Evolutionary and Structural Analysis of KdpD Proteins

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Abbreviations

5-Aminolevulinic acid	ALA
6His/His tag	Six histindine tag
Ap^R	Ampicillin resistance
ATP	Adenosine triphosphate
BCIP	5-bromo-4-chloro-3-indolyl-phosphate
c-di-AMP	3′,5′-Cyclic diadenylic acid
cDNA	Complementary DNA
Cip	CipA or CipB protein
cryo-EM	Cryo-electron microscopy (cryo-EM)/electron cryomicroscopy
DM	n-dodecyl b-D-maltoside
DMPC	1,2-dimyristoyl-*sn*-glycero-3-phosphocholine
DPPC	1,2-Dipalmitoyl-*sn*-glycero-3-phosphocholine
DUF XXX (e.g DUF4118)	Domain of unknown function
EAL	Putative diguanylate phosphodiesterase
EBP	Enhancer binding protein
Em^R	Erythromycin resistance
E-value	Expect value
FM	Fluorescence microscopy
GAF	cGMP-specific phosphodiesterases, adenylyl cyclases and FhlA
GFP	Green fluorescent protein
HAMP	(Histidine kinases, Adenylyl cyclases, Methyl binding proteins, Phosphatases) domain
HATPase_C	Histidine kinase-like ATPase, C-terminal domain
HDc	Metal dependent phosphohydrolases with conserved 'HD' motif
HGT	Horizontal gene transfer
HisKA	His Kinase A (phospho-acceptor) domain
HK	Histidine kinase
HK^{K+}	Histidine kinase perceives K^+ signal
HMM	Hidden Markov Model
HPLC	High-performance liquid chromatography
HPT	Histidine phosphotransferase
HTH	Helix-turn-helix

kDa	Kilodalton
Km^R	Kanamycin resistance
LDAO	lauryldimethylamine oxide
MSA	Multiple sequence alignment
MSP	Membrane scaffold protein
NAD(P)+	β-Nicotinamide adenine dinucleotide (2′-phosphate)
NADB_Rossmann	Rossmann-fold $NAD(P)^+$-binding
NMR	Nuclear magnetic resonance
NTB	Nitro blue tetrazolium
Nucleotidyl_cyc_IIIyl_cyc_III	Class III nucleotidyl cyclases
OD600	Optical density measured at a wavelength of 600 nm
ORF	Open reading frame
PAC	Motif C-terminal to PAS motifs (likely to contribute to PAS structural domain)
PAS	Per Arnt Sim
PCI(s)	Protein crystalline inclusion(s)
PCM	Phase contrast microscopy
PCR	Polymerase chain reaction
POPC	1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine
PTS_EIIA_2	Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2
qPCR	Real-Time PCR/Quantitative PCR
qRT-PCR	Quantitative reverse transcription polymerase chain reaction
REC	Signal receiver domain
RNAP	RNA polymerase
RR	Response regulator
RR^{K+}	Response regulator involves in K^+ signal responding
SD sequence	Shine-Dalgarno sequence
SDS-PAGE	Sodium dodecyl sulfate-polyacrylamide gel electrophoresis
SK	Sensor kinase
Sm^R	Streptomycin resistance
TCS	Two component system
Tet^R	Tetracycline resistance
URP	UniProt reference proteomes
Usp	Universal stress protein
v/v	Volume per volume
w/v	Weight per volume

Nomenclature

●Promoter of an operon: "$P_{\text{operon name}}$", for example promoter of the *kdp* operon P_{kdp}.

●Deletion of gene *A*, "Δ*A"*.

●DNA element insertion between gene *A* and gene *B*: "*A*::inserted DNA element::*B*".

●Gene *A*/promoter *A* replaced by a new DNA element, "Δ A/P_A::new DNA element".

● Gene/protein fusion between *A* and *B* with *A* located at the N or 5' terminus, "*gene A-gene B*"/"protein A-protein B". No linker was used for the fusion, for example *cipA-gfp* or CipA-GFP.

●Several genes/proteins separately fused to a same gene *X*/protein X, with *X* located at the N or 5' terminus:" gene *X*-(*gene A*,*gene B*,*gene C*)" or "protein X-(protein A, protein B, protein C)", for example *cipA*-(*vioA*,*vioB*) or CipA-(VioA,VioB).

●Amino acids are denoted with three letter codes or one letter code.

Contribution

1. Section 3.1.5, the related Figure 14 and Table 5 were contibuted by the collabrators: Prof. Dr. Dirk Metzler, Dr. Noémie Becker and Dr. Sonja Grath, Evolutionary Biology, LMU Munich.
2. The plasmid pNBU1-PKdp-NanoLuc (in Table 2 of section 2.2.4) used for the construction of *B. fragilis* Wlu reporter stain was generated by Dr. Mark Mimee from the group Prof. Dr. Timothy Lu, MIT.
3. Mass spectrometry of KdpD 38-380 (in Figure 22B) was performed by Dr. Markus Hartl, Plant Science of LMU Munich
4. Expression of CipA-GFP and CipB-GFP in insect cells (Figure 25) and serial crystallography of PCIs were performed by the collabrator Dr. Lars Redecke, Universitäten Lübeck und Hamburg.

1 Introduction

1.1 Bacterial signal transduction and two component system (TCS)

Bacterial cells face various environmental changes on nutrients, toxicity, temperature, light, osmolality, pH, and in some occasions they need intraspecies or interspecies cell to cell communications (Galperin 2004, Waters and Bassler 2005). These activities depend on different signal transduction mechanisms. The most prevalent signal transduction pathways are one-component system and two-component system (TCS) (Ulrich, Koonin et al. 2005). The TCS is typically composed of a sensor histidine kinase (HK) and a cognate response regulator (RR) (Figure 1).

HK has a dimerization and phosphoacceptor domain (HisKA domain) as well as an ATP binding HATPase_c domain, as the output region. The output region of the HK is bifunctional that can carry out both autophosphorylation and dephosphorylation of the conserved histidine residue in the HiskA domain (Kennelly 2002, Klumpp and Krieglstein 2002). Besides, HK generally has a signal input region composed of various protein domains like transmembrane helices, periplasmic domains or cytoplasmic domains including GAF, PAS, HAMP *etc* (Mascher, Helmann et al. 2006). The signal input domain perceives extra- and/or intracellular signals and hence regulates the kinase and phosphatase activities of the output region (Schramke, Wang et al. 2016).

RR of TCS typically has a signal receiver domain (REC domain) which could be phosphorylated by the HK and an effector domain which may be a DNA-binding domain (helix-turn-helix domain, HTH) or an enzymatic domain. In a few case, the REC domain protein can be a stand-alone protein which participates in protein-protein interactions, for example the CheY protein of bacteria chemotaxis system (Galperin 2006). Typically, a phosphoryl group is transferred from ATP to the HisKA domain of HK by the catalysis of HATPase_c domain and subsequently to the conserved aspartate in the REC domain of RR. Phosphorylation may

cause the dimerization of RR and activates/enhances its DNA-binding capability or modulate the enzyme activity of the effector domain (Galperin 2006, Capra and Laub 2012). When the output domain of the RR is the HTH domain, the response activity of RR is generally a transcriptional initiation of one or serval operons via interacting with the sigma factor and the RNA polymerases (RNAP) (Figure 1).

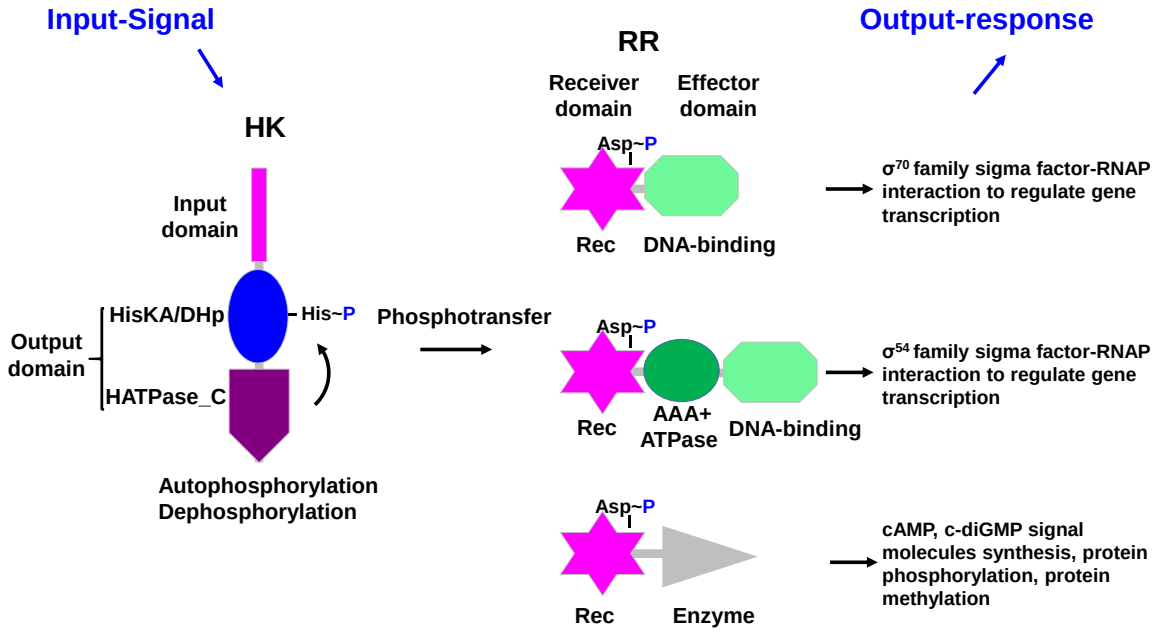


Figure 1: Schematic of the typical mechanism of TCS. The core elements of bacterial TCS comprise HK and RR. HK perceives extra- and/or intracellular signals and processes them into phosphorylation and dephosphorylation reactions to the REC domain of the RR. Phosphorylated RR may exhibit altered DNA-binding affinities, enzymatic activities or protein interaction capabilities to regulate the response of the cells.

1.2 K^+ transport and the K^+ responding TCS -- KdpD/KdpE

K^+ is the most abundant cation in cells and participates in turgor regulation, metabolism, virulence and intercellular communication (Epstein 2003, Su, Gong et al. 2009, Arlehamn, Pétrilli et al. 2010, Xue, You et al. 2011, Prindle, Liu et al. 2015). K^+ transporters with low and high affinities, different uptake kinetics and expression patterns have been identified. In *E. coli,* the constitutively expressed Trk systems, which include TrkA-TrkH-TrkE and TrkA-TrkG-TrkE

complexes (Dosch, Helmer et al. 1991, Schlosser, Meldorf et al. 1995) and Kup (Schleyer and Bakker 1993, Trchounian and Kobayashi 1999), represent low-affinity K^+ transport systems, while KdpFABC operates as a high-affinity transporter (Figure 2). Expression of the *kdpFABC* operon is induced in response to K^+ limitation (Walderhaug, Polarek et al. 1992, Altendorf, Voelkner et al. 1994, Heermann, Weber et al. 2009, Heermann and Jung 2010, Freeman, Dorus et al. 2013, Laermann, Ćudić et al. 2013) under the control of the histidine kinase/response regulator (HK/RR) system KdpD/KdpE.

1.3 Domain composition of the KdpD proteins

1.3.1 "Full-length" KdpD with kinase function

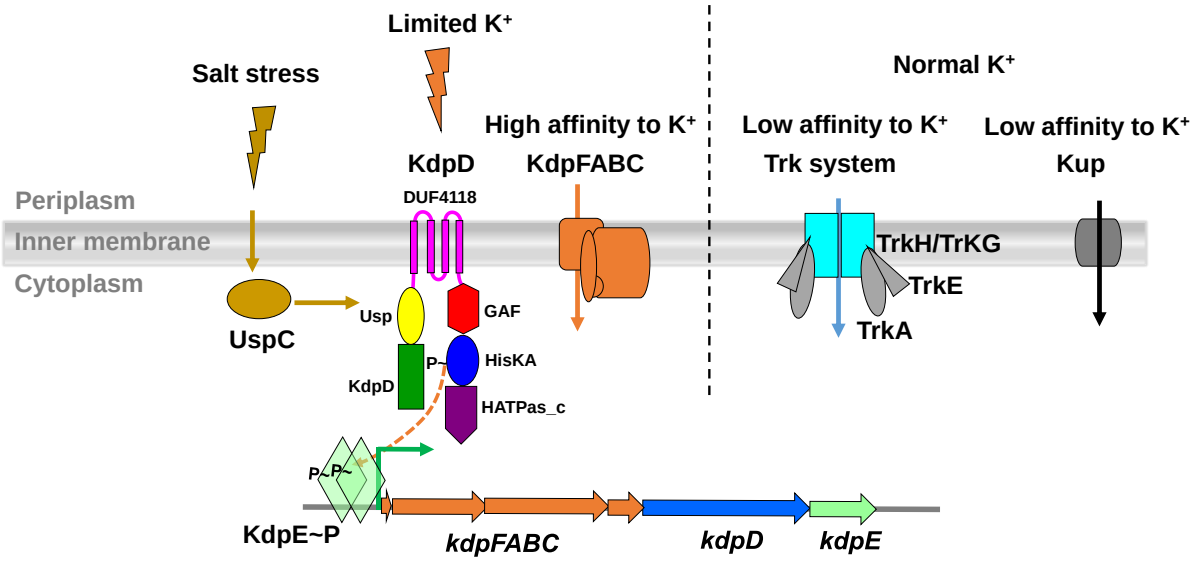


Figure 2: Components of the Kdp system of *E. coli*. KdpFABC is a high-affinity K^+ transporter. Its expression is regulated by the HK/RR--KdpD/KdpE system in response to K^+ availability and the cell's demand for K^+. KdpD consists of the following domains: KdpD, Usp, DUF4118, GAF, HisKA and HATPase_c. K^+ limitation causes autophosphorylation of KdpD and transfer of the phosphoryl group to KdpE. Phosphoryated KdpE dimerizes and activates the $P_{kdpFABC}$ promoter to promote the production of KdpFABC transport, which in turn relieve the stress of K^+ limitation.

As discussed above KdpD protein was firstly known from *E. coli*, as HK. Comparing to the other bacterial HKs, the stimulus-perceiving region of *E. coli* histidine kinase KdpD is rather

unique (Jung and Altendorf 2002, Mascher, Helmann et al. 2006). It is made up of four domains: the cytosolic N-terminal KdpD (PF02702) and Usp (PF00582) domains, the four-helix transmembrane domain, DUF4118 (PF13493), and a GAF (PF01590) domain (also found in c**G**MP-specific phosphodiesterases, **a**denylyl cyclases and **F**hlA). It is connected to the C-terminal signal transmitter module [comprising HisKA (PF00512) and HATPase_c (PF02518) domains), which contains the autophosphorylation site (Figure 2). The N-terminal region comprising KdpD and Usp domain is localized in the cytoplasm and is important for stabilizing the KdpE-DNA complex and integrating the salt stress signal via interaction with UspC, which acts as a scaffold protein (Figure 2) (Heermann, Altendorf et al. 2003, Heermann, Lippert et al. 2009). The transmembrane domain DUF4118 was found to be important for K^+ and osmostress sensing, and its conformation determines the spatial relationship between the N- and C-terminal cytoplasmic domains of KdpD (Heermann, Fohrmann et al. 2003, Zimmann, Steinbrügge et al. 2007, Heermann and Jung 2010). NMR analysis indicates that the DUF4118 domain forms a tightly packed four-helix bundle (Maslennikov, Klammt et al. 2010).

1.3.2 "Truncated" KdpD without kinase function

In several bacterial species, e.g. *Anabaena* sp. strain L31, *Synechocystis* sp. strain PCC 6803 and *Deinococcus radiodurans*, the cytosolic N-terminal domain of KdpD is encoded as an independent protein. It is often described as "truncated KdpD", because comparing to the *E. coli* KdpD, these KdpD proteins have much shorter length and the transmembrane domain and the essential kinase module (HiskA and HATPase_c domain) are "missing" (Ballal and Apte 2005, Ballal, Bramkamp et al. 2005, Ballal, Basu et al. 2007, Nanatani, Shijuku et al. 2015). That is to say, in these bacteria, the KdpD domain-containing proteins (will be called as KdpD proteins) are literally not histidine kinases.

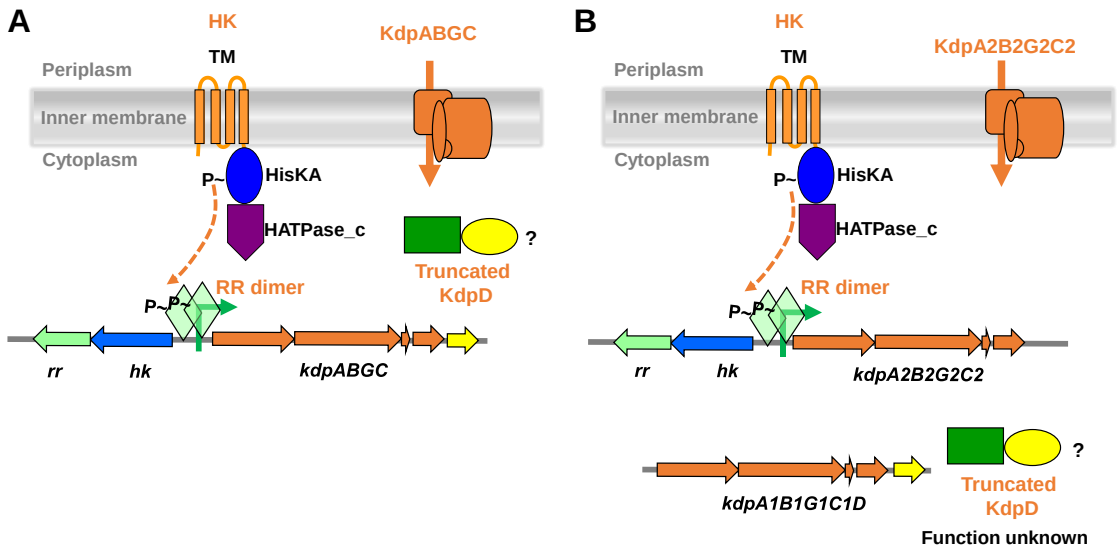


Figure 3: Models of Kdp system in *Cyanobacteria*. (A) Kdp system of *Synechocystis* sp. strain PCC 6803. In response to K^+ concentration, the expression of high-affinity K^+ transporter KdpABGC is regulated by the HK^{K+}/RR^{K+} encoded at its upstream. Deletion of *kdpD* genes does not affect the response of *kdp* operon to K^+. **(B)** Kdp system of *Anabaena* sp. strain L-31. *Anabaena* sp. strain L-31 has two *kdp* operons. The *kdpD* ORF is included in one the *kdp* operons whose expression is not efficiently induced by low K^+ [Modified based on (Ballal and Apte 2005)]. "Truncated KdpD" in both *Synechocystis* sp. strain PCC 6803 and *Anabaena* sp. strain L-31 consist of two domains--KdpD and Usp. The function of "truncated KdpD" in these cyanobacterial species is unknown.

1.4 Alternative HK/RR involved in K^+ response

It is apparent that the "truncated KdpD" described above cannot functionalize as HK without the fundamental output domains of HiskA and HATPase_c. However, genes for a HK that lacks KdpD and Usp domains and a RR that is homologous to KdpE were found in the vicinity of the gene for the "truncated KdpD" in *Anabaena* sp. strain L31 and *Synechocystis* sp. strain PCC 6803 (Figure 3). Deletion of the *kdpD* genes encoding the "truncated KdpD" in *D. radiodurans* and *Synechocystis* sp. strain PCC 6803 does not affect the *kdp* operons expression (Ballal, Basu et al. 2007, Nanatani, Shijuku et al. 2015). Conversely, the HK/RR encoded in genomic neighborhood of *kdpD* have been shown essential for K^+ sensing (Ballal and Apte 2008, Nanatani, Shijuku et al. 2015). For simplicity, the alternative HK/RR, which have been proved or predicted to involve in K^+ response, will be called alternative HK^{K+}/RR^{K+}.

In *E. coli*, various cyanobacterial species and in *S. aureus*, the RR that regulates expression of *kdpFABC* (or *kdpABGC*), functions together with the σ^{70} family sigma factor for transcriptional initiation. In contrast, it was suggested that the *kdp* promoter in *Desulfovibrio vulgaris* Hildenborough can be recognized by σ^{54}-dependent transcriptional activators (Rajeev, Luning et al. 2011).

1.5 *Bacteroides fragilis*

B. fragilis attracts lots of attentions and concerns (Wexler 2007). The main habitat of this species is the mammal gut, which is an anaerobic and K^+ rich environment. While Kdp system, as described above, is commonly equipped to the species to cope with K^+ limitation. From this respect, there seems no point for this bacterium to preserve the Kdp system. However, as will be discussed in the results section, many proteomes of the *Bacteroidetes/Chlorobi* group species, including *B. fragilis* were found to contain both KdpD and KdpA proteins. Until now, there is no report on the Kdp system in *Bacteroides fragilis*.

1.6 Structure of KdpD protein

As a multidomain protein, the tertiary structure of KdpD has not been elucidated. But the structures of DUF4118 and (KdpD 397-502) and GAF domains (KdpD 515-646[3920]) of *E. coli* KdpD have been resolved by NMR and crystallography, respectively (PBD IDs: 2KSF and 4QPR) (Maslennikov, Klammt et al. 2010). Moreover, the KdpD domain structure (KdpD 19-243) of *Pseudomonas syringae* pv. *tomato* str. DC3000 HK KdpD was also published (PDB ID: 2R8R). The DUF4118 domain has four-helix bundle, the helices were sperated by very short loops (Figure 4A). The GAF domain has four α-helices and four β-sheet strands. Especially the last α-helix is quite long and comprises 35 amino acids (Figure 4B). The KdpD domain is composed of seven α-helices and six β-sheet strands. They were crystallized with binding SO_4^{2-} ion (Figure 4C) (Berman, Westbrook et al. 2000).

The architecture of the HisKA and HATPase_c domain are better research. For example, these two domains contained in *E. coli* kinases QseC, EnvZ, CpxA have been analysed via crystallography.

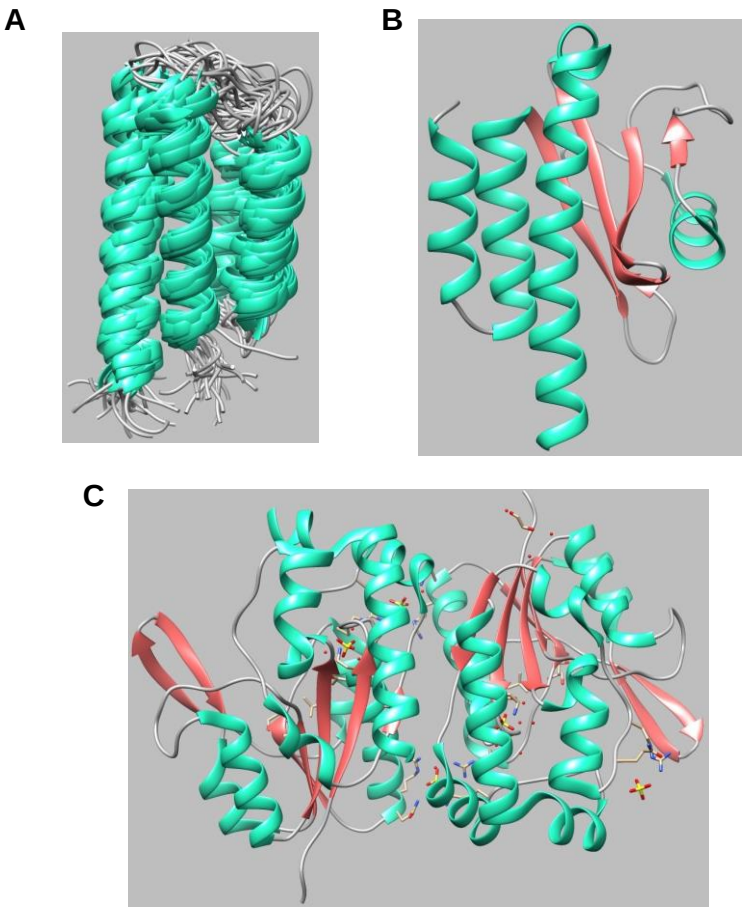


Figure 4: **Three dimensional structure of DUF4118, GAF and KdpD domains. (A)** NMR structure of the transmembrane domain DUF4118 of *E. coli* KdpD protein. **(B)** Crystal structure of the GAF domain of *E. coli* KdpD protein. **(C)** Crystal structure of the KdpD domain dimer (with binding $SO4^{2-}$ ion) of *Pseudomonas syringae* KdpD protein. These three figures are snapshots of the corresponding three dimensional structures downloaded from PDB database (Berman, Westbrook et al. 2000).

1.7 *In vivo* protein organization and protein crystallization

As described in section 1.6, even though there are different methods to determine the protein structures, crystallography is still the most successful strategy to study protein structures. In addition to the common crystallization setups, *in vivo* protein crystallization is a clever trick to

get diffractive crystals for solving protein structures (Koopmann, Cupelli et al. 2012). Protein crystals formed *in vivo* may be considered as protein complexes or protein crystalline inclusions (PCIs), which assemble automatically in the cytoplasm.

Proteins can be organized *in vivo* into various structures--compartments such as carboxysomes (Yeates, Kerfeld et al. 2008, Kerfeld and Melnicki 2016) and gas vesicles (Pfeifer 2012), or protein inclusions like the parasporal crystalline inclusion (Bt crystals) (Agaisse and Lereclus 1995, Schnepf, Crickmore et al. 1998) and refractile body (R body) (Pond, Gibson et al. 1989, Polka and Silver 2016). Some special proteins can automatically assemble into diffractive PCIs (*in vivo* protein crystals) in cells. For example, two *in vivo* protein crystals formed respectively in insect cells and in *Bacillus thuringiensis* have been successfully used for protein structure determinations with serial femtosecond X-ray free-electron lasers (Boutet, Lomb et al. 2012, Sawaya, Cascio et al. 2014).

1.8 CipA and CipB and their application potentials as scaffolds for *in vivo* protein crystallization

CipA and CipB are small proteins of 104 and 100 amino acids respectively, which are found in the entomopathogenic bacterium *Photorhabdus luminescens* (Figure 5A) (Bintrim and Ensign 1998, Bowen and Ensign 2001). CipA and CipB PCIs appear refractile when viewed by phase-contrast microscopy, and exhibit polyhedral configurations in the scanning or transmission electron microscope (Bintrim and Ensign 1998, Bowen and Ensign 2001). The mechanism underlying their organization into PCIs is unknown. The hydrophobicity is speculated to be the primary driving force, because both proteins contain high proportions of hydrophobic amino acids (CipA and CipB comprise, respectively, 49.0 % and 51.0% hydrophobic amino acids, Figure 5B).

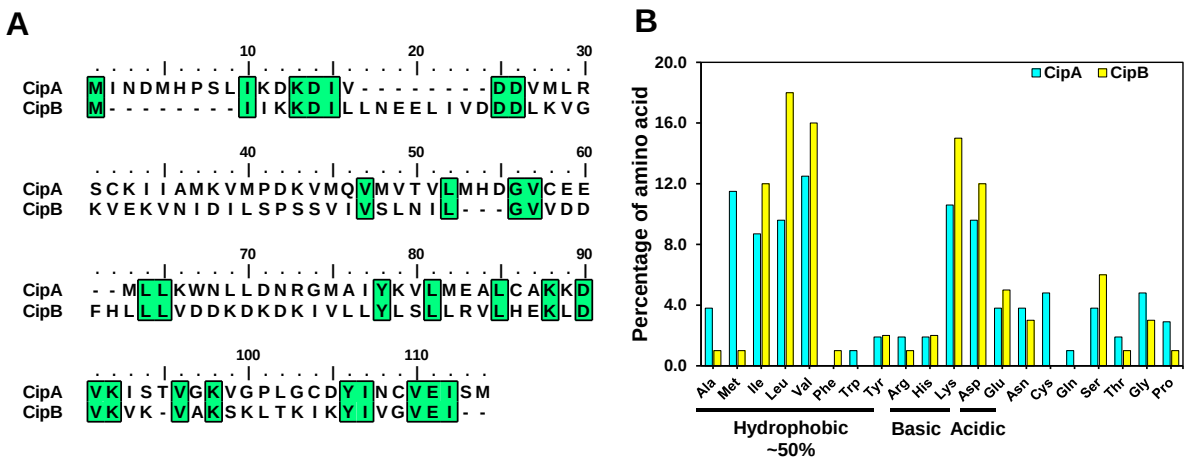


Figure 5: CipA and CipB protein sequences analysis. (A) Sequence comparison of CipA and CipB (indentical amino acids are highlighted in green). **(B)** Relative abundance of individual amino acids in CipA and CipB. (Hydrophobic, acidic and basic amino acids are underlined).

1.8.1 CipA and CipB as scaffolds to boost protein *in vivo* crystallization

As shown above, there are two *in vivo* grown crystals, which have been used for structural analysis. They are actually composed of natural proteins without any artificial design (Boutet, Lomb et al. 2012, Sawaya, Cascio et al. 2014). *In vivo* protein crystallization is particularly mystifying and the relevant mechanism remains unexplored.

Considering the small sizes of CipA and CipB and their PCIs forming capabilities, they may be potentially used as protein tags or scaffolds to bring other proteins into diffractive protein crystals *in vivo*, so that the method of *in vivo* crystallization could be extended to more proteins.

1.8.2 CipA and CipB as scaffolds to organize enzymes into PCIs for biotechnological applications

Based on the principles of natural protein organization, various types of synthetic protein scaffolds have been developed to artificially organize proteins with a view to promoting *in vivo* or *in vitro* biotechnological processes (Whitaker and Dueber 2011, Lee, DeLoache et al. 2012) or mimicking the function of organelles (Kim and Tullman-Ercek 2013, Huber, Schreiber et al.

2015). For example, to fine-tune metabolic flux through mevalonate and glucaric acid biosynthetic pathways, the related enzymes have been spatially organized into supramolecules via the scaffolding of signaling protein interaction domains (Dueber, Wu et al. 2009). At subcellular scales, a lipid-containing scaffold has recently been developed that can co-organize two enzymes involved in indigo biosynthesis into lipid-bound compartments in *Escherichia coli* for the purpose of metabolic engineering (Myhrvold, Polka et al. 2016). The cohesin-dockerin scaffold has been used to display multiple enzymes on bacterial outer membrane vesicles for *in-vitro* cascade reactions (Park, Sun et al. 2014). An ethanol bioreactor was generated by incorporating the corresponding enzymes into an intracellular compartment normally devoted to 1,2-propanediol utilization in *Citrobacter freundii* (Lawrence, Frank et al. 2014). Moreover, a method for scaffold-free self-assembly of the octameric leucine dehydrogenase and dimeric formate dehydrogenase has been developed (Gao, Yang et al. 2014).

Simililarily, CipA and CipB may be developed in to protein scaffolds to bring enzymes into PCIs for biotechnological applications.

1.9 Scope of the thesis

The overall scope of the thesis is aimed to reveal the evolutionary routes and the three dimensional structure of KdpD proteins.

Evolutionary analysis of KdpD proteins is aimed to: **(i)** Systematically analyze the distribution, architecture and evolution of KdpD domain-containing proteins (“KdpD proteins”) in the three domains of life; **(ii)** Predict and prove new alternative HK^{K+}/RR^{K+} involved in *kdp* operon regulation in various bacterial species.

As shown above, there are two versions of KdpD proteins, “full-length” and “truncated KdpD proteins. The structure of the former one is aimed to be analyzed via protein crystallization or

cryo-EM in membrane lipid bilayer. “Truncated” KdpD protein is composed of KdpD and Usp domains without any transmembrane helix. Therefore, “truncated” KdpD will be purified and crystallized as soluble proteins.

CipA and CipB, as the original aspiration, will be tested as scaffolds to bring “truncated” KdpD proteins into *in vivo crystals* for the purpose of X-ray crystallography. In addition, the biotechnological applications of CipA and CipB proteins shall be evaluated.

2 Materials and Methods

2.1 Bioinformatic analyses

2.1.1 Identification and collection of proteins containing KdpD, KdpA, TrkH or DUF4118 domain

A database was created from UniProt reference proteomes 2015_10 (URP), which provides broad coverage of all three domains of life as well as high-quality annotation of protein sequences (UniProt 2015). HMMER 3.0 was utilized to construct Hidden-Markov Models (HMM) and query URP for proteins containing KdpD (PF02702), KdpA (PF03814), TrkH (PF02386) or DUF4118 (PF13493) domains with the respective cut-off values defined by Pfam 26.0 (Finn, Clements et al. 2011, Finn, Bateman et al. 2014). Proteins containing KdpD, KdpA or TrkH domains related to K^+ sensing/uptake were collected and grouped as KdpD, KdpA and TrkH proteins, respectively.

Domain architectures of entire KdpD proteins or proteins containing a DUF4118 domain were annotated with CDD v3.14 (the interface of CDD database is CD-search), using a cut-off *E*-value of 0.01 (Marchler-Bauer, Derbyshire et al. 2015). When domains were predicted to be overlapping, the one with the lowest *E*-value was adopted.

2.1.2 Phylogeny reconstruction and detection of selection pressure

Protein sequence alignments were performed with Mafft and gaps were removed with trimAl v1.2 (Capella-Gutierrez, Silla-Martinez et al. 2009). All Maximum Likelihood protein trees were constructed with PhyML 3.0 (Anisimova and Gascuel 2006, Guindon, Dufayard et al. 2010). Nucleotide sequences for the KdpD proteins were retrieved from the protein sequences using tBlast (Altschul, Gish et al. 1990) and Entrez queries. Program CodonPhyML was used to infer the phylogeny of nucleotide sequences (Gil, Zanetti et al. 2013).

Selection pressure was tested using the program CODEML from the PAML v4.8 package (Yang 2007), which uses the ratio ω of the rates of non-synonymous and synonymous mutations to test for selection on specific branches of the tree.

2.1.3 Prediction of protein structures and display phylogenetic trees

Transmembrane regions were predicted with TMHMM 2.0 (Krogh, Larsson et al. 2001) and DAS (Cserzo, Wallin et al. 1997); The three dimensional structure of the outer membrane porin KdpO was predicted with HHpred (Soding, Biegert et al. 2005). The secondary structures of CipA and CipB were predicted with PSIPRED server (Jones 1999).

All trees were displayed using iTOL v3 (Letunic and Bork 2016).

2.2 Experimental analyses

2.2.1 Common methods and chemicals

2.2.1.1 Genomic DNA and plasmid extraction

Genomic DNA was extracted with UltraClean Microbial DNA Isolation Kit of Mo Bio. Plasmid was extracted using the Hi Yield MINI Plasmid DNA Extraction Kit of Süd-Laborbedarf. Genomic DNA samples and plasmids were stored at -20 °C.

2.2.1.2 PCR reaction

PCR reactions with high fidelity (for gene deletion and vector construction) were performed with Phusion® High-Fidelity DNA Polymerase of New England Biolabs. Colony PCR reactions were performed with OneTaq® DNA Polymerase of New England Biolabs.

2.2.1.3 DNA restriction and ligation

DNA restrictions and ligations were performed with the specific restriction enzymes and T4 DNA ligase purchased from New England Biolabs following the manufacturer's instructions.

Before each ligation, dephosphorylation of 5´ and 3´ ends of restricted vectors was performed with the calf intestinal alkaline phosphatase of New England Biolabs.

2.2.1.4 DNA purification/isolation

After PCR or DNA restriction, the target DNA were separated with DNA agarose gel electrophoresis (in Tris-HCl-acetate EDTA buffer, pH 8.3). Agarose slices with desired DNA bands were dissolved for sample recovery with Hi Yield Gel/PCR DNA Fragment Extraction Kits of Süd-Laborbedarf.

2.2.1.5 DNA sequence analysis

DNA sequencing experiments were performed in the Department of Genetics of LMU Munich with the BigDye v3.1 protocol of Thermo Fisher Scientific.

2.2.1.6 Preparation of *E. coli* competent cells and transformation of DNA

E. coli competent cells were prepared with calcium chloride, following the protocol described before (Seidman, Struhl et al. 1997). Transformations of *E. coli* strains with plasmids were performed with the heat shock method (Seidman, Struhl et al. 1997). Transformations of *E. coli* strains with liner DNA were performed with electro-transformed into *E. coli* strains as described in Quick & Easy *E. coli* Gene Deletion Kit (Gene Bridges).

2.2.1.7 SDS-PAGE and gel development

Denaturing protein gel electrophoresis (SDS-PAGE) was performed as described (Laemmli 1970). Unless specified, the polyacrylamide concentration of the gels used in this thesis was set to12.5% (w/v). Gels may be either stained by Coomassie Brilliant Blue R-250 (stained with 50% (v/v) methanol, 10% (v/v) acetic acid in H_2O for two hours and destained with 5% methanol (v/v), 7.5% acetic acid (v/v) in H_2O until background disappeared) or Coomassie Brilliant Blue G-250 (in water with ~10mM of H_2SO_4) for visualization of the bands or transferred

to methanol activated PVDF membrane (300 mA for 90 min in 25mM Tris-HCl, 192 mM glycine and 20% methanol) for Western blot.

Table 1 lists the common chemicals used in this study. The other chemicals or materials not listed were purchased from Carl Roth, Fluka, Sigma-Aldrich, or Merck Millipore.

Table 1: Common materials and chemicals

Material	Manufacturer
>98% violacein (>=85%) and deoxyviolacein	Sigma-Aldrich
2-Log DNA-Ladder	New England Biolabs
5-Aminolevulinic acid hydrochloride	Sigma-Aldrich
5-Bromo-4-Chloro-3-Indoxyl Phosphate (BCIP)	AppliChem
Acetonitrile	Fluka
Acrylamide Protogel	Biozym Diagnostik
Agarose	Serva
All Restriction Nucleases	New England Biolabs
Ammonium Persulfate (APS)	National Diagnostics
Ampicillin (sodium salt)	Carl Roth
Anti-GFP Antibody	Thermo Fisher Scientific
Anti-Mouse Secondary Antibodies	Rockland Immunochemicals
Anti-Rabbit Secondary Antibodies	Rockland Immunochemicals
Bovine Serum Albumin (BSA)	AppliChem
Brain Heart Infusion	BD Bacto
Brillant Blau G250	Carl Roth
Brillant Blau R250	Carl Roth
Calf Intestinal Phosphatase (CIP)	New England Biolabs
Chloramphenicol	Sigma-Aldrich
Chloroform	Carl Roth
Congo red	Merck Millipore
DNA oligonucleotides	Sigma-Aldrich
DNase I	Sigma-Aldrich
dNTPs (deoxynucleotide triphosphates)	Invitrogen
Erythromycin	Sigma-Aldrich
Folin-Ciocalteu's phenol reagent (2N)	Merck Millipore
Glycerol	Carl Roth
Hemin Chloride	Carl Roth
Hi Yield PCR Clean-Up & Gel-Extraction Kit	Süd-Laborbedarf
Hi Yield Plasmid Mini Kit	Süd-Laborbedarf
Hybond-P protein transfer membrane	GE Healthcare
iQ SYBR Green Supermix	Bio-Rad

Material	Manufacturer
Kanamycin (sulfate)	Carl Roth
L-(+)-Arabinose	Carl Roth
N,N,N′,N′-Tetramethylethylenediamine (TEMED)	Carl Roth
Nano-Glo Luciferase Assay System	Promega
Ni-NTA agarose	Qiagen
Nitro Blue Tetrazolium (NBT)	Biomol
Nitrocellulose membrane	GE Healthcare
o-Nitrophenyl β-D-galactopyranoside (*o*NPG)	Carl Roth
Page Ruler Prestained Protein Ladder	Fermentas
Penta·His Antibody	Qiagen
Phenol/Chloroform/Isoamylalcohol (25/24/1)	Carl Roth
Phenol-Chloroform	Carl Roth
Phenylmethylsulfonyl fluoride (PMSF)	Sigma-Aldrich
Phusion DNA Polymerase	New England Biolabs
Quick & Easy *E. coli* Gene Deletion Kit	Gene Bridges
RevertAid H Minus First Strand cDNA Synthesis Kit	ThermoFisher
Ribonuclease	Carl Roth
T4-DNA ligase	New England Biolabs
Tetracycline Hydrochloride	Sigma-Aldrich
Vitamin K1	Sigma-Aldrich

2.2.2 Medium and cultivation

Strains used in this part of study are listed in Table 2. *E. coli* DH5α was used to construct all the plasmids. *E. coli* S17-1 λpir or *E. coli* ST18 (Strand, Lale et al. 2014) were used for conjugation plasmids into *B. fragilis* and *P. luminescens* strains. LB medium (10 g/L NaCl, 10 g/L Tryptone, 5 g/L yeast extract) (Bertani 1951) was used to cultivate *E. coli* strains. For cultivation of *E. coli* ST18, a *hemA* deficient strain, 5-aminolevulinic acid (50 µg/mL) was always supplemented. When necessary, 100 µg/mL ampicillin and/or 25 µg/mL chloramphenicol were supplemented.

All *B. fragilis* strains were cultivated in BHIS [Brain Heart Infusion supplemented with 5 g/L yeast extract, 1 µg/mL vitamin K1, 0.5 g/L cysteine chloride (pH=6.5), 5 µg/L hemin] or in a modified anaerobic minimal medium with glucose [AMMgluc medium; 5 g/L of glucose, 0.5 g/L cysteine chloride (pH=6.5), 0.4 g/L Na_2CO_3, 0.79 g/L $(NH4)_2SO_4$, 5% (v/v) mineral solution

stock (1.06 g/L $CaCl_2 \cdot 2H_2O$, 0.8 g/L $MgCl_2 \cdot 6H_2O$, 0.4 g/L $MnCl_2 \cdot 4H_2O$, 0.04 g/L $CoCl_2 \cdot 6H_2O$, autoclaved separately),1 µg/mL vitamin K_1, 0.5 µg/mL vitamin B_{12}, 5 µg/mL hemin, 0.4 µg/L $FeSO_4 \cdot 7H_2O$, 100 mM phosphate buffer, pH 7.2, in a gas atmosphere of 5% CO_2, 10% H_2, and 85% N_2 (Linde AG)] (Varel and Bryant 1974, Baughn and Malamy 2002). Depending on the requirement on variable K^+ concentrations, the potassium phosphate was replaced by same mole of sodium phosphate. For growth of *thyA* deletion *B. fragilis* mutants, 50 µg/mL of thymine was additionally provided. Cultivation of *B. fragilis* was carried out in an anaerobic jar or anaerobically in Hungate tubes (Hungate 1969) at 37 °C. When necessary, 50 µg/mL gentamicin, 2 µg/mL tetracycline and/ or 100 µg/mL trimethoprim were supplemented (Baughn and Malamy 2002).

All *P. luminescens* strains were grown in casein-soya-peptone (CASO) medium at 30°C (Munch, Stingl et al. 2008). When necessary, the medium was supplemented with 25 µg/mL kanamycin.

Chromobacterium violaceum DSM 30191 was grown in LB medium at 30°C overnight for genomic DNA extraction.

Table 2: Strains and plasmids

Strain/Plasmid name	Feature	Source
E. coli DH5α	F^- Φ80*lacZ*ΔM15 Δ(*lacZYA-argF*)U169 *recA*1 *endA*1 *hsdR*17 (rK^-, mK^+) *phoA supE*44 λ^- thi-1 gyrA96 *relA*1.	Invitrogen
E. coli BL21(DE3)	Strain B F^- *ompT gal dcm lon hsdS*$_B$($r_B^- m_B^-$) λ(DE3 [*lacI lacUV5-T7p07 ind1 sam7 nin5*]) [*malB*$^+$]$_{K\text{-}12}$(λ^S).	NEB
E. coli HAK006	Δ*kdpFABC*::*neo* Δ*kdpD*161-726 $P_{kdpFABC}$:*lacZ* Δ(*lac-pro*) *ara thi*	*(Nakashima, Sugiura et al. 1993)*, lab stock
E. coli ST18	F^- *RP4-2(Km::Tn7,Tc::Mu-1) pro-82 λpir recA1 endA1 thiE1 hsdR17 creC510 ΔhemA*.	(Thoma and Schobert 2009), lab stock
E. coli HB101	*E. coli* K-12 lyophilized *E. coli* K-12 for amplification and storage of pJST61 and its derivate	(Meehan, Baughn et al. 2012)
E. coli LF2	*E. coli* MG1655 *rpsL150 Plac*::*rpsL-kan/neo*::*lacZ*, Km^R Sm^s	(Fried, Lassak et al. 2012), lab stock
E. coli YW1	*E. coli* MG1655 *rpsL150* ΔP_{lac}::$P_{kdpB.fragilis}$, Km^s Sm^R	This study
E. coli YW2	*E. coli* YW1 Δ*kdpDE*::FRT-*PGK-gb2-neo*-FRT, Km^R Sm^R	This study
E. coli Vio0	*E. coli* DH5α transformed with the plasmids pBAD18 and pBAD33.	This study

Strain/Plasmid name	Feature	Source
E. coli Vio1	*E. coli* DH5α transformed with the plasmids pBAD-free-(vioA,vioB) and pBAD-free-(vioC,vioD,vioE).	This study
E. coli Vio2	*E. coli* DH5α transformed with the plasmids pBAD-cipA-(vioA,vioB) and pBAD-free-(vioC,vioD,vioE).	This study
E. coli Vio3	*E. coli* DH5α transformed with the plasmids pBAD-cipA-(vioA,vioB) and pBAD-free-(vioC)-cipA-(vioD,vioE).	This study
E. coli Vio4	*E. coli* DH5α transformed with the plasmids pBAD-free-(vioA,vioB) and pBAD-free-(vioC)-cipA-(vioD,vioE).	This study
E. coli Vio5	*E. coli* DH5α transformed with the plasmids pBAD-free-(vioA,vioB) and pBAD-cipA-(vioC,vioD,vioE).	This study
E. coli Vio6	*E. coli* DH5α transformed with the plasmids pBAD-cipA-(vioA,vioB) and pBAD-cipA-(vioC,vioD,vioE).	This study
B. fragilis NCTC 9343	Wild type strain. synonym: DSM 2151, ATCC 25285, JCM 11019	DSMZ
B. fragilis WLu	*B. fragilis* NCTC 9343 attB2::pNBU1-PKdp-NanoLuc	This study
*Photorhabdus luminescens sub*sp. *laumondii* TT01	Type strain, Synonym DSM 15139.	Lab stock
P. luminescens cip$^-$	*P. luminescens sub*sp. *laumondii* TT01 Δ*cipA* Δ*cipB*.	This study
P. luminescens cip$^-$ P_{cipA}-*cipA-gfp*	*P. luminescens cip*$^-$ with genomically integrated pPINT-P_{cipA}-cipA-gfp.	This study
P. luminescens cip$^-$ P_{cipB}-*cipB-gfp*	*P. luminescens cip* $^-$ with genomically integrated pPINT-P_{cipA}-cipA-gfp.	This study
Chromobacterium violaceum DSM 30191	Type strain, Synonym ATCC 12472, NCTC 9757.	DSMZ
pBAD18	Ap^R, pBR322 ori, *araBAD* promoter, *araC*	(Guzman, Belin et al. 1995), lab stock
pBAD24	Ap^R, pBR322 ori, *araBAD* promoter, *araC*	(Guzman, Belin et al. 1995), lab stock
pBAD33	Cm^R, pACYC ori, *araBAD* promoter, *araC*	(Guzman, Belin et al. 1995), lab stock
pBAD-gfp	pBAD18 vector harboring *gfp* gene	Lab stock
pBAD18	pBR322 ori, *araBAD* promoter, *araC*, Ap^R.	(Guzman, Belin et al. 1995), lab stock
pNBU1	*E. coli – B. fragilis* shuttle vector, Ap^R, Em^R. The intN1 tyrosine integrase encoded on the vector catalyzes the recombination between the attN site of pNBU1 and one of two attBT sites on the *B. fragilis* chromosome.	(Wang, Wang et al. 2001, Mimee, Tucker et al. 2015)
pYT102	p15A *ori*, RP4 *oriT*; *B. fragilis* suicide vector, *thyA*$^+$, Cm^R,Tet^R.	(Meehan, Baughn et al. 2012)
pJST61	*E. coli – B. fragilis* shuttle vector, pBR322 *oriV*, pRK2 *oriT,* with *endRI* under the control of the promoter of phage lambda, Em^R, Ap^R.	(Meehan, Baughn et al. 2012)
pBAD-rrK+	The gene (*rr*$^{K+}$) encoding the putative response regulator of Kdp system is expressed from P_{BAD} on the pBAD18 backbone, Ap^R. Six-histidine codons are added to the 5' terminus of the *rr*$^{K+}$ gene (locus: BF9343_0503).	This study
pBAD-hkK+	The gene (*hk*$^{K+}$) encoding the putative histidine kinase of Kdp system is expressed from P_{BAD} on the pBAD18 backbone, Ap^R. Six-histidine codons was added to the 3' terminus of the *hk* gene (locus: BF9343_0509).	This study
pBAD-rrK+-hkK+	The genes *rr*$^{K+}$ and *hk*$^{K+}$ are express from P_{BAD}, pBAD18 backbone.	This study
pBAD-rrK+-hkK+-kdpD	The genes *rr*$^{K+}$ and *hk*$^{K+}$ and *kdpD* are expressed from P_{BAD}, pBAD18 backbone, Ap^R. Six-histidine codons are add to the 5' of the *rr*$^{K+}$ gene and to the 3' terminus of the *hk*$^{K+}$ and *kdpD* (locus: BF9343_0508) genes, respectively.	This study
pNBU1-PKdp-NanoLuc	Nanoluc luciferase gene is expressed from the native P_{Kdp} of *B. fragilis* NCTC 9343, pNBU1 backbone.	By Mark Mimee
pNBU1-PKdp(mu)-NanoLuc	Nanoluc luciferase gene is expressed from mutated (putative -12 and -24 motifs are mutated) P_{Kdp} of *B. fragilis* NCTC 9343, pNBU1 backbone.	This study
pYT102-ΔthyA	Vector for gene deletion of *thyA* (gene locus BF9343_3430), pYT102 backbone.	This study

Strain/Plasmid name	Feature	Source
pYT102-ΔrrK+	Vector for gene deletion of *rr*$^{K+}$, pYT102 backbone	This study
pYT102-ΔkdpA	Vector for gene deletion of *kdpA* (*kdpA* gene locus BF9343_0504), pYT102 backbone.	This study
pYT102-ΔkdpO	Vector for gene deletion of *kdpO* (*kdpO* gene locus BF9343_0507), pYT102 backbone.	This study
pYT102-ΔkdpD	Vector for gene deletion of *kdpD*, pYT102 backbone.	This study
pYT102-ΔhkK+	Vector for gene deletion of *hk*$^{K+}$, pYT102 backbone	This study
pPV5-3 R511Q-6His	Vector for protein overproduction of *E. coli* KdpD-R511Q-6His, Ap^R, P_{tac} pBR322 origin.	(Jung and Altendorf 1998), lab stock
pBAD24/HS	pBAD24 backboned vector carrying a gene mutant encoding *E.coli* KdpD ΔTM1-4-6His (KdpD soluble mutant). Construction of pBAD24-KdpD-WrbA-6His is based on this vector	Lab stock
pBAD24-KdpD-WrbA-6His	Vector for protein overproduction of *E. coli* KdpD-WrbA-6His, pBAD24 backbone	This study
pBD (1-395)/6his	Vector for protein overproduction of *E. coli* KdpD 1-395-6His, pBAD18 backbone	(Heermann, Altendorf et al. 2000), Lab stock
pBD2 DeinoD-6His	Vector for protein overproduction of *D. radiodurans* KdpD-6His. This KdpD protein is naturally "truncated" KdpD.	Lab stock
pBD5-3	pBAD18 backboned vector with *kdpD* gene under the control of arabinose promoter. Used as template for *E. coli kdpD* gene fragment PCR amplification.	(Jung, Heermann et al. 1998), lab stock
pKJ2-6His	Vector for protein overproduction of *E. coli* KdpD-6His, Ap^R, P_{tac} , pKK223-3 backbone.	(Jung, Tjaden et al. 1997), lab stock
pBAD24-KdpD(Met+38-380)-6His	pBAD24 backboned vector for protein overproduction of *E. coli* KdpD (38-380)-6His, which wasidentified as stable fragemt by limited proteolysis. "ATG" start codon was added in front of the codon of KdpD 38T.	This study
pMSP1E3D1	pET 28a backboned vector, Km^R, T7_promoter	(Denisov, Baas et al. 2007)
pNPTS-138-R6KT	versatile suicide vector.	(Lassak, Henche et al. 2010)
pNPTS-138-R6KT-del-cipA	pNPTS-138-R6KT containing regions homologous to upstream and downstream of the *P. luminescens cipA*, designed for clean deletion of *cipA*.	This study
pNPTS-138-R6KT-del-cipB	pNPTS-138-R6KT containing regions homologous to upstream and downstream of the *P. luminescens cipB*, designed for clean deletion of *cipB*.	This study
pPINT	pNPTS-138-R6KT containing *rpmE* and *glmS* homologous regions of the *P. luminescens*, designed for gene integration into *P. luminescens* genome.	(Glaeser and Heermann 2015)
pPINT-P_{cipA}-cipA-gfp	pPINT containing overlap PCR product of P_{cipA}-*cipA-gfp,* designed for *cipA-gfp* integration into *P. luminescens cip*$^-$ genome.	This study
pPINT-P_{cipB}-cipB-gfp	pPINT containing overlap PCR product of P_{cipB}-*cipB-gfp,* designed for *cipA-gfp* integration into *P. luminescens cip*$^-$ genome.	This study
pFasBac1	Vector for protein productions in insect cells using the baculovirus system.pUC origin, pH promoter (Polyhedrin promoter) Ap^R ,Gm^R	Thermo Fisher Scientific
pFastBac1-cipA-gfp	pFastBac1 backoned, for expression of *cipA-gfp* gene fusion from, pH promoter.	This study
pFastBac1-cipB-gfp	pFastBac1 backoned, for expression of *cipB-gfp* gene fusion from, pH promoter.	This study
pBAD-6his-lacZ	pBAD18 vector harboring *E. coli* derived *lacZ* gene, with 6 histidine codons fused to the 5' end of *lacZ*.	Lab stock
pBAD-cipA-6his	pBAD18 vector harboring c*ipA* gene with 6 histidine codons at its 3' end.	This study
pBAD-cipB-6his	pBAD18 vector harboring c*ipB* gene with 6 histidine codons at its 3' end.	This study

Strain/Plasmid name	Feature	Source
pBAD-gfp-cipA	pBAD18 vector harboring the gene hybrid *gfp-cipA*.	This study
pBAD-gfp-cipB	pBAD18 vector harboring the gene hybrid *gfp-cipB*.	This study
pBAD-cipA-gfp	pBAD18 vector harboring the gene hybrid *cipA-gfp*.	This study
pBAD-cipB-gfp	pBAD18 vector harboring the gene hybrid *cipB-gfp*.	This study
pBAD-cipA-lacZ	pBAD18 vector harboring the gene hybrid *cipA-lacZ*.	This study
pBAD-cipB-lacZ	pBAD18 vector harboring the gene hybrid *cipB-lacZ*.	This study
pBAD-cipA-(gfp,lacZ)	pBAD18 vector harboring the hybrids *cipA-gfp and cipA-lacZ*.	This study
pBAD-cipB-(gfp,lacZ)	pBAD18 vector harboring the hybrids *cipB-gfp and cipB-lacZ*.	This study
pBAD-free-(vioA,vioB)	pBAD18 vector harboring the genes of *vioA* and *vioB*.	This study
pBAD-cipA-(vioA,vioB)	pBAD18 vector harboring the hybrids of *cipA-vioA* and *cipA-vioB*.	This study
pBAD-free-(vioC,vioD,vioE)	pBAD33 vector harboring the genes of *vioC*, *vioD* and *vioE*.	This study
pBAD-free-(vioC)-cipA-(vioD,vioE)	pBAD33 vector harboring the gene of *vioC*, and hybrids of *cipA-vioD* and *cipA-vioE*.	This study
pBAD-cipA-(vioC,vioD,vioE)	pBAD33 vector harboring the hybrids of *cipC-vioC*, *cipA-vioD* and *cipA-vioE*.	This study
pBAD-cipA(1-47)-gfp	pBAD18 vector harboring the gene hybrid *cipA(1-47)-gfp*.	This study
pBAD-cipA(1-32)-gfp	pBAD18 vector harboring the gene hybrid *cipA(1-32)-gfp*.	This study
pBAD-cipA(1-23)-gfp	pBAD18 vector harboring the gene hybrid *cipA(1-23)-gfp*.	This study
pBAD-cipB(1-59)-gfp	pBAD18 vector harboring the gene hybrid *cipB(1-59)-gfp*.	This study
pBAD-cipB(1-33)-gfp	pBAD18 vector harboring the gene hybrid *cipB(1-33)-gfp*.	This study
pBAD-cipB(1-17)-gfp	pBAD18 vector harboring the gene hybrid *cipB(1-17)-gfp*.	This study

2.2.3 Plasmid construction

Plasmids used in this study are listed in Table 2, and the primers used for PCR amplification of the DNA fragments needed to generate these plasmids are listed in Table 3. All gene fusions (*e.g.* the Δ*thyA*-gene fusion composing two DNA fragments homologous separately to upstream and downstream of *thyA* gene. It was generated for *thyA* gene deletion) were created with overlap PCR.

To construct plasmids pBAD-rrK+, pBAD-hkK+, pBAD-rrK+-hkK+, pBAD-rrK+-hkK+-kdpD, pYT102-ΔthyA, pYT102-ΔrrK+, pYT102-ΔkdpA, pYT102-ΔkdpO, pYT102-ΔkdpD and pYT102-ΔhkK+, the respective genes or gene fusions were amplified using chromosomal DNA of *B. fragilis* NCTC 9343 as template. The amplified DNA fragments were then digested and ligated into the correspondingly restricted vector pBAD18 (Guzman, Belin et al. 1995) or pYT102 (Meehan, Baughn et al. 2012).

Plasmid pNBU1-PKdp-NanoLuc was created by placing the luciferase gene *Nluc* under the control of *B. fragilis kdp* promoter $P_{kdpB.\ fragilis}$. pNBU1-PKdp(mu)-NanoLuc was created from pNBU1-PKdp-NanoLuc by replacing the native promoter with a mutant (wild type, TGGCACGCATTTGGCAT; mutant, TAATACGCATTTAATAT) to destroy the predicted σ^{54} recognition motif.

To construct the *kdpD-wrbA* gene fusion, *wrbA* gene was amplified with *E. coli* MG1655 genome DNA with the primers listed in Table 3. Fragments of *kdpD* upstream and downstream of the first periplasmic loop coding regions were amplified separately with pBD5-3 as the template. Subsequently, these two fragments were fused to upstream and downstream of the amplified *wrbA* gene via overlap PCR. To generate the pBAD24-KdpD-WrbA-6His (for overproduction of KdpD-WrbA-6His), the produced *kdpD-wrbA* gene fusion was digested with *Sac*I and *Nde*I and ligated into equally treated pBAD24/HS vector backbone. To generate pBAD24-KdpD(Met+38-380)-6His, *kdpD* gene fragment encoding KdpD 38-380 (identified as stable fragment via limited proteolysis and sequenced via mass spectrometry) was amplified with pBD5-3 as template and ligated into pBAD24 vector after restriction.

To create pPINT-P_{cipA}-cipA-gfp and pPINT-P_{cipB}-cipB-gfp, P_{cipA}-*cipA-gfp* or P_{cipB}-*cipB-gfp* (synthesized by overlap PCR; P_{cipA} or P_{cipB} stands for the native promoters of *cipA* and *cipB*) was ligated into the pPINT vector (Glaeser and Heermann 2015). Gene fusions *cipA-gfp* and *cipB-gfp* were amplified from pPINT-P_{cipA}-cipA-gfp and pPINT-P_{cipB}-cipB-gfp with primers Insect CipA- BamHI-Sense/Insect CipB-BamHI-sense and gfp-HindIII-anti (see Table 3) and ligated into pFastBac1 to creat pFastBac1-cipA-gfp and pFastBac1-cipB-gfp. To generate plasmid pBAD-cipA-6His, pBAD-cipB-6his, pBAD-gfp-cipA, pBAD-gfp-cipB, pBAD-cipA-gfp, pBAD-cipB-gfp, pBAD-cipA-lacZ, and pBAD-cipB-lacZ, pBAD-cipA(1-47)-gfp, pBAD-cipA(1-32)-gfp, pBAD-cipA(1-23)-gfp, pBAD-cipB(1-59)-gfp, pBAD-cipB(1-33)-gfp, pBAD-cipB(1-17)-gfp, the respective genes or gene fragments were amplified using chromosomal DNA of *P. luminescens*, *E. coli* or pBAD-gfp as template. Gene fusions were constructed by overlap PCR.

Herein, His-tag was added to the N-terminus of LacZ and to the C-terminus of CipA and CipB, respectively. The DNA fragments were then digested and ligated into the correspondingly resected vector pBAD18 (Guzman, Belin et al. 1995). Plasmids pBAD-cipA-(gfp,lacZ) and pBAD-cipB-(gfp,lacZ) were generated by successively ligating *cipA-gfp* and *cipA-lacZ* or *cipB-gfp* and *cipB-lacZ* into pBAD18. To generate the pBAD-free-(vioA,vioB) and pBAD-cipA-(vioA,vioB) constructs, *vioA* and *vioB* genes or c*ipA-vioA* and *cipA-vioB* fusions were amplified from chromosomal DNA of *P. luminescens* or *C. violaceum* DSM 30191. DNA fragments were digested and then ligated successively into the appropriately digested pBAD18. In the same way, pBAD-free-(vioC,vioD,vioE), pBAD-free-(vioC)-cipA-(vioD,vioE) and pBAD-cipA-(vioC,vioD,vioE) plasmids were constructed by successively ligating *vioC*, *vioD* and *vioE* genes, either alone or as c*ipA-vioC*, *cipA-vioD*, *cipA-vioE* fusions, into the pBAD33 vector (pBAD18 compatible) (Guzman, Belin et al. 1995).

Unless specified, all restriction digests of PCR-amplified DNA fragments and pBAD18, pBAD24, pBAD33, pNBU1 and pYT102 vectors were performed with the enzymes indicated in the names of the primers used for gene amplification (Table 3). All multiple genes or gene fusions ligated into common vectors can be expressed by induction of the arabinose-dependent P_{BAD} promoter encoded on the vector backbone, but retain their own Shine-Dalgarno sequences and stop codons. Note that, in every case where a protein was tagged with a Cip scaffold, no intervening linker of any kind was used. While flexible glycine-serine linkers “GGSGGSG” were added to the two interfaces between WrbA and KdpD proteins.

Table 3: Primers

Name	Sequence (5' to 3')	Reference
wrbA-sense	GGTGGCAGCGGTGGAAGCGGTATGGCTAAAGTTC TGGTGCTTTA	Amplification of *wrbA* gene of *E. coli* MG1655 for construction of the gene fusion of *kdpD-wrbA*
wrbA-anti	ACCACTTCCACCGCTGCCACCGCCGTTAAGTTTAA CTGCCAGAC	
KdpDup-sense-SacI	GCGCGAGCTCGCACTGCGCCGTACTG	amplification of kdpD gene fragment upstream of the first periplasmic loop coding region (with
kdpD-wrbA-periup-anti	CATACCGCTTCCACCGCTGCCACCCGCCATCAGCC ACTGCATGGCAAT	

Name	Sequence (5' to 3')	Reference
		wrbA homolgous overhang)
KdpDperidown-sense	GGCGGTGGCAGCGGTGGAAGTGGTTTTGATGCCG CCAACCTGGTGAT	amplification of kdpD gene fragment downstream of the first periplasmic loop coding region (with wrbA homolgous overhang)
KdpDdown-antisense-NdeI	CGGCCATATGCATATCCTCATGAAATTCTTCAAG	
KdpDNld(38-380)-NcoI-sense	ATACCATGGCAACCTGGGCGATGCTGGCAGAAGC	Amplification of *E. coli* kdpD gene fragments encoding KdpD (38-380)
KdpDNld(38-380)-6his-HindIII-anti	CGCAAGCTTTTAGTGGTGATGGTGATGATGGCGGG CGGGTGGTTCATCAAGCG	
del-thyA-upsen-BamHI	ACGGGATCCAATAGGATATACCGGCGGAATG	Deletion of *B. fragilis thyA*
del-thyA-upanti	GCGAATGGTATACTTCTTGGGT	
del-thyA-downsen	ACCCAAGAAGTATACCATTCGCTAATCCCCATCGG ACTATGAGT	
del-thyA-downanti-HindIII	AGTAAGCTTGAGTATGTCATCGACCCGGAGA	
thyA-check-upsen	GCGATGTTCGATGCATTCGGTA	
thyA-check-downanti	AGACGAGCAGATTCTGAAGTTG	
del-rr-upsen-BamHI	TGTGGATCCCATTGGTCGACTTATGCTCTGC	Deletion of *B. fragilis rr*$^{K+}$
del-rr-upanti	GGCAACGATATTCACGCGCGACCTGATAAGTTAAA ATGTGAATGGT	
del-rr-downsen	GTCGCGCGTGAATATCGTTGCC	
del-rr-downanti-HindIII	CATAAGCTTCAGACCACTCTCACCGCTGTAG	
rr-check-upsen	GGTCACAACTGTGCAACTCT	
rr-check-downanti	GCGGTAACAGAATACGTGTGCA	
del-kdpA-upsen-BamHI	TCGGGATCCACTTTCACATCCGGTCAATAGG	Deletion of *B. fragilis kdpA*
del-kdpA-upanti	CGATCGGAATAAACCGACTCAGGACAATCTGCACC GCCACTCCTA	
del--kdpA-downsen	CTGAGTCGGTTTATTCCGATCG	
del-kdpA-downanti-HindIII	AAGAAAGCTTTCGCCCGGTTGC	
kdpA-check-upsen	CAAGATAGGTGACACGAAGC	
kdpA-check-downanti	CTTTGTAATCACATTGGCACGC	
del-kdpO-upsen-HindIII	CCGAAGCTTGGCGCTGAAAGGAGTACAATAT	Deletion of *B. fragilis kdpO*
del-kdpO-upanti	CTCACTCTGAAGGGATAGTTGAATTTCATCTTTACT TTCTATCTG	
del-kdpO-downsen	TTCAACTATCCCTTCAGAGTGAG	
del-kdpO-downanti-HindIII	CTCATTCAAGCTTCCTTCCACA	
kdpO-check-upsen	CGACCTCGATAATGACCCAAC	
kdpO-check-downanti	CCCATCACAACCTCATTCTCT	
del-kdpD-upsen-BamHI	AGAGGATCCTTGGAATGATGTGCTTCTGGGG	Deletion of *B. fragilis kdpD*
del-kdpD-upanti	AATCTATGTTCGCTTGTGCCAGCTGTACACTTTCTT CTCTATCC	
del-kdpD-downsen	CTGGCACAAGCGAACATAGATT	
del-kdpD-downanti-HindIII	CGCAAGCTTGTTCGTGGGAGATGGTAGAGAT	
kdpD-check-upsen	GCATGAATGTGGAAGAGGTGAG	
kdpD-check-downanti	CTTCCACCTGCGTCATGTTCA	
del-hk-upsen-HindIII	AAGGAAGCTTGAATGAGAAACG	Deletion of *B. fragilis hk*$^{K+}$
del-hk-upanti	CAATATTCCAATGCCGAAAAGT	
del--hk-downsen	ACTTTTCGGCATTGGAATATTGTGATAATGCTGGAA ATTATGGAG	
del-hk-downanti-BamHI	TACGGATCCGATGTACTCTTTCCACCACCCC	
hk-check-upsen	GAAGCCCTGTTGAAAGGTTTAC	
hk-check-downanti	GCTCTCAGCGTTTGATGTTC	
61RAB	GGCGCGCCGTAAGGAAAGTGGCTCTCAG	(Meehan, Baughn et al. 2012)
1842	CAAGGCGACAAGGTGCTGATGC	(Meehan, Baughn et al. 2012)

Name	Sequence (5' to 3')	Reference
rr-bind-upsen(FAM)	GGCAATAAAACAGAAGCAGC	For EMSA
rr-bind-upanti	AGGAAAGAAGCATAAAACTC	
pNBU-Pkdp-upsen-EcoRI	GACATGGGAATTCCCCTCCACCG	Mutation σ^{54} recognition motif of $P_{kdp\ B.\ fragilis}$. From TGGCACGCATTTGGCAT to TAATACGCATTTAATAT
pNBU-Pkdp-downanti-StuI	GCTCAGGCCTTCGTACGGGAT	
rr-bind-downsen	GAGTTTTATGCTTCTTTCCTCTTTTCATAATGATAGGGTATCTT	
Pkdpb.framu-anti-up	AGAAACAGTCAAGGATAAGATAA	
Pkdpb.framu3-sens-down	TTATCTTATCCTTGACTGTTTCTAATACGCATTTAATATGAAGAGTTACA	
rr -sen-6his-1	CATCATCACCATCACCACATGAGTAAAATTCTGATTATTGA	Primers for *E. coli* reporter construction or relevant plasmids construction
rr-sen-6his-2-KpnI	AGTGGTACCCACATTTTAACTTATCAGATATGCATCATCACCATCACCACATGA	
rr-anti- PstI	ATCCTGCAGTTAGAGCTTATATTCTTCTATTTTTCG	
rr-seq-sen	CCGGAAAAGAGGTGTTTGCC	
KdpD-sen-NheI	TGAGCTAGCGTATAAAAATTGAAGAAAAGATGGA	
KdpD-6his-anti-EcoRI	ATCGAATTCTTAGTGGTGATGGTGATGATGTGCAAGTATAATCAAATCTATGTTC	
hk-sen-EcoRI	TGAGAATTCTTTAGTCTTAGTTATCCATTATGAA	
hk-6his-anti-KpnI	ATCGGTACCTTAGTGGTGATGGTGATGATGTGCCTTCAACCTTATCACAAAGCA	
kdpOb.fra-6his-*HindIII*-anti	CTCAAGCTTCAGTGGTGATGGTGATGATGTGGCTTTAAAGTAATACCAA	
KdpFbfra-gfp-anti-nonstop	AAAGTTCTTCTCCTTTACTCATAAACTTCTCTGGACGAATGAGCA	
lacI-Pkdp-sen	GACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTTACGTAATGTAATCGAACGCAGCCT	
Pkdp-lacZ-anti	CAGTCACGACGTTGTAAAACGACGGCCAGTGAATCCGTAATCATGGTCATTGCTTTATTTTCAAATTAAAACTTC	
lacI-check-sen	ACTCTCTCAGGGCCAGGCG	
lacZ-check-anti	CTGCGCAACTGTTGGGAAGG	
QRT-kdpD-sen	GATTGATAACGGGGTGGATG	Primers for qRT-PCR of the regulator or structure genes of Kdp *B. fragilis* system
QRT-kdpD-anti	CATTGGTATGTGCCAGTTCG	
QRT-hk-sen	AATGGCCGAGTAGTGATTGG	
QRT-hk-anti	AATGTCCCTCCATGTGCTTC	
QRT-rr-sen	TCAAGAACGGAGCTTTCGAT	
QRT-rr-anti	CCGCTTCTTTCAATGCTTTC	
QRT-kdpA-sen	ACCGCTTTCATTGGTGGTAG	
QRT-kdpA-anti	AACGGATGCGAAGAATTGAC	
QRT-kdpB-sen	CCATTACCGGTGAATCTGCT	
QRT-kdpB-anti	TATCTCGTTCGGCGTCTTCT	
QRT-kd-sen	TCGGCAGGTAGCAATAAAGG	
QRT-kd-anti	GCGCCACTCTTTTCACTTGT	
QRT-kdpO-sen	CACCGATTTTGACGGAACTT	
QRT-kdpO-anti	ATAAGCCACTCCTGCCTCAA	
QRT-recA-sen	GAATTGCCGCTTTCATTGAT	
QRT- recA-anti	GTCAAGGCGGCTACAGAGTC	
Insect CipA- BamHI-Sense	CGCGGATCCAATGATTAATGACATGCATCCTTC	For generation of pFastBac1-cipA-gfp and pFastBac1-cipB-gfp
Insect CipB-BamHI-sense	CTAGGATCCAATGATAATTAAGAAAGATATTTTG	
cipA-RBS-NheI-sen	CCGGCTAGCAGGAGGTCTATATGATTAATGACATGCATCCTTC	
cipB-RBS-NheI-sen	CCGGCTAGCAGGAGGTCTATATGATAATTAAGAAAGATATTT	
cipA-RBS-KpnI-sen	CAGGGTACCAGGAGGTCTATATGATTAATGACATGCATCCTTC	

Name	Sequence (5' to 3')	Reference
cipB-RBS-KpnI-sen	CAGGGTACCAGGAGGTCTATATGATAATTAAGAAA GATATTT	Amplification of *cipA* and *cipB* genes and generation of pBAD-cipA-6his and pBAD-cipB-6his plasmids.
cipA-RBS-SalI-sen	CACGTCGACAGGAGGTCTATATGATTAATGACATG CATCCTTC	
cipB-RBS-SalI-sen	CACGTCGACAGGAGGTCTATATGATAATTAAGAAA GATATTT	
cipA-RBS-HindIII-sen	GCGAAGCTTAGGAGGTCTATATGATTAATGACATG CATCCTTC	
cipB-RBS-HindIII-sen	GCGAAGCTTAGGAGGTCTATATGATAATTAAGAAAG ATATTT	
cipA-anti	CATAGAGATTTCTACGCAATTAA	
cipB-anti	AATTTCAACACCTACTATATATT	
cipA-6his-HindIII-anti	GCTAAGCTTAGTGATGGTGATGGTGATGCATAGAG ATTTCTACGCAATTA	
cipB-6his-HindIII-anti	GCTAAGCTTAGTGATGGTGATGGTGATGAATTTCAA CACCTACTATATAT	
gfp-sense	ATGAGTAAAGGAGAAGAACTTT	Generation of *gfp-cipA*, *gfp-cipB*,*cipA-gfp* and *cipB-gfp* gene fusions for pBAD-cipA-gfp, pBAD-cipB-gfp, pBAD-cipA-(gfp,lacZ) and pBAD-cipB-(gfp,lacZ) plasmids
gfp-HindIII-anti	CTAAGCTTATTTGTATAGTTCATCCATGC	
gfp-cipA-sense	ACATGGCATGGATGAACTATACAAAATGATTAATGA CATGCATCCTTC	
gfp-cipB-sense	CATGGCATGGATGAACTATACAAAATGATAATTAAG AAAGATATTTTGTT	
cipA-gfp-anti	AAAGTTCTTCTCCTTTACTCATCATAGAGATTTCTAC GCAATTA	
cipB-gfp-anti	AAAGTTCTTCTCCTTTACTCATAATTTCAACACCTAC TATATAT	
gfp-XmaI-anti	ACTCCCGGGTTATTTGTATAGTTCATCCATGC	
gfp-RBS-EcoR1-sense	CGCGAATTCAGGAGGATACTAATGAGTAAAGGAGA AGAACTTTTC	
cipA-lacZ-anti	CAGTGAATCCGTAATCATGGTCATCATAGAGATTTC TACGCAATTAA	Generation of *cipA-lacZ* and *cipB-lacZ* gene fusions for pBAD-cipA-lacZ, pBAD-cipB-lacZ, pBAD-cipA-(gfp,lacZ) and pBAD-cipB-(gfp,lacZ) plasmids
cipB-lacZ-anti	CAGTGAATCCGTAATCATGGTCATAATTTCAACACC TACTATATATT	
lacZ-Sense	ATGACCATGATTACGGATTCAC	
lacZ-HindIII-anti	CGCAAGCTTATTTTTGACACCAGACCAACT	
cipA-vioA-sen	ATTAATTGCGTAGAAATCTCTATGATGAAGCATTCT TCCGATATCTGC	Generation of *cipA-vio* gene gene fusions for pBAD-cipA-(vioA,vioB), pBAD-free-(vioC)-cipA-(vioD,vioE) and pBAD-cipA-(vioC,vioD,vioE) plasmids
vioA-SacI-anti	GTCGAGCTCACGCGGCGATGCGCTGCAGC	
cipA-vioB-sen	ATTAATTGCGTAGAAATCTCTATGATGAGCATTCTG GATTTTCCACGC	
vioB-KpnI-anti	CTGGGTACCTCAGGCCTCTCTAGAAAGCTTTCC	
cipA-vioC-sen	ATTAATTGCGTAGAAATCTCTATGATGAAAAGAGCA ATCATAGTCGGAG	
vioC-SalI-anti	CCTGTCGACTCAGTTGACCCTCCCTATCTTGTA	
cipA-vioD-sen	ATTAATTGCGTAGAAATCTCTATGATGAAGATTCTG GTCATCGGCGCGG	
vioD-HindIII-anti	CGCAAGCTTCAGCGTTGCAGCGCGTAGCGCA	
cipA-vioE-sen	ATTAATTGCGTAGAAATCTCTATGATGGAAAACCGG GAACCGCCGCTG	
vioE-HindIII-anti	CTCAAGCTTCTAGCGCTTGGCGGCGAAGACGGC	
vioA-RBS-NheI-sen	CCGGCTAGCAGGAGGTCTATATGAAGCATTCTTCC GATATCTGC	Amplification of *vio* genes for generation of pBAD-free-(vioA,vioB), pBAD-free-(vioC,vioD,vioE) and pBAD-free-(vioC)-cipA-(vioD,vioE) plasmids
vioB-RBS-KpnI-sen	CAGGGTACCAGGAGGTCTATATGAGCATTCTGGAT TTTCCACGC	
vioC-RBS-KpnI-sen	CAGGGTACCAGGAGGTCTATATGAAAAGAGCAATC ATAGTCGGAG	
vioD-RBS-SalI-sen	CACGTCGACAGGAGGTCTATATGAAGATTCTGGTC ATCGGCGCGG	
vioE-RBS-HindIII-sen	GCGAAGCTTAGGAGGTCTATATGGAAAACCGGGAA CCGCCGCTG	

Name	Sequence (5' to 3')	Reference
Del-cipA-upstream-PstI-sen	CTCTGCAGCATAGAATAGTGAATTCTAAT	Generation of pNPTS-138-R6KT-del-cipA and pNPTS-138-R6KT-del-cipB plasmids
Del-cipA-upstream-up-anti	AAGCATTTCAACAATCAATTATTAATGTAAACTCCAAAATATAATG	
Del-cipA-downstream-sen	AATAATTGATTGTTGAAATGC	
Del-cipA-downstream-BamHI- anti	GCGGATCCTATATGACTGCAATCTCTGAA	
Del-cipB-upstream-PstI-sen	ATTCTGCAGGTGGAAGTGAAGGGGCAGTGG	
Del-cipB-upstream-up-anti	TAGAAATTTAACAAATACTTCGACATAAACTCCAAAATTTAA	
Del-cipB-downstream-sen	GAAGTATTTGTTAAATTTCT	
Del-cipB-downstream-NheI-anti	ATAACGGGAACGCCATGCTAGCGG	
Promoter-cipA-PstI-sens	GGCCTGCAGTTACTCCAATACAATTTATCCTT	Generation of pPINT-P_{cipA}-cipA-gfp and pPINT-P_{cipB}-cipB-gfp plasmids (gfp-sense, cipA-gfp-anti and cipB-gfp-anti are also required here)
Promoter-cipB-PstI-sens	GGCCTGCAGCGTGGTATAGTTAAAATTGACA	
gfp-EagI-anti	CTAAGCTTCGGCCGTTATTTGTATAGTTCATCCATGC	
cipA-N47-anti-HindIII	GCTAAGCTTAATCATGCATTAATACAGTCACCA	CipA truncation
cipA-N47-gfp-anti	AAAGTTCTTCTCCTTTACTCATATCATGCATTAATACAGTCACCATA	
cipA-N32-gfp-anti	AAAGTTCTTCTCCTTTACTCATCATAACTTTCATTGCAATGATTTTA	
cipA-N23-gfp-anti	AAAGTTCTTCTCCTTTACTCATGCTACGTAGCATTACGTCATCTACT	
cipB-N59-HindIII-anti	GCTAAGCTTAATCTTTATCATCAACTAGTAATA	CipB truncation
cipB-N59-gfp-anti	AAAGTTCTTCTCCTTTACTCATATCTTTATCATCAACTAGTAATAG	
cipB-N33-gfp-anti	AAAGTTCTTCTCCTTTACTCATTGACAGAATATCAATATTGACCTTC	
cipB-N17-gfp-anti	AAAGTTCTTCTCCTTTACTCATATCATCGACAATCAGCTCTTCATTT	

2.2.4 Strain construction

2.2.4.1 Construction of *E. coli* reporter for testing *B. fragilis* Kdp system

An *E. coli* reporter strain was constructed by the method described (Fried, Lassak et al. 2012), to place the native chromosomal *lacZ* under the control of *B. fragilis kdp* promote $P_{kdp\ B.fragilis}$. Briefly, the fragment containing $P_{kdp\ B.fragilis}$ was amplified with the primers LacI-Pkdp-sen and Pkdp-lacZ-anti (see Table 3) from the genomic DNA and electro-transformed into *E. coli* LF2 to replace the P_{lac}::*rpsL-neo-kan*, cassette to generate *E. coli* YW1. Then the native *kdpD* and *kdpE* gene in the *E. coli* YW1 were deleted together with the method described in Quick & Easy *E. coli* Gene Deletion Kit (Gene Bridges), to generate the finial reporter strain *E. coli* YW2.

2.2.4.2 Conjugation of shuttle vectors from *E. coli* to *B. fragilis* and gene deletions in *B. fragilis*

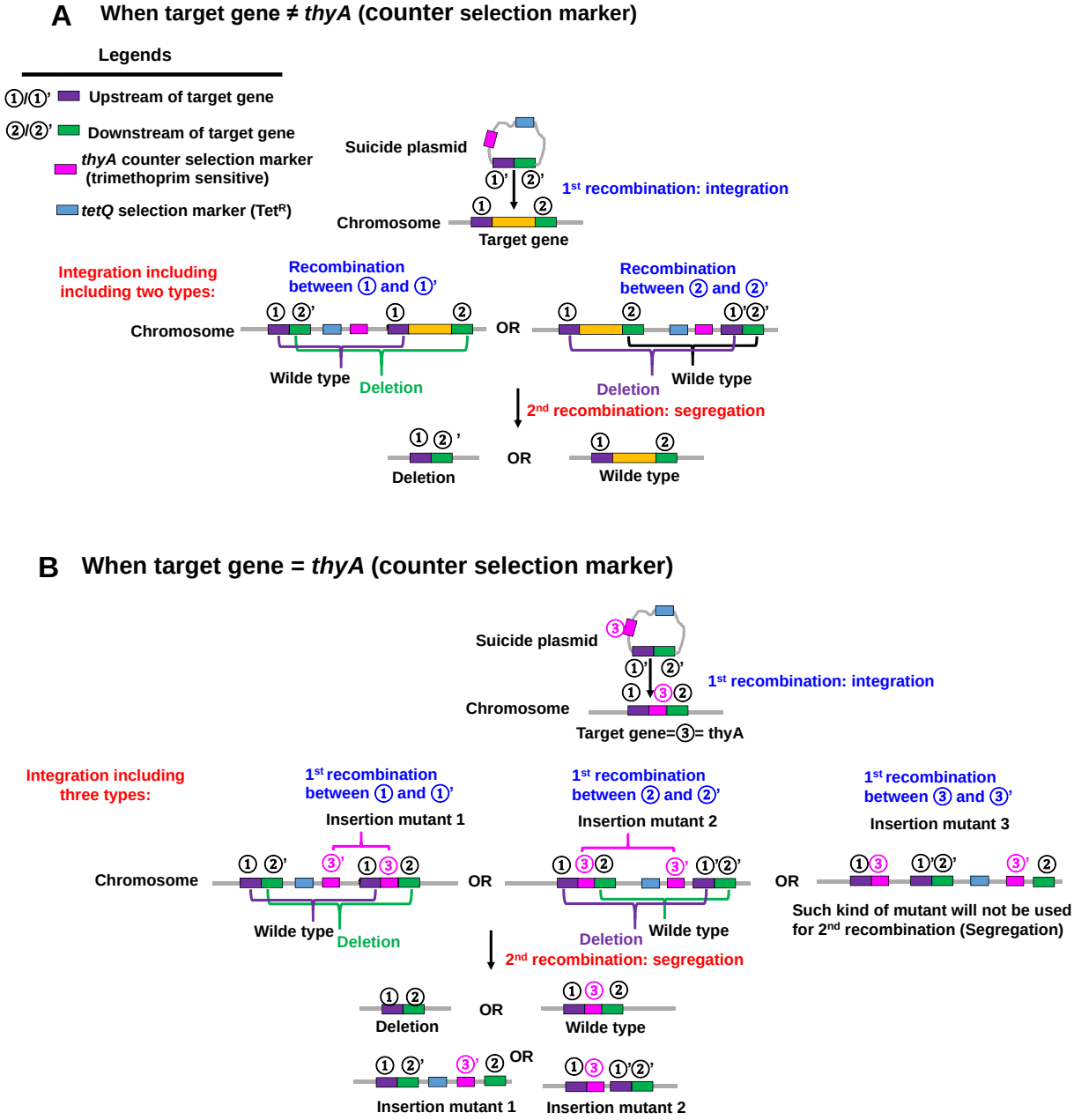


Figure 6: Schematics of gene deletion in *B. fragilis* with pYT102 backboned plasmids. (A) Deletion of a gene in *B. fragilis thyA* mutant stain. **(B)** Deletion of chromosomal *thyA* gene from the wild type strain *B. fragilis* NCTC 9343 with pYT102-ΔthyA. Gene deletion of *thyA* has priority than any other gene deletion steps, to make the counter selection work properly.

Plasmids backboned with pNBU1 were mobilized from *E. coli* ST18 (or *E. coli* S17-1 λpir) to *B. fragilis* strains by biparental mating (Choi, Herrou et al. 2016). Briefly, *E. coli* strains harboring desired plasmids were cultivated in LB medium overnight from single colony. Preculture was transfer to fresh LB and cultivated to the early exponential stage. *B. fragilis* was inoculated into BHIS and overnight culture was transferred to fresh BHIS and cultivated to the late exponential stage. Pellet 250 µL of *E. coli* and *B. fragilis* at 5,000×*g* for 5 minutes and washed once with BHIS. Mixture of them was resuspended with 50 uL fresh BHIS and spotted on BHIS plate without antibiotics (5-aminolevulinic acid and thymine is required by *E. coli* ST18 and *B. fragilis thyA* deletion mutants, respectively) and incubated anaerobically overnight at 37 °C. The lawn was collected, resuspended with BHIS and plated on BHIS containing gentamicin and erythromycin or tetracycline, and grown anaerobically. Integration of the vector was confirmed by colony PCR. The *B. fragilis* WLu reporter was constructed in such a way.

When the shuttle vectors (pYT102 backboned vectors) were designed for gene deletion (this part of experiment is still ongoing), an additional second step recombination was performed as described (Baughn and Malamy 2002). Cointegrants from the first step of recombination were grown anaerobically in BHIS supplemented with thymine (gene deletion of *B. fragilis* should be carried out in a *thyA* mutant). Overnight cultures were plated on AMMgluc plate containing thymine and trimethoprim to select for segregation of the vector and deletion of the target gene (Figure 6A).

However, to make the counter-selection (*thyA* as the marker) work properly, all the gene deletions should be carried out in *thyA* mutants. Therefore, *thyA* gene should be deleted before the deletions of *kdpA*, *kdpD*, *rr*$^{k+}$ *etc.* Principally, *thyA* mutant could be obtained by random mutation, as well as by gene deletion with the pYT102 back-boned plasmids. One may ask how the chromosomal *thyA* gene could be deleted by using the pYT102 *thyA* as counter selection marker. Even though the recombination procedures are more complicated and trickier, this is theoretically indeed possible (Figure 6B).

2.2.4.3 Construction of *P. luminescens* Δ*cipA* and/or Δ*cipB* and CipA-GFP or CipB-GFP production strains

To generate a clean deletion of *cipA* or *cipB* in *P. luminescens*, two 700-bp fragments homologous to the upstream and downstream regions of the *cipA* and *cipB* genes, respectively, were amplified using *P. luminescens* chromosomal DNA and the appropriate primers listed in Table 3. The resulting products were then combined into one DNA fragment via a second PCR step, and inserted into the suicide vector pNPTS-138-R6KT(Lassak, Henche et al. 2010) to obtain pNPTS-138-R6KT-del-cipA and pNPTS-138-R6KT-del-cipB, respectively. *E. coli* ST18 (Thoma and Schobert 2009) transformed with these plasmids was used for conjugation of *P. luminescens* TT01, and chromosomal integrants were selected on the basis of their kanamycin resistance (Glaeser and Heermann 2015). These cells were grown in CASO medium and then plated on CASO agar containing 10% (w/v) sucrose in the absence of kanamycin to select for segregation of the plasmid backbone from the chromosome. Single colonies were tested for deletion of *cipA* or *cipB* and loss of the marker gene *sacB*, which confers sucrose sensitivity (Blomfield, Vaughn et al. 1991). The overall principals are quite similar as shown in Figure 6. *P. luminescens cip*$^-$ was generated by successive deletion of *cipA* and *cipB,* and each recombination step was confirmed by colony PCR. Plasmids pPINT-P_{cipA}-cipA-gfp and pPINT-P_{cipB}-cipB-gfp were separately conjugated from *E. coli* ST18 into *P. luminescens cip*$^-$ and integrated into the genome as described (Glaeser and Heermann 2015). Recombination events were verified by colony PCR.

2.2.4.4 Construction of the strains *E. coli* Vio1 to Vio6

Violacein production strains *E. coli* Vio1 to Vio6 were generated by co-transformation of *E. coli* DH5α with the respective pBAD18 and pBAD33 derivatives containing free or *cipA*-fused *vio* genes as listed in Table 2. For use as a negative control strain for violacein production, *E. coli*

Vio0 was obtained by co-transformation of *E. coli* DH5α with the empty vectors pBAD18 and pBAD33.

2.2.5 Test the reporter strains to different signals

2.2.5.1 Fuctional analysis of KdpD-WrbA-6His in *E. coli* reporter HAK006

To test the functional performance of KdpD-WrbA-6His in comparison with the wild type KdpD, *E. coli* HAK006 transformed with pBD5-3 or pBAD24-KdpD-WrbA-6His were cultivated at 37 °C in phosphate-buffered minimal medium containing different concentrations of K^+ (Epstein and Kim 1971) for about seven hours. After measuring OD_{600}, cells were collected and frozen at -20°C. β-Galactosidase activities were measured as described (Miller 1972, Schramke, Laermann et al. 2017). β-Galactosidase activity per OD_{600} was used to demonstrate the expression level of *kdp* operon.

2.2.5.2 Test the *E. coli* reporter of *B. fragilis* Kdp system

Reporter strain *E. coli* YW2 was transformed respectively with pBAD18, pBAD-rr, pBAD-hk, pBAD-rr-hk, pBAD-rr-hk-kdpD. These strains were then cultivated at 37 °C in phosphate-buffered minimal medium containing various K^+ concentrations (Epstein and Kim 1971). When testing the response of strains to osmostress or salt stress, different amounts of sucrose (0 M, 0.2 M, 0.4 M, 0.6 M, 0.8 M) or NaCl (0 M, 0.1 M, 0.2 M, 0.3 M, 0.4 M) were added to the same minimal medium with K^+ adjusted to 10 mM. To demonstrate the transcription level of *B. fragilis kdp* operon in the reporter strain, β-galactosidase activity were assayed as described (Miller 1972, Schramke, Laermann et al. 2017).

2.2.5.3 Test the *B. fragilis* WLu reporter strain to different signals

B. fragilis WLu was cultivated overnight at 37 °C in **(i)** AMMgluc containing 0.1 mM, 1 mM, 2.5 mM, 7.5 mM, 10 mM, or 100 mM K^+ to test the response of its Kdp system to K^+ and **(ii)** AMMgluc (10mM K^+) supplemented with 0.1 M, 0.2 M, 0.4 M NaCl or with 0.2 M, 0.4 M, 0.6 M

and 0.8 M sucrose to test the response of its Kdp system to salt stress or osmostress, respectivly. Briefly, *B. fragilis* WLu was cultivated in the media described above for 9 hours. After measuring of the OD_{600}, cells were lysed and the released luciferase was mixed up with the substrate of Nano-Glo Luciferase Assay kit. Luminescence intensity per OD_{600} was used as measure for the transcriptional level of *kdp* operon.

2.2.6 Isolation of total RNA, cDNA synthesis and qRT-PCR

B. fragilis NCTC 9343 was cultivated at 37 °C in AMMgluc containing 0.1 mM or 10 mM K^+ for about 14 hours. Cells were collected and total RNA was extracted as described (Aiba, Adhya et al. 1981). The total RNA was treated with DNase to remove any genomic DNA contamination.

Subsequently, random hexamers and the isolated RNA were used to synthesize the first strand of cDNA with the RevertAid H Minus First Strand cDNA Synthesis Kit (Thermo Fisher). The relative levels of cDNA *rr*$^{K+}$, *kdpA*, *kdpC*, *kdpO*, *kdpD* and *hk*$^{K+}$ in different samples were measured with iQ™ SYBR® Green Supermix (Bio-Rad) and *recA* gene was chosen as the reference.

2.2.7 Purification of *kinase* KdpD protein

Production of wild type KdpD-6His, KdpD-R511Q-6His and KdpD-WrbA-6His was carried out with *E. coli* BL21 (DE3). Production of these proteins was induced with 0.25 mM of IPTG or 0.3% (w/v) L-arabinose (when cell density reached OD_{600} ~1.0) for three hours at 37 °C or overnight (for about 16 hours) at 16 °C. Cells were collected at 4°C and lysed with high-pressure cell disruptions in the lysis buffer (50 mM Tris-HCl, pH 7.0, 10 % (v/v) glycerol, 10 mM $MgCl_2$, 1 mM DTT, and 0.5 mM PMSF, 1 µg/mL DNase). Cell debris was removed with low speed centrifugation (14,461×*g* at 4 °C for 20 min). Supernatant was transferred to ultracentrifugation (212,605×*g* at 4 °C for 20 min) to separate the cytoplasm and the cytoplasmic membrane fractions. The isolated membrane vesicles were washed and frozen at

-80 °C. KdpD protein solubilization and purification from membrane vesicles were performed as described (Jung, Tjaden et al. 1997). Protein concentration was determined with the Lowry method (Lowry, Rosebrough et al. 1951).

2.2.8 Purification of nanodiscs MSP (MSP1E3D1)

Single colony of *E. coli* BL21 (DE3) transformed with the plasmid pMSP1E3D1 was cultivated at 30°C overnight in LB medium containing 25 µg/mL kanamycin. The overnight culture was used to inoculate LB medium (supplemented with 25 µg/mL kanamycin and pre-warmed to 37°C) loaded in two 2-liter flask. To induce the production of MSP1E3D1, 0.5 mM IPTG was added when cell density reached OD_{600} ~1.0. One hour later, the temperature was shifted from 37°C to 28°C. After three hours' further cultivation at this lower temperature, cells were collected by centrifugation and stored at -80°C. Cells was lysed in 20 mM phosphate buffer with 1% (v/v) Triton X-100. Protein purification steps were performed using Ni-NTA affinity resin. MSP shows affinity to membrane fractions, therefore 1% (v/v) Triton X-100 or 50 mM Na-cholate was added to the wash buffer (40 mM Tris-HCl, pH 8.0, 0.3 M NaCl, 20 mM imidazole) (Ritchie, Grinkova et al. 2009). Protein concentration was determined by measuring the absorbance at wavelength 280 nm with PEQLAB Nano Drop ND-1000 Spectrophotometer [(molar extinction coefficient ε280 = 29,400 $M^{-1}cm^{-1}$) (Luthra, Gregory et al. 2013)].

2.2.9 Nanodiscs assembly

Preparation of the phospholipid solution and assembly of nanodiscs was carried out as described (Hornschemeyer, Liss et al. 2016). Modifications were made at the following three points, **(i)** the membrane scaffold protein used in study is MSP1E3D1; **(ii)** ratios between MSP, target protein and phospholipid were modified to 1:130 and 4:130 **(iii)** two times more β-cyclodextrin was added to remove the DM detergent wrapping KdpD proteins. Size-exclusion chromatography was performed with Superdex 200 Increase 10/300 GL column and ÄKTA Protein Purification Systems of GE Healthcare Life Sciences, by following the manufacturer's

manual and calibration instruction (Sample injection 500 µL). Peaks were detected with UV-Vis monitor. Column calibration was performed by the Gel Filtration Calibration Kit (GE Healthcare) with the protein markers, ferritin, aldolase, conalbumin, ovalbumin, carbonic anhydrase, ribonuclase and aprotinin.

2.2.10 Purification of *non-kinase* KdpD protein

E. coli KdpD 1-395-6His, *E. coli* KdpD 38-380-6His and *D. radiodurans* KdpD-6His were produced with *E. coli* BL21 (DE3). Production of these protein was induced with 0.3% (w/v) L-arabinose for three hours at 37 °C. Cells were lysed and membrane fractions were isolated as described in 2.2.8.1. *E. coli* KdpD 1-395-6His and *D. radiodurans* KdpD-6His were extracted from membrane vesicles and purified with Ni-NTA agarose affinity chromatography as described (Heermann, Altendorf et al. 2000). Protein concentration was determined with the Lowry method (Lowry, Rosebrough et al. 1951).

2.2.11 Limited proteolysis of *non-kinase* KdpD

Purified KdpD 1-395-6His (~0.5 mg/mL) was treated with 0.1, 0.01, and 0.001 mg/mL proteinase K, trypsin or subtilisin [reaction buffer, 20 mM HEPES, pH 7.5, 50 mM NaCl, 10 mM $MgSO_4$] at room temperature or on ice for 30 min, respectively. To stop the reaction, 5×SDS loading buffer was added to the proteolysis mixture and the mixtures were subsequently applied to SDS-PAGE. Under optimal conditions, proteolysis was followed in a timecourse (reaction time 15 min, 30 min, 45 min, 60 min). Stable peptides were extracted and sent to the collaborator Dr. Markus Hartl for sequence analysis by mass spectrometry.

2.2.12 Isolation and characterization of PCIs

To isolate PCIs, cells were collected by centrifugation, resuspended in ice-cold Na-phosphate buffer (20 mM sodium phosphate buffer, pH 7.0, 8.5 mM KCl), and disrupted by three passages

through a French press (Thermo IEC Laboratory Press) at 0.4 kbar. PCIs were collected by centrifugation for 15 min at 4.000×*g*, and washed three times with the same buffer (Figure 7).

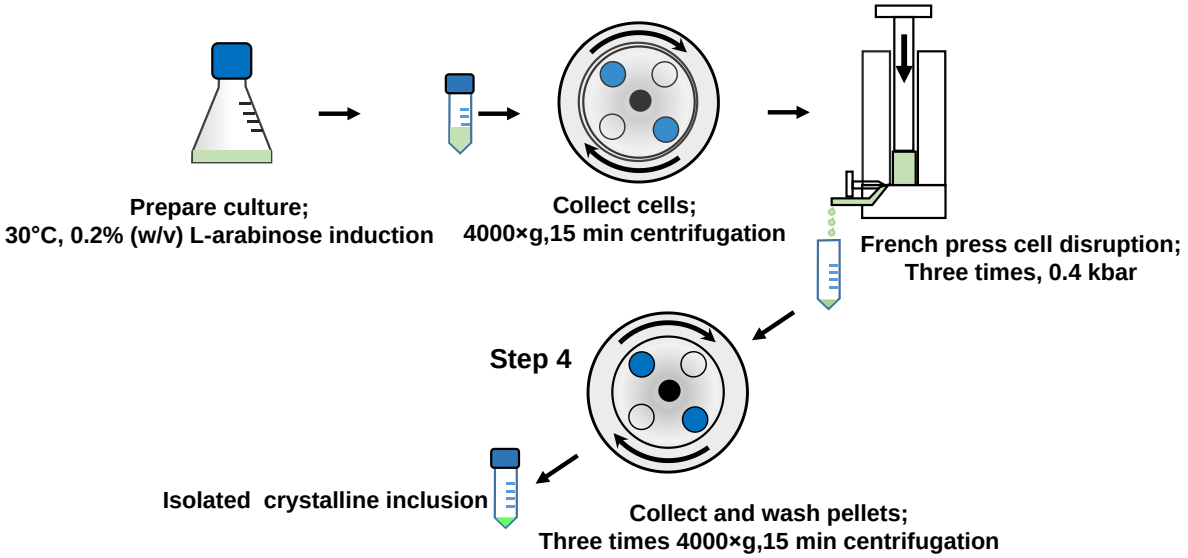


Figure 7: Schematic of production and isolation of the PCIs. Cells producing PCIs were collected by centrifugation. Cells were lysed by French press and insoluble fractions containing the PCIs were recovered by centrifugation and washed three times whith Na-phosphate buffer.

Thermal stability studies were performed in Na-phosphate buffer. The isolated CipA-GFP and CipB-GFP PCIs were incubated for 10 min at 30°C, 40°C, 50°C, 60°C, 70°C, 80°C, 90°C and 100°C, respectively, and PCIs shape and fluorescence intensity were subsequently determined by microscopy.

The solubility of PCIs was analyzed by following the method described (Bowen and Ensign 2001). CipA-GFP and CipB-GFP PCIs were resuspended at an OD_{600} of 20-60 in deionized water. Then, 10 µL of this suspension was added to, and gently mixed with 1 mL of the following solutions: **(i)** deionized water; **(ii)** 150 mM NaCl, pH 1.0, 3.0, 5.0, 7.0, 9.0, 11.0 or 13.0; **(iii)** 1 M, 2 M, 3 M, and 4 M NaCl, pH 7.0; **(iv)** 2 M, 4 M, 6 M, 8 M urea; **(v)** 100 mM EDTA, pH 7.0; **(vi)** 10% (w/v) SDS, pH 7.0; **(vii)** 100% (v/v) methanol, and **(viii)** 50% (v/v) glycerol, respectively. The OD_{600} was then monitored periodically and set in relation to that of the

corresponding control (PCIs in deionized water), which was set to 100% (Bowen and Ensign 2001).

Measuring the absorption spectra of Congo Red was performed as described (Upadhyay, Murmu et al. 2012). Briefly CipA-LacZ, CipB-LacZ, CipA-GFP&CipA-LacZ or CipB-GFP&CipB-LacZ PCIs as well as the soluble protein His-LacZ were separately diluted in reaction Na-phosphate buffer to final protein concentration of 50 µg/ml. Congo Red was added to this mixtures to a final concentration of 20 µM (Upadhyay, Murmu et al. 2012). After 30 minutes or 16 hours of incubation at room temeperature, 200 µl of these mixtures were loaded separately into 96-Well plate (Corning, Clear Bottom Black). The absorption spectra of Congo Red measured from wavelength 400 to 800 nm with Infinite M200 Plate Reader (Tecan). Congo Red alone exhibits maximum light absorbance at the wavelength of 490 nm. Upon binding to the repeated β-sheet structure in the inclusion body, its maximum light absorbance will be shifted to longer wave length of around 540 nm.

2.2.13 Overproduction, purification and assay of β-galactosidase (LacZ)

The production and isolation of CipA-LacZ or CipB-LacZ PCIs were performed as described in Figure 7. To purify LacZ in a soluble state, N-terminally 6His-tagged LacZ (His-LacZ) was produced in *E. coli* DH5α. An overnight culture (20 mL) of cells carrying pBAD-6his-lacZ was used to inoculate three 2-l flasks, each containing 500 ml of LB medium supplemented with 100 µL/mL ampicillin. When the cell density reached OD_{600} 0.8, 0.2% (w/v) L-arabinose was added to induce gene expression, and the cultures were further incubated at 37°C for 6 h. Cells were then harvested by centrifugation, suspended in lysis buffer (50 mM Tris-HCl, pH 7.0, 300 mM NaCl, 10 mM β-mercaptoethanol, 10 mM imidazole, 10 mM $MgCl_2$, EDTA-free protease inhibitor cocktail), and disrupted in a French press. Cell debris was removed by centrifugation for 20 min at 14,500×*g*, and the supernatant was loaded onto 4 ml of Ni-NTA resin previously equilibrated with binding buffer (50 mM Tris-HCl, pH 7.0, 300 mM NaCl, 10

mM β-mercaptoethanol, 10 mM imidazole, 20 mM $MgCl_2$). Columns were washed with 100 ml of washing buffer (binding buffer containing 20 mM imidazole), and His-LacZ was eluted with 20 ml of elution buffer (binding buffer containing 200 mM imidazole). Imidazole was later removed by dialysis of the protein against buffer (20 mM Tris-HCl, pH 7.0, 150 mM NaCl, 10 mM β-mercaptoethanol, 5 mM $MgCl_2$).

β-Galactosidase activity assays were performed at 30°C in modified buffer Z and quantified as described before (Miller 1972). One unit equals the amount of enzyme needed to hydrolyze 2-nitrophenyl β-D-galactopyranoside (*o*NPG) to 1 µmol of *o*-nitrophenol in 1 min at 30°C. The total protein content of PCI samples and purified His-LacZ was determined by using the Lowry method (Lowry, Rosebrough et al. 1951) Specific enzyme activity was defined as units of enzyme activity/mg of His-LacZ, or CipA-LacZ or CipB-LacZ PCIs (see the unit definition above).

To test the influence of, pH on the activity of His-LacZ, CipA-LacZ PCIs and CipB-LacZ PCIs, the, pH of modified buffer Z (chloroform and SDS were ignored) was adjusted to 5.0, 6.0, 7.0, 8.0, 9.0, and 10.0 (by adjusting the ratio between base and acid compositions), and β-galactosidase activity assays were performed at 30°C as described above. The enzyme activities measured at the different, pH values were expressed relative to the activity measured at, pH 7.0. To determine temperature dependence, the reaction temperature was adjusted to 22°C, 30°C, 37°C, 42°C, 47°C, 52°C, 57°C and 62°C, and measured activities were expressed relative to that at 30°C.

2.2.14 Western blot

For Western blot with KdpD polyclonal antiserum as the first antibody, the PVDF membrane was pre-blocked for 1 hour at room temperature with 5% (w/v) of milk powder in the buffer A (55 mM Tris-HCl, pH= 7.4, 154 mM NaCl). While for Western blot with Penta·His Antibody or anti-GFP antibody as the first antibody, the membrane was pre-blocked for 1 hour at room

temperature with 3% (w/v) of BSA in buffer A. The bands one the membrane were developed colorimetricly via the alkaline phosphatase activity of the second antibody (BCIP in conjunction with NBT as substrate) (Dejong, Vankesselvanvark et al. 1985).

2.2.15 Violacein/deoxyviolacein production and quantification

To determine the appropriate concentration of inducer for violacein production, cultures of the engineered strains (*E. coli* Vio1 to *E. coli* Vio6) in early exponential phase were diluted with LB to an OD_{600} of 0.05 and drops were placed on LB plates containing 0%, 0.01%, 0.02%, 0.05%, 0.1% and 0.4% (w/v) of L-arabinose. After overnight cultivation at 30°C, the appropriate inducer concentration was found to be in the range of 0.01% (w/v) to 0.05% (w/v) according to the pigment accumulation. The violacein production was induced with 0.01% (w/v) and 0.05% (w/v) L-arabinose.

To quantify violacein/desoxyviolacein production *E. coli* strains Vio1-Vio6 were aerobically incubated in LB medium, supplemented with 100 µg/mL ampicillin, 15 µg/mL chloramphenicol and 0.05% (w/v) L-arabinose, at 30°C. Aliquots (1 ml) were taken at the indicated time points, centrifuged, and the pellets were resuspended in 1 ml of 95% (v/v) methanol, vortexed, and cell debris was removed by centrifugation. The concentration of the violacein + deoxyviolacein mixture was determined based on absorbance at A_{577nm}, based on a molar extinction coefficient of 1.7×10^4 L mol^{-1} cm^{-1} (Sneath 1956). To determine the proportions of violacein and deoxyviolacein in the methanol extracts, a HPLC protocol was used as described (Lee, Aswani et al. 2013), but with modifications for use with the Hypersil GOLD aQ column (Thermo Scientific). Briefly, two solvents were used to perform gradient elution. Solvent A was 0.1% (v/v) formic acid in water; solvent B was 0.1% (v/v) formic acid in acetonitrile. The column was equilibrated with 95% (v/v) A + 5% (v/v) B for 6 min; 50 µL methanol extract was then injected; the solvent gradient was started 7 min after injection, and over a period of 10 min, B was increased to 98%; the 2% (v/v) A + 98% (v/v) B mixture was kept constant for 7 min and then

replaced by 95% (v/v) A + 5% (v/v) B for 2 min. Light absorbance of the peaks was analyzed with a UV/VIS detector at a wavelength of 567 nm (Lee, Aswani et al. 2013). Since pure violacein is not commercially available, a mixture of violacein (>85%) and deoxyviolacein was used as standard.

3 Results

3.1 Bioinformatics analysis on KdpD protein evolution

3.1.1 Distribution of KdpD and KdpA proteins in the three domains of life

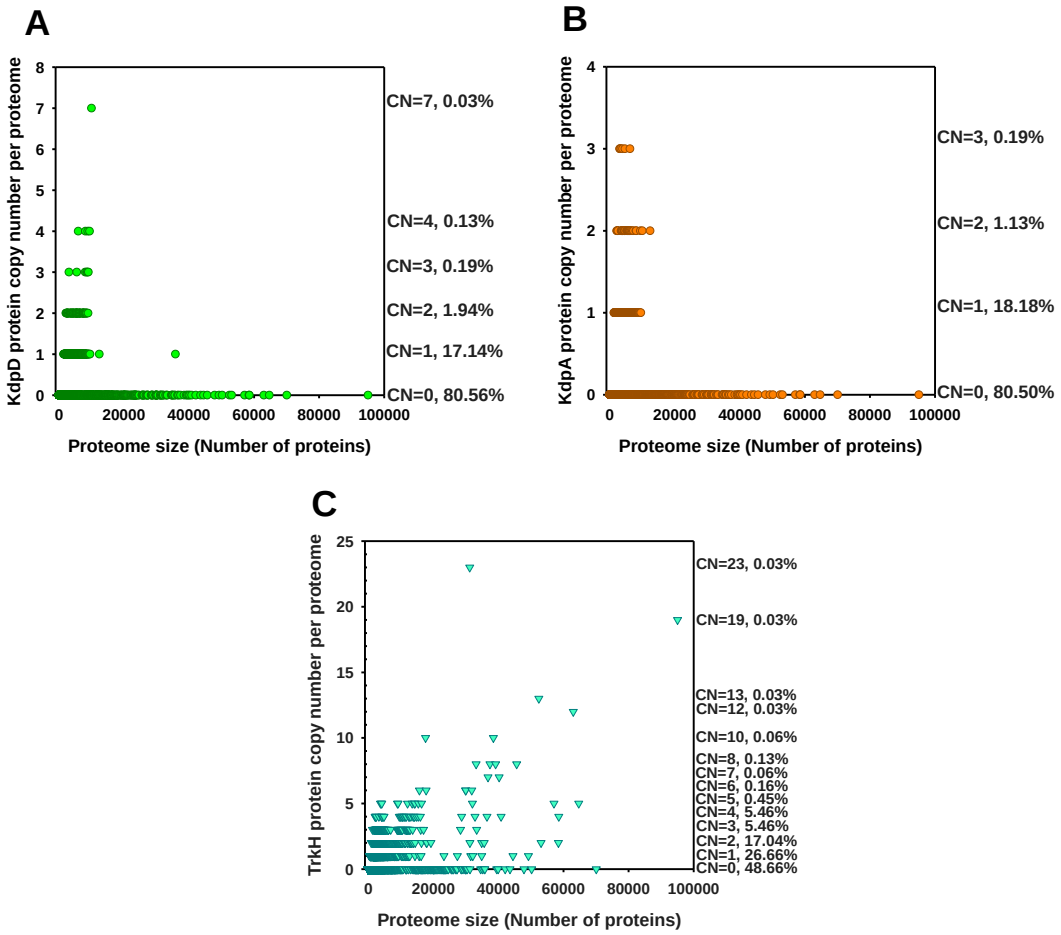


Figure 8: Abundancy of the KdpA, KdpD and the TrkH proteins in single proteomes. X-axes show the individual proteome sizes indicated by the protein numbers, while the Y-axes mark the copies of KdpD, KdpA, and TrKH proteins detected in each examined proteomes. No correlation was detected between the proteome sizes and copy numbers of KdpD, KdpA and TrkH proteins.

All proteins containing at least one KdpD domain (PF02702) were retrieved from the UniProt reference proteomes database 2015_10 (RFP) and defined as KdpD proteins (Data set-sheet 1 gives the proteome IDs and species of origin listed in the RFP database. Total number of reference proteomes for each domain of life: Archaea, 124; Bacteria, 2118; Eukaryote, 427).

In addition, all sequences of KdpA (PF03814), the translocating subunit of the inducible high-affinity K^+ transporter KdpFABC, and TrkH (PF02386), the ion channel of the constitutively expressed low-affinity transporter Trk (Figure 2), were recovered from the same database.

A total of 692 KdpD proteins were detected with HMMER 3.0 in one eukaryotic phylum (Data set-sheet 3, green rows), one archaeal phylum (Data set-sheet 3, red rows) and eighteen bacterial groups/phyla (Data set-sheet 2 and 3 black or grey rows).

Noticebaly, about 2% of all proteomes queried contained more than one KdpD or KdpA protein (all the identified KdpA protein is listed in Data set-sheet 4), while multiple TrkH (all the identified TrkH protein is listed in Data set-sheet 5) were present in about 24% of them [Figures 8 A, B and C, with copy number (CN) >1)]. No correlation between the copy number of these proteins and overall proteome size was detectable.

With one exception -- a KdpD protein (entry ID: X1X445_ACYPI) detected in the RFP of the eukaryote *Acyrthosiphon pisum* (the pea aphid) -- KdpD proteins are restricted to archaeal and bacterial proteomes.

KdpD and KdpA proteins were detected in 28.2% and 27.6% of the bacterial proteomes, respectively, and show a strong tendency to occur together in these bacterial groups/phyla, which underlines their functional relationship (Figures 9A and 9B). Frequencies of coordinated occurrence of KdpD and KdpA were lower in the phylum *Firmicutes* than in *Proteobacteria* and *Actinobacteria* (Figure 9B), implying that the coordinated function of KdpD and KdpA proteins is less important for survival in the first phylum. Notably, there is hardly any KdpD, KdpA or TrkH proteins among unclassified bacteria (Figure 9B).

In addition to their coordinated occurrence on population level, instances of coordinated occurrence and absence of KdpD and KdpA were also detected in individual bacterial proteomes. They were both present in 26.3% of individual bacterial proteomes and were both

absent in 70.5% of individual bacterial proteomes. In contrast, only a small percentage of individual bacterial proteomes contain KdpD but no KdpA (1.8%) or KdpA but no KdpD (1.3%) (Figure 9C).

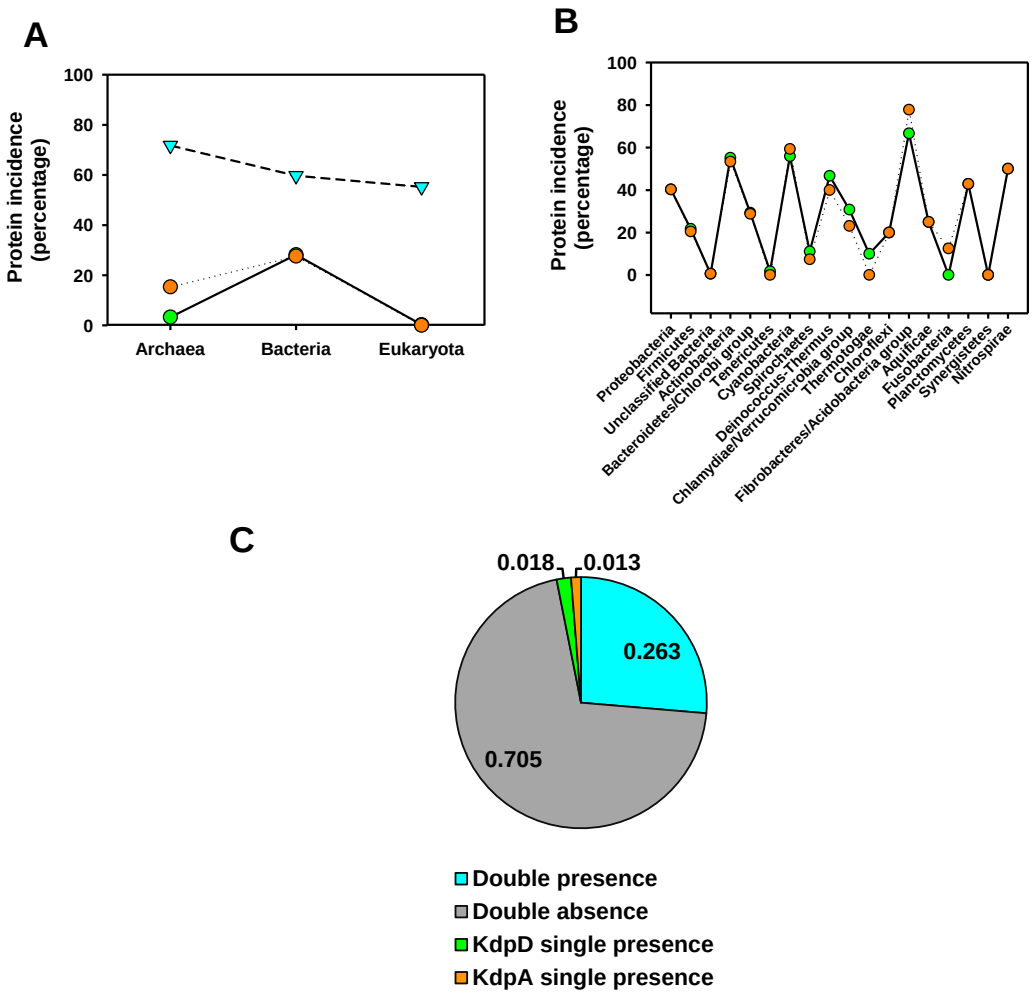


Figure 9: Coordinated distribution of KdpD and KdpA in bacterial species. Distribution of KdpD, KdpA, and TrkH proteins in reference proteomes drawn from the three domains of life. **(A)** Prevalence of KdpD, KdpA and TrkH in proteomes from the three domains of life. **(B)** Prevalence of KdpD and KdpA proteins in proteomes of the major bacterial groups/phyla (only those bacterial groups and phyla are shown that contain at least five reference proteomes): green, KdpD; orange, KdpA; cyan, TrkH. **(C)** Co-occurrence of KdpD and KdpA in individual bacterial proteomes.

In archaeal proteomes, KdpA proteins are more prevalent than KdpD proteins (Figure 9A, KdpD proteins occur in only 3.2% of proteomes, while the figure for KdpA is 15.3%). This

finding can be explained by the existence of KdpD-independent Kdp systems in this domain of life. For example, the only experimentally investigated archaeal Kdp system -- in *Halobacterium salinarum* -- does not recruit KdpD as a regulator, but employs a protein called KdpQ, which consists of two Usp domains. Although the regulatory mechanism used by KdpQ is still unclear, expression of the *kdp* operon in response to K^+ was found to be similar to that in *E. coli* (Kixmuller, Strahl et al. 2011). Genes for KdpQ homologs were also found associated with other archaeal *kdp* operons. KdpQ are actually more prevalent thank KdpD in Archaea (Figures 10 and A1, yellow colored genes marked “kdpQ”).

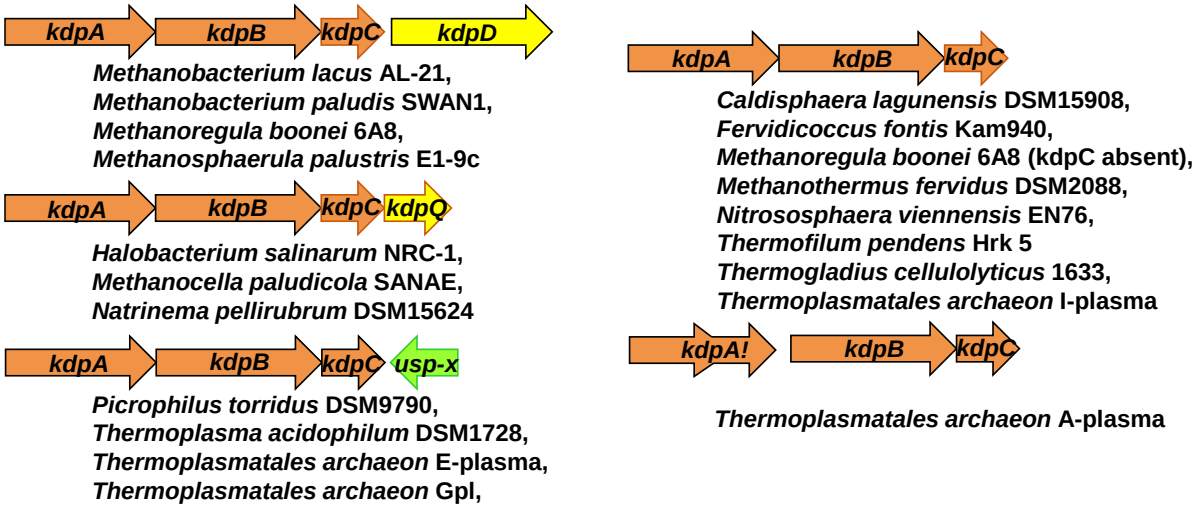


Figure 10: Genes encoding the archaeal *Kdp* systems. The species with similar *kdp* genomic neigbohoods were grouped and the species names were demonstrated under the operon icons. The *kdpD* and *kdpQ* genes were marked with yellow colors. The “*usp-x*” gene encodes a protein with domain architecture of Usp domain plus an unpredicted domain (X domain). “*kdpA!*” encodes the two parts of a split KdpA protein (due to frame shift mutation) of one KdpA protein. These two parts of KdpA were detected by HMMER as two copies of KdpA protein.

As a comparison, the distribution of TrkH proteins were also analyzed. TrkH has much wider distribution than KdpA and was observed in all the three domain of life. No correlation between the distributions of KdpD and TrkH proteins was found (Figure 9A).

Taking together the Kdp system of Archaea and Bacteria, KdpD proteins are the most common, but not the only regulator of the *kdp* operon.

3.1.2 Functional classification of KdpD proteins

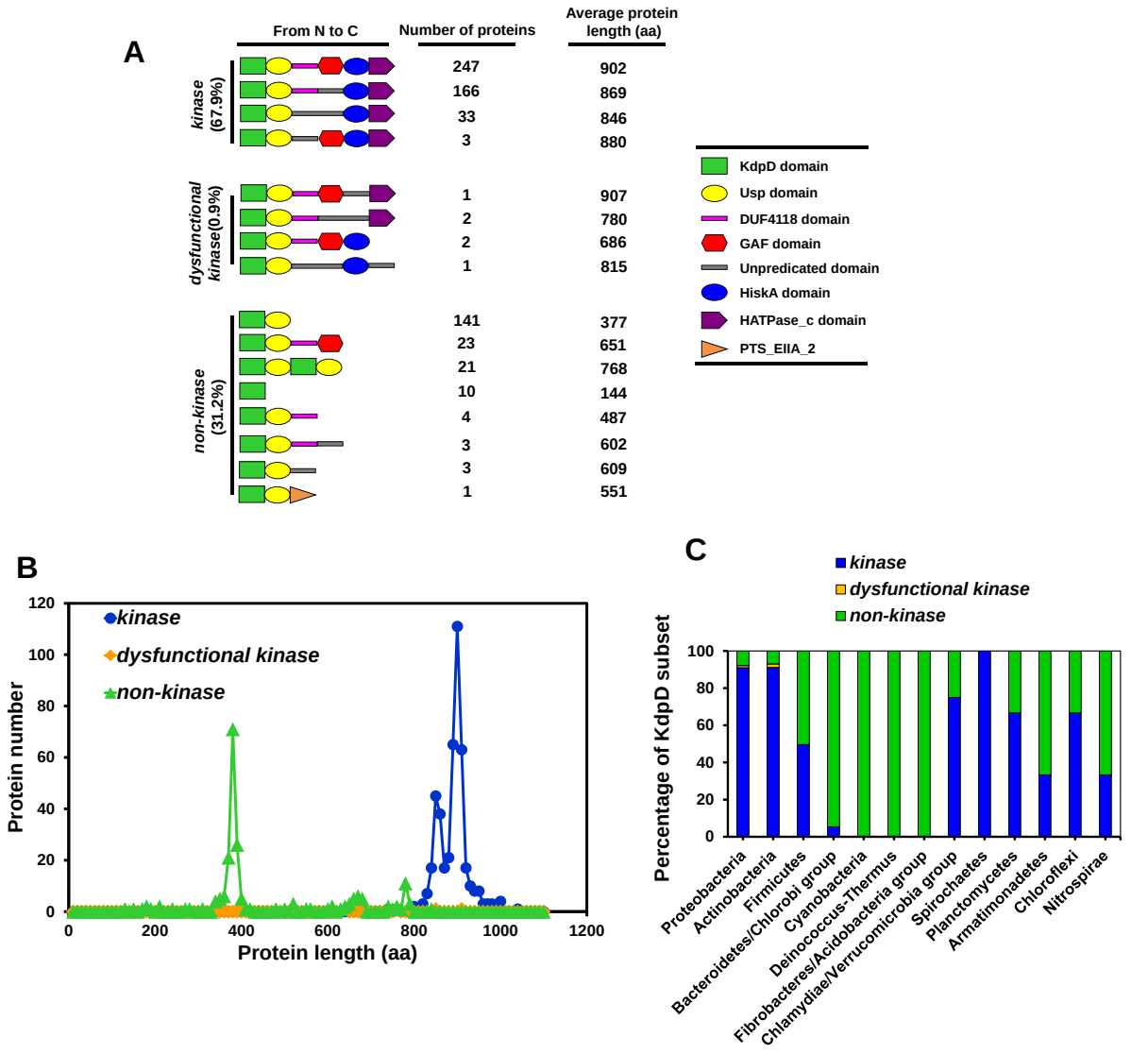


Figure 11: Functional classification of KdpD proteins according to the domain architecture of the overall proteins. (A) KdpD proteins were classified into three groups (*kinase*, *dysfunctional kinase* and *non-kinase*) on the basis of their domain architecture. **(B)** Length [in amino acids (aa)] variations of KdpD proteins. **(C)** Distribution of the three groups of KdpD proteins among bacterial groups/phyla (only those bacterial groups and phyla are shown that contain at least three KdpD proteins).

Before carrying out further analysis of the predicted 692 KdpD proteins detected by HMMER 3.0, all of them were examined with CDD v3.14 (CD-search as the interface) to annotate the domains contained in each sequence as well as refining the protein list. The cut-off *E*-value was set to 0.001, and 661 out of 692 proteins detected by HMMER 3.0 were predicted by CDD v3.14 to have at least one KdpD domain (Data set-sheet 3). These 661 proteins were retained as the refined list and their lengths, domain architectures and distributions were subsequently analyzed. Based on domain architecture, they were classified into three groups: *kinase*, *dysfunctional kinase* and *non-kinase* (Figure 11A). In terms of length, they fall into two major groups: one has 370-400 amino acids and the other consists of about 850-900 residues (Figure 11B). *Kinase*s and *non-kinase*s make up the majority of KdpD proteins, accounting for 67.5% and 31.2%, respectively, of the set surveyed here (Figure 11A).

The *kinases* necessarily contain HisKA and HATPase_c domains, *dysfunctional kinases* contain either one or the other, and *non-kinases* lack both of these domains (due to either gene truncation or the essential asparate amino acid was substituted). The KdpD of *E. coli* is a typical example of the *kinase* group, consisting of KdpD and Usp domains, the four-helix transmembrane domain (DUF4118), a GAF domain and the HisKA and HATPase_c domains.

Non-kinase KdpD proteins are usually much shorter, and include the truncated KdpD of *Anabaena* sp. strain L31, *Synechocystis* sp. strain PCC 6803 and *D. radiodurans* (Ballal and Apte 2005, Nanatani, Shijuku et al. 2015). Most of the *non-kinase* KdpD comprise two domains: KdpD-Usp. However, there are two versions of special *non-kinase* KdpD with domain architectures of KdpD-Usp-KdpD-Usp and KdpD-Usp-DUF4118-GAF, respectively (Figure 11B). As will be discussed later, these two versions of *non-kinase* KdpD are meanly found in *Firmicutes*, indicating quite diverse evolution events of their KdpD proteins.

The *dysfunctional kinase* just have six KdpD sequences. Five of them have quite similar protein length to that of the *kinase*. However, there is no predicted HiskA or HATPase_c domain in

these five KdpD, because the conserved amino acids of either of these two domains were replaced. The other *dysfunctional kinase* has shorter protein sequence (686 amino acid sequences), indicating the HATPase_c domain was deleted.

The two major groups of KdpD proteins are preferentially represented in different bacterial groups/phyla (Figure 11C). For example, the *kinase* KdpD account for more than 80% all KdpD detected in *Proteobacteria* and *Actinobacteria*, and examples of *non-kinase* KdpD are rare (Figure 11C). In contrast, KdpD were predominantly detected as *non-kinase* in the *Bacteroidetes/Chlorobi* group, *Cyanobacteria* and *Deinococcus-Thermus*. *Firmicutes* have both *non-kinase* and *kinase* KdpD at an equal proportion.

3.1.3 Lineage-specific KdpD evolution events

Having shown the distribution pattern of KdpD proteins and disparate preferences of bacterial specices for *kinase* or *non-kinase* KdpD (Figure 11B). The next step is to infer the evolution of the KdpD proteins and reveal the evolutionary relationship between the *kinase* and *non-kinase* KdpD. To reconstructed the KdpD protein tree, amino acid sequences of the predicted 682 KdpD domains and 672 Usp domains were extracted (see Figure 11A) and aligned with Mafft L-INS-i. The aligned columns with more than 95% of gaps were removed with trimAl v1.2 (Capella-Gutierrez, Silla-Martinez et al. 2009) and the aligned KdpD domains and Usp domains were concatenated. Tidy alignments were used for Maximum Likelihood tree reconstructions with the PhyML 3.0 [(LG+ estimated invariable sites + 4 substitution rate categories, branch support value was estimated with approximate likelihood ratio test (aLRT), tree topology was improved with Nearest Neighbor Interchange (NNI)] (Anisimova and Gascuel 2006, Guindon, Dufayard et al. 2010).

On the constructed Maximum Likelihood tree (Figures 12 and A2), the most distinguished feature is that the presence of horizontal gene transfer (HGT).

(i) KdpD of Archaea have short-branch length and disperse at different positions on the tree. This results indicates that the *kdpD* genes were not inherited from the common ancestor of bacteria and archaea, but rather from bacterial species, via HGT. Therefore, the archaeal KdpD proteins cannot be used to root the whole protein tree.

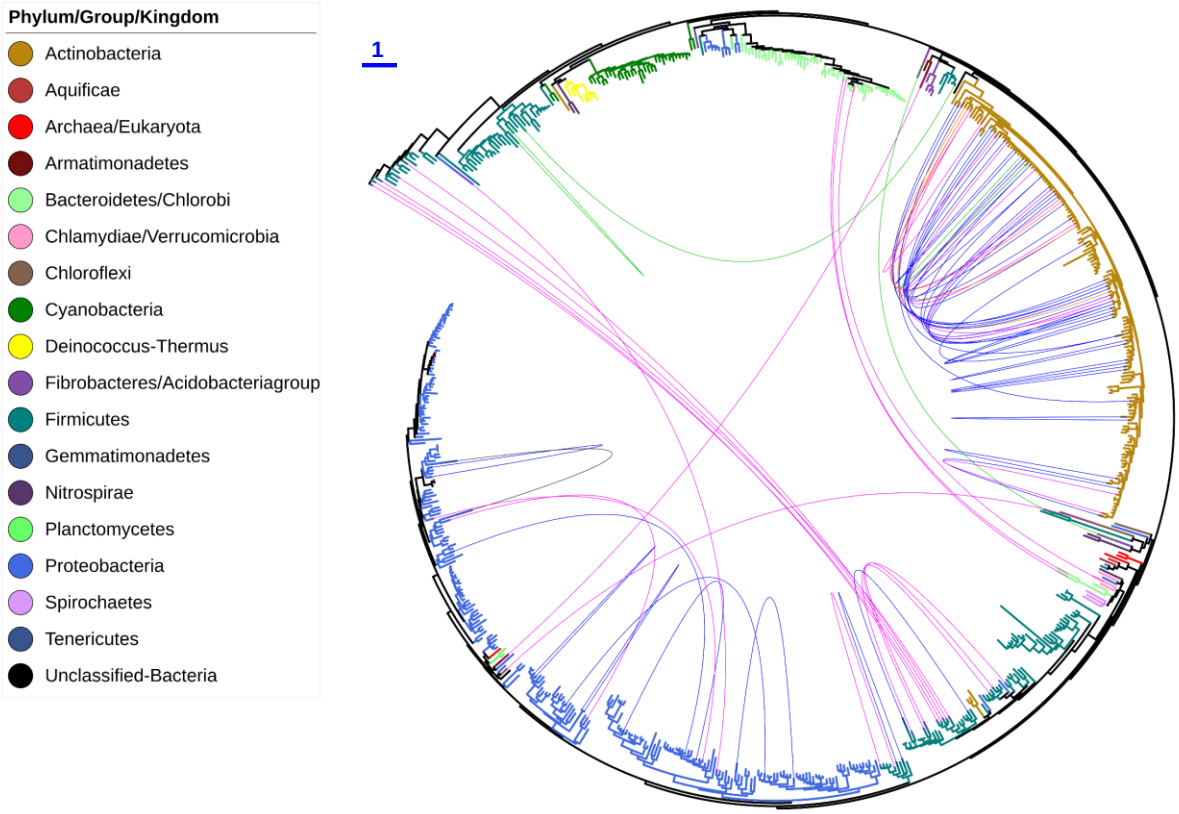


Figure 12: Unrooted Maximum Likelihood KdpD protein constructed from concatenated KdpD and Usp MSA. Color of the branches designate the bacterial phylum or group (red color branches stands for archaeal KdpD). Curves connecting KdpD proteins belong to the same species (acquire via KdpD duplication or HGT). Blues curves connecting two *kinase* KdpD; Magenta curves connecting *kinase* and *non-kinase* KdpD; Orange colors connecting *kinase* KdpD and *dysfunctional* KdpD.

(ii) *Firmicutes* do not form unique phyletic group, but two major groups and several small clusters (Figures 12 and A2). The first big group is staying together with cyanobacterial KdpD. While the second group obviously is in conflict with the life tree (see Figure 13B), interjects between *Chlamydiae/Verrucomicrobia*, *Nitrospirae* and the large proteobacterial KdpD cluster.

This group suggests the presence of either “genuine paralogs” or “pseudoparalogs” (Koonin 2005) of KdpD in *Firmicutes*. Suppose the paralogs were “genuine”, the duplication of *kdpD* genes should have occurred before the generation of *Firmicutes* divergence. In other words, this would mean subsequent widespread lose events of one of the paralogs in most of the other bacterial species, because most of bacterial phyla do not possess multi-phyletic groups. Conversely, supposed the paralogs are pseudoparalogs, the *Firmicutes* KdpD, which is sharing closer relation with *Proteobacteria*, *Chlamydiae/Verrucomicrobia* and *Nitrospirae*, should be obtained via HGT from the species appeared between the divergence of *Chlamydiae/Verrucomicrobia*, *Nitrospirae* and the prevalence of *Proteobacteria* on the earth.

(iii) Like the *Firmictues*, 50% *Deltaproteobacteria* KdpD do not form unique cluster on the proteins tree. One cluster is clamping with the KdpD of *Bacteroidetes/Chlorobi* group, which also suggests either the presence of genuine paralogs or HGT.

In addition to probable HGT, KdpD protein duplications were also observed in some species (Figures 12 and A2, KdpD proteins connected by colored curves). Moreover, duplication of KdpD are different from phylum to phylum.

(i) Duplication of KdpD is most obvious in *Actinobacteria* and almost all actinobacterial KdpD proteins are arranged into one phyletic group (Figures 12 and A2). This results indicates the KdpD duplication occurs after the *Actinobacteria* divergence or HGT within the phylum.

(ii) Inner phyletic duplication of KdpD was also found in *Firmicutes*. Moreover, some *Firmicutes* species also have multiple KdpD proteins being localized into separated two groups. As described above, this should be caused either by gene duplication or HGT.

These results suggest that KdpD proteins have quite various evolution trajectories in the bacterial species.

3.1.4 Domain shuffling (recombination) between Usp and DUF4118 domains shapes the evolution of KdpD proteins.

Evolution occurs on multiple levels with different molecular mechanism. In addition to the nucleotide insertions, deletions, substitutions, gene recombinations can speed up drastically the evolution of a gene. Gene recombination would cause rearrangements of protein domain (domain shuffling) or domain duplications, especially to the multi-domain proteins. As the basic evolution unit, protein domains have been undergoing extensive duplication and recombination during the evolution course--2/5-3/5 of the proteins in prokaryotes are composed of multiple domains (Han, Batey et al. 2007).

As shown above, 98.5% of KdpD proteins are multi-domain proteins (Figure 11A). Only 10 KdpD proteins were identified to be composed of stand-alone KdpD domain, some of which may be rather due to short-gun sequencing interruption. Interestingly, all the other KdpD domains are only connecting to the Usp domain, but not to any of the other domains. This finding indicates the strong evolutionary and functional relationship between these two domains.

In addition to the essential domains HisKA and HATPase_c, DUF4118 domain is also important to distinguish *kinase* KdpD from *non-kinase* KdpD. DUF4118 domain in *E. coli* KdpD is known essential for the K^+ sensing (Zimmann, Steinbrugge et al. 2007, Schramke, Tostevin et al. 2016). Moreover, more than 92% of *kinase* KdpD have a DUF4118 domain, while only 14.6% of the *non-kinase* KdpD contain this domain [(all such proteins exhibit KdpD-Usp-DUF4118-(X) or KdpD-Usp-DUF4118-GAF domain architectures (Figure 11B)]. This results indicates that domain shuffling between Usp domain and DUF4118 domain drastically shapes the evolution of KdpD proteins and mediates the interconversion between *kinase* and *non-kinase* KdpD.

To illustrate the evolution process of KdpD proteins, all the DUF4118 domain-containing proteins (DUF4118 proteins) were also collected with HMMER 3.0. Actually, only 51.4% DUF4118 domains are incorporated into KdpD proteins [(A protein with KdpD domain would be preferentially called KdpD protein) (Table 4 and Data set-sheet 6)]. The following table shows the diverse domain compositions of the other proportion of DUF4118 proteins, which accounts for a percentage of 48.6 % but does not fuse to KdpD and Usp domains. For simplicity, they are called “non-KdpD DUF4118 proteins”. Some of the *non-KdpD DUF4118* proteins (Table 4, rows in bold) are identical to the C-terminal of *kinase* KdpD (Figure 11B). It principally makes the interconversion between *kinase* and *non-kinase* KdpD rather sample and it does not require multiple-step recombination.

Table 4: Domain composition of *non-KdpD DUF4118 proteins*
(x stands for unpredicted domain)

Domain composition of *non-KdpD DUF4118 proteins*	**Number of Sequence**	**Property and proportion**
DUF4118;HisKA	1	Kinase or hybrid kinase activity (32.6%)
DUF4118;X;HATPase_c	5	
DUF4118;HisKA;HATPase_c	89	
DUF4118;X;HisKA;HATPase_c	61	
DUF4118;GAF;HisKA;HATPase_c	31	
Usp;DUF4118;GAF;HisKA;HATPase_c	10	
Usp;DUF4118;X;HisKA;HATPase_c	24	
DUF4118;X;PAS;HisKA;HATPase_c	1	
DUF4118;PAS;X;HATPase_c	2	
DUF4118;PAS;HisKA;HATPase_c	8	
DUF4118;(PAS)2;HisKA;HATPase_c	1	
DUF4118;X;(PAS)2;HisKA;HATPase_c	1	
DUF4118;(PAS)3;HisKA;HATPase_c	2	
DUF4118;PAS;GAF;PAS;HisKA;HATPase_c	1	
DUF4118;(PAS)2;GAF;HisKA;HATPase_c	2	
DUF4118;(PAS)2;GAF;(PAS)2;HisKA;HATPase_c	1	
DUF4118;PAS;X;GAF;X;(PAS)2;HisKA;HATPase_c	1	
DUF4118;(PAS)4;X;PAS;HisKA;HATPase_c	1	
DUF4118;(PAS)7;HisKA;HATPase_c	1	
DUF4118;HisKA;HATPase_c;REC	1	
DUF4118;PAS;HisKA;HATPase_c;REC	2	
DUF4118;PAS;X;HisKA;HATPase_c;REC	1	
DUF4118;GAF;X;PAS;GAF;HisKA;HATPase_c;REC	1	
DUF4118;PAS;X;(PAS)2;HisKA;HATPase_c;REC	2	
DUF4118;(PAS)3;HisKA;HATPase_c;REC	1	
DUF4118;PAS;X;(PAS)3;HisKA;HATPase_c;REC	1	
DUF4118;(PAS)5;HisKA;HATPase_c;REC	1	
DUF4118;X;GAF;X;PAS;(GAF)2;HisKA;HATPase_c;REC	1	
DUF4118;X;PAS;GAF;X;PAS;X;PAS;HisKA;HATPase_c;REC	1	
DUF4118;PAS;GAF;X;(PAS)3;GAF;(PAS)2;HisKA;HATPase_c;REC	1	
DUF4118;X;PAS;GAF;X;PAS;(GAF)2;HisKA;HATPase_c;REC	1	
DUF4118;PAS;GAF;PAS;X;PAC;PAS;X;PAS;(GAF)2;HisKA;HATPase_c;REC	1	
DUF4118;PAS;X;PAS;X;(PAS)3;GAF;HisKA;HATPase_c;REC	1	

Domain composition of *non-KdpD DUF4118 proteins*	Number of Sequence	Property and proportion
DUF4118;X;(PAS)2;(GAF)2;HisKA;HATPase_c;REC	1	
DUF4118;X;HATPase_c;REC;(PAS)2;X;HisKA;HATPase_c;REC	1	
DUF4118;PAS;X;PAS;HisKA;HATPase_c;REC;HPT	1	
DUF4118;PAS;HisKA;HATPase_c;REC;REC;HPT	1	
DUF4118	8	No predicted function (10.0%)
DUF4118;X	18	
DUF4118;GAF	2	
DUF4118;GAF;X	42	
DUF4118;X;GAF;X	2	
DUF4118;Usp	2	
Usp;DUF4118;GAF	1	
Usp;DUF4118;X	3	
DUF4118;PAS	1	
DUF4118;(PAS)2;X	1	
DUF4118;(PAS)3;X;PAS;X	1	
DUF4118;GAF;Nucleotidyl_cyc_III	4	Cyclic nucleotide metabolism (2.5%)
DUF4118;Nucleotidyl_cyc_III	1	
DUF4118;Nucleotidyl_cyc_III;HDc	8	
DUF4118;HDc	5	
DUF4118;(PAS)2;Nucleotidyl_cyc_III;EAL	1	
DUF4118;X;EAL	1	
NADB_Rossmann;DUF4118;GAF;X	17	$NAD(P)^+$-binding activities (3.5%)
NADB_Rossmann;DUF4118;X	2	
NADB_Rossmann;DUF4118;X;GAF;X	1	
NADB_Rossmann;X;DUF4118;GAF;X	7	
NADB_Rossmann;X;DUF4118;X	1	

Theoretical routes of domain shuffling between the KdpD-Usp and DUF4118 proteins, which support the interconversion between *kinase* KdpD and *non-kinase* KdpD were proposed (Figure 13A). Additionally, KdpD domain was duplicated in some *non-kinase* KdpD. It is a process independent of the DUF4118 proteins and results in the KdpD variants with the domain architecture of KdpD-Usp-KdpD-Usp. In parallel, DUF4118 domain might have undergone domain shuffling events that are independent of the KdpD and Usp domains (Figure 13A).

All the domain architectures of KdpD and DUF4118 proteins were also plotted on the newly published ribosome protein life tree (Hug, Baker et al. 2016). The domain composition and availability of *non-KdpD DUF4118 proteins* are very distinct among the bacterial phyla (Figure 13B). In some phyla, low abundances or even the absence of the *non-KdpD DUF4118 proteins* should prevent interconversion between *kinase* and *non-kinase* KdpD proteins, such as in *Bacteroidetes/Chlorobi* group, *Deinococcus-Thermus*. However, there are also some phyla containing plenty of *non-KdpD DUF4118 protein*s, but almost all of their KdpD proteins are *non-kinase*, such as the *Fibrobacteres/Acidobacteria* group and *Cyanobacteria*.

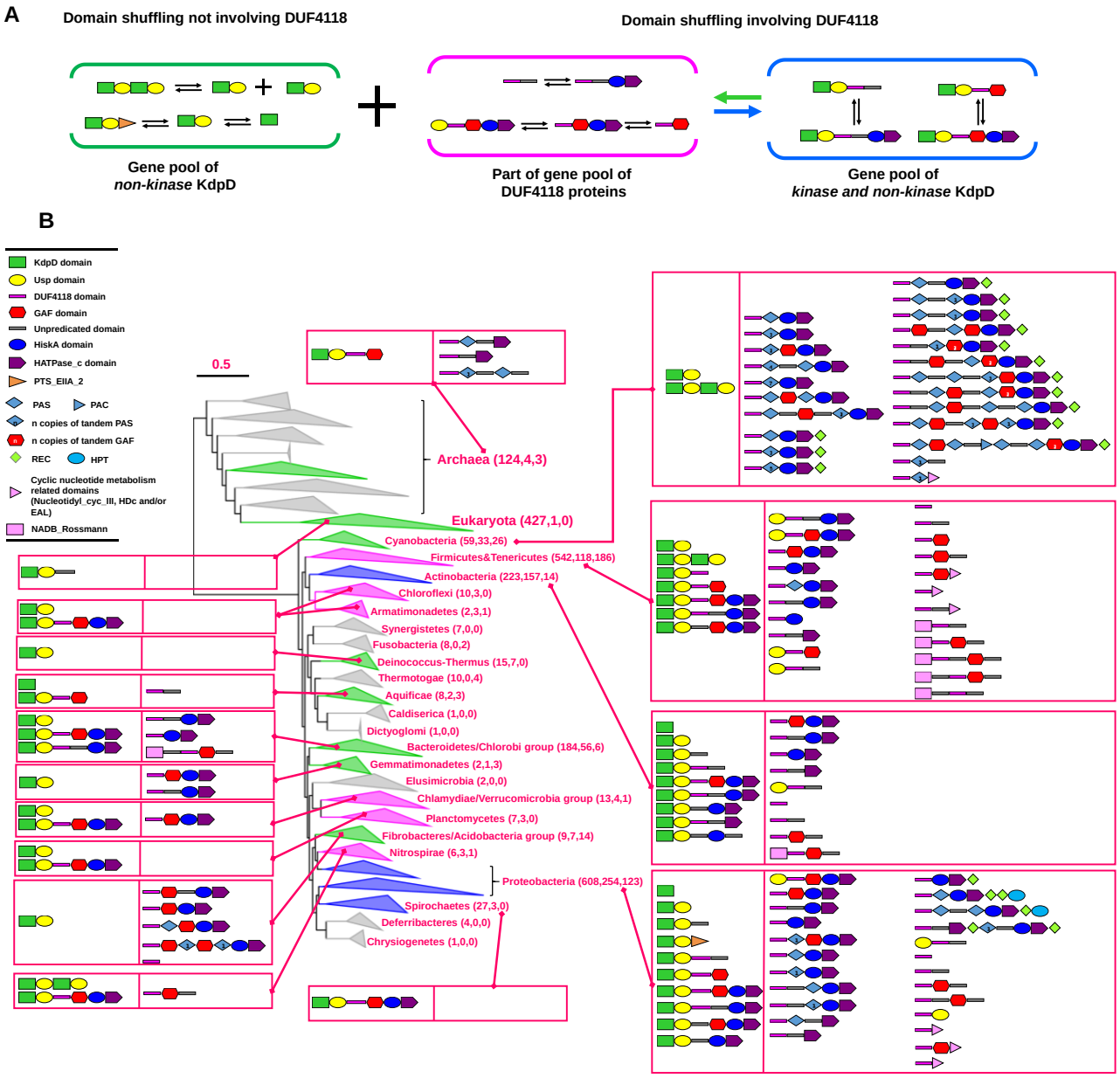


Figure 13: KdpD-Usp and DUF4118 domain recombinatorial routes. (A) Schematic of theoretical domain shuffling between KdpD-Usp and *DUF4118 domain proteins*. There are also domain shuffling events of *non-kinase* KdpD and *non-KdpD DUF4118 proteins* that are independent of each other. **(B)** Domain architectures of KdpD (left columns of the frames) and DUF4118 proteins (right columns of the frames) plotted on the concatenated-ribosomal-protein life tree (unclassified bacteria and the two KdpD proteins belonging to them were not shown; *non-KdpD DUF4118 protein* of the phyla without detected KdpD proteins were exclued). Backbone of the tree was created by modifying the published ribosome protein life tree (Hug, Baker et al. 2016). Leaves of the tree were marked with the taxon names, and in brackets successively, the numbers of reference proteomes and number of detected KdpD proteins and *non-KdpD DUF4118 proteins* in the relevant taxon. Colors of the leaves indicate the proportion of two groups of KdpD (*dysfunctional kinase* was considered as *kinase*); green, ≥90% of the KdpD are *non-kinase*; blue, ≥90% of the KdpD are *kinase*; magenta, both *non-kinase* and *kinase* KdpD accounts for comparable proportions.

In next step it was figured out whether the interconvertsion between *kinase* and *non-kinase* KdpD are purely random events or whether some selection pressure affecting the domain shuffling between Usp and DUF4118 domains.

3.1.5 Global purifying selection / localized positive selection constraints / buttresses interconversion between *kinase* and *non-kinase* KdpD

Nucleotide sequences for the KdpD proteins were retrieved from the protein sequences using tBlast (Altschul, Gish et al. 1990) and Entrez queries. The nucleotide sequences were re-translated into protein sequences and annotated with domains, using CDD v3.14 with a cut-off *E*-value of 0.01 (Marchler-Bauer, Derbyshire et al. 2015).

To infer the phylogeny of the *kdpD* genes, DNA sequences encoding the KdpD domain, the Usp domain and the DUF4118 domain were collected. Only sequences of bacterial accession numbers for which there is exactly one DNA sequence available for the KdpD domain, exactly one DNA sequence for the Usp domain, at most one DNA sequence of the DUF4118 domain were used. The protein sequence alignments obtained from the Pfam profile HMM were mapped to the DNA sequences and concatenated the three domains for each taxon. An alignment of 216 sequences, all of which contained the KdpD domain and the Usp domain, and 141 also contained the DUF4118 domain, were obtained. Program CodonPhyML was used to infer the phylogeny of these sequences (Gil, Zanetti et al. 2013).

KdpD and Usp domains were separately tested for evidence of selection using the program CODEML from the PAML v4.8 package (Yang 2007) with the F3x4 model of codon frequencies and a single value of ω that was inferred simultaneously with the tree and the ratio of transition and transversion rates. A null model that did not allow for variation in ω between the branches of the phylogeny was used for the first CODEML run. Then, a parsimonious set of branches in the *kdpD* gene phylogeny that separate the *kinase* and *dysfunctional kinase kdpD* genes from the *non-kinase kdpD* genes was identified [*dysfunctional kinase* was considered as *kinase*

herein, because *dysfunctional kinase* is a minority which has similar domain architecture to *kinase*]. It was tested whether ω was increased on these branches on the KdpD and Usp domains, which will indicate positive selection on these candidate branches associated with the conversion from *kinase* to *non-kinase* (or vice versa). For this, CODEML was applied to fit a model in which two different ω values were allowed, one for the candidate branches and one for all other branches. In addition a model with seven ω values, one for each candidate branch and one for all other branches, was fitted. These models were fitted separately to the KdpD domain sequence alignment and to the Usp domain sequence alignment. In addition to the differences between synonymous and non-synonymous, mutations differences in the rates of transitions and transversions were taken into consideration. The mutation rates were estimated within the CODEML analyses.

With the null model, in which only one value of ω was allowed throughout the tree, the average ratios of non-synonymous to synonymous mutation rates (ω) for the entire phylogeny were 0.099 for the KdpD domain and 0.075 for the Usp domain. These values indicate that these domains are under strong purifying selection.

When a different ω value was allowed on the six candidate branches that separate *kinases* from *non-kinases* (Figure 14, marked with rectangle, circle, or star), the estimated values on the candidate branches were ω=0.295 for the KdpD domain and ω=0.128 on the Usp domain, whereas the ω values on the other branches remained similar to the values inferred with the null model (0.098 for the KdpD domain and 0.074 for the Usp domain). This model fitted significantly better for the KdpD domain but not for the Usp domain (p values $<10^{-9}$ for the KdpD domain, 0.17 for the Usp domain; likelihood-ratio test, with χ^2 approximation, df=1).

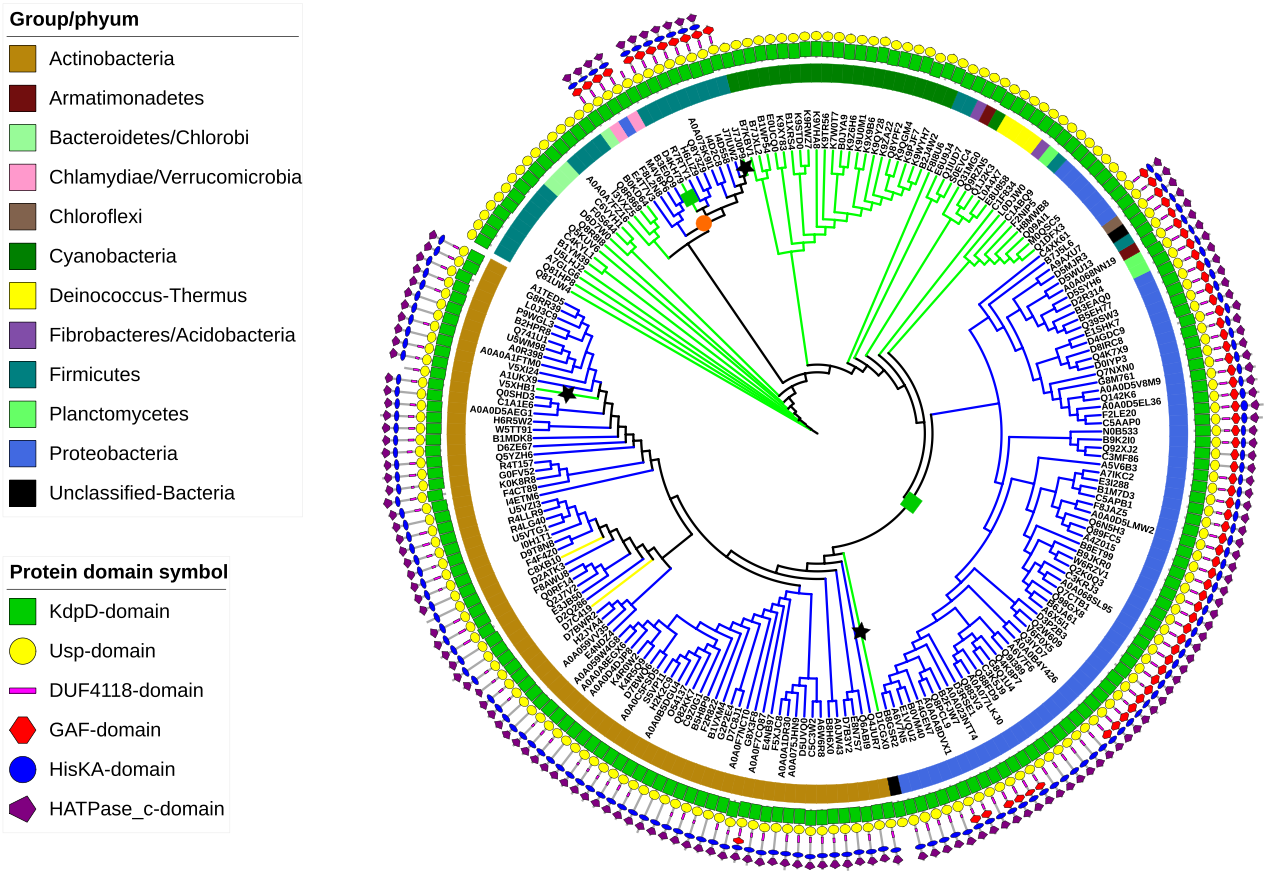


Figure 14: Selection pressure analysis on KdpD and Usp domains. Backbone of the tree was constructed with CodonPhyML (see the chapter of Materials and Methods). Branch color demonstrates the type of analyzed KdpD protein (blue, *kinase* KdpD; yellow, *dysfunctional kinase* KdpD; green, *non-kinase* KdpD). Colored ring indicates the bacterial taxa (see Data set-sheet 7 for species names). Domain architectures of KdpD were predicted with CDD v3.14. Branches with positive selection on KdpD domain were marked with green rectangles, and those with positive selection on both KdpD and Usp domains were marked with orange circles. Black stars indicate the candidate branches which may support the interconversion between *kinase* and *non-kinase* but without detected positive selection on either KdpD domain or Usp domain.

For the KdpD domain the model in which each of the six candidate branches was allowed to have its own value of ω (in addition to one ω for all non-candidate branches) fitted significantly better than the model with only two ω values (p value < 10^{-12}, df=5). For the Usp domain this model was compared to the model with only one ω value for all branches as this model was not rejected in the comparison to the model with two ω values. It was found that the model with different ω values for the candidate branches fits significantly better (p value 0.035, df=5). With

this model, *ω* was estimated to be greater than 1 (indicating positive selection) for both domains on the branch that is marked with an orange circle in Figure 14 (Table 5). On the two branches that are marked with a green rectangle only the *ω* values for the KdpD were estimated to be greater than 1 (Table 5). One of them leads to a single taxon (D4KH79, *Megamonas hypermegale*). On this branch the value for the Usp domain (0.444) was still substantially higher than the value for the non-candidate branches (0.075 with this model) (Table 5).

Table 5: Selection pressure analysis on KdpD and Usp domains

Branch	KdpD domain			Usp domain		
	N•dN[a]	S•dS[b]	*ω* (dN/dS)	N•dN[a]	S•dS[b]	*ω* (dN/dS)
Internal A	24.202	0.011	633.058	0	0	0.0001
Internal B	52.998	0.011	965.763	14.776	0.005	999
V5XHB1	48.568	62.44	0.218	3.109	1449.532	0.001
D1CGX0	90.695	916.39	0.028	28.579	1423.992	0.008
D4KH79	116.497	31.627	1.031	20.262	17.188	0.444
J7J0P9	19.772	77.857	0.071	2.692	15.463	0.066
All other	8068.716	22842.98	0.099	1756.113	8795.949	0.075

Numbers of non-synonymous ([a]) and synonymous ([b]) mutation and *ω* values as estimated by CodeML with a model that allowed for different dN and dS values on six candidate branches. The internal branch A was marked with a green rectangle in Figure 14. Internal branch B was marked with an orange circle in Figure 14. For branches that lead to only one taxon the identifier of the taxon was given (See also Data set-sheet 7). Note that large values given by CodeML should be taken with caution. E.g., 999.000 was the maximum value given by CodeML, just indicating that there is evidence for non-synonymous mutations but not for synonymous mutations.

3.2 Alternative HK^{K+}/RR^{K+} regulate Kdp system

3.2.1 Prediction of new alternative HK^{K+}/RR^{K+}

The fact that *non-kinase* KdpD proteins lack the output domain of HisKA and HATPase_c raises the question of how the expression of *kdp* operons might be regulated in these species. In light of earlier work on the Kdp system in *Cyanobacteria* (Ballal and Apte 2008, Nanatani, Shijuku et al. 2015), the genomic neighborhoods (within ±15 kbp of the *kdpD* start codon and

stop codon) of all *non-kinase kdpD* genes were checked (genomic neighborhoods of some of the *non-kinase kdpD* genes were depicted in Figure A3). Genes for three major types of HK^{K+} were identified in these regions: **(i)** DUF4118-GAF(X)-HK^{K+} (mainly found in *Firmicutes* and the *Fibrobacteres/Acidobacteria* group; X stands for an unpredicted domain); **(ii)** 4TM(2TM)-HK^{K+} (found in *Cyanobacteria* and *Deinococcus-Thermus*); and **(iii)** 2TM-HAMP-PAS(X)-HK^{K+} (X stands for an unpredicted domain), which might phosphorylate σ^{70} family sigma factors related RR (found in some *Firmicutes*) or σ^{54}-dependent transcriptional activator (found in some deltaproteobacterial species and in the *Bacteroidetes/Chlorobi* group) (Figure 15, Data set-sheet 8).

In agreement with this idea, it has been experimentally proven that a HK which has the domain architecture of 4TM(2TM)-HK^{K+} can mediate the regulation of *kdp* genes in cyanobacteria (Ballal and Apte 2008, Nanatani, Shijuku et al. 2015). Moreover, the C-terminal portion of *E. coli* KdpD, which is homologous to DUF4118-GAF(X)-HK^{K+}, is able to sense extracellular K^+ (Rothenbucher, Facey et al. 2006, Schramke, Tostevin et al. 2016).

Sigma factors are essential for bacterial RNA polymerase (RNAP) to recognize promoters (Gruber and Gross 2003, Kazmierczak, Wiedmann et al. 2005, Filloux 2012). There are two families of sigma factors. The σ^{70} family includes housekeeping sigma factors as well various alternative sigma factors. The σ^{54} family differs in sequence and structure from all other sigma factors and contains exclusively the σ^{54} (Lonetto, Gribskov et al. 1992, Gruber and Gross 2003). As assumed above, HK^{K+} of the *non-kinase* KdpD might phosphorylate a σ^{54}-dependent RR^{K+} (σ^{54}-dependent transcriptional activator) in some species of the *Deltaproteobacteria* and the *Bacteroidetes/Chlorobi* group (Figure 15, Data set-sheet 8).

In agreement with this assumption, DNA-affinity-purified-chip assay has shown that two σ^{54}-dependent transcriptional activators DVU0596 and DVU3305 bind to the upstream of *kdp* operon in *Desulfovibrio vulgaris* Hildenborough, a typical deltaproteobacteria strain (Rajeev,

Luning et al. 2011). Moroever, as will be proved, the RR^{K+} of *Bacteroides fragilis* KdpD, a σ^{54}-dependent transcriptional activator was also found affecting the expression of *B. fragilis kdp* operon (See section 3.2.2, Figure 17 for details). Tighter regulation of σ^{54} factor dependent *kdp* operons could be expected, since ATP hydrolysis by these transcriptional activators is required to overcome the kinetic barrier and form the open complex at the promoter (Rombel, North et al. 1998, Buck, Gallegos et al. 2000, Studholme and Dixon 2003, Bush and Dixon 2012).

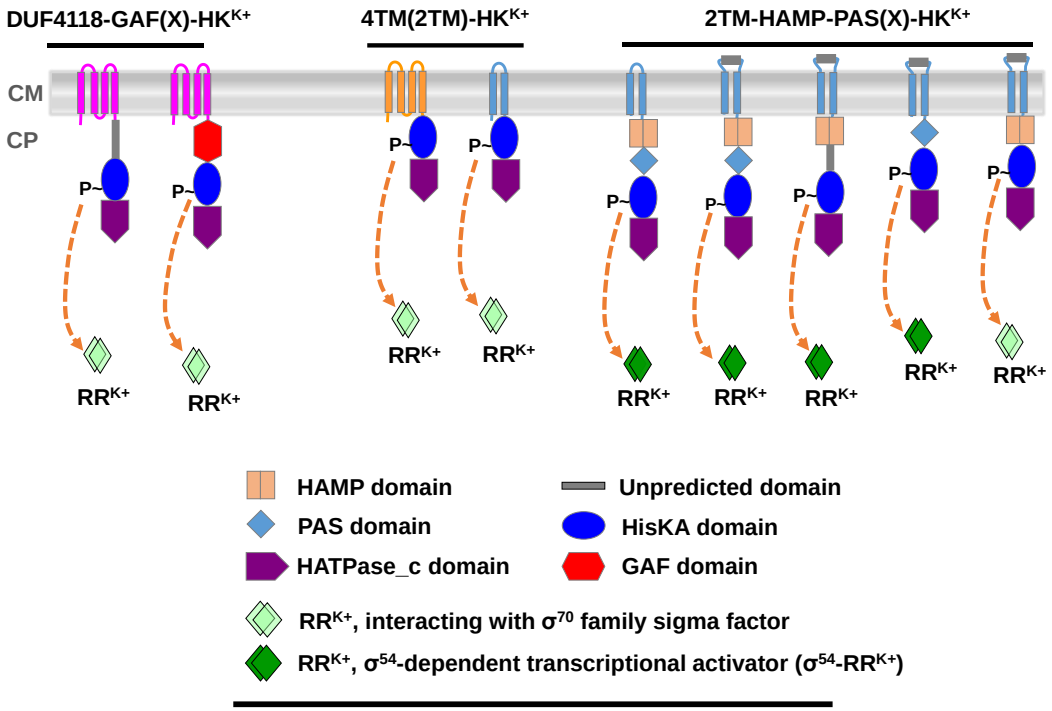


Figure 15: Alternative HK^{K+}/RR^{K+} pairs found in the genomic neighborhoods of *kdp* operons. Representative domain architectures of HK^{K+} and RR^{K+} are shown. CM, cytoplasmic membrane; CP, cytoplasm; X, unpredicted domain; DUF4118 (four-helix transmembrane domain with K^+ binding site, magnate); 4TM, four-helix transmembrane domain (orange); 2TM, two-helix transmembrane domain (pale blue).

3.2.2 Characterization of the Kdp system of *B. fragilis*

As described above, some Kdp systems equipped with *non-kinase* KdpD may recruit putative alternative HK^{K+}/RR^{K+} to transcriptionally regulate the *kdp* operons. It is aimed subsequently to verify the roles of 2TM-HAMP-PAS(X)-HK^{K+} and σ^{54}-dependent transcriptional activator, σ^{54}-

RR^{K+} (Figure 15), which is especially interesting and was mainly found in some *Delta-proteobacteria* and *Bacteroidetes/Chlorobi* species. The *B. fragilis* was chosen because **(i)** *B. fragilis* is an important intestinal commensal bacteria as well as an opportunistic pathogen highly related to human health concerns, while Kdp system is believed to participating the pathogenicity is some bacteria (Freeman, Dorus et al. 2013); **(ii)** Human colon is generally a K^+ rich environment. It is aimed to disclose the role of Kdp system encoded in the *B. fragilis* genome.

3.2.2.1 Prediction of the components of *B. fragilis* Kdp system

The Kdp system of *B. fragilis* is predicted to have *kdpFABCO* as the structural genes and hk^{K+}/rr^{K+} as the core regulating components (Figure 16A). KdpF is a short peptide which was annotated in the genome of *E. coli* but not in the genome *B. fragilis*. But a typical SD sequence was found upstream of *kdpA*, followed by a putative ORF starting with “ATG” and ending with “TAA” codons (Figure 16A). The amino acid sequence translated from this short ORF shows high similarity to the *E. coli* KdpF. They both should have the structure of hydrophobic α-helix (Figure 16D).These findings suggest KdpF should be also encoded in the *B. fragilis kdp* operon.

As described in 3.2.1, the RR^{K+} was predicted to be a σ^{54}-dependent transcriptional activator and the HK^{K+} was predicted to be 2TM-HAMP-PAS-HK^{K+} (Figure 16C). Unlike the *E. coli* or cyanobacterial Kdp system, the genes encoding the HK^{K+} and RR^{K+} do not share the same operon (Figure 16 indicated with blue and green arrows). Moreover, the putative σ^{54} recognition motif was found in the promoter of *B. fragilis kdp*. It is about 170 bp upstream of the start codon of the predicted *kdpF.* In the Dataset-sheet 9, 23 more *kdp* operons were found to have similar motifs in their promoters. All these *kdp* operons were equipped with *non-kinase* KdpD and were found in sixteen *Bacteroidetes* and seven *Deltaproteobacteria.* The σ^{54} recognition motif is quite different from that of σ^{70}, the house keeping sigma factor (Francke, Groot Kormelink et al. 2011). Moreover, the transcriptional initiation at of σ^{54} dependent promoter strictly requires

the hydrolysis of ATP to form initiation complexes (Rombel, North et al. 1998, Buck, Gallegos et al. 2000, Studholme and Dixon 2003, Bush and Dixon 2012). Such kind of transcription initiation mechanism leads to tighter regulation of the Kdp system of *B. fragilis*, which principally has very low probability to face K^+ limitation.

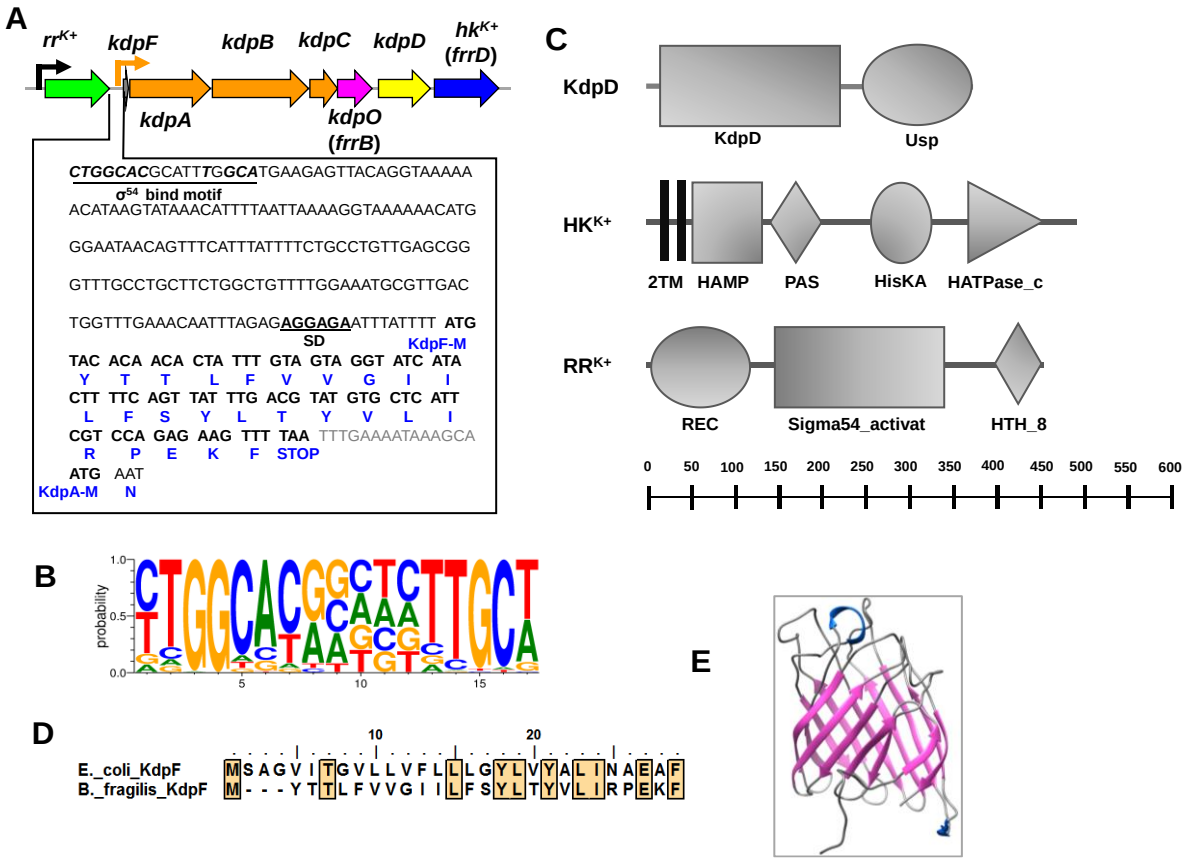


Figure 16: Predicted elements of Kdp system in *B. fragilis* (A) Predicted genes that encode the Kdp system in *B. fragilis*. Amino acid sequence of the predicted KdpF is marked with blue color. Underline sequences designate the putative σ^{54} regonization motif (italic) and the SD sequence (bold) of the *kdpF* gene, respectively. **(B)** DNA sequence logo constructed from known σ^{54} recognition motif (Barrios, Valderrama et al. 1999). **(C)** Predicted domain architectures of KdpD, RR^{K+} and HK^{K+}. **(D)** Sequence comparision between the KdpF of *E. coli* MG1655 and the predicted KdpF of *B. fragilis.* Identical amino acid are highlighted with backgroup color. **(E)** Three dimensional structure model of KdpO (FrrD).

In addition, between *kdpC* and *kdpD* there is an ORP (*frrB*) encoding a putative outer membrane porin, which is composed of 14 predicted β-strands (Figure 16E). In this thesis, this

protein was renamed as KdpO. KdpO may increase the permeability of the K^+ from extracellular environment to the periplasm to speed up the uptake K^+ by the KdpFABC located in the inner membrane.

3.2.2.2 Test the stimuli of Kdp system in *B. fragilis* reporter

As described above, the signal molecules of the *B. fragilis* Kdp system is rather mysterious, since this bacterium habits the K^+ rich mammal colon. To test the stimulus of *B. fragilis* Kdp system, a *B. fragilis* reporter strain *B. fragilis* Wlu was constructed (Figure 17A), in which the luciferase gene *Nluc* is under the control of *B. fragilis kdp* promoter $P_{kdp\ B.\ fragilis}$. Luminescence intensity per OD_{600} is used to demonstrate *kdp* promoter activities. The reporter was tested to three kinds of possible signals: K^+ concentration, osmostress (by sucrose) or salt stress (by NaCl). Briefly, the *B. fragilis* Wlu reporter strain was cultivated in AMMgluc medium with different concentrations of K^+ or AMMgluc medium added with indicated amount of sucrose or NaCl (K^+ was set to 10 mM) for 9 hours. Luminescence intensity per OD_{600} was measured as an indication of the *kdp* operon expression.

Interestingly, Kdp system of *B. fragilis* is indeed reponsing to K^+ limitation. The expression of *kdp* operon could be strongly induced by low K^+ and was switched off when K^+ is higher than 5 mM (Figure 17B). Conversely, the expression of *kdp* operon was slightly increased by osmostress or salt stress (about one fold increase, Figures 17C and 17D). This result suggests that the expression of *B. fragilis kdp* operon shows unspecifical responses to osmostress or salt stress. High concentration of sucrose (>=0.6 M) and NaCl (>=0.3 M) strongly inhibit the growth of *B. fragilis* reporter strain. Therefore, the relevant luminescence intensities could not be measured (Figures 17C and 17D).

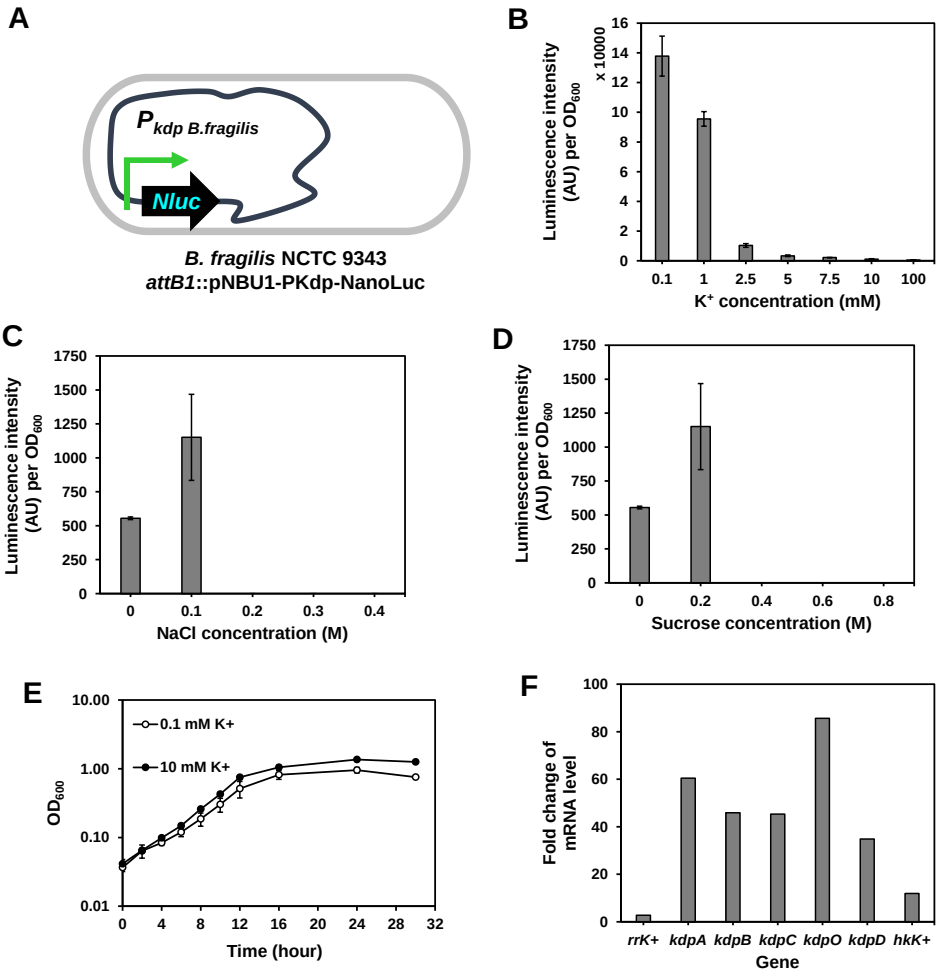


Figure 17: Test the stimuli of Kdp system in *B. fragilis*. (A) Construction of the *B. fragilis* Wlu reporter strain. In the reporter luciferase gene was located under the control of $P_{kdp\ B.\ fragilis}$ on the backbone of shuttle vector pNBU1, which was integrated into the *attB1* site on chromosome of *B. fragilis* NCTC 9343. **(B)-(D)** Test the response of Kdp system to K^+ concentration, salt stress and sucrose osmostress, respectively. High concentration of sucrose (>=0.6 M) and NaCl (>=0.3 M) stongly inhibit the growth of *B. fragilis* reporter strain. **(E)** Impact of K^+ on the growth of *B. fragilis* wild type strain. **(F)** Change of mRNA level of the predicted *kdp* genes in response to K^+ limitation. Cells were cultivated in AMMgluc medium with indicated K^+ concentrations for 14 hours and were collected for total RNA isolation. The expression of gene *recA* was selected as the reference for qRT-PCR.

To further confirm the stimulus of *B. fragilis* Kdp system is K^+ limitation, qRT-PCR was used to measure the transcriptional alternations of the *kdpA*, *kdpB*, *kdpC*, *kdpO*, *kdpD*, rr^{K+} and hk^{K+} in response to K^+ concentrations. In agreement with the luciferase reporter assay, expression levels of *kdpA*, *kdpB*, *kdpC*, *kdpO*, *kdpD* were strongly stimulated by 30 to 90 folds, when cells

were grown under K^+ limitation (0.1 mM). Additionally, this finding also indicates that these five genes sharing the same operon. The transcription of *hk*$^{K+}$ was also stimulated by low K^+ but less significantly (10 folds increase) (Figure 17E). To verify whether *hk*$^{K+}$ is also included into the *kdp* operon, further experiment, *e.g.* Northern blot, is required to measure the structure of the *B. fragilis kdp* operon composition. Growth of the *B. fragilis* wild type strain was also tested the in minimal medium with 0.1 mM and 10 mM K^+. Low K^+ causes dimished biomass formation (Figure 17F) of this bacterium. This result indicates that the *B. fragilis* species requires proper K^+ concentration (~10 mM) for normal growth.

3.2.2.3 Test the role of the putative Kdp-regulating HK^{K+}/RR^{K+} in *E. coli* reporter

In order to confirm the regulation role of the predicted KdpD, HK^{K+}/RR^{K+} in Figure 15, these three genes were expressed under control of arabinose promoter P_{BAD} individually or in combination in the reporter strain *E. coli* YW2, in which the native promoter of chromosomal *lacZ* gene has been replace by the $P_{kdp\ B.\ fragilis}$ (Figure 18A). β-Galactosidase per OD_{600} is used to demonstrate the activity of the *kdp* promoter in the reporter strain. *E. coli* YW2 transformed with the listed genes was cultivated in minimal medium with various concentrations of K^+ (see 2.2.6). Increase of β-galactosidase was observed, when *rr*$^{K+}$ and *rr*$^{K+}$ and *hk*$^{K+}$ were expressed from the arabinose promorter leakage. However such kind of increase is not in response to K^+ (Figure 18B). Considering *kdpO* gene was not found in the *E. coli kdp* operon, in order to check its potential effect on the K^+ sensing capability of HK^{K+}/RR^{K+}, this gene was also expressed on the pBAD33 vector from P_{BAD} in combination with *hk*$^{K+}$/*rr*$^{K+}$ in the *E. coli* YW2. However, KdpO does not endow the K^+ response capability of HK^{K+}/RR^{K+} in *E. coli* reporter. The deregulation of the HK^{K+}/RR^{K+} in *E. coli* may due to two reasons. **(i)** Essential co-sensor of the HK^{K+}/RR^{K+} is not available in *E. coli*; **(ii)** *The B. fragilis kdp* operon includes the *hk*$^{K+}$. This would mean a positive feedback amplification of *kdp* operon. In responding to low K^+, *hk*$^{K+}$ needs to increase the expression of itself to amplify the low K^+ signal to increase efficently the expression of

kdpFABC. Such kind of positive feedback amplification may be destroyed in the *E. coli* reporter because the hk^{K+} expression is constantly from P_{BAD} (Figure 18D).

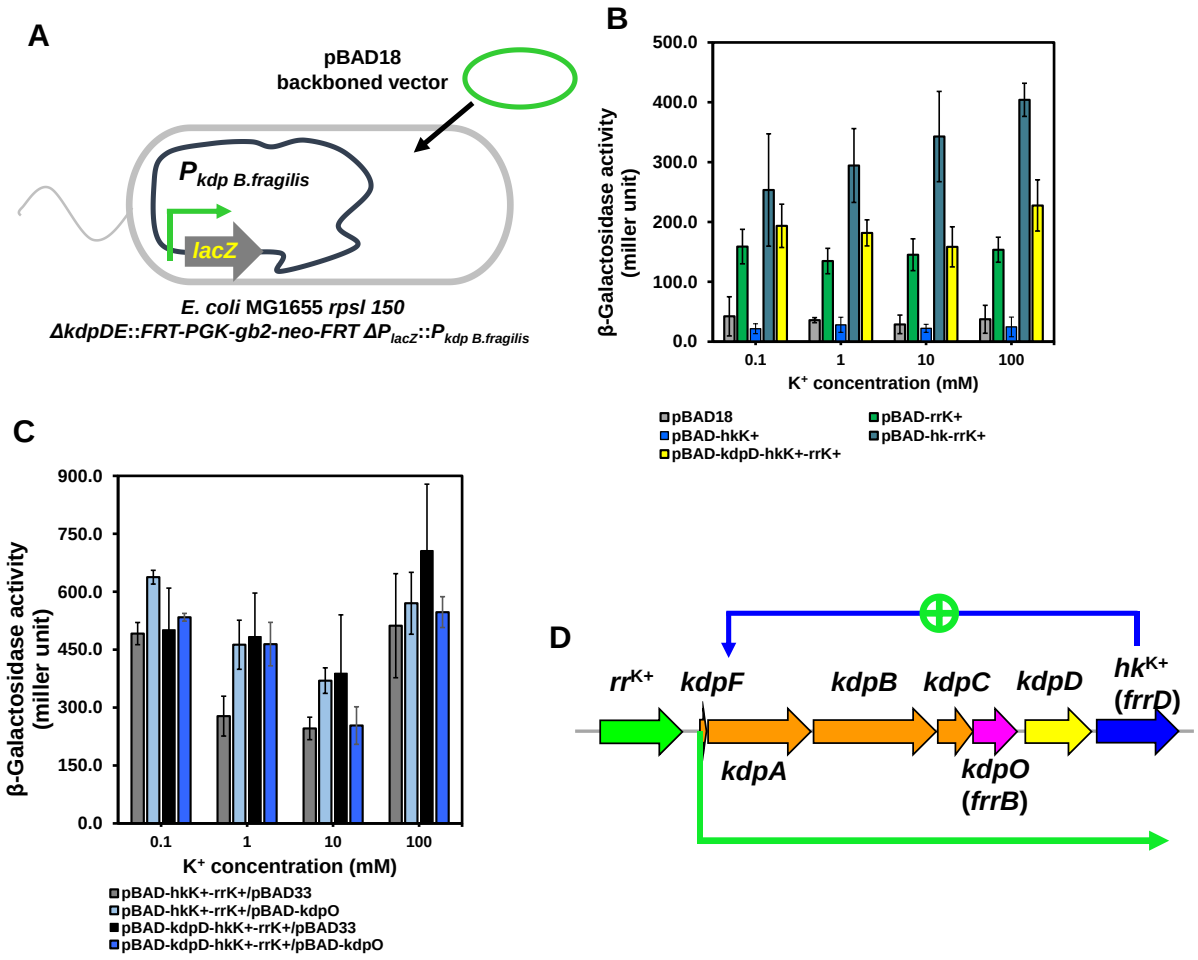


Figure 18: Test the role of the putative Kdp-regulating H^{K+}/RR^{K+} in *E. coli* reporter. (A) Construction of the *E. coli* reporter strain. In the *E. coli* reporter the native *kdpDE* system was removed and the chromosomal *lacZ* was under the control of $P_{kdp\ B.\ fragilis}$. **(B)** rr^{K+}, hk^{K+}, rr^{K+}& hk^{K+}, rr^{K+}& hk^{K+}& *kdpD* were expressed individually or in combination from the P_{BAD} promoter leakage. **(C)** Gene *kdpO* was expressed on pBAD33 vector in combination with hk^{K+}/rr^{K+} or with $kdpD/hk^{K+}/rr^{K+}$. KdpO does not endow the HK^{K+}/RR^{K+} K^+ response capability in *E. coli* reporter. **(D)** Suppose hk^{K+} is involved in the *kdp* operon, there would be a positive feedback loop. This loop may be interrupted when the related genes were expressed on the vector while the *kdp* promoter was integrated into *E. coli* genome.

3.3 Structural analysis of KdpD proteins

3.3.1 Purification of "full-length" *E. coli* KdpD proteins and crystallization trials

It is conceivable that the wild type *kinase* KdpD should have flexible conformational transition, because its kinase and phosphatase activities are altered instantly by the change of K^+ concentrations. This accordingly raises the obstacle for crystallization setups. Therefore, a variant with constant kinase activity (indicating more rigid in conformational transition), KdpD-R511Q (Jung and Altendorf 1998), was chosen as the candidate for initial crystallization setups. The KdpD-R511Q-6His was successfully purified from membrane vesicles as described in the chapter of Materials and Methods, with more than 90% purity (Figure 19). The sample was subsequently sent to the collaborator, Prof. Dr. Jörg Stetefeld, for crystallization. Unfortunately, after several rounds of trials, the protein precipitated and no crystals were obtained.

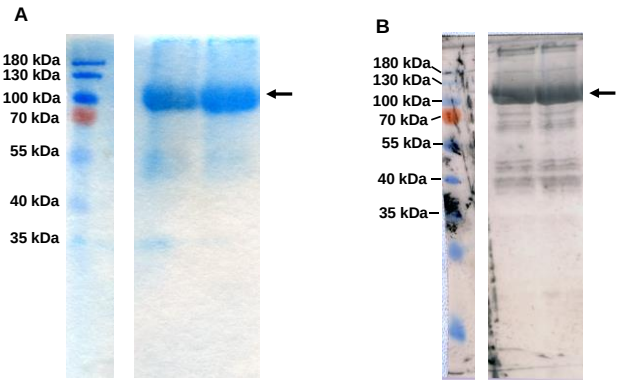


Figure 19: Purified KdpD-R511Q used for initial crystallization setups. **(A)** Coomassie Brilliant Blue G-250 staining and (**B)** Western blot with KdpD polyclonal antiserum as the first antibody. Arrow indicates the purified KdpD-R511Q-6His.

As shown in Figures 2 and 20A, *kinase* KdpD protein integrated into lipid bilayers are very asymmetric. KdpD, Usp, GAF, HiskA and HATPase_C domains are located one side of the membrane (cytoplasm), while there are just two small loops of the DUF4118 domain on the other side (Figures 2 and 20A). The first periplasmic loop is very short, with four amino acids,

while the second periplasmic loop is longer and essential for K^+ sensing (Schramke, Tostevin et al. 2016). Such kind of asymmetry may hinder the formation of crystal lattice.

To increase the molecular symmetry and therefore support the downstream crystallization experiments, WrbA, a soluble flavodoxin protein, was inserted into the first periplasmic of *E. coli* KdpD. WrbA is a NAD(P)H:quinone oxidoreductase with 198 amino acids (20.6 kDa). Each of the WrbA monomer binds FMN as the cofactor and the protein has been crystallized successfully as yellow colored bipyramid (Patridge and Ferry 2006, Kishko, Carey et al. 2013). To protect the folding independence of the KdpD and WrbA, flexible glycine and serine linkers were inserted between the WrbA and KdpD periplasmic loop.

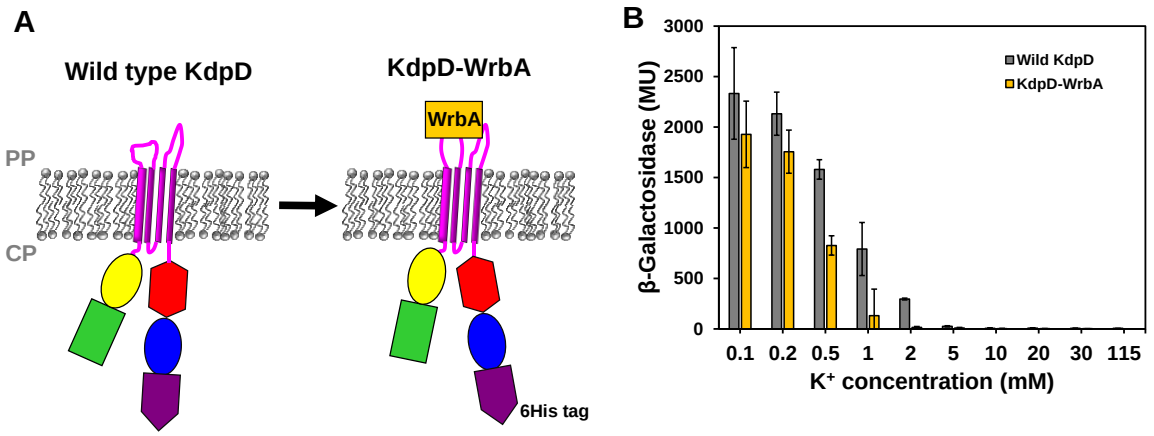


Figure 20: Construction and functional assay of KdpD-WrbA. **(A)** Schematic of the wild type KdpD and the KdpD-WrbA hybrid protein in to the lipid bilayers. Six histidine tag was attached to the C-terminal end of HisKA_c domain for subsequent protein affinity chromatography. PP, periplasm; CP, cytoplasm. **(B)** Test the response of the KdpD-WrbA to K^+ concentrations in comparison to the wild type KdpD. Standard deviations were calculated based on three parallel measurement.

The functionality of this hybrid protein was firstly determined to make sure the overall structure of the protein was not destroyed by the insertion of the WrbA into the K^+-sensing domain, DUF4118. β-Galactosidase assays suggest the KdpD-WrbA protein works properly. This

hybrid protein responses to the decreased K^+ concentration like the wild type *E. coli* KdpD (Figure 20B).

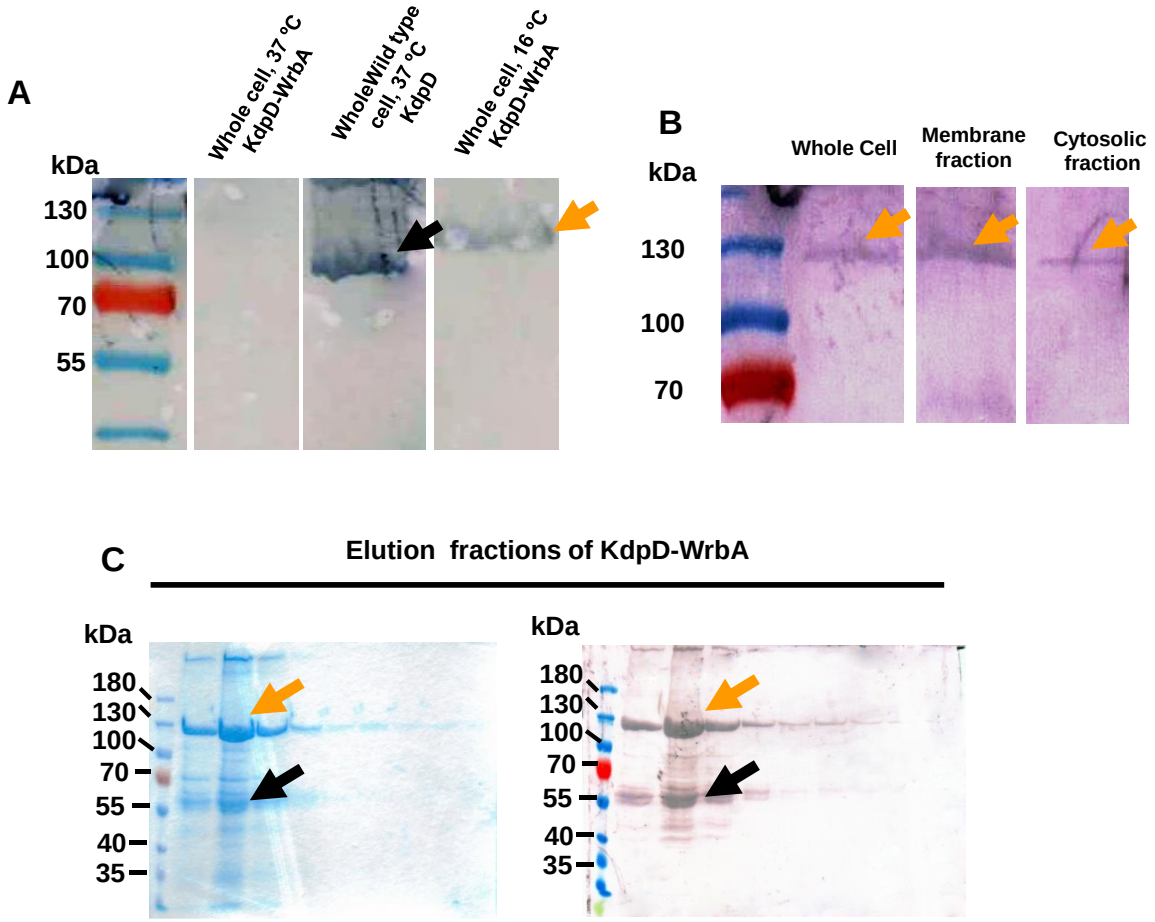


Figure 21: Localization analysis and purification of KdpD-WrbA hybrid. **(A)** KdpD-WrbA production was carried out with *E. coli* BL21 (DE3) induced with 0.3% (w/v) L-arabinose at 37°C for 3 hours or at 16°C for 15 hours. Equal volume (25 µL) of the cultures were loaded on SDS-gel. The wild type KdpD (black arrow) can be accumulated efficiently in the cells at 37 ºC, while KdpD-WrbA hybrid (yellow arrow) must be produced at lower temperature of 16 ºC. **(B)** KdpD-WrbA is mainly located into the cytoplasmic membrane. Cell were lysed with sonication and cytoplasmic membrane and cytoplasm fractions were separated with ultracentrifugation as described. Membrane fraction was resupended to the same volume of cytoplasm fraction, and equal volume (25 µL) of membrane and cytoplasm fraction were loaded on the SDS-gel. **(C)** Evaluation of the KdpD-WrbA elution fraction from affinity chromatograph. Left, Coomassie Brilliant Blue G-250 stained; right, Western blot (KdpD polyclonal antiserum as the first antibody). Large proportions of KdpD-WrbA were truncated (black arrow). All Western blots were performed with KdpD polyclonal antiserum as the first antibody.

However, when cultivation of the *E. coli* B21(DE3) carrying the pBAD24-KdpD-WrbA-6His vector was carried out at 37 °C with the induction of 0.3% (w/v) L-arabinose, the production of the hybrid protein could be hardly detected by Western blot. When the cultivation was performed at low temperature (16 ºC), production KdpD-WrbA hybrid was detected, but to a level which is much lower than that of the wild type KdpD (Figure 21A). Moreover, not all of the KdpD-WrbA proteins were incorporated successfully into the cytoplasmic membrane. Hybrid protein was also detected in the cytoplasmic fraction (Figure 21B). KdpD-WrbA proteins could be purified with the same protocol adopted for purification of KdpD-R511Q. However, compared to KdpD-R511Q, KdpD-WrbA is quite unstable. About 30% of the proteins were degradated or truncated by premature translation-termination (Figure 21C). Considering the very high requirements to purity and stability in crystallization setups, KdpD-WrbA was not used.

3.3.2 In search of soluble KdpD for crystallization

Since all the trials on crystallization of *kinase* KdpD were not fruitful thus for, any soluble and stable fragment of the *non-kinase* part of KdpD would be embraced as alternative candidate. *Non-kinase* KdpD with the domain architecture of KdpD-Usp was supposed to be located in the cytoplasm (see section 1.3.2). However, *E. coli kinase* KdpD by artificial truncation (*E. coli* KdpD 1-395 amino acids) was found to be attached to the membrane (Heermann, Altendorf et al. 2000). Similarly, native occurring *non-kinase* KdpD of *D. radiodurans* (see section 3.1.2, *Deinococcus-Thermus* has only *non-kinase* KdpD) also has poor solubility and a high tendency to bind to the cytoplasmic membrane (Figure 22A). It is not wise to apply these *non-kinase* KdpD straightly to crystallization setups, considering their hydrophobic features. In order to find a readily soluble and stable fragments of KdpD proteins, the *E. coli* KdpD 1-395 was purified and treated with limited proteolysis. Stable fragments were anticipated to gain better solubility. When *E. coli* KdpD 1-395 were digested respectively with proteinase K, trypsin and subtilisin, a stable fragment was identified with molecular mass of about 35 kDa (Figure 22B).

This band was extracted and tested with mass spectrometry. The composition of this band was found to be KdpD 38-380. The coding region of KdpD 38-380 was subsequently amplified as an ORF and overexpressed in *E. coli* BL21(DE3). Unfortunately, this protein variant still show affinity to the cytoplasmic membrane (Figure 22C), and therefore not suitable for crystallization setups.

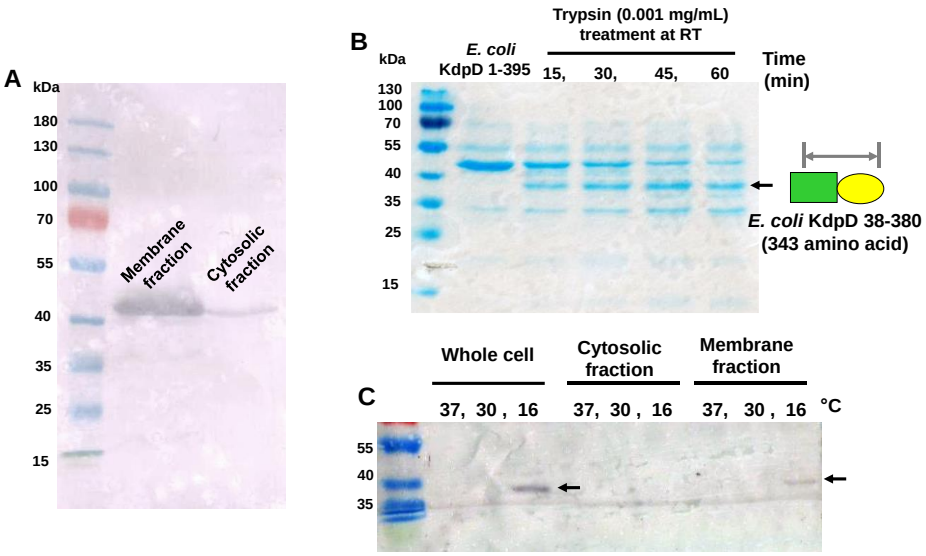


Figure 22: In search of soluble KdpD fragments. (A) *E. coli* BL21(DE3) cells producing the native *non-kinase* KdpD of *D. radiodurans* protein were lysed and cytoplasmic membrane and cytoplasm were separated via ultracentrifugation. Cytoplasmic membrane was resuspended with lysis buffer to the same volume of the cytoplasm fraction, and 25 µL of these two fractions were loaded on SDS-gel. Western blot was performed using Penta·His Antibody as the first antibody**. (B)** Trypsin limited proteolysis of KdpD were performed at room temperature for indicated times. Reactions were stopped by adding the 5×SDS loading dye. Reaction mixtures (25µL) were subsequently loaded on SDS-gel. Stable band indicated with the arrow was cut and analysed by mass spectrometry. This stable fragment was found to be composed of KdpD 38-380. **(C)** *E. coli* BL21(DE3) carrying pBAD24-KdpD(Met+38-380)-6His was cultivated overnight in LB [with 0.1 % (w/v) arabinose] at the indicated temperatures. Cytoplasmic membrane and cytoplasm fractions were sparated as described in (A). After adding with 5×SDS loading dye into LB culture, resuspended membrane vesicles and cytoplasm fraction, 25µL of the mixtures were loaded on SDS-gel. Western blot was performed using KdpD polyclonal antiserum as the first antibody.

3.3.3 Assembly of *E. coli kinase* KdpD into nanodiscs for single particle cryo-EM

Compared to crystallization trials, the single particle cryo-EM might be more advisable for probing the structure of *kinase* KdpD protein. Membrane proteins may be extracted with detergent and visualized by cryo-EM directly in the micelles or after reconstitution into nanodiscs or liposomes (Vinothkumar 2015). Compared to nanodiscs, liposomes are easier to obtain, but much larger and less stable. Moreover, it is hard to accurately control the size and the lipid to protein ratio (Bayburt and Sligar 2010).

Assembly of KdpD protein into nanodiscs was preliminarily tested. There are several MSP available with increasing protein lengths such as MSP1, MSP1E1, MSP1E2, MSP1E3 (and their variants), which can support the assembly of nanodiscs with increasing diameters (for empty nandiscs, ranging from 9.5 to 12.8 nm) (Denisov, Grinkova et al. 2004). The empty nanodiscs with the MSP1E3D1 [MSP1E3 derivate, two slight differences from MSP1E3, **(i)** at the N-terminal end there is a 7-histidine tag instead of 6 His, and **(ii)** there is a TEV protease cleavage site following the 7-histidine tag)] as the belts have an average diameter of 12.1nm.

The MSP and *E. coli kinase* KdpD protein were purified separately as described in the chapter of Materials and Methods. As the first trial of nanodiscs assembly, the 7-His tag attaching to the MSP protein was kept for the point of future Western blot and total lipid extract of *E. coli* was used as the lipid substrate [other commonly used lipids are DPPC, DMPC and POPC (Nath, Atkins et al. 2007)] . The MSP and lipid were firstly mixed with a molar ratio of 1:130 and 4:130 to check the formation of empty nanodiscs. According to the estimated protein size (~163 kDa) (Figures 23B and 23D, blue arrow) via size-exclusion chromatography, the formation of empty nanodiscs seemed to be successful (theoretical size ~ 232 kDa). When the stoichiometric ratio was set to 1:130, most of the lipid and MSP were incorporated into liposomes (Figure 23C, red arrow marked peak on the grey curve; Figure 23D). When this ratio

was adjusted to 4:130, the formation of nanodiscs was promoted and the formation of liposomes diminished (Figure 23C, black curve).

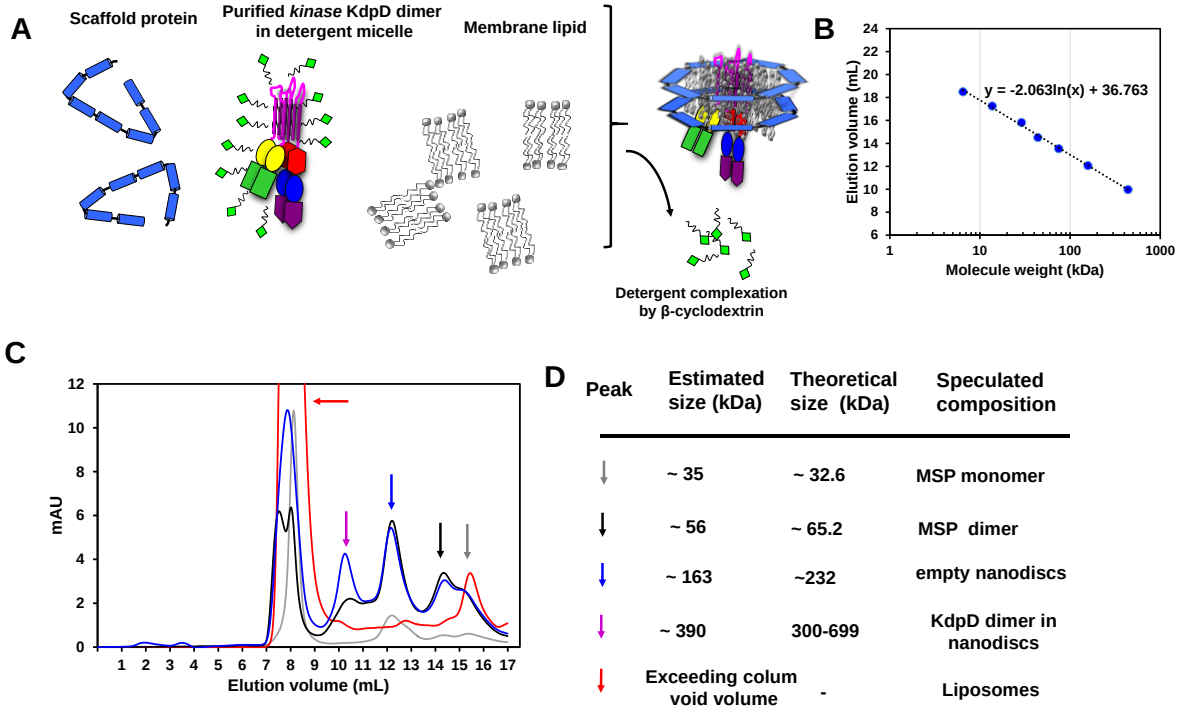


Figure 23: Integration of *E. coli kinase* KdpD into nanodiscs. (A) Schematic of assembling purified *kinase* KdpD into nanodiscs. **(B)** Calibration curve of Superdex 200 Increase 10/300 GL column for the size-exclusion chromatography. Column calibration was performed by the proteins were used for the calibration ferritin (440 kDa), aldolase (158 kDa), conalbumin (75 kDa), ovalbumin (44 kDa), carbonic anhydrase (29 kDa), ribonuclease (13.7 kDa) and aprotinin (6.5 kDa). **(C)** Size-exclusion chromatography analysis of four nanodiscs assembly mixtures. Grey and Black curves: MSP and lipid molar ratio = 1:130 and = 4:130, respectively [MSP should assemble into empty nanodiscs (blue arrow), liposomes (red arrow) and protein dimer (black arrow)]. Red and blue curves: KdpD, MSP and lipid molar ratio = 0.2:1:130 and = 0.05:4:130, respectively [MSP should assemble into empty nanodiscs and nanodiscs containing KdpD dimer (violet arrow), MSP dimer (black arrow)]. Moreover, KdpD may be attracted by lipids to form liposomes (red arrow), while some MSP stays as monomer (grey arrow)]. **(D)** Speculated composition of the peak fraction in (C), according to the estimated and theoretical molecule sizes.

In parallel, to assemble KdpD into nanodiscs, KdpD was added into the MSP and lipid mixture with two kinds of stoichiometric proportion, KdpD:MSP:lipid = 0.2:1:130 (Figure 23C, red curve) and 0.05:4:130 (Figure 23C, blue curve). To make the KdpD protein more accessible to lipid,

the wrapping detergent was chelated with four folds concentration of β-cyclodextrin (Hornschemeyer, Liss et al. 2016). According to the size-exclusion chromatography analysis, the stoichiometric proportion of 0.2:1:130 could not support the formation of empty nanodiscs or nanodiscs with KdpD dimer. Instead, all the KdpD proteins assembled with lipid as liposomes (Figures 23B and 23D, red arrows). When less KdpD protein and more MSP were supplied into the reaction mixture (stoichiometric proportion 0.05:4:130), two new peaks appeared, indicating empty nanodiscs and nanodics loaded with KdpD dimer, respectively (Figure 23C, blue and violet arrows on blue curve).

These results suggest KdpD dimer may have already been assembled into nanodiscs. However, when the fractions were evaluated with SDS-PAGE and Western blot, very faint signal was detected (data not shown). Further verifications are required.

3.3.4 Exploring CipA and CipB as scaffolds for *in vivo* crystallization

In addition to the common methods to get the structure of KdpD, *in vivo* crystallization offers another opportunity. Since both *kinase* and *non-kinase* KdpD are targeted to cytoplasmic membrane, in order to get the KdpD proteins crystallized, a scaffold protein is required to keep in them cytosol.

It has been known that CipA and CipB form independent PCIs with different shapes in *P. luminescens* (Bintrim and Ensign 1998, Bowen and Ensign 2001). But there is no report whether they would function as a scaffold to bring heterogeneous proteins into PCIs. In order to verfy this speculation, the *cipA* or *cipB* genes was first deleted individually. Basing on the single deletion of *cipA* and *cipB*, *cipA*$^{-}$ *cipB*$^{-}$ double deletion mutant of *P. luminescens* was aslo generated and designated as *P. luminescens cip*$^{-}$ (see materials and methods). This strain could be used for production of *in vivo* crystals of desired proteins.

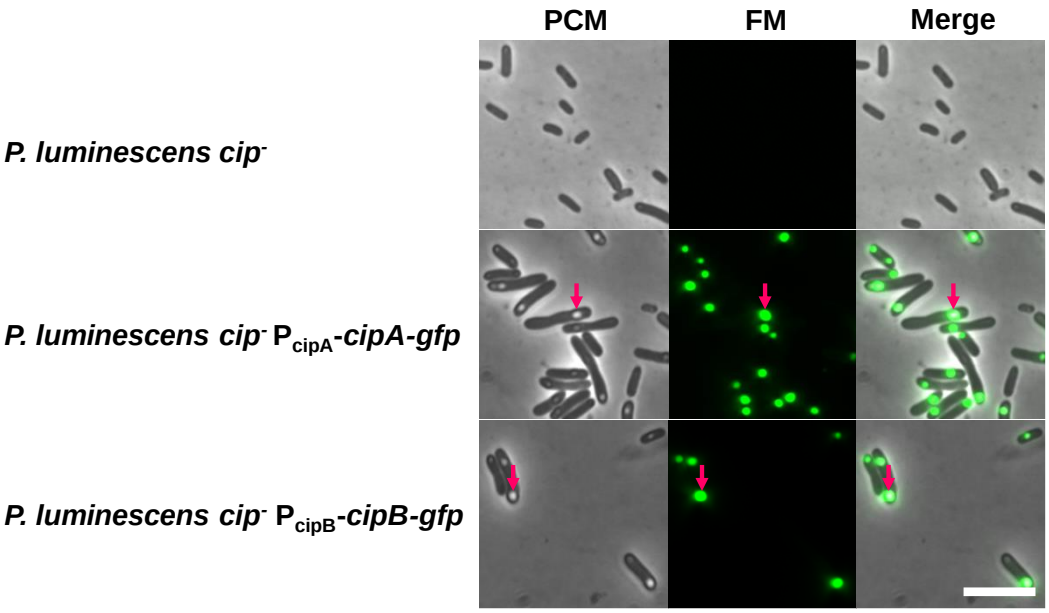


Figure 24: CipA-GFP and CipB-GFP hybrids are organized into PCIs in *P. luminescens cip*- cells. After 56 h of growth on LB plates at 30°C, *P. luminescens cip*-, *P. luminescens cip*-, *P. luminescens cip*- P_{cipA}-*cipA-gfp*, *P. luminescens cip*- P_{cipB}-*cipB-gfp* cells were collected and resuspended in fresh LB medium for microscopy. The fusion genes *cipA-gfp* and *cipB-gfp* were expressed under the control of the native promoters of *cipA* and *cipB*, respectively. Arrows indicate PCIs. PCM, phase-contrast microscopy; FM, fluorescence microscopy. Scale bar, 7.5 µm.

The scaffold funcation of CipA and CipB was subsequently evaluated via organizing the GFP reporter into PCIs. Gene fusions *cipA-gfp* or *cipB-gfp* (under control of their respective native promoters) coding either for CipA-GFP or CipB-GFP, were integrated into the chromosome of *P. luminescens cip*-. Then, the cells were grown for 56 h on LB agar at 30°C, and *in vivo* formation of fluorescent CipA-GFP or CipB-GFP PCIs were observed (Figure 24). This experiment proves that both CipA and CipB can act independently as scaffolds in their native host.

Subsequently, the CipA, CipB, CipA-GFP and CipB-GFP was isolated as shown in Figure 7, and shipped to the collaborator Dr. Lars Redecke (Universitäten Lübeck und Hamburg, current position Universität zu Lübeck) for serial crystallography synchrotron beamline SPring-8

(Japan). Unfortunately, diffraction pattern was only observed from the CipB PCIs (at resolution of 6 Å, data not shown).

It is conceivable that larger *in vivo* PCIs may support better diffractions. In order to get lager PCIs, the vectors pFastBac1-cipA-gfp and pFastBac1-cipA-gfp were constructed. CipA-GFP and CipB-GFP hybrid proteins were subsequently produced in Sf9 insect cells from the polyhedrin (P_H) promoter, by the collaborator Dr. Lars Redecke. Even though the *in vivo* assembly of these two proteins were observed. The roundish complexes are analogous to the organelles of eukaryotic cells, but are not PCIs (Figure 25). Therefore, they could not be used as crystals for protein structural analysis.

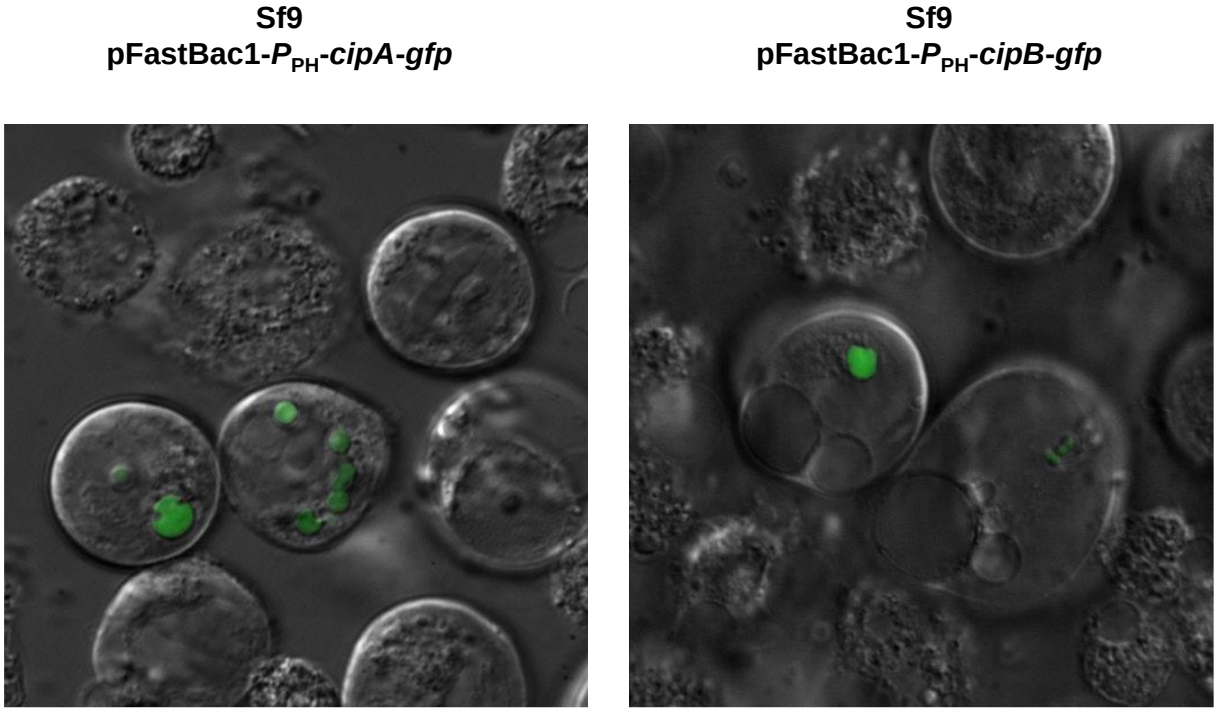


Figure 25: CipA-GFP and CipB-GFP assemble into roundish complexes in the insect cells. (A) CipA-GFP, **(B)** CipB-GFP. Gene fusions *cipA-gfp* and *cipB-gfp* were expressed from the baculovirus polyhedrin (P_H) promoter in insect Sf9 cell line.

3.4 Evaluation of CipA and CipB as protein scaffolds for biotechnological applications

3.4.1 Cip scaffolds bring single proteins into PCIs

3.4.1.1 CipA-6His and CipB-6His form PCIs in *E. coli*

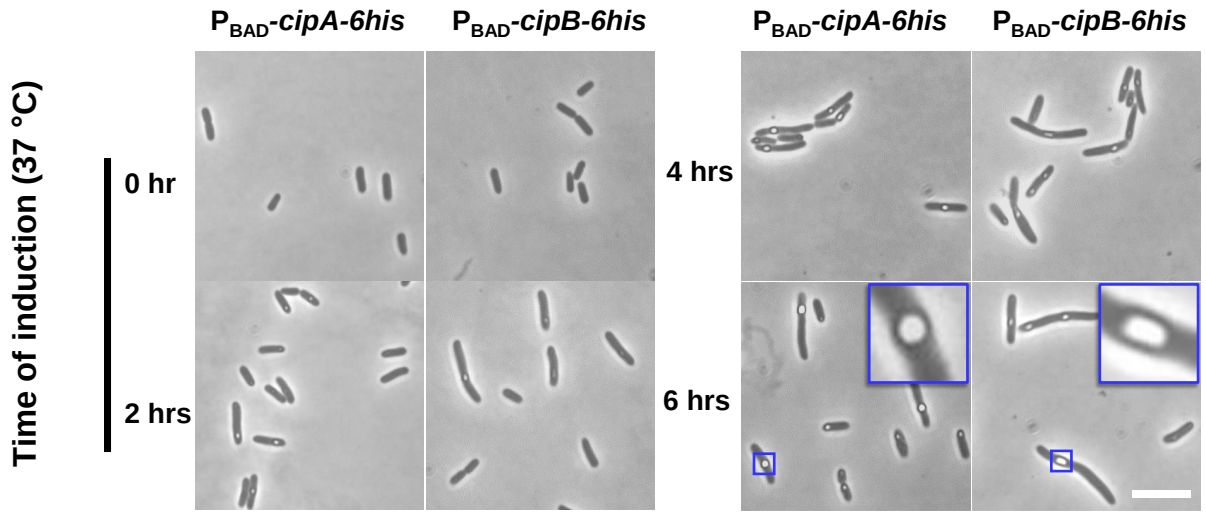


Figure 26: CipA-6His and CipB-6His self-organize into PCIs in *E. coli* DH5α. Production of CipA-6His and CipB-6His in *E. coli* DH5α was induced with 0.2% (w/v) L-arabinose at 37°C, when the cell density reached OD_{600}=0.6. Cells were subsequently analyzed every 2 h by microscopy. The PCIs in the areas marked by the small boxes (bottom row) are shown at higher magnification at the top right.

Formation of CipA-GFP and CipB-GFP PCIs in *P. luminescens* generally takes 2-3 days (Figure 24), and the factors that control the native *cip* promoters are still unknown. To circumvent these drawbacks the Cip scaffolds were tested in *E. coli*. First, *cipA-his* and *cipB-his* were expressed in *E. coli* DH5α under the control of the arabinose inducible promoter P_{BAD}. When cells were grown at 37°C, PCIs with diameters of 0.1-0.3 µm were detected by phase-contrast microscopy after induction of fusion gene expression with L-arabinose for 2 h (Figure 26). This confirmed that PCIs can be produced heterologously in *E. coli*.

3.4.1.2 Cip organize GFP into PCIs in *E. coli*

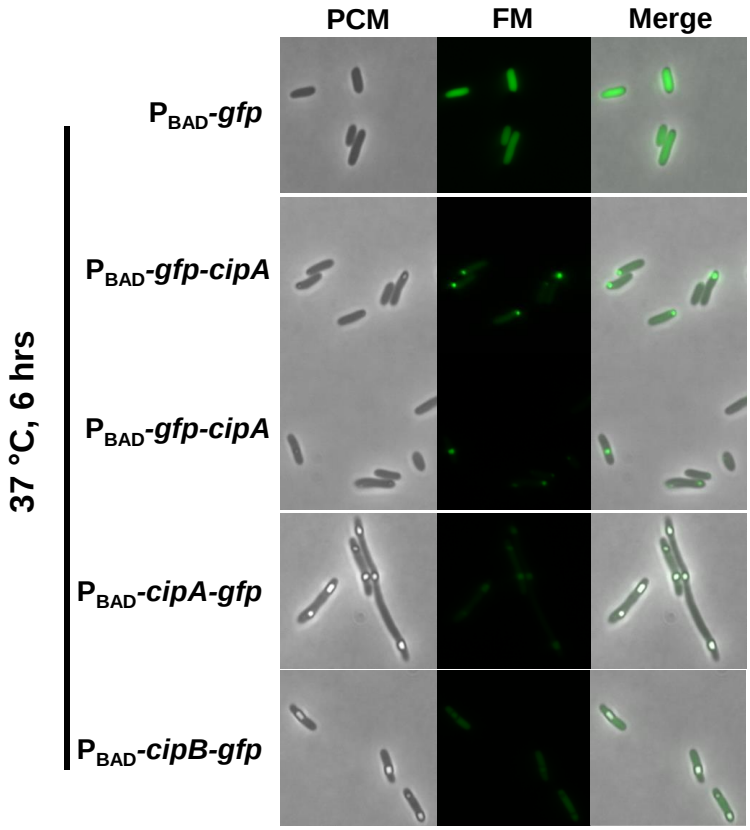


Figure 27: Production of CipA-GFP and CipB-GFP PCIs at 37°C**.** *E. coli* DH5α was induced with 0.2% (w/v) L-arabinose at 37°C, when the cell density reached OD_{600}=0.6. Cells were subsequently analyzed by microscopy 6 h after the supplement of L-arabinose.

GFP produced in *E. coli* is normally homogenously distributed (Figure 27). Cip scaffolds were then tested for their competences of subcellularly organize GFP. CipA-GFP and CipB-GFP, GFP-CipA and GFP-CipB were produced at different growth temperatures in *E. coli*. As shown in Figure 27, with the assistance of Cip scaffolds, GFP can be assemble into PCIs.

When the Cip scaffolds was placed to the C-terminal of GFP, very small fluorescent foci were observed. When the Cip scaffolds placed to the N-terminal of GFP, very large PCIs form in *E. coli* cells, while they are barely fluorescent (Figure 27). Therefore in the following experiments, Cip scaffolds are uniformly placed to the N-terminal of interested proteins.

3.4.1.3 Temperature impact on the formation of PCIs in *E. coli*

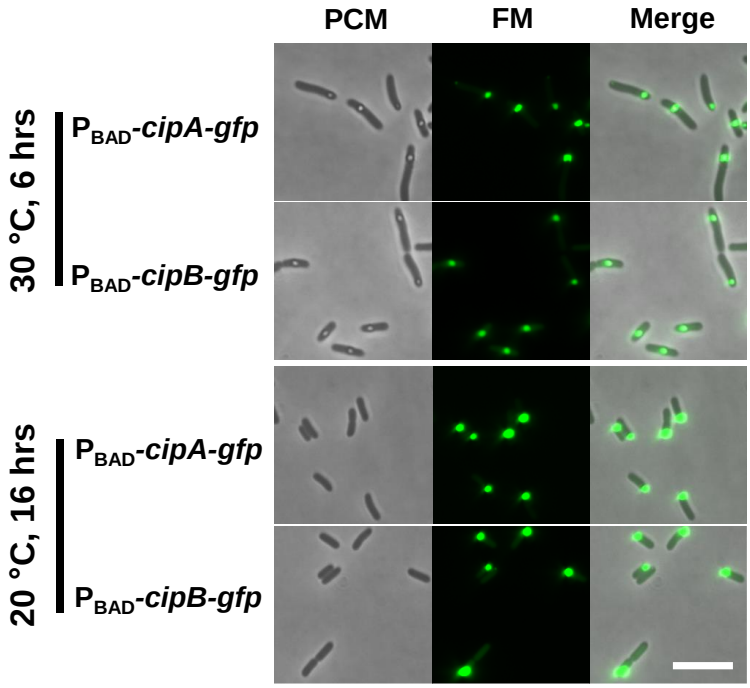


Figure 28: Production of fluorescent GFP complex at lower temperature. Production of CipA-GFP and CipB-GFP in *E. coli* DH5α was induced with 0.2% (w/v) L-arabinose at 30°C and 20°C, respectively, when the cell density reached OD_{600}=0.6. Cells were analyzed by microscopy 6 h after the supplement of L-arabinose.

As shown above cells grown at 37°C had highly refractile, but weakly fluorescent GFP PCIs (Figure 27). When cells were grown at 30°C, phase-bright and fluorescent CipA-GFP or CipB-GFP PCIs were detectable (Figure 28). A further decrease in the growth temperature to 20°C permitted subcellular organization of CipA-GFP and CipB-GFP hybrids to be visualized as highly fluorescent areas, which were not detectable in phase-contrast micrographs (Figure 28).

These results suggest that the protein complexes formed at 30°C/37°C are densely organized and therefore can shift the phase of incident light, whereas the complexes produced at 20°C seem to be less tightly packed. The low fluorescence of PCIs produced at 37°C is likely to be the result of rapid assembly of the CipA-GFP or Cip-GFP molecules, which might exceed the maturation rate of the chromophores.

3.4.1.4 Impact of inducer concentration on the formation of PCIs

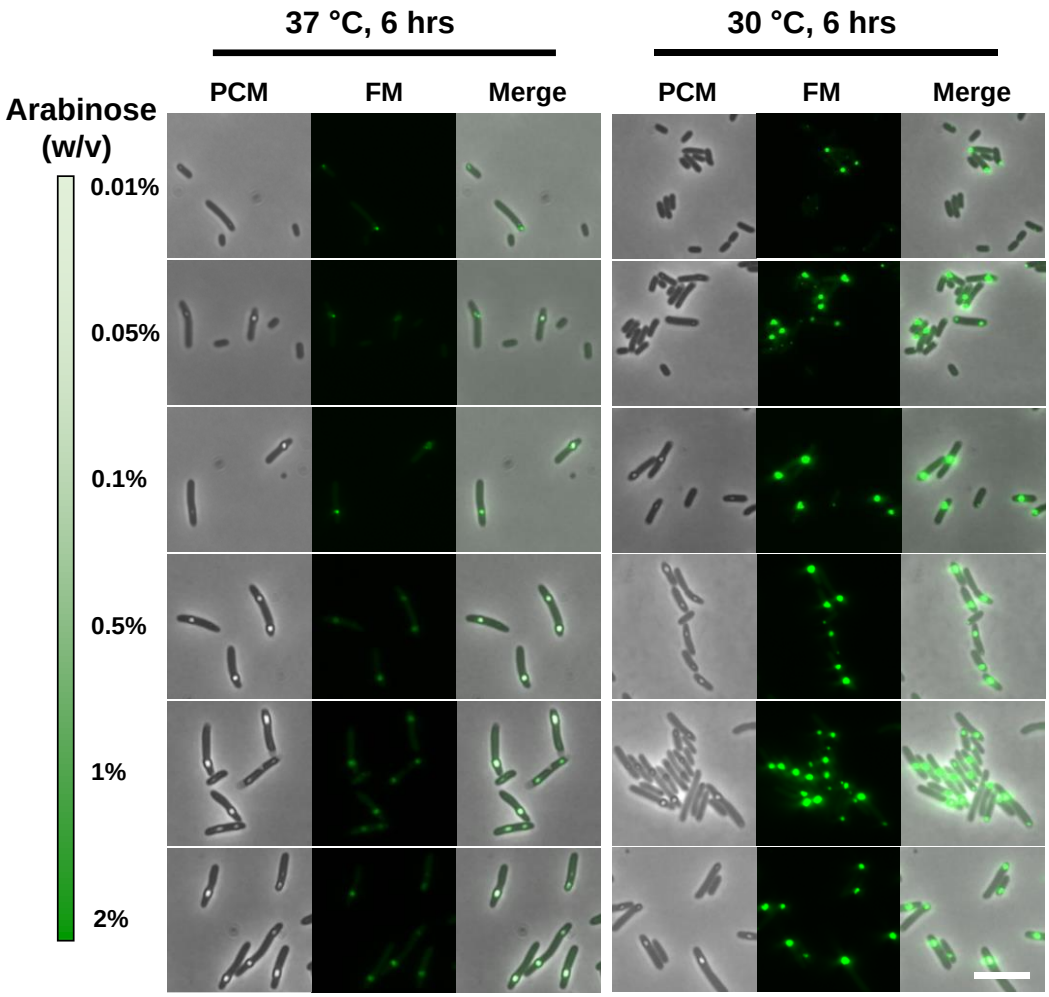


Figure 29: Influence of inducer concentration on formation of CipA-GFP PCIs in *E. coli*. The cultivation procedure (at 37°C or 30°C) was the same as described in Figure 27, but different L-arabinose concentrations [from 0.01% to 2% (w/v)] were tested. PCM, phase-contrast microscopy; FM, fluorescence microscopy. Scale bar, 7.5 µm.

In addition to the temperature, the effect of inducer concentration was also test on Cip scaffolds protein organization. When the L-arabinose concentration was reduced to 0.05% (w/v) or 0.01% (w/v), the PCIs formed by CipA-GFP were quite smaller, but their fluorescence intensity was not affected (Figure 29). This result implies that the inducer concentration has an impact on the rate of synthesis of CipA-GFP molecules, but - unlike temperature - has no influence on the organization of the hybrid protein.

3.4.1.5 *In vivo* stability of the GFP PCIs

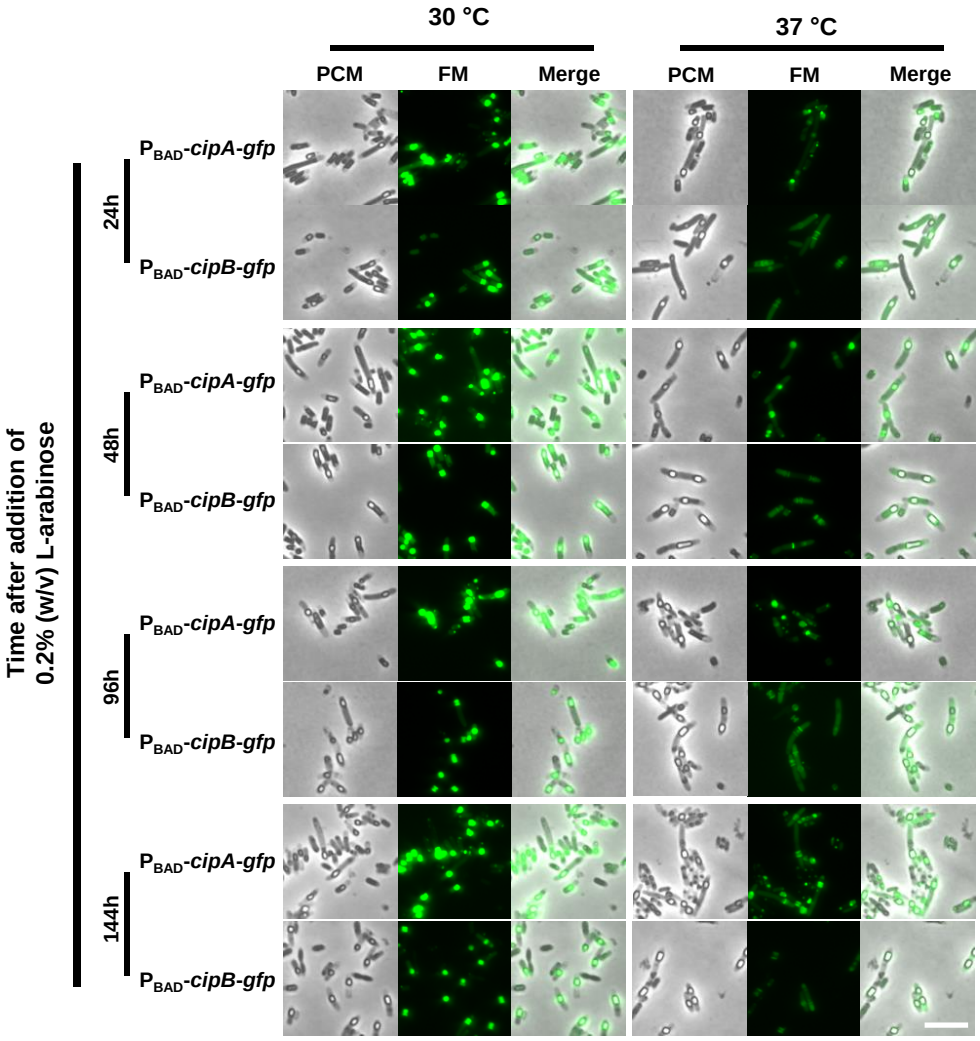


Figure 30: Stability of CipA-GFP and CipB-GFP PCIs in *E. coli* cells. Production of the CipA-GFP and CipB-GFP PCIs in *E. coli* was initiated as described by addition of 0.2% (w/v) L-arabinose (PCM, phase-contrast microscopy; FM, fluorescence microscopy). Cultures were grown at 30°C and 37°C, respectively. Scale bar, 7.5 µm.

To study the PCIs stability *in vivo*, the production of the GFP PCIs was induced at 30 and 37°C as described in Figures 27 and 28, but the cultivation time was much more extended. During this period, there was no fresh medium was provided for the PCI producing cell. Cells were checked at the indicated timepoints (Figure 30). After 6 days cultivation, the PCIs are still clearly visible. This results indicates that the PCIs are very stable *in vivo*.

3.4.1.6 Formation of PCIs in defined medium

In addition to the LB medium, a defined medium modified from M9 medium (Noyes, Meng et al. 2008), can also support the formation of PCIs in *E. coli* cells. As shown in Figure 31, CipA-GFP and CipB-GFP assembled into fluorescent PCIs that were clearly visible under the microscope. This offers the opportunity to balance and apply advanced feeding schemes. Because for large scale factory productions, cheaper and poorer media are commonly used than the medium used in the laboratory.

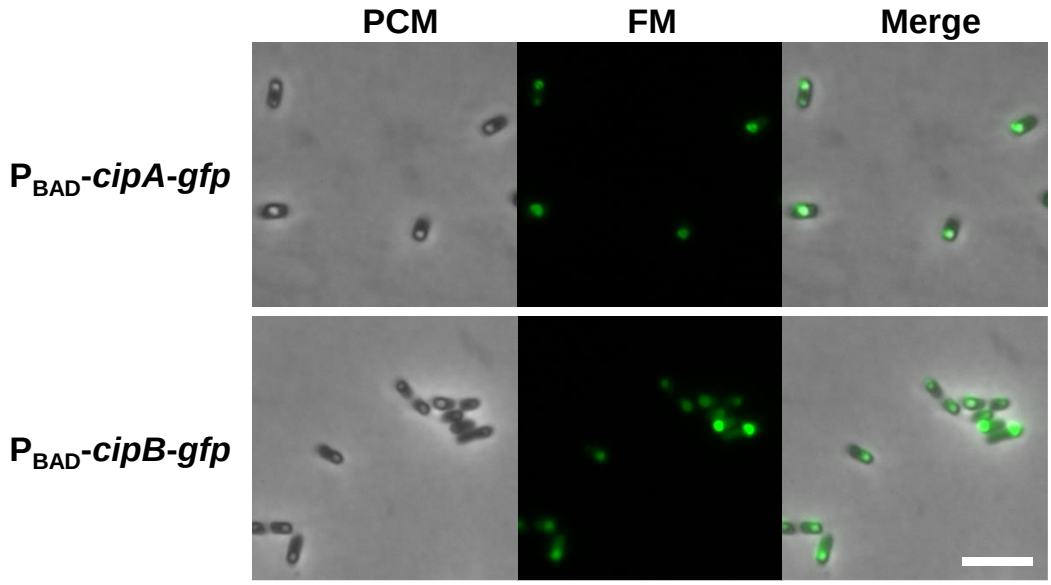


Figure 31: Cip scaffolds organize GFP into PCIs in *E. coli* cells cultivated in a defined medium (Noyes, Meng et al. 2008)**.** Production of CipA-GFP and CipB-GFP at 37°C was induced with 0.2% (w/v) L-arabinose at the beginning of cultivation. Micrographs were taken after 16 hours of induction. PCM, phase-contrast microscopy; FM, fluorescence microscopy. Scale bar, 7.5 µm.

3.4.1.7 Isolation and characterization of CipA-GFP and CipB-GFP PCIs from *E. coli*

To isolate CipA-GFP and CipB-GFP PCIs from *E. coli*, cells were passed three times through a French press at 0.4 kbar. Then the PCIs were collected by centrifugation and washed three times with Na-phosphate buffer (Figure 7). CipA-GFP and CipB-GFP protein complexes

produced at 20°C could not be isolated by this procedure as they broke up during cell disruption and could not be pelleted by centrifugation (Figure 32A).

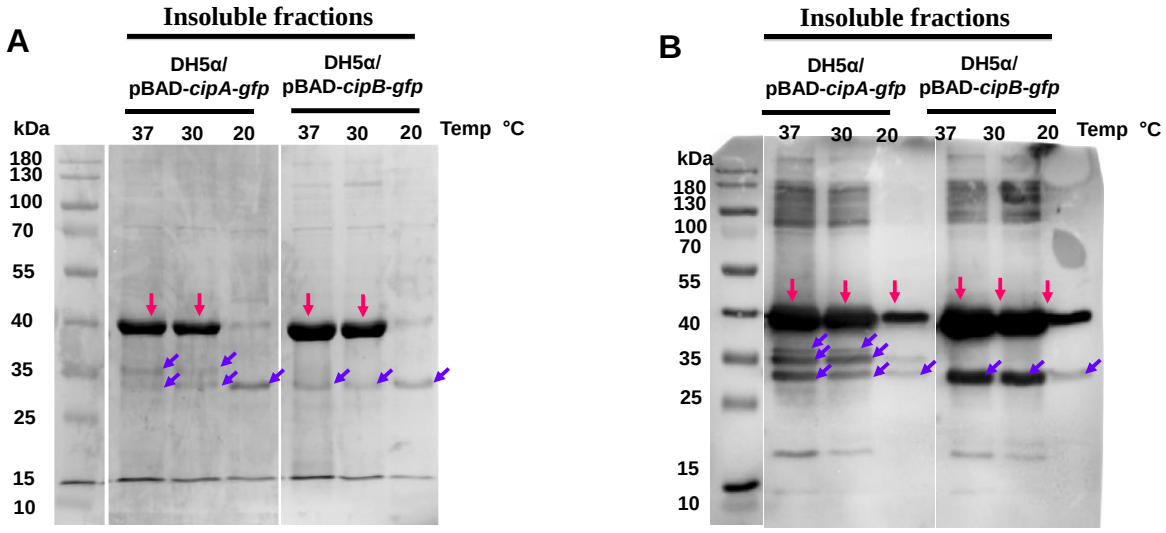


Figure 32: SDS-PAGE and Western blot of the CipA-GFP and CipB-GFP protein complexes. *E. coli* cells were cultivated at 37°C, 30°C and 20°C to produce CipA-GFP and CipB-GFP complexes as described in Figures 27 and 28. Cells were collected and lysed as described in Figure 7. Insoluble fractions were collected and washed three times with Na-phosphate buffer, and resuspended in an equal final volume compared to the supernatant. Equal volumes (24 µL) of washed pellets were loaded on the SDS-PAGE. Gels were stained with Coomassie Brilliant Blue R-250 **(A)** or applied to Western blot using anti-GFP antibody **(B).** Magenta and blue arrows mark CipA-GFP and CipB-GFP monomers and early translation termination or protein degradation bands, respectively.

To check the purities of the isolated PCIs, the insoluble fractions were applied to SDS-PAGE. As shown on the stained SDS-gels, the isolated PCIs were already about 90% pure (Figure 32A). However, some bands that may indicate early translation termination or protein degradation were observed when the isolated PCIs were analyzed by Western blot with anti-GFP antibody (Figure 32B). The early translation termination or protein degradation seems not to be affected by different cultivation temperatures.

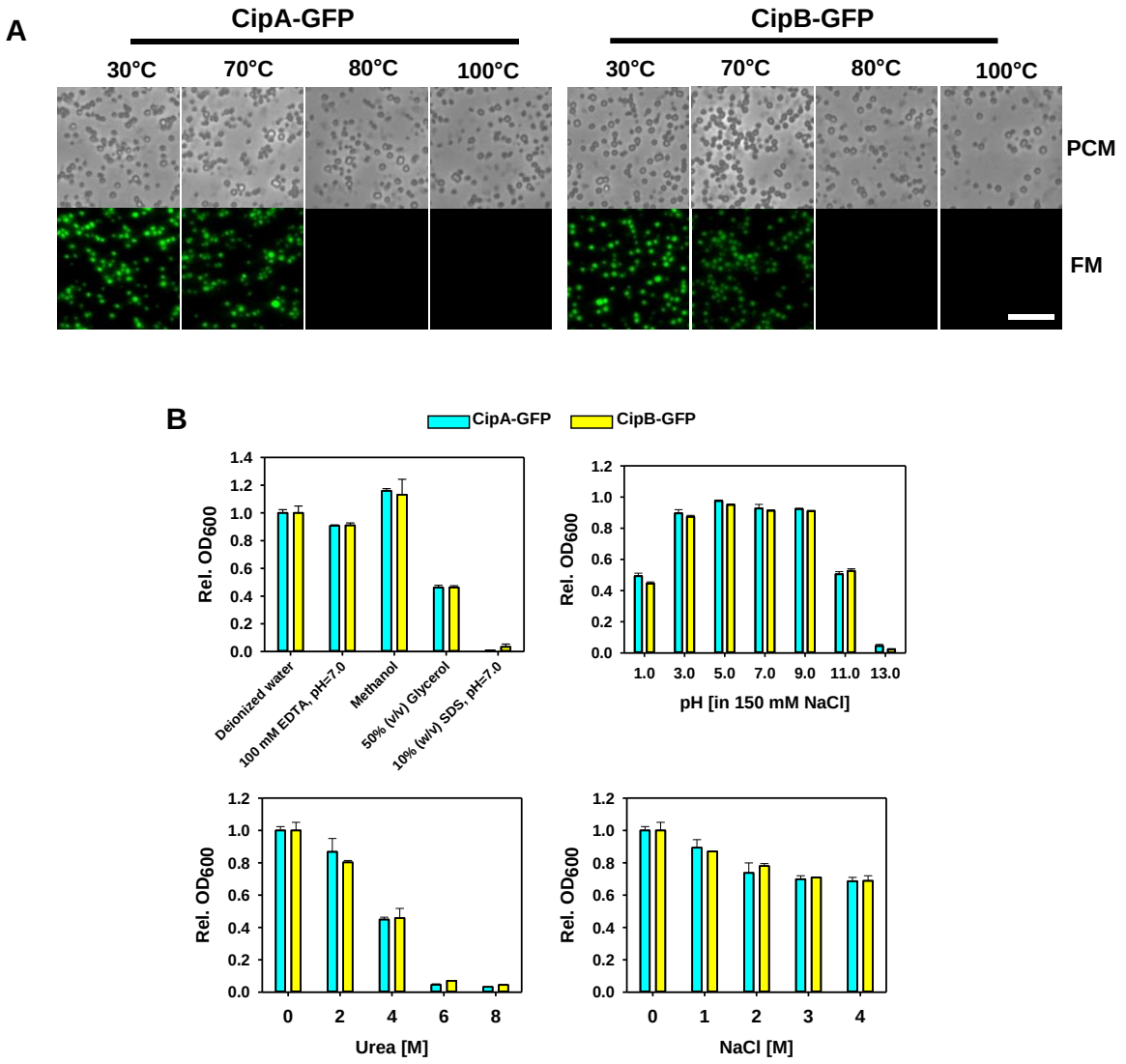


Figure 33: Isolation and characterization of GFP PCIs. (A) Thermal stability of isolated PCIs. Micrographs were taken after a 10-min incubation at the indicated temperature (PCM, phase contrast microscopy; FM, fluorescence microscopy). Scale bar, 7.5 µm. **(B)** Solubility of PCI in various solutes. The degree of solubilization of PCIs was estimated by the relative decrease in initial optical density. The value for PCIs in deionized water was set to 1.0.

To study their thermal stability, the isolated PCIs were exposed to different temperatures for 10 min. It was found that the fluorescence signals emitted by CipA-GFP and CipB-GFP PCIs vanished at 80°C, but PCIs remained structurally undisturbed even after 10 min at 100°C (Figure 33A). Thus, high temperature affects the activity of the tagged protein or enzyme but does not influence PCI structure *per se*.

To determine their solubility, CipA-GFP and CipB-GFP PCIs were resuspended in different solutions. The initial optical density (OD_{600}) was measured and any subsequent decrease was taken to reflect solubilization of PCIs (Figure 33B). It was found that PCIs could be dissolved in denaturing solutions such as 10% (w/v) SDS or 8 M urea, and under acidic (pH 3) or alkaline (pH 11) conditions, but also (partially) in 50% (v/v) glycerol. In contrast, high concentrations of NaCl or EDTA had no effect (Figure 33B).

In fact, PCIs organized by Cip scaffolds, like many other crystals produced *in vivo*, differ markedly in some physical characteristics from crystals produced *in vitro*. For example, the crystals of *Trypanosoma brucei* cathepsin produced in Sf9 insect cells have been reported to be stable in deionized water, salt solutions or alkaline buffers, but soluble in buffers at, pH below 4 (Koopmann, Cupelli et al. 2012). Bt crystals also remain stable in mildly acidic conditions, but can be dissolved at alkaline, pH (Sawaya, Cascio et al. 2014). In summary, it has been clearly shown that the Cip-based PCIs produced *in vivo* are very stable. Easy isolation of stable proteins is an essential prerequisite for most biotechnological applications *in vitro*.

3.4.1.8 Cip scaffolds organize LacZ into enzymatically active PCIs

In the next step, the β-galactosidase (LacZ) derived from *E. coli* was tagged separately with CipA and CipB and produced in *E. coli* DH5α at 37°C. Similarly, CipA-LacZ and CipB-LacZ were organized into refractile PCIs (Figure 34A), which could be isolated as easily as the CipA-GFP and CipB-GFP PCIs. In parallel, soluble 6His-tagged LacZ (His-LacZ) was purified by affinity chromatography. In the next step, enzymatic activities were determined. Yields of CipA-LacZ and CipB-LacZ were higher relative to that of the soluble His-LacZ (Figure 34B). Conversely, the specific activity of the soluble His-LacZ was higher than that of Cip-tagged LacZ. This might indicate that only molecules on the surface of PCIs are accessible to the substrate *o*-nitrophenyl-β-D-galactopyranoside.

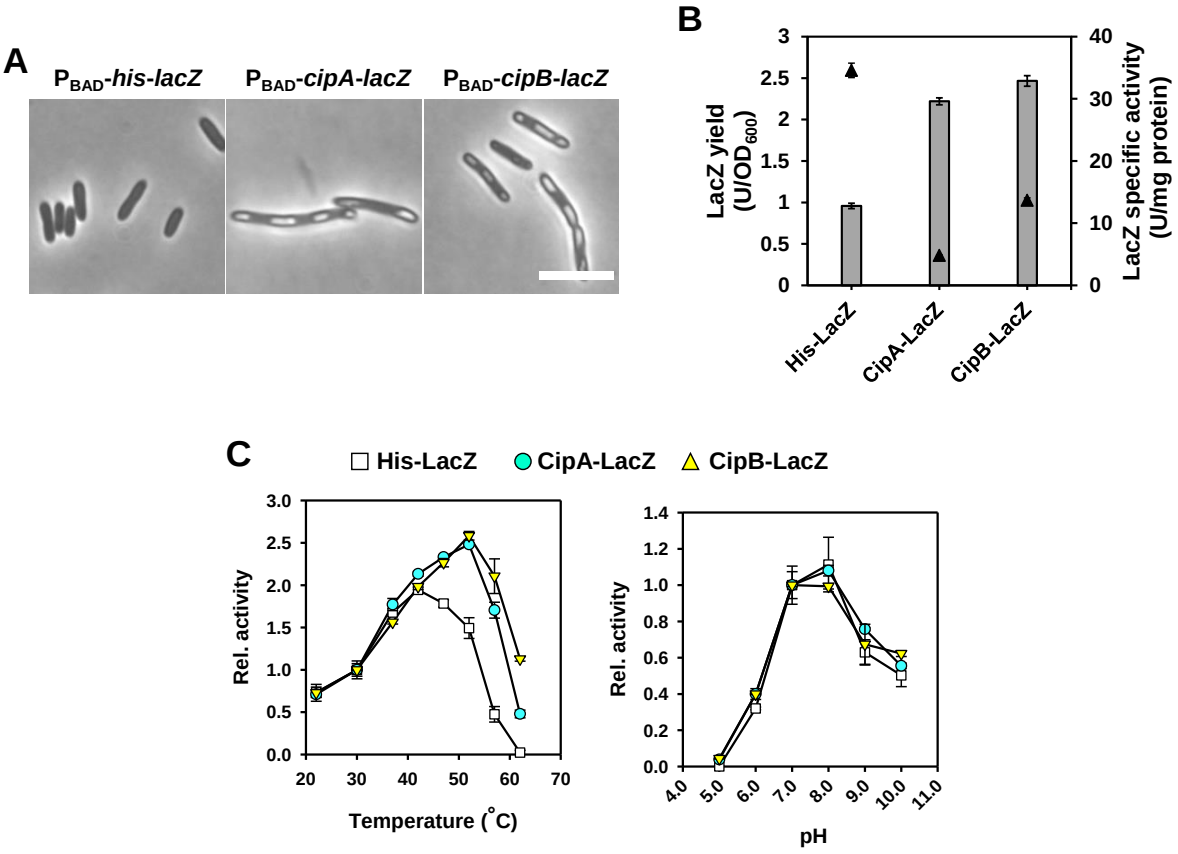


Figure 34: Cip scaffolds organize LacZ into PCIs in *E. coli*. (A) Micrographs of His-LacZ, CipA-LacZ or CipB-LacZ-producing *E. coli* cells. Synthesis of His-LacZ, CipA-LacZ or CipB-LacZ in *E. coli* DH5α was induced with 0.2% (w/v) L-arabinose at 37°C for 6 h (scale bar, 7.5 µm). **(B)** LacZ yield (grey column) and specific activity (black triangle) of His-LacZ, CipA-LacZ PCIs and CipB-LacZ PCIs. **(C)** Effects of temperature and, pH on the activity of His-LacZ, CipA-LacZ PCIs and CipB-LacZ PCIs. The β-galactosidase activity measured at 30°C and, pH 7.0, respectively, was set to 1.0.

The optimum temperature for His-LacZ activity was determined to be 42°C, while the activities of CipA-LacZ and CipB-LacZ PCIs peaked at 52°C (Figure 34C, left). The, pH profiles were similar for LacZ in soluble and PCI forms, all showing an optimal activity at, pH 8.0 (Figure 34C, right). This demonstrates that Cip scaffolds are useful tools to stabilize enzymes. Furthermore, Cip scaffolds can functionally organize proteins of large size (LacZ = 116 kDa) into PCIs.

3.4.2 Cip scaffolds bring multiple proteins into PCIs

3.4.2.1 Cip scaffolds co-organize GFP and LacZ into bioactive PCIs

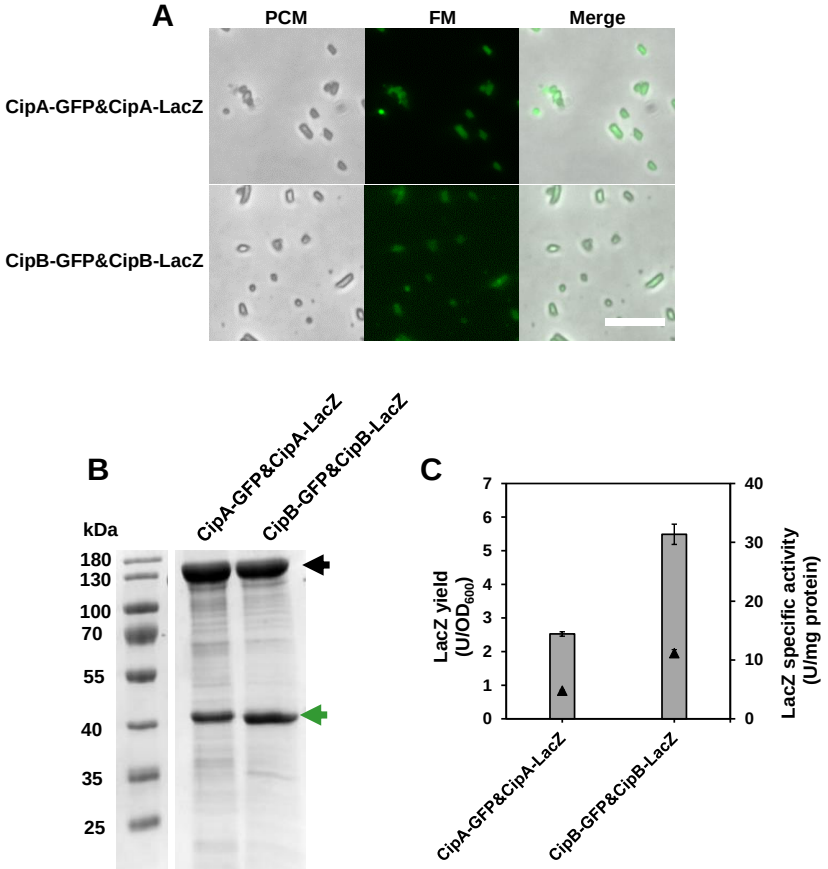


Figure 35: Cip scaffolds co-organize GFP and LacZ into PCIs in *E. coli*. (A) Isolated CipA-GFP&CipA-LacZ and CipB-GFP&CipB-LacZ PCIs. CipA-GFP and CipA-LacZ or CipB-GFP and CipB-LacZ were co-produced as PCIs, which were released from the cells as described in methods. Scale bar, 7.5 µm. **(B)** SDS-PAGE of CipA-GFP&CipA-LacZ and CipB-GFP&CipB-LacZ PCIs. The black arrow indicates CipA-LacZ or CipB-LacZ and the green arrow indicates CipA-GFP or CipB-GFP. **(C)** β-Galactosidase yields (grey column) of CipA-GFP&CipA-LacZ and CipB-GFP&CipB-LacZ PCIs and their corresponding specific activities (indicated by the black triangle).

Most metabolic pathways employ multiple enzymes to transform substrates into products. It will be interesting to know, in addition to organizing single types of proteins, Cip scaffolds could also co-organize multiple proteins. For this purpose, GFP and LacZ (two reporter proteins that share no sequence or structural similarity and differ in molecular weight) were tagged separately with CipA and CipB. CipA-GFP and CipA-LacZ or CipB-GFP and CipB-LacZ were

produced in combination in *E. coli* and the PCIs were isolated as described above and analyzed by microscopy.

It was found that each of the isolated PCI particles was fluorescent (Figure 35A), indicating that GFP molecules had been incorporated into all PCIs. The isolated PCIs were also analyzed by SDS-PAGE, which clearly revealed two major bands corresponding to CipA-LacZ (or CipB-LacZ) and CipA-GFP (or CipB-GFP) in similar molar ratios (Figure 35B). Moreover, the isolated PCIs also had similar β-galactosidase activities (Figure 35C). Thus, it could be concluded that Cip scaffolds can organize GFP and LacZ proteins into mixed PCIs, which are both fluorescent and enzymatically active. This suggested that Cip scaffolds might also be capable of organizing multiple enzymes into metabolic pathways.

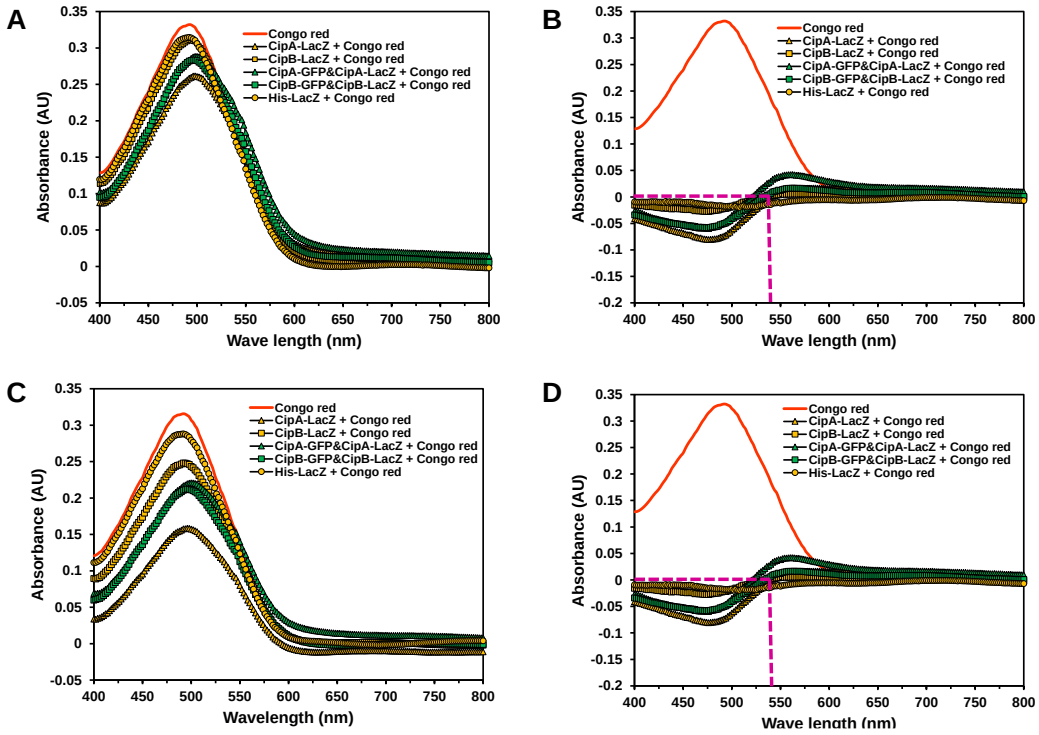


Figure 36: Congo Red absorption spectra shift assay. LacZ PCIs and the soluble His-LacZ were incubated separately with Congo Red for 30 min [**(A)** and **(B)],** and 16 hours [**(C)** and **(D)**]. No spectral shift was detected by measuring the absorbance spectra [(A) and (C)]. No obvious difference was detected on the difference spectra at the wavelengths around 540nm [(B) and (D) (marked with magenta dash lines)].

LacZ PCIs in Figure 34 and Figure 35 show much decreased specific activities. This raises the question whether the CipA-LacZ and CipB-LacZ molecules are mis-folded and the PCIs are protein inclusion bodies. Before further experiment, this speculation needed to be verified. Protein inclusion bodies are generally rich of β-sheet structure (cross-β structure) (Fink 1998, Wang 2009). Such kind of structure can be detected by measuring the absorption spectra of Congo Red (Wang, Maji et al. 2008, Upadhyay, Murmu et al. 2012). Congo Red alone exhibits maximum light absorbance at the wavelength of 490 nm. Upon binding to the repeated β-sheet structure in the inclusion body, its maximum light absorbance will be shifted to longer wave length of around 540 nm.

The absorption spectra of Congo Red supplemented with CipA-LacZ, CipB-LacZ, CipA-GFP&CipA-LacZ or CipB-GFP&CipB-LacZ PCIs as well as the soluble protein His-LacZ were separately measured with the procedure described by Upadhyay *et al* (Upadhyay, Murmu et al. 2012). No specific spectral shift, which would indicate the repeated β-sheet structure in an inclusion body, was observed when the incubation time was extended to 16 hours (Figure 36). This proves that the PCIs are different from inclusion bodies.

3.4.2.2 The CipA scaffold brings together multiple enzymes involved in violacein biosynthetic pathway

To prove that Cip scaffolds can be used to organize multiple enzymes required for successive steps in a biosynthetic pathway and thus to enhance metabolite production, the enzymes of the violacein biosynthetic pathway (Vio enzymes) were separately tagged with the CipA scaffolf. Violacein is a bisindole compound that is naturally produced by several Gram-negative bacteria i.e*. Chromobacterium violaceum*, *Janthinobacterium lividum* and *Pseudoalteromonas tunicata.* Due to its potential applications in medicine, its complex synthetic pathway has been well studied.(Sanchez, Brana et al. 2006, Hoshino 2011) Violacein synthesis starts from L-tryptophan, and involves the five enzymes VioA, VioB, VioE, VioC, VioD (Vio enzymes) (Figure

37A). Protodeoxyviolaceinic acid is the common precursor of violacein and deoxyviolacein. Deoxyviolacein is an unwanted product, as its formation reduces the amount of protodeoxyviolaceinic acid available for synthesis of violacein (Figure 37A). Organization of the Vio enzymes with the aid of a CipA-based scaffold should bring the Vio enzymes close together in space, which in turn might increase the intermediate concentration close to the enzyme active sites and facilitate the rapid conversion of unstable metabolites.

A series of production strains, designated *E. coli* Vio1-Vio6, were generated in which none (Vio1), all (Vio6) or some (Vio2, Vio3, Vio4, Vio5) of the five enzymes in the pathway were individually fused to CipA (Figure 37B).

VioA and VioB are the two enzymes that catalyze the two-step conversion of L-tryptophan into indole-3-pyruvic acid imine dimer. The intermediate produced by VioA, indole-3-pyruvic acid imine, could be easily hydrolyzed.(Sanchez, Brana et al. 2006) Therefore, VioA and VioB were combined (strains *E. coli* Vio2, Vio3 and Vio6) with the aim to promote rapid conversion of indole-3-pyruvic acid imine into the dimer. VioC, VioD and VioE catalyze the downstream part of the metabolic pathway. The intermediates protodeoxyviolaceinic acid and protoviolaceinic acid are also very unstable.(Hoshino 2011) Therefore, VioC, VioD, VioE were combined in strains *E. coli* Vio5 and *E. coli* Vio6 to promote the rapid conversion of these intermediates. Finally, VioC is the most special Vio enzyme. It is not only required for conversion of protoviolaceinic acid into violacein, but is also involved in converting protodeoxyviolaceinic acid into the side product deoxyviolacein. Therefore, strains were designed to include VioC into the PCIs (*E. coli* Vio5 and Vio6) or to exclude it from the PCIs (*E. coli* Vio2, *E. coli* Vio3 and *E. coli* Vio4). The corresponding genes were placed under the control of the P_{BAD} promoter.

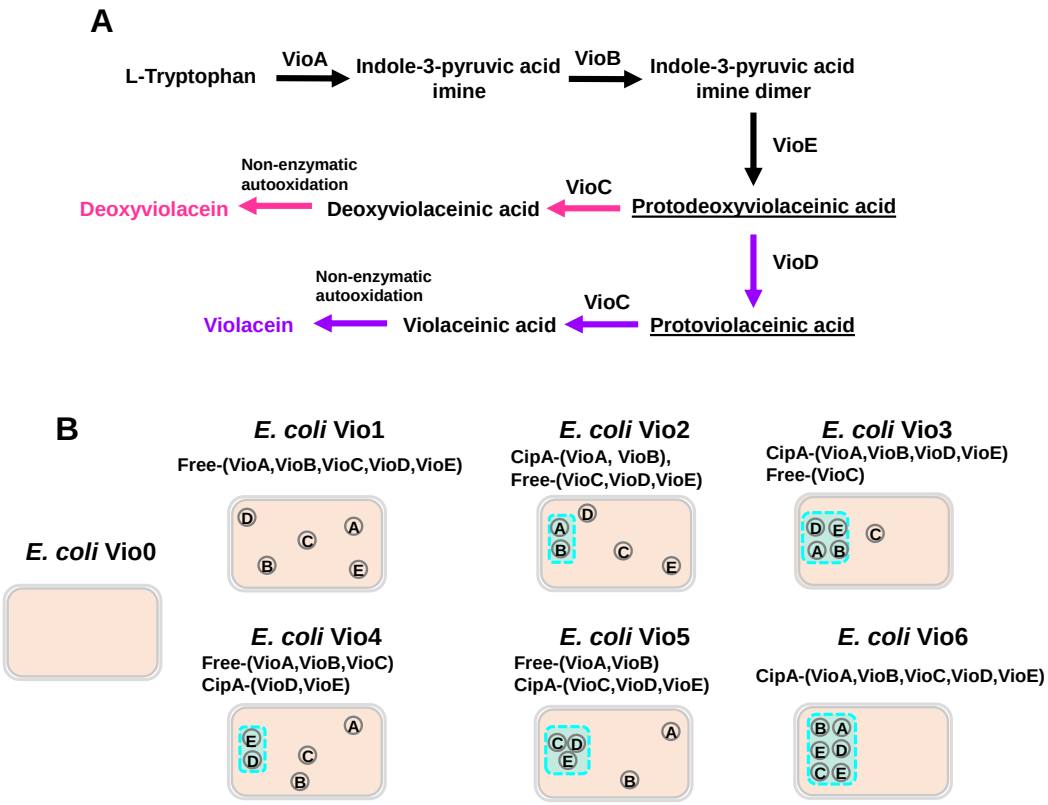


Figure 37: Engineering the violacein production metabolic pathway. (A) The biosynthetic pathway that converts L-tryptophan into violacein. The underlined compounds are reported to be very unstable intermediates. **(B)** Vio enzymes framed with box were separately tagged by CipA to be brought together into PCIs

First, appropriate inducer concentration for violacein production was determined the. Cultures of the engineered strains (*E. coli* Vio1 to *E. coli* Vio6) in early exponential phase were diluted with LB to an OD_{600} of 0.05 and drops were placed on LB plates containing 0%, 0.01%, 0.02%, 0.05%, 0.1% and 0.4% (w/v) of L-arabinose. After overnight cultivation at 30°C, the appropriate inducer concentration was found to be in the range of 0.01% (w/v) to 0.05% (w/v) according to the pigment accumulation (Figure 38A). The violacein production was induced with 0.01% (w/v) and 0.05% (w/v) L-arabinose. *E. coli* Vio4 and *E. coli* Vio5 produced more violacein and deoxyviolacein with 0.05% (w/v) L-arabinose while the other strains show less difference in the yields between these two inducer concentrations (Figure 38C). Therefore, unless specidied, violacein production was induced with 0.05% (w/v) L-arabinose.

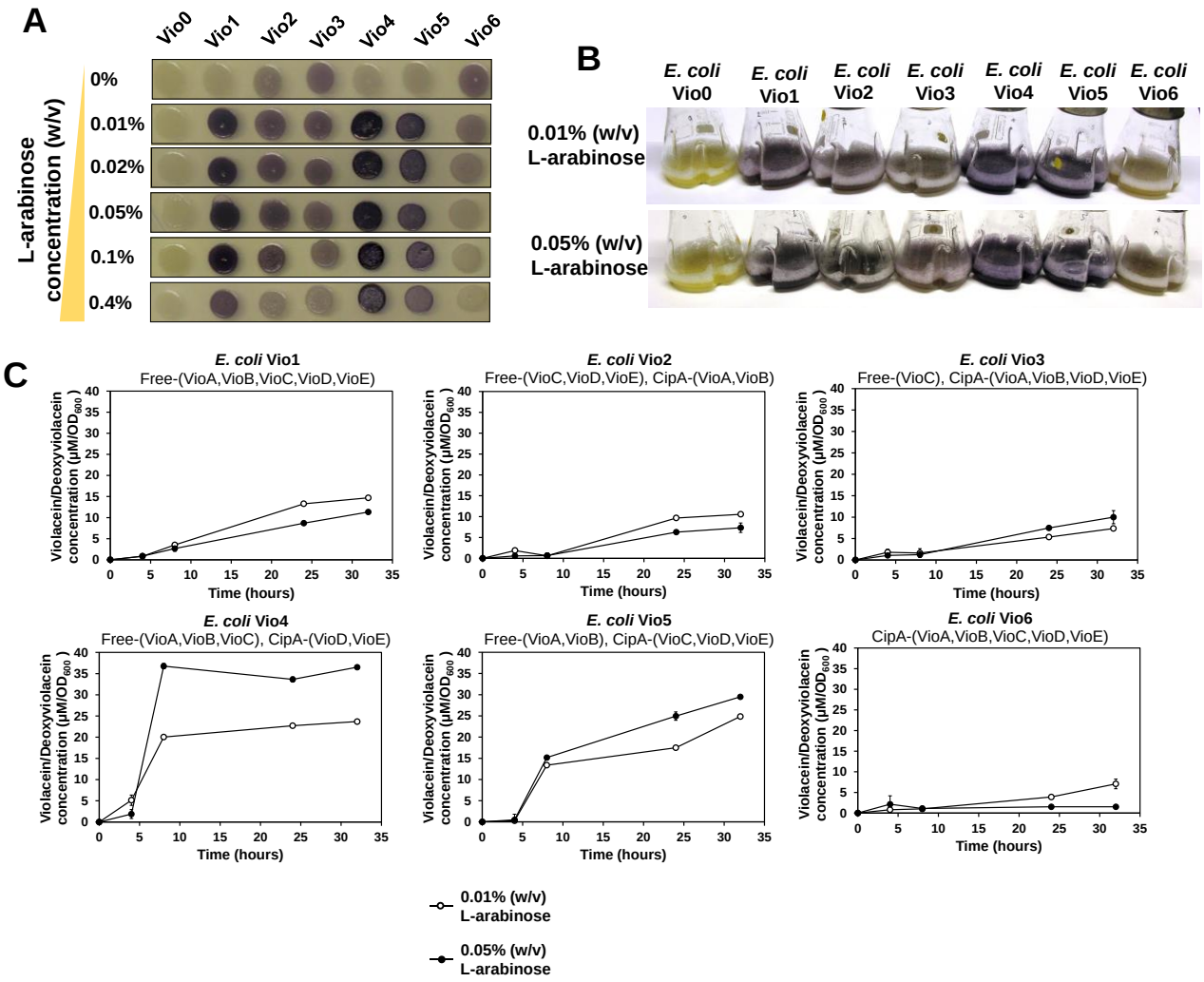


Figure 38: Batch cultivation of Vio strains for production of Violacein (A) Precultures of the engineered strains in Figure 37 were diluted with LB to an OD_{600} of 0.05 and dripped to LB plates containing indicated concentrations of L-arabinose and cultivated at 30°C overnight to stationary phase. The inducer concentration was selected according to the pigment accumulation. **(B)** Cultivation of *E. coli* Vio0 to *E. coli* Vio6 in LB medium supplemented with 0.01% (w/v) and 0.05% (w/v) L-arabinose for 32 h. Different levels of pigment accumulation were observed. **(C)**Time course of violacein and deoxyviolacein synthesis (mixture) in cultures of the engineered *E. coli* strains supplemented with 0.01% (w/v) or 0.05% (w/v) L-arabinose. Strain names and characteristics are given above the plots (see scheme in Figure 37).

Briefly, the final yields of violacein + deoxyviolacein were 11.3 µM/OD_{600} (Vio1: all Vio enzymes free), 7.3 µM/OD_{600} [Vio2: CipA-(VioA,VioB), all other enzymes free] 10.0 µM/OD_{600} [Vio3: CipA-(VioA,VioB,VioD,VioE); VioC free], 36.5 µM/OD_{600} [Vio4: CipA-(VioD,VioE), others free],

29.5 µM/OD_{600} [Vio5: CipA-(VioC,VioD,VioE); VioA and VioB free] and 1.5 µM/OD_{600} (Vio6: CipA-all Vio enzymes) (Figure 38C). These results show that productivity is very much improved in *E. coli* strains Vio4 and Vio5 in comparison to Vio1. However, *E. coli* Vio6 shows lower violacein and deoxyviolacein yield. This may be due to that the advantages by organizing Vio enzymes into into PCIs--increasing the intermediate concentration close to the enzyme active sites and facilitating the conversion of unstable metabolites--were counteracted by the disadvantages--decreasing the specific activities of the involved enzymes (as also shown in Figure 34 and 35).

The maximum rate of synthesis of violacein + deoxyviolacein for *E. coli* Vio1 was 0.4 µM/h per OD_{600}, it was 22.2-fold higher (8.7 µM/h per OD_{600}) and 8.8-fold higher (3.7 µM/h per OD_{600}) in strains *E. coli* Vio4 and *E. coli* Vio5, respectively.

In the next step, the ratios of violacein to deoxyviolacein were determined by HPLC (Figure 39). *E. coli* strains Vio3 and Vio6 had the lowest level of the by-product, but the overall yield was much lower than in *E. coli* strain Vio4 (Figure 38C). Overall, however, *E. coli* Vio5 was characterized to show the highest production of violacein, which was determined to be 183.2 µM (calculated from Figures 38C and 39B). In this strain VioC, VioD and VioE were organized into PCIs, while VioA and VioB were synthesized as free enzymes. Since VioE and VioD are, respectively, responsible for synthesis of the unstable intermediates PDVA and PVA, while VioC converts these into deoxyviolacein and violacein, respectively, encapsulation of the three enzymes clearly enhances both the overall productivity of the pathway - and selectivity for violacein.

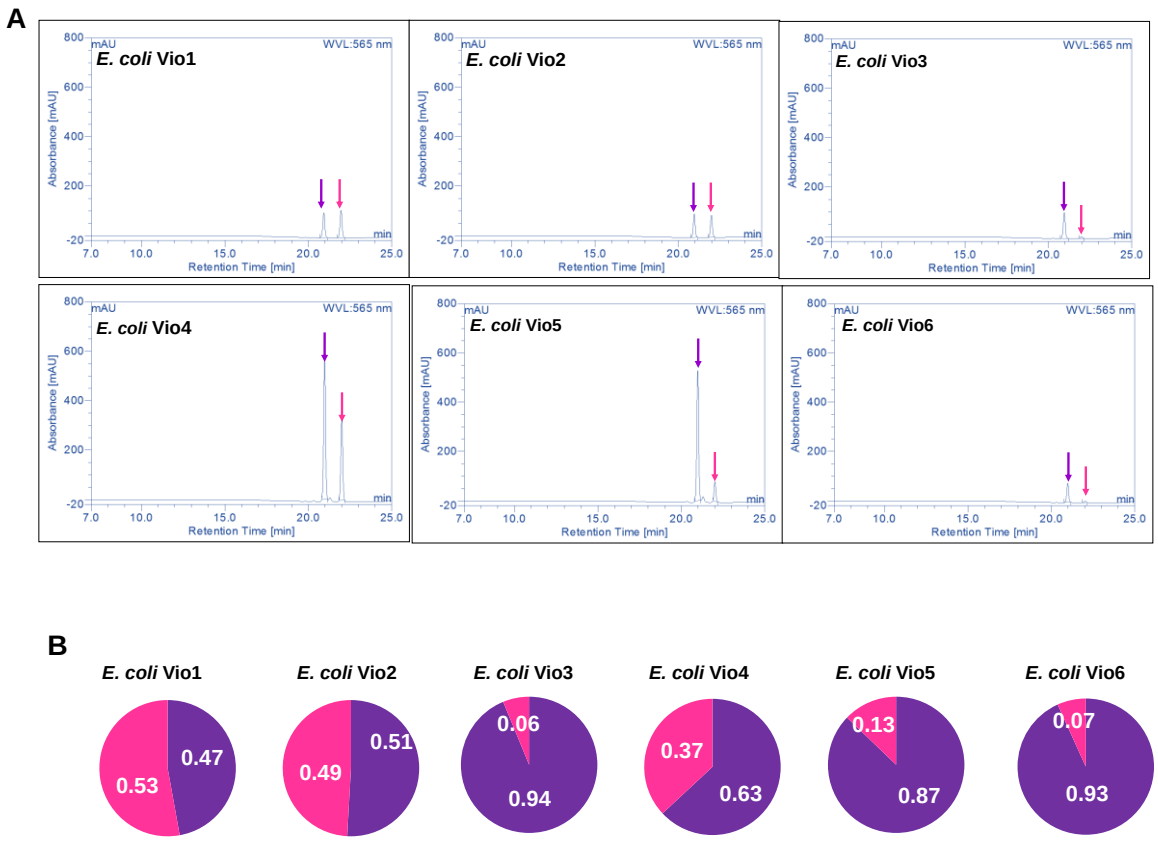


Figure 39: The ratios of violacein (violet) to deoxyviolacein (red) in the final product. (A) HPLC was performed as described in the chapter of Materials and Methods to analyse of the methanol-extracted violacein/deoxyviolacein mixtures produced by *E. coli* Vio1 to *E. coli* Vio6 strains. Fraction peaks of violacein (retention time 21 min) and deoxyviolacein (retention time 22 min) were marked with colored arrows. **(B)** Calaculated violacein and deoxyviolacein ratios in the methanol extracts of the listed six *E. coli* Vio strains

Additionally, the incorporation of Vio enzymes into PCIs was confirmed in strains *E. coli* Vio2-Vio6 by phase contrast microscopy and SDS-PAGE analysis of the insoluble fraction fater cell disruption (Figures 40A and 40B).

These results indicate that the VioA scaffold can organize multiple protein into PCIs *in vivo*. PCIs composed of multiple enzymes may play parts of the roles of organelles, which can bring related enzymes closer to each other and therefore enhance the metabolic flux to desired products.

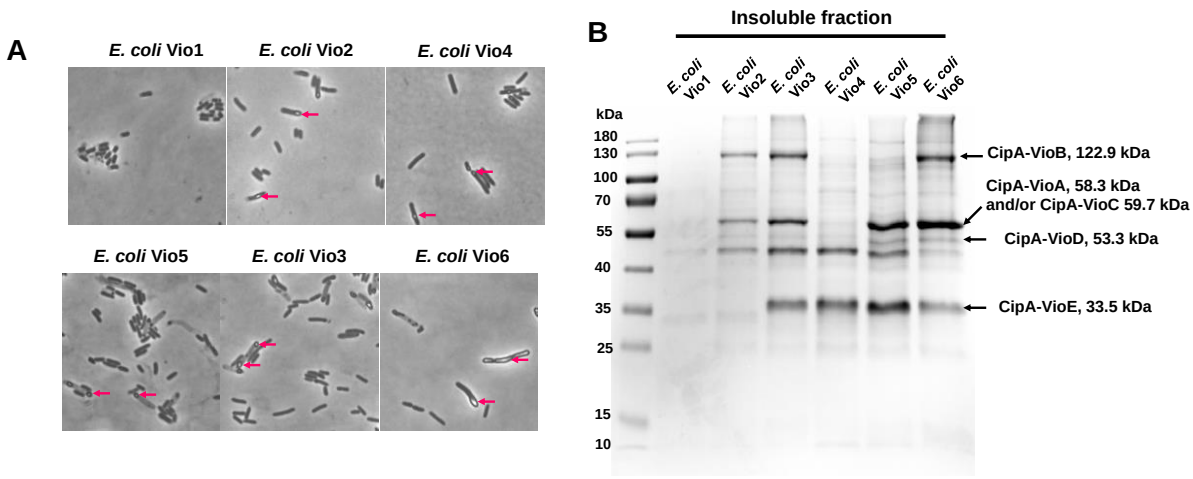


Figure 40: CipA scaffold organizes Vio enzymes into PCIs. (A) Vio enzymes were organized into PCIs (indicated by arrows) by CipA scaffold. Cells were collected at the 32 h time point and analyzed by microscope. Scale bar, 7.5 µm. **(B)** Cells of *E. coli* Vio1 to *E. coli* Vio6 were lysed after 32 h cultivation and insoluble fractions were collected and washed as described in the methods. Equal volumes (25 µL) of washed pellets were loaded on the SDS-PAGE. Gels were stained with Coomassie Brilliant Blue R-250. Arrows mark the Cip-Vio enzymes.

3.4.3 Truncation of Cip scaffolds

Despite native CipA/CipB have good performance in assembling proteins, they are generally much longer comparing to the commonly used protein tags, such as polyhistindine or FLAG octapeptiden tags, which have lengths ranging from six to around fifty amino acids. Therefore experiments were designed to investigate whether Cip scaffolds can be truncated while maintaining the scaffold functionality.

Firstly, the secondary structures of CipA and CipB were predicted with the PSIPRED software (Jones 1999). To protect secondary structures which may be important for the scaffold functionality, the truncation sites were chosen at their predicted loop regions (Figure 41A). The truncated versions of CipA and CipB were designed to be produced from the first methionine of the proteins to the amino acids at the indicated truncation sites (Figure 41A). The truncated Cip scaffolds were designated as CipA*1 [CipA(1-47)], CipA*2 [CipA(1-32)], CipA*3 [CipA(1-23)] and CipB*1 [CipB(1-59)], CipB*2 [CipB(1-33)], CipB*3 [CipB(1-17)], respectively.

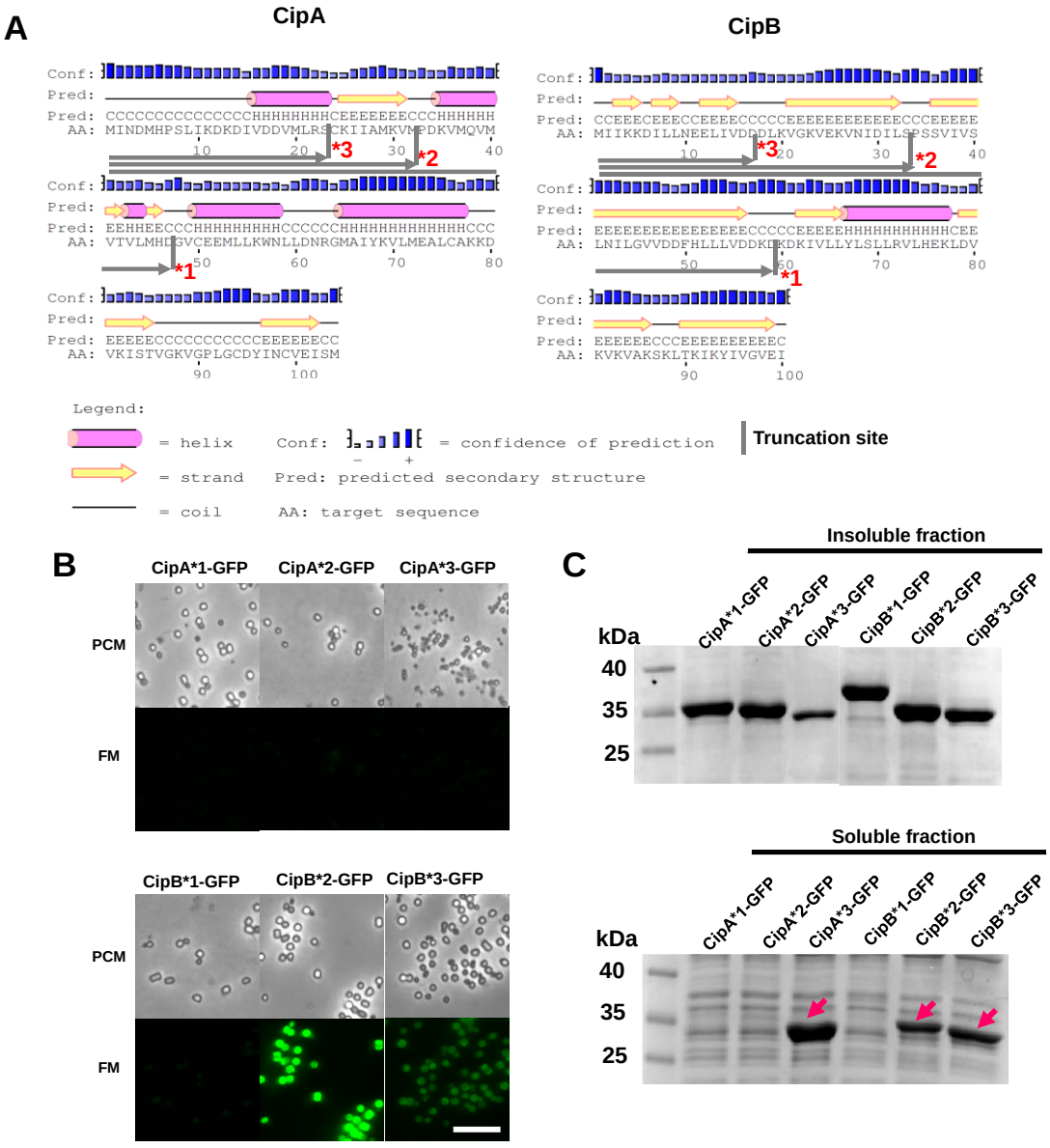


Figure 41: Truncated of Cip scaffolds bring GFP into PCIs. (A) Predicted secondary structures of CipA and CipB. Numbers with red asterisks demonstrate the truncation sites. The truncated scaffolds were produced from the first methionine until the amino acid at the indicated truncation sites. **(B)** Protein hybrids between CipA*1 [CipA(1-47)], CipA*2 [CipA(1-32)], CipA*3 [CipA(1-23)] , CipB*1 [CipB(1-59)], CipB*2 [CipB(1-33)] or CipB*3 [CipB(1-17)] and GFP were separately produced in *E. coli* at 37°C as described in Figure 27. GFP PCIs were isolated as described in (C) and used for microscopy. PCM, phase contrast microscopy; FM, fluorescence microscopy. Scale bar, 7.5 µm. **(C)** Cell producing GFP PCIs were lysed and soluble fractions and insoluble fractions were subsequently separated as described in Figure 7. The insoluble fractions were washed three times and resuspended with Na-phosphate buffer to the same volume of soluble fractions. Equal volume (25 µL) of soluble fractions and insoluble fractions were loaded on SDS-gel, which was stained with Coomassie Brilliant Blue R-250. Arrows mark the bands composed of CipA3*-GFP CipB*2-GFP and CipB*3-GFP, which were detected in both soluble and insoluble fractions.

Protein hybrids between GFP and truncated Cip scaffolds were produced in *E. coli* at 37°C as described in Figure 27. The PCIs were subsequently isolated as described in Figure 7 and inspected under microscope. All the truncated vriants of Cip scaffolds, can support the assembly of GFP into PCIs, even when two of them were truncated to lengths of about 20 amino acids (Figure 41B).

However, the PCIs assembled by the truncated CipB scaffold show very distinct fluorescence intensities, while PCIs assembled by the truncated CipA scaffolds show less differences (Figure 41B). Such kind of difference should be caused by the distinct secondary structurs of CipA and CipB. Both CipB and GFP are rich of β-sheet secondary structures, while CipA mainly composes of α-helix (Yang, Moss et al. 1996). When CipB was truncated, originial interaction between the β-sheets of wild type CipB might be replaced by the intermolecular interaction between the β-sheets of truncated variants of CipB and that of GFP, which in turns, affects the GFP structure and its fluorescence properties.

Moreover, there were large proportions of CipA*3-GFP, CipB*2-GFP and CipB*3-GFP detected in the soluble fraction via SDS-PAGE, indicating the lower assembly efficiencies of the Cip scaffold variants (Figure 41C).

4 Discussion

4.1 The evolutionary analysis of KdpD proteins

4.1.1 Classification of KdpD proteins

Current knowledge on KdpD proteins are mainly based on the research on the Kdp systems of four species: *E. coli*, *S. aureus*, *Synechocystis* sp. strain PCC 6803 and *Anabaena* sp. strain L-31. Since KdpD protein was firstly known from *E. coli* as a histidine kinase (Walderhaug, Polarek et al. 1992), the KdpD proteins identified later from the two cyanobacterial species were therefore named as “truncated” KdpD, due to the missing transmembrane domain and the essential elements of kinase, HiskA and HATPase_c domains. However, it is a bit arbitrary to speculate that KdpD protein ought to be a “*kinase*” and the shorter version of KdpD proteins were just “truncated” (Importantly, in the current study, the “KdpD protein” is defined by the presence of KdpD domain). Moreover, it was demonstrated that the domain architectures of KdpD domain-containing proteins are rather diverse (Figure 11) and, therefore should extend beyond the previously reported “full-length KdpD” of *E. coli* and “truncated KdpD” of *Cyanobacteria* (Ballal and Apte 2005, Ballal, Bramkamp et al. 2005, Ballal, Basu et al. 2007, Nanatani, Shijuku et al. 2015).

Based on the analysis of the sequences of 661 KdpD domain-containing proteins (“KdpD proteins”) described above, they were classified into three groups (Figure 11). The *kinase* KdpD comprise the largest group, with 449 proteins, followed by the *non-kinase* KdpD (206 proteins). The *dysfunctional kinase* group is a very small group with only 6 representatives, and its domain architecture is quite similar to that of the *kinase* KdpD (Figure 11A).

4.1.2 Function of KdpD proteins

Regardless the domain compositions, coordinated distribution of KdpD and KdpA proteins was found in a broad range of bacterial species (Figure 9). This finding suggests the function of KdpD protein is highly related to the Kdp system. However, there are two inevitable questions

regarding to the exact function of KdpD proteins: **(i)** How does *non-kinase* KdpD performs its regulatory role without any signal output domain of either TCS (HisKA and HATPase_c domains) or that of one-component system (*e.g.* HTH domain which can potentially binds to DNA sequences), especially when all the knowledge regarding to the regulation of the Kdp system is transcriptional regulation; **(ii)** Why are bacterial species equipped with KdpD proteins with different domain architectures (Figure 13A).

To answer question one, the assumption is that the *non-kinase* KdpD is an auxiliary protein to the alternative HK^{K+}/RR^{K+}, while KdpD-Usp domain of *kinase* KdpD is an "auxiliary part". There are several evidences in favor of this assumption.

Firstly, according to some reports, the *non-kinase* KdpD is not really essential for the expression of *kdp* operon in response to K^+, at least in two cyanobacterial species (Figure 3) (Ballal and Apte 2008, Nanatani, Shijuku et al. 2015).

Secondly, there are several reports on the "auxiliary" function of the KdpD and/or Usp domains. **(i)** *E. coli* KdpD domain was report to contain a modified of 'Walker-type' ATP-binding site which is able to stabilize the complex formed between the phosphorylated KdpE dimer and the DNA (Jung and Altendorf 1998, Heermann, Altendorf et al. 2003); **(ii)** The Usp domain associated with KdpD proteins is known to mediate different functions in several bacteria. For example, the Usp domain in *E. coli* KdpD is recognized by UspC, which serves a scaffolding function under salt stress (Heermann, Weber et al. 2009). In *Staphylococcus aureus* the Usp domain in KdpD binds c-di-AMP (Moscoso, Schramke et al. 2016).

All these reported functions are based on the presence of the histidine kinase module (HiskA and HATPase_c domains).

To answer question two, it was attempted to identify some relations between the domain architecture of KdpD proteins and the phenotypes, lifestyles or the habitats of host cells, *e.g*. free-living vs. host-associated, potassium-rich vs. potassium-poor habitats, and pathogens vs.

nonpathogens. However, there is no obvious correlation found (Table 6). Different bacterial species also show specific preferences to *kinase* or *non-kinase* KdpD, which further complicates the question (Figure 13C). All in all, there was no evidence detected that the *kinase* and *non-kinase* KdpD are more profitable to the host cells than the other.

Table 6: No correlation was found between the domain architectures of KdpD proteins and host lifestyles

Species	KdpD architecture (form N to C terminus)	Habitat	Virulence/ Pathogenicity
Myxococcus xanthus	KdpD-Usp	soil, decaying plant	no
Synechocystis sp. PCC6803		freshwater, both heterotrophic and photosynthetic	no
Bacteroides fragilis		normal flora of the human colon	causing anaerobic infections
Propionibacterium acnes HL060PA1	KdpD-Usp-DUF4118-X-HiskA-HATPase	commensal of human skin	causing inflammation, acne vulgaris
Streptomyces coelicolor A3(2)		soil, metabolizing other organism's remains	no
Mycobacterium tuberculosis		intracellular pathogens	causing tuberculosis
Escherichia coli K-12	KdpD-Usp-DUF4118-GAF-HiskA-HATPase	commonly found in the lower intestine of warm-blooded organisms	no
Pseudomonas putida F1		found in most soil and water habitats	no
Burkholderia mallei savp1		soil and associating with animals	human and animal pathogen causing glanders

4.1.3 DUF4118 domain containing proteins

The DUF4118 domain, comprising the four transmembrane helices, is crucial for stimulus perception by KdpD, as it includes the binding site for external K^+ in *E. coli* (Zimmann, Steinbrugge et al. 2007, Schramke, Tostevin et al. 2016). Moreover, the DUF4118 domain is certainly important for the function of *kinase* KdpD, since 413 out of 449 *kinase* KdpD contain this domain (Figure 13A). From another angle, there are about ~50% of DUF4118 domains not incorporated into KdpD proteins (Table 4 and Data set-sheet 6). Although DUF4118 domain-containing HK are encoded in the genomes of cyanobacterial species, these bacteria

recruits, nevertheless, 4TM(2TM)-HK^{K+} to regulate the expression of the *kdp* operon (Figure 17).

DUF4118 domain is more versatile than the KdpD domain, and should participate in other signaling activities. For example, some DUF4118 domains were found to be connected to class III nucleotidyl cyclase domains (nucleotidyl_cyc_III superfamily) or phosphohydrolases with a conserved 'HD' motif (HDc) and might play a role in second messenger metabolism (Table 4 and Data set-sheet 6).

4.1.4 Multiple factors contribute to the evolution of KdpD proteins

The evolution of KdpD proteins is a very complicate process. It involves many kinds of evolutionary events such as gene loss or gene drift, duplication, recombination, HGT and nucleotide mutations. Moreover, KdpD proteins do not have uniform evolution scenarios among the investigated bacterial species.

(i) *kdpD* and *kdpA* are undergoing widespread gene drift or gene loss events. The KdpD and KdpA proteins have been detected with widespread existence in bacterial phyla/group [(Data set-sheet 2, 18 out 26 bacterial phyla/group have detected KdpD]. Some bacterial phyla/group have no detected KdpD. This is likely due to their low proteome sampling number in the selected RFP (Data set-sheet 2). However, KdpA and KdpD protein show very low prevalence in the three domains of life (Figure 11). On average about 20% bacterial species have KdpD and KdpA (Figure 11C). These findings suggest that the KdpD and KdpA proteins are undergoing gene drift or gene loss events (see also the following 4.1.5, discussion on the Kdp system of *Firmicutes*)

(ii) Lineage-specific evolution events of KdpD proteins

Lineage-specific evolution events of KdpD proteins have been shown on the following aspects.

Firstly, different bacterial phyla or groups have quite distinct prevalences of KdpD proteins (Figure 11B).

Secondly, different bacterial phyla or groups have different proportions of *kinase*, *dysfunctional kinase* and *non-kinase* KdpD (Figure 11C).

Thirdly, domain architecture of the KdpD proteins are not uniform among the bacteria phyla/group (Figure 13B).

Fourthly, intensive KdpD duplications were detected (including protein duplication and domain duplication) in *Firmicutes* and *Actinobacteria*, but not detected in the other bacterial groups/phyla. The KdpD protein duplication, as *kinase*, occurred after the divergence of *Actinobacteria*, because as observed, the duplicated proteins are clustering into one group (Figures 12 and A2). While KdpD domain duplication in *non-kinase* KdpD proteins should also have occurred after the divergence of *Firmicutes*, because almost all the KdpD with the domain architecture KdpD-Usp-KdpD-Usp were detected in this phylum. Such kind of special structure should be generated via domain duplication of KdpD-Usp.

Fifthly, HGT involves in the evolution of KdpD protein. In addition to the archaeal KdpD (see section 3.1.1), *Firmicutes* KdpD proteins do not form unique phyletic groups (Figure 12) on the protein tree. This should be due to either *kdpD* gene paralogs or HGT. The latter one may be more approaching to the truth. This is because one group of *Firmicutes* KdpD proteins that have close phylogenic relations with *Proteobacteria* KdpD, also show quite similar domain architectures to *Proteobacteria* KdpD (see Figure A2).

(iii) Domain shuffling/recombination mediate the interconversion between *kinase* and *non-kinase* KdpD.

KdpD protein evolution is not only a matter of KdpD domain itself. It is also involves the *DUF4118 domain protein*. As shown in 3.1.4, domain shuffling between Usp and DUF4118

domains clearly supports the interconversion between *kinase* and *non-kinase* KdpD. Focusing on the interconversion of *non-kinase* and *kinase kdpD* genes, one can envisage **(i)** the transformation of a *kinase kdpD* into a *non-kinase kdpD* by gene fission or **(ii)** the converse transition from *non-kinase* to *kinase kdpD* by recombination with a *hk*$^{K+}$ sequence (gene fusion).

Several lines of evidence argue in favor of the predominance of the second route. Firstly, various types of *hk*$^{K+}$ were detected in the genomic vicinity of *non-kinase kdpD* genes, which encode, for example, HK^{K+} with a HAMP and/or a PAS domain [2TM-HAMP-PAS(X)-HK^{K+}] (Figure 15). But corresponding *kinase* KdpD that contained a HAMP or PAS domain were not found (Figure 11A), which could potentially be converted into a *non-kinase* KdpD and HK^{K+} with HAMP and/or PAS domain by fission of its encoding gene. Sencondly, *non-kinase kdpD* genes are always located adjacent to *kdp* operons, but the orientations of *hk*$^{K+}$ and *rr*$^{K+}$ genes and their positions with respect to *non-kinase kdpD* and *kdp* operons vary in different species (Figure A3). This finding suggests that these *hk*$^{K+}$ and *rr*$^{K+}$ do not share the same operon as the *E. coli kdpDE* and may be separately derived from different *hk/rr* pairs via gene duplication and divergence, but not from the fission of *kinase kdpD* genes. Furthermore, as reported by Kummerfeld *et al.*, during the evolution of multidomain proteins, gene fusion events occur four times more often than gene fission events (Kummerfeld and Teichmann 2005).

The results described in 3.1.5 reveal also that three KdpD domains have evolved under strong purifying selection, which demonstrates that the corresponding gene is essential as non-synonymous mutations are rapidly eliminated. In addition, there is clear evidence for several instances of positive selection on branches of the phylogenetic tree where switches from *non-kinase* to *kinase* (or the reverse) must have occurred. Three of the four branches under positive selection are branches leading to *kinase* KdpD (Figure 14), which shows that the switch has occurred in evolution, and consequently this gain of function can confer a selective advantage for bacteria cells.

4.1.5 The most special case--Firmicutes Kdp system

In comparison with other major bacterial phyla (Proteobacteria and *Actinobacteria*), the *Firmicutes* exhibits the greatest diversity of KdpD protein architectures (Figure 11B) but the species of *Firmicutes* are less likely to have KdpD- and KdpA domain-containing proteins (Figure 9B). This phylum has almost equal proportions of the *kinase* and *non-kinase* KdpD proteins (Figure 11C). All these findings indicate that the KdpD proteins of *Firmicutes* have followed a very distinct evolutionary trajectory, and imply that the Kdp-based system of potassium may play a less significant role in this phylum.

For example, it has been reported that deletion of the Kdp transporter encoding operon or the gene of *non-kinase* KdpD protein in *Bacillus cereus* does not affect cell growth under potassium-limited conditions (Mellegard, Kovacs et al. 2011). Moreover, the genome of *B. subtilis* encodes neither a Kdp potassium transporter nor KdpD proteins. In contrast, two Ktr potassium transport systems, KtrAB and KtrCD, have been identified in this species. The membrane-integrated KtrB and KtrD in *B. subtilis*, as well as membrane subunits of the two Trk systems in *E. coli* (TrkH and TrkG), all belong to the TrkH superfamily. They have been detected by the HMMER 3.0 with the HMM model of the TrkH domain and are listed (in green) in Data set-sheet 5. With regard to their affinities for K^+, KtrAB and KtrCD have K_m values of 1 mM and 10 mM (Holtmann, Bakker et al. 2003), while the two Trk systems (Figure 1) in *E. coli* have K_m values of 1 mM or less (Schlosser, Meldorf et al. 1995). This results indicates that *B. subtilis*, as a typical representative of the *Firmicutes*, either has less need for potassium or uses other strategies, such as sporulation or biofilm formation, to cope with K^+ limitation (Grau, de Ona et al. 2015).

4.1.6 Alternative HK^{K+}/RR^{K+} and the *B. fragilis* Kdp system

As have discussed above, the core regulator of the Kdp system should be the kinase module of *kinase* KdpD and the cognate RR (for Kdp system equipped with *kinase* KdpD) or the

HK^{K+}/RR^{K+} (for *Kdp* system equipped with *non-kinase* KdpD). According to this assumption, the genomic neighborhoods of Kdp systems equipped with *non-kinase* KdpD were compared to each other, and in the selected regions some operons which may potentially encode the HK^{K+}/RR^{K+} (Data set-sheet 8 and Figure A3) were found. Their domain architectures were predicted with CDD v3.14 and the transmembrane domain with TMHMM 2.0 (Krogh, Larsson et al. 2001) and DAS (Cserzo, Wallin et al. 1997) (see 2.1.4). The HK^{K+}/RR^{K+} pairs were classified into three groups (Figure 15).

Among the three types of alternative HK^{K+}/RR^{K+}, the third pair (Figure 15) is mostly interesting, which was found mainly in some *Deltaproteobacteria* and *Bacteroidetes*. This is because the RR^{K+} was predicted to be σ^{54} dependent transcriptional activator and the HK^{K+} was predicted to have two transmembrane helices (DUF4118 domain has four transmembrane helices) (Figures 15, A3A, and Data set-sheet 8). The σ^{54} factor differs in sequence and structure from that of σ^{70} family sigma factors (Lonetto, Gribskov et al. 1992, Gruber and Gross 2003).

The *B. fragilis* was chosen as the object to study on the σ^{54} -dependent *kdp* operon, because **(i)** It associates mutually with humans and other mammals, as an opportunistic pathogen, while Kdp system has been found to integrate K^+ homeostasis and virulence (Freeman, Dorus et al. 2013); **(ii)** It lives in a potassium rich niche, but preserves the low potassium response system.

Here, preliminary studies were performed to characterize the *B. fragilis* Kdp system. The expression of *B. fragilis kdp* operon was confirmed to be in response to low K^+ (Figure 16). The K^+ limitation faced by this bacterium may be caused by the formation of biofilms, which is mainly made of multiple layers of *Firmicutes*, *Bacteroidetes*, *Proteobacteria* in the large intestine (Jandhyala, Talukdar et al. 2015, Johnson, Dejea et al. 2015). *B. fragilis* Kdp system recruits σ^{54} factor transcriptional activator as the RR^{K+} may indicate tighter transcriptional regulation. *E. coli* reporter assay gives some evidences that the predicted HK^{K+}/RR^{K+} should invovle in the regulation of *B. fragilis kdp* operon, because the expression of hk^{K+}/rr^{K+} increase

the expression level of the reporter gene *lac*Z (Figure 18). But more straightforward experiments like deletion of related genes (see Figure 16) are certainly required.

4.2 Structural analysis of KdpD proteins

There are generally three common methods which have been used for the determination of protein structures.

(i) Nuclear magnetic resonance (NMR) spectroscopy can determine the structure of small proteins in the solutions or that of membrane proteins in lipid bilayers or detergent micelles (as described above for the structure determination of the DUF4118 domain). Analyzing protein structure with NMR does not require protein crystallization and could detect the conformational changes of proteins. However, application of NMR is limited by upper molecular size (protein molecules should be smaller than 30 kDa. Membrane protein dissolved in detergent micelles should be even smaller) and low resolutions.

(ii) Reconstruction of the protein structure of protein complexes with single-particle cryo-EM has recently attracted very intensive attention. It is considered to be a very promising method for protein structural analysis (Vinothkumar 2015, Doerr 2016, Skiniotis and Southworth 2016, Frank 2017). In the past few years, this method has been being steadily improved. It enables successful reconstruction of the structure of enzyme complexes, virus particles, ribosomes, ion channels with “large, fragile, or flexible structures” to near-atomic resolution (Scheiner 2015). Protein samples ould be treated with negative staining or cryogenic freezing, and as designated by the name, no protein crystallizition is needed. However, careful preparation of samples is required to keep them homogeneous in solutions. Moreover, the size of the molecule should be larger than 150 kDa (Thompson, Walker et al. 2016).

Smaller membrane protein may be embedded into liposomes or nanodiscs. The later one is a self-assembled discoidal particle composed of lipid bilayers surrounded with membrane

protein scaffold (MSP) as the belts. Nanodiscs are soluble in aqueous solutions, with a diameter of 8–16 nm (depends on the lenth of MSP and the inserted protein size) and therefore can afford the native environment for the membrane proteins and assistant particle recognition during cryo-EM (Denisov and Sligar 2016). Assembly of the nanodiscs is an automatic process (Bayburt, Grinkova et al. 2002, Denisov, Grinkova et al. 2004).

(ii) X-ray crystallography has been the most prevalent strategy of protein structure determination. It requires protein crystallization, which is always a big obstacle, especially for membrane protein. Proteins integrated into the membrane have very hydrophobic surfaces and very flexible conformations (Carpenter, Beis et al. 2008). There are actually challenges at almost every step before coming to the crystallization of membrane proteins, such as low production, instability, aggregation. Membrane proteins can be extracted from the membrane lipid with detergent into aqueous solutions for the purpose of crystallization. Meanwhile, there are also other careful designs to promote the crystallization of membrane proteins, such as fusing soluble protein to stabilize transmembrane domain loop and increase solubility (Chun, Thompson et al. 2012).

The biggest obstacle of crystallizing KdpD lays at the hydrophobic feature of these proteins. On one hand, the DUF4118 domain is entirely embedded into the lipid bilayers. On the other hand the natively occurring *non-kinase* KdpD composed of KdpD and Usp domains, even containing no transmembrane helix, shows high affinity to the cytoplasmic membrane (Figure 22). It has also been shown that the KdpD-Usp domain can make the GFP protein approach to the cytoplasmic membrane (Maier, Hubich et al. 2008) .

The topology of the *kinase* KdpD was speculated in Figure 42 (Jung, Tjaden et al. 1997). The stress signal acting on membrane may be perceived via tight interaction between KdpD-Usp and the cell membrane. Crystallization of proteins does not only requires the sample to be pure but also must be homogenous and stable. The hydrophobicity of KdpD proteins makes their

molecules very aggregation-prone, and accordingly the precipitation during crystallization setups of KdpD-R511Q. Artificial design was aimed to promote the asymmetry of *kinase* KdpD via inserting the WrbA protein to the first periplasm loop of the DUF4118 domain. It, nevertheless, causes the accumulation of truncated proteins (Figure 21). The introduction of WrbA may interrupt the insertion of the transmembrane helices and therefore causes premature translation termination. All in all, crystallography does not seem to be the proper way to resolve the KdpD structure.

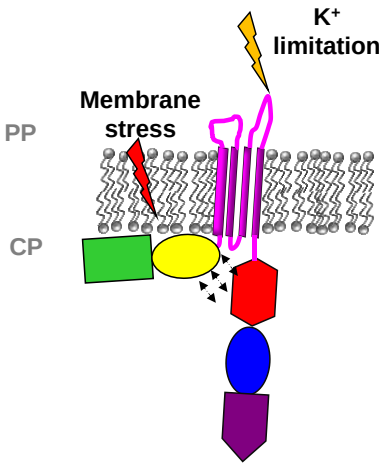


Figure 42: Assumed topology of the *kinase* KdpD basing on its hydrophobicity. KdpD and Usp domains have very high affinity to the cytoplasmic membranes. The interaction between KdpD-Usp and lipid bilayer may make the convergence of membrane stress to the kinase module. While the secondary periplasmic loop is known for sening K^+ limitation. PP: periplasm, CP: cytoplasm.

Single particle cryo-EM seems to be a quite promising practice to solve the structure of *kinase* KdpD. The functional form of *kinase* KdpD is a dimer with a molecular weight of ~200 kDa (Heermann, Altendorf et al. 1998), while the lower limit protein (complexes) size of protein cryo-EM at current stage is about 150 kDa (Thompson, Walker et al. 2016). If the dimer could be successfully assembled into nanodiscs, there is good reason to expect that the structure of *kinase* KdpD could be solved by cryo-EM. Since time was limited, only very preliminary trials were performed to assemble KdpD protein into nanodiscs (Figure 23). Further experiments are required to check the assembly is successful. Moreover, intensive optimization of the KdpD,

MSP and lipid stoichiometric ratios is certainly required, to make sure that the samples are homogeneous.

4.3 The biotechnological application of Cip scaffolds

4.3.1 Protein subcellular structures

Proteins can be natively organized *in vivo* into various structures with different biological functions. Their formation are under tight regulations of cells' demands. For example in some autotrophic bacteria like *Phormidium uncinatum* and *Halothiobacillus neapolitanus*, their predominant enzymes catalyzing carbon fixation --ribulose-1,5-biphosphate carboxylase and the oxygenase -- can form polyhedral protein inclusions, known as carboxysome (Tsai, Sawaya et al. 2007, Yeates, Kerfeld et al. 2008). In order to get buoyancy, some planktonic microorganism produce proteins such as GvpA and GvpC which can assemble together into gas vesicles (Pfeifer 2012). Cry and Cyt proteins of *Bacillus thuringiensis* can assemble into parasporal crystalline inclusion, commonly known as Bt crystals, which have pesticidal activities (Agaisse and Lereclus 1995, Schnepf, Crickmore et al. 1998, Parker and Feil 2005, Bravo, Gill et al. 2007).

4.3.2 The CipA and CipB proteins

CipA and CipB are short proteins with respectively 104 and 100 amino acids and they also assemble into two distinct types of crystalline inclusions with polyhedral configurations in the primary cells of entomopathogenic *Photorhabdus luminescens*. The formation of CipA and CipB crystalline inclusion production is tightly regulated by the native host cell (Bintrim and Ensign 1998, Bowen and Ensign 2001, Heermann and Fuchs 2008). Besides, the sister genus of *Photorhabdus*, *Xenorhabdus nematophila* also produce two types of crystalline inclusions named IP1 (methionine-rich PixA inclusion with 185 amino acids and encoded by *pixA*) and IP2 (encoded by uncharacterized gene) (Couche and Gregson 1987). The common feature of CipA, CipB and PixA is that they all have high percentage of (~50%) hydrophobic amino acids.

In contrast to the Bt crystals and the carboxysome, the functions of crystalline inclusions produced in *Photorhabdus* and *Xenorhabdus* remain ambiguous (Goetsch, Owen et al. 2006, Goodrich-Blair and Clarke 2007).

The formation of CipA, CipB, and PixA might be also driven by hydrophobic amino acid, but this is different from the formation of protein inclusion bodies. The formation of the PCIs in the native producer *P. luminescens* are tightly regulated, while the formation of protein inclusion bodies are generally out of the control of the producer. As described, at lower temperature of 20 °C, the organization of CipA-GFP and CipB-GFP as non-refractile protein complexes were still visibile (Figure 28), and they can be disassembled by mechanical cell disruption into soluble proteins (Figure 32). This result suggests the proteins are correctly folded and the organization process of the proteins is not caused by the mis-folding of the proteins, but due to the scaffold function of CipA and CipB. Additionally, Congo Red absorption spectra shift assay has shown that the LacZ PCIs do not have the enriched β-sheet structure, which is commonly found in protein inclusion bodies.

4.3.3 *In vitro* application of Cip scaffolds

By hybridizing the reporter GFP to Cip, it was found that the assembled complexes could be compact crystalline inclusion or loose textures (Figures 27 and 28). The isolation of the PCIs complexes is effortless and can be finished within 2-3 hours (Figures 7 and 43).

Genearlly, it is important to improve the solubility of recombinant proteins in some applications. On the opposite, there are also significant efforts being spent on decreasing the solubility of a protein, like immobilizing enzymes, which also has very practical importance such as enhancing stability of the enzyme during catalysis and simplifying the recovery & reusing of the enzymes at the downstream processing (Mohamad, Marzuki et al. 2015). Cip scaffolds can immbolize enzymes in to PCIs. Moreover this process can be carried out *in vivo* by the cells. As have been shown that CipA-LacZ and CipB-LacZ PCIs are more thermal resistant that the

soluble His-LacZ (Figure 34). Moreover, these PCIs can be recovered by centrifugation for recycling. These advantages are very useful for practical applications.

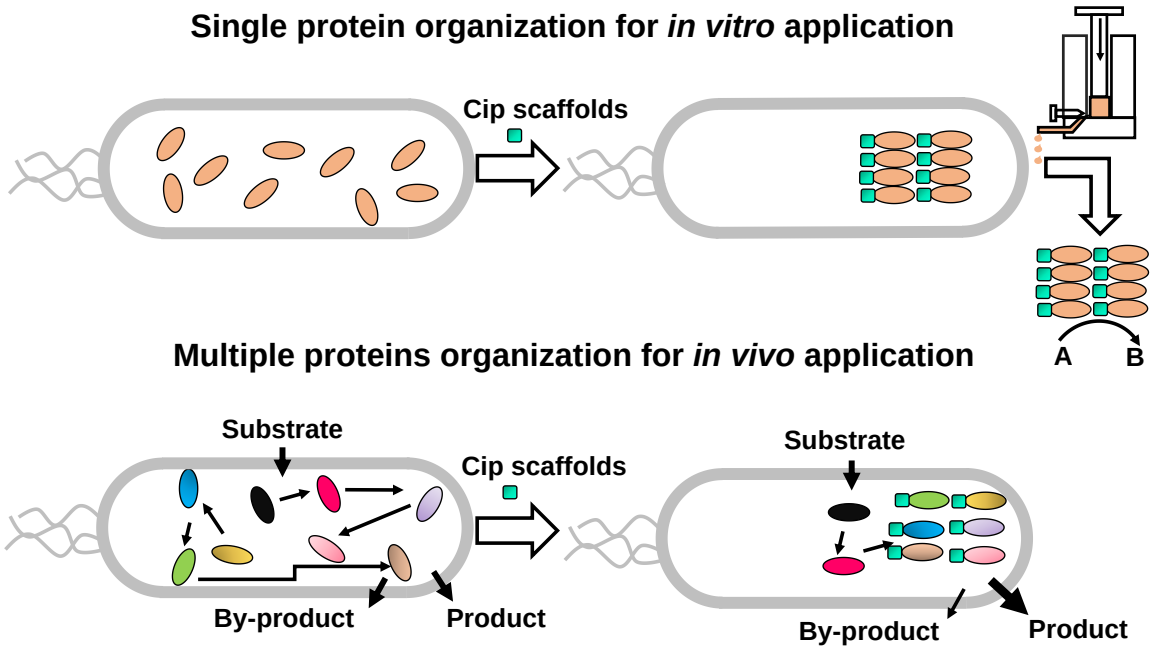


Figure 43: Schematic of *in vitro* and *in vivo* applications of Cip scaffolds. For *in vitro* applications PCIs can be isolated easily after cell disruptions. For *in vivo* applications multiple enzymes could be brought closer to each to promote the rapid conversion of unstable intermediates and therefore increase the production of desired products.

4.3.4 *In vivo* application of Cip scaffolds

For *in vivo* applications, the use of Cip scaffolds enables flexible organization of multiple enzymes into complexes (Figure 43). Such kind of complexes are not aimed for isolation and *in vitro* catalysis application. Therefore, they do not have to be in the PCIs state (see the GFP complexes form at 20 ºC, Figure 28). The multiple enzyme complexes may be considered as a kind of no-membrane-bound organelles, which can bring multiple enzymes spatically closer to each other. This can help to speed up the conversion of unstable intermediates and avoid the unwanted diffusion of toxic metabolites (Dueber, Wu et al. 2009, Yadav, De Mey et al. 2012, Proschel, Detsch et al. 2015).

As shown here for violacein biosynthesis, bringing the multiple Vio enzymes together via CipA has improved the overall yield of the desired product and reduced side-product accumulation (Figures 38 and 39). This holds significant importance in the field of synthetic biology and metabolic engineering.

Cip scaffolds can organize proteins into PCIs with versatile applications. The resulting protein complexes can **(i)** retain the original enzyme activities, **(ii)** remain stable during product synthesis, **(iii)** and can be easily isolated for *in vitro* applications or be capable of organizing multiple proteins for *in vivo* usages.

5 Summary

KdpD/KdpE is a pair of histidine kinase/response regulator (HK/RR) systems sensing K^+ limitation and mediating intracellular K^+ homeostasis. The KdpD of *Escherichia coli* is a multi-domain membrane protein with an unusual cytosolic N-terminal region, which contains a unique KdpD domain. KdpE controls expression of the high-affinity K^+ uptake system KdpFABC. In this work, all proteins containing the special KdpD domain were collected as KdpD proteins. According to the domain architectures, KdpD proteins were classified into *kinase*, *non-kinase* and *dysfunctional kinase*, which do not distribute uniformly among bacterial phyla. Lineage-specific evolutionary events such as *kdpD* gene duplication and intensive horizontal gene transfer were detected. Besides, domain shuffling and selective pressure on nucleotide sequences were found to promote the interconversion between the *kinase* and *non-kinase* KdpD.

The investigation of the genomic contexts of *non-kinase kdpD* genes in different bacteria revealed several types of alternative HK and RR, designated as alternative HK^{K+}/ RR^{K+}, which might regulate induction of the *kdp* operon in response to K^+ limitation. Some of the alternative RR^{K+} were predicted to be σ^{54}-dependent transcriptional activators. To confirm the prediction, the K^+ responsive elements of the Kdp system of *Bacteroides fragilis* were investigated.

Several approaches were used to determine the structure of *kinase* or *non-kinase* KdpD proteins via crystallography, but no promising results were obtained. A protocol was established to incorporate the *kinase* KdpD into nanodiscs as prerequisite for single particle cryo-EM.

CipA and CipB are two small proteins that form protein crystalline inclusions (PCIs) in the cytoplasm of *Photorhabdus luminescens*. CipA and CipB were originally developed as Cip scaffolds to organize proteins, such as *non-kinase* KdpD, into PCIs for the purpose of crystallography. However, most of the obtained PCIs did not show a diffraction signal.

Therefore, the biotechnological application potential of Cip scaffolds was evaluated in *E. coli*. On the one hand proteins such as LacZ, could be incorporated into PCIs and readily isolated for *in vitro* applications, because the PCIs are insoluble in water and resistant to high temperature. On the other hand, Cip scaffolds could organize multiple enzymes into functional complexes *in vivo* and are therefore useful tools for metabolic engineering, as revealed by improving the production of violacein.

6 Zusammenfassung

Das aus Histidinkinase und Antwortregulator (histidine kinase HK/respones regulator RR) bestehende Zweikomponentensystem KdpD/KdpE reagiert auf K+ Limitierung und vermittelt durch eine Signaltransduktion eine intrazelluläre K+ Homöostase. Das *Escherichia coli* KdpD ist ein Multidomänen-Membranprotein mit einer ungewöhnlichen N-terminalen Region, die eine besondere KdpD Domäne enthält. KdpE reguliert die Expression des hochaffinen K+ Aufnahmesystems KdpFABC.

In dieser Arbeit wurden alle Proteine mit KdpD Domäne als KdpD Proteine zusammengefasst. Entsprechend ihrer Domänenarchitektur wurden KdpD Proteine in Kinasen, Nicht-Kinasen und dysfunktionale Kinasen eingeteilt, wobei die drei Gruppen nicht gleichmäßig innerhalb der Bakterienphyla verteilt sind. Es konnten verschiedene linienspezifische, evolutionäre Ereignisse, wie *kdpD* Genduplikation und häufiger horizontaler Gentransfer, nachgewiesen werden. Zudem wurde gezeigt, dass Domänenverschiebungen (*domain shuffling*) und Selektionsdruck auf Nukleotidsequenzen eine Umwandlung zwischen Kinasen und Nicht-Kinasen KdpD begünstigt. Durch eine Analyse des genomischen Kontextes von Nicht-Kinasen *kdpD* Genen in verschiedenen Bakterien wurden mehrere Arten von alternativen HK und RR entdeckt, die als alternative HK^{K+}/ RR^{K+} bezeichnet wurden und die möglicherweise die Induktion des *kdp* Operons als Antwort auf K^+ Limitierung regulieren. Einige der alternativen RR^{K+} wurden vorhergesagt, σ^{54}-abhängige Transkriptionsfaktoren zu sein. Um diese Vorhersage zu überprüfen, wurden K^+ sensitive Elemente des Kdp Systems von *Bacteroides fragilis* näher untersucht.

Um die Struktur der Kinasen oder Nicht-Kinasen KdpD Proteine mittels Kristallographie zu ermitteln wurden verschiedene Methoden angewendet, es konnte jedoch kein vielversprechendes Ergebnis erzielt werden. Aus diesem Grund wurde ein Protokoll entwickelt, um Kinasen KdpD für eine Cryo-EM in Nanodiscs einzuschließen.

CipA und CipB sind zwei niedermolekulare Proteine, die kristalline Proteineinschlüsse (protein crystalline inclusions, PCI) im Cytoplasma von *Photorhabdus luminescens* bilden. CipA und CipB wurden anfangs als Gerüst verwendet, um Proteine wie Nichtkinasen KdpD für die Kristallographie in PCIs zu organisieren. Die Mehrzahl der nachgewiesenen PCIs zeigte jedoch kein Beugungssignal.

Deshalb wurde das generelle biotechnologische Anwendungspotential von Cip Gerüsten in *E. coli* evaluiert. Auf der einen Seite konnten Proteine wie LacZ in PCIs eingeschlossen werden und *in vitro* isoliert werden, da PCIs wasserunlöslich und unempfindlich gegenüber hohen Temperaturen sind. Auf der anderen Seite konnte am Beispiel von Violacein gezeigt werden, dass es möglich ist, verschiedene Enzyme mit Hilfe von Cip Gerüste in funktionale Komplexe zu organisieren. Dies macht Cip Gerüste zu einem nützlichen Werkzeug für die Konstruktion metabolischer Prozesse (*metabolic engineering*).

7 Literature

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8 Appendix

The appendix contains the following files and has been provided in the attached compact disc.

Figure A1: Archaeal *kdp* operon compositions. All *kdpD* genes (yellow colored arrows marked with “kdpD”) encode KdpD proteins with the domain architecture of KdpD-Usp-DU4118-GAF. HP, hypothetic protein, Usp-X, Usp-domain connecting with unpredicted domain.

Figure A2: KdpD-Usp protein tree with assigned KdpD domain architectures. This is supplementary to Figure 12 with additionally included KdpD domain architectures, protein IDs (in bracket) as well as species names. For branch color, blue: *kinase*, yellow: *dysfunctional kinase*, green: *non-kinase*. Proteins with domain architecture of KdpD-Usp-KdpD-Usp have two branches, because of two copies of “KdpD-Usp” (see the reason in Figure 11A) and the selected part for MSA is colored, while the other part is grey. Curves connecting KdpD proteins belong to the same species.

Figure A3: Genomic neighborhoods of some *non-kinase kdpD* genes. (A) Genomic neighborhoods of *non-kinase kdpD* genes encoding KdpD proteins with the domain architecture KdpD-Usp (yellow arrows marked “kdpD”) or KdpD-Usp-KdpD-Usp (yellow-green arrows marked “kdpD”). **(B)** Genomic neighborhoods of *non-kinase kdpD* genes encoding KdpD proteins with the domain architecture KdpD-Usp-DUF4118-GAF (yellow arrows marked “kdpD”) or KdpD-Usp-DUF4118 (yellow-green arrows marked “kdpD”). The genes encoding HK^{K+} and RR^{K+} are depicted as different colored arrows marked “hk” and “rr” or “sigma 54-related rr”, respectively. Domain architectures of corresponding HK^{K+} are also included (the “X” stands for an unpredicted domain). HP, hypothetical protein; OMP, outer membrane porin.

Data set:

Content of the appendix data set (including 9 sheets)	
Sheet Name	**Description**
Sheet 1	List of proteome IDs and taxon in the RFP
Sheet 2	Bacterial groups/phyla with KdpD protein(s)
Sheet 3	All KdpD proteins retrieved from the RFP
Sheet 4	All KdpA proteins retrieved from the RFP
Sheet 5	All TrkH proteins retrieved from the RFP
Sheet 6	All DUF4118 proteins retrieved from the RFP
Sheet 7	Taxonomy information of 216 KdpD proteins used for selection pressure analysis in Figure 14
Sheet 8	HK^{K+} and RR^{K+} of *non-kinase* KdpD
Sheet 9	σ^{54}-recognition motif detected in the *kdp* promoter in some *Bacteroidetes/Chlorobi* group and *Deltaproteobacteria*

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感谢我的家人和我的爱人对我无时无刻的支持与鼓励。

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EDUCATION

Ph.D, Microbiology, Department of Biology I. LMU Munich. Martinsried, Germany. Expected, *May 2017.*

Dissertation: "Evolutionary and Structural Analysis of KdpD Proteins". *Advisor:* Prof. Dr. Kirsten Jung

M.A., Shandong University. Ji'nan, China. Metabolic Engineering and Synthetic Biology, State Key Laboratory of Microbial Technology. *July 2012.*

Thesis: "Metabolic Engineering of *Escherichia coli* and *Corynebacterium glutamicum* for Efficient Production of 5-Aminolevulinic Acid" (In Chinese). *Advisor:* Prof. Dr. Qingsheng Qi

B.S., Microbiology and Bioengineering, School of Life Science. Shandong Agricultural University. Tai'an, China. *July 2009.*

RESEARCH EXPERIENCE

2012.9-2017.3 Bioinformatics analysis the evolution history of KdpD proteins.

2015.12-2017.3 Characterization of the K^+- responding Kdp system of *Bacteroides fragilis*.

2012.9-2015.12 Structural analysis of KdpD proteins via protein crystallization and single particle cryo-EM.

2013.6-2014.12 Development of scaffold for organizing single or multiple proteins into *in vivo* protein crystalline inclusions for biotechnological applications.

2009.9-2012.7 Metabolic engineering of *Escherichia coli* and *Corynebacterium glutamicum* for high level production of 5-aminolevulinic acid or N-acetylneuraminic acid.

FELLOWSHIPS AND AWARDS

China Scholarship, 2012-2016

Guanghua scholarship, Shandong University, 2011

National Inspirational Scholarship, Shandong Agricultural University 2008

National Inspirational Scholarship, Shandong Agricultural University 2007

PUBLICATIONS

Select peer-reviewed articles

1. Classification and evolutionary analysis of KdpD proteins. **Yang Wang**, Noémie Becker, Sonja Grath, Ileana Sáenz Soto, Dirk Metzler, Kirsten Jung. (In submission)
2. CipA and CipB as scaffolds to organize proteins into crystalline inclusions. **Yang Wang,** Ralf Heermann, Kirsten Jung. *ACS Synthetic Biology*. 2017 Feb 10. doi: 10.1021/acssynbio.6b00323. [Epub ahead of print]
3. Constitutive expression of RyhB regulates the heme biosynthesis pathway and increases the 5-aminolevulinic acid accumulation in *Escherichia col.* Fangfang Li, **Yang Wang**, Kai Gong, Qian Wang, Quanfeng Liang and Qingsheng Qi. *FEMS Microbiology Letters*. 2014 Jan;350(2):209-15
4. Engineering of an N-acetylneuraminic acid synthetic pathway in *Escherichia coli*. Junhua Kanga, Pengfei Gu, **Yang Wang**, Yikui Li, Fan Yang, Qian Wang, Qingsheng Qi. *Metabolic Engineering*. 2012 Nov;14(6):623-9
5. Metabolic engineering to improve 5-aminolevulinic acid production. Zhen Kang, **Yang Wang**, Qiang Wang , Qingsheng Qi. *Bioengineered*. 2011 Nov-Dec;2(6):342-5.
6. Engineering *Escherichia coli* for efficient production of 5-aminolevulinic acid from glucose. Zhen Kang, **Yang Wang**, Pengfei Gu, Qian Wang, Qingsheng Qi. *Metabolic Engineering*. 2011 Sep;13(5):492-8.

Book chapter

Hannah Schramke, **Yang Wang**, Ralf Heermann and Kirsten Jung. Stimulus perception by histidine kinases. 2016. *In* Stress and environmental regulation of gene expression and adaptation in bacteria (pp 282–300). Frans J. de Bruijn (Ed). John Wiley & Sons, Inc publisher.

Patents

1. **Yang Wang**, Ralf Heermann and Kirsten Jung. CipA, CipB and PixA as scaffolds to organize proteins into crystalline inclusions. 2016. Application Number EP 16202046.5

2. Qingsheng Qi, Zhen Kang, **Yang Wang**, Qian Wang. Recombinant *E. coli* and use thereof in producing 5-aminolevulinic acid. 2012. Pub. No.: WO/2012/129748

ATTENDED CONFERENCES

15-16 September 2016. CIPSM Fest of Chemical Biology 2016. Martinsried, Germany.

13-16 March 2016. Annual Conference 2016 of the Association for General and Applied Microbiology (VAAM 2016). Jena, Germany

14 November 2014. Synthetic biology workshop: Application of Synthetic Biology in Medicine. Munich, Germany.

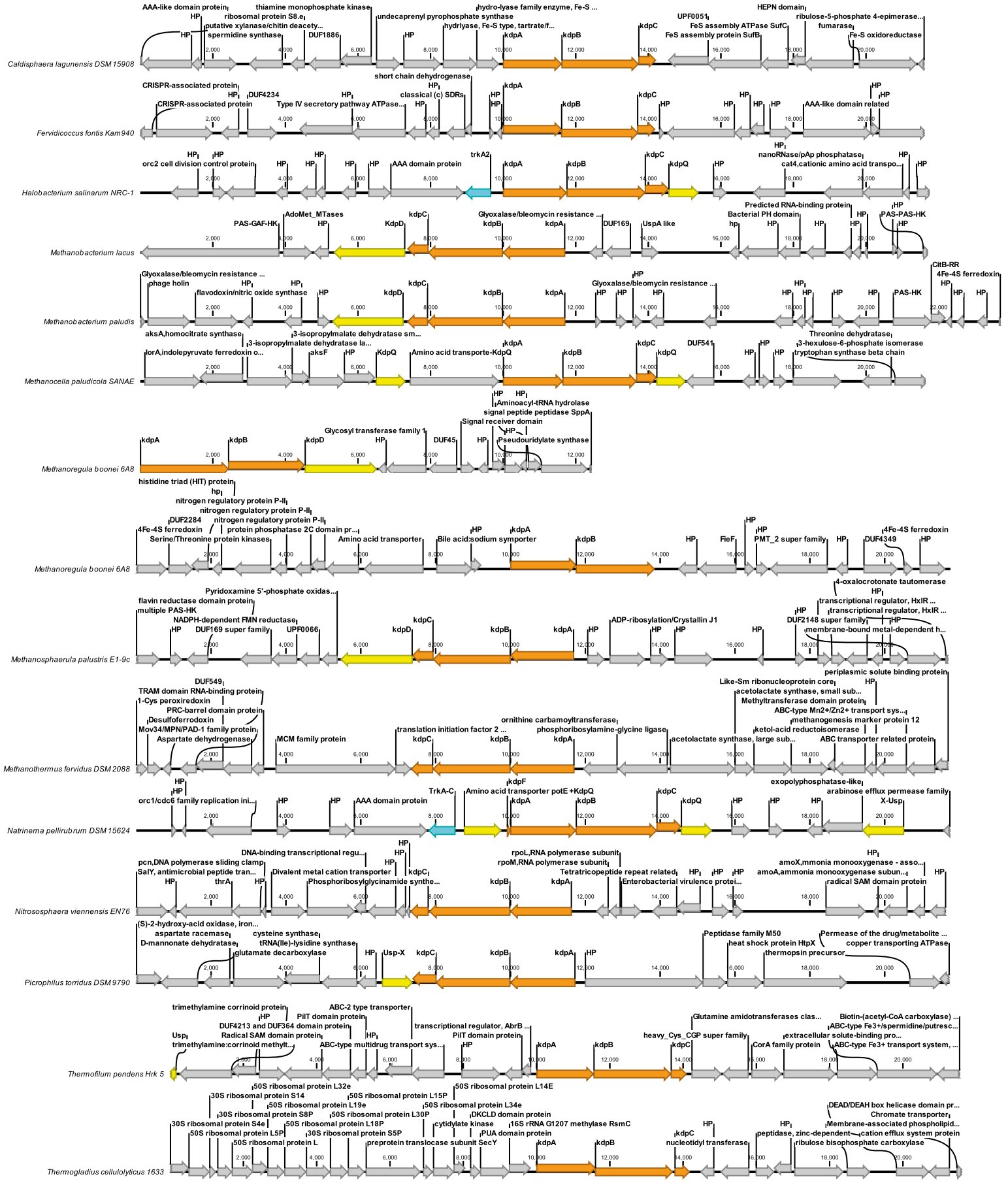


Figure A1 Page 1

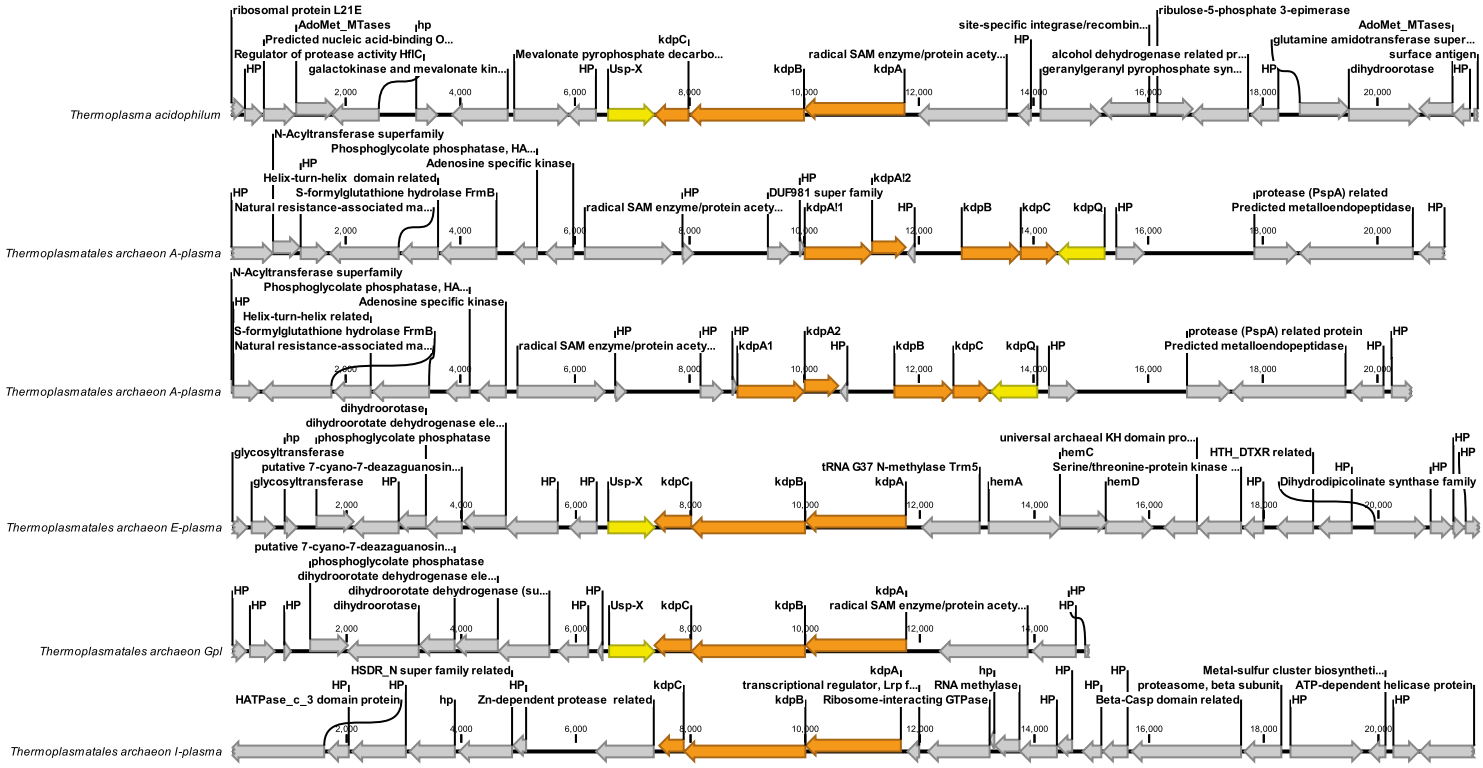


Figure A1 Archaeal *kdp* operons. All *kdpD* genes (yellow arrows) encode KdpD proteins with the domain architecture KdpD-Usp-DU4118-GAF. *kdpQ* genes encode proteins with domain architecture of Usp-Usp. Usp-X, Usp-domain linked to an unpredicted domain. HP, hypothetical protein.

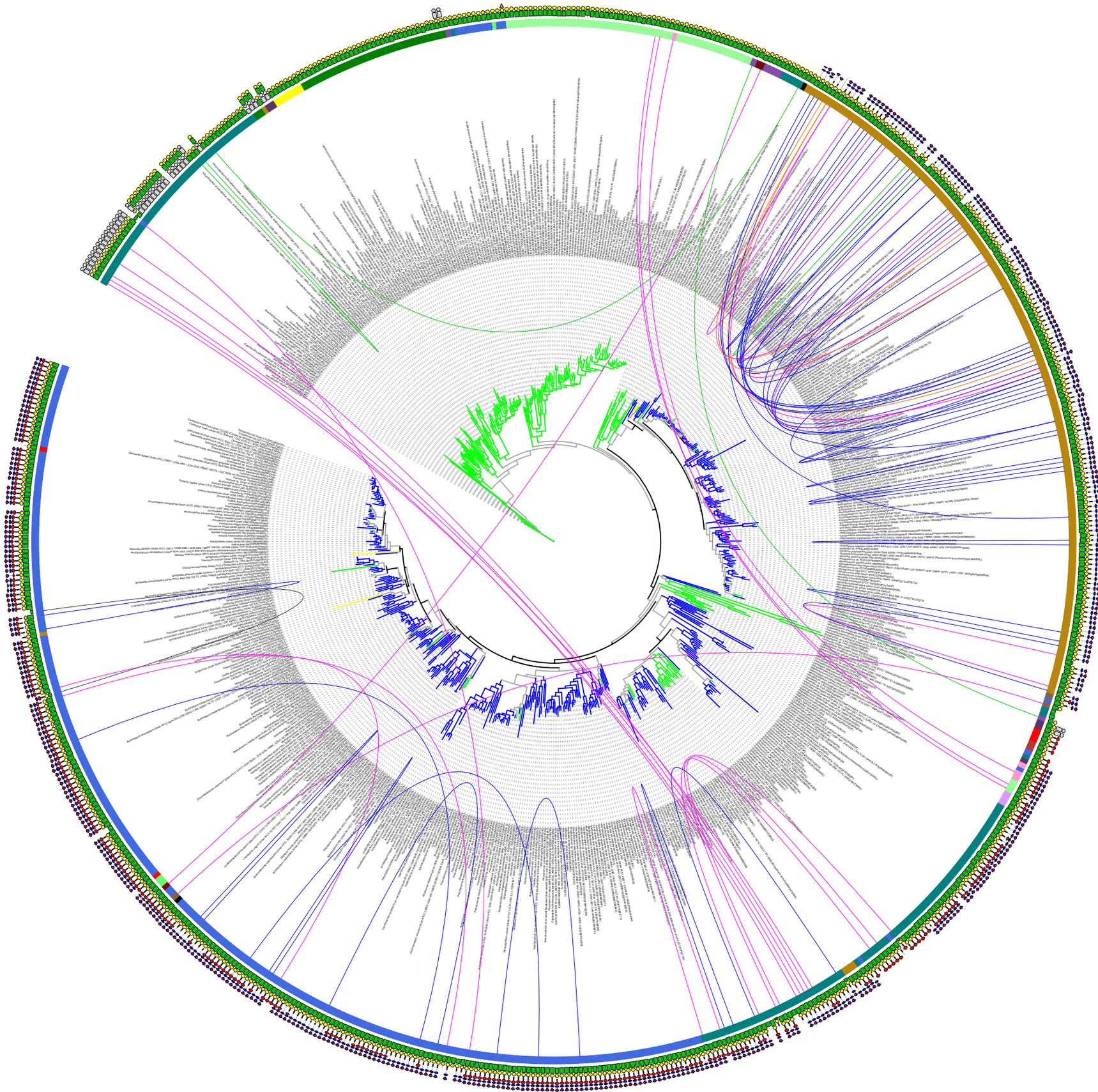
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Phylum/Group/Kingdom

- Actinobacteria
- Aquificae
- Archaea/Eukaryota
- Armatimonadetes
- Bacteroidetes/Chlorobi
- Chlamydiae/Verrucomicrobia
- Chloroflexi
- Cyanobacteria
- Deinococcus-Thermus
- Fibrobacteres/Acidobacteriagroup
- Firmicutes
- Gemmatimonadetes
- Nitrospirae
- Planctomycetes
- Proteobacteria
- Spirochaetes
- Tenericutes
- Unclassified-Bacteria

Protein domain symbol

- KdpD-domain
- Usp-domain
- DUF4118-domain
- GAF-domain
- HisKA-domain
- HATPase_c-domain
- PTS_EIIA_2-domain



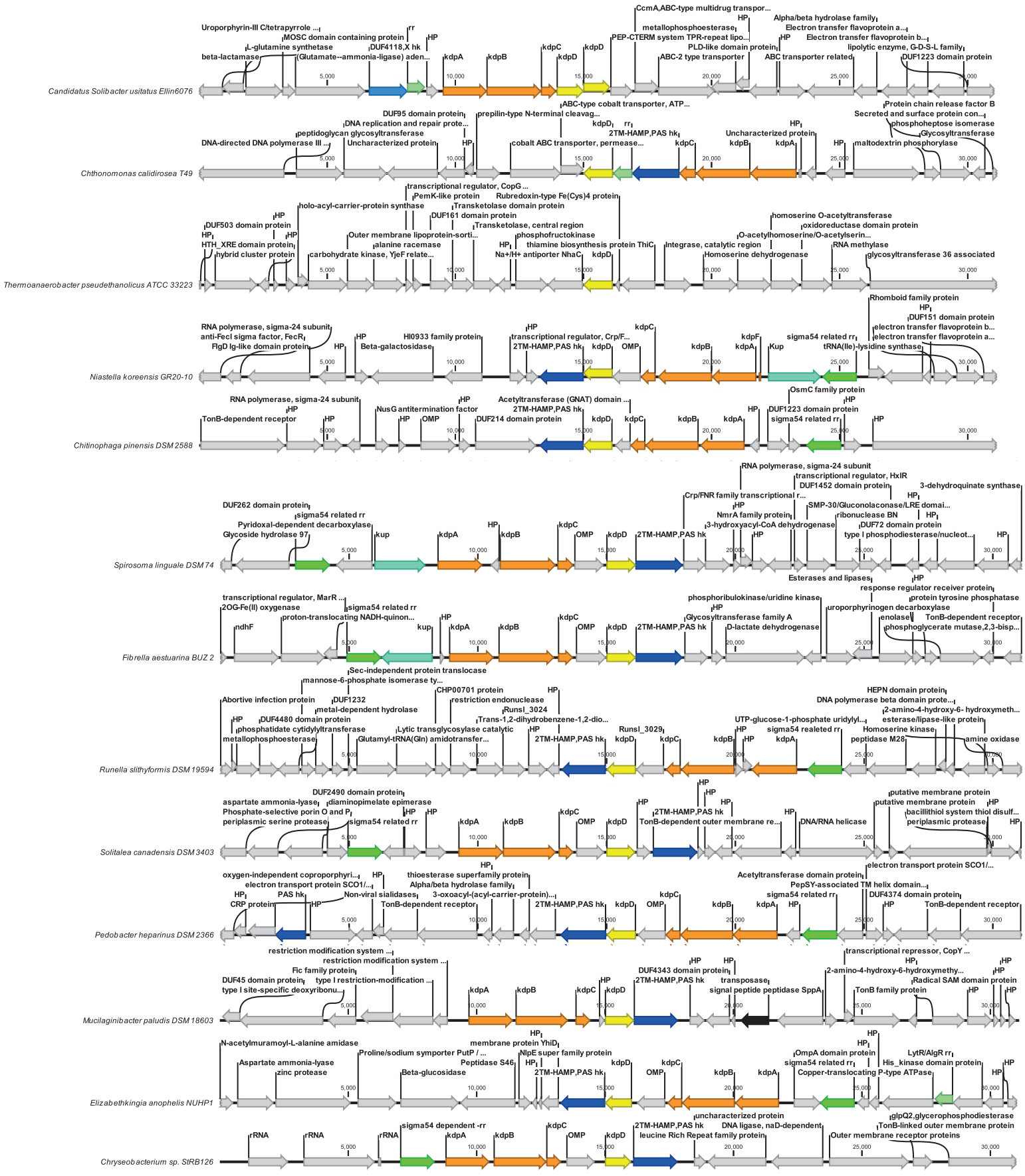


Figure A3A Page 1

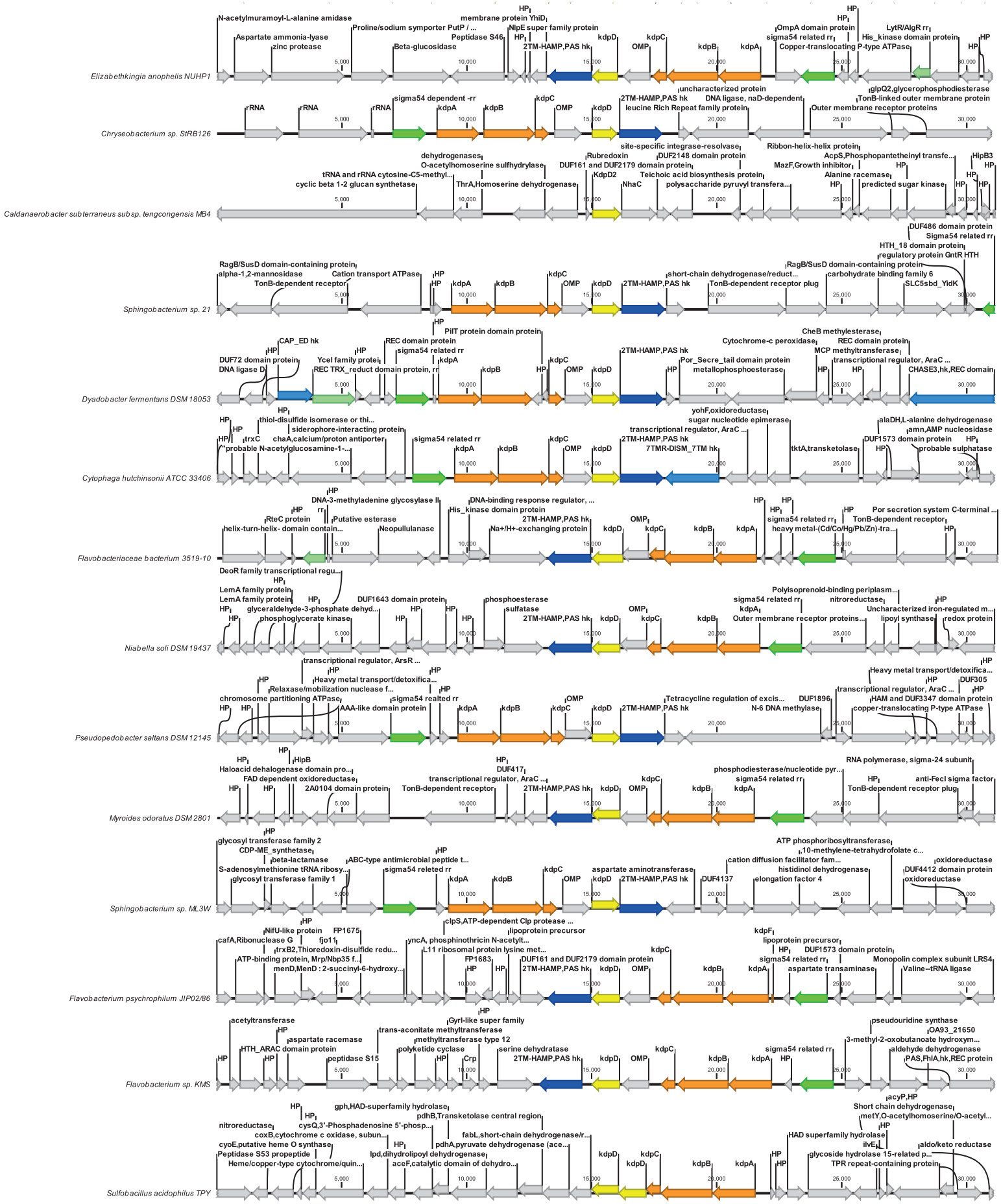


Figure A3A Page 2

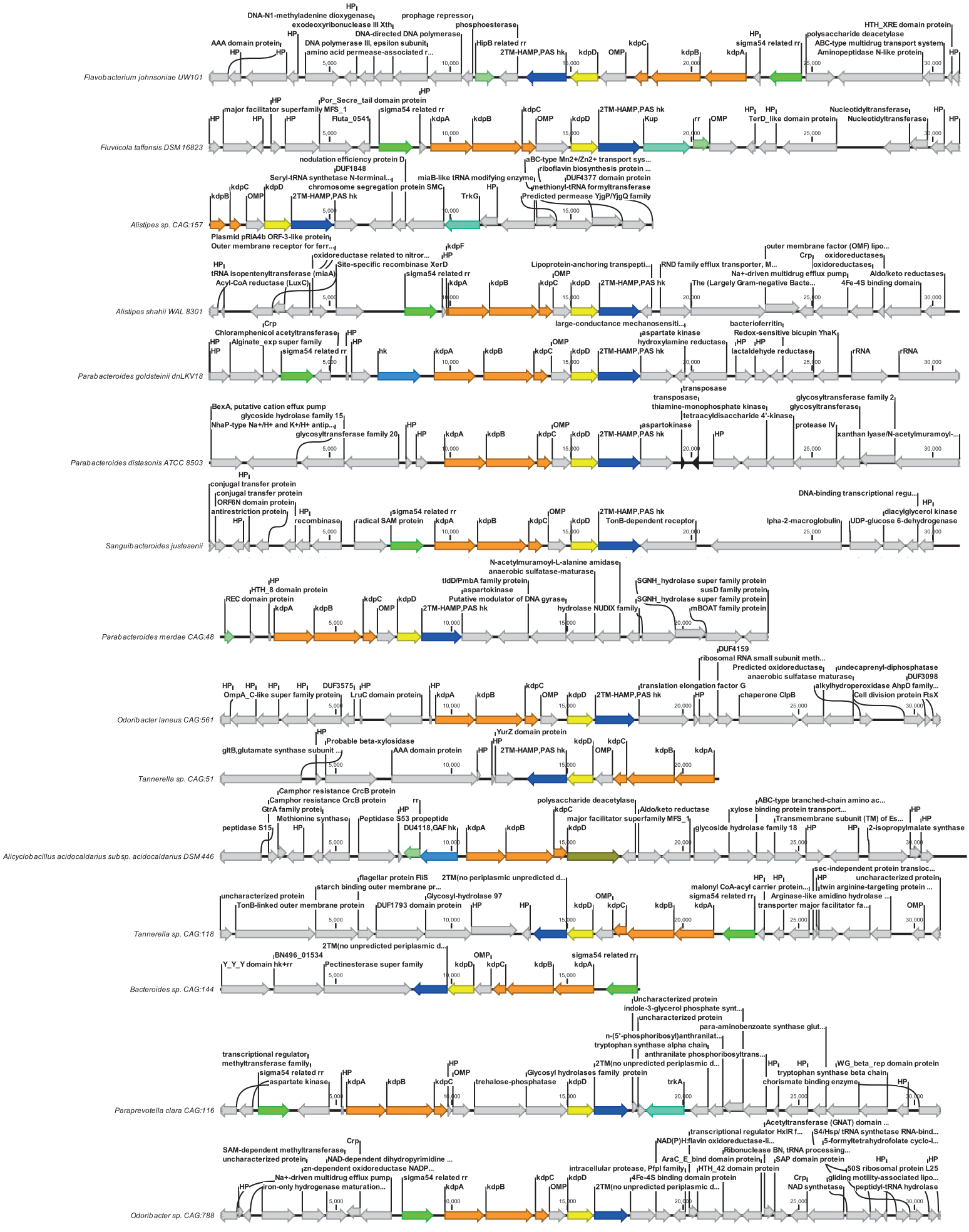


Figure A3A Page 3



Figure A3A Page 4

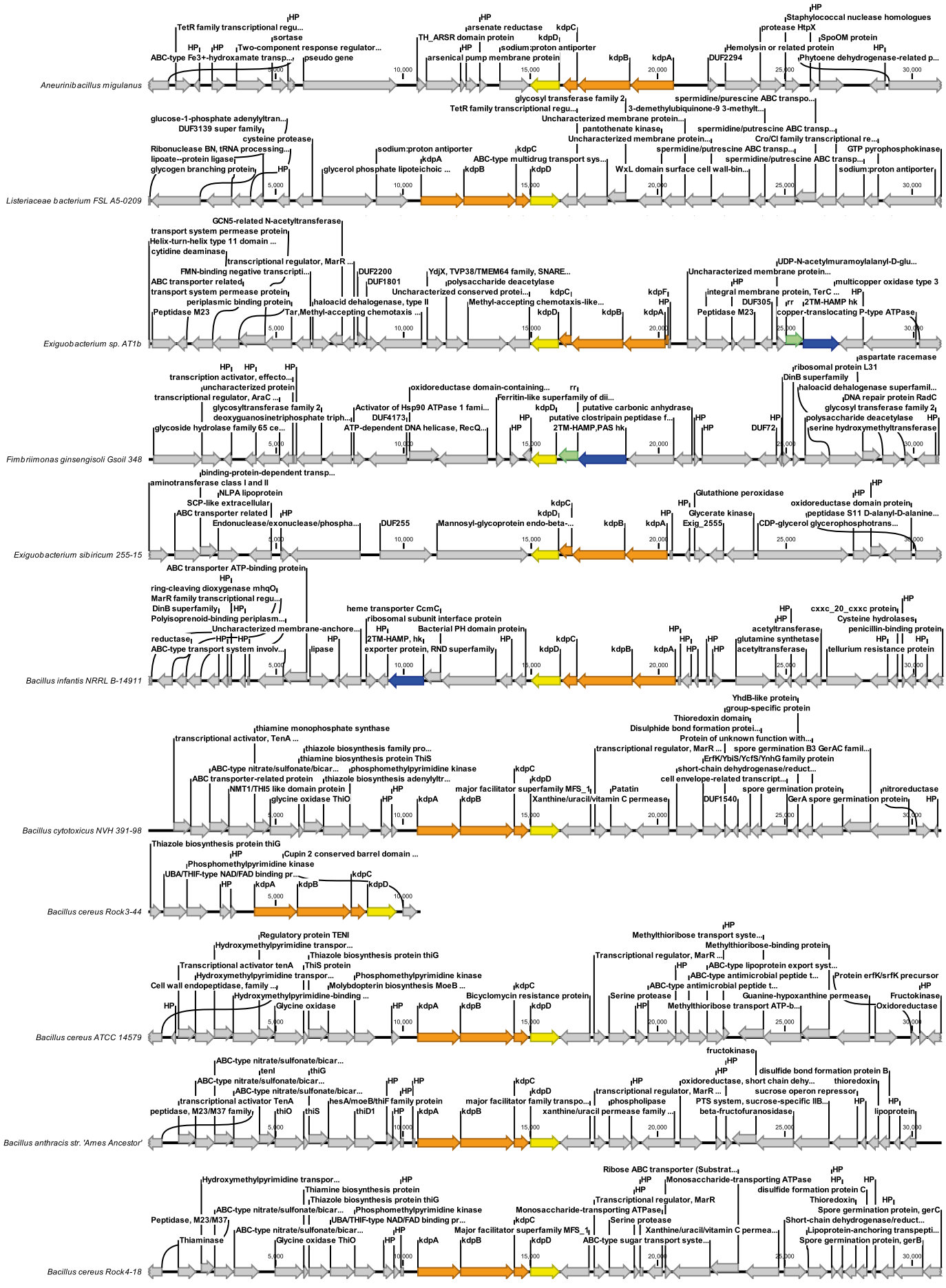


Figure A3A Page 5



Figure A3A Page 6

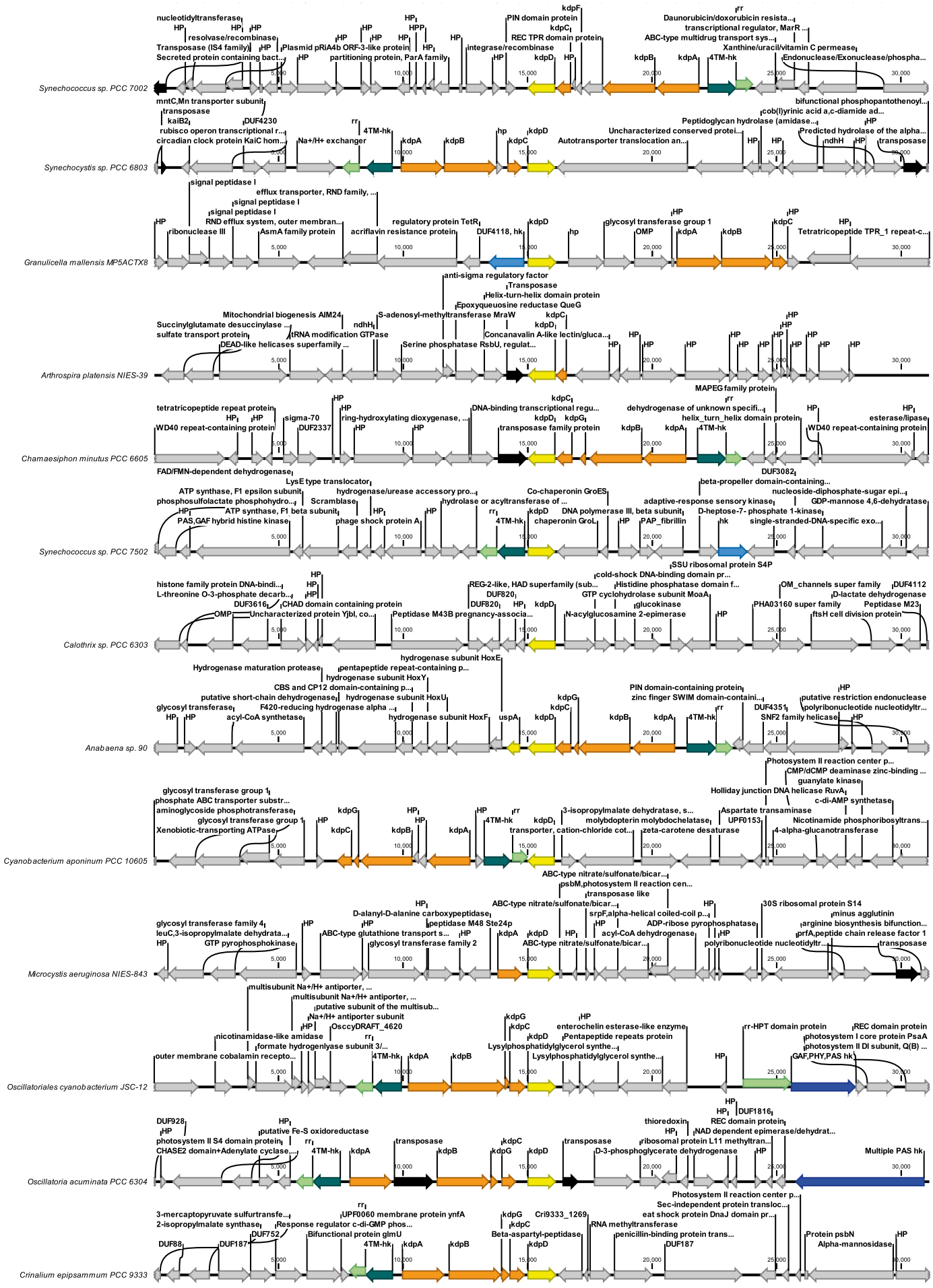


Figure A3A Page 7

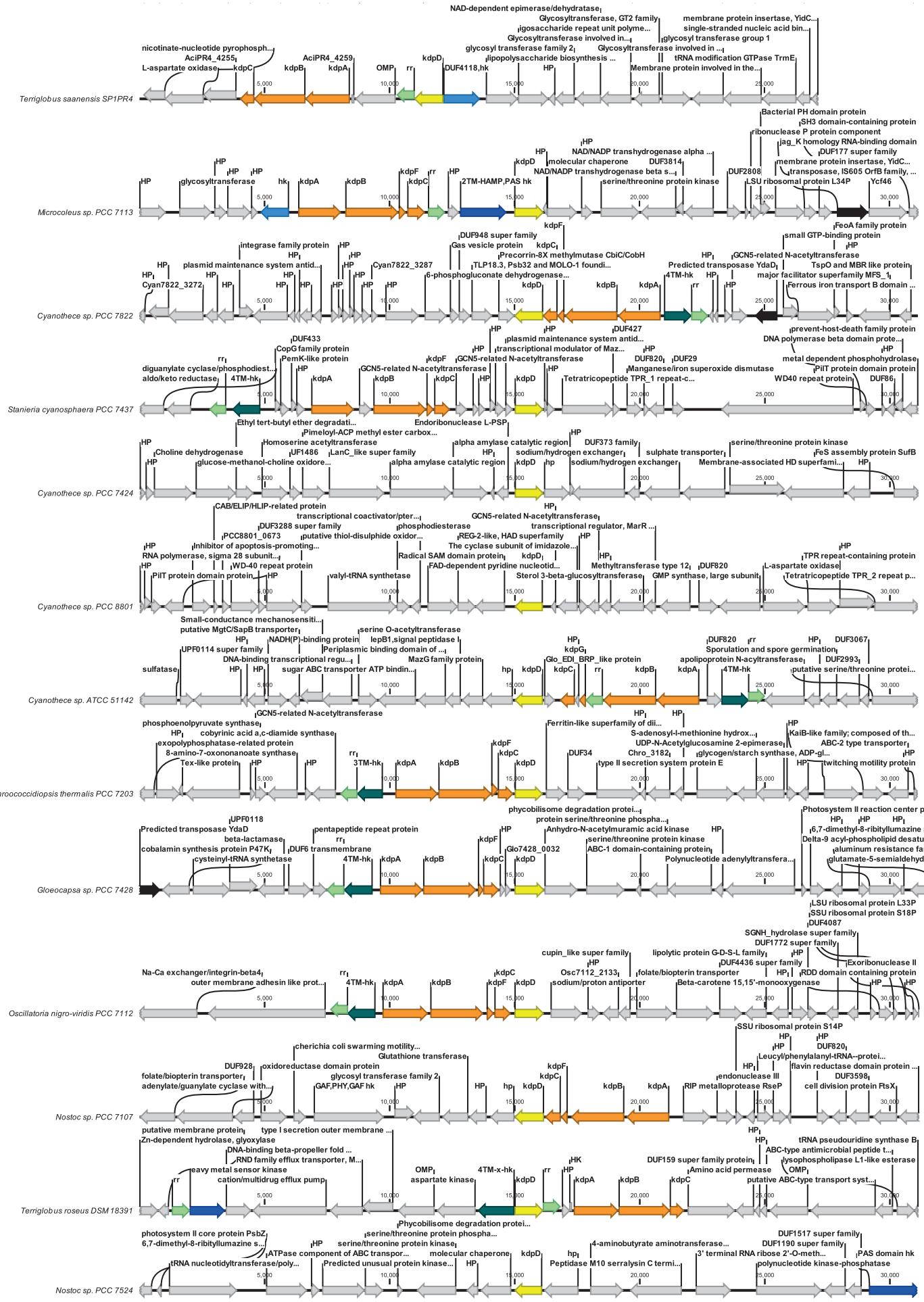


Figure A3A Page 8

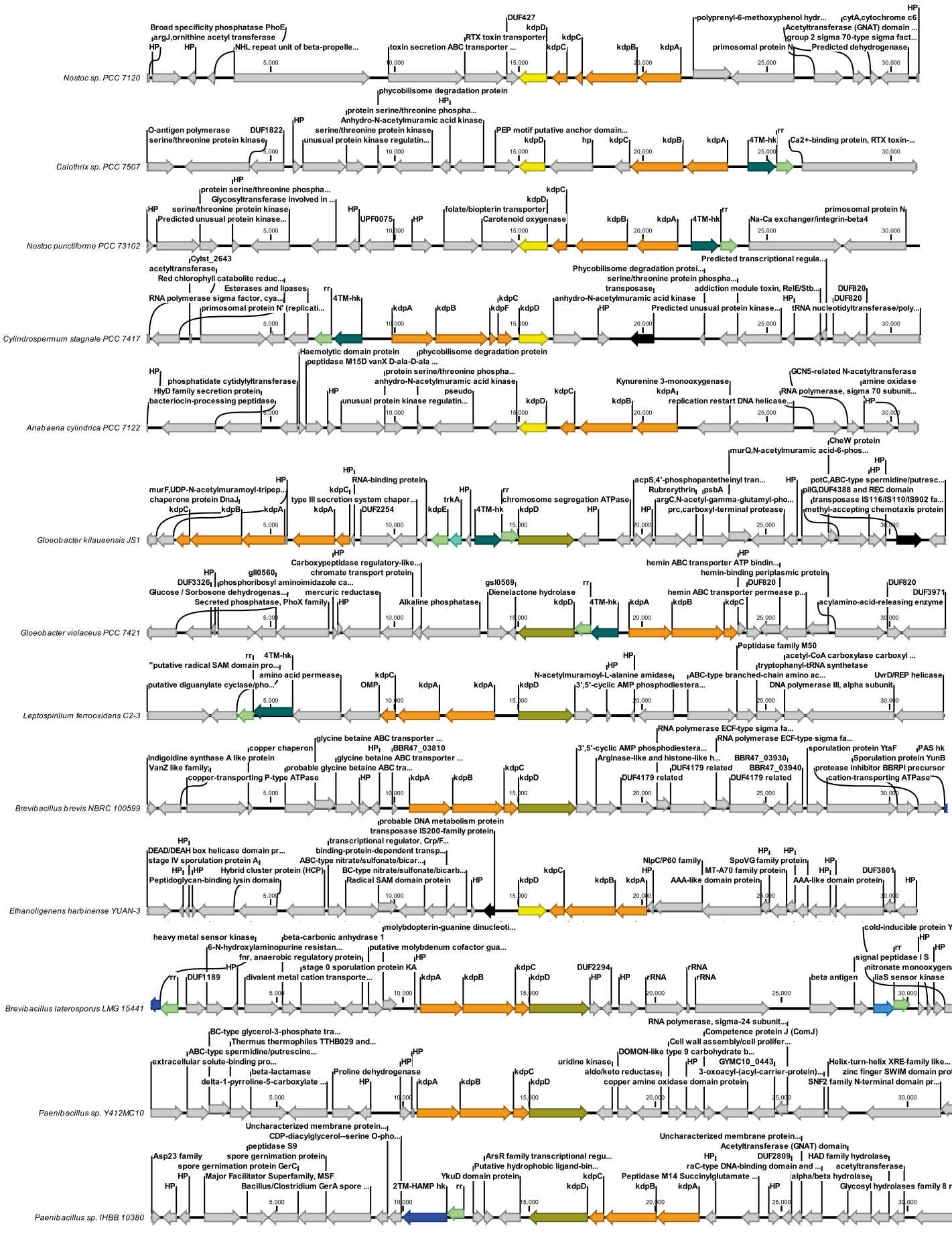


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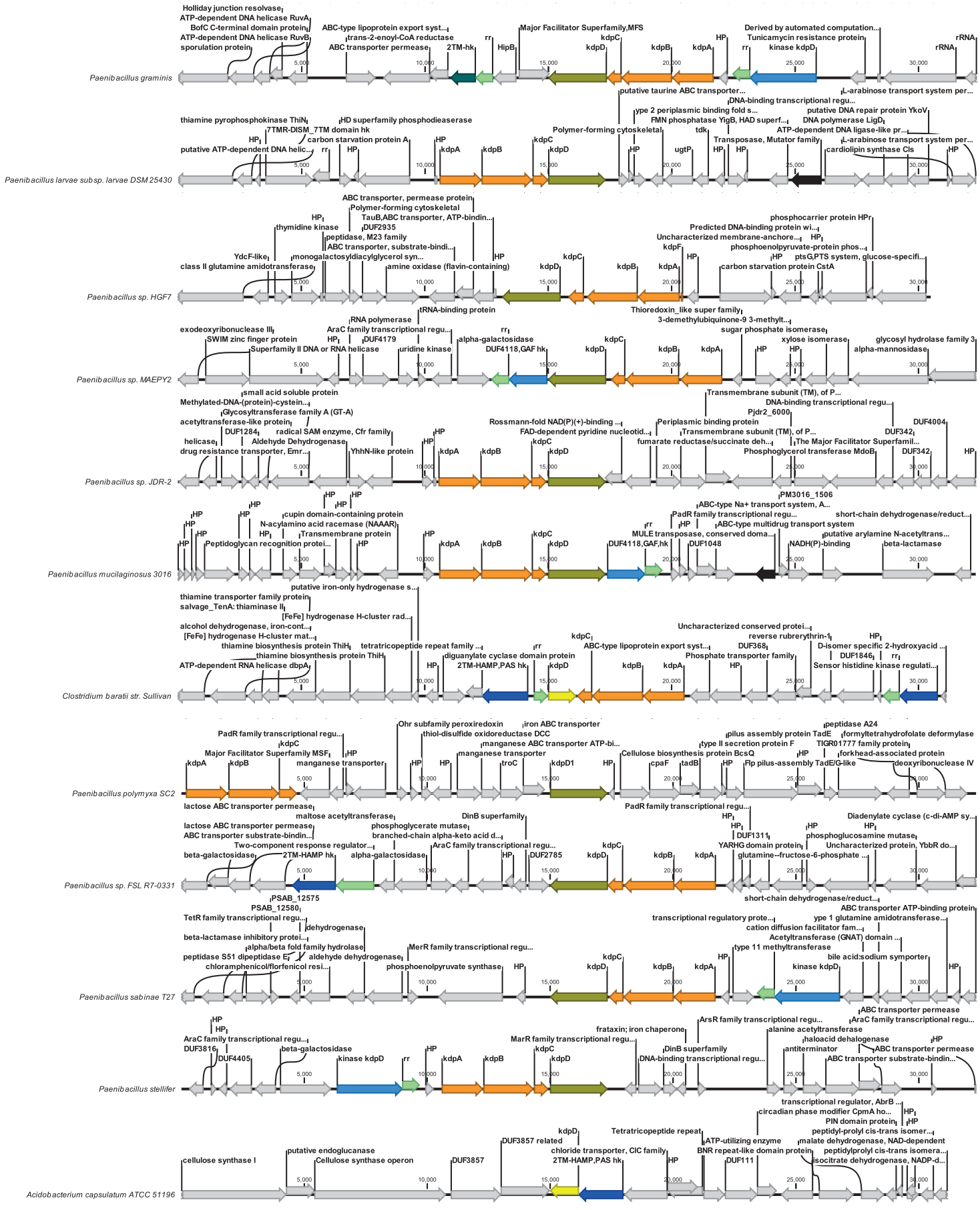


Figure A3A Page 10

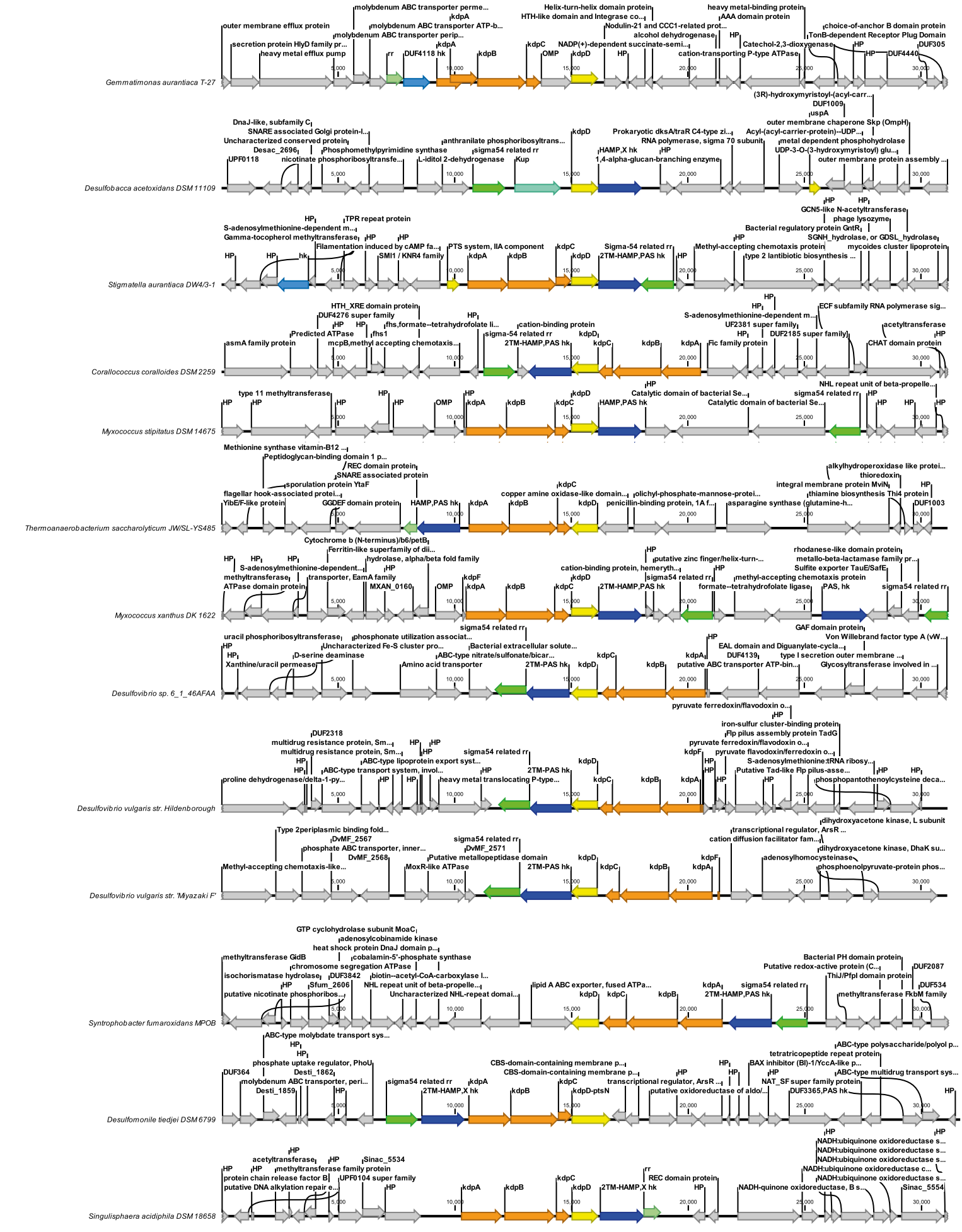


Figure A3A Page 11

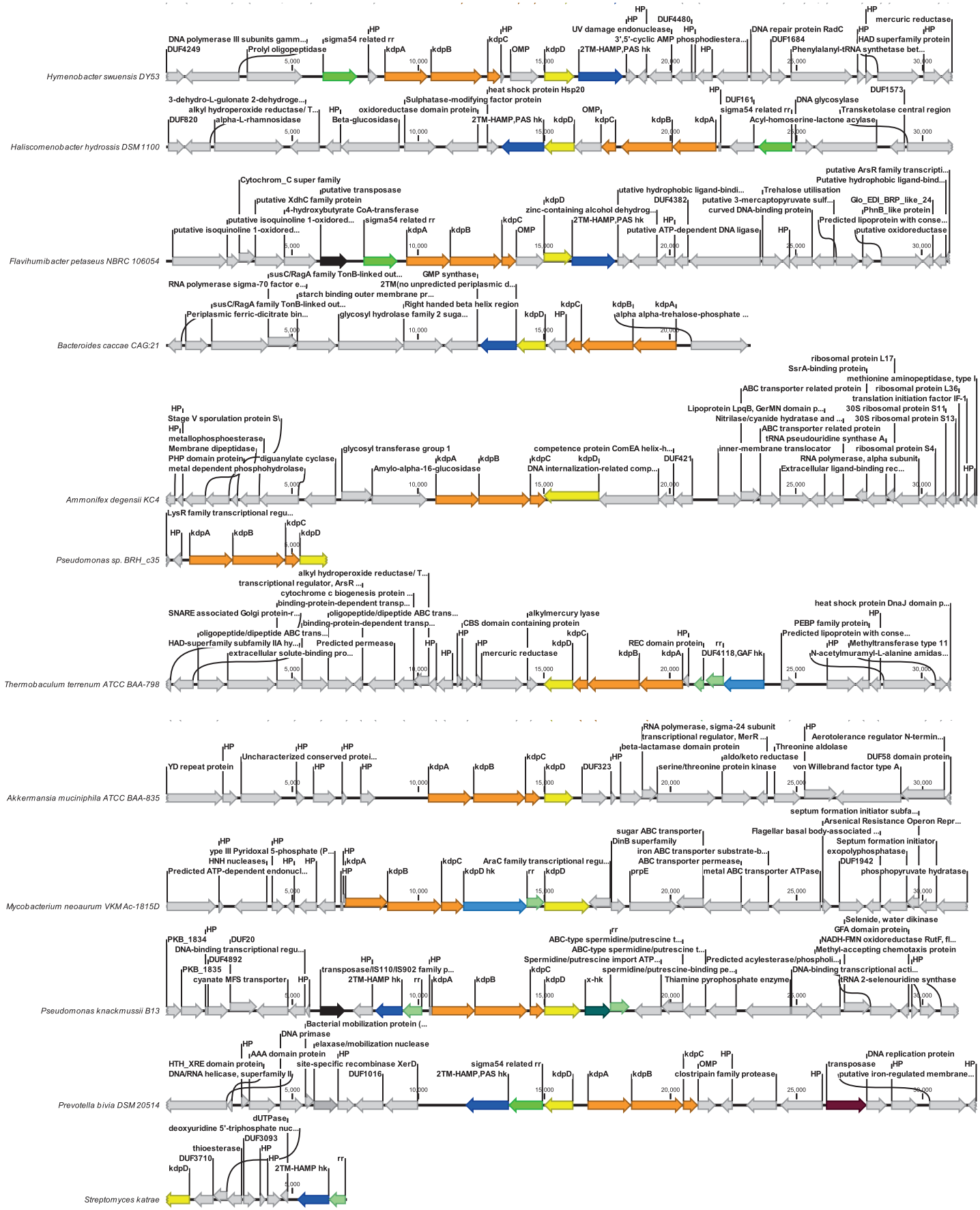


Figure A3A Page 12

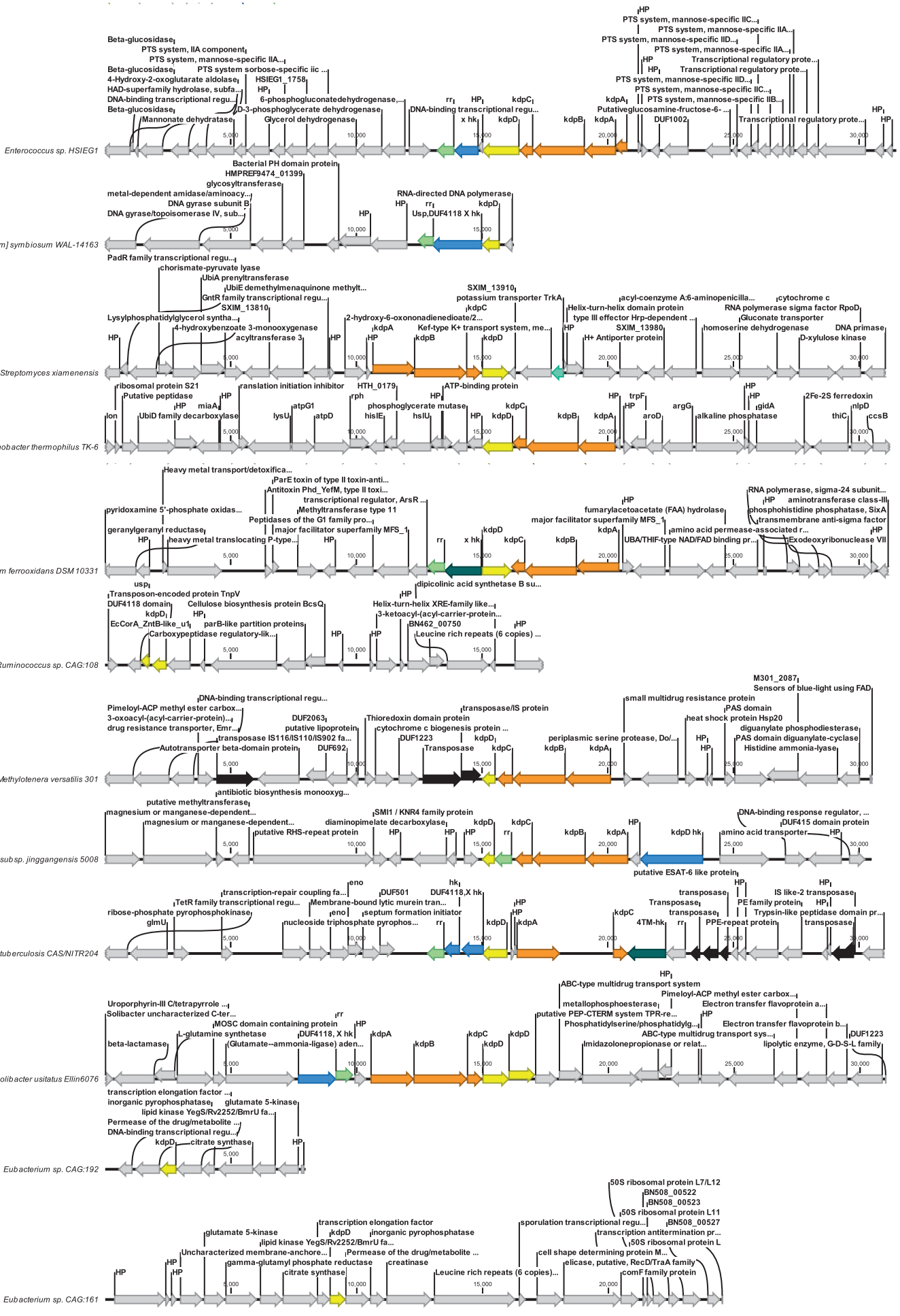


Figure A3A Page 13

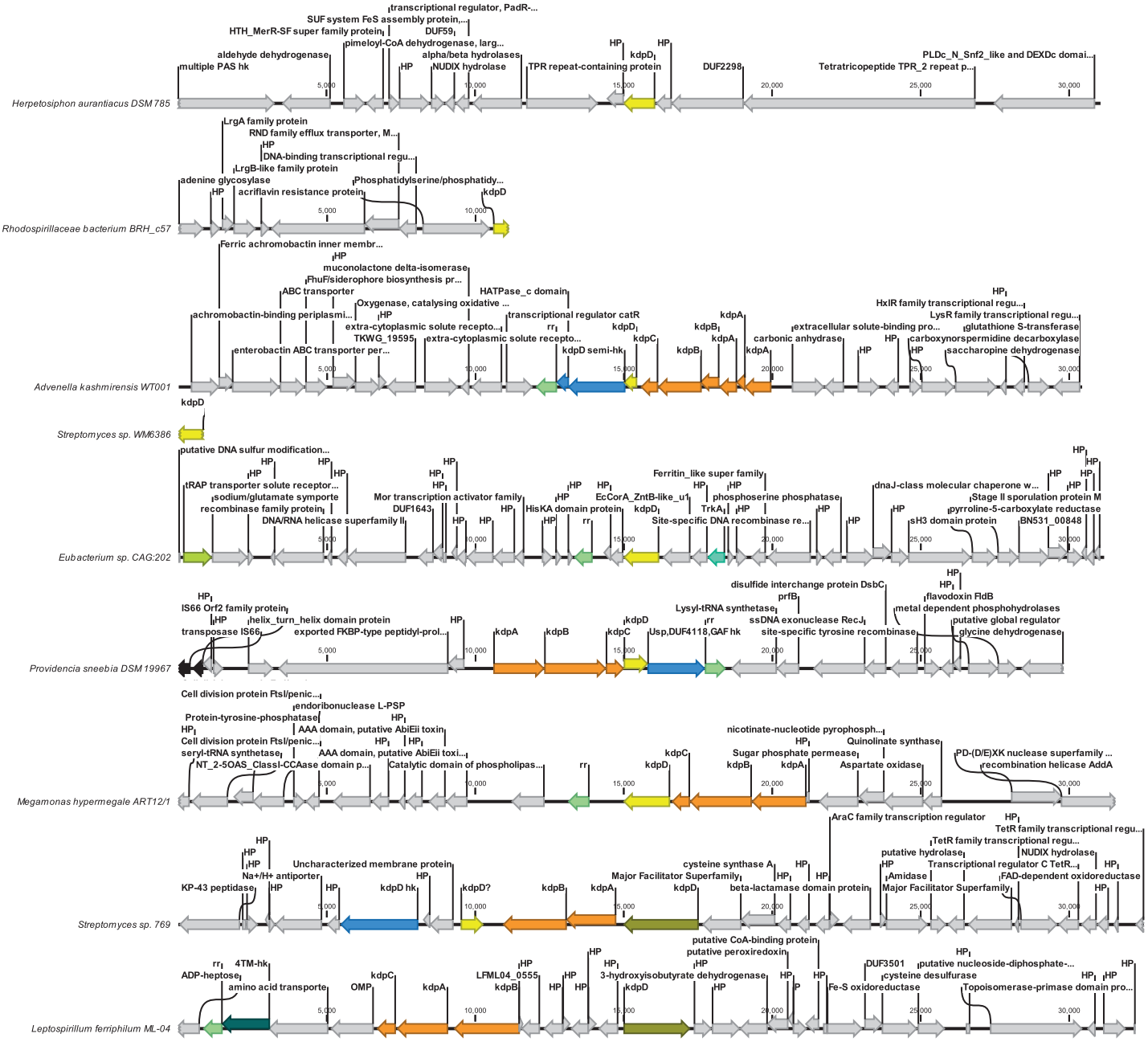


Figure A3A Page 14

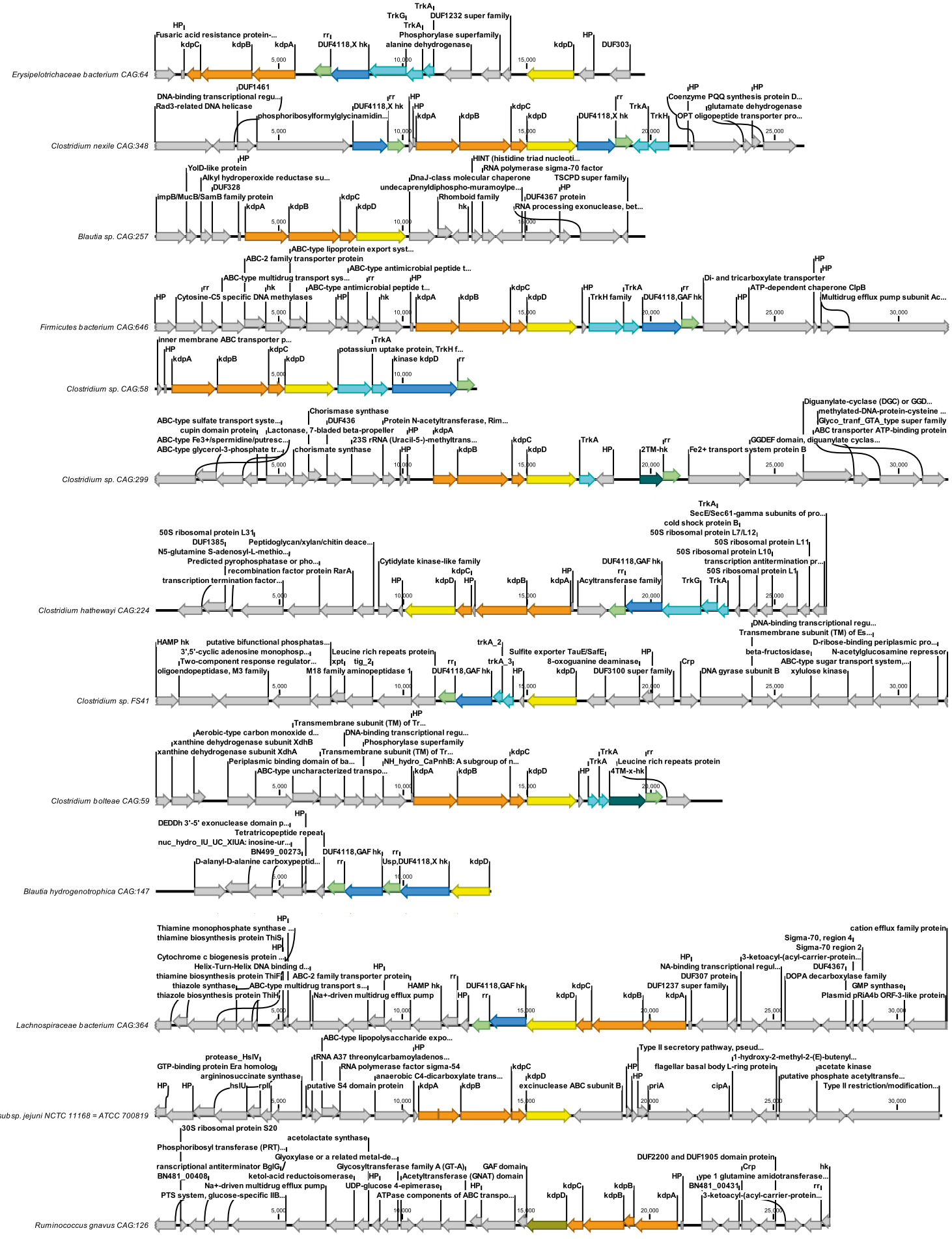


Figure A3B Page 1

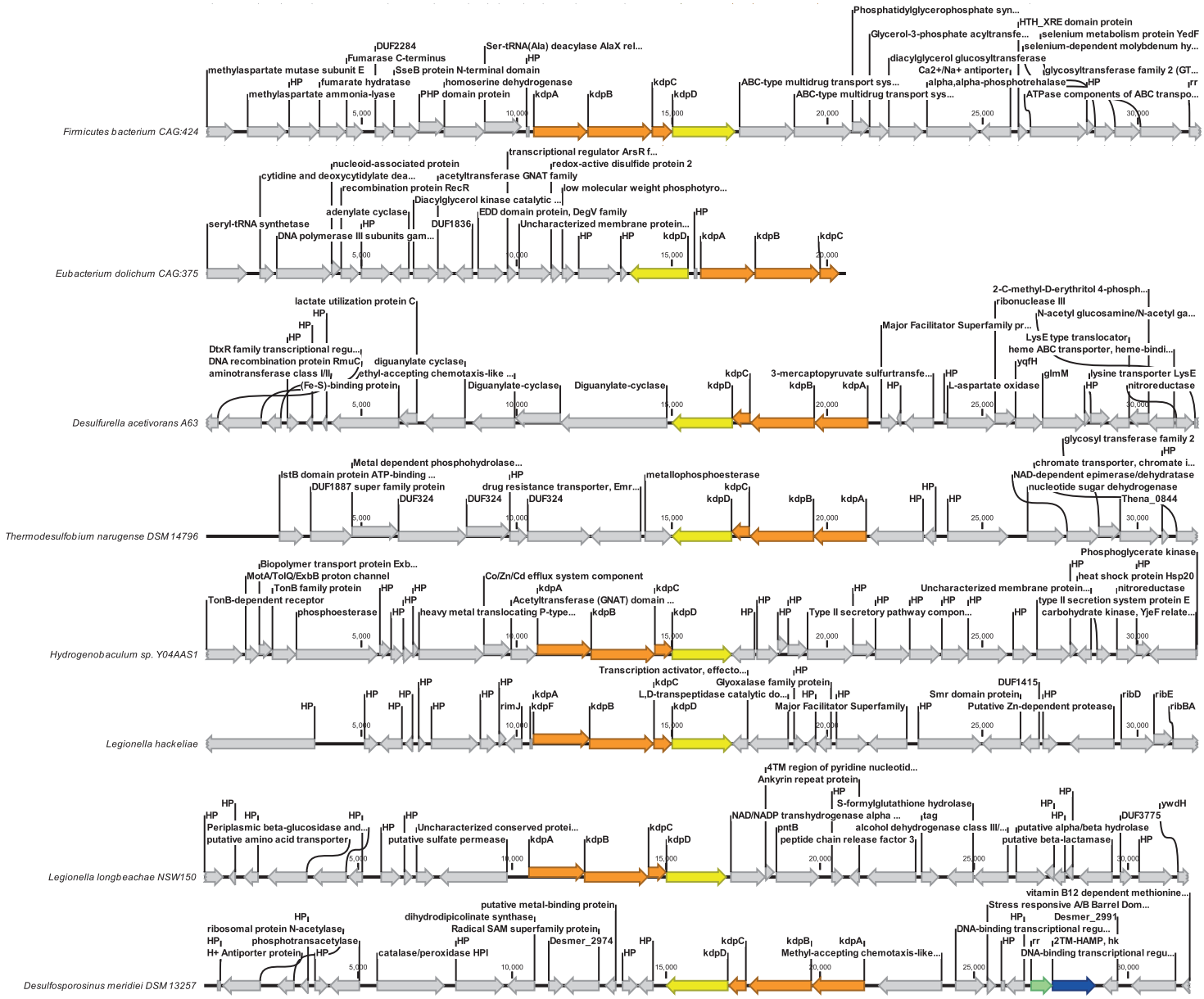


Figure A3B Page 2

Figure A3: Genomic neighborhoods of some *non-kinase kdpD* genes. (A) Genomic neighborhoods of *non-kinase kdpD* genes encoding KdpD proteins with the domain architecture KdpD-Usp (yellow arrows marked “kdpD”) or KdpD-Usp-KdpD-Usp (yellow-green arrows marked “kdpD”). **(B)** Genomic neighborhoods of *non-kinase kdpD* genes encoding KdpD proteins with the domain architecture KdpD-Usp-DUF4118-GAF (yellow arrows marked “kdpD”) or KdpD-Usp-DUF4118 (yellow-green arrows marked “kdpD”). The genes encoding HK^{K+} and RR^{K+} are depicted as different colored arrows marked “hk” and “rr” or “sigma 54-related rr”, respectively. Domain architectures of corresponding HK^{K+} are also included (the “X” stands for an unpredicted domain). HP, hypothetical protein; OMP, outer membrane porin.

Content of the appendix data set S1 (including 9 sheets)	
Sheet Name	**Description**
Sheet 1	List of proteome IDs and taxon in the RFP
Sheet 2	Bacterial groups/phyla with KdpD protein(s)
Sheet 3	All KdpD proteins retrieved from the RFP
Sheet 4	All KdpA proteins retrieved from the RFP
Sheet 5	All TrkH proteins retrieved from the RFP
Sheet 6	All DUF4118 proteins retrieved from the RFP
Sheet 7	Taxonomy information of 216 KdpD proteins used for selection pressure analysis in Figure 16
Sheet 8	HK^{K+} and RR^{K+} of non-kinase KdpD
Sheet 9	Sigma 54 recognition motif detected in the *kdp* promoter in some *Bacteroidetes/Chlorobi* group and *Deltaproteobacteria*

Sheet 1

List of proteome IDs and species of origin in the Uniprot reference proteomes 2015_10 (RFP)								
Proteome ID	**Organism (and Synonym)**	**Organism ID**	**Last modified**	**Protein count**	**Taxname (NCBI taxonomy)**	**Lineage retrieved with NCBI taxonomy**	**Domain of Life**	**Group/phylums**
UP000002518	Aeropyrum pernix (strain ATCC 700893 / DSM 11879 / JCM 9820 / NBRC 100138 / K1)	272557	7/30/2015	1700	Aeropyrum pernix K1	272557 56636 56635 2272 114380 183924 28889 2157 131567	Archaea	
UP000000429	Helicobacter pylori (strain ATCC 700392 / 26695) (Campylobacter pylori)	85962	8/2/2015	1553	Helicobacter pylori 26695	85962 210 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000554	Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	64091	8/2/2015	2426	Halobacterium sp. NRC-1	64091 2242 2239 2236 2235 183963 28890 2157 131567	Archaea	
UP000000558	Escherichia coli O157:H7	83334	8/2/2015	5303	Escherichia coli O157:H7	83334 562 561 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000579	Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd)	71421	8/2/2015	1707	Haemophilus influenzae Rd KW20	71421 727 724 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002524	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	243230	8/2/2015	3085	Deinococcus radiodurans R1	243230 1299 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000001806	Buchnera aphidicola subsp. Acyrthosiphon pisum (strain APS) (Acyrthosiphon pisum symbiotic bacterium)	107806	7/30/2015	572	Buchnera aphidicola str. APS (Acyrthosiphon pisum)	107806 118099 9 32199 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000799	Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	192222	7/30/2015	1623	Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819	192222 32022 197 194 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000005640	Homo sapiens (Human)	9606	8/9/2015	70071	Homo sapiens	9606 9605 207598 9604 314295 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000805	Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) (Methanococcus jannaschii)	243232	8/2/2015	1787	Methanocaldococcus jannaschii DSM 2661	243232 2190 196118 196117 2182 183939 28890 2157 131567	Archaea	
UP000000806	Mycobacterium leprae (strain TN)	272631	8/2/2015	1603	Mycobacterium leprae TN	272631 1769 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008062	Zymoseptoria tritici (strain CBS 115943 / IPO323) (Speckled leaf blotch fungus) (Septoria tritici)	336722	7/30/2015	10972	Zymoseptoria tritici IPO323	336722 1047171 1047167 93133 134362 451867 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000803	Drosophila melanogaster (Fruit fly)	7227	8/2/2015	22011	Drosophila melanogaster	7227 32351 32346 32341 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000808	Mycoplasma pneumoniae (strain ATCC 29342 / M129)	272634	7/30/2015	687	Mycoplasma pneumoniae M129	272634 2104 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000002196	Lactococcus lactis subsp. lactis (strain IL1403) (Streptococcus lactis)	272623	8/2/2015	2225	Lactococcus lactis subsp. lactis Il1403	272623 1360 1358 1357 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002199	Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126)	224325	8/2/2015	2400	Archaeoglobus fulgidus DSM 4304	224325 2234 2233 2232 2231 183980 28890 2157 131567	Archaea	
UP000000625	Escherichia coli (strain K12)	83333	7/30/2015	4305	Escherichia coli K-12	83333 562 561 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001584	Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)	83332	8/2/2015	3991	Mycobacterium tuberculosis H37Rv	83332 1773 77643 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001570	Bacillus subtilis (strain 168)	224308	8/2/2015	4197	Bacillus subtilis subsp. subtilis str. 168	224308 135461 1423 653685 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000002438	Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	208964	8/2/2015	5563	Pseudomonas aeruginosa PAO1	208964 287 136841 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000811	Treponema pallidum (strain Nichols)	243276	8/2/2015	1028	Treponema pallidum subsp. pallidum str. Nichols	243276 161 160 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000001425	Synechocystis sp. (strain PCC 6803 / Kazusa)	1111708	8/2/2015	3507	Synechocystis sp. PCC 6803 substr. Kazusa	1111708 1148 1142 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000005223	Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NBRC 100330 / Delta H) (Methanobacterium thermoautotrophicum)	187420	8/2/2015	1868	Methanothermobacter thermautotrophicus str. Delta H	187420 145262 145260 2159 2158 183925 28890 2157 131567	Archaea	
UP000000431	Chlamydia trachomatis (strain D/UW-3/Cx)	272561	8/2/2015	895	Chlamydia trachomatis D/UW-3/CX	272561 813 810 1113537 809 51291 204429 204428 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000001258	Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)	272558	7/30/2015	4006	Bacillus halodurans C-125	272558 86665 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000008183	Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)	243274	8/2/2015	1852	Thermotoga maritima MSB8	243274 2336 2335 188709 2419 188708 200918 2 131567	Bacteria	Thermotogae
UP000001974	Sulfolobus solfataricus (strain ATCC 35092 / DSM 1617 / JCM 11322 / P2)	273057	8/2/2015	2938	Sulfolobus solfataricus P2	273057 2287 2284 118883 2281 183924 28889 2157 131567	Archaea	
UP000002480	Rickettsia prowazekii (strain Madrid E)	272947	8/2/2015	834	Rickettsia prowazekii str. Madrid E	272947 782 114292 780 33988 775 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001940	Caenorhabditis elegans	6239	8/2/2015	26066	Caenorhabditis elegans	6239 6237 55885 6243 55879 6236 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000812	Xylella fastidiosa (strain 9a5c)	160492	7/30/2015	2772	Xylella fastidiosa 9a5c	160492 2371 2370 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000528	Mycoplasma pulmonis (strain UAB CTIP)	272635	7/30/2015	778	Mycoplasma pulmonis UAB CTIP	272635 2107 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes

UP000001807	Borrelia burgdorferi (strain ATCC 35210 / B31 / CIP 102532 / DSM 4680)	224326	8/2/2015	1290	Borrelia burgdorferi B31	224326 139 64895 138 1643685 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000000584	Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	243277	8/2/2015	3784	Vibrio cholerae O1 biovar El Tor str. N16961	243277 686 127906 666 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000425	Neisseria meningitidis serogroup B (strain MC58)	122586	8/2/2015	2001	Neisseria meningitidis	122586 491 487 482 481 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000798	Aquifex aeolicus (strain VF5)	224324	8/2/2015	1553	Aquifex aeolicus VF5	224324 63363 2713 64898 32069 187857 200783 2 131567	Bacteria	Aquificae
UP000001024	Thermoplasma acidophilum (strain ATCC 25905 / DSM 1728 / JCM 9062 / NBRC 15155 / AMRC-C165)	273075	8/2/2015	1482	Thermoplasma acidophilum DSM 1728	273075 2303 2302 46659 2301 183967 28890 2157 131567	Archaea	
UP000000814	Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	272562	8/2/2015	3847	Clostridium acetobutylicum ATCC 824	272562 1488 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001014	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	99287	8/2/2015	4533	Salmonella enterica subsp. enterica serovar Typhimurium str. LT2	99287 90371 59201 28901 590 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000586	Streptococcus pneumoniae (strain ATCC BAA-255 / R6)	171101	7/30/2015	2030	Streptococcus pneumoniae R6	171101 1313 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001976	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	266834	8/2/2015	6169	Sinorhizobium meliloti 1021	266834 382 28105 227292 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002483	Nostoc sp. (strain PCC 7120 / UTEX 2576)	103690	7/30/2015	6070	Nostoc sp. PCC 7120	103690 1177 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000000750	Streptococcus pyogenes serotype M1	301447	8/9/2015	1690	Streptococcus pyogenes serotype M1	301447 1314 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000589	Mus musculus (Mouse)	10090	8/14/2015	49220	Mus musculus	10090 862507 10088 39107 10066 337687 33553 9989 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001436	Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	267608	7/30/2015	5002	Ralstonia solanacearum GMI1000	267608 305 48736 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001015	Sulfolobus tokodaii (strain DSM 16993 / JCM 10545 / NBRC 100140 / 7)	273063	7/30/2015	2805	Sulfolobus tokodaii str. 7	273063 111955 2284 118883 2281 183924 28889 2157 131567	Archaea	
UP000000815	Yersinia pestis	632	8/2/2015	3909	Yersinia pestis	632 1649845 629 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002485	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	284812	8/2/2015	5121	Schizosaccharomyces pombe 972h-	284812 4896 4895 4894 34346 147554 451866 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000813	Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	176299	8/2/2015	5344	Agrobacterium fabrum str. C58	176299 1176649 1183400 357 227290 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000809	Pasteurella multocida (strain Pm70)	272843	8/2/2015	2015	Pasteurella multocida subsp. multocida str. Pm70	272843 44283 747 745 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000819	Encephalitozoon cuniculi (strain GB-M1) (Microsporidian parasite)	284813	7/30/2015	2008	Encephalitozoon cuniculi GB-M1	284813 6035 6033 36734 6032 6029 4751 33154 2759 131567	eukaryotes	
UP000001816	Caulobacter crescentus (strain ATCC 19089 / CB15)	190650	8/2/2015	3720	Caulobacter crescentus CB15	190650 155892 75 76892 204458 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002487	Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A)	188937	8/2/2015	4468	Methanosarcina acetivorans C2A	188937 2214 2207 2206 94695 224756 28890 2157 131567	Archaea	
UP000000555	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	273068	7/30/2015	2545	Caldanaerobacter subterraneus subsp. tengcongensis MB4	273068 119072 911092 249529 186814 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000001973	Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	100226	7/30/2015	8038	Streptomyces coelicolor A3(2)	100226 1902 1477431 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001010	Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	190485	7/30/2015	4127	Xanthomonas campestris pv. campestris str. ATCC 33913	190485 340 339 338 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001007	Chlorobium tepidum (strain ATCC 49652 / DSM 12025 / NBRC 103806 / TLS)	194439	7/30/2015	2250	Chlorobium tepidum TLS	194439 1097 256319 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002521	Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131)	190304	8/2/2015	2046	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	190304 76856 851 848 203492 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000000821	Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R)	208435	7/30/2015	2105	Streptococcus agalactiae 2603V/R	208435 216466 1311 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000440	Thermosynechococcus elongatus (strain BP-1)	197221	7/30/2015	2451	Thermosynechococcus elongatus BP-1	197221 146786 146785 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000000818	Clostridium perfringens (strain 13 / Type A)	195102	7/30/2015	2721	Clostridium perfringens str. 13	195102 1502 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000817	Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	169963	7/30/2015	2844	Listeria monocytogenes EGD-e	169963 1639 1637 186820 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000000439	Bifidobacterium longum (strain NCC 2705)	206672	8/2/2015	1725	Bifidobacterium longum NCC2705	206672 216816 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000562	Wigglesworthia glossinidia brevipalpis	36870	7/27/2015	617	Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis	36870 51229 51228 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002512	Streptococcus mutans serotype c (strain ATCC 700610 / UA159)	210007	8/2/2015	1953	Streptococcus mutans UA159	210007 1309 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008089	Ovine adenovirus D serotype 7 (isolate OAV287) (OAdV-7) (Ovine adenovirus 7)	114430	7/30/2015	30	Ovine adenovirus 7	114430 130327 100953 10508 35237 10239	Vruses	
UP000001408	Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	189518	8/2/2015	3676	Leptospira interrogans serovar Lai str. 56601	189518 57678 173 171 170 1643688 203692 203691 2 131567	Bacteria	Spirochaetes

UP000000423	Ureaplasma parvum serovar 3 (strain ATCC 700970)	273119	7/30/2015	611	Ureaplasma parvum serovar 3 str. ATCC 700970	273119 38504 134821 2129 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000000556	Pseudomonas putida (strain KT2440)	160488	7/30/2015	5313	Pseudomonas putida KT2440	160488 303 136845 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001409	Corynebacterium efficiens (strain DSM 44549 / YS-314 / AJ 12310 / JCM 11189 / NBRC 100395)	196164	7/30/2015	2945	Corynebacterium efficiens YS-314	196164 152794 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000601	Buchnera aphidicola subsp. Baizongia pistaciae (strain Bp)	224915	7/30/2015	507	Buchnera aphidicola str. Bp (Baizongia pistaciae)	224915 135842 9 32199 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001412	Clostridium tetani (strain Massachusetts / E88)	212717	8/2/2015	2415	Clostridium tetani E88	212717 1513 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002200	Tropheryma whipplei (strain Twist) (Whipple's bacillus)	203267	7/30/2015	805	Tropheryma whipplei str. Twist	203267 2039 2038 577468 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000012045	Botryotinia fuckeliana (strain BcDW1) (Noble rot fungus) (Botrytis cinerea)	1290391	7/30/2015	11022	Botrytis cinerea BcDW1	1290391 40559 33196 28983 5178 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001415	Enterococcus faecalis (strain ATCC 700802 / V583)	226185	7/30/2015	3240	Enterococcus faecalis V583	226185 1351 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002671	Coxiella burnetii (strain RSA 493 / Nine Mile phase I)	227377	8/2/2015	1815	Coxiella burnetii RSA 493	227377 777 776 118968 118969 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000428	Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	227882	7/30/2015	7664	Streptomyces avermitilis MA-4680 = NBRC 14893	227882 33903 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001416	Nitrosomonas europaea (strain ATCC 19718 / NBRC 14298)	228410	7/30/2015	2375	Nitrosomonas europaea ATCC 19718	228410 915 914 206379 32003 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001417	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	226900	8/2/2015	5240	Bacillus cereus ATCC 14579	226900 1396 86661 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000000552	Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	266835	7/30/2015	7255	Mesorhizobium loti MAFF303099	266835 381 68287 69277 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008186	Shewanella oneidensis (strain MR-1)	211586	7/30/2015	4068	Shewanella oneidensis MR-	211586 70863 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001826	Methanopyrus kandleri (strain AV19 / DSM 6324 / JCM 9639 / NBRC 100938)	190192	8/2/2015	1687	Methanopyrus kandleri AV19	190192 2320 2319 183713 68985 183988 28890 2157 131567	Archaea	
UP000002526	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	224911	8/2/2015	8253	Bradyrhizobium diazoefficiens USDA 110	224911 1355477 374 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000432	Lactobacillus plantarum (strain ATCC BAA-793 / NCIMB 8826 / WCFS1)	220668	7/30/2015	3088	Lactobacillus plantarum WCFS1	220668 1590 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001418	Mycoplasma gallisepticum (strain R(low / passage 15 / clone 2))	710127	8/2/2015	761	Mycoplasma gallisepticum str. R(low)	710127 233150 2096 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000001013	Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1)	186497	7/30/2015	2045	Pyrococcus furiosus DSM 3638	186497 2261 2260 2259 2258 183968 28890 2157 131567	Archaea	
UP000002495	Helicobacter hepaticus (strain ATCC 51449 / 3B1)	235279	7/30/2015	1872	Helicobacter hepaticus ATCC 51449	235279 32025 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002494	Rattus norvegicus (Rat)	10116	8/2/2015	29887	Rattus norvegicus	10116 10114 39107 10066 337687 33553 9989 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002439	Pyrobaculum aerophilum (strain ATCC 51768 / IM2 / DSM 7523 / JCM 9630 / NBRC 100827)	178306	7/30/2015	2590	Pyrobaculum aerophilum str. IM2	178306 13773 2276 2267 2266 183924 28889 2157 131567	Archaea	
UP000002493	Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	223926	7/30/2015	4821	Vibrio parahaemolyticus RIMD 2210633	223926 670 717610 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002676	Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	257313	8/2/2015	3258	Bordetella pertussis Tohama I	257313 520 517 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001422	Synechococcus sp. (strain WH8102)	84588	7/30/2015	2512	Synechococcus sp. WH	84588 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000002522	Mycoplasma penetrans (strain HF-2)	272633	7/30/2015	1028	Mycoplasma penetrans HF-	272633 28227 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000002515	Pseudomonas syringae pv. tomato (strain DC3000)	223283	7/30/2015	5431	Pseudomonas syringae pv. tomato str. DC3000	223283 323 251701 136849 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001022	Haemophilus ducreyi (strain 35000HP / ATCC 700724)	233412	7/30/2015	1694	Haemophilus ducreyi 35000HP	233412 730 724 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001420	Prochlorococcus marinus (strain SARG / CCMP1375 / SS120)	167539	7/30/2015	1881	Prochlorococcus marinus subsp. marinus str. CCMP1375	167539 142554 1219 1218 1217 1212 1117 2 131567	Bacteria	Cyanobacteria
UP000001025	Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1)	243090	8/4/2015	7271	Rhodopirellula baltica SH 1	243090 265606 265488 126 112 203683 203682 2 131567	Bacteria	Planctomycetes
UP000000822	Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)	221109	7/30/2015	3490	Oceanobacillus iheyensis HTE831	221109 182710 182709 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001423	Prochlorococcus marinus (strain MIT 9313)	74547	8/2/2015	2830	Prochlorococcus marinus str. MIT 9313	74547 1219 1218 1217 1212 1117 2 131567	Bacteria	Cyanobacteria
UP000000557	Gloeobacter violaceus (strain PCC 7421)	251221	8/2/2015	4406	Gloeobacter violaceus PCC 7421	251221 33072 33071 307595 307596 1117 2 131567	Bacteria	Cyanobacteria
UP000000588	Porphyromonas gingivalis (strain ATCC BAA-308 / W83)	242619	7/30/2015	1863	Porphyromonas gingivalis W83	242619 837 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000012065	Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)	1108050	7/30/2015	12197	Rhizoctonia solani AG-1 IB	1108050 456999 1322061 34425 5250 36064 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000002675	Vibrio vulnificus (strain YJ016)	196600	7/30/2015	4990	Vibrio vulnificus YJ016	196600 672 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001026	Prochlorococcus marinus subsp. pastoris (strain CCMP1986 / MED4)	59919	7/30/2015	1942	Prochlorococcus marinus subsp. pastoris str. CCMP1986	59919 142479 1219 1218 1217 1212 1117 2 131567	Bacteria	Cyanobacteria

UP000002514	Photorhabdus luminescens subsp. laumondii (strain TT01)	243265	7/30/2015	4556	Photorhabdus luminescens subsp. laumondii TTO1	243265 141679 29488 29487 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000291	Sulfobacillus acidophilus (strain TPY)	1051632	7/30/2015	3722	Sulfobacillus acidophilus TPY	1051632 53633 28033 539000 538999 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002198	Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis)	257309	7/30/2015	2265	Corynebacterium diphtheriae NCTC 13129	257309 1717 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000422	Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W) (Vibrio succinogenes)	273121	8/2/2015	2028	Wolinella succinogenes DSM 1740	273121 844 843 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000595	Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) (Methanosarcina frisia)	192952	8/2/2015	3303	Methanosarcina mazei Go1	192952 2209 2207 2206 94695 224756 28890 2157 131567	Archaea	
UP000002192	Blochmannia floridanus	203907	7/27/2015	583	Candidatus Blochmannia floridanus	203907 203804 84564 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001424	Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	243365	7/30/2015	4397	Chromobacterium violaceum ATCC 12472	243365 536 535 90153 1499392 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000030301	Arthrobacter sp. PAMC25486	1494608	7/27/2015	4345	Arthrobacter sp. PAMC25486	1494608 1663 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000030300	Nocardioides simplex (Arthrobacter simplex)	2045	8/2/2015	5426	Pimelobacter simplex	2045 2044 85015 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000030307	Pantoea sp. PSNIH1	1484158	7/27/2015	3922	Pantoea sp. PSNIH1	1484158 53335 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001450	Plasmodium falciparum (isolate 3D7)	36329	8/2/2015	5353	Plasmodium falciparum 3D7	36329 5833 418107 5820 1639119 5819 422676 5794 33630 2759 131567	eukaryotes	
UP000012076	Thermoplasmatales archaeon BRNA1	1054217	8/4/2015	1528	Thermoplasmatales archaeon BRNA1	1054217 74967 2301 183967 28890 2157 131567	Archaea	
UP000012082	Pseudomonas denitrificans ATCC 13867	1294143	8/7/2015	5045	Pseudomonas denitrificans ATCC 13867	1294143 43306 136844 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000030314	Treponema sp. OMZ 838	1539298	7/27/2015	2218	Treponema sp. OMZ 838	1539298 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000001414	Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	226186	7/30/2015	4782	Bacteroides thetaiotaomicron VPI-5482	226186 818 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001027	Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	257310	8/2/2015	4961	Bordetella bronchiseptica RB50	257310 518 517 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000030310	Pantoea sp. PSNIH2	1484157	7/27/2015	4329	Pantoea sp. PSNIH2	1484157 53335 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001426	Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	258594	7/30/2015	4811	Rhodopseudomonas palustris CGA009	258594 1076 1073 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008888	Methylomonas methanica (strain MC09)	857087	7/30/2015	4435	Methylomonas methanica MC09	857087 421 416 403 135618 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008898	Zobellia galactanivorans (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)	63186	7/30/2015	4708	Zobellia galactanivorans	63186 112040 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000578	Nanoarchaeum equitans (strain Kin4-M)	228908	7/30/2015	536	Nanoarchaeum equitans Kin4-M	228908 160232 193568 192989 2157 131567	Archaea	
UP000000577	Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	243231	8/2/2015	3402	Geobacter sulfurreducens PCA	243231 35554 28231 213422 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000580	Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	262316	7/30/2015	4316	Mycobacterium avium subsp. paratuberculosis K-10	262316 1770 1764 120793 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008212	Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222)	243275	7/30/2015	2753	Treponema denticola ATCC 35405	243275 158 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000012174	Eutypa lata (strain UCR-EL1) (Grapevine dieback disease fungus) (Eutypa armeniacae)	1287681	7/30/2015	11684	Eutypa lata UCREL1	1287681 97096 97095 42364 37989 222545 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001016	Mycoplasma mycoides subsp. mycoides SC (strain PG1)	272632	7/30/2015	978	Mycoplasma mycoides subsp. mycoides SC str. PG1	272632 44101 2103 2102 656088 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000000582	Corynebacterium glutamicum (strain ATCC 13032 / DSM 20300 / JCM 1318 / LMG 3730 / NCIMB 10025)	196627	8/2/2015	3093	Corynebacterium glutamicum ATCC 13032	196627 1718 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000581	Lactobacillus johnsonii (strain CNCM I-12250 / La1 / NCC 533)	257314	7/30/2015	1809	Lactobacillus johnsonii NCC 533	257314 33959 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002523	Onion yellows phytoplasma (strain OY-M)	262768	7/30/2015	730	Onion yellows phytoplasma OY-M	262768 100379 85620 33926 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000006657	Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) (Bacteroides splanchnicus)	709991	7/30/2015	3479	Odoribacter splanchnicus DSM 20712	709991 28118 283168 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006135	Acidithiobacillus caldus (strain SM-1)	990288	7/30/2015	3062	Acidithiobacillus caldus SM-1	990288 33059 119977 225058 225057 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006659	Corynebacterium variabile (strain DSM 44702 / JCM 12073 / NCIMB 30131) (Corynebacterium mooreparkense)	858619	7/30/2015	2972	Corynebacterium variabile DSM 44702	858619 1727 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006138	Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	713604	7/30/2015	9551	Amycolatopsis mediterranei S699	713604 33910 1813 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000030340	Mycobacterium sp. VKM Ac-1817D	1273687	7/27/2015	6100	Mycobacterium sp. VKM Ac-1817D	1273687 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000030341	Pseudoalteromonas sp. OCN003	1348114	7/27/2015	3997	Pseudoalteromonas sp. OCN003	1348114 53246 267888 135622 1236 1224 2 131567	Bacteria	Proteobacteria

UP000008392	Collimonas fungivorans (strain Ter331)	1005048	7/30/2015	4429	Collimonas fungivorans Ter331	1005048 158899 202907 75682 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008983	Ichthyophthirius multifiliis (strain G5) (White spot disease agent) (Ich)	857967	7/30/2015	8049	Ichthyophthirius multifiliis strain G5	857967 5932 5931 37090 31277 6020 431838 5878 33630 2759 131567	eukaryotes	
UP000008080	Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100)	264462	8/7/2015	3583	Bdellovibrio bacteriovorus HD100	264462 959 958 213483 213481 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000008895	Capnocytophaga canimorsus (strain 5)	860228	7/30/2015	2394	Capnocytophaga canimorsus Cc5	860228 28188 1016 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008393	Candidatus Tremblaya princeps PCVAL	1053648	7/27/2015	115	Candidatus Tremblaya princeps PCVAL	1053648 189385 189384 119066 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008984	Hypocrea jecorina (strain QM6a) (Trichoderma reesei)	431241	7/30/2015	9114	Trichoderma reesei QM6a	431241 51453 5543 5129 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000590	Methanococcus maripaludis (strain S2 / LL)	267377	7/30/2015	1722	Methanococcus maripaludis S2	267377 39152 2184 2183 2182 183939 28890 2157 131567	Archaea	
UP000000591	Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / FGSC 9923 / NRRL Y-1056) (Yeast) (Eremothecium gossypii)	284811	7/30/2015	4760	Eremothecium gossypii ATCC 10895	284811 33169 33170 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008066	Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719)	759272	7/30/2015	7182	Chaetomium thermophilum var. thermophilum DSM 1495	759272 285224 209285 5149 35718 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008068	Caenorhabditis brenneri (Nematode worm)	135651	7/30/2015	29982	Caenorhabditis brenneri	135651 6237 55885 6243 55879 6236 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000529	Protochlamydia amoebophila (strain UWE25)	264201	7/30/2015	2023	Candidatus Protochlamydia amoebophila UWE25	264201 362787 282132 92713 51291 204429 204428 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000000304	Drosophila simulans (Fruit fly)	7240	7/27/2015	15359	Drosophila simulans	7240 32351 32346 32341 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002194	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	882	7/30/2015	3517	Desulfovibrio vulgaris str. Hildenborough	882 881 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000593	Photobacterium profundum (Photobacterium sp. (strain SS9))	74109	7/30/2015	5328	Photobacterium profundum	74109 657 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000594	Bacillus anthracis	1392	7/30/2015	5493	Bacillus anthracis	1392 86661 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000030624	Geoglobus acetivorans	565033	7/27/2015	2213	Geoglobus acetivorans	565033 190818 2232 2231 183980 28890 2157 131567	Archaea	
UP000030635	Clostridium baratii str. Sullivan	1415775	7/27/2015	3167	Clostridium baratii str. Sullivan	1415775 1561 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000030636	Bifidobacterium pseudolongum PV8-2	1447715	7/27/2015	1578	Bifidobacterium pseudolongum PV8-2	1447715 1694 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000030625	Bifidobacterium kashiwanohense PV20-2	1447716	8/14/2015	1870	Bifidobacterium kashiwanohense PV20-2	1447716 630129 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000030653	Dacryopinax sp. (strain DJM 731) (Brown rot fungus)	745407	7/27/2015	10233	Dacryopinax sp. DJM-731 SS1	745407 139276 5254 28997 452332 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000030634	Deinococcus swuensis	1182571	7/27/2015	2886	Deinococcus swuensis	1182571 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000030665	Trichuris trichiura (Whipworm) (Trichocephalus trichiurus)	36087	7/27/2015	9625	Trichuris trichiura	36087 36086 119093 6329 1457286 119088 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000030669	Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) (Brown rot fungus)	670483	7/27/2015	11735	Gloeophyllum trabeum ATCC 11539	670483 104355 40443 452340 452339 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000030673	Plasmodium falciparum (isolate NF54)	5843	7/27/2015	5920	Plasmodium falciparum NF54	5843 5833 418107 5820 1639119 5819 422676 5794 33630 2759 131567	eukaryotes	
UP000005893	Enterobacteria phage phiX174 (Isolate Sanger) (Bacteriophage phi-X174)	1217068	7/27/2015	10	Enterobacteria phage phiX174 isolate Sanger	1217068 10847 374840 10842 10841 29258 10239	Vruses	
UP000030689	Eutrema salsugineum (Saltwater cress) (Sisymbrium salsugineum)	72664	7/27/2015	28349	Eutrema salsugineum	72664 98005 981100 3700 3699 91836 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000030680	Galdieria sulphuraria (Red alga)	130081	7/27/2015	7035	Galdieria sulphuraria	130081 83373 265316 265318 2797 2763 2759 131567	eukaryotes	
UP000001635	Cyclobacterium marinum (strain ATCC 25205 / DSM 745) (Flectobacillus marinus)	880070	8/7/2015	4983	Cyclobacterium marinum DSM 745	880070 104 68288 563798 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001636	Arthromitus sp. (strain SFB-mouse-Japan)	1029718	7/30/2015	1487	Candidatus Arthromitus sp. SFB-mouse-Japan	1029718 49118 49082 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001640	Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) (Yeast) (Saccharomyces castellii)	1064592	7/30/2015	5565	Naumovozyma castellii CBS 4309	1064592 27288 278028 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000012651	Atopobium minutum 10063974	997872	7/27/2015	1539	Atopobium minutum 10063974	997872 1381 1380 1643824 84999 84998 201174 2 131567	Bacteria	Actinobacteria
UP000030742	Dendroctonus ponderosae (Mountain pine beetle)	77166	7/27/2015	12251	Dendroctonus ponderosae	77166 77156 55867 7042 71529 41088 41084 7041 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000012672	Candidatus Methanomethylophilus alvus Mx1201	1236689	7/27/2015	1643	Candidatus Methanomethylophilus alvus Mx1201	1236689 1291540 1291539 1577788 1235850 183967 28890 2157 131567	Archaea	
UP000030745	Saprolegnia parasitica (strain CBS 223.65)	695850	7/27/2015	20052	Saprolegnia parasitica CBS 223.65	695850 101203 4769 4764 4763 4762 33634 2759 131567	eukaryotes	

UP000012675	Enterococcus casseliflavus EC20	565655	7/27/2015	3112	Enterococcus casseliflavus EC20	565655 37734 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002489	Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	660025	7/30/2015	17784	Fusarium oxysporum Fo5176	660025 5507 171631 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000030763	Eimeria maxima (Coccidian parasite)	5804	7/27/2015	6057	Eimeria maxima	5804 5800 5799 423054 75739 5796 1280412 5794 33630 2759 131567	eukaryotes	
UP000030748	Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	4155	7/27/2015	28677	Erythranthe guttata	4155 1502711 41399 4143 91888 71274 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000030787	Candidatus Methanoplasma termitum	1577791	7/27/2015	1393	Candidatus Methanoplasma termitum	1577791 1607807 1577788 1235850 183967 28890 2157 131567	Archaea	
UP000008520	Lactococcus garvieae (strain Lg2) (Enterococcus seriolicida)	420890	7/30/2015	1938	Lactococcus garvieae Lg2	420890 1363 1357 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000689	Naumovozyma dairenensis (strain ATCC 10597 / BCRC 20456 / CBS 421 / NBRC 0211 / NRRL Y-12639) (Saccharomyces dairenensis)	1071378	7/30/2015	5523	Naumovozyma dairenensis CBS 421	1071378 27289 278028 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000030789	Hymenobacter sp. DG25B	1385664	7/27/2015	3153	Hymenobacter sp. DG25B	1385664 89966 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000030746	Lottia gigantea (Giant owl limpet)	225164	7/27/2015	23675	Lottia gigantea	225164 72691 69676 216260 69675 6448 6447 1206795 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007041	Clostridium sticklandii (strain ATCC 12662 / DSM 519 / JCM 1433 / NCIB 10654)	499177	7/30/2015	2572	[Clostridium] sticklandii DSM 519	499177 1511 1481960 186804 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001037	Pyrolobus fumarii (strain DSM 11204 / 1A)	694429	7/30/2015	1967	Pyrolobus fumarii 1A	694429 54252 54251 2307 114380 183924 28889 2157 131567	Archaea	
UP000001645	Meleagris gallopavo (Common turkey)	9103	7/27/2015	16534	Meleagris gallopavo	9103 9102 466552 9005 8976 1549675 8825 8782 436492 436491 436489 436486 8492 1329799 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001073	Nomascus leucogenys (Northern white-cheeked gibbon) (Hylobates leucogenys)	61853	7/27/2015	19734	Nomascus leucogenys	61853 325165 9577 314295 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000515	Drosophila x virus (isolate Chung/1996) (DXV)	654931	7/30/2015	3	Drosophila x virus (isolate Chung)	654931 48981 39752 10993 35325 10239	Vruses	
UP000000702	Trypanosoma congolense (strain IL3000)	1068625	7/30/2015	5906	Trypanosoma congolense IL3000	1068625 5692 47569 5690 5654 5653 33682 2759 131567	eukaryotes	
UP000007528	Chicken anemia virus (isolate Germany Cuxhaven-1) (CAV)	73475	7/30/2015	3	Chicken anemia virus Cuxhaven-1/Germany	73475 12618 227307 39724 29258 10239	Vruses	
UP000000516	Lymphocystis disease virus 1 (isolate Darai) (LCDV-1)	654922	7/30/2015	1	Lymphocystis disease virus 1 (isolate Darai)	654922 36363 10494 10486 35237 10239	Vruses	
UP000001074	Myotis lucifugus (Little brown bat)	59463	7/27/2015	20651	Myotis lucifugus	59463 9434 9431 30560 9397 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007020	Rachiplusia ou multiple nucleopolyhedrovirus (strain R1) (RoMNPV)	654904	7/30/2015	149	Rachiplusia ou MNPV (strain R1)	654904 80366 307456 558016 10442 35237 10239	Vruses	
UP000007022	Bovine parvovirus (isolate pAT153/1986) (BPV)	648243	7/30/2015	3	Bovine parvovirus pAT153/1986	648243 10784 1511873 1507401 40119 10780 29258 10239	Vruses	
UP000000514	Acidianus filamentous virus 1 (isolate United States/Yellowstone) (AFV-1)	654909	7/30/2015	40	Acidianus filamentous virus 1 (isolate Yellowstone)	654909 235266 341941 10477 1511857 35237 10239	Vruses	
UP000007018	Mastomys natalensis papillomavirus (isolate African multimammate rat) (MnPV)	654915	7/30/2015	6	Mastomys natalensis papillomavirus (isolate African multimammate rat)	654915 10567 325456 151340 35237 10239	Vruses	
UP000007017	Sulfolobus islandicus filamentous virus (isolate Iceland/Hveragerdi) (SIFV)	654908	7/30/2015	73	Sulfolobus islandicus filamentous virus (isolate Hveragerdi)	654908 176106 341940 10477 1511857 35237 10239	Vruses	
UP000007023	Porcine circovirus 1 (isolate China) (PCV1)	654929	7/30/2015	2	Porcine circovirus 1 (isolate China)	654929 133704 39725 39724 29258 10239	Vruses	
UP000007024	His1 virus (isolate Australia/Victoria) (His1V) (Haloarcula hispanica virus 1)	654912	7/30/2015	35	His1 virus (isolate Victoria)	654912 128708 352476 35237 10239	Vruses	
UP000000513	Acidianus bottle-shaped virus (isolate Italy/Pozzuoli) (ABV)	654911	7/30/2015	54	Acidianus bottle-shaped virus (isolate Pozzuoli)	654911 437444 573054 573053 35237 10239	Vruses	
UP000007021	Ostreid herpesvirus 1 (isolate France) (OsHV-1) (Pacific oyster herpesvirus)	654903	7/30/2015	116	Ostreid herpesvirus 1 (isolate France)	654903 261939 548686 548685 548681 35237 10239	Vruses	
UP000001646	Anolis carolinensis (Green anole) (American chameleon)	28377	7/27/2015	19110	Anolis carolinensis	28377 28376 81957 8515 8511 1329911 1329912 1329950 1329961 8509 8504 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007025	Apple chlorotic leaf spot virus (isolate plum P863) (ACLSV)	73473	7/30/2015	3	Apple chlorotic leaf spot virus (isolate PLUM P863)	73473 12175 40276 675068 675063 35278 439488 10239	Vruses	
UP000008908	Muricauda ruestringensis (strain DSM 13258 / LMG 19739 / B1)	886377	7/30/2015	3425	Muricauda ruestringensis DSM 13258	886377 111501 111500 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000030902	Candidatus Saccharibacteria oral taxon TM7x	1476577	7/27/2015	692	Candidatus Saccharibacteria oral taxon TM7x	1476577 95818 2323 2 131567	Bacteria	Unclassified Bacteria

UP000007019	Murine minute virus (strain MVM prototype) (MVM) (Murine minute virus (strain MVM(p)))	648235	8/2/2015	8	Murine minute virus strain MVM prototype	648235 10794 1511908 1506574 40119 10780 29258 10239	Vruses	
UP000001075	Cricetulus griseus (Chinese hamster) (Cricetulus barabensis griseus)	10029	7/27/2015	23884	Cricetulus griseus	10029 10028 10026 337677 337687 33553 9989 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000030907	Sphingopyxis fribergensis	1515612	7/27/2015	4797	Sphingopyxis fribergensis	1515612 165697 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000009072	Mycoplasma mobile (strain ATCC 43663 / 163K / NCTC 11711)	267748	7/30/2015	628	Mycoplasma mobile 163K	267748 2118 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000001610	Cordyceps militaris (strain CM01) (Caterpillar fungus)	983644	7/30/2015	9651	Cordyceps militaris CM01	983644 73501 45234 474943 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008784	Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) (Nematode-trapping fungus) (Didymozoophaga oligospora)	756982	7/30/2015	11478	Arthrobotrys oligospora ATCC 24927	756982 13349 261301 47022 47021 189479 189478 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000709	Spathaspora passalidarum (strain NRRL Y-27907 / 11-Y1)	619300	7/30/2015	5973	Spathaspora passalidarum NRRL Y-27907	619300 340170 412764 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001611	Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	498257	7/30/2015	10530	Verticillium dahliae VdLs.17	498257 27337 1036719 1033979 1033978 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000030854	Uncinula necator (Grape powdery mildew)	52586	7/27/2015	6482	Erysiphe necator	52586 5121 34371 5120 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001275	Sphingobium sp. SYK-6	627192	7/27/2015	4050	Sphingobium sp. SYK-6	627192 165695 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001279	Lactobacillus ruminis (strain ATCC 27782 / RF3)	1069534	7/30/2015	1851	Lactobacillus ruminis ATCC 27782	1069534 1623 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000707	Candida tenuis (strain ATCC 10573 / BCRC 21748 / CBS 615 / JCM 9827 / NBRC 10315 / NRRL Y-1498 / VKM Y-70) (Yeast)	590646	7/30/2015	6051	Candida tenuis ATCC 10573	590646 45596 1539853 766765 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001274	Pseudogulbenkiania sp. (strain NH8B)	748280	7/30/2015	3958	Pseudogulbenkiania sp. NH8B	748280 568394 1499392 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008178	Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	585394	7/30/2015	3351	Roseburia hominis A2-183	585394 301301 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000009186	Flavobacterium branchiophilum (strain FL-15)	1034807	7/30/2015	2848	Flavobacterium branchiophilum FL-15	1034807 55197 237 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000030944	Candidatus Nitrosopelagicus brevis	1410606	7/27/2015	1444	Candidatus Nitrosopelagicus brevis	1410606 1593364 651142 651137 2157 131567	Archaea	
UP000030901	Frischella perrara	1267021	7/27/2015	2270	Frischella perrara	1267021 1335631 1240483 1240482 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001285	Lactobacillus sanfranciscensis (strain TMW 1.1304)	714313	7/30/2015	1263	Lactobacillus sanfranciscensis TMW	714313 1625 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000007646	Loxodonta africana (African elephant)	9785	7/30/2015	25624	Loxodonta africana	9785 9784 9780 9779 311790 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007648	Sarcophilus harrisii (Tasmanian devil) (Sarcophilus laniarius)	9305	7/27/2015	22388	Sarcophilus harrisii	9305 9304 9277 38608 9263 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008909	Clonorchis sinensis (Chinese liver fluke)	79923	7/27/2015	13606	Clonorchis sinensis	79923 79922 6196 6194 6193 6179 6178 6157 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008911	Aeropyrum pernix ovoid virus 1 (APOV1)	1032474	7/27/2015	21	Aeropyrum pernix ovoid virus 1	1032474 1298634 324686 35237 10239	Vruses	
UP000031036	Toxocara canis (Canine roundworm)	6265	7/27/2015	18499	Toxocara canis	6265 6264 33259 33256 6249 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008313	Trypanosoma cruzi	5693	7/30/2015	10806	Trypanosoma cruzi	5693 47570 5690 5654 5653 33682 2759 131567	eukaryotes	
UP000007635	Gasterosteus aculeatus (Three-spined stickleback)	69293	7/27/2015	27249	Gasterosteus aculeatus	69293 69292 69291 1490020 8100 8111 1489922 1489872 123369 123368 123367 123366 123365 1489388 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000009286	Micavibrio aeruginosavorus (strain ARL-13)	856793	7/30/2015	2432	Micavibrio aeruginosavorus ARL-13	856793 349221 213485 82117 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002640	Phytophthora sojae (strain P6497) (Soybean stem and root rot agent) (Phytophthora megasperma f. sp. glycines)	1094619	7/27/2015	25721		67593 4783 4776 4762 33634 2759 131567	eukaryotes	
UP000002654	Thermoproteus tenax (strain ATCC 35583 / NBRC 100435 / JCM 9277 / Kra 1)	768679	7/30/2015	2047	Thermoproteus tenax Kra 1	768679 2271 2270 2267 2266 183924 28889 1783275 2157 131567	Archaea	
UP000031100	Bacillus sp. X1(2014)	1565991	7/27/2015	2943	Bacillus sp. X1(2014)	1565991 1386 186817 1385 91061 1239 1783272 2 131567	Bacteria	firmicutes
UP000005219	Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	693746	7/30/2015	4593	Oscillibacter valericigenes Sjm18-20	693746 351091 459786 216572 186802 186801 1239 1783272 2 131567	Bacteria	firmicutes
UP000009283	Bacillus coagulans 36D1	345219	7/27/2015	3275	Bacillus coagulans 36D1	345219 1398 1386 186817 1385 91061 1239 1783272 2 131567	Bacteria	firmicutes
UP000009282	Glaciecola nitratireducens (strain JCM 12485 / KCTC 12276 / FR1064)	1085623	7/30/2015	3653	Glaciecola nitratireducens FR1064	1085623 300231 89404 72275 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002663	Tetragenococcus halophilus (strain DSM 20338 / JCM 20259 / NCIMB 9735 / NBRC 12172) (Pediococcus halophilus)	945021	7/30/2015	2507	Tetragenococcus halophilus NBRC 12172	945021 51669 51668 81852 186826 91061 1239 1783272 2 131567	Bacteria	firmicutes
UP000002815	Streptococcus infantis ATCC 700779	889204	7/27/2015	1927	Streptococcus infantis ATCC 700779	889204 68892 1301 1300 186826 91061 1239 2 131567	Bacteria	firmicutes

UP000031104	Francisella guangzhouensis	594679	7/30/2015	1417	Francisella guangzhouensis	594679 262 34064 72273 1236 1224 2 131567	Bacteria	Proteobacteria
UP000031113	Streptomyces sp. 769	1262452	7/27/2015	9427	Streptomyces sp. 769	1262452 1883 2062 85011 1760 201174 1783272 2 131567	Bacteria	Actinobacteria
UP000031121	Coriobacteriaceae bacterium 68-1-3	1531429	7/27/2015	1405	Coriobacteriaceae bacterium 68-1-3	1531429 84113 84107 84999 84998 201174 1783272 2 131567	Bacteria	Actinobacteria
UP000012960	Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	214687	8/2/2015	36474	Musa acuminata subsp. malaccensis	214687 4641 4640 4637 4618 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000012984	Mycoplasma putrefaciens Mput9231	1292033	7/27/2015	666	Mycoplasma putrefaciens Mput9231	1292033 2123 2093 2092 2085 31969 544448 1783272 2 131567	Bacteria	Tenericutes
UP000007093	Acidaminococcus intestini (strain RyC-MR95)	568816	7/30/2015	2386	Acidaminococcus intestini RyC-MR95	568816 187327 904 909930 1843488 909932 1239 1783272 2 131567	Bacteria	Tenericutes
UP000012987	Mannheimia haemolytica M42548	1316932	7/27/2015	2705	Mannheimia haemolytica M42548	1316932 75985 75984 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008315	Methylomicrobium alcaliphilum (strain DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z)	1091494	7/30/2015	4041	Methylomicrobium alcaliphilum 20Z	1091494 271065 39773 403 135618 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006908	Gallibacterium anatis (strain UMN179) (Pasteurella anatis)	1005058	7/30/2015	2482	Gallibacterium anatis UMN179	1005058 750 155493 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008316	Burkholderia gladioli (strain BSR3)	999541	7/30/2015	7351	Burkholderia gladioli BSR3	999541 28095 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000031138	Xanthomonas sacchari	56458	7/27/2015	3736	Xanthomonas sacchari	56458 338 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007432	Bombyx mori densovirus 5 (isolate Shinshu) (BmDNV-5)	648251	7/30/2015	4	Bombyx mori densovirus 5 isolate Shinshu		Vruses	
UP000009022	Trichoplax adhaerens (Trichoplax reptans)	10228	7/30/2015	11520	Trichoplax adhaerens	10228 10227 10226 33208 33154 2759 131567	eukaryotes	
UP000008854	Schistosoma mansoni (Blood fluke)	6183	7/30/2015	11723	Schistosoma mansoni	6183 6181 31245 31244 6180 6179 6178 6157 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000009027	Trypanosoma vivax (strain Y486)	1055687	7/27/2015	3778	Trypanosoma vivax Y486	1055687 5699 47571 5690 5654 5653 33682 2759 131567	eukaryotes	
UP000006141	Rhodotorula glutinis (strain ATCC 204091 / IIP 30 / MTCC 1151) (Yeast)	1001064	7/30/2015	2816	Rhodotorula glutinis ATCC 204091	1001064 5286 5533 1799696 231213 162481 29000 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000007730	Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	504832	7/30/2015	3624	Oligotropha carboxidovorans OM5	504832 40137 40136 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008850	Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	1082931	7/30/2015	3875	Pelagibacterium halotolerans B2	1082931 531813 1082930 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006813	Heterocephalus glaber (Naked mole rat)	10181	7/27/2015	21449	Heterocephalus glaber	10181 10180 10167 33550 9989 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008513	Neurospora tetrasperma (strain FGSC 2509 / P0656)	510952	7/30/2015	11177	Neurospora tetrasperma FGSC 2509	510952 40127 5140 5148 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000009038	Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	380704	7/30/2015	10949	Aspergillus niger ATCC 1015	380704 5061 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000009130	Macaca fascicularis (Crab-eating macaque) (Cynomolgus monkey)	9541	7/27/2015	17396	Macaca fascicularis	9541 9539 9528 9527 314294 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000031368	Rhizobium gallicum bv. gallicum R602	1418105	7/27/2015	7034	Rhizobium gallicum bv. gallicum R602	1418105 142627 56730 379 227290 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000031386	Parvimonas micra	33033	7/27/2015	1418	Parvimonas micra	33033 543311 1570339 1737405 1737404 1239 1783272 2 131567	Bacteria	Firmicutes
UP000013026	Meiothermus ruber (strain ATCC 35948 / DSM 1279 / VKM B-1258 / 21) (Thermus ruber)	504728	7/27/2015	3037	Meiothermus ruber DSM 1279	504728 277 65551 188786 68933 188787 1297 1783272 2 131567	Bacteria	Deinococcus-Thermus
UP000009131	Mixia osmundae (strain CBS 9802 / IAM 14324 / JCM 22182 / KY 12970)	764103	7/30/2015	6725	Mixia osmundae IAM 14324	764103 34349 34348 165795 432026 432025 29000 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000031392	Neisseria elongata subsp. glycolytica ATCC 29315	546263	7/27/2015	2073	Neisseria elongata subsp. glycolytica ATCC 29315	546263 88719 495 482 481 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006812	Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	1033177	7/30/2015	11491	Aspergillus kawachii IFO 4308	1033177 40384 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000031443	Chelonia mydas (Green sea-turtle) (Chelonia agassizi)	8469	7/27/2015	18960	Chelonia mydas	8469 8468 8465 27791 1579336 1579337 8464 8459 1329799 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000031449	Jeotgalibacillus sp. D5	1508404	7/27/2015	4426	Jeotgalibacillus sp. D5	1508404 157226 186818 1385 91061 1239 1783272 2 131567	Bacteria	firmicutes
UP000031466	Flavobacterium sp. KMS	1566023	7/27/2015	4503	Flavobacterium sp. KMS	1566023 237 49546 200644 117743 976 68336 1783270 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000013140	Thauera sp. 27	305700	7/27/2015	4271	Thauera sp. 27	305700 33057 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007319	Azospirillum brasilense Sp245	1064539	7/27/2015	7541	Azospirillum brasilense Sp245	1064539 192 191 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000031496	Planococcus sp. PAMC 21323	1526927	7/27/2015	3084	Planococcus sp. PAMC 21323	1526927 1372 186818 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000031501	Streptomyces pluripotens	1355015	7/27/2015	12399	Streptomyces pluripotens	1355015 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000013117	Acinetobacter gerneri DSM 14967 = CIP 107464	1120926	7/27/2015	4174	Acinetobacter gerneri DSM 14967 = CIP 107464	1120926 202952 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000013121	Acinetobacter guillouiae CIP 63.46	1217655	7/27/2015	4594	Acinetobacter guillouiae CIP 63.46	1217655 106649 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000005667	Azospirillum lipoferum (strain 4B)	862719	7/30/2015	6062	Azospirillum lipoferum 4B	862719 193 191 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria

UP000005870	Pseudoxanthomonas spadix (strain BD-a59)	1045855	7/30/2015	3147	Pseudoxanthomonas spadix BD-a59	1045855 415229 83618 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000005868	Thermovirga lienii (strain ATCC BAA-1197 / DSM 17291 / Cas60314)	580340	7/30/2015	1853	Thermovirga lienii DSM 17291	580340 336261 336260 649777 649776 649775 508458 2 131567	Bacteria	Synergistetes
UP000006346	Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	768706	8/4/2015	5217	Desulfosporosinus orientis DSM 765	768706 1563 79206 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000006860	Rubinisphaera brasiliensis (strain ATCC 49424 / DSM 5305 / JCM 21570 / NBRC 103401 / IFAM 1448) (Planctomyces brasiliensis)	756272	7/30/2015	4710	Rubinisphaera brasiliensis DSM 5305	756272 119 1649490 126 112 203683 203682 2 131567	Bacteria	Planctomycetes
UP000005877	Methanosaeta harundinacea (strain 6Ac)	1110509	7/30/2015	2358	Methanosaeta harundinacea 6Ac	1110509 301375 2222 143067 94695 224756 28890 2157 131567	Archaea	
UP000000517	Fibrobacter succinogenes (strain ATCC 19169 / S85)	59374	7/30/2015	2870	Fibrobacter succinogenes subsp. succinogenes S85	59374 834 833 832 204431 218872 204430 65842 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000005666	Tetrapisispora phaffii (strain ATCC 24235 / CBS 4417 / NBRC 1672 / NRRL Y-8282 / UCD 70-5) (Yeast) (Fabospora phaffii)	1071381	7/30/2015	5238	Tetrapisispora phaffii CBS 4417	1071381 113608 113604 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006866	Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL)	572479	7/30/2015	2055	Halanaerobium praevalens DSM 2228	572479 2331 2330 972 53433 186801 1239 2 131567	Bacteria	Firmicutes
UP000006868	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	886882	7/30/2015	5377	Paenibacillus polymyxa SC2	886882 1406 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000006871	Ketogulonicigenium vulgare (strain Y25)	880591	7/30/2015	3209	Ketogulonicigenium vulgare Y25	880591 92945 92944 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006873	Eubacterium limosum (strain KIST612)	903814	7/30/2015	4506	Eubacterium limosum KIST612	903814 1736 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000006875	Ilyobacter polytropus (strain DSM 2926 / CuHBu1)	572544	7/30/2015	2859	Ilyobacter polytropus DSM 2926	572544 167642 167639 203492 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000006876	Achromobacter xylosoxidans (strain A8)	762376	8/2/2015	6798	Achromobacter xylosoxidans A8	762376 85698 222 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006878	Arthrobacter arilaitensis (strain DSM 16368 / CIP 108037 / JCM 13566 / Re117)	861360	7/30/2015	3380	Arthrobacter arilaitensis Re117	861360 256701 1663 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006631	Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	712898	7/30/2015	4590	Pantoea vagans C9-1	712898 470934 53335 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006539	Solenopsis invicta (Red imported fire ant) (Solenopsis wagneri)	13686	7/27/2015	14193	Solenopsis invicta	13686 13685 144017 34695 36668 34725 7434 7400 7399 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007248	Infectious pancreatic necrosis virus (strain Jasper) (IPNV)	11003	7/30/2015	3	Infectious pancreatic necrosis virus - Jasper	11003 11002 39750 10993 35325 10239	Vruses	
UP000007249	Avian infectious bursal disease virus (isolate Chicken/UK/UK661/1989) (IBDV) (Gumboro disease virus)	644440	7/30/2015	3	Infectious bursal disease virus chicken/UK/UK661/1989	644440 10995 39751 10993 35325 10239	Vruses	
UP000007250	Blotched snakehead virus (BSNV) (Channa lucius virus)	311176	7/27/2015	3	Blotched snakehead virus	311176 564643 10993 35325 10239	Vruses	
UP000007251	Cryphonectria hypovirus 1 (strain EP713) (CHV-1/EP713) (Chestnut blight fungus hypovirulence-associated virus)	12478	7/30/2015	2	Cryphonectria hypovirus 1-EP713	12478 40281 39749 39748 35325 10239	Vruses	
UP000007252	Human picobirnavirus (strain Human/Thailand/Hy005102/-) (PBV)	647332	7/30/2015	3	Human picobirnavirus strain Hy005102	647332 145856 104394 585893 35325 10239	Vruses	
UP000007253	Reovirus type 1 (strain Lang) (T1L) (Mammalian orthoreovirus 1)	10884	7/30/2015	11	Mammalian orthoreovirus 1 Lang	10884 538120 351073 10882 689831 10880 35325 10239	Vruses	
UP000007662	Bluetongue virus 10 (isolate USA) (BTV 10)	10900	7/30/2015	11	Bluetongue virus (serotype 10 / American isolate)	10900 10906 40051 10892 689832 10880 35325 10239	Vruses	
UP000007663	Rotavirus B (isolate Human/China/ADRV-N J19/1997) (RV ADRV-N) (Rotavirus (isolate novel adult diarrhea rotavirus-J19))	335103	7/30/2015	11	Adult diarrheal rotavirus strain J19	335103 1348384 10912 689832 10880 35325 10239	Vruses	
UP000007664	Rotavirus C (isolate Human/United Kingdom/Bristol/1989) (RV-C)	31567	7/30/2015	11	Human rotavirus (group C / strain Bristol)	31567 10943 36427 10912 689832 10880 35325 10239	Vruses	
UP000002311	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	559292	8/2/2015	6721	Saccharomyces cerevisiae S288c	559292 4932 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000031515	Chaetura pelagica (Chimney swift)	8897	7/27/2015	3162	Chaetura pelagica	8897 8896 8893 8892 8825 8782 436492 436491 436489 436486 8492 1329799 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002315	Methanothermus fervidus (strain ATCC 43054 / DSM 2088 / JCM 10308 / V24 S)	523846	7/30/2015	1283	Methanothermus fervidus DSM 2088	523846 2180 2179 2178 2158 183925 28890 2157 131567	Archaea	
UP000013307	Archaeoglobus sulfaticallidus PM70-1	387631	7/27/2015	2213	Archaeoglobus sulfaticallidus PM70-1	387631 1316941 2233 2232 2231 183980 28890 2157 131567	Archaea	
UP000013300	Bacillus sp. 1NLA3E	666686	7/27/2015	4384	Bacillus sp. 1NLA3E	666686 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000008177	Botryotinia fuckeliana (strain T4) (Noble rot fungus) (Botrytis cinerea)	999810	7/30/2015	16338	Botrytis cinerea T4	999810 40559 33196 28983 5178 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000007151	Danaus plexippus (Monarch butterfly)	13037	7/27/2015	16253	Danaus plexippus	13037 151542 13036 344705 30248 127218 33415 37572 104431 37567 41197 41196 41191 7088 85604 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007106	Azoarcus sp. KH32C	748247	8/4/2015	5176	Azoarcus sp. KH32C	748247 12960 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007113	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	682795	7/30/2015	4804	Granulicella mallensis MP5ACTX8	682795 940614 940557 204434 204433 204432 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000007112	Blattabacterium sp. (Cryptocercus punctulatus) str. Cpu	1075399	7/27/2015	548	Blattabacterium sp. (Cryptocercus punctulatus) str. Cpu	1075399 164514 34098 39782 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007115	Hypocrea virens (strain Gv29-8 / FGSC 10586) (Gliocladium virens) (Trichoderma virens)	413071	7/30/2015	12389	Trichoderma virens Gv29-8	413071 29875 5543 5129 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005627	Torulaspora delbrueckii (strain ATCC 10662 / CBS 1146 / NBRC 0425 / NCYC 2629 / NRRL Y-866) (Yeast) (Candida colliculosa)	1076872	7/30/2015	4966	Torulaspora delbrueckii CBS 1146	1076872 4950 4948 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005633	Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	640081	7/30/2015	3432	Dechlorosoma suillum PS	640081 146939 146937 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000005634	Pseudovibrio sp. (strain FO-BEG1)	911045	7/30/2015	5456	Pseudovibrio sp. FO-BEG1	911045 258255 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000005631	Owenweeksia hongkongensis (strain DSM 17368 / JCM 12287 / NRRL B-23963)	926562	7/30/2015	3471	Owenweeksia hongkongensis DSM 17368	926562 253245 267986 246874 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000005632	Sphaerochaeta pleomorpha (strain ATCC BAA-1885 / DSM 22778 / Grapes)	158190	7/30/2015	3150	Sphaerochaeta pleomorpha str. Grapes	158190 1131707 399320 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000005426	Hypocrea atroviridis (strain ATCC 20476 / IMI 206040) (Trichoderma atroviride)	452589	7/30/2015	11815	Trichoderma atroviride IMI 206040	452589 63577 5543 5129 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005435	Clostridium clariflavum (strain DSM 19732 / NBRC 101661 / EBR45)	720554	7/30/2015	3774	[Clostridium] clariflavum DSM 19732	720554 288965 1508657 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000005437	Pseudomonas fluorescens F113	1114970	7/27/2015	5837	Pseudomonas fluorescens F113	1114970 294 136843 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000005438	Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10)	700598	7/30/2015	7171	Niastella koreensis GR20-10	700598 354356 354354 563835 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000005436	Tannerella forsythia (strain ATCC 43037 / JCM 10827 / FDC 338) (Bacteroides forsythus)	203275	7/30/2015	2978	Tannerella forsythia 92A2	203275 28112 195950 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007148	Piriformospora indica (strain DSM 11827)	1109443	7/30/2015	11780	Piriformospora indica DSM 11827	1109443 65672 65702 1506295 297313 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000005442	Mycobacterium rhodesiae (strain NBB3)	710685	7/30/2015	6105	Mycobacterium rhodesiae NBB3	710685 36814 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007322	Thielavia heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) (Myceliophthora thermophila)	573729	7/30/2015	9081	Myceliophthora thermophila ATCC 42464	573729 78579 49009 35718 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005440	Actinoplanes sp. (strain ATCC 31044 / CBS 674.73 / SE50/110)	134676	7/30/2015	8249	Actinoplanes sp. SE50/110	134676 1865 28056 85008 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006934	Australian bat lyssavirus (isolate Bat/AUS/1996) (ABLV)	446561	7/30/2015	5	Australian bat lyssavirus bat/AUS/1996	446561 90961 11286 11270 11157 35301 439488 10239	Vruses	
UP000013523	Clostridium pasteurianum BC1	86416	7/27/2015	4454	Clostridium pasteurianum BC1	86416 1501 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007844	Desulfovibrio africanus str. Walvis Bay	690850	7/27/2015	3699	Desulfovibrio africanus str. Walvis Bay	690850 873 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000005444	Pediococcus claussenii (strain ATCC BAA-344 / DSM 14800 / JCM 18046 / KCTC 3811 / P06)	701521	7/30/2015	1877	Pediococcus claussenii ATCC BAA-344	701521 187452 1253 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000007845	Desulfovibrio desulfuricans ND132	641491	7/27/2015	3451	Desulfovibrio desulfuricans ND132	641491 876 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000013520	Desulfotomaculum gibsoniae DSM 7213	767817	7/27/2015	4313	Desulfotomaculum gibsoniae DSM 7213	767817 102134 1562 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000013521	Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	1287680	7/30/2015	10365	Neofusicoccum parvum UCRNP2	1287680 310453 407951 45131 451869 159987 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005638	Flavobacterium columnare (strain ATCC 49512 / CIP 103533 / TG 44/87)	1041826	7/30/2015	2617	Flavobacterium columnare ATCC 49512	1041826 996 237 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000005225	Otolemur garnettii (Small-eared galago) (Garnett's greater bushbaby)	30611	7/27/2015	19931	Otolemur garnettii	30611 30610 40297 376917 376911 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007842	Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	1003195	7/30/2015	7537	Streptomyces cattleya NRRL 8057 = DSM 46488	1003195 29303 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005447	Cavia porcellus (Guinea pig)	10141	7/30/2015	19923	Cavia porcellus	10141 10140 10139 33550 9989 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000013541	Actinoplanes sp. N902-109	649831	7/27/2015	8211	Actinoplanes sp. N902-109	649831 1865 28056 85008 1760 201174 2 131567	Bacteria	Actinobacteria
UP000013548	Mycobacterium tuberculosis CAS/NITR204	1310114	7/30/2015	3927	Mycobacterium tuberculosis CAS/NITR204	1310114 1306413 1773 77643 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000013561	Serratia symbiotica str. 'Cinara cedri'	568817	8/4/2015	672	Serratia symbiotica str. 'Cinara cedri'	568817 138074 613 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008181	Thielavia terrestris (strain ATCC 38088 / NRRL 8126) (Acremonium alabamense)	578455	7/30/2015	9760	Thielavia terrestris NRRL 8126	578455 35720 35719 35718 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000009010	Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	745277	7/30/2015	4841	Rahnella aquatilis CIP 78.65 = ATCC 33071	745277 34038 34037 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007161	Marinitoga piezophila (strain DSM 14283 / JCM 11233 / KA3)	443254	7/30/2015	2044	Marinitoga piezophila KA3	443254 149715 160798 1643949 1643947 188708 200918 2 131567	Bacteria	Thermotogae
UP000007742	Oceanimonas sp. (strain GK1)	511062	7/30/2015	3190	Oceanimonas sp. GK1	511062 129577 84642 135624 1236 1224 2 131567	Bacteria	Proteobacteria
UP000013777	Enterococcus asini ATCC 700915	1158606	7/27/2015	2389	Enterococcus asini ATCC 700915	1158606 57732 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000013782	Enterococcus pallens ATCC BAA-351	1158607	7/27/2015	5181	Enterococcus pallens ATCC BAA-351	1158607 160454 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000013776	Taphrina deformans (strain PYCC 5710 / ATCC 11124 / CBS 356.35 / IMI 108563 / JCM 9778 / NBRC 8474) (Peach leaf curl fungus) (Lalaria deformans)	1097556	7/30/2015	4659	Taphrina deformans PYCC 5710	1097556 5011 5010 5009 5008 147555 451866 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000013785	Enterococcus phoeniculicola ATCC BAA-412	1158610	7/27/2015	3510	Enterococcus phoeniculicola ATCC BAA-412	1158610 154621 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000005226	Takifugu rubripes (Japanese pufferfish) (Fugu rubripes)	31033	7/27/2015	47858	Takifugu rubripes	31033 31032 31031 32517 31028 31022 1489922 1489872 123369 123368 123367 123366 123365 1489388 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000013827	Emiliania huxleyi CCMP1516	280463	8/2/2015	35608	Emiliania huxleyi	280463 2903 2902 418966 73020 2830 2759 131567	eukaryotes	
UP000006791	Chloracidobacterium thermophilum (strain B)	981222	7/30/2015	3053	Chloracidobacterium thermophilum B	981222 458033 458032 1562566 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000013858	Enterococcus haemoperoxidus ATCC BAA-382	1158608	7/27/2015	3209	Enterococcus haemoperoxidus ATCC BAA-382	1158608 155618 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000006790	Eremothecium cymbalariae (strain CBS 270.75 / DBVPG 7215 / KCTC 17166 / NRRL Y-17582) (Yeast)	931890	7/30/2015	4429	Eremothecium cymbalariae DBVPG#7215	931890 45285 33170 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006793	Thermodesulfatator indicus (strain DSM 15286 / JCM 11887 / CIR29812)	667014	7/30/2015	2184	Thermodesulfatator indicus DSM 15286	667014 171695 241192 188711 188710 67799 200940 2 131567	Bacteria	Thermodesulfobacteria
UP000006794	Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6)	797210	7/30/2015	4221	Halopiger xanaduensis SH-6	797210 387343 387342 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000006800	Vibrio anguillarum (strain ATCC 68554 / 775) (Listonella anguillarum)	882102	7/30/2015	3722	Vibrio anguillarum 775	882102 42323 55601 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006804	Pseudothermotoga thermarum DSM 5069	688269	7/27/2015	1928	Pseudothermotoga thermarum DSM 5069	688269 119394 1643951 188709 2419 188708 200918 2 131567	Bacteria	Thermotogae
UP000006801	Burkholderia sp. Yi23	1097668	7/27/2015	7767	Burkholderia sp. Yi23	1097668 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006803	Arthrospira platensis (strain NIES-39 / IAM M-135) (Spirulina platensis)	696747	7/30/2015	6009	Arthrospira platensis NIES-39	696747 118562 35823 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000006810	Mycoplasma fermentans (strain ATCC 19989 / NBRC 14854 / NCTC 10117 / PG18)	496833	7/30/2015	891	Mycoplasma fermentans PG18	496833 2115 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000013893	Candidatus Saccharimonas aalborgensis	1332188	7/27/2015	1033	Candidatus Saccharimonas aalborgensis	1332188 1331051 95818 2323 2 131567	Bacteria	Unclassified Bacteria
UP000006811	Buchnera aphidicola (Cinara tujafilina)	261317	7/27/2015	359	Buchnera aphidicola (Cinara tujafilina)	261317 9 32199 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007174	Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)	759273	7/30/2015	16110	Colletotrichum higginsianum IMI 349063	759273 80884 5455 681950 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007110	Strongylocentrotus purpuratus (Purple sea urchin)	7668	7/27/2015	28593	Strongylocentrotus purpuratus	7668 7664 31181 7675 7674 7638 7625 7624 133551 7586 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000005237	Caenorhabditis japonica	281687	7/30/2015	35063	Caenorhabditis japonica	281687 6237 55885 6243 55879 6236 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007170	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	1133850	7/30/2015	9046	Streptomyces hygroscopicus subsp. jinggangensis 5008	1133850 311982 1912 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005220	Kazachstania africana (strain ATCC 22294 / BCRC 22015 / CBS 2517 / CECT 1963 / NBRC 1671 / NRRL Y-8276) (Yeast) (Kluyveromyces africanus)	1071382	7/30/2015	5354	Kazachstania africana CBS 2517	1071382 432096 71245 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008190	Nocardia cyriacigeorgica (strain GUH-2)	1127134	7/30/2015	5473	Nocardia cyriacigeorgica GUH-2	1127134 135487 1817 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005238	Phytophthora ramorum (Sudden oak death agent)	164328	7/30/2015	15349	Phytophthora ramorum	164328 4783 4776 4762 33634 2759 131567	eukaryotes	
UP000008798	Coprococcus catus GD/7	717962	7/27/2015	2985	Coprococcus catus GD/7	717962 116085 33042 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008803	[Eubacterium] siraeum 70/3	657319	7/27/2015	2347	[Eubacterium] siraeum 70/3	657319 39492 1508657 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007059	Faecalibacterium prausnitzii SL3/3	657322	7/27/2015	2744	Faecalibacterium prausnitzii SL3/3	657322 853 216851 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008804	Faecalibacterium prausnitzii L2-6	718252	7/27/2015	2755	Faecalibacterium prausnitzii L2-6	718252 853 216851 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000005239	Pristionchus pacificus (Parasitic nematode)	54126	7/30/2015	29080	Pristionchus pacificus	54126 54125 54124 50827 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008792	Drosophila virilis (Fruit fly)	7244	7/30/2015	14456	Drosophila virilis	7244 32335 32281 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008953	Roseburia intestinalis XB6B4	718255	7/27/2015	3629	Roseburia intestinalis XB6B4	718255 166486 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes

UP000008801	Faecalitalea cylindroides T2-87	717960	7/27/2015	1442	Faecalitalea cylindroides T2-87	717960 39483 1573534 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000008956	Ruminococcus torques L2-14	657313	7/27/2015	2797	Ruminococcus torques L2-	657313 33039 572511 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008957	Fretibacterium fastidiosum	651822	7/27/2015	1434	Fretibacterium fastidiosum	651822 1434006 649777 649776 649775 508458 2 131567	Bacteria	Synergistetes
UP000008805	Gordonibacter pamelaeae 7-10-1-b	657308	7/27/2015	2027	Gordonibacter pamelaeae 7-10-1-b	657308 471189 644652 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000008795	Bacteroides xylanisolvens XB1A	657309	8/4/2015	4407	Bacteroides xylanisolvens XB1A	657309 371601 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008797	[Clostridium] cf. saccharolyticum K10	717608	7/27/2015	3073	[Clostridium] cf. saccharolyticum K10	717608 84030 1506553 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008793	Erwinia billingiae (strain Eb661)	634500	7/30/2015	4915	Erwinia billingiae Eb661	634500 182337 551 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008961	butyrate-producing bacterium SS3/4	245014	7/27/2015	2993	butyrate-producing bacterium SS3/4	245014 39779 186813 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008960	Anaerostipes hadrus	649756	7/31/2015	2771	Anaerostipes hadrus	649756 207244 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008193	Treponema pallidum subsp. pertenue (strain CDC2)	491079	7/30/2015	1065	Treponema pallidum subsp. pertenue str. CDC2	491079 168 160 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000007055	Ruminococcus sp. SR1/5	657323	7/27/2015	3260	Ruminococcus sp. SR1/5	657323 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008959	butyrate-producing bacterium SM4/1	245012	7/27/2015	1684	butyrate-producing bacterium SM4/1	245012 39779 186813 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008806	Megamonas hypermegale ART12/1	657316	7/27/2015	2118	Megamonas hypermegale ART12/1	657316 158847 158846 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000008796	Butyrivibrio fibrisolvens 16/4	657324	7/27/2015	2904	Butyrivibrio fibrisolvens 16/4	657324 831 830 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007054	Ruminococcus champanellensis (strain DSM 18848 / JCM 17042 / 18P13)	213810	7/30/2015	2114	Ruminococcus champanellensis 18P13 = JCM 17042	213810 1161942 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008955	Blautia obeum A2-162	657314	7/27/2015	3155	Blautia obeum A2-162	657314 40520 572511 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008794	Alistipes shahii WAL 8301	717959	7/27/2015	2563	Alistipes shahii WAL 8301	717959 328814 239759 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008963	Halobacteriovorax marinus (strain ATCC BAA-682 / DSM 15412 / SJ) (Bacteriovorax marinus)	862908	7/30/2015	3230	Halobacteriovorax marinus SJ	862908 97084 1652133 1652132 213481 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000008972	Bombyx mori densovirus 3 (isolate Silkworm/China/Zhenjiang/-) (BmDNV-3)	648412	7/30/2015	7	Bombyx mori densovirus 3 isolate VD1/VD2	648412 328668 1285589 1285588 1285587 686617 10239	Vruses	
UP000007076	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	452652	7/30/2015	7443	Kitasatospora setae KM-6054	452652 2066 2063 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000009154	Gordonia polyisoprenivorans (strain DSM 44266 / VH2)	1112204	7/30/2015	5097	Gordonia polyisoprenivorans VH2	1112204 84595 2053 85026 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007177	Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	931626	7/30/2015	3445	Acetobacterium woodii DSM 1030	931626 33952 33951 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000006543	Subterranean clover stunt virus (strain F) (SCSV)	291607	7/30/2015	8	Subterranean clover stunt virus (strain F)	291607 36772 104766 251095 29258 10239	Vruses	
UP000006540	Mouse mammary tumor virus (strain C3H) (MMTV)	11759	7/30/2015	5	Mouse mammary tumor virus (STRAIN C3H)	11759 11757 140052 327045 11632 35268 10239	Vruses	
UP000006542	Beet curly top virus (strain California/Logan) (BCTV)	268960	7/30/2015	7	Beet curly top virus - California [Logan]	268960 10840 10813 10811 29258 10239	Vruses	
UP000009269	Citrus psorosis virus (isolate Spain/P-121) (CPsV) (Citrus ringspot virus)	652963	7/30/2015	4	Citrus ringspot virus isolate P-121	652963 88130 73561 88129 568247 35301 439488 10239	Vruses	
UP000006898	Candidatus Methylomirabilis oxyfera	671143	7/27/2015	3057	Candidatus Methylomirabilis oxyfera	671143 1170227 640293 2323 2 131567	Bacteria	Unclassified Bacteria
UP000007068	Tomato pseudo-curly top virus (TPCTV)	49267	7/27/2015	6	Tomato pseudo-curly top virus	49267 220339 10811 29258 10239	Vruses	
UP000013963	Spiroplasma syrphidicola EA-1	1276229	7/27/2015	1006	Spiroplasma syrphidicola EA-1	1276229 216945 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000013968	Amycolatopsis orientalis HCCB10007	1156913	7/27/2015	8161	Amycolatopsis orientalis HCCB10007	1156913 31958 1813 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006541	Maize streak virus genotype A (isolate South Africa) (MSV)	10824	7/30/2015	4	Maize streak virus - [South Africa]	10824 10821 10812 10811 29258 10239	Vruses	
UP000006831	Periplaneta fuliginosa densovirus (isolate Guo/2000) (PfDNV)	648333	7/30/2015	7	Periplaneta fuliginosa densovirus Guo/2000	648333 97344 1513184 10806 40120 10780 29258 10239	Vruses	
UP000007070	Human rhinovirus A serotype 89 (strain 41467-Gallo) (HRV-89)	650130	7/30/2015	1	Human rhinovirus 89 ATCC VR-1199	650130 12132 147711 12059 12058 464095 35278 439488 10239	Vruses	
UP000006840	Psittacid herpesvirus 1 (isolate Amazon parrot/-/97-0001/1997) (PsHV-1) (Pacheco's disease virus)	670426	7/30/2015	71	Psittacid herpesvirus 1 Amazon parrot/1997	670426 50294 180255 10293 10292 548681 35237 10239	Vruses	
UP000007875	Ciona savignyi (Pacific transparent sea squirt)	51511	7/27/2015	20004	Ciona savignyi	51511 7718 7717 7716 183770 7713 7712 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007303	Tetraodon nigroviridis (Spotted green pufferfish) (Chelonodon nigroviridis)	99883	7/27/2015	23075	Tetraodon nigroviridis	99883 47144 31031 32517 31028 31022 1489922 1489872 123369 123368 123367 123366 123365 1489388 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000014064	Wallemia ichthyophaga (strain EXF-994 / CBS 113033)	1299270	7/30/2015	4834	Wallemia ichthyophaga EXF-994	1299270 245174 148959 431959 431958 431957 5302 5204 451864 4751 33154 2759 131567	eukaryotes	

UP000014066	Methanobrevibacter sp. AbM4	224719	7/27/2015	1663	Methanobrevibacter sp. AbM4	224719 2172 2159 2158 183925 28890 2157 131567	Archaea	
UP000008672	Latimeria chalumnae (West Indian ocean coelacanth)	7897	7/27/2015	23434	Latimeria chalumnae	7897 7896 7895 7894 118072 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008651	Red clover necrotic mosaic virus (RCNMV)	12267	7/27/2015	3	Red clover necrotic mosaic virus	12267 12266 39738 35278 439488 10239	Vruses	
UP000008649	Rabies virus (strain Pasteur vaccins / PV) (RABV)	103929	7/30/2015	5	Rabies virus strain Pasteur vaccin	103929 11292 11286 11270 11157 35301 439488 10239	Vruses	
UP000014071	Pseudozyma hubeiensis (strain SY62) (Yeast)	1305764	7/30/2015	7472	Pseudozyma hubeiensis SY62	1305764 327079 63298 85578 5268 5267 5257 452284 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000014072	Salinarchaeum sp. Harcht-Bsk1	1333523	7/27/2015	3013	Salinarchaeum sp. Harcht-Bsk1	1333523 1269201 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000014070	Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1	1295009	7/27/2015	1826	Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1	1295009 1406512 1080709 1577788 1235850 183967 28890 2157 131567	Archaea	
UP000007304	Exophiala dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) (Black yeast) (Wangiella dermatitidis)	858893	7/30/2015	9391	Exophiala dermatitidis NIH/UT8656	858893 5970 5583 43219 34395 451870 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005221	Candida parapsilosis (strain CDC 317 / ATCC MYA-4646) (Yeast) (Monilia parapsilosis)	578454	7/30/2015	5777	Candida parapsilosis CDC317	578454 5480 1535326 1535325 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000014127	Enterococcus dispar ATCC 51266	1139219	7/27/2015	2622	Enterococcus dispar ATCC 51266	1139219 44009 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000014136	Enterococcus saccharolyticus ATCC 43076	1139996	7/27/2015	2573	Enterococcus saccharolyticus ATCC 43076	1139996 41997 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000005622	Nematocida sp. 1 (strain ERTm2 / ATCC PRA-371) (Nematode killer fungus)	944018	7/30/2015	2769	Nematocida sp. 1 ERTm2	944018 1155007 586132 469895 6029 4751 33154 2759 131567	eukaryotes	
UP000014140	Parabacteroides goldsteinii dnLKV18	1235789	7/27/2015	5574	Parabacteroides goldsteinii dnLKV18	1235789 328812 375288 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000014113	Enterococcus columbae DSM 7374 = ATCC 51263	1121865	7/27/2015	2315	Enterococcus columbae DSM 7374 = ATCC 51263	1121865 1355 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000007523	Paenibacillus mucilaginosus 3016	1116391	8/8/2015	7018	Paenibacillus mucilaginosus 3016	1116391 61624 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000005222	Pichia sorbitophila (strain ATCC MYA-4447 / BCRC 22081 / CBS 7064 / NBRC 10061 / NRRL Y-12695) (Hybrid yeast)	559304	7/30/2015	8851	Millerozyma farinosa CBS 7064	559304 4920 766502 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000014104	Enterococcus avium ATCC 14025	1140002	7/27/2015	4469	Enterococcus avium ATCC 14025	1140002 33945 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008005	Rickettsia amblyommii (strain GAT-30V)	1105111	7/30/2015	1377	Candidatus Rickettsia amblyommii str. GAT-30V	1105111 33989 114277 780 33988 775 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008022	Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	7/27/2015	45592	Oryza rufipogon	4529 4527 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000014199	Enterococcus durans ATCC 6056	1140001	7/27/2015	2991	Enterococcus durans ATCC 6056	1140001 53345 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000007517	Blastococcus saxobsidens (strain DD2)	1146883	7/30/2015	4791	Blastococcus saxobsidens DD2	1146883 138336 38501 85030 1643682 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005234	Frateuria aurantia (strain ATCC 33424 / DSM 6220 / NBRC 3245 / NCIMB 13370) (Acetobacter aurantius)	767434	7/30/2015	3098	Frateuria aurantia DSM 6220	767434 81475 70411 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000014227	Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	1303518	7/27/2015	2809	Chthonomonas calidirosea T49	1303518 454171 1077265 1077264 1077263 1077257 67819 2 131567	Bacteria	Armatimonadetes
UP000005204	Bombyx mori (Silk moth)	7091	8/2/2015	14767	Bombyx mori	7091 7090 475327 7089 37569 104431 37567 41197 41196 41191 7088 85604 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000005205	Atta cephalotes (Leafcutter ant)	12957	7/27/2015	18080	Atta cephalotes	12957 12956 143999 34695 36668 34725 7434 7400 7399 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000005203	Apis mellifera (Honeybee)	7460	8/2/2015	15323	Apis mellifera	7460 7459 83321 70987 7458 34735 7434 7400 7399 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007519	Saprospira grandis (strain Lewin)	984262	7/30/2015	4218	Saprospira grandis str. Lewin	984262 1008 1007 89374 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000014254	Mucor circinelloides f. circinelloides (strain 1006PhL) (Mucormycosis agent) (Calyptromyces circinelloides)	1220926	7/30/2015	12143	Mucor circinelloides f. circinelloides 1006PhL	1220926 70416 36080 4830 34489 1344963 4827 451507 112252 4751 33154 2759 131567	eukaryotes	
UP000014074	Togninia minima (strain UCR-PA7) (Esca disease fungus) (Phaeoacremonium aleophilum)	1286976	7/30/2015	8833	Togninia minima UCRPA7	1286976 223192 93810 93809 93808 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007575	Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	745776	7/30/2015	4329	Deinococcus gobiensis I-0	745776 502394 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000007587	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	1144275	7/30/2015	8019	Corallococcus coralloides DSM 2259	1144275 184914 83461 31 80811 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria

UP000007590	Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) (Flexibacter canadensis)	929556	7/30/2015	4304	Solitalea canadensis DSM 3403	929556 995 929509 84566 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007879	Amphimedon queenslandica (Sponge)	400682	7/27/2015	29758	Amphimedon queenslandica	400682 178513 178475 6049 6042 6040 33208 33154 2759 131567	eukaryotes	
UP000007599	Flavobacterium indicum (strain DSM 17447 / CIP 109464 / GPTSA100-9)	1094466	7/30/2015	2649	Flavobacterium indicum GPTSA100-9 = DSM 17447	1094466 312277 237 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000005446	Glarea lozoyensis (strain ATCC 74030 / MF5533)	1104152	7/30/2015	7926	Glarea lozoyensis 74030	1104152 101852 101851 5181 5178 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007883	Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	983917	7/30/2015	4686	Rubrivivax gelatinosus IL144	983917 28068 28067 224471 119065 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007887	Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421)	927704	7/30/2015	3481	Selenomonas ruminantium subsp. lactilytica TAM6421	927704 114197 971 970 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000007880	Caldilinea aerophila (strain DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1)	926550	7/30/2015	4097	Caldilinea aerophila DSM 14535 = NBRC 104270	926550 133453 233191 475964 475963 475962 200795 2 131567	Bacteria	Chloroflexi
UP000007881	Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	1142394	7/30/2015	3269	Phycisphaera mikurensis NBRC 102666	1142394 547188 666508 666507 666506 666505 203682 2 131567	Bacteria	Planctomycetes
UP000004793	Caldisericum exile (strain DSM 21853 / NBRC 104410 / AZM16c01)	511051	7/30/2015	1566	Caldisericum exile AZM16c01	511051 693075 693074 693073 693072 693071 67814 2 131567	Bacteria	Caldiserica
UP000007882	Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	512565	7/30/2015	8113	Actinoplanes missouriensis 431	512565 1866 1865 28056 85008 1760 201174 2 131567	Bacteria	Actinobacteria
UP000014417	Propionimicrobium lymphophilum ACS-093-V-SCH5	883161	7/27/2015	2076	Propionimicrobium lymphophilum ACS-093-V-SCH5	883161 33012 203133 31957 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007305	Zea mays (Maize)	4577	8/8/2015	58417	Zea mays	4577 4575 1648029 147429 1648033 147369 147370 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000007382	Leptospirillum ferrooxidans (strain C2-3)	1162668	7/30/2015	2413	Leptospirillum ferrooxidans C2-3	1162668 180 655606 179 189779 189778 203693 40117 2 131567	Bacteria	Nitrospirae
UP000007306	Oryza glaberrima (African rice)	4538	7/30/2015	31807	Oryza glaberrima	4538 4527 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000032891	Candidatus Phytoplasma solani	69896	7/27/2015	520	Candidatus Phytoplasma solani	69896 85632 33926 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000014480	Colletotrichum orbiculare (strain 104-T / ATCC 96160 / CBS 514.97 / LARS 414 / MAFF 240422) (Cucumber anthracnose fungus) (Colletotrichum lagenarium)	1213857	7/30/2015	13345	Colletotrichum orbiculare MAFF 240422	1213857 5465 5455 681950 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000014500	Strigamia maritima (European centipede) (Geophilus maritimus)	126957	8/4/2015	14972	Strigamia maritima	126957 126956 126955 60154 115407 115405 7540 61985 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007394	Ignavibacterium album (strain DSM 19864 / JCM 16511 / NBRC 101810 / Mat9-16)	945713	7/30/2015	3169	Ignavibacterium album JCM 16511	945713 591197 795750 795749 795748 795747 1134404 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007383	Spirochaeta africana (strain ATCC 700263 / DSM 8902 / Z-7692)	889378	7/30/2015	2766	Spirochaeta africana DSM 8902	889378 46355 146 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000007397	Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	866895	7/30/2015	4100	Halobacillus halophilus DSM 2266	866895 1570 45667 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000009136	Bos taurus (Bovine)	9913	8/2/2015	24107	Bos taurus	9913 9903 27592 9895 35500 9845 91561 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000009138	Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) (Mucormycosis agent) (Rhizopus arrhizus var. delemar)	246409	7/30/2015	16971	Rhizopus delemar RA 99-880	246409 936053 4842 1344955 1344963 4827 451507 112252 4751 33154 2759 131567	eukaryotes	
UP000007391	Fervidicoccus fontis (strain DSM 19380 / VKM B-2539 / Kam940)	1163730	7/30/2015	1384	Fervidicoccus fontis Kam940	1163730 683846 685950 685949 685948 183924 28889 2157 131567	Archaea	
UP000005012	Providencia stuartii (strain MRSN 2154)	1157951	7/30/2015	4220	Providencia stuartii MRSN 2154	1157951 588 586 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000014632	Candidatus Tremblaya phenacola PAVE	1266371	7/27/2015	175	Candidatus Tremblaya phenacola PAVE	1266371 1010676 189384 119066 28216 1224 2 131567	Bacteria	Proteobacteria
UP000009144	Methylophaga nitratireducenticrescens (strain ATCC BAA-2433 / DSM 25689 / JAM1)	754476	7/30/2015	3011	Methylophaga nitratireducenticrescens	754476 40222 135616 72273 1236 1224 2 131567	Bacteria	Proteobacteria
UP000009145	Methylophaga frappieri (strain ATCC BAA-2434 / DSM 25690 / JAM7)	754477	7/30/2015	2689	Methylophaga frappieri	754477 40222 135616 72273 1236 1224 2 131567	Bacteria	Proteobacteria
UP000005207	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)	8128	8/2/2015	26756	Oreochromis niloticus	8128 8139 1315725 318546 319095 8113 1489911 1489910 1489908 1489872 123369 123368 123367 123366 123365 1489388 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	

UP000005215	Ictidomys tridecemlineatus (Thirteen-lined ground squirrel) (Spermophilus tridecemlineatus)	43179	7/27/2015	19966	Ictidomys tridecemlineatus	43179 1141640 337730 337726 55153 33553 9989 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007437	Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454)	882378	7/30/2015	3859	Burkholderia rhizoxinica HKI 454	882378 412963 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007435	Leadbetterella byssophila (strain DSM 17132 / KACC 11308 / 4M15)	649349	7/30/2015	3429	Leadbetterella byssophila DSM 17132	649349 316068 319458 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006563	Sendai virus (strain Ohita) (SeV)	302272	7/30/2015	9	Sendai virus (strain Ohita)	302272 11191 186938 11159 11158 11157 35301 439488 10239	Vruses	
UP000001955	Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	630626	7/30/2015	3870	Shimwellia blattae DSM 4481 = NBRC 105725	630626 563 1335483 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002872	Nematocida parisii (strain ERTm3) (Nematode killer fungus)	935791	7/30/2015	2724	Nematocida parisii ERTm3	935791 586133 586132 469895 6029 4751 33154 2759 131567	eukaryotes	
UP000007434	Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	656519	7/30/2015	2250	Halanaerobium hydrogeniformans	656519 2330 972 53433 186801 1239 2 131567	Bacteria	Firmicutes
UP000002866	Tetrapisispora blattae (strain ATCC 34711 / CBS 6284 / DSM 70876 / NBRC 10599 / NRRL Y-10934 / UCD 77-7) (Yeast) (Kluyveromyces blattae)	1071380	7/30/2015	5385	Tetrapisispora blattae CBS 6284	1071380 1071379 113604 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002875	Emticicia oligotrophica (strain DSM 17448 / GPTSA100-15)	929562	7/30/2015	4251	Emticicia oligotrophica DSM 17448	929562 312279 312278 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002881	Mesotoga prima MesG1.Ag.4.2	660470	7/27/2015	2499	Mesotoga prima MesG1.Ag.4.2	660470 1184387 1184396 1643948 1643946 188708 200918 2 131567	Bacteria	Thermotogae
UP000008867	Sporisorium reilianum (strain SRZ2) (Maize head smut fungus)	999809	7/30/2015	6673	Sporisorium reilianum SRZ2	999809 72558 63265 5268 5267 5257 452284 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000007192	Murine coronavirus (strain A59) (MHV-A59) (Murine hepatitis virus)	11142	7/30/2015	11	Murine hepatitis virus strain A59	11142 11138 694005 694002 693995 11118 76804 35278 439488 10239	Vruses	
UP000014824	Chlamydia psittaci 02DC14	1112253	7/30/2015	1714	Chlamydia psittaci 02DC14	1112253 83554 810 1113537 809 51291 204429 204428 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000006461	Modestobacter marinus (strain BC501)	1144889	7/30/2015	5435	Modestobacter marinus BC501	1144889 88139 88138 85030 1643682 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006691	Solibacillus silvestris (strain StLB046) (Bacillus silvestris)	1002809	7/30/2015	3812	Solibacillus silvestris StLB046	1002809 76853 648800 186818 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000006469	Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (Halobacterium mediterranei)	523841	7/30/2015	3826	Haloferax mediterranei ATCC 33500	523841 2252 2251 1644056 1644055 183963 28890 2157 131567	Archaea	
UP000009181	Pelagibacter sp. (strain IMCC9063)	1002672	7/30/2015	1447	Candidatus Pelagibacter sp. IMCC9063	1002672 198251 1655514 54526 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006851	Coriobacterium glomerans (strain ATCC 49209 / DSM 20642 / JCM 10262 / PW2)	700015	7/30/2015	1768	Coriobacterium glomerans PW2	700015 33871 33870 84107 84999 84998 201174 2 131567	Bacteria	Actinobacteria
UP000000483	Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	880072	7/30/2015	2859	Desulfobacca acetoxidans DSM 11109	880072 60893 60892 213468 213462 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006852	Treponema succinifaciens (strain ATCC 33096 / DSM 2489 / 6091)	869209	7/30/2015	2561	Treponema succinifaciens DSM 2489	869209 167 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000000278	Dugbe virus (isolate ArD44313) (DUGV)	766194	7/30/2015	3	Dugbe virus (isolate ArD44313)	766194 11595 11592 11571 35301 439488 10239	Vruses	
UP000007206	European bat lyssavirus 2 (strain Human/Scotland/RV1333/2002) (EBLV2)	453116	7/30/2015	5	European bat lyssavirus 2 strain RV1333	453116 57482 11286 11270 11157 35301 439488 10239	Vruses	
UP000008926	European bat lyssavirus 1 (strain Bat/Germany/RV9/1968) (EBLV1)	453115	7/30/2015	5	European bat lyssavirus 1 strain RV9	453115 57482 11286 11270 11157 35301 439488 10239	Vruses	
UP000001461	Cocksfoot mottle virus (isolate Dactylis glomerata/Norway/CfMV-NO/1995) (CfMV)	1005059	7/30/2015	4	Cocksfoot mottle virus Dactylis glomerata/Norway/CfMV-NO/1995	1005059 40979 12137 35278 439488 10239	Vruses	
UP000007030	Marinithermus hydrothermalis (strain DSM 14884 / JCM 11576 / T1)	869210	7/30/2015	2194	Marinithermus hydrothermalis DSM 14884	869210 186192 186191 188786 68933 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000006854	Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	953739	8/7/2015	7451	Streptomyces venezuelae ATCC 10712	953739 54571 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007209	Zaire ebolavirus (strain Mayinga-76) (ZEBOV) (Zaire Ebola virus)	128952	7/30/2015	9	Ebola virus - Mayinga, Zaire, 1976	128952 1570291 186538 186536 11266 11157 35301 439488 10239	Vruses	
UP000005258	Tistrella mobilis (strain KA081020-065)	1110502	7/30/2015	5778	Tistrella mobilis KA081020-065	1110502 171437 171436 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000005242	Wallemia sebi (strain ATCC MYA-4683 / CBS 633.66)	671144	7/30/2015	5262	Wallemia mellicola CBS 633.66	671144 1708541 148959 431959 431958 431957 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000008927	Groundnut rosette virus (strain MC1) (GRV)	1005060	7/30/2015	3	Groundnut rosette virus	1005060 47740 39734 39738 35278 439488 10239	Vruses	
UP000008308	Verrucosispora maris (strain AB-18-032)	263358	7/30/2015	5998	Verrucosispora maris AB-18-032	263358 1003110 84593 28056 85008 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005267	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	1036672	7/30/2015	3933	Advenella kashmirensis WT001	1036672 310575 290425 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002497	Coccidioides posadasii (strain RMSCC 757 / Silveira) (Valley fever fungus)	443226	7/30/2015	10212	Coccidioides posadasii str. Silveira	443226 199306 5500 34383 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005269	Enterococcus faecium DO	333849	7/27/2015	3059	Enterococcus faecium DO	333849 1352 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes

UP000005270	Thermogladius cellulolyticus (strain 1633)	1184251	7/30/2015	1414	Thermogladius cellulolyticus 1633	1184251 1200300 477695 2272 114380 183924 28889 2157 131567	Archaea	
UP000002499	Metarhizium acridum (strain CQMa 102)	655827	7/30/2015	9830	Metarhizium acridum CQMa 102	655827 92637 5529 34397 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002498	Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	655844	7/30/2015	11684	Metarhizium robertsii ARSEF 23	655844 568076 5529 34397 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006173	Bifidobacterium bifidum BGN4	484020	7/27/2015	1834	Bifidobacterium bifidum BGN4	484020 1681 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006174	Ustilago hordei (strain Uh4875-4) (Barley covered smut fungus)	1128400	7/30/2015	7111	Ustilago hordei Uh4857-4	1128400 120017 5269 5268 5267 5257 452284 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000006178	Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	1094508	7/30/2015	2778	Thermoanaerobacterium saccharolyticum JW/SL-YS485	1094508 28896 28895 543371 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000008627	Hantaan virus (strain 76-118) (Korean hemorrhagic fever virus)	11602	7/30/2015	3	Hantaan virus 76-118	11602 11599 11598 11571 35301 439488 10239	Vruses	
UP000006048	Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) (Leptospira parva)	869212	7/30/2015	4092	Turneriella parva DSM 21527	869212 29510 338321 170 1643688 203692 203691 2 131567	Bacteria	Spirochaetes
UP000000673	Anopheles darlingi (Mosquito)	43151	7/27/2015	10447	Anopheles darlingi	43151 44552 44546 44545 44543 7164 43816 7157 41827 43786 7148 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006052	Alistipes finegoldii (strain DSM 17242 / JCM 16770 / AHN 2437 / CCUG 46020 / CIP 107999)	679935	7/30/2015	3055	Alistipes finegoldii DSM 17242	679935 214856 239759 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006050	Belliella baltica (strain DSM 15883 / CIP 108006 / LMG 21964 / BA134)	866536	7/30/2015	3609	Belliella baltica DSM 15883	866536 232259 232244 563798 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006051	Ornithobacterium rhinotracheale (strain ATCC 51463 / DSM 15997 / CCUG 23171 / LMG 9086)	867902	7/30/2015	2138	Ornithobacterium rhinotracheale DSM 15997	867902 28251 28250 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006056	Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63)	926566	7/30/2015	3936	Terriglobus roseus DSM 18391	926566 392734 392733 204434 204433 204432 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000006055	Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	706587	7/30/2015	5412	Desulfomonile tiedjei DSM 6799	706587 2358 2357 213468 213462 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006061	Anaerobaculum mobile (strain ATCC BAA-54 / DSM 13181 / NGA)	891968	7/30/2015	2004	Anaerobaculum mobile DSM 13181	891968 97477 46613 649777 649776 649775 508458 2 131567	Bacteria	Synergistetes
UP000006054	Flexibacter litoralis (strain ATCC 23117 / DSM 6794 / NBRC 15988 / NCIMB 1366 / Sio-4)	880071	7/30/2015	3832	Flexibacter litoralis DSM 6794	880071 999 992 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006062	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	765911	7/30/2015	4192	Thiocystis violascens DSM 198	765911 73141 13724 1046 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000014978	Spraguea lophii (strain 42_110) (Microsporidian parasite)	1358809	7/30/2015	2499	Spraguea lophii 42_110	1358809 51541 51540 227310 6032 6029 4751 33154 2759 131567	eukaryotes	
UP000000438	Picrophilus torridus (strain ATCC 700027 / DSM 9790 / JCM 10055 / NBRC 100828)	263820	7/30/2015	1535	Picrophilus torridus DSM 9790	263820 82076 46631 46630 2301 183967 28890 2157 131567	Archaea	
UP000014984	Spiroplasma taiwanense CT-1	1276220	7/27/2015	1007	Spiroplasma taiwanense CT-1	1276220 2145 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000007639	Epstein-Barr virus (strain AG876) (HHV-4) (Human herpesvirus 4)	82830	7/30/2015	80	Epstein-barr virus strain ag876	82830 10376 10375 10374 10292 548681 35237 10239	Vruses	
UP000007640	Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4)	10377	7/30/2015	118	Human herpesvirus 4 (strain B95-8)	10377 10376 10375 10374 10292 548681 35237 10239	Vruses	
UP000014983	Spiroplasma diminutum CUAS-1	1276221	7/27/2015	858	Spiroplasma diminutum CUAS-1	1276221 216936 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000006049	Aequorivita sublithincola (strain DSM 14238 / LMG 21431 / ACAM 643 / 9-3)	746697	7/30/2015	3134	Aequorivita sublithincola DSM 14238	746697 101385 153265 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007212	Infectious hematopoietic necrosis virus (strain WRAC) (IHNV)	429314	7/30/2015	6	Infectious hematopoietic necrosis virus - WRAC	429314 11290 186778 11270 11157 35301 439488 10239	Vruses	
UP000007643	Ictalurid herpesvirus 1 (strain Auburn) (IcHV-1) (Channel catfish herpesvirus)	766178	7/30/2015	76	Ictalurid herpesvirus 1 (strain Auburn)	766178 10401 172653 548682 548681 35237 10239	Vruses	
UP000006826	Mokola virus (MOKV)	12538	7/27/2015	5	Mokola virus	12538 11286 11270 11157 35301 439488 10239	Vruses	
UP000002892	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	646529	8/4/2015	4469	Desulfosporosinus acidiphilus SJ4	646529 885581 79206 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002895	Enterococcus hirae (strain ATCC 9790 / DSM 20160 / JCM 8729 / LMG 6399 / NBRC 3181 / NCIMB 6459 / NCDO 1258)	768486	7/30/2015	2743	Enterococcus hirae ATCC 9790	768486 1354 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008718	Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	694427	7/30/2015	3020	Paludibacter propionicigenes WB4	694427 185300 346096 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007039	Calditerrivibrio nitroreducens (strain DSM 19672 / NBRC 101217 / Yu37-1)	768670	7/30/2015	2089	Calditerrivibrio nitroreducens DSM 19672	768670 477976 545865 191394 191393 68337 200930 2 131567	Bacteria	Deferribacteres
UP000008720	Marivirga tractuosa (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43) (Microscilla tractuosa) (Flexibacter tractuosus)	643867	7/30/2015	3748	Marivirga tractuosa DSM 4126	643867 1006 869806 200667 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008721	Sulfuricurvum kujiense (strain ATCC BAA-921 / DSM 16994 / JCM 11577 / YK-1)	709032	7/30/2015	2794	Sulfuricurvum kujiense DSM 16994	709032 148813 286130 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000008722	Oceanithermus profundus (strain DSM 14977 / NBRC 100410 / VKM B-2274 / 506)	670487	7/30/2015	2372	Oceanithermus profundus DSM 14977	670487 187137 208447 188786 68933 188787 1297 2 131567	Bacteria	Deinococcus-Thermus

UP000007771	Lake Victoria marburgvirus (strain Musoke-80) (MARV) (Marburg virus (strain Kenya/Musoke/1980))	33727	7/30/2015	7	Marburg virus - Musoke, Kenya, 1980	33727 11269 186537 11266 11157 35301 439488 10239	Vruses	
UP000000310	Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	762903	7/30/2015	3780	Pseudopedobacter saltans DSM 12145	762903 151895 1649482 84566 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007804	Borna disease virus (strain V) (BDV)	928296	7/30/2015	5	Borna disease virus-V	928296 12455 186458 178830 11157 35301 439488 10239	Vruses	
UP000007254	Spirochaeta thermophila (strain ATCC 700085 / DSM 6578 / Z-1203)	869211	7/30/2015	2249	Spirochaeta thermophila DSM 6578	869211 154 146 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000015100	Dactylellina haptotyla (strain CBS 200.50) (Nematode-trapping fungus) (Monacrosporium haptotylum)	1284197	7/30/2015	10959	Dactylellina haptotyla CBS 200.50	1284197 430498 314122 54032 47021 189479 189478 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000003118	Propionibacterium propionicum (strain F0230a)	767029	7/30/2015	2931	Propionibacterium propionicum F0230a	767029 1750 1743 31957 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008589	Cowpea mosaic virus (strain SB) (CPMV)	928299	7/30/2015	5	Cowpea mosaic virus strain SB	928299 12264 12258 675075 675072 464095 35278 439488 10239	Vruses	
UP000007431	Schizophyllum commune (strain H4-8 / FGSC 9210) (Split gill fungus)	578458	7/30/2015	13128	Schizophyllum commune H4-8	578458 5334 5333 5332 5338 452333 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000015106	Triticum urartu (Red wild einkorn) (Crithodium urartu)	4572	8/2/2015	33313	Triticum urartu	4572 4564 1648030 147389 1648038 147368 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000008591	Hepatitis B virus genotype C subtype ayr (isolate Human/Japan/Okamoto/-) (HBV-C)	928302	7/30/2015	5	Hepatitis B virus C/ayr human/Japan/Okamoto	928302 489466 10407 10405 10404 35268 10239	Vruses	
UP000008590	Cricket paralysis virus (isolate Teleogryllus commodus/Australia/CrPVVIC/1968) (CrPV)	928300	7/30/2015	2	Cricket paralysis virus Teleogryllus commodus/Australia/CrPVVIC/ 1968	928300 12136 144051 232795 464095 35278 439488 10239	Vruses	
UP000006625	Moloney murine leukemia virus (isolate Shinnick) (MoMLV)	928306	7/30/2015	3	Moloney murine leukemia virus isolate Shinnick	928306 11801 11786 353210 353212 153135 327045 11632 35268 10239	Vruses	
UP000008026	Tacaribe virus (strain Franze-Fernandez) (TCRV)	928313	7/30/2015	4	Tacaribe virus strain Franze-Fernandez	928313 11631 1653394 11617 35301 439488 10239	Vruses	
UP000008588	Bovine ephemeral fever virus (strain BB7721) (BEFV)	928297	7/30/2015	12	Bovine ephemeral fever virus strain BB7721	928297 11303 32613 11270 11157 35301 439488 10239	Vruses	
UP000008592	Lettuce necrotic yellows virus (isolate 318) (LNYV)	928304	7/30/2015	6	Lettuce necrotic yellows virus isolate 318	928304 32612 11305 11270 11157 35301 439488 10239	Vruses	
UP000008595	Uukuniemi virus (strain S23) (Uuk)	487099	7/30/2015	4	Uukuniemi virus S23	487099 11591 11584 11571 35301 439488 10239	Vruses	
UP000008593	Maize mosaic virus (isolate Maize/United States/Reed/2005) (MMV)	928305	7/30/2015	6	Maize mosaic virus maize/USA/Reed/2005	928305 279896 11306 11270 11157 35301 439488 10239	Vruses	
UP000008597	Fowlpox virus (strain NVSL) (FPV)	928301	7/30/2015	251	Fowlpox virus strain NVSL	928301 10261 10260 10241 10240 35237 10239	Vruses	
UP000008594	Nodamura virus (strain Mag115) (NoV)	914672	7/30/2015	3	Nodamura virus Mag115	914672 12288 143920 12283 35278 439488 10239	Vruses	
UP000008915	Thermaerobacter marianensis (strain ATCC 700841 / DSM 12885 / JCM 10246 / 7p75a)	644966	7/30/2015	2324	Thermaerobacter marianensis DSM 12885	644966 73919 73918 539000 538999 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000006514	Auricularia delicata (strain TFB10046) (White-rot fungus)	717982	7/30/2015	5290	Auricularia subglabra TFB-10046 SS5	717982 1331295 5230 5227 5226 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000015104	Tetranychus urticae (Two-spotted spider mite)	32264	7/27/2015	18082	Tetranychus urticae	32264 32263 32262 83146 188550 83145 6947 83136 6946 6933 6854 6843 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006624	Human parvovirus B19 (strain HV) (HPV B19)	648237	7/30/2015	5	Human parvovirus B19 strain HV	648237 10798 1511900 40121 40119 10780 29258 10239	Vruses	
UP000015101	Helobdella robusta (Californian leech)	6412	8/2/2015	23328	Helobdella robusta	6412 6411 6407 6406 6403 55824 42113 6340 1206795 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008596	Yaba monkey tumor virus (strain VR587) (YMTV)	928314	7/30/2015	140	Yaba monkey tumor virus strain VR587	928314 38804 10282 10241 10240 35237 10239	Vruses	
UP000004208	Corynebacterium genitalium ATCC 33030	585529	7/27/2015	2216	Corynebacterium genitalium ATCC 33030	585529 38288 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008914	Intrasporangium calvum (strain ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP)	710696	7/30/2015	3551	Intrasporangium calvum DSM 43043	710696 53358 53357 85021 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008120	Candidatus Caldiarchaeum subterraneum	311458	7/27/2015	2154	Candidatus Caldiarchaeum subterraneum	311458 1048752 651142 651137 2157 131567	Archaea	
UP000006823	Trichinella spiralis (Trichina worm)	6334	7/30/2015	16041	Trichinella spiralis	6334 6333 6332 6329 1457286 119088 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007934	Helicobacter felis (strain ATCC 49179 / NCTC 12436 / CS1)	936155	7/30/2015	1649	Helicobacter felis ATCC 49179	936155 214 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000015102	Megaselia scalaris (Humpbacked fly) (Phora scalaris)	36166	7/27/2015	11463	Megaselia scalaris	36166 36165 192434 43831 36164 43739 43737 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000015103	Rhodnius prolixus (Triatomid bug)	13249	8/2/2015	15217	Rhodnius prolixus	13249 13248 70999 27479 33356 33354 33351 33349 33347 33345 33343 35568 35567 7524 33342 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008771	Hendra virus (isolate Horse/Autralia/Hendra/1994)	928303	7/30/2015	9	Hendra virus horse/Australia/Hendra/1994	928303 63330 260964 11159 11158 11157 35301 439488 10239	Vruses	
UP000008770	Frog virus 3 (isolate Goorha) (FV-3)	654924	7/30/2015	98	Frog virus 3 (isolate Goorha)	654924 10493 10492 10486 35237 10239	Vruses	

UP000008772	Infectious salmon anemia virus (isolate Atlantic salmon/Norway/810/9/99) (ISAV)	652965	7/30/2015	10	Infectious salmon anemia virus isolate 810/9/99	652965 55987 324913 11308 35301 439488 10239	Vruses	
UP000008773	Infectious spleen and kidney necrosis virus (isolate Mandarin fish/China/Nanhai/1998) (ISKNV)	654923	7/30/2015	125	Infectious spleen and kidney necrosis virus (isolate Nanhai)	654923 180170 308906 10486 35237 10239	Vruses	
UP000008775	Rosellinia necatrix mycoreovirus 3 (isolate W370) (RnMYRV-3) (Rosellinia anti-rot virus)	311229	7/30/2015	12	Mycoreovirus 3	311229 311227 689831 10880 35325 10239	Vruses	
UP000008776	Neodiprion lecontei nucleopolyhedrovirus (strain Canada) (NeleNPV)	654906	7/30/2015	89	Neodiprion lecontei NPV (strain Canada)	654906 249151 558018 10442 35237 10239	Vruses	
UP000006635	Culex nigripalpus nucleopolyhedrovirus (isolate Florida/1997) (CuniNPV)	645993	7/30/2015	109	Culex nigripalpus NPV Florida/1997	645993 1233169 558019 10442 35237 10239	Vruses	
UP000006636	Torque teno tupaia virus (isolate Tbc-TTV14)	766185	7/30/2015	3	Torque teno tupaia virus (isolate Tbc-TTV14)	766185 687381 687334 687329 29258 10239	Vruses	
UP000008769	Bean golden yellow mosaic virus (isolate Puerto Rico-Japan) (BGYMV)	222449	7/30/2015	9	Bean golden yellow mosaic virus-[Puerto Rico-Japan]	222449 220340 10814 10811 29258 10239	Vruses	
UP000008767	Crimean-Congo hemorrhagic fever virus (strain Nigeria/IbAr10200/1970) (CCHFV)	652961	7/30/2015	3	Crimean-Congo hemorrhagic fever virus strain IbAr10200	652961 11593 11592 11571 35301 439488 10239	Vruses	
UP000008779	Torque teno mini virus 1 (isolate TLMV-CBD279)	766183	7/30/2015	3	Torque teno mini virus 1 (isolate TLMV-CBD279)	766183 687369 687332 687329 29258 10239	Vruses	
UP000007078	Torque teno midi virus 1 (isolate MD1-073)	766184	7/30/2015	2	Torque teno midi virus 1 (isolate MD1-073)	766184 687379 687333 687329 29258 10239	Vruses	
UP000007079	Torque teno sus virus 1 (isolate Sd-TTV31)	766190	7/30/2015	3	Torque teno sus virus 1a (isolate Sd-TTV31)	766190 687386 687339 687329 29258 10239	Vruses	
UP000008768	Bunyavirus La Crosse (isolate Human/United States/L78/1978)	796210	7/30/2015	4	La Crosse virus L78	796210 11577 35305 11572 11571 35301 439488 10239	Vruses	
UP000008778	Torque teno virus 1 (isolate TA278)	766182	7/30/2015	2	Torque teno virus 1 (isolate TA278)	766182 687340 687331 687329 29258 10239	Vruses	
UP000008780	Torque teno tamarin virus (isolate So-TTV2)	766186	7/30/2015	4	Torque teno tamarin virus (isolate So-TTV2)	766186 687382 687335 687329 29258 10239	Vruses	
UP000015216	Candidatus Profftella armatura	669502	7/27/2015	372	Candidatus Profftella armatura	669502 1381133 119066 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007081	Walleye dermal sarcoma virus (WDSV)	39720	7/27/2015	6	Walleye dermal sarcoma virus	39720 153137 327045 11632 35268 10239	Vruses	
UP000003044	Yokenella regensburgei ATCC 43003	1002368	7/30/2015	4709	Yokenella regensburgei ATCC 43003	1002368 158877 158876 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008781	Torque teno felis virus (isolate Fc-TTV4)	766188	7/30/2015	3	Torque teno felis virus-Fc-TTV4	766188 687384 687337 687329 29258 10239	Vruses	
UP000003045	Mobiluncus mulieris ATCC 35239	871571	7/27/2015	2379	Mobiluncus mulieris ATCC 35239	871571 2052 2050 2049 2037 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001295	Torque teno canis virus (isolate Cf-TTV10)	766189	7/30/2015	3	Torque teno canis virus (isolate Cf-TTV10)	766189 687385 687338 687329 29258 10239	Vruses	
UP000008774	Murid herpesvirus 1 (strain Smith) (MuHV-1) (Mouse cytomegalovirus)	10367	7/30/2015	15	Murine cytomegalovirus (strain Smith)	10367 10366 10365 10357 10292 548681 35237 10239	Vruses	
UP000008777	Pyrobaculum spherical virus (isolate United States/Yellowstone) (PSV)	654907	7/30/2015	48	Pyrobaculum spherical virus (isolate Yellowstone)	654907 270161 564645 292638 35237 10239	Vruses	
UP000007080	Torque teno douroucouli virus (isolate At-TTV3)	766187	7/30/2015	3	Torque teno douroucouli virus (isolate At-TTV3)	766187 687383 687336 687329 29258 10239	Vruses	
UP000003678	Brucella ceti str. Cudo	595497	7/30/2015	3100	Brucella ceti str. Cudo	595497 120577 234 118882 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000003242	Megasphaera genomosp. type_1 str. 28L	699218	7/27/2015	1610	Megasphaera genomosp. type_1 str. 28L	699218 699192 906 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000008631	Isosphaera pallida (strain ATCC 43644 / DSM 9630 / IS1B)	575540	7/30/2015	3721	Isosphaera pallida ATCC 43644	575540 128 127 126 112 203683 203682 2 131567	Bacteria	Planctomycetes
UP000008783	Puccinia graminis f. sp. tritici (strain CRL 75-36-700-3 / race SCCL) (Black stem rust fungus)	418459	7/30/2015	15808	Puccinia graminis f. sp. tritici CRL 75-36-700-3	418459 56615 5297 5296 5262 5258 162484 29000 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000008634	Cellulophaga algicola (strain DSM 14237 / IC166 / ACAM 630)	688270	7/30/2015	4114	Cellulophaga algicola DSM 14237	688270 59600 104264 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008633	Nitratifractor salsuginis (strain DSM 16511 / JCM 12458 / E9I37-1)	749222	7/30/2015	2076	Nitratifractor salsuginis DSM 16511	749222 269261 269260 438853 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000015241	Fomitopsis pinicola (strain FP-58527) (Brown rot fungus)	743788	7/27/2015	13806	Fomitopsis pinicola FP-58527 SS1	743788 40483 34474 83233 5303 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000008125	Pseudomonas phage PB1 (isolate Pseudomonas aeruginosa/Scotland/Bradley/1968) (PB1) (Bacteriophage PB1)	1283339	7/27/2015	93	538398 1198980 10662 28883 35237 10239		Vruses	
UP000015268	Streptococcus lutetiensis 033	1076934	7/27/2015	1872	Streptococcus lutetiensis 033	1076934 150055 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008630	Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	693979	7/30/2015	3240	Bacteroides helcogenes P 36-108	693979 290053 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008635	Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	709986	7/30/2015	3262	Deinococcus maricopensis DSM 21211	709986 309887 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000008782	Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) (Maize anthracnose fungus) (Glomerella graminicola)	645133	7/30/2015	12019	Colletotrichum graminicola M1.001	645133 31870 5455 681950 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000008632	Pseudoxanthomonas suwonensis (strain 11-1)	743721	7/30/2015	3068	Pseudoxanthomonas suwonensis 11-1	743721 314722 83618 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001067	Pyrenophora teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)	861557	7/30/2015	11705	Pyrenophora teres f. teres 0-1	861557 97479 53485 5027 28556 715340 92860 451868 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000015332	Candidatus Carsonella ruddii DC	667013	7/27/2015	206	Candidatus Carsonella ruddii DC	667013 114186 114185 114403 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000003445	Paenibacillus sp. HGF7	944559	7/27/2015	5992	Paenibacillus sp. HGF7	944559 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000015382	Candidatus Nasuia deltocephalinicola str. NAS-ALF	1343077	7/27/2015	137	Candidatus Nasuia deltocephalinicola str. NAS-ALF	1343077 1160784 1301080 119066 28216 1224 2 131567	Bacteria	Proteobacteria
UP000015388	Corynebacterium maris DSM 45190	1224163	7/27/2015	2584	Corynebacterium maris DSM 45190	1224163 575200 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000015381	Halorhabdus tiamatea SARL4B	1033806	7/27/2015	2988	Halorhabdus tiamatea SARL4B	1033806 430914 146825 2236 2235 183963 28890 2157 131567	Archaea	
UP000003217	Streptococcus pseudoporcinus LQ 940-04	875093	7/27/2015	2026	Streptococcus pseudoporcinus LQ 940-04	875093 361101 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000003191	Bifidobacterium breve DSM 20213 = JCM 1192	518634	7/27/2015	2262	Bifidobacterium breve DSM 20213 = JCM 1192	518634 1685 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000015423	Streptomyces collinus Tu 365	1214242	8/6/2015	6681	Streptomyces collinus Tu 365	1214242 42684 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002970	[Clostridium] symbiosum WAL-14163	742740	7/27/2015	4668	[Clostridium] symbiosum WAL-14163	742740 1512 1506553 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000015464	Schizosaccharomyces cryophilus (strain OY26 / ATCC MYA-4695 / CBS 11777 / NBRC 106824 / NRRL Y48691) (Fission yeast)	653667	7/30/2015	5150	Schizosaccharomyces cryophilus OY26	653667 866546 4895 4894 34346 147554 451866 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000015441	Blumeria graminis f. sp. hordei (strain DH14) (Barley powdery mildew) (Oidium monilioides f. sp. hordei)	546991	7/27/2015	6486	Blumeria graminis f. sp. hordei DH14	546991 62688 34373 34372 34371 5120 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000015480	Paracoccus aminophilus JCM 7686	1367847	7/27/2015	4462	Paracoccus aminophilus JCM 7686	1367847 34003 265 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000004245	Rhodococcus equi ATCC 33707	525370	8/14/2015	5029	Rhodococcus equi ATCC 33707	525370 43767 1827 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000004198	Clostridium carboxidivorans P7	536227	7/27/2015	5458	Clostridium carboxidivorans P7	536227 217159 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000004291	Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43)	411684	8/19/2015	4185	Hoeflea phototrophica DFL-43	411684 244596 274591 69277 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000015503	Pseudomonas resinovorans NBRC 106553	1245471	8/7/2015	5795	Pseudomonas resinovorans NBRC 106553	1245471 53412 136841 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000015502	Thermococcus litoralis (strain ATCC 51850 / DSM 5473 / JCM 8560 / NS-C)	523849	7/30/2015	2506	Thermococcus litoralis DSM 5473	523849 2265 2263 2259 2258 183968 28890 2157 131567	Archaea	
UP000015562	endosymbiont of unidentified scaly snail isolate Monju	1248727	7/27/2015	2228	endosymbiont of unidentified scaly snail isolate Monju	1248727 33811 118884 1236 1224 2 131567	Bacteria	Proteobacteria
UP000015530	Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	1237896	7/30/2015	16388	Colletotrichum gloeosporioides Cg-14	1237896 474922 5455 681950 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000015559	Sulfuricella denitrificans skB26	1163617	7/27/2015	3071	Sulfuricella denitrificans skB26	1163617 649841 935200 1559980 1559979 28216 1224 2 131567	Bacteria	Proteobacteria
UP000005985	Hydrogenophaga sp. PBC	795665	7/27/2015	4964	Hydrogenophaga sp. PBC	795665 47420 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000004938	Neisseria weaveri LMG 5135	1051985	8/1/2015	2233	Neisseria weaveri LMG	1051985 28091 482 481 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000004946	Parascardovia denticolens DSM 10105 = JCM 12538	864564	8/2/2015	1679	Parascardovia denticolens DSM 10105 = JCM 12538	864564 78258 196082 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000015620	Treponema pedis str. T A4	1291379	7/27/2015	2775	Treponema pedis str. T A4	1291379 409322 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000004959	Oenococcus kitaharae DSM 17330	1045004	7/27/2015	1818	Oenococcus kitaharae DSM 17330	1045004 336988 46254 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000003714	Vibrio mimicus VM573	671076	7/27/2015	3744	Vibrio mimicus VM573	671076 674 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007938	Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	596154	7/30/2015	4620	Alicycliphilus denitrificans K601	596154 179636 201096 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007809	Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	675635	7/30/2015	6620	Pseudonocardia dioxanivorans CB1190	675635 240495 1847 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007808	Sphingobacterium sp. (strain 21)	743722	7/30/2015	5132	Sphingobacterium sp. 21	743722 28453 84566 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007807	Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) (Methanothrix concilii)	990316	7/30/2015	2791	Methanosaeta concilii GP6	990316 2223 2222 143067 94695 224756 28890 2157 131567	Archaea	
UP000005177	Lactobacillus jensenii JV-V16	525329	7/27/2015	1436	Lactobacillus jensenii JV-	525329 109790 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000007939	Sphaerochaeta coccoides (strain ATCC BAA-1237 / DSM 17374 / SPN1) (Spirochaeta coccoides)	760011	7/30/2015	1819	Sphaerochaeta coccoides DSM 17374	760011 273376 399320 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000008737	Pusillimonas sp. (strain T7-7)	1007105	7/30/2015	3751	Pusillimonas sp. T7-7	1007105 305976 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008297	Lacinutrix sp. (strain 5H-3-7-4)	983544	7/30/2015	2958	Lacinutrix sp. 5H-3-7-4	983544 291183 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008290	Dokdonia sp. (strain 4H-3-7-5) (Krokinobacter sp. (strain 4H-3-7-5))	983548	7/30/2015	2978	Dokdonia sp. 4H-3-7-5	983548 326319 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group

UP000006545	Porphyromonas asaccharolytica (strain ATCC 25260 / DSM 20707 / VPI 4198) (Bacteroides asaccharolyticus)	879243	7/30/2015	1672	Porphyromonas asaccharolytica DSM 20707	879243 28123 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000005380	Thioalkalimicrobium aerophilum AL3	717772	7/27/2015	2067	Thioalkalimicrobium aerophilum AL3	717772 92245 92244 135616 72273 1236 1224 2 131567	Bacteria	Proteobacteria
UP000005952	Hyphomicrobium denitrificans 1NES1	670307	7/27/2015	3832	Hyphomicrobium denitrificans 1NES1	670307 53399 81 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006546	Treponema brennaborense (strain DSM 12168 / CIP 105900 / DD5/3)	906968	7/30/2015	2522	Treponema brennaborense DSM 12168	906968 81028 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000005388	Streptococcus urinalis 2285-97	764291	7/27/2015	2206	Streptococcus urinalis 2285-97	764291 149016 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000015924	Adlercreutzia equolifaciens DSM 19450	1384484	7/27/2015	2281	Adlercreutzia equolifaciens DSM 19450	1384484 446660 447020 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000015929	Prevotella sp. oral taxon 299 str. F0039	575614	7/27/2015	1947	Prevotella sp. oral taxon 299 str. F0039	575614 652716 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000005580	Prevotella oralis ATCC 33269	873533	7/27/2015	2479	Prevotella oralis ATCC 33269	873533 28134 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000015934	Streptococcus sp. HSISB1	1316409	7/27/2015	2160	Streptococcus sp. HSISB1	1316409 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000006408	Bifidobacterium angulatum DSM 20098 = JCM 7096	518635	7/27/2015	1724	Bifidobacterium angulatum DSM 20098 = JCM 7096	518635 1683 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000015933	Streptococcus sp. HSISM1	1316408	7/27/2015	2219	Streptococcus sp. HSISM1	1316408 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000006424	Desulfovibrio sp. 6_1_46AFAA	665942	7/27/2015	3312	Desulfovibrio sp. 6_1_46AFAA	665942 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000015939	Enterococcus sp. HSIEG1	1316414	7/27/2015	3882	Enterococcus sp. HSIEG1	1316414 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000015961	Enterococcus sulfureus ATCC 49903	1140003	7/27/2015	2176	Enterococcus sulfureus ATCC 49903	1140003 1356 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000015971	Nocardioides sp. CF8	110319	7/27/2015	3893	Nocardioides sp. CF8	110319 1839 85015 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002938	Turicibacter sanguinis PC909	702450	7/27/2015	2779	Turicibacter sanguinis PC909	702450 154288 191303 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000005850	Brevibacillus laterosporus LMG 15441	1042163	7/27/2015	4532	Brevibacillus laterosporus LMG 15441	1042163 1465 55080 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000006431	Sulfurimonas gotlandica (strain DSM 19862 / JCM 16533 / GD1)	929558	7/27/2015	2865	Sulfurimonas gotlandica GD1	929558 1176482 202746 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000003070	Lactobacillus oris PB013-T2-3	908339	7/27/2015	2038	Lactobacillus oris PB013-T2-3	908339 1632 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000003081	Clostridium butyricum E4 str. BoNT E BL5262	632245	7/27/2015	4245	Clostridium butyricum E4 str. BoNT E BL5262	632245 1492 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000003112	Prevotella buccae ATCC 33574	873513	7/27/2015	2896	Prevotella buccae ATCC 33574	873513 28126 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000016160	Formosa agariphila KMM 3901	1347342	7/27/2015	3557	Formosa agariphila KMM 3901	1347342 320324 225842 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008922	Anaerolinea thermophila (strain DSM 14523 / JCM 11388 / NBRC 100420 / UNI-1)	926569	7/30/2015	3110	Anaerolinea thermophila UNI-1	926569 167964 233189 292628 292629 292625 200795 2 131567	Bacteria	Chloroflexi
UP000003111	Aeromicrobium marinum DSM 15272	585531	7/27/2015	3077	Aeromicrobium marinum DSM 15272	585531 219314 2040 85015 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007469	Staphylococcus pseudintermedius (strain HKU10-03)	937773	7/30/2015	2449	Staphylococcus pseudintermedius HKU10-03	937773 283734 1279 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000007472	Taylorella equigenitalis (strain MCE9)	937774	7/30/2015	1556	Taylorella equigenitalis MCE9	937774 29575 29574 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006229	Mycoplasma canis UFG4	1131455	7/27/2015	642	Mycoplasma canis UFG4	1131455 29555 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000006365	Desulfobulbus propionicus (strain ATCC 33891 / DSM 2032 / 1pr3)	577650	7/30/2015	3259	Desulfobulbus propionicus DSM 2032	577650 894 893 213121 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006362	Thermovibrio ammonificans (strain DSM 15698 / JCM 12110 / HB-1)	648996	7/30/2015	1812	Thermovibrio ammonificans HB-1	648996 228745 171868 558314 1485951 187857 200783 2 131567	Bacteria	Aquificae
UP000007468	Filifactor alocis (strain ATCC 35896 / D40 B5) (Fusobacterium alocis)	546269	7/30/2015	1616	Filifactor alocis ATCC 35896	546269 143361 44259 186804 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008673	Ogataea parapolymorpha (strain DL-1 / ATCC 26012 / NRRL Y-7560) (Yeast) (Hansenula polymorpha)	871575	7/30/2015	5338	Ogataea parapolymorpha DL-1	871575 1005962 461281 1156497 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008153	Leishmania infantum	5671	7/30/2015	8045	Leishmania infantum	5671 38574 38568 5658 1286322 5654 5653 33682 2759 131567	eukaryotes	
UP000006237	Corynebacterium glucuronolyticum ATCC 51866	548478	7/27/2015	2733	Corynebacterium glucuronolyticum ATCC 51866	548478 39791 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007471	Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)	765698	7/30/2015	6260	Mesorhizobium ciceri biovar biserrulae WSM1271	765698 278148 39645 68287 69277 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000007258	Leishmania braziliensis	5660	7/30/2015	8084	Leishmania braziliensis	5660 37617 37616 5658 1286322 5654 5653 33682 2759 131567	eukaryotes	
UP000016233	Streptococcus intermedius B196	862967	7/27/2015	1812	Streptococcus intermedius B196	862967 1338 671232 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000003586	Niabella soli DSM 19437	929713	7/27/2015	4110	Niabella soli DSM 19437	929713 446683 379899 563835 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006468	Komagataeibacter hansenii ATCC 23769	714995	7/27/2015	3303	Komagataeibacter hansenii ATCC 23769	714995 436 1434011 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria

UP000005275	Marichromatium purpuratum 984	765910	7/27/2015	3249	Marichromatium purpuratum 984	765910 37487 85076 1046 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000003813	Opitutaceae bacterium TAV5	794903	7/27/2015	6011	Opitutaceae bacterium TAV5	794903 278955 134623 415000 414999 74201 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000016412	Treponema socranskii subsp. socranskii VPI DR56BR1116 = ATCC 35536	1125725	7/27/2015	2624	Treponema socranskii subsp. socranskii VPI DR56BR1116 = ATCC 35536	1125725 69715 53419 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000004057	Spiroplasma melliferum KC3	570509	7/27/2015	1154	Spiroplasma melliferum	570509 2134 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000004324	Pelosinus fermentans B4	1149862	7/27/2015	4690	Pelosinus fermentans B4	1149862 365349 365348 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000004115	Lactobacillus iners DSM 13335	525328	7/27/2015	1214	Lactobacillus iners DSM 13335	525328 147802 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000016497	Alcaligenes sp. EGD-AK7	1386079	7/27/2015	3991	Alcaligenes sp. EGD-AK7	1386079 507 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000004595	Halobacterium sp. DL1	751944	7/27/2015	3265	Halobacterium sp. DL1	751944 2239 2236 2235 183963 28890 2157 131567	Archaea	
UP000003148	Bradyrhizobiaceae bacterium SG-6C	709797	7/27/2015	4236	Bradyrhizobiaceae bacterium SG-6C	709797 81426 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000016587	Desulfovibrio gigas DSM 1382 = ATCC 19364	1121448	7/29/2015	3319	Desulfovibrio gigas DSM 1382 = ATCC 19364	1121448 879 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000004889	Leptospira licerasiae serovar Varillal str. VAR 010	1049972	8/4/2015	3927	Leptospira licerasiae serovar Varillal str. VAR 010	1049972 447107 447106 171 170 1643688 203692 203691 2 131567	Bacteria	Spirochaetes
UP000016666	Anas platyrhynchos (Mallard) (Anas boschas)	8839	7/27/2015	16378	Anas platyrhynchos	8839 8835 8830 8826 1549675 8825 8782 436492 436491 436489 436486 8492 1329799 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000016601	Oscillibacter sp. KLE 1745	1226323	7/27/2015	4293	Oscillibacter sp. KLE 1745	1226323 459786 216572 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000003612	Neisseria mucosa C102	435832	8/1/2015	2026	Neisseria mucosa C102	435832 488 482 481 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000016665	Ficedula albicollis (Collared flycatcher) (Muscicapa albicollis)	59894	7/27/2015	15922	Ficedula albicollis	59894 36292 36291 9126 8825 8782 436492 436491 436489 436486 8492 1329799 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000016617	Streptococcus sobrinus W1703	1227275	7/27/2015	2210	Streptococcus sobrinus W1703	1227275 1310 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000003919	Algoriphagus machipongonensis	388413	8/4/2015	3932	Algoriphagus machipongonensis	388413 246875 563798 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000430	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	62977	7/30/2015	3263	Acinetobacter sp. ADP1	62977 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007966	Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	218491	7/30/2015	4459	Pectobacterium atrosepticum SCRI1043	218491 29471 122277 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002428	Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) (Yeast) (Torulopsis glabrata)	284593	7/30/2015	5200	Candida glabrata CBS 138	284593 5478 600669 374468 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008952	Bartonella tamiae Th239	1094558	7/27/2015	1978	Bartonella tamiae Th239	1094558 373638 773 772 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000598	Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) (Yeast) (Candida sphaerica)	284590	7/30/2015	5071	Kluyveromyces lactis NRRL Y-1140	284590 28985 4910 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001300	Yarrowia lipolytica (strain CLIB 122 / E 150) (Yeast) (Candida lipolytica)	284591	7/30/2015	6453	Yarrowia lipolytica CLIB122	284591 4952 4951 34353 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000599	Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) (Yeast) (Torulaspora hansenii)	284592	7/30/2015	6284	Debaryomyces hansenii CBS767	284592 58641 4959 4958 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000600	Paramecium tetraurelia	5888	7/30/2015	39461	Paramecium tetraurelia	5888 5884 340080 33825 6020 431838 5878 33630 2759 131567	eukaryotes	
UP000009005	Mycoplasma wenyonii (strain Massachusetts) (Eperythrozoon wenyonii)	1197325	7/30/2015	651	Mycoplasma wenyonii str. Massachusetts	1197325 65123 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000009011	Melioribacter roseus (strain JCM 17771 / P3M-2)	1191523	7/30/2015	2833	Melioribacter roseus P3M-2	1191523 1134405 1134403 1334117 795748 795747 1134404 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000602	Desulfotalea psychrophila (strain LSv54 / DSM 12343)	177439	7/30/2015	3233	Desulfotalea psychrophila LSv54	177439 84980 109168 213121 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000603	Propionibacterium acnes (strain KPA171202 / DSM 16379)	267747	7/30/2015	2294	Propionibacterium acnes KPA171202	267747 1747 1743 31957 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006647	Mesoplasma florum (strain ATCC 33453 / NBRC 100688 / NCTC 11704 / L1) (Acholeplasma florum)	265311	7/30/2015	683	Mesoplasma florum L1	265311 2151 46239 33925 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000001306	Leifsonia xyli subsp. xyli (strain CTCB07)	281090	7/30/2015	2001	Leifsonia xyli subsp. xyli str. CTCB07	281090 59736 1575 110932 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006039	Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	644352	7/30/2015	14328	Gaeumannomyces graminis var. tritici R3-111a-1	644352 36779 29850 29849 81093 639021 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000417	Symbiobacterium thermophilum (strain T / IAM 14863)	292459	7/30/2015	3313	Symbiobacterium thermophilum IAM 14863	292459 2734 2733 543349 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000006036	Helicobacter cinaedi ATCC BAA-847	1206745	7/27/2015	2315	Helicobacter cinaedi ATCC BAA-847	1206745 213 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000005240	Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)	630390	7/30/2015	11515	Puccinia triticina 1-1 BBBD Race 1	630390 208348 5296 5262 5258 162484 29000 5204 451864 4751 33154 2759 131567	eukaryotes	

UP000000607	Mannheimia succiniciproducens (strain MBEL55E)	221988	7/30/2015	2367	Mannheimia succiniciproducens MBEL55E	221988 157673 697331 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006507	Natrinema sp. (strain J7-2)	406552	7/30/2015	4296	Natrinema sp. J7-2	406552 88723 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000006821	Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	243233	7/30/2015	2925	Methylococcus capsulatus str. Bath	243233 414 413 403 135618 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006820	Nocardia farcinica (strain IFM 10152)	247156	7/30/2015	5941	Nocardia farcinica IFM	247156 37329 1817 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006502	Mycoplasma haemolamae (strain Purdue)	1212765	7/30/2015	923	Candidatus Mycoplasma haemolamae str. Purdue	1212765 141391 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000000609	Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513)	272624	7/30/2015	2930	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	272624 91891 446 445 444 118969 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006038	Oryza brachyantha	4533	8/2/2015	31989	Oryza brachyantha	4533 4527 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000006040	Acute bee paralysis virus (strain Rothamsted) (ABPV)	1217067	7/30/2015	3	Acute bee paralysis virus strain Rothamsted	1217067 92444 1213379 232795 464095 35278 439488 10239	Vruses	
UP000000605	Burkholderia pseudomallei (strain K96243)	272560	7/30/2015	5717	Burkholderia pseudomallei K96243	272560 28450 111527 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000016801	Claviceps purpurea (strain 20.1) (Ergot fungus) (Sphacelia segetum)	1111077	7/30/2015	8814	Claviceps purpurea 20.1	1111077 5111 5110 34397 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001168	Bacillus clausii (strain KSM-K16)	66692	8/7/2015	4082	Bacillus clausii KSM-K16	66692 79880 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000016800	Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	1279085	8/3/2015	14792	Fusarium fujikuroi IMI 58289	1279085 5127 171627 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000606	Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	279010	7/30/2015	4164	Bacillus licheniformis DSM 13 = ATCC 14580	279010 1402 653685 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000002914	Phaeobacter inhibens (strain ATCC 700781 / DSM 17395 / CIP 105210 / NBRC 16654 / BS107)	391619	7/27/2015	3853	Phaeobacter inhibens DSM 17395	391619 221822 302485 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001169	Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) (Halobacterium marismortui)	272569	7/30/2015	4234	Haloarcula marismortui ATCC 43049	272569 2238 2237 2236 2235 183963 28890 2157 131567	Archaea	
UP000007516	Wolbachia endosymbiont of Onchocerca ochengi	100901	7/27/2015	647	Wolbachia endosymbiont of Onchocerca ochengi	100901 953 952 942 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000016895	Vibrio nigripulchritudo	28173	7/27/2015	5540	Vibrio nigripulchritudo	28173 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008460	Cellulomonas fimi (strain ATCC 484 / DSM 20113 / JCM 1341 / NBRC 15513 / NCIMB 8980 / NCTC 7547)	590998	8/2/2015	3760	Cellulomonas fimi ATCC 484	590998 1708 1707 85016 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008458	Acidianus hospitalis (strain W1)	933801	7/30/2015	2329	Acidianus hospitalis W1	933801 563177 12914 118883 2281 183924 28889 2157 131567	Archaea	
UP000001170	Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311)	264199	7/30/2015	1577	Streptococcus thermophilus LMG 18311	264199 1308 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001172	Geobacillus kaustophilus (strain HTA426)	235909	7/30/2015	3516	Geobacillus kaustophilus HTA426	235909 1462 129337 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000016900	Candidatus Pantoea carbekii	1235990	7/27/2015	825	Candidatus Pantoea	1235990 53335 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008457	Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	697281	7/30/2015	2858	Mahella australiensis 50-1 BON	697281 252966 252965 543372 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000016901	Plautia stali symbiont	891974	7/27/2015	5007	Plautia stali symbiont	891974 36866 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008456	Melissococcus plutonius (strain ATCC 35311 / CIP 104052 / LMG 20360 / NCIMB 702443)	940190	7/30/2015	1876	Melissococcus plutonius ATCC 35311	940190 33970 33969 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000006552	Aromatoleum aromaticum (strain EbN1) (Azoarcus sp. (strain EbN1))	76114	7/30/2015	4483	Aromatoleum aromaticum EbN1	76114 551760 551759 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000683	Alteromonas sp. (strain SN2)	715451	7/30/2015	4342	Alteromonas sp. SN2	715451 226 72275 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008461	Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	760192	7/30/2015	6704	Haliscomenobacter hydrossis DSM 1100	760192 2350 2349 89374 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006548	Arabidopsis thaliana (Mouse-ear cress)	3702	8/2/2015	31493	Arabidopsis thaliana	3702 3701 980083 3700 3699 91836 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000001174	Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4)	177416	7/30/2015	1528	Francisella tularensis subsp. tularensis SCHU S4	177416 119856 263 262 34064 72273 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001171	Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	283942	7/30/2015	2608	Idiomarina loihiensis L2TR	283942 135577 135575 267893 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001173	Zymomonas mobilis subsp. mobilis (strain ATCC 31821 / ZM4 / CP4)	264203	7/30/2015	1779	Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821	264203 120045 542 541 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000686	Pseudomonas fulva (strain 12-X)	743720	8/7/2015	4459	Pseudomonas fulva 12-X	743720 47880 136845 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001023	Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) (Silicibacter pomeroyi)	246200	8/4/2015	4269	Ruegeria pomeroyi DSS-3	246200 89184 97050 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006968	Saccharomyces arboricola (strain H-6 / AS 2.3317 / CBS 10644) (Yeast)	1160507	7/30/2015	3653	Saccharomyces arboricola H-6	1160507 706196 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016926	Rhodosporidium toruloides (strain NP11) (Yeast) (Rhodotorula gracilis)	1130832	7/30/2015	8138	Rhodosporidium toruloides NP11	1130832 5286 5285 231213 162481 29000 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000007796	Grosmannia clavigera (strain kw1407 / UAMH 11150) (Blue stain fungus) (Graphiocladiella clavigera)	655863	7/30/2015	8311	Grosmannia clavigera kw1407	655863 226899 360145 5152 5151 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000000437	Danio rerio (Zebrafish) (Brachydanio rerio)	7955	8/26/2015	43550	Danio rerio	7955 7954 7953 30727 7952 186627 186626 32519 186634 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000531	Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	176279	7/30/2015	2492	Staphylococcus epidermidis RP62A	176279 1282 1279 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000016929	Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	1229665	7/30/2015	14157	Fusarium oxysporum f. sp. cubense race 4	1229665 61366 5507 171631 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016924	Coniosporium apollinis (strain CBS 100218) (Rock-inhabiting black yeast)	1168221	7/30/2015	9306	Coniosporium apollinis CBS 100218	1168221 61459 61458 43219 34395 451870 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016922	Glarea lozoyensis (strain ATCC 20868 / MF5171)	1116229	7/30/2015	13082	Glarea lozoyensis ATCC 20868	1116229 101852 101851 5181 5178 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008142	Ajellomyces capsulatus (strain H88) (Darling's disease fungus) (Histoplasma capsulatum)	544711	7/30/2015	9445	Histoplasma capsulatum H88	544711 5037 5036 299071 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000003936	secondary endosymbiont of Ctenarytaina eucalypti	1199245	7/27/2015	918	secondary endosymbiont of Ctenarytaina eucalypti	1199245 146507 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000016923	Ophiostoma piceae (strain UAMH 11346) (Sap stain fungus)	1262450	7/30/2015	8878	Ophiostoma piceae UAMH 11346	1262450 61273 5159 5152 5151 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016925	Malassezia sympodialis (strain ATCC 42132) (Atopic eczema-associated yeast)	1230383	7/30/2015	3318	Malassezia sympodialis ATCC 42132	1230383 76777 55193 742845 162474 1538075 452284 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000003937	secondary endosymbiont of Heteropsylla cubana	134287	7/27/2015	576	secondary endosymbiont of Heteropsylla cubana	134287 146507 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000016927	Nosema bombycis (strain CQ1 / CVCC 102059) (Microsporidian parasite) (Pebrine of silkworm)	578461	7/30/2015	4398	Nosema bombycis CQ1	578461 27978 27977 27974 6032 6029 4751 33154 2759 131567	eukaryotes	
UP000016935	Setosphaeria turcica (strain 28A) (Northern leaf blight fungus) (Exserohilum turcicum)	671987	7/30/2015	11687	Setosphaeria turcica Et28A	671987 93612 39952 28556 715340 92860 451868 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016933	Dothistroma septosporum (strain NZE10 / CBS 128990) (Red band needle blight fungus) (Mycosphaerella pini)	675120	8/7/2015	12414	Dothistroma septosporum NZE10	675120 64363 242508 93133 134362 451867 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016932	Pseudocercospora fijiensis (strain CIRAD86) (Black leaf streak disease fungus) (Mycosphaerella fijiensis)	383855	7/30/2015	13062	Pseudocercospora fijiensis CIRAD86	383855 83344 131324 93133 134362 451867 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002149	Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) (Filobasidiella neoformans)	214684	7/30/2015	6436	Cryptococcus neoformans var. neoformans JEC21	214684 40410 5207 552466 5206 5215 5234 155616 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000016931	Sphaerulina musiva (strain SO2202) (Poplar stem canker fungus) (Septoria musiva)	692275	7/30/2015	10154	Sphaerulina musiva SO2202	692275 85929 237179 93133 134362 451867 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016928	Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	1229664	7/30/2015	15355	Fusarium oxysporum f. sp. cubense race 1	1229664 61366 5507 171631 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016934	Cochliobolus sativus (strain ND90Pr / ATCC 201652) (Common root rot and spot blotch fungus) (Bipolaris sorokiniana)	665912	7/30/2015	12174	Bipolaris sorokiniana ND90Pr	665912 45130 33194 28556 715340 92860 451868 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006375	Gluconobacter oxydans (strain 621H) (Gluconobacter suboxydans)	290633	7/30/2015	2626	Gluconobacter oxydans 621H	290633 442 441 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000016936	Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis)	701091	7/30/2015	12857	Bipolaris maydis C5	701091 5016 33194 28556 715340 92860 451868 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006381	Lactobacillus acidophilus (strain ATCC 700396 / NCK56 / N2 / NCFM)	272621	7/30/2015	1859	Lactobacillus acidophilus NCFM	272621 1579 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000016930	Ceriporiopsis subvermispora (strain B) (White-rot fungus)	914234	7/30/2015	12078	Gelatoporia subvermispora B	914234 42742 98757 83233 5303 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000006735	Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85)	291331	7/30/2015	4382	Xanthomonas oryzae pv. oryzae KACC 10331	291331 64187 347 338 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000535	Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090)	242231	8/2/2015	2106	Neisseria gonorrhoeae FA 1090	242231 485 482 481 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002753	Saccharomyces kudriavzevii (strain ATCC MYA-4449 / AS 2.2408 / CBS 8840 / NBRC 1802 / NCYC 2889) (Yeast)	226230	7/30/2015	3745	Saccharomyces kudriavzevii IFO 1802	226230 114524 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000016943	Corynebacterium argentoratense DSM 44202	1348662	7/27/2015	1870	Corynebacterium argentoratense DSM 44202	1348662 42817 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000532	Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579)	300852	7/30/2015	2227	Thermus thermophilus HB8	300852 274 270 188786 68933 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000002975	Fusobacterium gonidiaformans 3-1-5R	469605	7/27/2015	1890	Fusobacterium gonidiaformans 3-1-5R	469605 849 848 203492 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000003961	Brucella abortus bv. 9 str. C68	520455	7/30/2015	3192	Brucella abortus bv. 9 str. C68	520455 1567505 235 234 118882 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006731	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	272559	7/30/2015	4234	Bacteroides fragilis NCTC 9343	272559 817 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002786	Prevotella bivia DSM 20514	868129	7/27/2015	2064	Prevotella bivia DSM 20514	868129 28125 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008975	Microbacterium testaceum (strain StLB037)	979556	7/30/2015	3671	Microbacterium testaceum StLB037	979556 2033 33882 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria

UP000003955	Streptomyces sp. Tu6071	355249	7/27/2015	6635	Streptomyces sp. Tu6071	355249 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007819	Acyrthosiphon pisum (Pea aphid)	7029	7/27/2015	35819	Acyrthosiphon pisum	7029 7028 33386 133076 27482 33385 143961 33380 33373 7524 33342 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000537	Vibrio fischeri (strain ATCC 700601 / ES114)	312309	7/30/2015	3813	Vibrio fischeri ES114	312309 668 511678 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000536	Thermococcus kodakarensis (strain ATCC BAA-918 / JCM 12380 / KOD1) (Pyrococcus kodakaraensis (strain KOD1))	69014	7/30/2015	2301	Thermococcus kodakarensis KOD1	69014 311400 2263 2259 2258 183968 28890 2157 131567	Archaea	
UP000002774	Mucilaginibacter paludis DSM 18603	714943	7/27/2015	6864	Mucilaginibacter paludis DSM 18603	714943 423351 423349 84566 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002785	Streptomyces sviceus ATCC 29083	463191	8/7/2015	8202	Streptomyces sviceus ATCC 29083	463191 285530 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006470	Polaribacter sp. MED152	313598	7/27/2015	2634	Polaribacter sp. MED152	313598 52959 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002759	Brenneria sp. EniD312	598467	7/27/2015	4386	Brenneria sp. EniD312	598467 71655 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007237	Saccharomyces cerevisiae (strain FostersO) (Baker's yeast)	764101	7/30/2015	3560	Saccharomyces cerevisiae FostersO	764101 4932 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000004671	Caldithrix abyssi DSM 13497	880073	7/27/2015	3674	Caldithrix abyssi DSM 13497	880073 187145 187144 2323 2 131567	Bacteria	Unclassified Bacteria
UP000000309	Saccharomyces cerevisiae (strain FostersB) (Baker's yeast)	764102	7/30/2015	3679	Saccharomyces cerevisiae FostersB	764102 4932 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007236	Saccharomyces cerevisiae (strain Lalvin QA23) (Baker's yeast)	764098	7/30/2015	4008	Saccharomyces cerevisiae Lalvin QA23	764098 4932 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000307	Saccharomyces cerevisiae (strain VIN 13) (Baker's yeast)	764099	7/30/2015	3916	Saccharomyces cerevisiae Vin13	764099 4932 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000003806	Jonquetella anthropi DSM 22815	885272	7/27/2015	1508	Jonquetella anthropi DSM 22815	885272 428712 428711 649777 649776 649775 508458 2 131567	Bacteria	Synergistetes
UP000002195	Dictyostelium discoideum (Slime mold)	44689	7/27/2015	12746	Dictyostelium discoideum	44689 5782 33083 142796 554915 2759 131567	eukaryotes	
UP000000306	Saccharomyces cerevisiae (strain AWRI796) (Baker's yeast)	764097	7/30/2015	3760	Saccharomyces cerevisiae AWRI796	764097 4932 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005785	Myroides odoratus DSM 2801	929704	7/27/2015	3687	Myroides odoratus DSM 2801	929704 256 76831 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002762	Beauveria bassiana (strain ARSEF 2860) (White muscardine disease fungus) (Tritirachium shiotae)	655819	7/30/2015	10363	Beauveria bassiana ARSEF 2860	655819 176275 5581 474943 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000004674	Burkholderiales bacterium JOSHI_001	864051	7/27/2015	4891	Burkholderiales bacterium JOSHI_001	864051 80841 119065 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007238	Saccharomyces cerevisiae (strain Zymaflore VL3) (Baker's yeast)	764100	7/30/2015	4014	Saccharomyces cerevisiae VL3	764100 4932 4930 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000005741	Methanoplanus limicola DSM 2279	937775	7/27/2015	2928	Methanoplanus limicola DSM 2279	937775 2315 2314 2194 2191 224756 28890 2157 131567	Archaea	
UP000005090	Methylomicrobium album BG8	686340	7/27/2015	3738	Methylomicrobium album BG8	686340 39775 39773 403 135618 1236 1224 2 131567	Bacteria	Proteobacteria
UP000005778	Desulfobacter postgatei 2ac9	879212	7/27/2015	3396	Desulfobacter postgatei 2ac9	879212 2293 2289 213119 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000008553	Plasmodium yoelii yoelii	73239	7/30/2015	7741	Plasmodium yoelii yoelii	73239 5861 418101 5820 1639119 5819 422676 5794 33630 2759 131567	eukaryotes	
UP000008549	Caenorhabditis briggsae	6238	7/30/2015	21750	Caenorhabditis briggsae	6238 6237 55885 6243 55879 6236 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000005087	Saccharomonospora glauca K62	928724	7/27/2015	4239	Saccharomonospora glauca K62	928724 40990 1851 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000004926	Saccharomonospora marina XMU15	882083	7/27/2015	5567	Saccharomonospora marina XMU15	882083 632569 1851 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005095	Methanofollis liminatans DSM 4140	28892	7/27/2015	2423	Methanofollis liminatans DSM 4140	28892 2201 81416 2194 2191 224756 28890 2157 131567	Archaea	
UP000002805	Streptomyces pristinaespiralis ATCC 25486	457429	8/7/2015	6866	Streptomyces pristinaespiralis ATCC 25486	457429 38300 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005753	[Eubacterium] cellulosolvens 6	633697	7/27/2015	2716	[Eubacterium] cellulosolvens 6	633697 29322 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000005106	Clostridium sp. DL-VIII	641107	7/27/2015	5645	Clostridium sp. DL-VIII	641107 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000005726	Candidatus Regiella insecticola LSR1	663321	7/27/2015	1368	Candidatus Regiella insecticola LSR1	663321 138073 568988 146507 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000539	Gallus gallus (Chicken)	9031	8/2/2015	17690	Gallus gallus	9031 9030 9072 9005 8976 1549675 8825 8782 436492 436491 436489 436486 8492 1329799 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000005096	Aminomonas paucivorans DSM 12260	584708	7/27/2015	2391	Aminomonas paucivorans DSM 12260	584708 81412 81411 649777 649776 649775 508458 2 131567	Bacteria	Synergistetes
UP000000542	Leishmania major	5664	7/30/2015	8038	Leishmania major	5664 38581 38568 5658 1286322 5654 5653 33682 2759 131567	eukaryotes	
UP000000543	Staphylococcus haemolyticus (strain JCSC1435)	279808	7/30/2015	2640	Staphylococcus haemolyticus JCSC1435	279808 1283 1279 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes

UP000000545	Corynebacterium jeikeium (strain K411)	306537	7/30/2015	2064	Corynebacterium jeikeium K411	306537 38289 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008540	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	220664	8/7/2015	6108	Pseudomonas protegens Pf-5	220664 380021 136843 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000005307	Octadecabacter antarcticus 307	391626	7/27/2015	4327	Octadecabacter antarcticus 307	391626 1217908 53945 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000003163	Edhazardia aedis (strain USNM 41457) (Microsporidian parasite)	1003232	7/30/2015	4208	Edhazardia aedis USNM 41457	1003232 70536 70535 322152 469895 6029 4751 33154 2759 131567	eukaryotes	
UP000005248	Streptococcus pyogenes M1 476	1207470	7/30/2015	1589	Streptococcus pyogenes M1 476	1207470 301447 1314 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000005263	Methylocystis sp. (strain SC2)	187303	7/30/2015	4040	Methylocystis sp. SC2	187303 133 31993 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001018	Sulfolobus acidocaldarius (strain ATCC 33909 / DSM 639 / JCM 8929 / NBRC 15157 / NCIMB 11770)	330779	7/30/2015	2221	Sulfolobus acidocaldarius DSM 639	330779 2285 2284 118883 2281 183924 28889 2157 131567	Archaea	
UP000017096	Corynebacterium sp. KPL1855	1203562	7/27/2015	2285	Corynebacterium sp. KPL1855	1203562 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000017101	Labrenzia sp. C1B10	1397530	8/4/2015	6397	Labrenzia sp. C1B10	1397530 478070 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000017102	Corynebacterium sp. KPL1989	1203622	8/4/2015	2066	Corynebacterium sp. KPL1989	1203622 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000005262	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	768704	8/4/2015	4340	Desulfosporosinus meridiei DSM 13257	768704 79209 79206 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017118	Clostridium saccharobutylicum DSM 13864	1345695	8/14/2015	4355	Clostridium saccharobutylicum DSM 13864	1345695 169679 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000546	Psychrobacter arcticus (strain DSM 17307 / 273-4)	259536	7/30/2015	2099	Psychrobacter arcticus 273-4	259536 334543 497 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000004810	Wuchereria bancrofti	6293	7/27/2015	19298	Wuchereria bancrofti	6293 6292 6296 6295 6274 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000547	Colwellia psychrerythraea (strain 34H / ATCC BAA-681) (Vibrio psychroerythus)	167879	7/30/2015	4872	Colwellia psychrerythraea 34H	167879 28229 28228 267889 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000017119	Mycoplasma parvum str. Indiana	1403316	7/27/2015	580	Mycoplasma parvum str. Indiana	1403316 984991 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000006352	Fibroporia radiculosa (strain TFFH 294) (Brown rot fungus) (Antrodia radiculosa)	1078123	7/30/2015	9251	Fibroporia radiculosa TFFH 294	1078123 599839 599838 5317 5303 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000000549	Mycoplasma synoviae (strain 53)	262723	7/30/2015	679	Mycoplasma synoviae 53	262723 2109 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000000548	Mycoplasma hyopneumoniae (strain J / ATCC 25934 / NCTC 10110)	262719	7/30/2015	671	Mycoplasma hyopneumoniae J	262719 2099 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000002528	Pelagibacter ubique (strain HTCC1062)	335992	7/30/2015	1354	Candidatus Pelagibacter ubique HTCC1062	335992 198252 198251 1655514 54526 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000559	Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)	237561	7/30/2015	9038	Candida albicans SC5314	237561 5476 1535326 1535325 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000550	Dechloromonas aromatica (strain RCB)	159087	7/30/2015	4155	Dechloromonas aromatica RCB	159087 259537 73029 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000009058	Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	242507	7/30/2015	12647	Magnaporthe oryzae 70-15	242507 318829 148303 81093 639021 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000561	Ustilago maydis (strain 521 / FGSC 9021) (Corn smut fungus)	237631	7/30/2015	6806	Ustilago maydis 521	237631 5270 5269 5268 5267 5257 452284 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000017175	Pseudomonas fluorescens NCIMB 11764	1221522	7/30/2015	6428	Pseudomonas fluorescens NCIMB 11764	1221522 294 136843 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000434	Thermobifida fusca (strain YX)	269800	7/30/2015	3085	Thermobifida fusca YX	269800 2021 83677 83676 85012 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008291	Thiobacillus denitrificans (strain ATCC 25259)	292415	7/30/2015	2826	Thiobacillus denitrificans ATCC 25259	292415 36861 919 206349 119069 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006078	Turicella otitidis ATCC 51513	883169	7/30/2015	1846	Turicella otitidis ATCC	883169 29321 144193 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006371	Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229)	342451	7/30/2015	2404	Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305	342451 147452 29385 1279 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000003281	Gordonia sp. KTR9	337191	7/27/2015	5161	Gordonia sp. KTR9	337191 2053 85026 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002531	Nitrobacter winogradskyi (strain Nb-255 / ATCC 25391)	323098	7/30/2015	2980	Nitrobacter winogradskyi Nb-255	323098 913 911 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008289	Dehalococcoides mccartyi (strain ATCC BAA-2266 / KCTC 15142 / 195) (Dehalococcoides ethenogenes (strain 195))	243164	7/30/2015	1502	Dehalococcoides mccartyi 195	243164 61435 61434 1202464 1202465 301297 200795 2 131567	Bacteria	Chloroflexi
UP000004994	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	4081	8/2/2015	34858	Solanum lycopersicum	4081 49274 4107 424574 424551 4070 4069 91888 71274 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000001805	Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987)	367110	8/2/2015	10258	Neurospora crassa OR74A	367110 5141 5140 5148 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000560	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	227321	7/30/2015	10555	Aspergillus nidulans FGSC A4	227321 162425 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000009057	Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	5518	8/2/2015	14213	Fusarium graminearum	5518 569360 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000004995	Setaria italica (Foxtail millet) (Panicum italicum)	4555	8/8/2015	39110	Setaria italica	4555 4554 1293361 147428 1648036 147369 147370 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000017184	Candidatus Symbiobacter mobilis CR	946483	7/27/2015	2609	Candidatus Symbiobacter mobilis CR	946483 1436290 1436289 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002535	Prochlorococcus marinus (strain NATL2A)	59920	7/30/2015	2142	Prochlorococcus marinus str. NATL2A	59920 1219 1218 1217 1212 1117 2 131567	Bacteria	Cyanobacteria
UP000002530	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	330879	7/30/2015	9649	Aspergillus fumigatus Af293	330879 746128 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000003779	Nocardiopsis alba (strain ATCC BAA-2165 / BE74)	1205910	7/30/2015	5500	Nocardiopsis alba ATCC BAA-2165	1205910 53437 2013 83676 85012 1760 201174 2 131567	Bacteria	Actinobacteria
UP000003996	Cardinium endosymbiont cEper1 of Encarsia pergandiella	1231626	7/27/2015	887	Cardinium endosymbiont cEper1 of Encarsia pergandiella	1231626 249402 273135 1501348 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006843	Pseudoalteromonas haloplanktis (strain TAC 125)	326442	7/30/2015	3484	Pseudoalteromonas haloplanktis TAC125	326442 228 53246 267888 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002698	Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) (Halobacterium pharaonis)	348780	7/30/2015	2765	Natronomonas pharaonis DSM 2160	348780 2257 63743 2236 2235 183963 28890 2157 131567	Archaea	
UP000006310	Kazachstania naganishii (strain ATCC MYA-139 / BCRC 22969 / CBS 8797 / CCRC 22969 / KCTC 17520 / NBRC 10181 / NCYC 3082) (Yeast) (Saccharomyces naganishii)	1071383	7/30/2015	5301	Kazachstania naganishii CBS 8797	1071383 588726 71245 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006838	Nitrosococcus oceani (strain ATCC 19707 / NCIMB 11848)	323261	7/30/2015	2995	Nitrosococcus oceani ATCC 19707	323261 1229 1227 1046 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000017200	Microbotryum violaceum (strain p1A1 Lamole) (Anther smut fungus) (Ustilago violacea)	683840	7/30/2015	7656	Microbotryum violaceum p1A1 Lamole	683840 5272 34416 55071 55070 162481 29000 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000017246	Echinococcus multilocularis (Fox tapeworm)	6211	7/27/2015	10336	Echinococcus multilocularis	6211 6209 6208 6201 6200 6199 6157 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008156	Methanosarcina barkeri (strain Fusaro / DSM 804)	269797	8/2/2015	3616	Methanosarcina barkeri str. Fusaro	269797 2208 2207 2206 94695 224756 28890 2157 131567	Archaea	
UP000002703	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	272943	7/30/2015	4285	Rhodobacter sphaeroides 2.4.1	272943 1063 1060 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002713	Thiomicrospira crunogena (strain XCL-2)	317025	7/30/2015	2187	Thiomicrospira crunogena XCL-2	317025 39765 933 135616 72273 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002708	Chlorobium chlorochromatii (strain CaD3)	340177	7/30/2015	1986	Chlorobium chlorochromatii CaD3	340177 337090 1091 274493 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002717	Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	1140	8/3/2015	2657	Synechococcus elongatus PCC 7942	1140 32046 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000002534	Pelobacter carbinolicus (strain DSM 2380 / Gra Bd 1)	338963	7/30/2015	3292	Pelobacter carbinolicus DSM 2380	338963 19 18 213423 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002718	Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849)	323848	7/30/2015	2732	Nitrosospira multiformis ATCC 25196	323848 1231 35798 206379 32003 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002706	Carboxydothermus hydrogenoformans (strain ATCC BAA-161 / DSM 6008 / Z-2901)	246194	7/30/2015	2615	Carboxydothermus hydrogenoformans Z-2901	246194 129958 129957 186814 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000002716	Shigella dysenteriae serotype 1 (strain Sd197)	300267	7/30/2015	3897	Shigella dysenteriae Sd197	300267 622 620 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002710	Desulfovibrio alaskensis (strain G20) (Desulfovibrio desulfuricans (strain G20))	207559	7/30/2015	3220	Desulfovibrio alaskensis G20	207559 58180 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002714	Sulfurimonas denitrificans (strain ATCC 33889 / DSM 1251) (Thiomicrospira denitrificans (strain ATCC 33889 / DSM 1251))	326298	7/30/2015	2084	Sulfurimonas denitrificans DSM 1251	326298 39766 202746 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000017242	Hymenolepis microstoma (Rodent tapeworm) (Rodentolepis microstoma)	85433	7/27/2015	9920	Hymenolepis microstoma	85433 6215 6214 6201 6200 6199 6157 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002707	Lactobacillus sakei subsp. sakei (strain 23K)	314315	7/30/2015	1872	Lactobacillus sakei subsp. sakei 23K	314315 214326 1599 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002709	Chlorobium luteolum (strain DSM 273 / 2530) (Pelodictyon luteolum)	319225	7/30/2015	2075	Chlorobium luteolum DSM 273	319225 1100 1099 274493 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002719	Brucella abortus (strain 2308)	359391	7/30/2015	3022	Brucella abortus 2308	359391 235 234 118882 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000007073	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	269799	7/30/2015	3502	Geobacter metallireducens GS-15	269799 28232 28231 213422 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000007058	Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	342108	7/30/2015	4514	Magnetospirillum magneticum AMB-1	342108 84159 13134 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001929	Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	269796	7/30/2015	3835	Rhodospirillum rubrum ATCC 11170	269796 1085 1081 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000238	Hahella chejuensis (strain KCTC 2396)	349521	7/30/2015	6751	Hahella chejuensis KCTC 2396	349521 158327 158481 224379 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007053	Moorella thermoacetica (strain ATCC 39073)	264732	7/30/2015	2451	Moorella thermoacetica ATCC 39073	264732 1525 44260 42857 186814 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000001930	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	271848	7/30/2015	5561	Burkholderia thailandensis E264	271848 57975 111527 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria

UP000007062	Anopheles gambiae (African malaria mosquito)	7165	7/30/2015	13072	Anopheles gambiae	7165 44542 44537 44534 7164 43816 7157 41827 43786 7148 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000004465	Facklamia hominis CCUG 36813	883111	7/27/2015	1717	Facklamia hominis CCUG 36813	883111 178214 66831 186827 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001931	Methanosphaera stadtmanae (strain ATCC 43021 / DSM 3091 / JCM 11832 / MCB-3)	339860	7/30/2015	1533	Methanosphaera stadtmanae DSM 3091	339860 2317 2316 2159 2158 183925 28890 2157 131567	Archaea	
UP000008674	Salinibacter ruber (strain DSM 13855 / M31)	309807	7/30/2015	2812	Salinibacter ruber DSM 13855	309807 146919 146918 563843 1100069 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000005408	Crassostrea gigas (Pacific oyster) (Crassostrea angulata)	29159	7/27/2015	25982	Crassostrea gigas	29159 6564 6563 98302 6562 6545 6544 6447 1206795 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001933	Syntrophus aciditrophicus (strain SB)	56780	7/30/2015	3145	Syntrophus aciditrophicus SB	56780 316277 43773 213468 213462 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001932	Sodalis glossinidius (strain morsitans)	343509	7/30/2015	2490	Sodalis glossinidius str. 'morsitans'	343509 63612 84565 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008808	Erythrobacter litoralis (strain HTCC2594)	314225	7/30/2015	2999	Erythrobacter litoralis HTCC2594	314225 39960 1041 335929 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001977	Bordetella avium (strain 197N)	360910	7/30/2015	3372	Bordetella avium 197N	360910 521 517 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008816	Staphylococcus aureus (strain NCTC 8325)	93061	7/30/2015	2889	Staphylococcus aureus subsp. aureus NCTC 8325	93061 46170 1280 1279 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001937	Frankia sp. (strain CcI3)	106370	7/30/2015	4441	Frankia sp. CcI3	106370 1854 74712 85013 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001935	Anaeromyxobacter dehalogenans (strain 2CP-C)	290397	7/30/2015	4345	Anaeromyxobacter dehalogenans 2CP-C	290397 161493 161492 1524215 80811 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001941	Methanospirillum hungatei JF-1 (strain ATCC 27890 / DSM 864 / NBRC 100397 / JF-1)	323259	7/30/2015	3087	Methanospirillum hungatei JF-1	323259 2203 2202 196137 2191 224756 28890 2157 131567	Archaea	
UP000001938	Synechococcus sp. (strain JA-2-3B'a(2-13)) (Cyanobacteria bacterium Yellowstone B-Prime)	321332	7/30/2015	2835	Synechococcus sp. JA-2-3B'a(2-13)	321332 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000001936	Rhizobium etli (strain CFN 42 / ATCC 51251)	347834	7/30/2015	5921	Rhizobium etli CFN 42	347834 29449 379 227290 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000007332	Lactobacillus buchneri CD034	1071400	7/27/2015	2369	Lactobacillus buchneri CD034	1071400 1581 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000009134	Novosphingobium aromaticivorans (strain DSM 12444 / F199)	279238	7/30/2015	3917	Novosphingobium aromaticivorans DSM 12444	279238 48935 165696 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000017396	Gloeobacter kilaueensis JS1	1183438	7/27/2015	4462	Gloeobacter kilaueensis	1183438 1416614 33071 307595 307596 1117 2 131567	Bacteria	Cyanobacteria
UP000007347	Desulfobacula toluolica (strain DSM 7467 / Tol2)	651182	7/30/2015	4189	Desulfobacula toluolica	651182 28223 28222 213119 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000017415	Enterococcus cecorum DSM 20682 = ATCC 43198	1121864	7/27/2015	2361	Enterococcus cecorum DSM 20682 = ATCC 43198	1121864 44008 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008320	Ehrlichia chaffeensis (strain ATCC CRL-10679 / Arkansas)	205920	7/30/2015	1100	Ehrlichia chaffeensis str. Arkansas	205920 945 106178 943 942 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000017469	Carnobacterium sp. WN1359	1266845	7/27/2015	2269	Carnobacterium sp.	1266845 2747 186828 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001942	Neorickettsia sennetsu (strain Miyayama)	222891	7/30/2015	932	Neorickettsia sennetsu str. Miyayama	222891 951 33993 942 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008326	Jannaschia sp. (strain CCS1)	290400	7/30/2015	4271	Jannaschia sp. CCS1	290400 188905 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001943	Anaplasma phagocytophilum (strain HZ)	212042	7/30/2015	1330	Anaplasma phagocytophilum str. HZ	212042 948 106179 768 942 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001946	Desulfitobacterium hafniense (strain Y51)	138119	7/30/2015	5014	Desulfitobacterium hafniense Y51	138119 49338 36853 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008332	Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) (Albidiferax ferrireducens)	338969	7/30/2015	4401	Rhodoferax ferrireducens T118	338969 192843 28065 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000017559	Moniliophthora roreri (strain MCA 2997) (Cocoa frosty pod rot fungus) (Crinipellis roreri)	1381753	7/30/2015	17976	Moniliophthora roreri MCA 2997	1381753 221103 221102 654221 654128 5338 452333 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000001948	Rhodopseudomonas palustris (strain BisB18)	316056	7/30/2015	4864	Rhodopseudomonas palustris BisB18	316056 1076 1073 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006559	Lactobacillus salivarius (strain UCC118)	362948	7/30/2015	1998	Lactobacillus salivarius UCC118	362948 1624 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001949	Theileria parva (East coast fever infection agent)	5875	7/30/2015	4071	Theileria parva	5875 5873 27994 5863 422676 5794 33630 2759 131567	eukaryotes	
UP000001947	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	203122	7/30/2015	3999	Saccharophagus degradans 2-40	203122 86304 316625 1706371 1706369 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006764	Alcanivorax pacificus W11-5	391936	7/27/2015	3686	Alcanivorax pacificus W11-	391936 1306787 59753 224372 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000017590	Clostridium autoethanogenum DSM 10061	1341692	8/14/2015	4013	Clostridium autoethanogenum DSM 10061	1341692 84023 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001953	Nitrobacter hamburgensis (strain X14 / DSM 10229)	323097	7/30/2015	4243	Nitrobacter hamburgensis X14	323097 912 911 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000239	Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)	290398	7/30/2015	3298	Chromohalobacter salexigens DSM 3043	290398 158080 42054 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001950	Theileria annulata	5874	7/30/2015	3790	Theileria annulata	5874 5873 27994 5863 422676 5794 33630 2759 131567	eukaryotes	
UP000006753	Marssonina brunnea f. sp. multigermtubi (strain MB_m1) (Marssonina leaf spot fungus)	1072389	7/30/2015	10037	Marssonina brunnea f. sp. 'multigermtubi' MB_m1	1072389 698441 698440 324777 76657 5178 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006564	Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	510516	7/30/2015	12072	Aspergillus oryzae RIB40	510516 5062 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006757	Trichosporon asahii var. asahii (strain CBS 8904) (Yeast)	1220162	7/30/2015	8515	Trichosporon asahii var. asahii CBS 8904	1220162 189963 82508 5552 415703 5234 155616 5302 5204 451864 4751 33154 2759 131567	eukaryotes	

UP000002427	Baumannia cicadellinicola subsp. Homalodisca coagulata	374463	8/5/2015	595	Baumannia cicadellinicola str. Hc (Homalodisca coagulata)	374463 186490 198346 118884 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002429	Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	266264	8/2/2015	6364	Cupriavidus metallidurans CH34	266264 119219 106589 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002430	Lawsonia intracellularis (strain PHE/MN1-00)	363253	7/30/2015	1342	Lawsonia intracellularis PHE/MN1-00	363253 29546 41707 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006578	Sphingopyxis alaskensis (strain DSM 13593 / LMG 18877 / RB2256) (Sphingomonas alaskensis)	317655	7/30/2015	3184	Sphingopyxis alaskensis RB2256	317655 117207 165697 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002431	Deinococcus geothermalis (strain DSM 11300)	319795	7/30/2015	3006	Deinococcus geothermalis DSM 11300	319795 68909 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000006097	alpha proteobacterium HIMB59	744985	7/27/2015	1493	alpha proteobacterium HIMB59	744985 1655516 1655514 54526 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002440	Methylobacillus flagellatus (strain KT / ATCC 51484 / DSM 6875)	265072	7/30/2015	2609	Methylobacillus flagellatus KT	265072 405 404 32011 206350 28216 1224 2 131567	Bacteria	Proteobacteria
UP000017642	Bacteroidales bacterium CF	1400053	7/27/2015	2289	Bacteroidales bacterium CF	1400053 185291 333046 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002432	Koribacter versatilis (strain Ellin345)	204669	7/30/2015	4771	Candidatus Koribacter versatilis Ellin345	204669 658062 658061 204434 204433 204432 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000006094	Clostridium acidurici (strain ATCC 7906 / DSM 604 / KCTC 5404 / 9a)	1128398	7/30/2015	2839	[Clostridium] acidurici 9a	1128398 1556 1505664 186813 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000636	Ruegeria sp. (strain TM1040) (Silicibacter sp.)	292414	7/30/2015	3849	Ruegeria sp. TM1040	292414 97050 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000017640	Spiribacter sp. UAH-SP71	1335757	7/27/2015	1861	Spiribacter sp. UAH-SP71	1335757 1335745 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001259	Lactobacillus delbrueckii subsp. bulgaricus (strain ATCC 11842 / DSM 20081 / JCM 1002 / NBRC 13953 / NCIMB 11778)	390333	7/30/2015	1519	Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842 = JCM 1002	390333 1585 1584 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002402	Myxococcus xanthus (strain DK 1622)	246197	7/30/2015	7314	Myxococcus xanthus DK 1622	246197 34 32 31 80811 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002051	Medicago truncatula (Barrel medic) (Medicago tribuloides)	3880	7/30/2015	57066	Medicago truncatula	3880 3877 163742 3814 3803 72025 91835 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000017720	Streptococcus iniae IUSA1	1273539	7/27/2015	2145	Streptococcus iniae IUSA1	1273539 1346 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000007015	Oryza sativa subsp. indica (Rice)	39946	7/30/2015	37386	Oryza sativa Indica Group	39946 4530 4527 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000006177	Leptospirillum ferriphilum (strain ML-04)	1048260	7/30/2015	2450	Leptospirillum ferriphilum ML-04	1048260 178606 261386 179 189779 189778 203693 40117 2 131567	Bacteria	Nitrospirae
UP000000763	Oryza sativa subsp. japonica (Rice)	39947	8/2/2015	62970	Oryza sativa Japonica Group	39947 4530 4527 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000006276	Riemerella anatipestifer RA-CH-1	1228997	8/3/2015	2187	Riemerella anatipestifer RA-CH-1	1228997 34085 34084 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017746	Actinoplanes friuliensis DSM 7358	1246995	7/27/2015	8558	Actinoplanes friuliensis DSM 7358	1246995 196914 1865 28056 85008 1760 201174 2 131567	Bacteria	Actinobacteria
UP000017667	Acinetobacter haemolyticus CIP 64.3	1217659	7/27/2015	3185	Acinetobacter haemolyticus CIP 64.3	1217659 29430 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008827	Glycine max (Soybean) (Glycine hispida)	3847	8/2/2015	64675	Glycine max	3847 1462606 3846 163735 3814 3803 72025 91835 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000017765	Streptomyces sp. PVA 94-07	1223307	7/27/2015	5894	Streptomyces sp. PVA 94-07	1223307 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007129	Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	1126212	7/30/2015	13801	Macrophomina phaseolina MS6	1126212 35725 35724 45131 451869 159987 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007127	Thalassospira xiamenensis M-5 = DSM 17429	1123366	7/27/2015	4340	Thalassospira xiamenensis M-5 = DSM 17429	1123366 220697 168934 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006282	Cycloclasticus sp. (strain P1)	385025	7/30/2015	2247	Cycloclasticus sp. P1	385025 34067 135616 72273 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006281	Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	1179773	7/30/2015	8423	Saccharothrix espanaensis DSM 44229	1179773 103731 2071 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000017805	Bacillus infantis NRRL B-14911	1367477	7/27/2015	5066	Bacillus infantis NRRL B-14911	1367477 324767 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000006294	Amphibacillus xylanus (strain ATCC 51415 / DSM 6626 / JCM 7361 / LMG 17667 / NBRC 15112 / Ep01)	698758	7/30/2015	2384	Amphibacillus xylanus NBRC 15112	698758 1449 29331 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000006304	Nocardia brasiliensis ATCC 700358	1133849	7/27/2015	8414	Nocardia brasiliensis ATCC 700358	1133849 37326 1817 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006306	Acidovorax sp. KKS102	358220	7/27/2015	4696	Acidovorax sp. KKS102	358220 12916 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006286	Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	930169	7/30/2015	4388	Alcanivorax dieselolei B5	930169 285091 59753 224372 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000017786	Mycobacterium kansasii ATCC 12478	557599	7/27/2015	5843	Mycobacterium kansasii ATCC 12478	557599 1768 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000017862	Candidatus Liberibacter americanus str. Sao Paulo	1261131	7/27/2015	978	Candidatus Liberibacter americanus str. Sao Paulo	1261131 309868 34019 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000017867	Methanobacterium sp. MB1	1379702	7/27/2015	2013	Methanobacterium sp. MB1	1379702 2160 2159 2158 183925 28890 2157 131567	Archaea	
UP000017904	Eubacterium sp. CAG:274	1262888	7/27/2015	2006	Eubacterium sp. CAG:274	1262888 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes

UP000017836	Amborella trichopoda	13333	7/27/2015	27371	Amborella trichopoda	13333 13332 22097 261009 232365 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000017881	Spiribacter salinus M19-40	1260251	7/27/2015	1684	Spiribacter salinus M19-40	1260251 1335746 1335745 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000017916	Bacteroides sp. CAG:598	1262743	7/27/2015	2776	Bacteroides sp. CAG:598	1262743 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017906	Bacteroides sp. CAG:754	1262750	7/27/2015	4054	Bacteroides sp. CAG:754	1262750 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017901	Brachyspira sp. CAG:700	1262760	7/27/2015	2280	Brachyspira sp. CAG:700	1262760 132529 29521 143786 1643686 203692 203691 2 131567	Bacteria	Spirochaetes
UP000017900	Ascaris suum (Pig roundworm) (Ascaris lumbricoides)	6253	7/27/2015	9213	Ascaris suum	6253 6251 6250 33256 6249 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000017907	Bacteroides sp. CAG:927	1262753	7/27/2015	2231	Bacteroides sp. CAG:927	1262753 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017905	Clostridium sp. CAG:138	1262775	7/27/2015	1746	Clostridium sp. CAG:138	1262775 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017918	Coraliomargarita sp. CAG:312	1262865	7/27/2015	2060	Coraliomargarita sp. CAG:312	1262865 1262864 442430 415002 415001 414999 74201 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000017921	Dorea sp. CAG:105	1262872	7/27/2015	2158	Dorea sp. CAG:105	1262872 286137 189330 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017920	Clostridium sp. CAG:533	1262818	7/27/2015	969	Clostridium sp. CAG:533	1262818 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017919	Clostridium sp. CAG:242	1262783	7/27/2015	2433	Clostridium sp. CAG:242	1262783 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017926	Clostridium sp. CAG:557	1262819	7/27/2015	1118	Clostridium sp. CAG:557	1262819 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017928	Firmicutes bacterium CAG:882	1262991	7/27/2015	2572	Firmicutes bacterium CAG:882	1262991 47928 1239 2 131567	Bacteria	Firmicutes
UP000017939	Clostridium sp. CAG:590	1262825	7/27/2015	2354	Clostridium sp. CAG:590	1262825 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017932	Firmicutes bacterium CAG:176	1263007	7/27/2015	1505	Firmicutes bacterium CAG:176	1263007 47928 1239 2 131567	Bacteria	Firmicutes
UP000017929	Clostridium sp. CAG:299	1262792	7/27/2015	2441	Clostridium sp. CAG:299	1262792 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017930	Acholeplasma sp. CAG:878	1262686	7/27/2015	1145	Acholeplasma sp. CAG:878	1262686 453121 2147 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000017925	Ruminococcus sp. CAG:403	1262958	7/27/2015	1971	Ruminococcus sp. CAG:403	1262958 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017943	Eubacterium sp. CAG:192	1262883	7/27/2015	1830	Eubacterium sp. CAG:192	1262883 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017913	Prevotella sp. CAG:255	1262923	7/27/2015	2771	Prevotella sp. CAG:255	1262923 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017917	uncultured Desulfofustis sp. PB-SRB1	1385624	7/27/2015	3578	uncultured Desulfofustis sp. PB-SRB1	1385624 543069 51194 213121 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000017936	Ruminococcus sp. CAG:353	1262955	7/27/2015	2331	Ruminococcus sp. CAG:353	1262955 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017924	Eubacterium sp. CAG:841	1262894	7/27/2015	1649	Eubacterium sp. CAG:841	1262894 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007978	Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	1028729	8/2/2015	12446	Fusarium pseudograminearum CS3096	1028729 101028 569360 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000017951	Clostridium sp. CAG:356	1262800	7/27/2015	1500	Clostridium sp. CAG:356	1262800 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017940	Eubacterium sp. CAG:86	1262895	7/27/2015	2189	Eubacterium sp. CAG:86	1262895 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017954	Eubacterium sp. CAG:38	1262889	7/27/2015	2436	Eubacterium sp. CAG:38	1262889 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017938	Firmicutes bacterium CAG:272	1263015	7/27/2015	2248	Firmicutes bacterium CAG:272	1263015 47928 1239 2 131567	Bacteria	Firmicutes
UP000017941	Clostridium bolteae CAG:59	1263064	7/27/2015	4862	Clostridium bolteae CAG:59	1263064 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017935	uncultured Thiohalocapsa sp. PB-PSB1	1385625	7/27/2015	6200	uncultured Thiohalocapsa sp. PB-PSB1	1385625 768989 85079 1046 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000017963	Firmicutes bacterium CAG:24	1263012	7/27/2015	2518	Firmicutes bacterium CAG:24	1263012 47928 1239 2 131567	Bacteria	Firmicutes
UP000017931	Thermoplasmatales archaeon I-plasma	667138	7/27/2015	1693	Thermoplasmatales archaeon I-plasma	667138 95865 2301 183967 28890 2157 131567	Archaea	
UP000017956	Prevotella sp. CAG:1124	1262920	7/27/2015	2441	Prevotella sp. CAG:1124	1262920 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017947	Clostridium sp. CAG:451	1262809	7/27/2015	1322	Clostridium sp. CAG:451	1262809 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017960	Coprobacillus sp. CAG:183	1262853	7/27/2015	2843	Coprobacillus sp. CAG:183	1262853 512291 100883 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000017968	Clostridium sp. CAG:288	1262791	7/27/2015	1500	Clostridium sp. CAG:288	1262791 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017959	Clostridium sp. CAG:678	1262831	7/27/2015	2250	Clostridium sp. CAG:678	1262831 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017958	Paraprevotella clara CAG:116	1263095	7/27/2015	2847	Paraprevotella clara CAG:116	1263095 910950 577309 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017945	Firmicutes bacterium CAG:308	1263016	7/27/2015	1735	Firmicutes bacterium CAG:308	1263016 47928 1239 2 131567	Bacteria	Firmicutes
UP000017942	Oscillibacter sp. CAG:155	1262910	7/27/2015	2148	Oscillibacter sp. CAG:155	1262910 876090 459786 216572 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007974	Thalassiosira oceanica (Marine diatom)	159749	7/27/2015	34547	Thalassiosira oceanica	159749 35127 29202 33847 33846 33836 2836 33634 2759 131567	eukaryotes	
UP000017955	Clostridium sp. CAG:762	1262837	7/27/2015	1127	Clostridium sp. CAG:762	1262837 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017957	Coprococcus comes CAG:19	1263070	7/27/2015	2198	Coprococcus comes	1263070 458252 33042 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017952	Collinsella sp. CAG:289	1262851	7/27/2015	1652	Collinsella sp. CAG:289	1262851 165189 102106 84107 84999 84998 201174 2 131567	Bacteria	Actinobacteria
UP000017966	Dialister invisus CAG:218	1263072	7/27/2015	1693	Dialister invisus CAG:218	1263072 135034 39948 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000017971	Streptomyces niveus NCIMB 11891	1352941	8/7/2015	7746	Streptomyces niveus NCIMB 11891	1352941 193462 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000017946	Clostridium sp. CAG:1024	1262770	7/27/2015	1915	Clostridium sp. CAG:1024	1262770 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017949	Coprococcus eutactus CAG:665	1263071	7/27/2015	2415	Coprococcus eutactus CAG:665	1263071 458252 33042 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes

UP000017964	Firmicutes bacterium CAG:822	1263032	7/27/2015	1377	Firmicutes bacterium CAG:822	1263032 47928 1239 2 131567	Bacteria	Firmicutes
UP000017977	Ruminococcus sp. CAG:624	1262965	7/27/2015	1963	Ruminococcus sp. CAG:624	1262965 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017983	Blautia sp. CAG:237	1262755	7/27/2015	2627	Blautia sp. CAG:237	1262755 765820 572511 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017970	Eubacterium sp. CAG:252	1262887	7/27/2015	2338	Eubacterium sp. CAG:252	1262887 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017961	Clostridium sp. CAG:230	1262782	7/27/2015	2209	Clostridium sp. CAG:230	1262782 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017965	Alistipes sp. CAG:435	1262695	7/27/2015	2286	Alistipes sp. CAG:435	1262695 538948 239759 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017975	Eubacterium sp. CAG:581	1262890	7/27/2015	1746	Eubacterium sp. CAG:581	1262890 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017984	Streptomyces roseochromogenus subsp. oscitans DS 12.976	1352936	8/7/2015	8885	Streptomyces roseochromogenus subsp. oscitans DS 12.976	1352936 149682 285450 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008037	Nitrososphaera gargensis (strain Ga9.2)	1237085	7/30/2015	3523	Candidatus Nitrososphaera gargensis Ga9.2	1237085 497727 497726 1033997 1033996 1643678 651137 2157 131567	Archaea	
UP000017992	Acetobacter sp. CAG:267	1262684	7/27/2015	1538	Acetobacter sp. CAG:267	1262684 114713 434 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000017979	Firmicutes bacterium CAG:321	1263018	7/27/2015	1220	Firmicutes bacterium CAG:321	1263018 47928 1239 2 131567	Bacteria	Firmicutes
UP000017974	Odoribacter laneus CAG:561	1263089	7/27/2015	2812	Odoribacter laneus CAG:561	1263089 876415 283168 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017980	Clostridium bartlettii CAG:1329	1263063	7/27/2015	2686	Clostridium bartlettii CAG:1329	1263063 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017996	Eubacterium sp. CAG:202	1262884	7/27/2015	1817	Eubacterium sp. CAG:202	1262884 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017993	Subdoligranulum sp. CAG:314	1262970	7/27/2015	1341	Subdoligranulum sp. CAG:314	1262970 512297 292632 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017987	Prevotella sp. CAG:1092	1262919	7/27/2015	2513	Prevotella sp. CAG:1092	1262919 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018000	Clostridium sp. CAG:1193	1262771	7/27/2015	1080	Clostridium sp. CAG:1193	1262771 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017997	Coprobacillus sp. CAG:826	1262857	7/27/2015	1394	Coprobacillus sp. CAG:826	1262857 512291 100883 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000008043	Streptomyces davawensis JCM 4913	1214101	8/7/2015	8553	Streptomyces davawensis JCM 4913	1214101 348043 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000017998	Ruminococcus torques CAG:61	1263108	7/27/2015	2019	Ruminococcus torques CAG:61	1263108 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018001	Byssochlamys spectabilis (strain No. 5 / NBRC 109023) (Paecilomyces variotii)	1356009	7/30/2015	8877	Byssochlamys spectabilis No. 5	1356009 264951 5092 1131624 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000018002	Coprococcus sp. CAG:782	1262863	7/27/2015	1959	Coprococcus sp. CAG:782	1262863 458252 33042 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018007	Lachnospiraceae bacterium CAG:215	1262985	7/27/2015	2481	Lachnospiraceae bacterium CAG:215	1262985 189703 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017988	Coprobacillus sp. CAG:605	1262855	7/27/2015	1211	Coprobacillus sp. CAG:605	1262855 512291 100883 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000018011	Firmicutes bacterium CAG:137	1263004	7/27/2015	2347	Firmicutes bacterium CAG:137	1263004 47928 1239 2 131567	Bacteria	Firmicutes
UP000018009	Clostridium clostridioforme CAG:132	1263065	7/27/2015	4152	Clostridium clostridioforme CAG:132	1263065 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007006	Bifidobacterium asteroides (strain PRL2011)	1147128	7/30/2015	1656	Bifidobacterium asteroides PRL2011	1147128 1684 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000017995	Ruminococcus sp. CAG:60	1262964	7/27/2015	2748	Ruminococcus sp. CAG:60	1262964 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018006	Bacteroides sp. CAG:1060	1262734	7/27/2015	1576	Bacteroides sp. CAG:1060	1262734 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018008	Clostridium sp. CAG:306	1262794	7/27/2015	2130	Clostridium sp. CAG:306	1262794 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018013	Ferroplasma sp. Type II	261388	7/27/2015	2671	Ferroplasma sp. Type II	261388 261387 74968 90142 2301 183967 28890 2157 131567	Archaea	
UP000017990	Bacteroides caccae CAG:21	1263037	7/27/2015	3543	Bacteroides caccae CAG:21	1263037 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018018	Bacteroides coprophilus CAG:333	1263041	7/27/2015	2352	Bacteroides coprophilus CAG:333	1263041 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000017986	Lachnospiraceae bacterium CAG:364	1262983	7/27/2015	2282	Lachnospiraceae bacterium CAG:364	1262983 189703 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018022	Clostridium sp. CAG:411	1262802	7/27/2015	2623	Clostridium sp. CAG:411	1262802 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008514	Psychroflexus torquis (strain ATCC 700755 / ACAM 623)	313595	7/30/2015	3457	Psychroflexus torquis ATCC 700755	313595 57029 83612 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018026	Alistipes putredinis CAG:67	1263036	7/27/2015	1913	Alistipes putredinis CAG:67	1263036 538948 239759 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018021	Firmicutes bacterium CAG:110	1263000	7/27/2015	2311	Firmicutes bacterium CAG:110	1263000 47928 1239 2 131567	Bacteria	Firmicutes
UP000018027	Ruminococcus sp. CAG:9	1262967	7/27/2015	2492	Ruminococcus sp. CAG:9	1262967 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018034	Parasutterella excrementihominis CAG:233	1263099	7/27/2015	2228	Parasutterella excrementihominis CAG:233	1263099 1263096 577310 995019 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000018032	Clostridium sp. CAG:75	1262836	7/27/2015	2286	Clostridium sp. CAG:75	1262836 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018014	Bacillus sp. CAG:988	1262708	7/27/2015	1397	Bacillus sp. CAG:988	1262708 65119 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000018037	Ruminococcus sp. CAG:108	1262950	7/27/2015	1917	Ruminococcus sp. CAG:108	1262950 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000017985	Dialister sp. CAG:486	1262870	7/27/2015	1926	Dialister sp. CAG:486	1262870 135034 39948 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000018038	Firmicutes bacterium CAG:791	1262993	7/27/2015	2175	Firmicutes bacterium CAG:791	1262993 47928 1239 2 131567	Bacteria	Firmicutes
UP000018040	Giardia intestinalis (Giardia lamblia)	5741	7/27/2015	6085	Giardia intestinalis	5741 5740 68459 5739 5738 207245 2759 131567	eukaryotes	

UP000018044	Firmicutes bacterium CAG:145	1263005	7/27/2015	1960	Firmicutes bacterium CAG:145	1263005 47928 1239 2 131567	Bacteria	Firmicutes
UP000018023	Clostridium sp. CAG:167	1262777	7/27/2015	1994	Clostridium sp. CAG:167	1262777 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018041	Clostridium sp. CAG:492	1262813	7/27/2015	1098	Clostridium sp. CAG:492	1262813 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018047	Clostridium sp. CAG:226	1262781	7/27/2015	2034	Clostridium sp. CAG:226	1262781 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000009223	Treponema primitia (strain ATCC BAA-887 / DSM 12427 / ZAS-2)	545694	7/30/2015	3512	Treponema primitia ZAS-2	545694 88058 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000009222	Treponema azotonutricium (strain ATCC BAA-888 / DSM 13862 / ZAS-9)	545695	7/30/2015	3457	Treponema azotonutricium ZAS-9	545695 150829 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000018025	Clostridium sp. CAG:127	1262774	7/27/2015	2463	Clostridium sp. CAG:127	1262774 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018042	Eggerthella sp. CAG:209	1262875	7/27/2015	1726	Eggerthella sp. CAG:209	1262875 293421 84111 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000018048	Acidaminococcus sp. CAG:917	1262688	7/27/2015	1276	Acidaminococcus sp. CAG:917	1262688 114562 904 909930 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000009224	Mycobacterium sinense (strain JDM601)	875328	7/30/2015	4332	Mycobacterium sinense	875328 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000018033	Ruminococcus sp. CAG:17	1262951	7/27/2015	2593	Ruminococcus sp. CAG:17	1262951 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018024	Anaerotruncus sp. CAG:528	1262700	7/27/2015	1705	Anaerotruncus sp. CAG:528	1262700 905010 244127 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018055	Clostridium sp. CAG:567	1262820	7/27/2015	1235	Clostridium sp. CAG:567	1262820 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018049	Mycoplasma sp. CAG:611	1262905	7/27/2015	943	Mycoplasma sp. CAG:611	1262905 167966 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000018039	Prevotella sp. CAG:732	1262934	7/27/2015	2409	Prevotella sp. CAG:732	1262934 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000009228	Lactobacillus kefiranofaciens (strain ZW3)	1033837	7/30/2015	2134	Lactobacillus kefiranofaciens ZW3	1033837 267818 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000018051	Firmicutes bacterium CAG:240	1263013	7/27/2015	1917	Firmicutes bacterium CAG:240	1263013 47928 1239 2 131567	Bacteria	Firmicutes
UP000018052	Thermoplasmatales archaeon E-plasma	667137	7/27/2015	1661	Thermoplasmatales archaeon E-plasma	667137 95865 2301 183967 28890 2157 131567	Archaea	
UP000018058	Bacteroides finegoldii CAG:203	1263045	7/27/2015	2825	Bacteroides finegoldii CAG:203	1263045 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018035	Firmicutes bacterium CAG:631	1262996	7/27/2015	1348	Firmicutes bacterium CAG:631	1262996 47928 1239 2 131567	Bacteria	Firmicutes
UP000018053	Acidiphilium sp. CAG:727	1262689	7/27/2015	1479	Acidiphilium sp. CAG:727	1262689 240134 522 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018056	Blautia sp. CAG:257	1262756	7/27/2015	2516	Blautia sp. CAG:257	1262756 765820 572511 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018046	Prevotella sp. CAG:386	1262925	7/27/2015	2132	Prevotella sp. CAG:386	1262925 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000009234	Desulfotomaculum ruminis (strain ATCC 23193 / DSM 2154 / NCIB 8452 / DL)	696281	7/30/2015	3763	Desulfotomaculum ruminis DSM 2154	696281 1564 1562 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000009226	Desulfotomaculum carboxydivorans (strain DSM 14880 / VKM B-2319 / CO-1-SRB)	868595	7/30/2015	2620	Desulfotomaculum carboxydivorans CO-1-SRB	868595 327817 1562 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018057	Prevotella sp. CAG:617	1262933	7/27/2015	1928	Prevotella sp. CAG:617	1262933 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000009229	Desulfotomaculum kuznetsovii (strain DSM 6115 / VKM B-1805 / 17)	760568	7/30/2015	3385	Desulfotomaculum kuznetsovii DSM 6115	760568 58135 1562 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018063	Bacteroides sp. CAG:462	1262740	7/27/2015	2834	Bacteroides sp. CAG:462	1262740 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018059	Ruminococcus obeum CAG:39	1263107	7/27/2015	2346	Ruminococcus obeum CAG:39	1263107 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018062	Prevotella sp. CAG:485	1262927	7/27/2015	1956	Prevotella sp. CAG:485	1262927 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000009227	Methanotorris igneus (strain DSM 5666 / JCM 11834 / Kol 5)	880724	7/30/2015	1753	Methanotorris igneus Kol 5	880724 2189 196119 196117 2182 183939 28890 2157 131567	Archaea	
UP000008641	Weeksella virosa (strain ATCC 43766 / DSM 16922 / JCM 21250 / NBRC 16016 / NCTC 11634 / CL345/78)	865938	7/30/2015	2045	Weeksella virosa DSM 16922	865938 1014 1013 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018045	Clostridium sp. CAG:568	1262821	7/27/2015	1211	Clostridium sp. CAG:568	1262821 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018050	Eimeria acervulina (Coccidian parasite)	5801	8/4/2015	6867	Eimeria acervulina	5801 5800 5799 423054 75739 5796 1280412 5794 33630 2759 131567	eukaryotes	
UP000018067	Clostridium sp. CAG:440	1262807	7/27/2015	1420	Clostridium sp. CAG:440	1262807 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000009236	Isoptericola variabilis (strain 225)	743718	7/30/2015	2879	Isoptericola variabilis 225	743718 139208 254250 85017 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000009231	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	868131	7/30/2015	2394	Methanobacterium paludis	868131 2160 2159 2158 183925 28890 2157 131567	Archaea	
UP000018065	Clostridium sp. CAG:245	1262784	7/27/2015	1330	Clostridium sp. CAG:245	1262784 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000009235	Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1)	443218	7/30/2015	4703	Amycolicicoccus subflavus DQS3-9A1	443218 639313 992401 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000018073	Firmicutes bacterium CAG:884	1262990	7/27/2015	1232	Firmicutes bacterium CAG:884	1262990 47928 1239 2 131567	Bacteria	Firmicutes
UP000018070	Faecalibacterium sp. CAG:82	1262898	7/27/2015	1856	Faecalibacterium sp. CAG:82	1262898 259314 216851 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018078	Prevotella sp. CAG:873	1262936	7/27/2015	2055	Prevotella sp. CAG:873	1262936 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018082	Ruminococcus sp. CAG:563	1262961	7/27/2015	2054	Ruminococcus sp. CAG:563	1262961 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018076	Clostridium sp. CAG:413	1262803	7/27/2015	2197	Clostridium sp. CAG:413	1262803 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018081	Clostridium sp. CAG:628	1262829	7/27/2015	1091	Clostridium sp. CAG:628	1262829 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes

UP000018064	Porphyromonas sp. CAG:1061	1262916	7/27/2015	1653	Porphyromonas sp. CAG:1061	1262916 134245 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018069	Eubacterium hallii CAG:12	1263078	7/27/2015	2309	Eubacterium hallii CAG:12	1263078 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000009242	Novosphingobium sp. PP1Y	702113	7/27/2015	4624	Novosphingobium sp. PP1Y	702113 165696 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018068	Bacteroides sp. CAG:714	1262749	7/27/2015	2561	Bacteroides sp. CAG:714	1262749 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018093	Eubacterium dolichum CAG:375	1263076	7/27/2015	1927	Eubacterium dolichum CAG:375	1263076 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018075	Butyrivibrio sp. CAG:318	1262761	7/27/2015	2127	Butyrivibrio sp. CAG:318	1262761 135026 830 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018074	Clostridium sp. CAG:448	1262808	7/27/2015	2084	Clostridium sp. CAG:448	1262808 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002669	Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	535722	7/30/2015	8907	Microsporum gypseum CBS 118893	535722 63402 34392 34384 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000018101	Firmicutes bacterium CAG:83	1262992	7/27/2015	1718	Firmicutes bacterium CAG:83	1262992 47928 1239 2 131567	Bacteria	Firmicutes
UP000018100	Odoribacter sp. CAG:788	1262909	7/27/2015	3078	Odoribacter sp. CAG:788	1262909 876415 283168 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018071	Clostridium sp. CAG:253	1262785	7/27/2015	2539	Clostridium sp. CAG:253	1262785 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018089	Sutterella wadsworthensis CAG:135	1263111	7/27/2015	2410	Sutterella wadsworthensis CAG:135	1263111 286132 40544 995019 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000018105	Sutterella sp. CAG:397	1262976	7/27/2015	1804	Sutterella sp. CAG:397	1262976 286132 40544 995019 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000018092	Roseburia sp. CAG:100	1262940	7/27/2015	2901	Roseburia sp. CAG:100	1262940 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018088	Eggerthella sp. CAG:368	1262877	7/27/2015	1381	Eggerthella sp. CAG:368	1262877 293421 84111 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000018107	Sutterella sp. CAG:351	1262975	7/27/2015	2202	Sutterella sp. CAG:351	1262975 286132 40544 995019 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000018084	Clostridium sp. CAG:470	1262812	7/27/2015	1535	Clostridium sp. CAG:470	1262812 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018104	Roseburia sp. CAG:182	1262942	7/27/2015	2523	Roseburia sp. CAG:182	1262942 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018094	Alistipes sp. CAG:831	1262698	7/27/2015	2179	Alistipes sp. CAG:831	1262698 538948 239759 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018113	Oscillibacter sp. CAG:241	1262911	7/27/2015	1823	Oscillibacter sp. CAG:241	1262911 876090 459786 216572 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018114	Ruminococcus gnavus CAG:126	1263106	7/27/2015	2588	Ruminococcus gnavus CAG:126	1263106 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018109	Dorea formicigenerans CAG:28	1263073	7/27/2015	2461	Dorea formicigenerans CAG:28	1263073 286137 189330 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018086	Clostridium sp. CAG:524	1262817	7/27/2015	1265	Clostridium sp. CAG:524	1262817 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007944	Erysipelothrix rhusiopathiae (strain Fujisawa)	650150	7/30/2015	1679	Erysipelothrix rhusiopathiae str. Fujisawa	650150 1648 1647 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000018090	Firmicutes bacterium CAG:114	1263001	7/27/2015	2222	Firmicutes bacterium CAG:114	1263001 47928 1239 2 131567	Bacteria	Firmicutes
UP000018116	Prevotella sp. CAG:474	1262926	7/27/2015	2297	Prevotella sp. CAG:474	1262926 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018115	Bacteroides sp. CAG:98	1262754	7/27/2015	2670	Bacteroides sp. CAG:98	1262754 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008144	Ciona intestinalis (Transparent sea squirt) (Ascidia intestinalis)	7719	7/27/2015	17309	Ciona intestinalis	7719 7718 7717 7716 183770 7713 7712 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000018098	Bacteroides sp. CAG:443	1262739	7/27/2015	2710	Bacteroides sp. CAG:443	1262739 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018087	Sporothrix schenckii (strain ATCC 58251 / de Perez 2211183) (Rose-picker's disease fungus)	1391915	7/30/2015	8673	Sporothrix schenckii ATCC 58251	1391915 29908 29907 5152 5151 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000018111	Prevotella sp. CAG:1320	1262922	7/27/2015	2035	Prevotella sp. CAG:1320	1262922 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018127	Eubacterium sp. CAG:786	1262893	7/27/2015	2502	Eubacterium sp. CAG:786	1262893 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018117	Mycoplasma sp. CAG:956	1262908	7/27/2015	1369	Mycoplasma sp. CAG:956	1262908 167966 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000018128	Clostridium sp. CAG:307	1262795	7/27/2015	1655	Clostridium sp. CAG:307	1262795 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018123	Firmicutes bacterium CAG:56	1263031	7/27/2015	2160	Firmicutes bacterium CAG:56	1263031 47928 1239 2 131567	Bacteria	Firmicutes
UP000018112	Firmicutes bacterium CAG:102	1262998	7/27/2015	2021	Firmicutes bacterium CAG:102	1262998 47928 1239 2 131567	Bacteria	Firmicutes
UP000018135	Anaerostipes sp. CAG:276	1262699	7/27/2015	3141	Anaerostipes sp. CAG:276	1262699 512317 207244 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018124	Eubacterium sp. CAG:156	1262880	7/27/2015	2092	Eubacterium sp. CAG:156	1262880 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018139	Firmicutes bacterium CAG:41	1263021	7/27/2015	2447	Firmicutes bacterium	1263021 47928 1239 2 131567	Bacteria	Firmicutes
UP000018136	Clostridium sp. CAG:964	1262848	7/27/2015	1860	Clostridium sp. CAG:964	1262848 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018137	Clostridium sp. CAG:62	1262828	7/27/2015	2452	Clostridium sp. CAG:62	1262828 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018120	Clostridium sp. CAG:510	1262816	7/27/2015	2541	Clostridium sp. CAG:510	1262816 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018110	Azospirillum sp. CAG:260	1262706	7/27/2015	1762	Azospirillum sp. CAG:260	1262706 114711 191 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000007952	Mycoplasma haemofelis (strain Ohio2)	859194	7/30/2015	1524	Mycoplasma haemofelis Ohio2	859194 29501 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000018141	Bacteroides pectinophilus CAG:437	1263051	7/27/2015	2278	Bacteroides pectinophilus CAG:437	1263051 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018148	Clostridium sp. CAG:343	1262796	7/27/2015	1443	Clostridium sp. CAG:343	1262796 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002668	Leptosphaeria maculans (strain JN3 / isolate v23.1.3 / race Av1-4-5-6-7-8) (Blackleg fungus) (Phoma lingam)	985895	7/30/2015	12608	Leptosphaeria maculans JN3	985895 225342 5022 220671 5021 34374 715340 92860 451868 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000018150	Tannerella sp. CAG:51	1262979	7/27/2015	2586	Tannerella sp. CAG:51	1262979 417613 195950 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018131	Ruminococcus sp. CAG:57	1262962	7/27/2015	2264	Ruminococcus sp. CAG:57	1262962 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018121	Bacteroides sp. CAG:633	1262744	7/27/2015	3004	Bacteroides sp. CAG:633	1262744 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018133	Firmicutes bacterium CAG:449	1263023	7/27/2015	1770	Firmicutes bacterium CAG:449	1263023 47928 1239 2 131567	Bacteria	Firmicutes
UP000018166	Ruminococcus sp. CAG:382	1262957	7/27/2015	1853	Ruminococcus sp. CAG:382	1262957 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007947	Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	1032480	7/30/2015	5305	Microlunatus phosphovorus NM-1	1032480 29405 29404 31957 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000018132	Faecalibacterium sp. CAG:1138	1262896	7/27/2015	1284	Faecalibacterium sp. CAG:1138	1262896 259314 216851 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018173	Roseburia sp. CAG:45	1262947	7/27/2015	2315	Roseburia sp. CAG:45	1262947 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008143	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)	8364	8/4/2015	23538	Xenopus (Silurana) tropicalis	8364 8363 8353 8360 8352 30319 8342 41666 8292 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000018182	Firmicutes bacterium CAG:95	1262988	7/27/2015	2767	Firmicutes bacterium CAG:95	1262988 47928 1239 2 131567	Bacteria	Firmicutes
UP000018183	Prevotella sp. CAG:1031	1262917	7/27/2015	2199	Prevotella sp. CAG:1031	1262917 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018181	Ruminococcus sp. CAG:254	1262953	7/27/2015	1961	Ruminococcus sp. CAG:254	1262953 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018187	Bacteroides sp. CAG:545	1262742	7/27/2015	2183	Bacteroides sp. CAG:545	1262742 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018185	Collinsella sp. CAG:398	1262852	7/27/2015	1833	Collinsella sp. CAG:398	1262852 165189 102106 84107 84999 84998 201174 2 131567	Bacteria	Actinobacteria
UP000018191	Bacteroides cellulosilyticus CAG:158	1263038	7/27/2015	4369	Bacteroides cellulosilyticus CAG:158	1263038 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018184	Prevotella sp. CAG:5226	1262930	7/27/2015	2309	Prevotella sp. CAG:5226	1262930 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018176	Clostridium sp. CAG:221	1262780	7/27/2015	2985	Clostridium sp. CAG:221	1262780 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018167	Firmicutes bacterium CAG:424	1263022	7/27/2015	2835	Firmicutes bacterium CAG:424	1263022 47928 1239 2 131567	Bacteria	Firmicutes
UP000018161	Firmicutes bacterium CAG:475	1263026	7/27/2015	1270	Firmicutes bacterium CAG:475	1263026 47928 1239 2 131567	Bacteria	Firmicutes
UP000018168	Clostridium leptum CAG:27	1263068	7/27/2015	2482	Clostridium leptum CAG:27	1263068 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018190	Clostridium sp. CAG:710	1262833	7/27/2015	1170	Clostridium sp. CAG:710	1262833 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018174	Mycoplasma sp. CAG:776	1262906	7/27/2015	1349	Mycoplasma sp. CAG:776	1262906 167966 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000018144	Pyronema omphalodes (strain CBS 100304) (Pyronema confluens)	1076935	7/30/2015	13306	Pyronema omphalodes CBS 100304	1076935 337075 47204 110846 5185 147549 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000018207	Firmicutes bacterium CAG:65	1262994	7/27/2015	2512	Firmicutes bacterium CAG:65	1262994 47928 1239 2 131567	Bacteria	Firmicutes
UP000018204	Blautia sp. CAG:37	1262757	7/27/2015	2353	Blautia sp. CAG:37	1262757 765820 572511 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018205	Clostridium sp. CAG:594	1262826	7/27/2015	1188	Clostridium sp. CAG:594	1262826 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018170	Clostridium sp. CAG:914	1262846	7/27/2015	1262	Clostridium sp. CAG:914	1262846 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018212	Roseburia inulinivorans CAG:15	1263105	7/27/2015	2653	Roseburia inulinivorans CAG:15	1263105 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018163	Blautia hydrogenotrophica CAG:147	1263061	7/27/2015	3087	Blautia hydrogenotrophica CAG:147	1263061 765820 572511 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018147	Prevotella sp. CAG:891	1262937	7/27/2015	2058	Prevotella sp. CAG:891	1262937 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018157	Bacteroides intestinalis CAG:564	1263049	7/27/2015	2827	Bacteroides intestinalis CAG:564	1263049 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018179	Erysipelotrichaceae bacterium CAG:64	1262981	7/27/2015	3917	Erysipelotrichaceae bacterium CAG:64	1262981 134224 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000018177	Blautia sp. CAG:52	1262758	7/27/2015	2465	Blautia sp. CAG:52	1262758 765820 572511 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018199	Parabacteroides sp. CAG:409	1262913	7/27/2015	2823	Parabacteroides sp. CAG:409	1262913 512311 375288 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018220	Firmicutes bacterium CAG:534	1263027	7/27/2015	2499	Firmicutes bacterium CAG:534	1263027 47928 1239 2 131567	Bacteria	Firmicutes
UP000018202	Thermoplasmatales archaeon Gpl	261391	7/27/2015	1917	Thermoplasmatales archaeon Gpl	261391 95865 2301 183967 28890 2157 131567	Archaea	
UP000018226	Bacteroides clarus CAG:160	1263039	7/27/2015	3005	Bacteroides clarus CAG:160	1263039 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018196	Coprobacillus sp. CAG:235	1262854	7/27/2015	2339	Coprobacillus sp. CAG:235	1262854 512291 100883 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000018193	Clostridium sp. CAG:921	1262847	7/27/2015	1350	Clostridium sp. CAG:921	1262847 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018213	Azospirillum sp. CAG:239	1262705	7/27/2015	1791	Azospirillum sp. CAG:239	1262705 114711 191 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018223	Clostridium sp. CAG:798	1262841	7/27/2015	1270	Clostridium sp. CAG:798	1262841 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008370	Phanerochaete carnosa (strain HHB-10118-sp) (White-rot fungus) (Peniophora carnosa)	650164	7/30/2015	13867	Phanerochaete carnosa HHB-10118-sp	650164 231932 5305 396331 5303 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000018230	Roseburia sp. CAG:18	1262941	7/27/2015	2378	Roseburia sp. CAG:18	1262941 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008493	Agaricus bisporus var. burnettii (strain JB137-S8 / ATCC MYA-4627 / FGSC 10392) (White button mushroom)	597362	7/30/2015	11211	Agaricus bisporus var. burnettii JB137-S8	597362 192524 5341 5340 5339 5338 452333 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	

UP000018232	Firmicutes bacterium CAG:345	1263020	7/27/2015	1462	Firmicutes bacterium CAG:345	1263020 47928 1239 2 131567	Bacteria	Firmicutes
UP000018225	Clostridium sp. CAG:1219	1262772	7/27/2015	1041	Clostridium sp. CAG:1219	1262772 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018228	Bacteroides sp. CAG:144	1262736	7/27/2015	2103	Bacteroides sp. CAG:144	1262736 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018237	Firmicutes bacterium CAG:94	1262989	7/27/2015	2410	Firmicutes bacterium CAG:94	1262989 47928 1239 2 131567	Bacteria	Firmicutes
UP000018231	Clostridium sp. CAG:349	1262797	7/27/2015	1346	Clostridium sp. CAG:349	1262797 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018241	Succinatimonas sp. CAG:777	1262974	7/27/2015	1970	Succinatimonas sp.	1262974 1262971 674963 83763 135624 1236 1224 2 131567	Bacteria	Proteobacteria
UP000018243	Ruminococcus sp. CAG:724	1262966	7/27/2015	1633	Ruminococcus sp. CAG:724	1262966 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018256	Corallococcus sp. CAG:1435	1262867	7/27/2015	1300	Corallococcus sp. CAG:1435	1262867 420968 83461 31 80811 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000018268	Clostridium sp. CAG:7	1262832	7/27/2015	2911	Clostridium sp. CAG:7	1262832 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018242	Clostridium sp. CAG:632	1262830	7/27/2015	2230	Clostridium sp. CAG:632	1262830 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018262	Dorea sp. CAG:317	1262873	7/27/2015	2206	Dorea sp. CAG:317	1262873 286137 189330 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018246	Clostridium hathewayi CAG:224	1263067	7/27/2015	4752	Clostridium hathewayi CAG:224	1263067 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018260	Firmicutes bacterium CAG:238	1263011	7/27/2015	2016	Firmicutes bacterium CAG:238	1263011 47928 1239 2 131567	Bacteria	Firmicutes
UP000018244	Clostridium sp. CAG:465	1262811	7/27/2015	1173	Clostridium sp. CAG:465	1262811 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018263	Clostridium sp. CAG:58	1262824	7/27/2015	2660	Clostridium sp. CAG:58	1262824 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018266	Eggerthella sp. CAG:298	1262876	7/27/2015	1581	Eggerthella sp. CAG:298	1262876 293421 84111 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000018259	Acetobacter sp. CAG:977	1262685	7/27/2015	1775	Acetobacter sp. CAG:977	1262685 114713 434 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018279	Firmicutes bacterium CAG:170	1263006	7/27/2015	2216	Firmicutes bacterium CAG:170	1263006 47928 1239 2 131567	Bacteria	Firmicutes
UP000018258	Halomonas sp. A3H3	1346287	7/27/2015	5279	Halomonas sp. A3H3	1346287 2745 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000018275	Prevotella sp. CAG:487	1262928	7/27/2015	2507	Prevotella sp. CAG:487	1262928 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018269	Firmicutes bacterium CAG:124	1263002	7/27/2015	2364	Firmicutes bacterium CAG:124	1263002 47928 1239 2 131567	Bacteria	Firmicutes
UP000018284	Clostridium sp. CAG:43	1262805	7/27/2015	2273	Clostridium sp. CAG:43	1262805 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018278	Clostridium sp. CAG:302	1262793	7/27/2015	1248	Clostridium sp. CAG:302	1262793 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018280	Mycoplasma sp. CAG:877	1262907	7/27/2015	1407	Mycoplasma sp. CAG:877	1262907 167966 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000018261	Peptostreptococcus anaerobius CAG:621	1263100	7/27/2015	1713	Peptostreptococcus anaerobius CAG:621	1263100 135073 1257 186804 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018274	Brachyspira sp. CAG:484	1262759	7/27/2015	2216	Brachyspira sp. CAG:484	1262759 132529 29521 143786 1643686 203692 203691 2 131567	Bacteria	Spirochaetes
UP000018299	Clostridium sp. CAG:575	1262823	7/27/2015	1338	Clostridium sp. CAG:575	1262823 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018282	Bacteroides uniformis CAG:3	1263055	7/27/2015	3570	Bacteroides uniformis CAG:3	1263055 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018290	Firmicutes bacterium CAG:103	1262999	7/27/2015	1809	Firmicutes bacterium CAG:103	1262999 47928 1239 2 131567	Bacteria	Firmicutes
UP000018281	Clostridium sp. CAG:277	1262790	7/27/2015	2689	Clostridium sp. CAG:277	1262790 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018292	Roseburia sp. CAG:309	1262945	7/27/2015	2223	Roseburia sp. CAG:309	1262945 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018300	Butyrivibrio crossotus CAG:259	1263062	7/27/2015	1976	Butyrivibrio crossotus CAG:259	1263062 135026 830 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018294	Firmicutes bacterium CAG:227	1263010	7/27/2015	2286	Firmicutes bacterium CAG:227	1263010 47928 1239 2 131567	Bacteria	Firmicutes
UP000018308	Catenibacterium sp. CAG:290	1262767	7/27/2015	1992	Catenibacterium sp. CAG:290	1262767 286141 135858 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000018319	Clostridium sp. CAG:452	1262810	7/27/2015	1317	Clostridium sp. CAG:452	1262810 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018295	Prevotella sp. CAG:604	1262932	7/27/2015	2073	Prevotella sp. CAG:604	1262932 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018289	Sutterella sp. CAG:521	1262977	7/27/2015	1632	Sutterella sp. CAG:521	1262977 286132 40544 995019 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000018309	Proteobacteria bacterium CAG:495	1262987	7/27/2015	1693	Proteobacteria bacterium CAG:495	1262987 47936 1224 2 131567	Bacteria	Proteobacteria
UP000018293	Bacteroides sp. CAG:709	1262748	7/27/2015	2178	Bacteroides sp. CAG:709	1262748 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018315	Ruminococcus sp. CAG:177	1262952	7/27/2015	1937	Ruminococcus sp. CAG:177	1262952 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018303	Clostridium sp. CAG:417	1262804	7/27/2015	1291	Clostridium sp. CAG:417	1262804 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018312	Eubacterium sp. CAG:603	1262891	7/27/2015	2287	Eubacterium sp. CAG:603	1262891 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018297	Coprobacillus sp. CAG:698	1262856	7/27/2015	1615	Coprobacillus sp. CAG:698	1262856 512291 100883 128827 526525 526524 1239 2 131567	Bacteria	Firmicutes
UP000018328	Faecalibacterium sp. CAG:74	1262897	7/27/2015	2464	Faecalibacterium sp.	1262897 259314 216851 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000006637	Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)	266117	7/30/2015	3127	Rubrobacter xylanophilus DSM 9941	266117 49319 42255 84997 255725 84996 84995 201174 2 131567	Bacteria	Actinobacteria
UP000018313	Clostridium sp. CAG:354	1262799	7/27/2015	1707	Clostridium sp. CAG:354	1262799 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018310	Clostridium sp. CAG:793	1262840	7/27/2015	1163	Clostridium sp. CAG:793	1262840 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018338	Firmicutes bacterium CAG:466	1263025	7/27/2015	2676	Firmicutes bacterium CAG:466	1263025 47928 1239 2 131567	Bacteria	Firmicutes
UP000018333	Dorea longicatena CAG:42	1263074	7/27/2015	2196	Dorea longicatena CAG:42	1263074 286137 189330 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018342	Clostridium sp. CAG:264	1262786	7/27/2015	2136	Clostridium sp. CAG:264	1262786 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes

UP000018345	Firmicutes bacterium CAG:212	1263009	7/27/2015	2078	Firmicutes bacterium CAG:212	1263009 47928 1239 2 131567	Bacteria	Firmicutes
UP000018302	Clostridium sp. CAG:169	1262778	7/27/2015	1970	Clostridium sp. CAG:169	1262778 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018350	Firmicutes bacterium CAG:270	1263014	7/27/2015	1695	Firmicutes bacterium CAG:270	1263014 47928 1239 2 131567	Bacteria	Firmicutes
UP000018332	Firmicutes bacterium CAG:536	1263028	7/27/2015	1621	Firmicutes bacterium CAG:536	1263028 47928 1239 2 131567	Bacteria	Firmicutes
UP000018359	Prevotella sp. CAG:520	1262929	7/27/2015	2171	Prevotella sp. CAG:520	1262929 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018318	Eubacterium sp. CAG:161	1262881	7/27/2015	2196	Eubacterium sp. CAG:161	1262881 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018358	Collinsella sp. CAG:166	1262850	7/27/2015	1601	Collinsella sp. CAG:166	1262850 165189 102106 84107 84999 84998 201174 2 131567	Bacteria	Actinobacteria
UP000018343	Prevotella sp. CAG:592	1262931	7/27/2015	2159	Prevotella sp. CAG:592	1262931 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018336	Roseburia sp. CAG:197	1262943	7/27/2015	2420	Roseburia sp. CAG:197	1262943 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018325	Clostridium sp. CAG:1000	1262768	7/27/2015	1142	Clostridium sp. CAG:1000	1262768 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018314	Prevotella sp. CAG:1058	1262918	7/27/2015	2263	Prevotella sp. CAG:1058	1262918 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018340	Clostridium sp. CAG:352	1262798	7/27/2015	2097	Clostridium sp. CAG:352	1262798 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018346	Alistipes sp. CAG:157	1262692	7/27/2015	1828	Alistipes sp. CAG:157	1262692 538948 239759 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018341	Acinetobacter sp. CAG:196	1262690	8/8/2015	2085	Acinetobacter sp. CAG:196	1262690 75661 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000018327	Clostridium sp. CAG:273	1262789	7/27/2015	1183	Clostridium sp. CAG:273	1262789 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018329	Alistipes sp. CAG:268	1262693	7/27/2015	2200	Alistipes sp. CAG:268	1262693 538948 239759 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018337	Thermoplasmatales archaeon A-plasma	667135	7/27/2015	2276	Thermoplasmatales archaeon A-plasma	667135 95865 2301 183967 28890 2157 131567	Archaea	
UP000018357	Prevotella sp. CAG:924	1262938	7/27/2015	2225	Prevotella sp. CAG:924	1262938 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018361	Prevotella copri CAG:164	1263102	7/27/2015	2331	Prevotella copri CAG:164	1263102 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018355	Roseburia sp. CAG:303	1262944	7/27/2015	2401	Roseburia sp. CAG:303	1262944 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018378	Roseburia sp. CAG:50	1262949	7/27/2015	2482	Roseburia sp. CAG:50	1262949 512313 841 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018368	Clostridium nexile CAG:348	1263069	7/27/2015	2321	Clostridium nexile CAG:348	1263069 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018364	Clostridium sp. CAG:217	1262779	7/27/2015	1746	Clostridium sp. CAG:217	1262779 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018382	Clostridium sp. CAG:1013	1262769	7/27/2015	2437	Clostridium sp. CAG:1013	1262769 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018387	Ruminococcus sp. CAG:579	1262963	7/27/2015	2155	Ruminococcus sp. CAG:579	1262963 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018385	Anaerotruncus sp. CAG:390	1262703	7/27/2015	2237	Anaerotruncus sp. CAG:390	1262703 905010 244127 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018390	Bacteroides sp. CAG:770	1262751	7/27/2015	2085	Bacteroides sp. CAG:770	1262751 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018384	Firmicutes bacterium CAG:194	1263008	7/27/2015	2310	Firmicutes bacterium CAG:194	1263008 47928 1239 2 131567	Bacteria	Firmicutes
UP000018363	Clostridium sp. CAG:269	1262788	7/27/2015	1540	Clostridium sp. CAG:269	1262788 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018392	Bacteroides sp. CAG:530	1262741	7/27/2015	2669	Bacteroides sp. CAG:530	1262741 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018393	Eggerthella sp. CAG:1427	1262874	7/27/2015	1937	Eggerthella sp. CAG:1427	1262874 293421 84111 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000018398	Firmicutes bacterium CAG:582	1262997	7/27/2015	1293	Firmicutes bacterium CAG:582	1262997 47928 1239 2 131567	Bacteria	Firmicutes
UP000018386	Firmicutes bacterium CAG:646	1262995	7/27/2015	2671	Firmicutes bacterium CAG:646	1262995 47928 1239 2 131567	Bacteria	Firmicutes
UP000018402	Firmicutes bacterium CAG:555	1263030	7/27/2015	1723	Firmicutes bacterium CAG:555	1263030 47928 1239 2 131567	Bacteria	Firmicutes
UP000018397	Fusobacterium sp. CAG:439	1262899	7/27/2015	2311	Fusobacterium sp.	1262899 127783 848 203492 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000018396	Tannerella sp. CAG:118	1262978	7/27/2015	2920	Tannerella sp. CAG:118	1262978 417613 195950 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018403	Firmicutes bacterium CAG:552	1263029	7/27/2015	1175	Firmicutes bacterium CAG:552	1263029 47928 1239 2 131567	Bacteria	Firmicutes
UP000018401	Clostridium sp. CAG:433	1262806	7/27/2015	1308	Clostridium sp. CAG:433	1262806 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018406	Bacteroides sp. CAG:189	1262737	7/27/2015	3866	Bacteroides sp. CAG:189	1262737 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018407	Parabacteroides merdae CAG:48	1263094	7/27/2015	2964	Parabacteroides merdae CAG:48	1263094 512311 375288 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018408	Mycoplasma sp. CAG:472	1262904	7/27/2015	1281	Mycoplasma sp. CAG:472	1262904 167966 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000018411	Eubacterium sp. CAG:180	1262882	7/27/2015	1742	Eubacterium sp. CAG:180	1262882 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018410	Firmicutes bacterium CAG:129	1263003	7/27/2015	1635	Firmicutes bacterium CAG:129	1263003 47928 1239 2 131567	Bacteria	Firmicutes
UP000018414	Eubacterium sp. CAG:251	1262886	7/27/2015	1717	Eubacterium sp. CAG:251	1262886 84372 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018374	Clostridium sp. CAG:780	1262839	7/27/2015	1194	Clostridium sp. CAG:780	1262839 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018383	Dialister sp. CAG:588	1262871	7/27/2015	1171	Dialister sp. CAG:588	1262871 135034 39948 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000018372	Bacteroides plebeius CAG:211	1263052	7/27/2015	2643	Bacteroides plebeius CAG:211	1263052 139043 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018389	Clostridium sp. CAG:609	1262827	7/27/2015	1196	Clostridium sp. CAG:609	1262827 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018377	Ruminococcus sp. CAG:330	1262954	7/27/2015	2234	Ruminococcus sp. CAG:330	1262954 129701 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes

UP000018370	Clostridium sp. CAG:571	1262822	7/27/2015	1620	Clostridium sp. CAG:571	1262822 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018360	Staphylococcus sp. CAG:324	1262969	7/27/2015	1476	Staphylococcus sp. CAG:324	1262969 129707 1279 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000018365	Dialister sp. CAG:357	1262869	7/27/2015	1809	Dialister sp. CAG:357	1262869 135034 39948 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000018347	Veillonella sp. CAG:933	1262980	7/27/2015	2777	Veillonella sp. CAG:933	1262980 135095 29465 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000018373	Firmicutes bacterium CAG:313	1263017	7/27/2015	1321	Firmicutes bacterium CAG:313	1263017 47928 1239 2 131567	Bacteria	Firmicutes
UP000001979	Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M)	259564	7/30/2015	2242	Methanococcoides burtonii DSM 6242	259564 29291 2225 2206 94695 224756 28890 2157 131567	Archaea	
UP000001983	Polaromonas sp. (strain JS666 / ATCC BAA-500)	296591	7/30/2015	5437	Polaromonas sp. JS666	296591 52972 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001982	Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013)	318161	7/30/2015	3727	Shewanella denitrificans OS217	318161 192073 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000018375	Prevotella sp. CAG:279	1262924	7/27/2015	2076	Prevotella sp. CAG:279	1262924 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018381	Clostridium sp. CAG:813	1262843	7/27/2015	1828	Clostridium sp. CAG:813	1262843 59619 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018439	Bacteroides coprosuis DSM 18011	679937	7/27/2015	2385	Bacteroides coprosuis DSM 18011	679937 151276 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000018353	Prevotella sp. CAG:755	1262935	7/27/2015	1936	Prevotella sp. CAG:755	1262935 84374 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001978	Peptoclostridium difficile (strain 630) (Clostridium difficile)	272563	7/30/2015	3762	Peptoclostridium difficile 630	272563 1496 1481960 186804 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001822	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	269798	7/30/2015	3771	Cytophaga hutchinsonii ATCC 33406	269798 985 978 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001975	Haloquadratum walsbyi (strain DSM 16790 / HBSQ001)	362976	7/30/2015	2551	Haloquadratum walsbyi DSM 16790	362976 293091 293431 1644056 1644055 183963 28890 2157 131567	Archaea	
UP000018461	Oribacterium parvum ACB1	796943	7/27/2015	2127	Oribacterium parvum ACB1	796943 1501329 265975 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001824	Clostridium perfringens (strain SM101 / Type A)	289380	7/30/2015	2558	Clostridium perfringens SM101	289380 1502 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000009183	Vitis vinifera (Grape)	29760	7/30/2015	29907	Vitis vinifera	29760 3603 3602 403667 91834 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000001820	Chelativorans sp. (strain BNC1)	266779	7/30/2015	4530	Chelativorans sp. BNC1	266779 449972 69277 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018418	Acinetobacter brisouii CIP 110357	1341683	7/27/2015	2927	Acinetobacter brisouii CIP 110357	1341683 396323 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000018419	Acinetobacter radioresistens SK82	596318	7/27/2015	3187	Acinetobacter radioresistens SK82	596318 40216 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001959	Hyphomonas neptunium (strain ATCC 15444)	228405	7/30/2015	3499	Hyphomonas neptunium ATCC 15444	228405 81032 85 69657 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000684	Shewanella frigidimarina (strain NCIMB 400)	318167	7/30/2015	3990	Shewanella frigidimarina NCIMB 400	318167 56812 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008878	Trichodesmium erythraeum (strain IMS101)	203124	7/30/2015	4342	Trichodesmium erythraeum IMS101	203124 1206 1205 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000007029	Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)	375451	7/30/2015	4118	Roseobacter denitrificans OCh 114	375451 2434 2433 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001981	Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087)	342610	7/30/2015	4271	Pseudoalteromonas atlantica T6c	342610 288 53246 267888 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008710	Rhodococcus jostii (strain RHA1)	101510	7/30/2015	9075	Rhodococcus jostii RHA1	101510 132919 1827 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001817	Burkholderia xenovorans (strain LB400)	266265	7/30/2015	8591	Burkholderia xenovorans LB400	266265 36873 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008210	Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	381666	7/30/2015	6614	Ralstonia eutropha H16	381666 106590 106589 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000018468	Lepisosteus oculatus (Spotted gar)	7918	8/2/2015	22463	Lepisosteus oculatus	7918 7916 7915 7914 1489100 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001968	Syntrophomonas wolfei subsp. wolfei (strain DSM 2245B / Goettingen)	335541	7/30/2015	2473	Syntrophomonas wolfei subsp. wolfei str. Goettingen G311	335541 370885 863 862 68298 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008871	Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2)	393595	7/30/2015	2752	Alcanivorax borkumensis SK2	393595 59754 59753 224372 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001055	Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	321614	8/2/2015	15998	Parastagonospora nodorum SN15	321614 13684 1351751 5020 715340 92860 451868 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000018467	Astyanax mexicanus (Blind cave fish) (Astyanax fasciatus mexicanus)	7994	7/27/2015	23669	Astyanax mexicanus	7994 7993 883878 533331 7992 1489739 7991 186628 186626 32519 186634 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000663	Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	351160	8/5/2015	3071	Methanocella arvoryzae MRE50	351160 1175445 570266 570265 570264 224756 28890 2157 131567	Archaea	
UP000001964	Maricaulis maris (strain MCS10)	394221	7/30/2015	3060	Maricaulis maris MCS10	394221 74318 74317 69657 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001652	Lactobacillus brevis (strain ATCC 367 / JCM 1170)	387344	8/2/2015	2201	Lactobacillus brevis ATCC 367	387344 1580 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes

UP000001962	Alkalilimnicola ehrlichii (strain ATCC BAA-1101 / DSM 17681 / MLHE-1)	187272	7/30/2015	2862	Alkalilimnicola ehrlichii MLHE-1	187272 351052 133193 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000657	Frankia alni (strain ACN14a)	326424	7/30/2015	6710	Frankia alni ACN14a	326424 1859 1854 74712 85013 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001056	Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	306901	7/30/2015	11041	Chaetomium globosum CBS 148.51	306901 38033 5149 35718 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000773	Pediococcus pentosaceus (strain ATCC 25745 / 183-1w)	278197	7/30/2015	1755	Pediococcus pentosaceus ATCC 25745	278197 1255 1253 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001963	Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	391165	7/30/2015	2430	Granulibacter bethesdensis CGDNIH1	391165 364410 364409 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001651	Lactobacillus casei (strain ATCC 334)	321967	8/2/2015	2708	Lactobacillus casei ATCC 334	321967 1582 655183 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001261	Coccidioides immitis (strain RS) (Valley fever fungus)	246410	8/2/2015	9712	Coccidioides immitis RS	246410 5501 5500 34383 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000671	Solibacter usitatus (strain Ellin6076)	234267	7/30/2015	7761	Candidatus Solibacter usitatus Ellin6076	234267 332163 332162 332161 332160 332159 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000000774	Oenococcus oeni (strain ATCC BAA-331 / PSU-1)	203123	7/30/2015	1682	Oenococcus oeni PSU-1	203123 1247 46254 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000669	Buchnera aphidicola subsp. Cinara cedri (strain Cc)	372461	7/30/2015	362	Buchnera aphidicola BCc	372461 261318 9 32199 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000755	Gramella forsetii (strain KT0803)	411154	7/30/2015	3554	Gramella forsetii KT0803	411154 411153 292691 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000362	Leuconostoc mesenteroides subsp. mesenteroides (strain ATCC 8293 / NCDO 523)	203120	7/30/2015	2002	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293	203120 33967 1245 1243 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000760	Campylobacter fetus subsp. fetus (strain 82-40)	360106	7/30/2015	1715	Campylobacter fetus subsp. fetus 82-40	360106 32019 196 194 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000758	Cenarchaeum symbiosum (strain A)	414004	7/30/2015	2022	Cenarchaeum symbiosum	414004 46770 46769 205957 205948 651137 2157 131567	Archaea	
UP000001819	Drosophila pseudoobscura pseudoobscura (Fruit fly)	46245	8/2/2015	16756	Drosophila pseudoobscura pseudoobscura	46245 7237 32358 32355 32341 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001784	Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	335543	7/30/2015	4012	Syntrophobacter fumaroxidans MPOB	335543 119484 29526 213465 213462 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000459	Methanolobus psychrophilus R15	1094980	7/27/2015	3132	Methanolobus psychrophilus R15	1094980 420950 2220 2206 94695 224756 28890 2157 131567	Archaea	
UP000000754	Arthrobacter sp. (strain FB24)	290399	7/30/2015	4453	Arthrobacter sp. FB24	290399 1663 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000759	Phaeodactylum tricornutum (strain CCAP 1055/1)	556484	7/30/2015	10465	Phaeodactylum tricornutum CCAP 1055/1	556484 2850 2849 38749 38748 33850 33849 2836 33634 2759 131567	eukaryotes	
UP000000674	Methanosaeta thermophila (strain DSM 6194 / JCM 14653 / NBRC 101360 / PT) (Methanothrix thermophila)	349307	7/30/2015	1673	Methanosaeta thermophila PT	349307 2224 2222 143067 94695 224756 28890 2157 131567	Archaea	
UP000000756	Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	380703	8/2/2015	4121	Aeromonas hydrophila subsp. hydrophila ATCC 7966	380703 196023 644 642 84642 135624 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000768	Sorghum bicolor (Sorghum) (Sorghum vulgare)	4558	8/8/2015	32798	Sorghum bicolor	4558 4557 1648028 147429 1648033 147369 147370 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000008702	Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a)	367928	8/2/2015	1629	Bifidobacterium adolescentis ATCC 15703	367928 1680 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008701	Chlorobium phaeobacteroides (strain DSM 266)	290317	7/30/2015	2579	Chlorobium phaeobacteroides DSM 266	290317 1096 1091 274493 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000757	Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	246196	7/30/2015	6601	Mycobacterium smegmatis str. MC2 155	246196 1772 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000466	Simiduia agarivorans (strain DSM 21679 / JCM 13881 / BCRC 17597 / SA1)	1117647	7/30/2015	3812	Simiduia agarivorans SA1 = DSM 21679	1117647 447471 447467 1706371 1706369 1236 1224 2 131567	Bacteria	Proteobacteria
UP000009175	Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)	326297	7/30/2015	3638	Shewanella amazonensis SB2B	326297 60478 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000998	Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)	351348	7/30/2015	4170	Marinobacter hydrocarbonoclasticus VT8	351348 2743 2742 72275 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000641	Thermofilum pendens (strain Hrk 5)	368408	7/30/2015	1876	Thermofilum pendens Hrk 5	368408 2269 2268 114378 2266 183924 28889 2157 131567	Archaea	
UP000000640	Nocardioides sp. (strain BAA-499 / JS614)	196162	7/30/2015	4888	Nocardioides sp. JS614	196162 1839 85015 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000637	Arthrobacter aurescens (strain TC1)	290340	7/30/2015	4565	Arthrobacter aurescens TC1	290340 43663 1663 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000643	Bartonella bacilliformis (strain ATCC 35685 / KC583)	360095	7/30/2015	1255	Bartonella bacilliformis KC583	360095 774 773 772 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000009159	Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	350058	8/7/2015	5902	Mycobacterium vanbaalenii PYR-1	350058 110539 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000639	Psychromonas ingrahamii (strain 37)	357804	7/30/2015	3530	Psychromonas ingrahamii	357804 357794 67572 267894 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000009170	Ostreococcus tauri	70448	7/30/2015	7745	Ostreococcus tauri	70448 70447 1525212 13792 1035538 3152 3041 33090 2759 131567	eukaryotes	
UP000000361	Paracoccus denitrificans (strain Pd 1222)	318586	8/2/2015	5019	Paracoccus denitrificans PD1222	318586 266 265 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000467	Thermacetogenium phaeum (strain ATCC BAA-254 / DSM 12270 / PB)	1089553	7/30/2015	2803	Thermacetogenium phaeum DSM 12270	1089553 85874 140458 186814 68295 186801 1239 2 131567	Bacteria	Firmicutes

UP000008221	Acidothermus cellulolyticus (strain ATCC 43068 / 11B)	351607	7/30/2015	2157	Acidothermus cellulolyticus 11B	351607 28049 28048 85032 1643683 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002596	Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	397945	7/30/2015	4602	Acidovorax citrulli AAC00-1	397945 80869 12916 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000482	Dehalobacter sp. CF	1131462	7/27/2015	2936	Dehalobacter sp. CF	1131462 56112 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000645	Acidovorax sp. (strain JS42)	232721	7/30/2015	4045	Acidovorax sp. JS42	232721 12916 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000374	Verminephrobacter eiseniae (strain EF01-2)	391735	7/30/2015	4911	Verminephrobacter eiseniae EF01-2	391735 364317 364316 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002588	Azoarcus sp. (strain BH72)	62928	7/30/2015	3981	Azoarcus sp. BH72	62928 12960 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000638	Mycobacterium sp. (strain KMS)	189918	7/30/2015	5893	Mycobacterium sp. KMS	189918 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002587	Ruthia magnifica subsp. Calyptogena magnifica	413404	8/7/2015	976	Candidatus Ruthia magnifica str. Cm (Calyptogena magnifica)	413404 386487 1541743 32036 118884 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000647	Halorhodospira halophila (strain DSM 244 / SL1) (Ectothiorhodospira halophila (strain DSM 244 / SL1))	349124	7/30/2015	2406	Halorhodospira halophila SL1	349124 1053 85108 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000365	Methanocorpusculum labreanum (strain ATCC 43576 / DSM 4855 / Z)	410358	7/30/2015	1739	Methanocorpusculum labreanum Z	410358 83984 2192 88404 2191 224756 28890 2157 131567	Archaea	
UP000000366	Methylibium petroleiphilum (strain PM1)	420662	7/30/2015	4359	Methylibium petroleiphilum PM1	420662 105560 316612 224471 119065 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000644	Polaromonas naphthalenivorans (strain CJ2)	365044	7/30/2015	4879	Polaromonas naphthalenivorans CJ2	365044 216465 52972 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000018523	Candidatus Saccharibacteria bacterium RAAC3_TM7_1	1394711	7/27/2015	920	Candidatus Saccharibacteria bacterium RAAC3_TM7_1	1394711 95818 2323 2 131567	Bacteria	Unclassified Bacteria
UP000008220	Clostridium novyi (strain NT)	386415	7/30/2015	2305	Clostridium novyi NT	386415 1542 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000018548	Pandoraea sp. RB-44	1380774	7/27/2015	4774	Pandoraea sp. RB-44	1380774 93217 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002586	Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1)	156889	7/30/2015	3594	Magnetococcus marinus MC-1	156889 1124597 162171 1191479 1191478 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018542	Hyphomicrobium nitrativorans NL23	1029756	7/27/2015	3330	Hyphomicrobium nitrativorans NL23	1029756 1427356 81 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018556	candidate division WWE3 bacterium RAAC2_WWE3_1	1394710	7/27/2015	871	candidate division WWE3 bacterium RAAC2_WWE3_1	1394710 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000018550	Spiroplasma apis B31	1276258	7/27/2015	992	Spiroplasma apis B31	1276258 2137 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000002593	Hyperthermus butylicus (strain DSM 5456 / JCM 9403 / PLM1-5)	415426	7/30/2015	1602	Hyperthermus butylicus DSM 5456	415426 54248 54247 2307 114380 183924 28889 2157 131567	Archaea	
UP000018580	Enterococcus mundtii QU 25	1300150	7/27/2015	3162	Enterococcus mundtii QU	1300150 53346 1350 81852 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000018680	Salinispira pacifica	1307761	7/27/2015	3350	Salinispira pacifica	1307761 1616789 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000018700	Candidatus Endolissoclinum faulkneri L5	1401328	7/27/2015	770	Candidatus Endolissoclinum faulkneri L5	1401328 1263979 1263978 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018745	Mycoplasma ovis str. Michigan	1415773	7/27/2015	834	Mycoplasma ovis str. Michigan	1415773 171632 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000018763	Mycobacterium neoaurum VKM Ac-1815D	700508	7/27/2015	4995	Mycobacterium neoaurum VKM Ac-1815D	700508 1795 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000018781	Rhodococcus pyridinivorans SB3094	1435356	8/14/2015	4825	Rhodococcus pyridinivorans SB3094	1435356 103816 1827 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000018780	Leisingera methylohalidivorans DSM 14336	999552	7/27/2015	4508	Leisingera methylohalidivorans DSM 14336	999552 133924 191028 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018769	Candidatus Babela massiliensis	673862	7/27/2015	981	Candidatus Babela massiliensis	673862 1551504 45456 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000715	Mustela putorius furo (European domestic ferret) (Mustela furo)	9669	7/30/2015	20056	Mustela putorius furo	9669 9668 9665 169418 9655 379584 33554 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002852	Xiphophorus maculatus (Southern platyfish) (Platypoecilus maculatus)	8083	7/30/2015	20451	Xiphophorus maculatus	8083 8082 586240 8079 8087 28738 1489913 1489908 1489872 123369 123368 123367 123366 123365 1489388 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000018838	Legionella oakridgensis ATCC 33761 = DSM 21215	1268635	7/27/2015	2907	Legionella oakridgensis ATCC 33761 = DSM 21215	1268635 29423 445 444 118969 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001713	Haemophilus phage HP1 (strain HP1c1) (Bacteriophage HP1)	1289570	7/27/2015	41	Haemophilus phage HP1c1	1289570 10690 1196844 857479 10662 28883 35237 10239	Vruses	
UP000001332	Oscillatoriales cyanobacterium JSC-12	864702	7/27/2015	4673	Oscillatoriales cyanobacterium JSC-12	864702 44887 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000018851	Sphingomonas sanxanigenens DSM 19645 = NX02	1123269	8/13/2015	6101	Sphingomonas sanxanigenens DSM 19645 =	1123269 397260 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002124	Streptomyces phage phiC31 (Bacteriophage phi-C31)	10719	7/30/2015	53	Streptomyces phage	10719 308912 10699 28883 35237 10239	Vruses	
UP000000840	Enterobacteria phage T7 (Bacteriophage T7)	10760	8/2/2015	57	Enterobacteria phage T7	10760 110456 542835 10744 28883 35237 10239	Vruses	
UP000009091	Bacillus phage SPbeta (Bacillus phage SPBc2) (Bacteriophage SP-beta)	66797	7/27/2015	185	Bacillus phage SPbeta	66797 680116 10699 28883 35237 10239	Vruses	
UP000002127	Enterobacteria phage MS2 (Bacteriophage MS2)	329852	7/27/2015	4	Enterobacteria phage MS2	329852 11990 11989 35278 439488 10239	Vruses	
UP000001835	Lactococcus phage c2	31537	7/27/2015	39	Lactococcus phage c2	31537 186532 10699 28883 35237 10239	Vruses	
UP000009092	Enterobacteria phage P2 (Bacteriophage P2)	10679	7/27/2015	43	Enterobacteria phage P2	10679 140410 857479 10662 28883 35237 10239	Vruses	
UP000002132	Enterobacteria phage N15 (Bacteriophage N15)	40631	7/27/2015	60	Enterobacteria phage N15	40631 308911 10699 28883 35237 10239	Vruses	

UP000002123	Mycobacterium phage L5 (Mycobacteriophage L5)	31757	7/27/2015	92	Mycobacterium phage L5	31757 186764 10699 28883 35237 10239	Vruses	
UP000001832	Enterobacteria phage MX1 (Bacteriophage MX1)	75723	7/27/2015	4	Enterobacteria phage MX1	75723 427703 12008 11989 35278 439488 10239	Vruses	
UP000001711	Enterobacteria phage lambda (Bacteriophage lambda)	10710	8/2/2015	66	Enterobacteria phage lambda	10710 186765 10699 28883 35237 10239	Vruses	
UP000018888	Rhizophagus irregularis (strain DAOM 181602 / DAOM 197198 / MUCL 43194) (Arbuscular mycorrhizal fungus) (Glomus intraradices)	747089	7/30/2015	29846	Rhizophagus irregularis DAOM 181602	747089 588596 1129544 36751 36750 214506 214504 4751 33154 2759 131567	eukaryotes	
UP000002125	Chlamydia phage 1 (Bacteriophage Chp1)	10857	7/27/2015	8	Chlamydia phage 1	10857 40274 686565 10841 29258 10239	Vruses	
UP000000854	Sulfolobus spindle-shape virus 1 (SSV1)	244589	8/2/2015	34	Sulfolobus spindle-shaped virus 1	244589 10475 10474 35237 10239	Vruses	
UP000001573	Acholeplasma phage L2 (Bacteriophage L2)	46014	7/27/2015	14	Acholeplasma phage L2	46014 10473 10472 35237 10239	Vruses	
UP000002611	Enterobacteria phage Mu (Bacteriophage Mu)	10677	7/27/2015	55	Enterobacteria phage Mu	10677 186777 10662 28883 35237 10239	Vruses	
UP000009087	Enterobacteria phage T4 (Bacteriophage T4)	10665	7/27/2015	273	Enterobacteria phage T4	10665 348604 10663 1198136 10662 28883 35237 10239	Vruses	
UP000002098	Pseudomonas phage phiKZ	169683	7/27/2015	369	Pseudomonas phage phiKZ	169683 680115 10662 28883 35237 10239	Vruses	
UP000002136	Pseudoalteromonas phage PM2 (Bacteriophage PM2)	10661	7/27/2015	21	Pseudoalteromonas phage PM2	10661 10660 10659 35237 10239	Vruses	
UP000001156	Enterobacteria phage T1 (Bacteriophage T1)	12355	7/27/2015	78	Enterobacteria phage T1	12355 187217 10699 28883 35237 10239	Vruses	
UP000001252	Spiroplasma virus SpV1-R8A2 B (SpV1) (Spiroplasma virus 1)	10854	7/27/2015	12	Spiroplasma phage 1-R8A2B	10854 10875 10860 29258 10239	Vruses	
UP000002101	Spiroplasma virus 4 (SpV4)	10855	7/27/2015	9	Spiroplasma phage 4	10855 10852 686565 10841 29258 10239	Vruses	
UP000002107	Escherichia phage T5 (Enterobacteria phage T5)	10726	7/27/2015	162	Escherichia phage T5	10726 187218 10699 28883 35237 10239	Vruses	
UP000018901	Barnesiella viscericola DSM 18177	880074	7/27/2015	2487	Barnesiella viscericola DSM 18177	880074 397865 397864 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000842	Enterobacteria phage phiKMV (Pseudomonas phage phiKMV)	204270	7/27/2015	49	Pseudomonas phage phiKMV	204270 477967 542835 10744 28883 35237 10239	Vruses	
UP000002111	Enterobacteria phage M13 (Bacteriophage M13)	10870	7/27/2015	9	Enterobacteria phage M13	10870 10861 10860 29258 10239	Vruses	
UP000018922	Magnetospirillum gryphiswaldense MSR-1 v2	1430440	7/27/2015	4154	Magnetospirillum gryphiswaldense MSR-1 v2	1430440 431944 55518 13134 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000018945	Bartonella quintana JK 73	1402976	7/30/2015	1313	Bartonella quintana JK 73	1402976 803 773 772 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001466	Staphylococcus phage Twort (strain DSM 17442) (Bacteriophage Twort)	1283338	7/27/2015	195	Staphylococcus phage Twort DSM 17442	1283338 55510 1198135 857473 10662 28883 35237 10239	Vruses	
UP000018936	Ophiophagus hannah (King cobra) (Naja hannah)	8665	7/27/2015	18387	Ophiophagus hannah	8665 8664 42168 8602 34989 8570 1329911 1329912 1329950 1329961 8509 8504 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006649	Clostridium phage phiCD119 (strain Clostridium difficile/United States/Govind/2006) (Bacteriophage phiCD119)	1283341	7/27/2015	79	Clostridium phage phiCD119 USA/Govind/2006	1283341 320122 1198989 10662 28883 35237 10239	Vruses	
UP000019024	Halostagnicola larsenii XH-48	797299	7/27/2015	4086	Halostagnicola larsenii XH-48	797299 353800 353799 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000019026	Spiroplasma mirum ATCC 29335	838561	7/27/2015	1091	Spiroplasma mirum ATCC 29335	838561 2144 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000001789	Enterobacteria phage N4 (Bacteriophage N4)	10752	7/27/2015	72	Escherichia phage N4	10752 371730 10744 28883 35237 10239	Vruses	
UP000019030	Serratia multitudinisentens RB-25	1441930	7/27/2015	4521	Chania multitudinisentens RB-25	1441930 1639108 1745211 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019028	Sodalis praecaptivus	1239307	7/27/2015	4281	Sodalis praecaptivus	1239307 84565 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019023	Desulfurella acetivorans A63	694431	7/27/2015	1825	Desulfurella acetivorans A63	694431 33002 33001 117942 213113 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002610	Pseudomonas phage phi6 (Bacteriophage phi-6)	10879	7/27/2015	13	Pseudomonas phage phi6	10879 10878 10877 35325 10239	Vruses	
UP000000730	Mycobacterium phage Bxz1 (Mycobacteriophage Bxz1)	205877	7/27/2015	225	Mycobacterium phage Bxz1	205877 1133560 680114 10662 28883 35237 10239	Vruses	
UP000007266	Tribolium castaneum (Red flour beetle)	7070	7/30/2015	16502	Tribolium castaneum	7070 7069 1304792 7065 71527 41088 41084 7041 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001785	Vibrio phage KVP40 (isolate Vibrio parahaemolyticus/Japan/Matsuzaki/1991) (KVP40) (Bacteriophage KVP40)	1283340	7/30/2015	380	Vibrio phage KVP40 Japan/Matsuzaki /1991	1283340 75320 1198137 1198136 10662 28883 35237 10239	Vruses	
UP000008091	Enterobacteria phage P1 (Bacteriophage P1)	10678	7/27/2015	110	Enterobacteria phage P1	10678 186789 10662 28883 35237 10239	Vruses	
UP000007478	Thermococcus barophilus (strain DSM 11836 / MP)	391623	7/30/2015	2265	Thermococcus barophilus MP	391623 55802 2263 2259 2258 183968 28890 2157 131567	Archaea	
UP000009070	Salmonella phage Felix O1 (isolate Felix O1-VT1) (Bacteriophage Felix O1)	1283336	7/27/2015	247	Salmonella phage Felix O1 VT1	1283336 77775 1198140 10662 28883 35237 10239	Vruses	
UP000008466	Sphaerochaeta globosa (strain ATCC BAA-1886 / DSM 22777 / Buddy) (Spirochaeta sp. (strain Buddy))	158189	7/30/2015	3007	Sphaerochaeta globosa str. Buddy	158189 1131703 399320 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000007484	Mycoplasma suis (strain Illinois)	768700	7/30/2015	844	Mycoplasma suis str. Illinois	768700 57372 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000007490	Methanobacterium lacus (strain AL-21)	877455	7/30/2015	2493	Methanobacterium lacus	877455 2160 2159 2158 183925 28890 2157 131567	Archaea	
UP000007102	Desulfurobacterium thermolithotrophum (strain DSM 11699 / BSA)	868864	7/30/2015	1496	Desulfurobacterium thermolithotrophum DSM 11699	868864 64160 64159 558314 1485951 187857 200783 2 131567	Bacteria	Aquificae
UP000007718	Deinococcus proteolyticus (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703 / MRP)	693977	7/30/2015	2652	Deinococcus proteolyticus MRP	693977 55148 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000001770	Salmonella phage epsilon15	215158	7/27/2015	51	Salmonella phage	215158 542960 10744 28883 35237 10239	Vruses	

UP000007488	Syntrophobotulus glycolicus (strain DSM 8271 / FlGlyR)	645991	7/30/2015	3105	Syntrophobotulus glycolicus DSM 8271	645991 51197 51196 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001765	Bordetella phage BPP-1	194699	7/27/2015	49	Bordetella phage BPP-1	194699 542959 10744 28883 35237 10239	Vruses	
UP000007462	Staphylococcus phage 44AHJD	204086	7/27/2015	21	Staphylococcus phage 44AHJD	204086 680287 542836 10744 28883 35237 10239	Vruses	
UP000001764	Spiroplasma virus SpV1-C74 (SpV1)	185959	7/27/2015	13	Spiroplasma phage 1-C74	185959 10875 10860 29258 10239	Vruses	
UP000007960	Enterobacteria phage P22 (Bacteriophage P22)	10754	7/30/2015	64	Enterobacteria phage P22	10754 186794 10744 28883 35237 10239	Vruses	
UP000007487	Cellulophaga lytica (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy l20)	867900	7/30/2015	3281	Cellulophaga lytica DSM 7489	867900 979 104264 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001721	Enterobacteria phage SP6 (Bacteriophage SP6)	194966	7/27/2015	52	Enterobacteria phage SP6	194966 542837 542835 10744 28883 35237 10239	Vruses	
UP000002143	Enterobacteria phage PRD1 (Bacteriophage PRD1)	10658	7/27/2015	30	Enterobacteria phage PRD1	10658 10657 10656 35237 10239	Vruses	
UP000007486	Bacteroides salanitronis (strain DSM 18170 / JCM 13567 / BL78)	667015	7/30/2015	3608	Bacteroides salanitronis DSM 18170	667015 376805 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007494	Neospora caninum (strain Liverpool)	572307	7/30/2015	7111	Neospora caninum Liverpool	572307 29176 29175 5809 423054 75739 5796 1280412 5794 33630 2759 131567	eukaryotes	
UP000002146	Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1)	368407	7/30/2015	2476	Methanoculleus marisnigri JR1	368407 2198 45989 2194 2191 224756 28890 2157 131567	Archaea	
UP000002145	Clostridium thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) (Ruminiclostridium thermocellum)	203119	8/2/2015	3105	Ruminiclostridium thermocellum ATCC 27405	203119 1515 1508657 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008524	Trypanosoma brucei brucei (strain 927/4 GUTat10.1)	185431	7/30/2015	8587	Trypanosoma brucei brucei TREU927	185431 5702 5691 39700 5690 5654 5653 33682 2759 131567	eukaryotes	
UP000007963	Aspergillus terreus (strain NIH 2624 / FGSC A1156)	341663	7/30/2015	10416	Aspergillus terreus NIH2624	341663 33178 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006643	Phytophthora infestans (strain T30-4) (Potato late blight fungus)	403677	7/30/2015	17609	Phytophthora infestans T30-4	403677 4787 4783 4776 4762 33634 2759 131567	eukaryotes	
UP000002150	Acidianus two-tailed virus (ATV)	315953	7/27/2015	72	Acidianus two-tailed virus	315953 680194 423358 35237 10239	Vruses	
UP000019095	Advenella mimigardefordensis DPN7	1247726	8/4/2015	4072	Advenella mimigardefordensis DPN7	1247726 302406 290425 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008387	Helicobacter bizzozeronii (strain CIII-1)	1002804	7/30/2015	1959	Helicobacter bizzozeronii CIII-1	1002804 56877 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000008385	Ramlibacter tataouinensis (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310)	365046	7/30/2015	3880	Ramlibacter tataouinensis TTB310	365046 94132 174951 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001432	Actinobacillus pleuropneumoniae serotype 5b (strain L20)	416269	8/3/2015	2004	Actinobacillus pleuropneumoniae serovar 5b str. L20	416269 44294 715 713 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019132	Pythium ultimum DAOM BR144	431595	7/30/2015	15153	Pythium ultimum DAOM BR144	431595 65071 4797 4782 121069 4762 33634 2759 131567	eukaryotes	
UP000006583	Thermodesulfobacterium geofontis (strain OPF15)	795359	7/30/2015	1594	Thermodesulfobacterium geofontis OPF15	795359 1295609 1740 188711 188710 67799 200940 2 131567	Bacteria	Thermodesulfobacteria
UP000019150	Nocardia nova SH22a	1415166	7/27/2015	7577	Nocardia nova SH22a	1415166 37330 1817 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000254	Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1)	399550	7/30/2015	1570	Staphylothermus marinus F1	399550 2280 2279 2272 114380 183924 28889 2157 131567	Archaea	
UP000002258	Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) (Yeast) (Pichia stipitis)	322104	7/30/2015	5797	Scheffersomyces stipitis CBS 6054	322104 4924 766733 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000019151	Gemmatirosa kalamazoonesis	861299	7/27/2015	6261	Gemmatirosa kalamazoonesis	861299 1706036 219687 219686 219685 142182 2 131567	Bacteria	Gemmatimonadetes
UP000001558	Shewanella loihica (strain ATCC BAA-1088 / PV-4)	323850	7/30/2015	3855	Shewanella loihica PV-4	323850 359303 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002270	Sulfolobus islandicus rod-shaped virus 1 (SIRV-1) (Sulfolobus virus SIRV-1)	157898	7/27/2015	43	Sulfolobus islandicus rod-shaped virus 1	157898 187213 157897 1511857 35237 10239	Vruses	
UP000006726	Cryptosporidium parvum (strain Iowa II)	353152	7/30/2015	3805	Cryptosporidium parvum Iowa II	353152 5807 5806 35082 423054 75739 5796 1280412 5794 33630 2759 131567	eukaryotes	
UP000019116	Triticum aestivum (Wheat)	4565	8/2/2015	95051	Triticum aestivum	4565 4564 1648030 147389 1648038 147368 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000006732	Pelobacter propionicus (strain DSM 2379)	338966	7/30/2015	3694	Pelobacter propionicus DSM 2379	338966 29543 18 213423 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000019226	Corynebacterium casei LMG S-19264	1285583	7/27/2015	2769	Corynebacterium casei LMG S-19264	1285583 160386 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006728	Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	405948	7/30/2015	7154	Saccharopolyspora erythraea NRRL 2338	405948 1836 1835 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000019205	Congregibacter litoralis KT71	314285	7/27/2015	3868	Congregibacter litoralis KT71	314285 393662 393661 1706372 1706369 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019231	Komagataeibacter xylinus E25	1296990	7/27/2015	3564	Komagataeibacter xylinus E25	1296990 28448 1434011 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001429	Candida albicans (strain WO-1) (Yeast)	294748	8/2/2015	5742	Candida albicans WO-1	294748 5476 1535326 1535325 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000019222	Corynebacterium vitaeruminis DSM 20294	1224164	7/27/2015	2565	Corynebacterium vitaeruminis DSM 20294	1224164 38305 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria

UP000019233	Bdellovibrio bacteriovorus W	765869	7/27/2015	2854	Bdellovibrio bacteriovorus W	765869 959 958 213483 213481 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006729	Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa)	3694	8/2/2015	44466	Populus trichocarpa	3694 3689 238069 3688 3646 91835 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000002280	Monodelphis domestica (Gray short-tailed opossum)	13616	8/2/2015	22244	Monodelphis domestica	13616 13615 126287 9265 38605 9263 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006706	Aspergillus niger (strain CBS 513.88 / FGSC A1513)	425011	7/30/2015	14068	Aspergillus niger CBS 513.88	425011 5061 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000212	Carnobacterium maltaromaticum LMA28	1234679	7/27/2015	3539	Carnobacterium maltaromaticum LMA28	1234679 2751 2747 186828 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000019232	Corynebacterium falsenii DSM 44353	1451189	7/27/2015	2243	Corynebacterium falsenii DSM 44353	1451189 108486 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000019229	Mycoplasma bovoculi M165/69	743966	7/27/2015	579	Mycoplasma bovoculi M165/69	743966 45362 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000002281	Equus caballus (Horse)	9796	8/2/2015	22718	Equus caballus	9796 35510 9789 9788 9787 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001556	Desulfotomaculum reducens (strain MI-1)	349161	7/30/2015	3220	Desulfotomaculum reducens MI-1	349161 59610 1562 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000214	Propionibacterium acidipropionici (strain ATCC 4875 / DSM 20272 / JCM 6432 / NBRC 12425 / NCIMB 8070)	1171373	7/30/2015	3316	Propionibacterium acidipropionici ATCC 4875	1171373 1748 1743 31957 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000019225	Kutzneria albida DSM 43870	1449976	7/27/2015	8775	Kutzneria albida DSM	1449976 43357 43356 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000223	Gluconobacter oxydans H24	1224746	7/27/2015	3696	Gluconobacter oxydans	1224746 442 441 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006718	Macaca mulatta (Rhesus macaque)	9544	8/2/2015	35626	Macaca mulatta	9544 9539 9528 9527 314294 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006697	Herminiimonas arsenicoxydans	204773	7/30/2015	3272	Herminiimonas arsenicoxydans	204773 303379 75682 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006701	Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	344612	7/30/2015	9140	Aspergillus clavatus NRRL 1	344612 5057 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000229	Pseudomonas mendocina (strain ymp)	399739	8/7/2015	4563	Pseudomonas mendocina ymp	399739 300 136841 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002277	Pan troglodytes (Chimpanzee)	9598	8/2/2015	20132	Pan troglodytes	9598 9596 207598 9604 314295 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002279	Ornithorhynchus anatinus (Duckbill platypus)	9258	8/2/2015	23553	Ornithorhynchus anatinus	9258 9257 9256 9255 9254 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000230	Enterobacter sp. (strain 638)	399742	7/30/2015	4236	Enterobacter sp. 638	399742 547 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000256	Caldicellulosiruptor saccharolyticus (strain ATCC 43494 / DSM 8903 / Tp8T 6331)	351627	7/30/2015	2629	Caldicellulosiruptor saccharolyticus DSM 8903	351627 44001 44000 543371 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000002287	Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))	269482	7/30/2015	7409	Burkholderia vietnamiensis G4	269482 60552 87882 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000009328	Wickerhamomyces ciferrii (strain F-60-10 / ATCC 14091 / CBS 111 / JCM 3599 / NBRC 0793 / NRRL Y-1031) (Yeast) (Pichia ciferrii)	1206466	7/30/2015	6698	Wickerhamomyces ciferrii NRRL Y-1031	1206466 1041607 599737 115784 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000242	Metallosphaera sedula (strain ATCC 51363 / DSM 5348)	399549	7/30/2015	2256	Metallosphaera sedula DSM 5348	399549 43687 41980 118883 2281 183924 28889 2157 131567	Archaea	
UP000000235	Salinispora tropica (strain ATCC BAA-916 / DSM 44818 / CNB-440)	369723	7/30/2015	4522	Salinispora tropica CNB-440	369723 168695 168694 28056 85008 1760 201174 2 131567	Bacteria	Actinobacteria
UP000009338	Providencia rettgeri Dmel1	1141663	7/27/2015	3847	Providencia rettgeri Dmel1	1141663 587 586 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006695	Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	351605	7/30/2015	4255	Geobacter uraniireducens Rf4	351605 351604 28231 213422 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000233	Pseudomonas stutzeri (strain A1501)	379731	7/30/2015	4092	Pseudomonas stutzeri A1501	379731 316 578833 136846 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006694	Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) (Cytophaga johnsonae)	376686	8/2/2015	5016	Flavobacterium johnsoniae UW101	376686 986 237 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000248	Dichelobacter nodosus (strain VCS1703A)	246195	7/30/2015	1273	Dichelobacter nodosus VCS1703A	246195 870 869 868 135615 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001566	Synechococcus sp. (strain WH7803)	32051	7/30/2015	2530	Synechococcus sp. WH	32051 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000000245	Acidiphilium cryptum (strain JF-5)	349163	7/30/2015	3521	Acidiphilium cryptum JF-5	349163 524 522 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001994	Bradyrhizobium sp. (strain ORS278)	114615	7/30/2015	6701	Bradyrhizobium sp. ORS 278	114615 374 41294 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001568	Ostreococcus lucimarinus (strain CCE9901)	436017	7/30/2015	7403	Ostreococcus lucimarinus CCE9901	436017 242159 70447 1525212 13792 1035538 3152 3041 33090 2759 131567	eukaryotes	
UP000006556	Pelotomaculum thermopropionicum (strain DSM 13744 / JCM 10971 / SI)	370438	7/30/2015	2884	Pelotomaculum thermopropionicum SI	370438 110500 191373 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes

UP000001565	Orientia tsutsugamushi (strain Boryong) (Rickettsia tsutsugamushi)	357244	7/30/2015	966	Orientia tsutsugamushi str. Boryong	357244 784 69474 33988 775 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000231	Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1)	312153	7/30/2015	2074	Polynucleobacter necessarius subsp. asymbioticus QLW-P1DMWA-1	312153 576611 576610 44013 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000243	Streptococcus suis (strain 05ZYH33)	391295	7/30/2015	2178	Streptococcus suis 05ZYH33	391295 1307 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000019265	Spiroplasma sabaudiense Ar-1343	1276257	7/27/2015	924	Spiroplasma sabaudiense Ar-1343	1276257 216944 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000001989	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	392499	7/30/2015	5313	Sphingomonas wittichii RW1	392499 160791 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000019267	Spiroplasma culicicola AES-1	1276246	7/27/2015	1071	Spiroplasma culicicola AES-	1276246 216935 2132 2131 186328 31969 544448 2 131567	Bacteria	Tenericutes
UP000001986	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	441771	8/14/2015	3590	Clostridium botulinum A str. Hall	441771 36826 1491 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001993	Psychrobacter sp. (strain PRwf-1)	349106	7/30/2015	2339	Psychrobacter sp. PRwf-1	349106 497 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001992	Methanobrevibacter smithii (strain PS / ATCC 35061 / DSM 861)	420247	7/30/2015	1783	Methanobrevibacter smithii ATCC 35061	420247 2173 2172 2159 2158 183925 28890 2157 131567	Archaea	
UP000006394	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	402612	7/30/2015	2421	Flavobacterium psychrophilum JIP02/86	402612 96345 237 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000009399	Mycoplasma hyorhinis SK76	1118964	7/27/2015	751	Mycoplasma hyorhinis	1118964 2100 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000001572	Alkaliphilus metalliredigens (strain QYMF)	293826	7/30/2015	4467	Alkaliphilus metalliredigens QYMF	293826 208226 114627 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001991	Lactobacillus reuteri (strain DSM 20016)	557436	7/30/2015	1865	Lactobacillus reuteri DSM 20016	557436 1598 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000006554	Roseiflexus sp. (strain RS-1)	357808	7/30/2015	4494	Roseiflexus sp. RS-1	357808 120961 1508635 1508595 32064 32061 200795 2 131567	Bacteria	Chloroflexi
UP000001996	Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) (Yeast) (Saccharomyces elongisporus)	379508	7/30/2015	5779	Lodderomyces elongisporus NRRL YB-4239	379508 36914 36913 1535325 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001997	Meyerozyma guilliermondii (strain ATCC 6260 / CBS 566 / DSM 6381 / JCM 1539 / NBRC 10279 / NRRL Y-324) (Yeast) (Candida guilliermondii)	294746	8/2/2015	5919	Meyerozyma guilliermondii ATCC 6260	294746 4929 766728 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000565	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) (Clostridium acetobutylicum)	290402	7/30/2015	5003	Clostridium beijerinckii NCIMB 8052	290402 1520 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001116	Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	266940	7/30/2015	4674	Kineococcus radiotolerans SRS30216 = ATCC BAA-149	266940 131568 33981 83778 622452 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001118	Nitratiruptor sp. (strain SB155-2)	387092	7/30/2015	1843	Nitratiruptor sp. SB155-2	387092 269258 34035 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006378	Sulfurovum sp. (strain NBC37-1)	387093	7/30/2015	2433	Sulfurovum sp. NBC37-1	387093 265570 34035 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006382	Anaeromyxobacter sp. (strain Fw109-5)	404589	7/30/2015	4461	Anaeromyxobacter sp. Fw109-5	404589 161492 1524215 80811 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001106	Methanococcus aeolicus (strain Nankai-3 / ATCC BAA-1280)	419665	7/30/2015	1490	Methanococcus aeolicus Nankai-3	419665 42879 2184 2183 2182 183939 28890 2157 131567	Archaea	
UP000001114	Actinobacillus succinogenes (strain ATCC 55618 / 130Z)	339671	8/3/2015	2077	Actinobacillus succinogenes 130Z	339671 67854 713 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001113	Marinomonas sp. (strain MWYL1)	400668	7/30/2015	4416	Marinomonas sp. MWYL1	400668 28253 135620 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002861	Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	435590	7/30/2015	3982	Bacteroides vulgatus ATCC 8482	435590 821 816 815 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001119	Rotavirus A (isolate Monkey/South Africa/SA11-H96/1958 G3-P5B[2]-I2-R2-C5-M5-A5-N5-T5-E2-H5) (RV-A) (Simian Agent 11 (isolate SI/South Africa/H96/58))	450149	7/30/2015	12	Simian rotavirus A/SA11-H96	450149 10923 444184 28875 10912 689832 10880 35325 10239	Vruses	
UP000002415	Fervidobacterium nodosum (strain ATCC 35602 / DSM 5306 / Rt17-B1)	381764	7/30/2015	1725	Fervidobacterium nodosum Rt17-B1	381764 2424 2422 1643950 2419 188708 200918 2 131567	Bacteria	Thermotogae
UP000006377	Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966)	402881	7/30/2015	3580	Parvibaculum lavamentivorans DS-1	402881 256618 256616 119043 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002418	Bdellovibrio phage phiMH2K (Bacteriophage phiMH2K)	145579	7/27/2015	11	Bdellovibrio phage phiMH2K	145579 10856 686565 10841 29258 10239	Vruses	
UP000001115	Synechococcus sp. (strain RCC307)	316278	7/30/2015	2528	Synechococcus sp.	316278 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000032900	Geofilum rubicundum JCM 15548	1236989	7/27/2015	4411	Geofilum rubicundum JCM 15548	1236989 472113 1236988 558415 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002417	Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	78245	7/30/2015	4971	Xanthobacter autotrophicus Py2	78245 280 279 335928 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000566	Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	435591	7/30/2015	3830	Parabacteroides distasonis ATCC 8503	435591 823 375288 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001110	Thermosipho melanesiensis (strain DSM 12029 / CIP 104789 / BI429)	391009	7/31/2015	1877	Thermosipho melanesiensis BI429	391009 46541 2420 1643950 2419 188708 200918 2 131567	Bacteria	Thermotogae
UP000001582	Pseudomonas aeruginosa (strain PA7)	381754	7/30/2015	6246	Pseudomonas aeruginosa PA7	381754 287 136841 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002407	Campylobacter hominis (strain ATCC BAA-381 / LMG 19568 / NCTC 13146 / CH001A)	360107	7/30/2015	1687	Campylobacter hominis ATCC BAA-381	360107 76517 194 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000019325	Nodularia spumigena CCY9414	313624	7/27/2015	5211	Nodularia spumigena CCY9414	313624 70799 159191 1162 1161 1117 2 131567	Bacteria	Cyanobacteria

UP000002301	Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	439375	7/30/2015	4757	Ochrobactrum anthropi ATCC 49188	439375 529 528 118882 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000006380	Campylobacter curvus (strain 525.92)	360105	7/30/2015	1928	Campylobacter curvus 525.92	360105 200 194 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002408	Methanoregula boonei (strain 6A8)	456442	7/30/2015	2450	Methanoregula boonei 6A8	456442 358766 395331 1198451 2191 224756 28890 2157 131567	Archaea	
UP000002411	Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	431943	7/30/2015	3828	Clostridium kluyveri DSM 555	431943 1534 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002300	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	315749	8/7/2015	3840	Bacillus cytotoxicus NVH 391-98	315749 580165 86661 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000000265	Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	272620	7/30/2015	5126	Klebsiella pneumoniae subsp. pneumoniae MGH 78578	272620 72407 573 570 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019375	Zygosaccharomyces bailii (strain CLIB 213 / ATCC 58445 / CBS 680 / CCRC 21525 / NBRC 1098 / NCYC 1416 / NRRL Y-2227)	1333698	7/30/2015	4722	Zygosaccharomyces bailii CLIB 213	1333698 4954 4953 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000260	Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	290339	7/30/2015	4421	Cronobacter sakazakii ATCC BAA-894	290339 28141 413496 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000262	Ignicoccus hospitalis (strain KIN4/I / DSM 18386 / JCM 14125)	453591	7/30/2015	1434	Ignicoccus hospitalis KIN4/I	453591 160233 54258 2272 114380 183924 28889 2157 131567	Archaea	
UP000019376	Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	933388	7/30/2015	9977	Penicillium oxalicum 114-2	933388 69781 5073 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001131	Streptococcus gordonii (strain Challis / ATCC 35105 / CH1 / DL1 / V288)	29390	7/30/2015	2050	Streptococcus gordonii str. Challis	29390 1302 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000007074	Serratia proteamaculans (strain 568)	399741	7/30/2015	4930	Serratia proteamaculans	399741 28151 613 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019373	Endocarpon pusillum (strain Z07020 / HMAS-L-300199) (Lichen-forming fungus)	1263415	7/30/2015	9228	Endocarpon pusillum Z07020	1263415 364733 364710 146292 146291 451870 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001355	Bacillus pumilus (strain SAFR-032)	315750	7/30/2015	3675	Bacillus pumilus SAFR-032	315750 1408 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001134	Acanthamoeba polyphaga mimivirus (APMV)	212035	7/27/2015	909	Acanthamoeba polyphaga mimivirus	212035 315393 549779 35237 10239	Vruses	
UP000002608	Shewanella pealeana (strain ATCC 700345 / ANG-SQ1)	398579	7/30/2015	4181	Shewanella pealeana ATCC 700345	398579 70864 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019374	Ophiocordyceps sinensis (strain Co18 / CGMCC 3.14243) (Yarsagumba caterpillar fungus) (Hirsutella sinensis)	911162	7/30/2015	6968	Ophiocordyceps sinensis CO18	911162 72228 474995 474942 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008148	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	290338	7/30/2015	5019	Citrobacter koseri ATCC BAA-895	290338 545 544 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019377	Pseudozyma brasiliensis (strain GHG001) (Yeast)	1392244	7/30/2015	5765	Pseudozyma brasiliensis	1392244 63298 85578 5268 5267 5257 452284 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000001137	Caldivirga maquilingensis (strain ATCC 700844 / DSM 13496 / JCM 10307 / IC-167)	397948	7/30/2015	1962	Caldivirga maquilingensis IC-167	397948 76887 76886 2267 2266 183924 28889 2157 131567	Archaea	
UP000001313	Frankia sp. (strain EAN1pec)	298653	7/30/2015	7133	Frankia sp. EAN1pec	298653 1854 74712 85013 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000268	Acaryochloris marina (strain MBIC 11017)	329726	7/30/2015	8172	Acaryochloris marina MBIC11017	329726 155978 155977 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000000269	Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	350688	7/30/2015	2828	Alkaliphilus oremlandii OhILAs	350688 461876 114627 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000270	Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	438753	7/30/2015	4708	Azorhizobium caulinodans ORS 571	438753 7 6 335928 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008561	Desulfococcus oleovorans (strain DSM 6200 / Hxd3)	96561	7/30/2015	3255	Desulfococcus oleovorans Hxd3	96561 181663 896 213119 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000781	Sulcia muelleri (strain GWSS)	444179	7/30/2015	227	Candidatus Sulcia muelleri GWSS	444179 336810 336809 313602 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002016	Pseudothermotoga lettingae (strain ATCC BAA-301 / DSM 14385 / NBRC 107922 / TMO) (Thermotoga lettingae)	416591	7/30/2015	2040	Pseudothermotoga lettingae TMO	416591 177758 1643951 188709 2419 188708 200918 2 131567	Bacteria	Thermotogae
UP000001151	Enterococcus phage phiEF24C (Enterococcus bacteriophage phi-EF24C)	442493	7/27/2015	221	Enterococcus phage phiEF24C	442493 1232680 857473 10662 28883 35237 10239	Vruses	
UP000000784	Delftia acidovorans (strain DSM 14801 / SPH-1)	398578	7/30/2015	5968	Delftia acidovorans SPH-1	398578 80866 80865 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007065	Mycoplasma agalactiae (strain PG2)	347257	7/30/2015	726	Mycoplasma agalactiae	347257 2110 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000000787	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	316274	7/30/2015	5254	Herpetosiphon aurantiacus DSM 785	316274 65 64 189773 189772 32061 200795 2 131567	Bacteria	Chloroflexi
UP000032941	Burkholderia cepacia JBK9	1395570	7/27/2015	4698	Burkholderia cepacia JBK9	1395570 292 87882 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001312	Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum)	665079	7/30/2015	14400	Sclerotinia sclerotiorum 1980 UF-70	665079 5180 5179 28983 5178 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000267	Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) (Kluyveromyces polysporus)	436907	7/30/2015	5353	Vanderwaltozyma polyspora DSM 70294	436907 36033 374469 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000789	Petrotoga mobilis (strain DSM 10674 / SJ95)	403833	7/30/2015	1890	Petrotoga mobilis SJ95	403833 69499 28236 1643949 1643947 188708 200918 2 131567	Bacteria	Thermotogae
UP000001136	Arcobacter butzleri (strain RM4018)	367737	7/30/2015	2254	Arcobacter butzleri RM4018	367737 28197 28196 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006833	Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12)	398580	7/30/2015	4086	Dinoroseobacter shibae DFL 12 = DSM 16493	398580 215813 309512 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria

UP000000788	Prochlorococcus marinus (strain MIT 9211)	93059	8/2/2015	1855	Prochlorococcus marinus str. MIT 9211	93059 1219 1218 1217 1212 1117 2 131567	Bacteria	Cyanobacteria
UP000002082	Pseudomonas phage LUZ24	484895	7/27/2015	68	Pseudomonas phage	484895 545932 10744 28883 35237 10239	Vruses	
UP000000792	Nitrosopumilus maritimus (strain SCM1)	436308	7/30/2015	1795	Nitrosopumilus maritimus SCM1	436308 338192 338191 338190 31932 651137 2157 131567	Archaea	
UP000000790	Lactobacillus helveticus (strain DPC 4571)	405566	7/30/2015	1580	Lactobacillus helveticus DPC 4571	405566 1587 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002084	Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	41514	8/11/2015	4500	Salmonella enterica subsp. arizonae serovar 62:z4,z23:-	41514 59203 28901 590 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000370	Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) (Lachnoclostridium phytofermentans)	357809	7/30/2015	3891	Lachnoclostridium phytofermentans ISDg	357809 66219 1506553 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002139	Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	448385	7/30/2015	9320	Sorangium cellulosum So ce56	448385 56 39643 49 80812 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001176	Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5)	272568	7/30/2015	3783	Gluconacetobacter diazotrophicus PA1 5	272568 33996 89583 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008558	Acholeplasma laidlawii (strain PG-8A)	441768	7/30/2015	1380	Acholeplasma laidlawii PG-8A	441768 2148 2147 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000002006	Enterobacteria phage Phieco32 (Escherichia coli phage phi32)	490103	7/27/2015	128	Enterobacteria phage Phieco32	490103 680277 10744 28883 35237 10239	Vruses	
UP000002083	Pseudomonas phage YuA	462590	7/27/2015	77	Pseudomonas phage YuA	462590 1299429 10699 28883 35237 10239	Vruses	
UP000002007	Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	288705	7/30/2015	3421	Renibacterium salmoninarum ATCC 33209	288705 1646 1645 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002008	Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl)	324602	7/30/2015	3850	Chloroflexus aurantiacus J-10-fl	324602 1108 1107 1106 1508594 32064 32061 200795 2 131567	Bacteria	Chloroflexi
UP000001510	Microcystis aeruginosa (strain NIES-843)	449447	7/30/2015	5981	Microcystis aeruginosa NIES-843	449447 1126 1125 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000001316	Caulobacter sp. (strain K31)	366602	7/30/2015	5373	Caulobacter sp. K31	366602 75 76892 204458 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001318	Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	31964	7/30/2015	3058	Clavibacter michiganensis subsp. sepedonicus	31964 28447 1573 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001319	Finegoldia magna (strain ATCC 29328) (Peptostreptococcus magnus)	334413	7/30/2015	1813	Finegoldia magna ATCC 29328	334413 1260 150022 1570339 1737405 1737404 1239 2 131567	Bacteria	Firmicutes
UP000008550	Heliobacterium modesticaldum (strain ATCC 51547 / Ice1)	498761	7/30/2015	2922	Heliobacterium modesticaldum Ice1	498761 35701 2697 31984 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001185	Methylobacterium sp. (strain 4-46)	426117	7/30/2015	6647	Methylobacterium sp. 4-46	426117 407 119045 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001179	Halomonas phage phiHAP-1 (isolate -/Gulf of Mexico/-/2001) (Bacteriophage phiHAP-1)	1283337	7/27/2015	46	Halomonas phage phiHAP-1 Gulf of Mexico/-/2001	1283337 499235 1198976 10662 28883 35237 10239	Vruses	
UP000008543	Histophilus somni (strain 2336) (Haemophilus somnus)	228400	7/30/2015	1971	Haemophilus somnus 2336	228400 731 214906 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001225	Bordetella petrii (strain ATCC BAA-461 / DSM 12804 / CCUG 43448)	340100	7/30/2015	4912	Bordetella petrii DSM 12804	340100 94624 517 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001357	Monosiga brevicollis (Choanoflagellate)	81824	7/30/2015	9188	Monosiga brevicollis	81824 81525 81524 28009 33154 2759 131567	eukaryotes	
UP000002156	Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	340099	7/30/2015	2193	Thermoanaerobacter pseudethanolicus ATCC 33223	340099 496866 1754 186814 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000001593	Nematostella vectensis (Starlet sea anemone)	45351	7/30/2015	24435	Nematostella vectensis	45351 45350 45349 6103 6102 6101 6073 6072 33208 33154 2759 131567	eukaryotes	
UP000008544	Desulforudis audaxviator (strain MP104C)	477974	7/30/2015	2136	Candidatus Desulforudis audaxviator MP104C	477974 471827 471826 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002164	Lysinibacillus sphaericus (strain C3-41)	444177	7/30/2015	4750	Lysinibacillus sphaericus C3-41	444177 1421 400634 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000002168	Shewanella woodyi (strain ATCC 51908 / MS32)	392500	7/30/2015	4865	Shewanella woodyi ATCC 51908	392500 60961 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001847	Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris)	456481	7/30/2015	3723	Leptospira biflexa serovar Patoc strain 'Patoc 1 (Paris)'	456481 145259 172 171 170 1643688 203692 203691 2 131567	Bacteria	Spirochaetes
UP000002166	Leuconostoc citreum (strain KM20)	349519	7/30/2015	1812	Leuconostoc citreum KM20	349519 33964 1243 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008030	Spodoptera frugiperda ascovirus 1a (SfAV-1a)	113370	7/30/2015	123	Spodoptera frugiperda ascovirus 1a	113370 43680 43682 35237 10239	Vruses	
UP000009294	Human herpesvirus 1 (strain 17) (HHV-1) (Human herpes simplex virus 1)	10299	7/30/2015	73	Herpes simplex virus (type 1 / strain 17)	10299 10298 10294 10293 10292 548681 35237 10239	Vruses	
UP000009295	Human herpesvirus 6A (strain Uganda-1102) (HHV-6 variant A) (Human B lymphotropic virus)	10370	7/30/2015	103	Human herpesvirus 6 (strain Uganda-1102)	10370 32603 40272 10357 10292 548681 35237 10239	Vruses	
UP000000587	Saimiriine herpesvirus 2 (strain 11) (SaHV-2) (Herpesvirus saimiri)	10383	7/30/2015	75	Herpesvirus saimiri (strain 11)	10383 10381 10379 10374 10292 548681 35237 10239	Vruses	
UP000001686	Korarchaeum cryptofilum (strain OPF8)	374847	7/30/2015	1602	Candidatus Korarchaeum cryptofilum OPF8	374847 498846 498845 51967 2157 131567	Archaea	
UP000006582	Polynucleobacter necessarius subsp. necessarius (strain STIR1)	452638	7/30/2015	1507	Polynucleobacter necessarius subsp. necessarius STIR1	452638 44014 576610 44013 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001693	Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) (Leptothrix discophora (strain SP-6))	395495	7/30/2015	4343	Leptothrix cholodnii SP-6	395495 34029 88 224471 119065 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001691	Uncultured termite group 1 bacterium phylotype Rs-D17	471821	7/27/2015	767	uncultured Termite group 1 bacterium phylotype Rs-D17	471821 167965 99260 74152 2 131567	Bacteria	Elusimicrobia

UP000009297	Ajellomyces capsulatus (strain NAm1 / WU24) (Darling's disease fungus) (Histoplasma capsulatum)	339724	7/30/2015	9252	Histoplasma capsulatum NAm1	339724 5037 5036 299071 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001192	Burkholderia phymatum (strain DSM 17167 / STM815)	391038	7/30/2015	7461	Burkholderia phymatum STM815	391038 148447 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000007013	Opitutus terrae (strain DSM 11246 / PB90-1)	452637	7/30/2015	4588	Opitutus terrae PB90-1	452637 107709 178440 134623 415000 414999 74201 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000001190	Mycobacterium marinum (strain ATCC BAA-535 / M)	216594	8/7/2015	5418	Mycobacterium marinum M	216594 1781 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001191	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	63737	7/30/2015	6573	Nostoc punctiforme PCC 73102	63737 272131 1177 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000001695	Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	395963	7/30/2015	3774	Beijerinckia indica subsp. indica ATCC 9039	395963 31994 533 532 45404 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001688	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	32049	7/30/2015	3179	Synechococcus sp. PCC 7002	32049 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000007137	Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	561007	8/25/2015	4940	Mycobacterium abscessus ATCC 19977	561007 36809 670506 670516 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006589	Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	426355	7/30/2015	6388	Methylobacterium radiotolerans JCM 2831	426355 31998 407 119045 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001861	Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) (Inky cap fungus) (Hormographiella aspergillata)	240176	7/30/2015	13335	Coprinopsis cinerea okayama7#130	240176 5346 184431 184208 5338 452333 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000001683	Natranaerobius thermophilus (strain ATCC BAA-1301 / DSM 18059 / JW/NM-WN-LF)	457570	7/30/2015	2847	Natranaerobius thermophilus JW/NM-WN-LF	457570 375929 375928 485255 485256 186801 1239 2 131567	Bacteria	Firmicutes
UP000001681	Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	262543	7/30/2015	3005	Exiguobacterium sibiricum 255-15	262543 332410 33986 539742 539002 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001029	Elusimicrobium minutum (strain Pei191)	445932	7/30/2015	1528	Elusimicrobium minutum Pei191	445932 423605 423604 641876 641854 641853 74152 2 131567	Bacteria	Elusimicrobia
UP000008838	Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)	378753	8/3/2015	2352	Kocuria rhizophila DC2201	378753 72000 57493 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001194	Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) (Bicoloured deceiver) (Laccaria laccata var. bicolor)	486041	7/30/2015	17895	Laccaria bicolor S238N-H82	486041 29883 29882 5351 5338 452333 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000001685	Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	455632	8/7/2015	7008	Streptomyces griseus subsp. griseus NBRC 13350	455632 67263 1911 1482596 629295 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008840	Stenotrophomonas maltophilia (strain K279a)	522373	7/30/2015	4365	Stenotrophomonas maltophilia K279a	522373 40324 995085 40323 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001031	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	349741	7/30/2015	2137	Akkermansia muciniphila ATCC BAA-835	349741 239935 239934 1647988 48461 203494 74201 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000008837	Malassezia globosa (strain ATCC MYA-4612 / CBS 7966) (Dandruff-associated fungus)	425265	7/30/2015	4274	Malassezia globosa CBS 7966	425265 76773 55193 742845 162474 1538075 452284 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000001195	Clostridium botulinum (strain Eklund 17B / Type B)	935198	8/14/2015	3473	Clostridium botulinum B str. Eklund 17B (NRP)	935198 36827 1491 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001201	Sulfurihydrogenibium sp. (strain YO3AOP1)	436114	7/30/2015	1712	Sulfurihydrogenibium sp. YO3AOP1	436114 212790 224027 32069 187857 200783 2 131567	Bacteria	Aquificae
UP000001203	Cyanothece sp. (strain ATCC 51142)	43989	7/30/2015	5239	Cyanothece sp. ATCC	43989 43988 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000009149	Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	481448	7/30/2015	2470	Methylacidiphilum infernorum V4	481448 511746 511745 717964 717963 326457 74201 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000033031	Citrobacter farmeri GTC 1319	1114922	7/30/2015	4558	Citrobacter farmeri GTC 1319	1114922 67824 544 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001741	Acinetobacter baumannii (strain SDF)	509170	7/30/2015	2767	Acinetobacter baumannii SDF	509170 470 909768 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033046	Verrucomicrobia bacterium IMCC26134	1637999	7/27/2015	2622	Verrucomicrobia bacterium IMCC26134	1637999 417295 326457 74201 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000001227	Amoebophilus asiaticus (strain 5a2)	452471	8/2/2015	1253	Candidatus Amoebophilus asiaticus 5a2	452471 281120 281119 1501348 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002420	Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	398767	7/30/2015	3644	Geobacter lovleyi SZ	398767 313985 28231 213422 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001228	Chlorobium phaeobacteroides (strain BS1)	331678	7/30/2015	2434	Chlorobium phaeobacteroides BS1	331678 1096 1091 274493 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001197	Podospora anserina (strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) (Pleurage anserina)	515849	7/30/2015	10527	Podospora anserina S mat+	515849 5145 5144 42302 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000033048	Methanococcoides methylutens MM1	1434104	7/27/2015	2203	Methanococcoides methylutens MM1	1434104 2226 2225 2206 94695 224756 28890 2157 131567	Archaea	
UP000033049	Methanosarcina sp. MTP4	1434100	7/27/2015	3238	Methanosarcina sp. MTP4	1434100 2207 2206 94695 224756 28890 2157 131567	Archaea	
UP000001594	Fowl adenovirus A serotype 1 (strain CELO / Phelps) (FAdV-1) (Avian adenovirus gal1 (strain Phelps))	10553	7/30/2015	38	Fowl adenovirus 1	10553 190061 10552 10508 35237 10239	Vruses	
UP000033070	Ferriphaselus amnicola	1188319	7/27/2015	2638	Ferriphaselus amnicola	1188319 1443590 90627 713636 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001205	Borrelia turicatae (strain 91E135)	314724	7/30/2015	818	Borrelia turicatae 91E135	314724 142 138 1643685 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000001036	Cellvibrio japonicus (strain Ueda107) (Pseudomonas fluorescens subsp. cellulosa)	498211	7/30/2015	3711	Cellvibrio japonicus Ueda107	498211 155077 10 1706371 1706369 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001207	Bacillus phage phi29 (Bacteriophage phi-29)	10756	7/27/2015	27	Bacillus phage phi29	10756 186846 542836 10744 28883 35237 10239	Vruses	
UP000033067	Pseudoxanthomonas suwonensis	314722	7/27/2015	3063	Pseudoxanthomonas suwonensis	314722 83618 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria

UP000008812	Mycoplasma arthritidis (strain 158L3-1)	243272	7/30/2015	631	Mycoplasma arthritidis 158L3-1	243272 2111 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000001726	Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	338565	7/30/2015	3618	Erwinia tasmaniensis	338565 551 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001035	Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) (Burkholderia cepacia (strain J2315))	216591	7/30/2015	6993	Burkholderia cenocepacia J2315	216591 95486 87882 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000008810	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	15368	8/2/2015	29942	Brachypodium distachyon	15368 15367 147385 147368 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000001208	Chloroherpeton thalassium (strain ATCC 35110 / GB-78)	517418	7/30/2015	2708	Chloroherpeton thalassium ATCC 35110	517418 100716 100715 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000033072	Methanosarcina lacustris Z-7289	1434111	7/30/2015	3201	Methanosarcina lacustris Z-7289	1434111 170861 2207 2206 94695 224756 28890 2157 131567	Archaea	
UP000031513	Plasmodium knowlesi (strain H)	5851	7/30/2015	5100	Plasmodium knowlesi strain H	5851 5850 418103 5820 1639119 5819 422676 5794 33630 2759 131567	eukaryotes	
UP000033094	Blochmannia endosymbiont of Polyrhachis (Hedomyrma) turneri	1505596	8/4/2015	589	Blochmannia endosymbiont of Polyrhachis (Hedomyrma) turneri	1505596 711328 203804 84564 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033103	Sneathia sp. Sn35	1069640	7/27/2015	1182	Sneathia sp. Sn35	1069640 168808 1129771 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000001727	Corynebacterium urealyticum (strain ATCC 43042 / DSM 7109)	504474	7/30/2015	2011	Corynebacterium urealyticum DSM 7109	504474 43771 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033109	Pontibacter korlensis	400092	7/27/2015	4103	Pontibacter korlensis	400092 323449 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002566	Ralstonia pickettii (strain 12J)	402626	7/30/2015	4890	Ralstonia pickettii 12J	402626 329 48736 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000033104	Blochmannia endosymbiont of Camponotus (Colobopsis) obliquus	1505597	7/27/2015	584	Blochmannia endosymbiont of Camponotus (Colobopsis) obliquus	1505597 711328 203804 84564 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019426	Clostridium bornimense	1216932	8/4/2015	3269	Clostridium bornimense	1216932 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000019423	Hymenobacter swuensis DY53	1227739	7/27/2015	4612	Hymenobacter swuensis DY53	1227739 1446467 89966 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000033121	Flavihumibacter petaseus NBRC 106054	1220578	7/27/2015	4759	Flavihumibacter petaseus NBRC 106054	1220578 549295 1004301 563835 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002724	Pelodictyon phaeoclathratiforme (strain DSM 5477 / BU-1)	324925	7/30/2015	2685	Pelodictyon phaeoclathratiforme BU-1	324925 34090 1099 274493 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002725	Prosthecochloris aestuarii (strain DSM 271 / SK 413)	290512	7/30/2015	2319	Prosthecochloris aestuarii DSM 271	290512 1102 1101 191412 191411 191410 1090 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000019442	Halorhodospira halochloris str. A	1354791	7/27/2015	2964	Halorhodospira halochloris str. A	1354791 1052 85108 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001863	Sputnik virophage	543939	7/27/2015	21	Sputnik virophage	543939 552364 10239	Vruses	
UP000019430	Campylobacter coli RM4661	1183379	7/30/2015	1815	Campylobacter coli	1183379 195 194 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001868	Phenylobacterium zucineum (strain HLK1)	450851	7/30/2015	3838	Phenylobacterium zucineum HLK1	450851 284016 20 76892 204458 28211 1224 2 131567	Bacteria	Proteobacteria
UP000019443	Rhizobium sp. LPU83	348824	8/4/2015	7493	Rhizobium sp. LPU83	348824 379 227290 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008825	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	404380	7/30/2015	4042	Geobacter bemidjiensis Bem	404380 225194 28231 213422 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001870	Alteromonas macleodii (strain DSM 17117 / Deep ecotype)	314275	7/30/2015	3938	Alteromonas macleodii str. 'Deep ecotype'	314275 28108 226 72275 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008820	Aedes aegypti (Yellowfever mosquito) (Culex aegypti)	7159	8/2/2015	16654	Aedes aegypti	7159 53541 7158 1056966 43817 7157 41827 43786 7148 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001872	Hydrogenobaculum sp. (strain Y04AAS1)	380749	7/30/2015	1626	Hydrogenobaculum sp. Y04AAS1	380749 168657 64898 32069 187857 200783 2 131567	Bacteria	Aquificae
UP000019450	Candidatus Hepatoplasma crinochetorum Av	1427984	7/27/2015	582	Candidatus Hepatoplasma crinochetorum Av	1427984 295596 295595 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000019474	Lactobacillus florum 8D	1221538	7/27/2015	1228	Lactobacillus florum 8D	1221538 640331 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008321	Salmonella gallinarum (strain 287/91 / NCTC 13346)	550538	7/30/2015	3943	Salmonella enterica subsp. enterica serovar Gallinarum str. 287/91	550538 594 59201 28901 590 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033166	Lactococcus piscium MKFS47	297352	8/4/2015	2361	Lactococcus piscium MKFS47	297352 1364 1357 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000718	Thermodesulfovibrio yellowstonii (strain ATCC 51303 / DSM 11347 / YP87)	289376	7/30/2015	1982	Thermodesulfovibrio yellowstonii DSM 11347	289376 28262 28261 189779 189778 203693 40117 2 131567	Bacteria	Nitrospirae
UP000000624	African swine fever virus (strain Badajoz 1971 Vero-adapted) (Ba71V) (ASFV)	10498	7/30/2015	152	African swine fever virus BA71V	10498 10497 39743 137992 35237 10239	Vruses	
UP000008319	Proteus mirabilis (strain HI4320)	529507	7/30/2015	3661	Proteus mirabilis HI4320	529507 584 583 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001732	Coprothermobacter proteolyticus (strain ATCC 35245 / DSM 5265 / BT)	309798	7/30/2015	1481	Coprothermobacter proteolyticus DSM 5265	309798 35786 68335 227387 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000008333	Plasmodium vivax (strain Salvador I)	126793	7/30/2015	5389	Plasmodium vivax Sal-1	126793 5855 418103 5820 1639119 5819 422676 5794 33630 2759 131567	eukaryotes	
UP000002019	Cloacimonas acidaminovorans (strain Evry)	459349	7/30/2015	1813	Candidatus Cloacimonas acidaminovorans str. Evry	459349 456827 456826 456828 2323 2 131567	Bacteria	Unclassified Bacteria
UP000008323	Phytoplasma australiense	59748	7/27/2015	633	Candidatus Phytoplasma australiense	59748 85632 33926 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes

UP000002020	Phytoplasma mali (strain AT)	482235	7/30/2015	448	Candidatus Phytoplasma mali AT	482235 37692 85630 33926 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000001590	Bacillus phage SP01 (Bacteriophage SP01)	10685	7/27/2015	204	Bacillus phage SPO1	10685 140409 857473 10662 28883 35237 10239	Vruses	
UP000001591	Rhodospirillum centenum (strain ATCC 51521 / SW)	414684	7/30/2015	3984	Rhodospirillum centenum SW	414684 34018 1081 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001471	Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis)	426418	7/30/2015	12062	Pyrenophora tritici-repentis Pt-1C-BFP	426418 45151 5027 28556 715340 92860 451868 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008129	Aerococcus urinae (strain ACS-120-V-Col10a)	866775	7/30/2015	1684	Aerococcus urinae ACS-120-V-Col10a	866775 1376 1375 186827 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008130	Polymorphum gilvum (strain LMG 25793 / CGMCC 1.9160 / SL003B-26A1)	991905	7/30/2015	4354	Polymorphum gilvum SL003B-26A1	991905 991904 991903 82117 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001062	Marinomonas mediterranea (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1)	717774	7/30/2015	4118	Marinomonas mediterranea MMB-1	717774 119864 28253 135620 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019522	Pseudomonas stutzeri (Pseudomonas perfectomarina)	316	7/27/2015	4145	Pseudomonas stutzeri	316 578833 136846 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000723	Azobacteroides pseudotrichonymphae genomovar. CFP2	511995	8/4/2015	847	Candidatus Azobacteroides pseudotrichonymphae genomovar. CFP2	511995 511435 511434 333046 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000008204	Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	41431	7/30/2015	4335	Cyanothece sp. PCC 8801	41431 43988 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000000716	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	360911	7/30/2015	3020	Exiguobacterium sp. AT1b	360911 33986 539742 539002 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000008206	Cyanothece sp. (strain PCC 7822)	497965	7/30/2015	6559	Cyanothece sp. PCC 7822	497965 43988 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000001038	Oryzias latipes (Japanese rice fish) (Japanese killifish)	8090	8/2/2015	24636	Oryzias latipes	8090 8089 8088 47757 28781 76071 1489913 1489908 1489872 123369 123368 123367 123366 123365 1489388 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000000724	Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)	500485	7/30/2015	12788	Penicillium rubens Wisconsin 54-1255	500485 1108849 254878 5073 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000033188	Babesia bigemina	5866	7/27/2015	4432	Babesia bigemina	5866 5864 32594 5863 422676 5794 33630 2759 131567	eukaryotes	
UP000002510	Paenibacillus sp. (strain JDR-2)	324057	7/30/2015	6210	Paenibacillus sp. JDR-2	324057 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000000738	Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) (Micrococcus lysodeikticus)	465515	7/30/2015	2207	Micrococcus luteus NCTC 2665	465515 1270 1269 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007719	Dictyoglomus turgidum (strain Z-1310 / DSM 6724)	515635	7/30/2015	1743	Dictyoglomus turgidum DSM 6724	515635 513050 13 203488 203487 203486 68297 2 131567	Bacteria	Dictyoglomi
UP000001349	Clostridium cellulolyticum (strain ATCC 35319 / DSM 5812 / JCM 6584 / H10)	394503	7/30/2015	3287	[Clostridium] cellulolyticum H10	394503 1521 1508657 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000033187	Candidatus Filomicrobium marinum	1608628	8/4/2015	4045	Candidatus Filomicrobium marinum	1608628 119044 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008207	Methylobacterium nodulans (strain ORS2060 / LMG 21967)	460265	7/30/2015	8128	Methylobacterium nodulans ORS 2060	460265 114616 407 119045 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002505	Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	452863	7/30/2015	4587	Arthrobacter chlorophenolicus A6	452863 85085 1663 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008136	Archaeoglobus veneficus (strain DSM 11195 / SNP6)	693661	7/27/2015	2065	Archaeoglobus veneficus SNP6	693661 58290 2233 2232 2231 183980 28890 2157 131567	Archaea	
UP000008137	Prevotella denticola (strain F0289)	767031	7/30/2015	2380	Prevotella denticola F0289	767031 28129 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000007463	Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	755732	7/30/2015	4016	Fluviicola taffensis DSM 16823	755732 191579 332102 246874 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002509	Plasmodium chabaudi	5825	7/30/2015	14614	Plasmodium chabaudi	5825 418101 5820 1639119 5819 422676 5794 33630 2759 131567	eukaryotes	
UP000008139	Hippea maritima (strain ATCC 700847 / DSM 10411 / MH2)	760142	7/30/2015	1653	Hippea maritima DSM 10411	760142 84405 84404 117942 213113 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000019587	Yersinia enterocolitica LC20	1443113	7/27/2015	5273	Yersinia enterocolitica LC20	1443113 630 629 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008141	Chlorella variabilis (Green alga)	554065	7/30/2015	9831	Chlorella variabilis	554065 3071 35461 35460 75966 3041 33090 2759 131567	eukaryotes	
UP000002511	Cyanothece sp. (strain PCC 7425 / ATCC 29141)	395961	7/30/2015	5232	Cyanothece sp. PCC 7425	395961 43988 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000007721	Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	316067	7/30/2015	3798	Geobacter daltonii FRC-32	316067 1203471 28231 213422 69541 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000033201	Sphingomonas sp. Ant20	104605	7/27/2015	3084	Sphingomonas sp. Ant20	104605 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000019593	Roseibacterium elongatum DSM 19469	1294273	7/27/2015	3433	Roseibacterium elongatum DSM 19469	1294273 159346 159345 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033200	Sphingomonas taxi	1549858	7/27/2015	3401	Sphingomonas taxi	1549858 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000019591	Eubacterium acidaminophilum DSM 3953	1286171	7/27/2015	2843	Eubacterium acidaminophilum DSM 3953	1286171 1731 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000007722	Methanococcus voltae (strain ATCC BAA-1334 / A3)	456320	7/30/2015	1658	Methanococcus voltae A3	456320 2188 2184 2183 2182 183939 28890 2157 131567	Archaea	
UP000002381	Geobacillus sp. (strain Y412MC10)	481743	7/30/2015	6237	Paenibacillus sp.	481743 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000000719	Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562)	373903	7/30/2015	2324	Halothermothrix orenii H 168	373903 31909 32636 972 53433 186801 1239 2 131567	Bacteria	Firmicutes
UP000002384	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	65393	7/30/2015	5656	Cyanothece sp. PCC 7424	65393 43988 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000002383	Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	396588	7/30/2015	3272	Thioalkalivibrio sulfidiphilus HL-EbGr7	396588 1033854 106633 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002382	Kosmotoga olearia (strain TBF 19.5.1)	521045	7/30/2015	2087	Kosmotoga olearia TBF 19.5.1	521045 651457 651456 1643948 1643946 188708 200918 2 131567	Bacteria	Thermotogae

UP000007720	Plasmodium berghei (strain Anka)	5823	7/30/2015	11656	Plasmodium berghei ANKA	5823 5821 418101 5820 1639119 5819 422676 5794 33630 2759 131567	eukaryotes	
UP000002386	Geobacillus sp. (strain WCH70)	471223	7/30/2015	3048	Geobacillus sp. WCH70	471223 129337 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000000271	Bacillus selenitireducens (strain ATCC 700615 / DSM 15326 / MLS10)	439292	7/30/2015	3231	[Bacillus] selenitireducens MLS10	439292 85683 663587 186821 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000002424	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	322710	7/30/2015	4990	Azotobacter vinelandii DJ	322710 354 352 351 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000007727	Campylobacter lari (strain RM2100 / D67 / ATCC BAA-1060)	306263	7/30/2015	1545	Campylobacter lari RM2100	306263 201 194 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000739	Desulfatibacillum alkenivorans (strain AK-01)	439235	7/30/2015	5198	Desulfatibacillum alkenivorans AK-01	439235 259354 218207 213119 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000033202	Sphingomonas changbaiensis NBRC 104936	1219043	7/27/2015	3151	Sphingomonas changbaiensis NBRC 104936	1219043 529705 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000740	Halorubrum lacusprofundi (strain ATCC 49239 / DSM 5036 / JCM 8891 / ACAM 34)	416348	7/30/2015	3495	Halorubrum lacusprofundi ATCC 49239	416348 2247 56688 1644056 1644055 183963 28890 2157 131567	Archaea	
UP000002257	Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	395965	7/30/2015	3816	Methylocella silvestris BL2	395965 199596 120652 45404 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000019656	Gilliamella apicola	1196095	7/27/2015	2784	Gilliamella apicola	1196095 1193503 1240483 1240482 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000742	Anoxybacillus flavithermus (strain DSM 21510 / WK1)	491915	7/30/2015	2819	Anoxybacillus flavithermus WK1	491915 33934 150247 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000000741	Moniliophthora perniciosa (strain FA553 / isolate CP02) (Witches'-broom disease fungus) (Marasmius perniciosus)	554373	7/30/2015	13649	Moniliophthora perniciosa FA553	554373 153609 221102 654221 654128 5338 452333 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000006743	Haemophilus parasuis serovar 5 (strain SH0165)	557723	7/30/2015	2002	Haemophilus parasuis SH0165	557723 738 724 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019675	Lysinibacillus varians	1145276	7/27/2015	4504	Lysinibacillus varians	1145276 400634 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000002598	Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	525146	7/30/2015	2345	Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774	525146 115117 876 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000019668	Snodgrassella alvi wkB2	1196094	7/27/2015	2295	Snodgrassella alvi wkB2	1196094 1196083 1193515 481 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002060	Variola virus (isolate Human/India/Ind3/1967) (VARV) (Smallpox virus)	587200	7/30/2015	199	Variola virus human/India/Ind3/1967	587200 10255 10242 10241 10240 35237 10239	Vruses	
UP000006903	Desulfurococcus kamchatkensis (strain 1221n / DSM 18924)	490899	7/30/2015	1470	Desulfurococcus kamchatkensis 1221n	490899 477693 2273 2272 114380 183924 28889 2157 131567	Archaea	
UP000002456	Bifidobacterium animalis subsp. lactis (strain AD011)	442563	7/30/2015	1525	Bifidobacterium animalis subsp. lactis AD011	442563 302911 28025 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002601	Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763)	526222	7/30/2015	3807	Desulfovibrio salexigens DSM 2638	526222 880 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002602	Varicella-zoster virus (strain Dumas) (HHV-3) (Human herpesvirus 3)	10338	7/30/2015	69	Human herpesvirus 3 strain Dumas	10338 10335 10319 10293 10292 548681 35237 10239	Vruses	
UP000002457	Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	521011	7/30/2015	2655	Methanosphaerula palustris E1-9c	521011 475088 475087 1198451 2191 224756 28890 2157 131567	Archaea	
UP000001362	Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	243159	7/30/2015	3120	Acidithiobacillus ferrooxidans ATCC 23270	243159 920 119977 225058 225057 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001361	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	883	7/30/2015	3178	Desulfovibrio vulgaris str. 'Miyazaki F'	883 881 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006906	Chlamydomonas reinhardtii (Chlamydomonas smithii)	3055	7/30/2015	14337	Chlamydomonas reinhardtii	3055 3052 3051 3042 3166 3041 33090 2759 131567	eukaryotes	
UP000000449	Streptococcus uberis (strain ATCC BAA-854 / 0140J)	218495	7/30/2015	1760	Streptococcus uberis 0140J	218495 1349 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000447	Thermomicrobium roseum (strain ATCC 27502 / DSM 5159 / P-2)	309801	7/30/2015	2858	Thermomicrobium roseum DSM 5159	309801 500 499 189777 189776 189775 200795 2 131567	Bacteria	Chloroflexi
UP000007307	Anaplasma marginale (strain Florida)	320483	7/30/2015	939	Anaplasma marginale str. Florida	320483 770 768 942 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000453	Variovorax paradoxus (strain S110)	543728	7/30/2015	6272	Variovorax paradoxus S110	543728 34073 34072 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001596	Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	311402	7/30/2015	5353	Agrobacterium vitis S4	311402 373 357 227290 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000448	Nautilia profundicola (strain ATCC BAA-1463 / DSM 18972 / AmH)	598659	7/30/2015	1730	Nautilia profundicola AmH	598659 244787 191291 224467 235899 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000009097	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	8/24/2015	31179	Fusarium oxysporum f. sp. lycopersici 4287	426428 59765 5507 171631 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001511	Nostoc azollae (strain 0708) (Anabaena azollae (strain 0708))	551115	7/30/2015	3646	'Nostoc azollae' 0708	551115 1164 264688 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000000442	Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2)	177437	7/30/2015	4846	Desulfobacterium autotrophicum HRM2	177437 2296 2295 213119 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000019755	Curtobacterium flaccumfaciens UCD-AKU	1292022	7/27/2015	3386	Curtobacterium flaccumfaciens UCD-AKU	1292022 2035 2034 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000009099	Thioalkalivibrio sp. (strain K90mix)	396595	7/30/2015	2823	Thioalkalivibrio sp. K90mix	396595 106633 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000444	Staphylococcus carnosus (strain TM300)	396513	7/30/2015	2460	Staphylococcus carnosus subsp. carnosus TM300	396513 147448 1281 1279 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001600	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	311403	7/30/2015	6674	Agrobacterium radiobacter K84	311403 358 1183400 357 227290 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria

UP000009096	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	7/30/2015	17589	Fusarium verticillioides 7600	334819 117187 171627 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000019772	Paenibacillus sabinae T27	1268072	8/8/2015	4776	Paenibacillus sabinae T27	1268072 365617 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001874	Human herpesvirus 2 (strain HG52) (HHV-2) (Human herpes simplex virus 2)	10315	7/30/2015	74	Human herpesvirus 2 strain HG52	10315 10310 10294 10293 10292 548681 35237 10239	Vruses	
UP000019763	Gregarina niphandrodes	110365	7/27/2015	6341	Gregarina niphandrodes	110365 35089 35088 35087 35086 1280412 5794 33630 2759 131567	eukaryotes	
UP000001803	Brachyspira hyodysenteriae (strain ATCC 49526 / WA1)	565034	7/30/2015	2642	Brachyspira hyodysenteriae WA1	565034 159 29521 143786 1643686 203692 203691 2 131567	Bacteria	Spirochaetes
UP000001595	Pongo abelii (Sumatran orangutan) (Pongo pygmaeus abelii)	9601	8/9/2015	22875	Pongo abelii	9601 9599 607660 9604 314295 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000019771	Trueperella pyogenes	1661	7/27/2015	1984	Trueperella pyogenes	1661 1069494 2049 2037 1760 201174 2 131567	Bacteria	Actinobacteria
UP000009102	Halothiobacillus neapolitanus (strain ATCC 23641 / c2) (Thiobacillus neapolitanus)	555778	7/30/2015	2353	Halothiobacillus neapolitanus c2	555778 927 109262 255526 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000019768	Bordetella holmesii ATCC 51541	1247649	7/27/2015	3755	Bordetella holmesii ATCC 51541	1247649 35814 517 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001366	Persephonella marina (strain DSM 14350 / EX-H1)	123214	7/30/2015	2048	Persephonella marina EX-H1	123214 309805 182899 224027 32069 187857 200783 2 131567	Bacteria	Aquificae
UP000009100	Vibrio tasmaniensis (strain LGP32) (Vibrio splendidus (strain Mel32))	575788	7/30/2015	4420	Vibrio tasmaniensis LGP32	575788 212663 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001368	Streptococcus equi subsp. zooepidemicus (strain H70)	553483	7/30/2015	1851	Steptococcus equi subsp. zooepidemicus H70	553483 40041 1336 119603 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001294	Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333)	441960	7/30/2015	10448	Talaromyces marneffei ATCC 18224	441960 37727 5094 28568 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001742	Enterocytozoon bieneusi (strain H348) (Microsporidian parasite)	481877	7/30/2015	3311	Enterocytozoon bieneusi H348	481877 31281 27971 27970 6032 6029 4751 33154 2759 131567	eukaryotes	
UP000001875	Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	332952	7/30/2015	13501	Aspergillus flavus NRRL3357	332952 5059 5052 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000033358	Candidatus Arcanobacter lacustris	1607817	8/8/2015	815	Candidatus Arcanobacter lacustris	1607817 1699066 210592 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001743	Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	561896	7/30/2015	8983	Postia placenta Mad-698-R	561896 104341 83235 83233 5303 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000001744	Schizosaccharomyces japonicus (strain yFS275 / FY16936) (Fission yeast)	402676	7/30/2015	4852	Schizosaccharomyces japonicus yFS275	402676 4897 4895 4894 34346 147554 451866 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001745	Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum)	441959	7/30/2015	13022	Talaromyces stipitatus ATCC 10500	441959 28564 5094 28568 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000033364	Orientia tsutsugamushi str. UT76	682184	7/30/2015	3693	Orientia tsutsugamushi str. UT76	682184 784 69474 33988 775 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002208	Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	546414	7/30/2015	3459	Deinococcus deserti VCD115	546414 310783 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000033406	Streptomyces sp. NRRL S-444	1609134	8/4/2015	8021	Streptomyces sp. NRRL S-444	1609134 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033378	Desulfobulbaceae bacterium BRH_c16a	1629713	7/30/2015	4871	Desulfobulbaceae bacterium BRH_c16a	1629713 231686 213121 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002207	Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	240015	7/30/2015	3363	Acidobacterium capsulatum ATCC 51196	240015 33075 33973 204434 204433 204432 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000002204	Rhodococcus erythropolis (strain PR4 / NBRC 100887)	234621	7/30/2015	6424	Rhodococcus erythropolis PR4	234621 1833 1827 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001879	Natrialba magadii (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) (Natronobacterium magadii)	547559	7/30/2015	4211	Natrialba magadii ATCC 43099	547559 13769 63742 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000007962	Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	471853	7/30/2015	4195	Beutenbergia cavernae DSM 12333	471853 84757 84756 125316 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033393	Lechevalieria aerocolonigenes (Nocardia aerocolonigenes) (Saccharothrix aerocolonigenes)	68170	8/4/2015	8237	Lechevalieria aerocolonigenes	68170 166974 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033409	Saccharothrix sp. ST-888	1427391	8/4/2015	5936	Saccharothrix sp. ST-888	1427391 2071 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033411	Devosia epidermidihirudinis	1293439	7/30/2015	3353	Devosia epidermidihirudinis	1293439 46913 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001877	Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	358681	8/1/2015	5887	Brevibacillus brevis NBRC 100599	358681 1393 55080 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000002209	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	379066	7/30/2015	3932	Gemmatimonas aurantiaca T-27	379066 173480 173479 219687 219686 219685 142182 2 131567	Bacteria	Gemmatimonadetes
UP000002009	Micromonas sp. (strain RCC299 / NOUM17) (Picoplanktonic green alga)	296587	7/30/2015	10115	Micromonas sp. RCC299	296587 38832 41873 13792 1035538 3152 3041 33090 2759 131567	eukaryotes	
UP000001054	Rhizobium sp. (strain NGR234)	394	7/30/2015	6274	Sinorhizobium fredii NGR234	394 380 663276 28105 227292 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001876	Micromonas pusilla (strain CCMP1545) (Picoplanktonic green alga)	564608	7/30/2015	10250	Micromonas pusilla CCMP1545	564608 38833 38832 41873 13792 1035538 3152 3041 33090 2759 131567	eukaryotes	
UP000033428	Candidatus Omnitrophus sp. SKK-01	1609969	7/30/2015	2573	Candidatus Omnitrophus sp. SKK-01	1609969 1431823 67812 2323 2 131567	Bacteria	Unclassified Bacteria

UP000033425	Microbacterium sp. SA39	1263625	8/4/2015	3732	Microbacterium sp. SA39	1263625 33882 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033423	Candidatus Magnetobacterium bavaricum	29290	7/30/2015	6447	Candidatus Magnetobacterium bavaricum	29290 40118 189779 189778 203693 40117 2 131567	Bacteria	Nitrospirae
UP000033431	Desulfatitalea sp. BRH_c12	1629708	7/30/2015	4424	Desulfatitalea sp. BRH_c12	1629708 1303912 213119 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000033434	Pseudoalteromonas luteoviolacea S4054	1129367	7/30/2015	5121	Pseudoalteromonas luteoviolacea S4054	1129367 43657 53246 267888 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002213	Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	446462	7/30/2015	6912	Actinosynnema mirum DSM 43827	446462 40567 40566 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001219	Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	526226	7/30/2015	4628	Gordonia bronchialis DSM 43247	526226 2054 2053 85026 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007967	Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	479435	7/30/2015	6940	Kribbella flavida DSM 17836	479435 182640 182639 85015 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000019805	Castellaniella defragrans 65Phen	1437824	7/27/2015	3575	Castellaniella defragrans 65Phen	1437824 75697 359336 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001052	Desulfohalobium retbaense (strain DSM 5692)	485915	7/30/2015	2500	Desulfohalobium retbaense DSM 5692	485915 45663 45662 213117 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000033439	Peptococcaceae bacterium BRH_c4a	1629716	7/30/2015	2917	Peptococcaceae bacterium BRH_c4a	1629716 208050 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002011	Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	471854	7/30/2015	5703	Dyadobacter fermentans DSM 18053	471854 94254 120831 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000033442	Desulfosporosinus sp. I2	1617025	7/30/2015	5500	Desulfosporosinus sp. I2	1617025 79206 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000033448	Microbacterium azadirachtae	582680	8/4/2015	3744	Microbacterium	582680 33882 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002010	Laribacter hongkongensis (strain HLHK9)	557598	7/30/2015	3208	Laribacter hongkongensis HLHK9	557598 168471 168470 1499392 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001377	Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (Eubacterium lentum)	479437	7/30/2015	3054	Eggerthella lenta DSM 2243	479437 84112 84111 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000033446	Peptococcaceae bacterium BRH_c4b	1629717	7/30/2015	3086	Peptococcaceae bacterium BRH_c4b	1629717 208050 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000628	Jonesia denitrificans (strain ATCC 14870 / DSM 20603 / CIP 55134) (Listeria denitrificans)	471856	7/30/2015	2495	Jonesia denitrificans DSM 20603	471856 43674 43673 85022 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002012	Denitrovibrio acetiphilus (strain DSM 12809 / N2460)	522772	7/30/2015	2901	Denitrovibrio acetiphilus DSM 12809	522772 118000 117999 191394 191393 68337 200930 2 131567	Bacteria	Deferribacteres
UP000033451	Microbacterium ginsengisoli	400772	8/4/2015	2779	Microbacterium ginsengisoli	400772 33882 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033452	Pseudoalteromonas rubra	43658	8/4/2015	4390	Pseudoalteromonas rubra	43658 53246 267888 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002255	Xylanimonas cellulosilytica (strain DSM 15894 / CECT 5975 / LMG 20990 / XIL07)	446471	7/30/2015	3441	Xylanimonas cellulosilytica DSM 15894	446471 186189 186188 85017 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033449	Salinivibrio sp. KP-1	1406902	7/30/2015	3027	Salinivibrio sp. KP-1	1406902 51366 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033454	Orientia tsutsugamushi str. Sido	1359174	7/30/2015	864	Orientia tsutsugamushi str. Sido	1359174 784 69474 33988 775 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001880	Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2)	502025	7/30/2015	6684	Haliangium ochraceum DSM 14365	502025 80816 162027 224464 224462 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001746	Halomicrobium mukohataei (strain ATCC 700874 / DSM 12286 / JCM 9738 / NCIMB 13541) (Haloarcula mukohataei)	485914	7/30/2015	3343	Halomicrobium mukohataei DSM 12286	485914 57705 203135 2236 2235 183963 28890 2157 131567	Archaea	
UP000033457	Corynebacterium kutscheri	35755	7/30/2015	2047	Corynebacterium kutscheri	35755 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033468	Rhodospirillaceae bacterium BRH_c57	1629718	7/30/2015	3397	Rhodospirillaceae bacterium BRH_c57	1629718 41296 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002077	Corynebacterium aurimucosum (strain ATCC 700975 / DSM 44827 / CN-1) (Corynebacterium nigricans)	548476	7/30/2015	2528	Corynebacterium aurimucosum ATCC 700975	548476 169292 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001383	Macrococcus caseolyticus (strain JCSC5402)	458233	7/30/2015	2059	Macrococcus caseolyticus JCSC5402	458233 69966 69965 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000033484	Streptomyces sp. NRRL S-495	1609133	8/4/2015	7273	Streptomyces sp. NRRL S-495	1609133 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000007968	Veillonella parvula (strain ATCC 10790 / DSM 2008 / JCM 12972 / Te3) (Veillonella alcalescens)	479436	7/30/2015	1843	Veillonella parvula DSM 2008	479436 29466 29465 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000033488	Clostridiaceae bacterium BRH_c20a	1629719	7/30/2015	3831	Clostridiaceae bacterium BRH_c20a	1629719 189971 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000033491	Lactobacillus spicheri	216463	7/30/2015	2336	Lactobacillus spicheri	216463 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000033495	Hyphomonadaceae bacterium BRH_c29	1629720	7/30/2015	3303	Hyphomonadaceae bacterium BRH_c29	1629720 69658 69657 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001213	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	521096	7/30/2015	4170	Tsukamurella paurometabola DSM 20162	521096 2061 2060 85028 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033493	Peptococcaceae bacterium BRH_c8a	1629715	7/30/2015	3440	Peptococcaceae bacterium BRH_c8a	1629715 208050 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001910	Leptotrichia buccalis (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249 / C-1013-b)	523794	7/30/2015	2218	Leptotrichia buccalis C-1013-b	523794 40542 32067 1129771 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000033503	Peptococcaceae bacterium BRH_c23	1629714	7/30/2015	5016	Peptococcaceae bacterium BRH_c23	1629714 208050 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000006654	Bacillus cereus Rock3-44	526986	7/30/2015	4750	Bacillus cereus Rock3-44	526986 1396 86661 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes

UP000033511	Pseudoalteromonas piscicida	43662	8/4/2015	4134	Pseudoalteromonas piscicida	43662 53246 267888 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033514	Devosia soli	361041	7/30/2015	3705	Devosia soli	361041 46913 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001384	Bacillus cereus Rock4-18	526988	7/27/2015	2841	Bacillus cereus Rock4-18	526988 1396 86661 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000006650	Capnocytophaga ochracea (strain ATCC 27872 / DSM 7271 / JCM 12966 / NCTC 12371 / VPI 2845) (Bacteroides ochraceus)	521097	7/30/2015	2171	Capnocytophaga ochracea DSM 7271	521097 1018 1016 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001916	Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	526227	7/30/2015	3383	Meiothermus silvanus DSM 9946	526227 52022 65551 188786 68933 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000006666	Kytococcus sedentarius (strain ATCC 14392 / DSM 20547 / CCM 314 / 541) (Micrococcus sedentarius)	478801	7/30/2015	2531	Kytococcus sedentarius DSM 20547	478801 1276 57499 145357 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033519	Devosia psychrophila	728005	7/30/2015	4000	Devosia psychrophila	728005 46913 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001917	Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	521098	7/30/2015	3059	Alicyclobacillus acidocaldarius subsp. acidocaldarius DSM 446	521098 1388 405212 29330 186823 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001918	Thermomonospora curvata (strain ATCC 19995 / DSM 43183 / JCM 3096 / NCIMB 10081)	471852	7/30/2015	4888	Thermomonospora curvata DSM 43183	471852 2020 2019 2012 85012 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006663	Halogeometricum borinquense (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3)	469382	7/30/2015	3894	Halogeometricum borinquense DSM 11551	469382 60847 60846 1644056 1644055 183963 28890 2157 131567	Archaea	
UP000001382	Geodermatophilus obscurus (strain ATCC 25078 / DSM 43160 / JCM 3152 / G-20)	526225	7/30/2015	4795	Geodermatophilus obscurus DSM 43160	526225 1861 1860 85030 1643682 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002294	Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) (Peptostreptococcus prevotii) (Peptococcus prevotii)	525919	7/30/2015	1795	Anaerococcus prevotii DSM 20548	525919 33034 165779 1570339 1737405 1737404 1239 2 131567	Bacteria	Firmicutes
UP000001358	Invertebrate iridescent virus 3 (IIV-3) (Mosquito iridescent virus)	345201	7/27/2015	126	Invertebrate iridescent virus 3	345201 10491 10486 35237 10239	Vruses	
UP000033558	Lactobacillus mellifer	1218492	7/30/2015	1592	Lactobacillus mellifer	1218492 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000033562	Candidatus Neoehrlichia lotoris str. RAC413	1359163	7/30/2015	1017	Candidatus Neoehrlichia lotoris str. RAC413	1359163 467750 467749 942 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033569	Streptomyces sp. NRRL F-4428	1609137	8/4/2015	5663	Streptomyces sp. NRRL F-4428	1609137 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033566	Corynebacterium camporealensis	161896	7/30/2015	2245	Corynebacterium camporealensis	161896 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033583	Brevundimonas sp. KM4	1628191	7/30/2015	2906	Brevundimonas sp. KM4	1628191 41275 76892 204458 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033581	Gammaproteobacteria bacterium BRH_c0	1629722	7/30/2015	2959	Gammaproteobacteria bacterium BRH_c0	1629722 33811 118884 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033572	Microbacterium foliorum	104336	8/4/2015	3324	Microbacterium foliorum	104336 33882 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033604	Clostridium sp. FS41	1609975	7/30/2015	5722	Clostridium sp. FS41	1609975 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000033603	Terrabacter sp. 28	1619947	8/4/2015	3812	Terrabacter sp. 28	1619947 53355 85021 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033602	Pseudomonas sp. BRH_c35	1629711	7/30/2015	3016	Pseudomonas sp. BRH_c35	1629711 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033608	Devosia limi DSM 17137	1121477	7/30/2015	3824	Devosia limi DSM 17137	1121477 288995 46913 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033607	Limnoraphis robusta CS-951	1637645	8/2/2015	0	Limnoraphis robusta CS-	1637645 1118279 1332112 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000033614	Avibacterium paragallinarum (Haemophilus gallinarum)	728	8/4/2015	2171	Avibacterium	728 292486 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033616	Orientia chuto str. Fuller	1359168	7/30/2015	1067	Orientia chuto str. Fuller	1359168 911112 69474 33988 775 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033551	Streptomyces katrae	68223	8/4/2015	7302	Streptomyces katrae	68223 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033618	Burkholderia andropogonis	28092	7/30/2015	4737	Burkholderia andropogonis	28092 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000033632	Devosia geojensis	443610	7/30/2015	3992	Devosia geojensis	443610 46913 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001548	Giardia intestinalis (strain ATCC 50803 / WB clone C6) (Giardia lamblia)	184922	7/30/2015	7154	Giardia lamblia ATCC 50803	184922 5741 5740 68459 5739 5738 207245 2759 131567	eukaryotes	
UP000033636	Thermoproteus sp. AZ2	1609232	7/30/2015	1702	Thermoproteus sp. AZ2	1609232 2270 2267 2266 183924 28889 2157 131567	Archaea	
UP000033640	Microbacterium oxydans	82380	8/4/2015	3588	Microbacterium oxydans	82380 33882 85023 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033633	Photobacterium halotolerans	265726	7/30/2015	3968	Photobacterium	265726 657 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033638	Pediococcus damnosus LMG 28219	1448143	7/30/2015	1996	Pediococcus damnosus LMG 28219	1448143 51663 1253 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000002296	Trypanosoma cruzi (strain CL Brener)	353153	7/30/2015	19242	Trypanosoma cruzi strain CL Brener	353153 5693 47570 5690 5654 5653 33682 2759 131567	eukaryotes	
UP000033642	Halomonas sp. S2151	579478	8/4/2015	4021	Halomonas sp. S2151	579478 2745 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033641	Streptomyces sp. WM6386	1415558	8/4/2015	8143	Streptomyces sp. WM6386	1415558 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033649	Devosia chinhatensis	429727	7/30/2015	3103	Devosia chinhatensis	429727 46913 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002297	Croceibacter atlanticus (strain ATCC BAA-628 / HTCC2559 / KCTC 12090)	216432	7/30/2015	2702	Croceibacter atlanticus HTCC2559	216432 313588 216431 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001351	Stigmatella aurantiaca (strain DW4/3-1)	378806	7/30/2015	8307	Stigmatella aurantiaca DW4/3-1	378806 41 40 39 80811 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000033664	Pseudoalteromonas ruthenica	151081	8/4/2015	3470	Pseudoalteromonas ruthenica	151081 53246 267888 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001302	Parvularcula bermudensis (strain ATCC BAA-594 / HTCC2503 / KCTC 12087)	314260	7/30/2015	2687	Parvularcula bermudensis HTCC2503	314260 208216 208215 255474 255473 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033651	Luteibacter yeojuensis	345309	7/30/2015	3844	Luteibacter yeojuensis	345309 242605 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001602	Maribacter sp. (strain HTCC2170 / KCCM 42371)	313603	7/30/2015	3411	Maribacter sp. HTCC2170	313603 252356 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000033676	Roseovarius sp. BRH_c41	1629709	7/30/2015	4456	Roseovarius sp. BRH_c41	1629709 74030 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033680	Sphingomonas sp. SRS2	133190	7/30/2015	4289	Sphingomonas sp. SRS2	133190 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria

UP000033681	Flavobacteriales bacterium BRH_c54	1629721	7/30/2015	2326	Flavobacteriales bacterium BRH_c54	1629721 403978 313602 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000009049	Robiginitalea biformata (strain ATCC BAA-864 / HTCC2501 / KCTC 12146)	313596	7/30/2015	3211	Robiginitalea biformata HTCC2501	313596 252307 252306 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000033695	Lactobacillus mellis	1218508	7/30/2015	1572	Lactobacillus mellis	1218508 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000033684	Methylococcaceae bacterium Sn10-6	1632867	7/30/2015	2947	Methylococcaceae bacterium Sn10-6	1632867 51352 403 135618 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033699	Streptomyces rubellomurinus	359131	8/4/2015	6267	Streptomyces	359131 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002173	Babesia bovis	5865	7/30/2015	3690	Babesia bovis	5865 5864 32594 5863 422676 5794 33630 2759 131567	eukaryotes	
UP000033718	Candidatus Magnetoovum chiemensis	1609970	7/30/2015	4107	Candidatus Magnetoovum chiemensis	1609970 995729 189779 189778 203693 40117 2 131567	Bacteria	Nitrospirae
UP000033732	Grimontia sp. AD028	1581149	8/4/2015	4746	Grimontia sp. AD028	1581149 246861 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033750	Mycoplasma meleagridis ATCC 25294	1264554	7/30/2015	505	Mycoplasma meleagridis ATCC 25294	1264554 29561 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000033741	Loktanella sp. S4079	579483	8/4/2015	3296	Loktanella sp. S4079	579483 245186 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033764	Aquitalea magnusonii	332411	7/30/2015	4103	Aquitalea magnusonii	332411 407217 1499392 206351 28216 1224 2 131567	Bacteria	Proteobacteria
UP000033772	Nocardioides luteus	1844	7/30/2015	5124	Nocardioides luteus	1844 1839 85015 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033747	Marinomonas sp. S3726	579484	8/4/2015	4618	Marinomonas sp. S3726	579484 28253 135620 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033765	Hyphomonas sp. BRH_c22	1629710	7/30/2015	3532	Hyphomonas sp. BRH_c22	1629710 85 69657 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033774	Elstera litoralis	552518	7/30/2015	3298	Elstera litoralis	552518 1091044 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033769	Orientia tsutsugamushi str. Gilliam	1359184	7/30/2015	2704	Orientia tsutsugamushi str. Gilliam	1359184 784 69474 33988 775 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002215	Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)	485918	7/30/2015	7179	Chitinophaga pinensis DSM 2588	485918 79329 79328 563835 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002220	Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	521674	7/30/2015	4258	Planctopirus limnophila DSM 3776	521674 120 1649480 126 112 203683 203682 2 131567	Bacteria	Planctomycetes
UP000002216	Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) (Desulfovibrio baculatus)	525897	7/30/2015	3421	Desulfomicrobium baculatum DSM 4028	525897 899 898 213116 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000852	Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290)	485917	8/1/2015	4249	Pedobacter heparinus DSM 2366	485917 984 84567 84566 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000851	Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897)	479433	7/30/2015	8909	Catenulispora acidiphila DSM 44928	479433 304895 414878 414877 414714 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002222	Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175)	525898	7/30/2015	2243	Sulfurospirillum deleyianum DSM 6946	525898 65553 57665 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002221	Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) (Rhodothermus obamensis)	518766	7/30/2015	2861	Rhodothermus marinus DSM 4252	518766 29549 29548 563843 1100069 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002219	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	446468	7/30/2015	5497	Nocardiopsis dassonvillei subsp. dassonvillei DSM 43111	446468 568208 2014 2013 83676 85012 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001359	Invertebrate iridescent virus 6 (IIV-6) (Chilo iridescent virus)	176652	7/27/2015	468	Invertebrate iridescent virus 6	176652 10487 10486 35237 10239	Vruses	
UP000000849	Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134)	446466	8/2/2015	3673	Cellulomonas flavigena DSM 20109	446466 1711 1707 85016 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002334	Hamiltonella defensa subsp. Acyrthosiphon pisum (strain 5AT)	572265	7/30/2015	2045	Candidatus Hamiltonella defensa 5AT (Acyrthosiphon pisum)	572265 138072 568987 146507 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002218	Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	479431	7/30/2015	5123	Nakamurella multipartita DSM 44233	479431 53461 53460 85031 1643684 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002217	Desulfotomaculum acetoxidans (strain ATCC 49208 / DSM 771 / VKM B-1644)	485916	7/30/2015	4016	Desulfotomaculum acetoxidans DSM 771	485916 58138 1562 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001231	Kangiella koreensis (strain DSM 16069 / KCTC 12182 / SW-125)	523791	7/30/2015	2630	Kangiella koreensis DSM 16069	523791 261964 261963 224372 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000845	Sebaldella termitidis (strain ATCC 33386 / NCTC 11300)	526218	7/30/2015	4124	Sebaldella termitidis ATCC 33386	526218 826 32068 1129771 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000002332	Pseudomonas fluorescens (strain SBW25)	216595	7/30/2015	6388	Pseudomonas fluorescens SBW25	216595 294 136843 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002026	Slackia heliotrinireducens (strain ATCC 29202 / DSM 20476 / NCTC 11029 / RHS 1) (Peptococcus heliotrinreducens)	471855	7/30/2015	2750	Slackia heliotrinireducens DSM 20476	471855 84110 84108 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000001919	Brachybacterium faecium (strain ATCC 43885 / DSM 4810 / NCIB 9860)	446465	7/30/2015	3062	Brachybacterium faecium DSM 4810	446465 43669 43668 85020 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000844	Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	446470	7/30/2015	6379	Stackebrandtia nassauensis DSM 44728	446470 283811 283810 85034 85014 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002027	Sphaerobacter thermophilus (strain DSM 20745 / S 6022)	479434	7/30/2015	3471	Sphaerobacter thermophilus DSM 20745	479434 2057 2056 85002 255728 85001 85000 189775 200795 2 131567	Bacteria	Chloroflexi
UP000002029	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	479432	7/30/2015	8955	Streptosporangium roseum DSM 43021	479432 2001 2000 2004 85012 1760 201174 2 131567	Bacteria	Actinobacteria
UP000009073	Tolumonas auensis (strain DSM 9187 / TA4)	595494	7/30/2015	3126	Tolumonas auensis DSM 9187	595494 43948 43947 84642 135624 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002339	Banana bunchy top virus (isolate Autralia) (BBTV)	645099	7/30/2015	7	Banana bunchy top virus isolate Autralia	645099 12585 251096 251095 29258 10239	Vruses	

UP000001473	Corynebacterium kroppenstedtii (strain DSM 44385 / CCUG 35717)	645127	7/30/2015	2018	Corynebacterium kroppenstedtii DSM 44385	645127 161879 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000841	Saccharomonospora viridis (strain ATCC 15386 / DSM 43017 / JCM 3036 / NBRC 12207 / P101)	471857	7/30/2015	3828	Saccharomonospora viridis DSM 43017	471857 1852 1851 2070 85010 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002030	Thermanaerovibrio acidaminovorans (strain ATCC 49978 / DSM 6589 / Su883) (Selenomonas acidaminovorans)	525903	7/30/2015	1737	Thermanaerovibrio acidaminovorans DSM 6589	525903 81462 81461 649777 649776 649775 508458 2 131567	Bacteria	Synergistetes
UP000001476	Eubacterium eligens (strain ATCC 27750 / VPI C15-48)	515620	7/30/2015	2761	[Eubacterium] eligens ATCC 27750	515620 39485 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000001477	Eubacterium rectale (strain ATCC 33656 / VPI 0990)	515619	7/30/2015	3545	Eubacterium rectale ATCC 33656	515619 39491 1730 186806 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002028	Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896)	504472	7/30/2015	6867	Spirosoma linguale DSM 74	504472 108 107 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000001485	Edwardsiella ictaluri (strain 93-146)	634503	8/3/2015	3686	Edwardsiella ictaluri 93-146	634503 67780 635 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000009082	Nosema ceranae (strain BRL01) (Microsporidian parasite)	578460	7/30/2015	2060	Nosema ceranae BRL01	578460 40302 27977 27974 6032 6029 4751 33154 2759 131567	eukaryotes	
UP000009080	Teredinibacter turnerae (strain ATCC 39867 / T7901)	377629	7/30/2015	4249	Teredinibacter turnerae T7901	377629 2426 2425 1706371 1706369 1236 1224 2 131567	Bacteria	Proteobacteria
UP000009081	Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	272630	8/7/2015	6233	Methylobacterium extorquens AM1	272630 408 578822 407 119045 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000009071	Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	573370	7/30/2015	4663	Desulfovibrio magneticus RS-1	573370 184917 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001491	Mycoplasma conjunctivae (strain ATCC 25834 / HRC/581 / NCTC 10147)	572263	7/30/2015	695	Mycoplasma conjunctivae HRC/581	572263 45361 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000001492	Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	573065	7/30/2015	3743	Asticcacaulis excentricus CB 48	573065 78587 76890 76892 204458 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002729	Aureococcus anophagefferens (Harmful bloom alga)	44056	7/30/2015	11501	Aureococcus anophagefferens	44056 44055 54409 35675 33634 2759 131567	eukaryotes	
UP000002730	Clostridium cellulovorans (strain ATCC 35296 / DSM 3052 / OCM 3 / 743B)	573061	8/14/2015	4211	Clostridium cellulovorans 743B	573061 1493 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002744	Liberibacter asiaticus (strain psy62)	537021	7/30/2015	1102	Candidatus Liberibacter asiaticus str. psy62	537021 34021 34019 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002741	Hodgkinia cicadicola (strain Dsem)	573234	7/30/2015	169	Candidatus Hodgkinia cicadicola Dsem	573234 573658 573657 119042 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002742	Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540)	583345	7/30/2015	2334	Methylotenera mobilis JLW8	583345 359408 359407 32011 206350 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001631	Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus) (Histoplasma capsulatum)	447093	7/30/2015	9214	Histoplasma capsulatum G186AR	447093 5037 5036 299071 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002743	Methylovorus glucosetrophus (strain SIP3-4)	582744	7/30/2015	2907	Methylovorus glucosetrophus SIP3-4	582744 266009 81682 32011 206350 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002745	Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418)	582402	7/30/2015	3187	Hirschia baltica ATCC 49814	582402 2724 2723 69657 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001628	Paracoccidioides brasiliensis (strain Pb18)	502780	7/30/2015	8399	Paracoccidioides brasiliensis Pb18	502780 121759 38946 34383 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001625	Sideroxydans lithotrophicus (strain ES-1)	580332	7/30/2015	2977	Sideroxydans lithotrophicus ES-1	580332 63745 314343 90627 713636 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002058	Uncinocarpus reesii (strain UAMH 1704)	336963	7/30/2015	7760	Uncinocarpus reesii 1704	336963 33188 33187 33184 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002059	Paracoccidioides lutzii (strain ATCC MYA-826 / Pb01) (Paracoccidioides brasiliensis)	502779	7/30/2015	8811	Paracoccidioides lutzii Pb01	502779 1048829 38946 34383 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008536	Zygosaccharomyces rouxii (strain ATCC 2623 / CBS 732 / NBRC 1130 / NCYC 568 / NRRL Y-229) (Candida mogii)	559307	7/30/2015	4987	Zygosaccharomyces rouxii CBS 732	559307 4956 4953 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000000314	Komagataella pastoris (strain GS115 / ATCC 20864) (Yeast) (Pichia pastoris)	644223	7/30/2015	5073	Komagataella phaffii GS115	644223 460519 460517 115784 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000001512	Flavobacteriaceae bacterium (strain 3519-10)	531844	7/30/2015	2533	Flavobacteriaceae bacterium 3519-10	531844 61432 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000002035	Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) (Microsporum canis)	554155	7/30/2015	8764	Arthroderma otae CBS 113480	554155 63405 63399 34384 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002039	Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) (Blastomyces dermatitidis)	559297	7/30/2015	9539	Blastomyces dermatitidis ER-3	559297 5039 229219 299071 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002036	Lachancea thermotolerans (strain ATCC 56472 / CBS 6340 / NRRL Y-8284) (Yeast) (Kluyveromyces thermotolerans)	559295	7/30/2015	5093	Lachancea thermotolerans CBS 6340	559295 381046 300275 4893 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002037	Candida tropicalis (strain ATCC MYA-3404 / T1) (Yeast)	294747	7/30/2015	6226	Candida tropicalis MYA-3404	294747 5482 1535326 1535325 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007703	Clavispora lusitaniae (strain ATCC 42720) (Yeast) (Candida lusitaniae)	306902	7/30/2015	5932	Clavispora lusitaniae ATCC 42720	306902 36911 36910 27319 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007083	Equine herpesvirus 2 (strain 86/87) (EHV-2)	82831	7/30/2015	79	Equid herpesvirus type 2 strain 86/87	82831 12657 548688 10374 10292 548681 35237 10239	Vruses	
UP000000941	Alcelaphine herpesvirus 1 (strain C500) (AlHV-1) (Malignant catarrhal fever virus)	654901	7/30/2015	70	Alcelaphine herpesvirus 1 strain C500	654901 35252 548687 10374 10292 548681 35237 10239	Vruses	

UP000000771	Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)	525909	7/30/2015	1935	Acidimicrobium ferrooxidans DSM 10331	525909 53635 53634 84994 84993 84992 201174 2 131567	Bacteria	Actinobacteria
UP000000942	Human herpesvirus 8 type P (isolate GK18) (HHV-8) (Kaposi's sarcoma-associated herpesvirus)	868565	7/30/2015	85	Human herpesvirus 8 strain GK18	868565 37296 10379 10374 10292 548681 35237 10239	Vruses	
UP000001514	Selaginella moellendorffii (Spikemoss)	88036	7/27/2015	33150	Selaginella moellendorffii	88036 3246 3245 3244 1521260 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000000948	Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)	634452	7/30/2015	2906	Acetobacter pasteurianus IFO 3283-01	634452 481145 438 434 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008072	Gallid herpesvirus 2 (strain Chicken/Md5/ATCC VR-987) (GaHV-2) (Marek's disease herpesvirus type 1)	10389	7/30/2015	90	Marek's disease herpesvirus type 1 strain MD5	10389 10390 180252 10293 10292 548681 35237 10239	Vruses	
UP000002185	Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	75379	7/30/2015	3134	Thiomonas intermedia K12	75379 926 32012 224471 119065 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001619	Accumulibacter phosphatis (strain UW-1)	522306	7/30/2015	4438	Candidatus Accumulibacter phosphatis clade IIA str. UW-1	522306 327160 327159 119066 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000954	Cryptobacterium curtum (strain ATCC 700683 / DSM 15641 / 12-3)	469378	7/30/2015	1355	Cryptobacterium curtum DSM 15641	469378 84163 84162 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000002187	Burkholderia glumae (strain BGR1)	626418	7/30/2015	5660	Burkholderia glumae BGR1	626418 337 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002186	Thauera sp. (strain MZ1T)	85643	7/30/2015	3927	Thauera sp. MZ1T	85643 33057 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000960	Atopobium parvulum (strain ATCC 33793 / DSM 20469 / JCM 10300 / VPI 0546) (Streptococcus parvulus) (Peptostreptococcus parvulus)	521095	7/30/2015	1353	Atopobium parvulum DSM 20469	521095 1382 1380 1643824 84999 84998 201174 2 131567	Bacteria	Actinobacteria
UP000001624	Pantoea sp. (strain At-9b)	592316	7/30/2015	5760	Pantoea sp. At-9b	592316 53335 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001508	Desulfurivibrio alkaliphilus (strain DSM 19089 / UNIQEM U267 / AHT2)	589865	7/30/2015	2595	Desulfurivibrio alkaliphilus AHT 2	589865 427923 427922 213121 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002613	Ferroglobus placidus (strain DSM 10642 / AEDII12DO)	589924	7/30/2015	2463	Ferroglobus placidus DSM 10642	589924 54261 54260 2232 2231 183980 28890 2157 131567	Archaea	
UP000000323	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	525904	7/30/2015	2827	Thermobaculum terrenum ATCC BAA-798	525904 166501 262406 2323 2 131567	Bacteria	Unclassified Bacteria
UP000000322	Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	446469	7/30/2015	3710	Sanguibacter keddieii DSM 10542	446469 60920 60919 145360 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002061	Methanocaldococcus infernus (strain DSM 11812 / JCM 15783 / ME)	573063	7/30/2015	1439	Methanocaldococcus infernus ME	573063 67760 196118 196117 2182 183939 28890 2157 131567	Archaea	
UP000001441	Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	572477	7/30/2015	3211	Allochromatium vinosum DSM 180	572477 1049 85072 1046 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002620	Ammonifex degensii (strain DSM 10501 / KC4)	429009	7/30/2015	2077	Ammonifex degensii KC4	429009 42838 42837 42857 186814 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000002072	Streptobacillus moniliformis (strain ATCC 14647 / DSM 12112 / NCTC 10651 / 9901)	519441	7/30/2015	1431	Streptobacillus moniliformis DSM 12112	519441 34105 34104 1129771 203491 203490 32066 2 131567	Bacteria	Fusobacteria
UP000001444	Streptomyces scabiei (strain 87.22)	680198	7/30/2015	8700	Streptomyces scabiei 87.22	680198 1930 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001449	Thalassiosira pseudonana (Marine diatom) (Cyclotella nana)	35128	7/30/2015	11718	Thalassiosira pseudonana	35128 35127 29202 33847 33846 33836 2836 33634 2759 131567	eukaryotes	
UP000005206	Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	660122	7/30/2015	15709	Nectria haematococca mpVI 77-13-4	660122 70791 140110 232080 5506 110618 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002624	Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	544712	7/30/2015	9545	Histoplasma capsulatum H143	544712 5037 5036 299071 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002569	Aggregatibacter actinomycetemcomitans serotype C (strain D11S-1) (Actinobacillus actinomycetemcomitans)	668336	7/30/2015	2276	Aggregatibacter actinomycetemcomitans D11S-1	668336 714 416916 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002629	Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (Mycoplana segnis)	509190	7/30/2015	4136	Caulobacter segnis ATCC 21756	509190 88688 75 76892 204458 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002630	Ectocarpus siliculosus (Brown alga)	2880	7/30/2015	16334	Ectocarpus siliculosus	2880 2879 2878 2877 2870 569578 33634 2759 131567	eukaryotes	
UP000001235	Gallionella capsiferriformans (strain ES-2) (Gallionella ferruginea capsiferriformans (strain ES-2))	395494	7/30/2015	2853	Gallionella capsiferriformans ES-2	395494 370405 96 90627 713636 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002631	Mycoplasma hominis (strain ATCC 23114 / NBRC 14850 / NCTC 10111 / PG21)	347256	7/30/2015	529	Mycoplasma hominis ATCC 23114	347256 2098 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000002696	Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (Caulobacter subvibrioides)	633149	7/30/2015	3326	Brevundimonas subvibrioides ATCC 15264	633149 74313 41275 76892 204458 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002191	Desulfovibrio aespoeensis (strain ATCC 700646 / DSM 10631 / Aspo-2)	643562	7/30/2015	3269	Desulfovibrio aespoeensis Aspo-2	643562 182210 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000002484	Frankia sp. (strain EuI1c)	298654	7/30/2015	7079	Frankia sp. EuI1c	298654 1854 74712 85013 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001881	Sordaria macrospora (strain ATCC MYA-333 / DSM 997 / K(L3346) / K-hell)	771870	7/30/2015	9890	Sordaria macrospora k-hell	771870 5147 5146 5148 5139 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000002190	Burkholderia sp. (strain CCGE1002)	640511	7/30/2015	6866	Burkholderia sp.	640511 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001396	Polysphondylium pallidum (Cellular slime mold)	13642	7/30/2015	12351	Polysphondylium pallidum	13642 13641 33083 142796 554915 2759 131567	eukaryotes	
UP000001542	Trichomonas vaginalis	5722	7/30/2015	50191	Trichomonas vaginalis	5722 5721 181550 37104 5719 2759 131567	eukaryotes	
UP000008698	Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) (Verticillium wilt of alfalfa) (Verticillium albo-atrum)	526221	7/30/2015	10233	Verticillium alfalfae VaMs.102	526221 1051613 1036719 1033979 1033978 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000008693	Bifidobacterium dentium (strain ATCC 27534 / DSM 20436 / JCM 1195 / Bd1)	401473	8/14/2015	2121	Bifidobacterium dentium Bd1	401473 1689 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001887	Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	530564	7/30/2015	4711	Pirellula staleyi DSM 6068	530564 125 123 126 112 203683 203682 2 131567	Bacteria	Planctomycetes
UP000008699	Measles virus (strain Ichinose-B95a) (MeV) (Subacute sclerose panencephalitis virus)	645098	7/30/2015	8	Measles virus strain Ichinose-B95a	645098 11234 11229 11159 11158 11157 35301 439488 10239	Vruses	
UP000001882	Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE)	304371	7/30/2015	2993	Methanocella paludicola SANAE	304371 570267 570266 570265 570264 224756 28890 2157 131567	Archaea	
UP000001397	Streptomyces sp. (strain SirexAA-E / ActE)	862751	7/30/2015	6354	Streptomyces sp. SirexAA-	862751 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001889	Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	637910	7/30/2015	4792	Citrobacter rodentium ICC168	637910 67825 544 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001883	Rothia mucilaginosa (strain DY-18) (Stomatococcus mucilaginosus)	680646	7/30/2015	1991	Rothia mucilaginosa DY-18	680646 43675 32207 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001890	Xanthomonas albilineans (strain GPE PC73 / CFBP 7063)	380358	7/30/2015	3190	Xanthomonas albilineans GPE PC73	380358 29447 338 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001401	Bacillus cellulosilyticus (strain ATCC 21833 / DSM 2522 / FERM P-1141 / JCM 9156 / N-4)	649639	8/2/2015	4253	Bacillus cellulosilyticus DSM 2522	649639 1413 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001398	Human metapneumovirus (strain CAN97-83) (HMPV)	694067	7/30/2015	9	Human metapneumovirus CAN97-83	694067 162145 162387 11244 11158 11157 35301 439488 10239	Vruses	
UP000001400	Aciduliprofundum boonei (strain DSM 19572 / T469)	439481	7/30/2015	1539	Aciduliprofundum boonei T469	439481 379547 379546 33867 28890 2157 131567	Archaea	
UP000001901	Archaeoglobus profundus (strain DSM 5631 / JCM 9629 / NBRC 100127 / Av18)	572546	7/30/2015	1822	Archaeoglobus profundus DSM 5631	572546 84156 2233 2232 2231 183980 28890 2157 131567	Archaea	
UP000001902	Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4)	591001	7/30/2015	2016	Acidaminococcus fermentans DSM 20731	591001 905 904 909930 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000001405	Atelocyanobacterium thalassa (isolate ALOHA)	713887	7/27/2015	1199	Candidatus Atelocyanobacterium thalassa	713887 1453359 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000001399	Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	648757	7/30/2015	3513	Rhodomicrobium vannielii ATCC 17100	648757 1069 1068 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000001903	Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (Halococcus turkmenicus)	543526	7/30/2015	5113	Haloterrigena turkmenica DSM 5511	543526 62320 121871 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000001544	Bacillus pseudofirmus (strain OF4)	398511	7/30/2015	4310	Bacillus pseudofirmus OF4	398511 79885 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000008229	Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	469383	7/30/2015	5912	Conexibacter woesei DSM 14684	469383 191495 191494 320583 588673 1497346 201174 2 131567	Bacteria	Actinobacteria
UP000002572	Desulfurispirillum indicum (strain ATCC BAA-1389 / S5)	653733	7/30/2015	2551	Desulfurispirillum indicum S5	653733 936456 393029 189770 189769 118001 200938 2 131567	Bacteria	Chrysiogenetes
UP000002574	Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6)	608538	7/30/2015	1892	Hydrogenobacter thermophilus TK-6	608538 940 939 64898 32069 187857 200783 2 131567	Bacteria	Aquificae
UP000008227	Sus scrofa (Pig)	9823	8/16/2015	26148	Sus scrofa	9823 9822 9821 35497 91561 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001908	Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	644283	7/30/2015	6204	Micromonospora aurantiaca ATCC 27029	644283 47850 1873 28056 85008 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001811	Oryctolagus cuniculus (Rabbit)	9986	8/2/2015	21184	Oryctolagus cuniculus	9986 9984 9979 9975 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002040	Azospirillum sp. (strain B510)	137722	7/30/2015	6092	Azospirillum sp. B510	137722 193 191 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008680	Methanobrevibacter ruminantium (strain ATCC 35063 / DSM 1093 / JCM 13430 / OCM 146 / M1) (Methanobacterium ruminantium)	634498	7/30/2015	2209	Methanobrevibacter ruminantium M1	634498 83816 2172 2159 2158 183925 28890 2157 131567	Archaea	
UP000008563	Streptococcus mitis (strain B6)	365659	7/30/2015	1971	Streptococcus mitis B6	365659 28037 1301 1300 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000001551	Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	663278	7/30/2015	2663	Ethanoligenens harbinense YUAN-3	663278 253239 253238 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008234	Mageeibacillus indolicus (strain UPII9-5) (Clostridiales genomosp. BVAB3 (strain UPII9-5))	699246	7/30/2015	1566	Mageeibacillus indolicus UPII9-5	699246 884684 1637257 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008225	Callithrix jacchus (White-tufted-ear marmoset)	9483	8/2/2015	42054	Callithrix jacchus	9483 9481 9480 9498 9479 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001549	Frankia symbiont subsp. Datisca glomerata	656024	7/27/2015	4063	Frankia symbiont of Datisca glomerata	656024 1854 74712 85013 1760 201174 2 131567	Bacteria	Actinobacteria
UP000001550	Burkholderia sp. (strain CCGE1003)	640512	7/30/2015	5983	Burkholderia sp.	640512 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001926	Entamoeba histolytica	5759	8/2/2015	7959	Entamoeba histolytica	5759 5758 33084 555406 554915 2759 131567	eukaryotes	
UP000008075	Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	406817	7/30/2015	4439	Xenorhabdus nematophila ATCC 19061	406817 628 626 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002045	Xenorhabdus bovienii (strain SS-2004)	406818	7/30/2015	4102	Xenorhabdus bovienii SS-2004	406818 40576 626 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002043	Thermocrinis albus (strain DSM 14484 / JCM 11386 / HI 11/12)	638303	7/30/2015	1592	Thermocrinis albus DSM 14484	638303 136094 75905 64898 32069 187857 200783 2 131567	Bacteria	Aquificae
UP000001453	Gardnerella vaginalis (strain ATCC 14019 / 317)	525284	8/14/2015	1365	Gardnerella vaginalis ATCC 14019	525284 2702 2701 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria

UP000001554	Branchiostoma floridae (Florida lancelet) (Amphioxus)	7739	8/2/2015	28544	Branchiostoma floridae	7739 7737 7736 7735 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001522	Helicobacter mustelae (strain ATCC 43772 / LMG 18044 / NCTC 12198 / 12198) (Campylobacter mustelae)	679897	7/30/2015	1400	Helicobacter mustelae 12198	679897 217 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001555	Ixodes scapularis (Black-legged tick) (Deer tick)	6945	7/30/2015	20473	Ixodes scapularis	6945 6944 426442 6939 297308 6935 6934 6933 6854 6843 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001702	Pantoea ananatis (strain LMG 20103)	706191	7/30/2015	4241	Pantoea ananatis LMG 20103	706191 553 53335 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001520	Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1)	639282	7/30/2015	2338	Deferribacter desulfuricans SSM1	639282 197162 53572 191394 191393 68337 200930 2 131567	Bacteria	Deferribacteres
UP000001519	Gorilla gorilla gorilla (Western lowland gorilla)	9595	8/14/2015	27296	Gorilla gorilla gorilla	9595 9593 9592 207598 9604 314295 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002320	Culex quinquefasciatus (Southern house mosquito) (Culex pungens)	7176	7/30/2015	18703	Culex quinquefasciatus	7176 518105 53527 7174 53550 43817 7157 41827 43786 7148 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001700	Riesia pediculicola (strain USDA)	515618	7/30/2015	540	Candidatus Riesia pediculicola USDA	515618 401619 401618 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008866	Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) (Trichophyton mentagrophytes)	663331	7/30/2015	7978	Arthroderma benhamiae CBS 112371	663331 63400 63399 34384 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008243	Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) (Halobacterium volcanii)	309800	7/30/2015	3987	Haloferax volcanii DS2	309800 2246 2251 1644056 1644055 183963 28890 2157 131567	Archaea	
UP000001845	Mycoplasma crocodyli (strain ATCC 51981 / MP145)	512564	7/30/2015	689	Mycoplasma crocodyli MP145	512564 50052 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000001844	Nitrosococcus halophilus (strain Nc4)	472759	7/30/2015	3770	Nitrosococcus halophilus Nc 4	472759 133539 1227 1046 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001060	Legionella longbeachae serogroup 1 (strain NSW150)	661367	7/30/2015	3460	Legionella longbeachae NSW150	661367 450 445 444 118969 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001059	Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP)	547558	7/30/2015	1986	Methanohalophilus mahii DSM 5219	547558 2176 2175 2206 94695 224756 28890 2157 131567	Archaea	
UP000007753	Sphingobium japonicum (strain NBRC 101211 / UT26S)	452662	7/30/2015	4347	Sphingobium japonicum UT26S	452662 332056 165695 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002350	Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)	637905	7/30/2015	4336	Shewanella violacea DSS12	637905 60217 22 267890 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000002349	Dehalogenimonas lykanthroporepellens (strain ATCC BAA-1523 / JCM 15061 / BL-DC-9)	552811	7/30/2015	1619	Dehalogenimonas lykanthroporepellens BL-DC-9	552811 552810 670486 301297 200795 2 131567	Bacteria	Chloroflexi
UP000007032	Helicobacter canadensis MIT 98-5491	537970	7/27/2015	1535	Helicobacter canadensis MIT 98-5491	537970 123841 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000007754	Taeniopygia guttata (Zebra finch) (Poephila guttata)	59729	8/2/2015	18141	Taeniopygia guttata	59729 59728 40155 37611 175121 9126 8825 8782 436492 436491 436489 436486 8492 1329799 32561 8457 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002356	Ovis aries (Sheep)	9940	8/16/2015	23133	Ovis aries	9940 9935 9963 9895 35500 9845 91561 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002360	Comamonas testosteroni (strain CNB-2)	688245	7/30/2015	4780	Comamonas testosteroni CNB-2	688245 543891 285 283 80864 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000002361	Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)	272942	7/30/2015	3632	Rhodobacter capsulatus SB 1003	272942 1061 1060 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002366	Aminobacterium colombiense (strain DSM 12261 / ALA-1)	572547	7/30/2015	1872	Aminobacterium colombiense DSM 12261	572547 81468 81466 649777 649776 649775 508458 2 131567	Bacteria	Synergistetes
UP000007460	Puniceispirillum marinum (strain IMCC1322)	488538	7/30/2015	2545	Candidatus Puniceispirillum marinum IMCC1322	488538 767892 767891 62654 82117 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002365	Bacillus megaterium (strain DSM 319)	592022	8/2/2015	5100	Bacillus megaterium DSM 319	592022 1404 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000001654	Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87)	655815	7/30/2015	4633	Zunongwangia profunda SM-A87	655815 398743 417127 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000927	Prevotella ruminicola (strain ATCC 19189 / JCM 8958 / 23)	264731	7/30/2015	2761	Prevotella ruminicola 23	264731 839 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000930	Moraxella catarrhalis (strain RH4)	749219	7/30/2015	1881	Moraxella catarrhalis RH4	749219 480 46226 475 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000925	Coraliomargarita akajimensis (strain DSM 45221 / IAM 15411 / JCM 23193 / KCTC 12865)	583355	7/30/2015	3110	Coraliomargarita akajimensis DSM 45221	583355 395922 442430 415002 415001 414999 74201 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000002368	Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	562970	7/30/2015	3135	Kyrpidia tusciae DSM 2912	562970 33943 1129704 186823 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000002357	Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	443255	8/7/2015	7290	Streptomyces clavuligerus ATCC 27064	443255 1901 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria

UP000002358	Nasonia vitripennis (Parasitic wasp)	7425	7/30/2015	17084	Nasonia vitripennis	7425 7424 272242 7423 7422 272201 7400 7399 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000008467	Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	642492	7/30/2015	4150	Clostridium lentocellum DSM 5427	642492 29360 698776 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002247	Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	640132	7/30/2015	3001	Segniliparus rotundus DSM 44985	640132 286802 286801 316606 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002376	Thermosphaera aggregans (strain DSM 11486 / M11TL)	633148	7/30/2015	1387	Thermosphaera aggregans DSM 11486	633148 54254 54253 2272 114380 183924 28889 2157 131567	Archaea	
UP000002377	Thermincola potens (strain JR)	635013	7/30/2015	2908	Thermincola potens JR	635013 863643 278993 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000939	Arcobacter nitrofigilis (strain ATCC 33309 / DSM 7299 / LMG 7604 / NCTC 12251 / CI) (Campylobacter nitrofigilis)	572480	7/30/2015	3125	Arcobacter nitrofigilis DSM 7299	572480 28199 28196 72294 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000006640	Thermobispora bispora (strain ATCC 19993 / DSM 43833 / CBS 139.67 / JCM 10125 / NBRC 14880 / R51)	469371	7/30/2015	3545	Thermobispora bispora DSM 43833	469371 2006 147067 1643818 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000378	Syntrophothermus lipocalidus (strain DSM 12680 / TGB-C1)	643648	7/30/2015	2311	Syntrophothermus lipocalidus DSM 12680	643648 86170 129001 68298 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000376	Arcanobacterium haemolyticum (strain ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018)	644284	7/30/2015	1717	Arcanobacterium haemolyticum DSM 20595	644284 28264 28263 2049 2037 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000377	Streptomyces bingchenggensis (strain BCW-1)	749414	8/7/2015	10019	Streptomyces bingchenggensis BCW-1	749414 379067 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006633	Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	639283	7/30/2015	4424	Starkeya novella DSM 506	639283 921 152053 335928 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000002226	Toxoplasma gondii	5811	8/2/2015	4727	Toxoplasma gondii	5811 5810 5809 423054 75739 5796 1280412 5794 33630 2759 131567	eukaryotes	
UP000000383	Methylotenera versatilis (strain 301)	666681	7/30/2015	2752	Methylotenera versatilis 301	666681 1055487 359407 32011 206350 28216 1224 2 131567	Bacteria	Proteobacteria
UP000000379	Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24)	649638	7/30/2015	2924	Truepera radiovictrix DSM 17093	649638 332249 332248 332247 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000000387	Rothia dentocariosa (strain ATCC 17931 / CDC X599 / XDIA)	762948	7/30/2015	2212	Rothia dentocariosa ATCC 17931	762948 2047 32207 1268 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000936	Propionibacterium freudenreichii subsp. shermanii (strain ATCC 9614 / CIP 103027 / CIRM-BIA1)	754252	7/30/2015	2310	Propionibacterium freudenreichii subsp. shermanii CIRM-BIA1	754252 1752 1744 1743 31957 85009 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000327	White spot syndrome virus (isolate Shrimp/China/Tongan/1996) (WSSV) (White spot bacilliform virus)	654913	7/30/2015	525	Shrimp white spot syndrome virus (isolate Tongan)	654913 92652 342409 249585 196937 35237 10239	Vruses	
UP000006742	Mobiluncus curtisii (strain ATCC 43063 / DSM 2711 / V125) (Falcivibrio vaginalis)	548479	7/30/2015	1904	Mobiluncus curtisii ATCC 43063	548479 2051 2050 2049 2037 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000391	Methanohalobium evestigatum (strain DSM 3721 / OCM 161 / Z-7303)	644295	7/30/2015	2250	Methanohalobium evestigatum Z-7303	644295 2322 2321 2206 94695 224756 28890 2157 131567	Archaea	
UP000000390	Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	795797	7/30/2015	3779	Halalkalicoccus jeotgali B3	795797 413810 332246 2236 2235 183963 28890 2157 131567	Archaea	
UP000001505	Waddlia chondrophila (strain ATCC VR-1470 / WSU 86-1044)	716544	7/30/2015	1919	Waddlia chondrophila WSU 86-1044	716544 71667 71666 92714 51291 204429 204428 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000000938	Human cytomegalovirus (strain Merlin) (HHV-5) (Human herpesvirus 5)	295027	7/30/2015	168	Human herpesvirus 5 strain Merlin	295027 10359 10358 10357 10292 548681 35237 10239	Vruses	
UP000006911	Tuber melanosporum (strain Mel28) (Perigord black truffle)	656061	7/30/2015	7494	Tuber melanosporum Mel28	656061 39416 36048 40289 5185 147549 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000006910	Lactobacillus fermentum (strain CECT 5716)	712938	7/30/2015	1043	Lactobacillus fermentum CECT 5716	712938 1613 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000000329	Herbaspirillum seropedicae (strain SmR1)	757424	8/2/2015	4732	Herbaspirillum seropedicae SmR1	757424 964 963 75682 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001660	Nitrospira defluvii	330214	7/27/2015	4263	Nitrospira defluvii	330214 1234 189779 189778 203693 40117 2 131567	Bacteria	Nitrospirae
UP000000333	Olsenella uli (strain ATCC 49627 / DSM 7084 / CIP 109912 / JCM 12494 / VPI D76D-27C) (Lactobacillus uli)	633147	7/30/2015	1739	Olsenella uli DSM 7084	633147 133926 133925 1643824 84999 84998 201174 2 131567	Bacteria	Actinobacteria
UP000009046	Pediculus humanus subsp. corporis (Body louse)	121224	7/30/2015	10763	Pediculus humanus corporis	121224 121225 121222 121221 30005 85819 33342 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000023152	Reticulomyxa filosa	46433	7/27/2015	39903	Reticulomyxa filosa	46433 46432 188961 1505960 29178 543769 2759 131567	eukaryotes	
UP000031521	Celeribacter indicus	1208324	7/27/2015	4665	Celeribacter indicus	1208324 875170 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000031524	Corynebacterium humireducens NBRC 106098 = DSM 45392	1223515	7/27/2015	2510	Corynebacterium humireducens NBRC 106098 = DSM 45392	1223515 1223514 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000031523	Streptomyces albus	1888	8/7/2015	7322	Streptomyces albus	1888 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000031526	Streptomyces nodosus	40318	8/5/2015	5863	Streptomyces nodosus	40318 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000031563	Bacillaceae bacterium MTCC 8252	1123719	7/30/2015	4016	Bacillaceae bacterium MTCC 8252	1123719 197483 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000031620	Lactobacillus hokkaidonensis	1193095	7/27/2015	2328	Lactobacillus	1193095 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000031623	Thioploca ingrica	40754	7/27/2015	3951	Thioploca ingrica	40754 40751 135617 72273 1236 1224 2 131567	Bacteria	Proteobacteria

UP000031627	Candidatus Tachikawaea gelatinosa	1410383	8/4/2015	613	Candidatus Tachikawaea gelatinosa	1410383 1682492 84563 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000023703	Corynebacterium glyciniphilum AJ 3170	1404245	7/27/2015	3270	Corynebacterium glyciniphilum AJ 3170	1404245 1404244 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000031625	cyanobacterium endosymbiont of Epithemia turgida isolate EtSB Lake Yunoko	1228987	7/27/2015	1720	cyanobacterium endosymbiont of Epithemia turgida isolate EtSB Lake Yunoko	1228987 718217 34079 1117 2 131567	Bacteria	Cyanobacteria
UP000031637	Sulfuritalea hydrogenivorans sk43H	1223802	7/27/2015	3578	Sulfuritalea hydrogenivorans sk43H	1223802 748811 1054211 75787 206389 28216 1224 2 131567	Bacteria	Proteobacteria
UP000031641	Mycoplasma canadense	29554	7/27/2015	481	Mycoplasma canadense	29554 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000031636	Winogradskyella sp. PG-2	754409	8/4/2015	3520	Winogradskyella sp. PG-2	754409 286104 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000031643	Methyloceanibacter caenitepidi	1384459	8/4/2015	3341	Methyloceanibacter caenitepidi	1384459 1484898 119042 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000031649	Burkholderiales bacterium GJ-E10	1469502	8/4/2015	2955	Burkholderiales bacterium GJ-E10	1469502 80841 119065 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000031651	Bacillus sp. (strain OxB-1)	98228	8/4/2015	3544	Bacillus sp. OxB-1	98228 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000031650	Chryseobacterium sp. StRB126	878220	8/5/2015	4811	Chryseobacterium sp. StRB126	878220 59732 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000031631	Thiolapillus brandeum	1076588	7/27/2015	2824	Thiolapillus brandeum	1076588 1608298 118884 1236 1224 2 131567	Bacteria	Proteobacteria
UP000031652	Pseudomonas sp. StFLB209	1028989	7/27/2015	5594	Pseudomonas sp.	1028989 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000023755	Neorickettsia helminthoeca str. Oregon	1286528	7/27/2015	868	Neorickettsia helminthoeca str. Oregon	1286528 33994 33993 942 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000031668	Thelohanellus kitauei (Myxosporean)	669202	7/27/2015	14792	Thelohanellus kitauei	669202 89725 35587 109802 35583 35582 35581 6073 6072 33208 33154 2759 131567	eukaryotes	
UP000023772	Draconibacterium orientale	1168034	7/27/2015	3940	Draconibacterium orientale	1168034 1471399 1471398 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000031760	Nonlabens marinus S1-08	1454201	7/27/2015	2790	Nonlabens marinus S1-08	1454201 930802 363408 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000031765	archaeon GW2011_AR20	1579378	7/27/2015	1010	archaeon GW2011_AR20	1579378 93506 29294 2157 131567	Archaea	
UP000031777	archaeon GW2011_AR10	1579370	7/27/2015	1339	archaeon GW2011_AR10	1579370 93506 29294 2157 131567	Archaea	
UP000031776	archaeon GW2011_AR15	1579373	7/27/2015	1308	archaeon GW2011_AR15	1579373 93506 29294 2157 131567	Archaea	
UP000031843	Cupriavidus basilensis	68895	7/27/2015	7643	Cupriavidus basilensis	68895 106589 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000031842	Myroides profundi	480520	7/27/2015	3534	Myroides profundi	480520 76831 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000031928	Corynebacterium marinum DSM 44953	1224162	7/27/2015	2547	Corynebacterium marinum DSM 44953	1224162 349751 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000031982	Bacillus badius	1455	7/27/2015	4479	Bacillus badius	1455 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000031980	Sanguibacteroides justesenii	1547597	7/27/2015	2587	Sanguibacteroides justesenii	1547597 1635148 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000032025	Sphingomonas paucimobilis NBRC 13935	1219050	7/27/2015	3995	Sphingomonas paucimobilis NBRC 13935	1219050 13689 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000032160	Candidatus Phaeomarinobacter ectocarpi	1458461	7/27/2015	3295	Candidatus Phaeomarinobacter ectocarpi	1458461 1541445 119043 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000032141	Brassica oleracea var. oleracea	109376	8/2/2015	58535	Brassica oleracea var. oleracea	109376 3712 3705 981071 3700 3699 91836 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000024387	Dyella jiangningensis	1379159	7/27/2015	4342	Dyella jiangningensis	1379159 231454 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000032180	Leersia perrieri	77586	7/27/2015	36775	Leersia perrieri	77586 35711 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000032229	Siansivirga zeaxanthinifaciens CC-SAMT-1	1454006	7/27/2015	2744	Siansivirga zeaxanthinifaciens CC-SAMT-	1454006 762954 1204360 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000032266	Gynuella sunshinyii YC6258	1445510	7/27/2015	5913	Gynuella sunshinyii YC6258	1445510 1445505 1445504 255527 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000032276	Aneurinibacillus migulanus (Bacillus migulanus)	47500	7/27/2015	5438	Aneurinibacillus migulanus	47500 55079 85151 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000032261	Ureaplasma diversum	42094	7/27/2015	625	Ureaplasma diversum	42094 2129 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000032303	Photobacterium gaetbulicola Gung47	658445	7/27/2015	4974	Photobacterium gaetbulicola Gung47	658445 1295392 657 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000032234	Streptomyces cyaneogriseus subsp. noncyanogenus	477245	7/27/2015	5829	Streptomyces cyaneogriseus subsp. noncyanogenus	477245 68192 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000032287	Weissella cibaria	137591	8/4/2015	2282	Weissella cibaria	137591 46255 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000024404	Onchocerca volvulus	6282	7/27/2015	12994	Onchocerca volvulus	6282 6281 6296 6295 6274 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000032300	Sphingomonas sp. WHSC-8	1609977	7/27/2015	4211	Sphingomonas	1609977 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000032320	Paenibacillus sp. IHBB 10380	1566358	7/27/2015	4588	Paenibacillus sp. IHBB 10380	1566358 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000007456	Vibrio furnissii (strain DSM 14383 / NCTC 11218)	903510	7/30/2015	4440	Vibrio furnissii NCTC 11218	903510 29494 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000024941	Rhodococcus sp. BCP1	931223	7/27/2015	5509	Rhodococcus sp. BCP1	931223 1827 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000033816	Parcubacteria bacterium GW2011_GWA2_46_39	1618836	7/30/2015	345	Parcubacteria bacterium GW2011_GWA2_46_39	1618836 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000025222	Stenotrophomonas rhizophila	216778	7/27/2015	3922	Stenotrophomonas rhizophila	216778 40323 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria

UP000033829	Parcubacteria bacterium GW2011_GWA2_45_30	1618834	7/30/2015	769	Parcubacteria bacterium GW2011_GWA2_45_30	1618834 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033819	Parcubacteria bacterium GW2011_GWA2_43_17	1618827	7/30/2015	1238	Parcubacteria bacterium GW2011_GWA2_43_17	1618827 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033821	Parcubacteria bacterium GW2011_GWA2_42_11	1618819	7/30/2015	545	Parcubacteria bacterium GW2011_GWA2_42_11	1618819 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033825	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWA2_49_56	1618670	7/30/2015	130	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWA2_49_56	1618670 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000025229	Rubrobacter radiotolerans	42256	7/27/2015	3148	Rubrobacter radiotolerans	42256 42255 84997 255725 84996 84995 201174 2 131567	Bacteria	Actinobacteria
UP000033838	Parcubacteria bacterium GW2011_GWA2_52_8	1618857	7/30/2015	470	Parcubacteria bacterium GW2011_GWA2_52_8	1618857 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033847	candidate division WWE3 bacterium GW2011_GWF1_42_14	1619138	7/30/2015	977	candidate division WWE3 bacterium GW2011_GWF1_42_14	1619138 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033822	Parcubacteria bacterium GW2011_GWD2_42_14	1618944	7/30/2015	1088	Parcubacteria bacterium GW2011_GWD2_42_14	1618944 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033854	Microgenomates (Collierbacteria) bacterium GW2011_GWA2_42_17	1618378	7/30/2015	800	Microgenomates (Collierbacteria) bacterium GW2011_GWA2_42_17	1618378 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033856	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWF2_41_8	1618667	7/30/2015	620	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWF2_41_8	1618667 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033842	candidate division TM6 bacterium GW2011_GWF2_28_16	1619077	7/30/2015	953	candidate division TM6 bacterium GW2011_GWF2_28_16	1619077 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033858	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_41_10	1618577	7/30/2015	595	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_41_10	1618577 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033846	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA2_44_10	1619024	7/30/2015	549	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA2_44_10	1619024 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033859	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWC2_41_9	1619029	7/30/2015	670	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWC2_41_9	1619029 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033860	Microgenomates (Beckwithbacteria) bacterium GW2011_GWB1_47_15	1618371	7/30/2015	1146	Microgenomates (Beckwithbacteria) bacterium GW2011_GWB1_47_15	1618371 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033869	candidate division CPR2 bacterium GW2011_GWC1_41_48	1618344	7/30/2015	1116	candidate division CPR2 bacterium GW2011_GWC1_41_48	1618344 1618339 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033866	candidate division WS6 bacterium GW2011_GWE1_34_7	1619093	7/30/2015	606	candidate division WS6 bacterium GW2011_GWE1_34_7	1619093 74243 2323 2 131567	Bacteria	Unclassified Bacteria
UP000025241	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	1301098	7/27/2015	5616	Pseudomonas knackmussii B13	1301098 65741 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000033870	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_56_11	1619044	7/30/2015	1162	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_56_11	1619044 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033876	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_37_5	1618742	7/30/2015	831	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_37_5	1618742 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033877	Microgenomates bacterium GW2011_GWC1_38_14	1618513	7/30/2015	392	Microgenomates bacterium GW2011_GWC1_38_14	1618513 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033875	Parcubacteria bacterium GW2011_GWB1_49_7	1618883	7/30/2015	442	Parcubacteria bacterium GW2011_GWB1_49_7	1618883 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033865	Parcubacteria (Uhrbacteria) bacterium GW2011_GWC2_53_7	1618986	7/30/2015	627	Parcubacteria (Uhrbacteria) bacterium GW2011_GWC2_53_7	1618986 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033884	Parcubacteria bacterium GW2011_GWA2_37_10	1618810	7/30/2015	832	Parcubacteria bacterium GW2011_GWA2_37_10	1618810 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033881	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_39_12	1618574	7/30/2015	1817	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_39_12	1618574 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033880	Microgenomates (Levybacteria) bacterium GW2011_GWB1_35_5	1618461	7/30/2015	589	Microgenomates (Levybacteria) bacterium GW2011_GWB1_35_5	1618461 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033901	Microgenomates (Curtissbacteria) bacterium GW2011_GWC1_44_33	1618413	7/30/2015	510	Microgenomates (Curtissbacteria) bacterium GW2011_GWC1_44_33	1618413 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria

UP000033896	Parcubacteria bacterium GW2011_GWA1_59_11	1618804	7/30/2015	754	Parcubacteria bacterium GW2011_GWA1_59_11	1618804 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033902	Microgenomates (Levybacteria) bacterium GW2011_GWB1_37_8	1618463	7/30/2015	796	Microgenomates (Levybacteria) bacterium GW2011_GWB1_37_8	1618463 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033903	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA2_41_22	1619023	7/30/2015	259	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA2_41_22	1619023 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033912	Parcubacteria bacterium GW2011_GWA2_47_10b	1618840	7/30/2015	878	Parcubacteria bacterium GW2011_GWA2_47_10b	1618840 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033913	Parcubacteria bacterium GW2011_GWA2_53_21	1618858	7/30/2015	512	Parcubacteria bacterium GW2011_GWA2_53_21	1618858 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033918	Parcubacteria (Wolfebacteria) bacterium GW2011_GWB1_41_12	1619006	7/30/2015	688	Parcubacteria (Wolfebacteria) bacterium GW2011_GWB1_41_12	1619006 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000009882	Penicillium digitatum (strain PHI26 / CECT 20796) (Green mold)	1170229	7/30/2015	9101	Penicillium digitatum PHI26	1170229 36651 5073 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000033909	Parcubacteria bacterium GW2011_GWC1_41_7	1618904	7/30/2015	534	Parcubacteria bacterium GW2011_GWC1_41_7	1618904 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033910	candidate division WWE3 bacterium GW2011_GWB2_43_22	1619118	7/30/2015	440	candidate division WWE3 bacterium GW2011_GWB2_43_22	1619118 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033894	Microgenomates bacterium GW2011_GWC1_44_23	1618523	7/30/2015	966	Microgenomates bacterium GW2011_GWC1_44_23	1618523 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033922	Microgenomates (Pacebacteria) bacterium GW2011_GWF2_38_9	1618472	7/30/2015	871	Microgenomates (Pacebacteria) bacterium GW2011_GWF2_38_9	1618472 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033908	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_41_12	1618440	7/30/2015	246	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_41_12	1618440 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033926	candidate division TM6 bacterium GW2011_GWF2_37_49	1619083	7/30/2015	1225	candidate division TM6 bacterium GW2011_GWF2_37_49	1619083 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033923	Parcubacteria (Nomurabacteria) bacterium GW2011_GWA1_35_8	1618727	7/30/2015	287	Parcubacteria (Nomurabacteria) bacterium GW2011_GWA1_35_8	1618727 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033935	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_39_13	1618995	7/30/2015	1082	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_39_13	1618995 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033930	Parcubacteria (Uhrbacteria) bacterium GW2011_GWC1_41_20	1618983	7/30/2015	882	Parcubacteria (Uhrbacteria) bacterium GW2011_GWC1_41_20	1618983 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033934	Berkelbacteria bacterium GW2011_GWA2_38_9	1618334	7/30/2015	842	Berkelbacteria bacterium GW2011_GWA2_38_9	1618334 1618330 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033936	Parcubacteria bacterium GW2011_GWB1_44_7	1618876	7/30/2015	663	Parcubacteria bacterium GW2011_GWB1_44_7	1618876 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033948	Microgenomates bacterium GW2011_GWC1_41_20	1618518	7/30/2015	553	Microgenomates bacterium GW2011_GWC1_41_20	1618518 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033945	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_44_26	1618648	7/30/2015	1054	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_44_26	1618648 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033954	Parcubacteria bacterium GW2011_GWA1_49_11	1618796	7/30/2015	326	Parcubacteria bacterium GW2011_GWA1_49_11	1618796 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033949	Parcubacteria (Nomurabacteria) bacterium GW2011_GWC2_41_8	1618755	7/30/2015	593	Parcubacteria (Nomurabacteria) bacterium GW2011_GWC2_41_8	1618755 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033953	Parcubacteria bacterium GW2011_GWB1_43_8	1618874	7/30/2015	664	Parcubacteria bacterium GW2011_GWB1_43_8	1618874 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033957	Peregrinibacteria bacterium GW2011_GWF2_38_29	1619066	7/30/2015	1162	Peregrinibacteria bacterium GW2011_GWF2_38_29	1619066 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033965	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWA2_49_19	1618669	7/30/2015	581	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWA2_49_19	1618669 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033966	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWA2_45_13	1618662	7/30/2015	657	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWA2_45_13	1618662 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033976	Parcubacteria bacterium GW2011_GWF2_42_7	1618966	7/30/2015	857	Parcubacteria bacterium GW2011_GWF2_42_7	1618966 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033973	Parcubacteria bacterium GW2011_GWA2_46_10	1618835	7/30/2015	603	Parcubacteria bacterium GW2011_GWA2_46_10	1618835 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria

UP000033978	Parcubacteria bacterium GW2011_GWA1_47_10	1618791	7/30/2015	837	Parcubacteria bacterium GW2011_GWA1_47_10	1618791 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033964	Parcubacteria bacterium GW2011_GWA2_56_7	1618860	7/30/2015	406	Parcubacteria bacterium GW2011_GWA2_56_7	1618860 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033982	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_50_22	1619043	7/30/2015	312	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_50_22	1619043 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033988	Parcubacteria bacterium GW2011_GWC1_40_11	1618902	7/30/2015	750	Parcubacteria bacterium GW2011_GWC1_40_11	1618902 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033990	alpha proteobacterium HIMB114	684719	7/30/2015	1321	alpha proteobacterium HIMB114	684719 1655516 1655514 54526 28211 1224 2 131567	Bacteria	Proteobacteria
UP000033958	bacterium GW2011_GWB1_45_10	1620411	7/30/2015	196	bacterium GW2011_GWB1_45_10	1620411 49928 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033995	Microgenomates (Woesebacteria) bacterium GW2011_GWA2_33_28	1618561	7/30/2015	1044	Microgenomates (Woesebacteria) bacterium GW2011_GWA2_33_28	1618561 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034000	Microgenomates (Levybacteria) bacterium GW2011_GWA2_37_36	1618457	7/30/2015	552	Microgenomates (Levybacteria) bacterium GW2011_GWA2_37_36	1618457 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034008	Parcubacteria bacterium GW2011_GWC1_45_9	1618916	7/30/2015	615	Parcubacteria bacterium GW2011_GWC1_45_9	1618916 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034006	Microgenomates (Collierbacteria) bacterium GW2011_GWB2_44_22	1618387	7/30/2015	1168	Microgenomates (Collierbacteria) bacterium GW2011_GWB2_44_22	1618387 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000033999	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_45_39	1619041	7/30/2015	869	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_45_39	1619041 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034004	Microgenomates (Roizmanbacteria) bacterium GW2011_GWC2_34_23	1618484	7/30/2015	783	Microgenomates (Roizmanbacteria) bacterium GW2011_GWC2_34_23	1618484 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034016	Microgenomates bacterium GW2011_GWA2_47_8	1618503	7/30/2015	782	Microgenomates bacterium GW2011_GWA2_47_8	1618503 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034020	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWB1_45_9b	1618653	7/30/2015	410	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWB1_45_9b	1618653 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034031	Microgenomates (Levybacteria) bacterium GW2011_GWA2_36_13	1618456	7/30/2015	452	Microgenomates (Levybacteria) bacterium GW2011_GWA2_36_13	1618456 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034025	Parcubacteria bacterium GW2011_GWA2_42_14	1618820	7/30/2015	1246	Parcubacteria bacterium GW2011_GWA2_42_14	1618820 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034024	'Deinococcus soli' Cha et al. 2014	1309411	7/30/2015	2935	'Deinococcus soli' Cha et al. 2014	1309411 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000034034	Streptomyces xiamenensis	408015	8/16/2015	5484	Streptomyces xiamenensis	408015 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000034032	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA2_44_9	1619025	7/30/2015	975	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA2_44_9	1619025 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034036	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWF2_42_19	1618659	7/30/2015	934	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWF2_42_19	1618659 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034033	Microgenomates (Curtissbacteria) bacterium GW2011_GWC2_41_21	1618415	7/30/2015	1141	Microgenomates (Curtissbacteria) bacterium GW2011_GWC2_41_21	1618415 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034044	Parcubacteria (Wolfebacteria) bacterium GW2011_GWC1_37_10	1619010	7/30/2015	597	Parcubacteria (Wolfebacteria) bacterium GW2011_GWC1_37_10	1619010 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034029	Salinicoccus halodurans	407035	7/30/2015	2634	Salinicoccus halodurans	407035 45669 90964 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000034038	Parcubacteria bacterium GW2011_GWF2_44_7	1618970	7/30/2015	420	Parcubacteria bacterium GW2011_GWF2_44_7	1618970 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032414	Tatlockia micdadei (Legionella micdadei)	451	7/27/2015	2989	Tatlockia micdadei	451 465 444 118969 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034043	Parcubacteria bacterium GW2011_GWA2_50_10b	1618854	7/30/2015	439	Parcubacteria bacterium GW2011_GWA2_50_10b	1618854 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032410	Rhodococcus sp. B7740	1564114	7/27/2015	5193	Rhodococcus sp. B7740	1564114 1827 85025 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000032409	Peptoniphilus sp. 1-1	875453	7/27/2015	1528	Peptoniphilus sp. 1-1	875453 162289 1570339 1737405 1737404 1239 2 131567	Bacteria	Firmicutes
UP000032417	Porphyromonadaceae bacterium ING2-E5B	1562970	7/27/2015	2391	Porphyromonadaceae bacterium ING2-E5B	1562970 361210 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000034050	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWB1_43_11	1618446	7/30/2015	1522	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWB1_43_11	1618446 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034056	candidate division TM6 bacterium GW2011_GWF2_43_87	1619086	7/30/2015	910	candidate division TM6 bacterium GW2011_GWF2_43_87	1619086 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032413	Streptomyces lydicus A02	1403539	8/7/2015	8500	Streptomyces lydicus A02	1403539 47763 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000034048	Parcubacteria (Falkowbacteria) bacterium GW2011_GWA2_39_24	1618634	7/30/2015	579	Parcubacteria (Falkowbacteria) bacterium GW2011_GWA2_39_24	1618634 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032420	Candidatus Evansia muelleri	1495769	7/27/2015	330	Candidatus Evansia	1495769 1495768 114403 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034063	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_44_17	1618444	7/30/2015	652	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_44_17	1618444 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034054	Parcubacteria (Uhrbacteria) bacterium GW2011_GWA2_52_8d	1618979	7/30/2015	785	Parcubacteria (Uhrbacteria) bacterium GW2011_GWA2_52_8d	1618979 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034059	Parcubacteria bacterium GW2011_GWC2_49_9	1618934	7/30/2015	1288	Parcubacteria bacterium GW2011_GWC2_49_9	1618934 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034062	Parcubacteria bacterium GW2011_GWB1_41_6	1618869	7/30/2015	667	Parcubacteria bacterium GW2011_GWB1_41_6	1618869 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034069	Microgenomates (Collierbacteria) bacterium GW2011_GWA1_44_12	1618376	7/30/2015	855	Microgenomates (Collierbacteria) bacterium GW2011_GWA1_44_12	1618376 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034072	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWE2_40_11	1619033	7/30/2015	792	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWE2_40_11	1619033 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034070	Parcubacteria (Campbellbacteria) bacterium GW2011_GWC1_35_31	1618629	7/30/2015	765	Parcubacteria (Campbellbacteria) bacterium GW2011_GWC1_35_31	1618629 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034071	Kangiella geojedonensis	914150	7/30/2015	2207	Kangiella geojedonensis	914150 261963 224372 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000032434	Acholeplasma oculi	35623	7/27/2015	1468	Acholeplasma oculi	35623 2147 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000034083	Parcubacteria bacterium GW2011_GWA2_36_10	1618808	7/30/2015	863	Parcubacteria bacterium GW2011_GWA2_36_10	1618808 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034086	Microgenomates (Woesebacteria) bacterium GW2011_GWE1_45_18	1618598	7/30/2015	682	Microgenomates (Woesebacteria) bacterium GW2011_GWE1_45_18	1618598 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032431	[Clostridium] cellulosi	29343	7/27/2015	2007	[Clostridium] cellulosi	29343 1508657 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000032438	Moritella viscosa	80854	7/27/2015	4219	Moritella viscosa	80854 58050 267891 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034081	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_38_8	1618570	7/30/2015	1394	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_38_8	1618570 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032430	Legionella fallonii LLAP-10	1212491	7/27/2015	3840	Legionella fallonii LLAP-10	1212491 96230 445 444 118969 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034096	Microgenomates (Woesebacteria) bacterium GW2011_GWC1_38_13	1618583	7/30/2015	1019	Microgenomates (Woesebacteria) bacterium GW2011_GWC1_38_13	1618583 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032448	Photobacterium iliopiscarium	56192	8/4/2015	3736	Photobacterium	56192 657 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034108	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_41_17	1619048	7/30/2015	770	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_41_17	1619048 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034107	Parcubacteria (Nomurabacteria) bacterium GW2011_GWA1_46_11	1618732	7/30/2015	975	Parcubacteria (Nomurabacteria) bacterium GW2011_GWA1_46_11	1618732 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034106	Dehalogenimonas sp. WBC-2	943347	8/4/2015	1717	Dehalogenimonas sp. WBC-2	943347 670486 301297 200795 2 131567	Bacteria	Chloroflexi
UP000034117	Parcubacteria bacterium GW2011_GWA2_47_16	1618842	7/30/2015	892	Parcubacteria bacterium GW2011_GWA2_47_16	1618842 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034112	Trichoderma harzianum (Hypocrea lixii)	5544	7/30/2015	11497	Trichoderma harzianum	5544 5543 5129 5125 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000032479	Photobacterium leiognathi	553611	8/4/2015	3854	Photobacterium leiognathi	553611 657 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034128	candidate division WWE3 bacterium GW2011_GWA2_44_16	1619110	7/30/2015	366	candidate division WWE3 bacterium GW2011_GWA2_44_16	1619110 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034130	Parcubacteria bacterium GW2011_GWA2_47_8b	1618848	7/30/2015	530	Parcubacteria bacterium GW2011_GWA2_47_8b	1618848 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034132	Parcubacteria bacterium GW2011_GWA2_47_64	1618845	7/30/2015	1097	Parcubacteria bacterium GW2011_GWA2_47_64	1618845 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034119	candidate division CPR1 bacterium GW2011_GWC1_49_13	1618342	7/30/2015	606	candidate division CPR1 bacterium GW2011_GWC1_49_13	1618342 1618338 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034137	Parcubacteria (Falkowbacteria) bacterium GW2011_GWF2_39_8	1618642	7/30/2015	1038	Parcubacteria (Falkowbacteria) bacterium GW2011_GWF2_39_8	1618642 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034136	Parcubacteria bacterium GW2011_GWC2_44_22	1618930	7/30/2015	1216	Parcubacteria bacterium GW2011_GWC2_44_22	1618930 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034140	candidate division WS6 bacterium GW2011_GWC1_36_11	1619090	7/30/2015	737	candidate division WS6 bacterium GW2011_GWC1_36_11	1619090 74243 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034135	Microgenomates (Daviesbacteria) bacterium GW2011_GWA1_42_6	1618420	7/30/2015	491	Microgenomates (Daviesbacteria) bacterium GW2011_GWA1_42_6	1618420 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034143	Parcubacteria bacterium GW2011_GWA1_50_14	1618798	7/30/2015	433	Parcubacteria bacterium GW2011_GWA1_50_14	1618798 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034158	Parcubacteria bacterium GW2011_GWB1_55_9	1618887	7/30/2015	602	Parcubacteria bacterium GW2011_GWB1_55_9	1618887 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034149	Microgenomates bacterium GW2011_GWC1_46_20	1618528	7/30/2015	903	Microgenomates bacterium GW2011_GWC1_46_20	1618528 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034161	Parcubacteria bacterium GW2011_GWC1_43_30	1618910	7/30/2015	850	Parcubacteria bacterium GW2011_GWC1_43_30	1618910 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034154	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_44_350	1619000	7/30/2015	1030	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_44_350	1619000 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034160	Microgenomates (Amesbacteria) bacterium GW2011_GWA2_42_12	1618356	7/30/2015	823	Microgenomates (Amesbacteria) bacterium GW2011_GWA2_42_12	1618356 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034155	Parcubacteria bacterium GW2011_GWC2_32_10	1618918	7/30/2015	1108	Parcubacteria bacterium GW2011_GWC2_32_10	1618918 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034173	Parcubacteria bacterium GW2011_GWC2_42_12	1618926	7/30/2015	962	Parcubacteria bacterium GW2011_GWC2_42_12	1618926 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034170	Parcubacteria bacterium GW2011_GWC1_43_12	1618909	7/30/2015	793	Parcubacteria bacterium GW2011_GWC1_43_12	1618909 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034167	Microgenomates bacterium GW2011_GWC1_39_12	1618514	7/30/2015	833	Microgenomates bacterium GW2011_GWC1_39_12	1618514 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034156	Nitrosomonas communis	44574	7/30/2015	3064	Nitrosomonas communis	44574 914 206379 32003 28216 1224 2 131567	Bacteria	Proteobacteria
UP000034175	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_46_17	1619042	7/30/2015	592	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_46_17	1619042 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034178	Microgenomates bacterium GW2011_GWC1_39_7b	1618516	7/30/2015	619	Microgenomates bacterium GW2011_GWC1_39_7b	1618516 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034176	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_34_13	1618434	7/30/2015	597	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_34_13	1618434 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034183	Peregrinibacteria bacterium GW2011_GWF2_33_10	1619065	7/30/2015	1394	Peregrinibacteria bacterium GW2011_GWF2_33_10	1619065 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034190	Parcubacteria (Falkowbacteria) bacterium GW2011_GWA2_41_14	1618635	7/30/2015	455	Parcubacteria (Falkowbacteria) bacterium GW2011_GWA2_41_14	1618635 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034181	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_38_5b	1618569	7/30/2015	970	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_38_5b	1618569 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034198	Parcubacteria bacterium GW2011_GWA1_33_6	1618781	7/30/2015	292	Parcubacteria bacterium GW2011_GWA1_33_6	1618781 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034197	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_40_263	1618996	7/30/2015	1041	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_40_263	1618996 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034191	Parcubacteria bacterium GW2011_GWC1_36_108	1618894	7/30/2015	1009	Parcubacteria bacterium GW2011_GWC1_36_108	1618894 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034192	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_44_11b	1618580	7/30/2015	305	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_44_11b	1618580 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034201	Parcubacteria (Adlerbacteria) bacterium GW2011_GWC1_50_9	1618608	7/30/2015	910	Parcubacteria (Adlerbacteria) bacterium GW2011_GWC1_50_9	1618608 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034204	Microgenomates bacterium GW2011_GWC1_43_11	1618520	7/30/2015	1121	Microgenomates bacterium GW2011_GWC1_43_11	1618520 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034208	Microgenomates bacterium GW2011_GWA2_39_19	1618498	7/30/2015	736	Microgenomates bacterium GW2011_GWA2_39_19	1618498 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034213	Microgenomates (Beckwithbacteria) bacterium GW2011_GWA2_43_10	1618369	7/30/2015	697	Microgenomates (Beckwithbacteria) bacterium GW2011_GWA2_43_10	1618369 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034207	candidate division CPR2 bacterium GW2011_GWC2_39_10	1618345	7/30/2015	1123	candidate division CPR2 bacterium GW2011_GWC2_39_10	1618345 1618339 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034212	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_47_8	1618438	7/30/2015	336	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_47_8	1618438 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034219	candidate division TM6 bacterium GW2011_GWA2_36_9	1619072	7/30/2015	1134	candidate division TM6 bacterium GW2011_GWA2_36_9	1619072 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034211	Microgenomates bacterium GW2011_GWA2_37_6	1618497	7/30/2015	516	Microgenomates bacterium GW2011_GWA2_37_6	1618497 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034231	Microgenomates (Shapirobacteria) bacterium GW2011_GWE1_38_10	1618488	7/30/2015	1056	Microgenomates (Shapirobacteria) bacterium GW2011_GWE1_38_10	1618488 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034235	Microgenomates (Daviesbacteria) bacterium GW2011_GWA2_38_24	1618422	7/30/2015	1234	Microgenomates (Daviesbacteria) bacterium GW2011_GWA2_38_24	1618422 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034251	Microgenomates bacterium GW2011_GWC1_37_12b	1618510	7/30/2015	1051	Microgenomates bacterium GW2011_GWC1_37_12b	1618510 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034246	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_39_21	1618550	7/30/2015	1069	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_39_21	1618550 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034250	Parcubacteria bacterium GW2011_GWB1_36_5	1618862	7/30/2015	649	Parcubacteria bacterium GW2011_GWB1_36_5	1618862 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034254	Parcubacteria bacterium GW2011_GWC1_39_29	1618900	7/30/2015	651	Parcubacteria bacterium GW2011_GWC1_39_29	1618900 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034258	Parcubacteria bacterium GW2011_GWF2_38_76	1618960	7/30/2015	919	Parcubacteria bacterium GW2011_GWF2_38_76	1618960 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034262	Parcubacteria bacterium GW2011_GWF2_38_8	1618961	7/30/2015	733	Parcubacteria bacterium GW2011_GWF2_38_8	1618961 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034272	Parcubacteria bacterium GW2011_GWA1_47_8	1618793	7/30/2015	891	Parcubacteria bacterium GW2011_GWA1_47_8	1618793 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034269	Parcubacteria bacterium GW2011_GWC1_38_17	1618896	7/30/2015	699	Parcubacteria bacterium GW2011_GWC1_38_17	1618896 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034284	Parcubacteria bacterium GW2011_GWB1_56_8	1618888	7/30/2015	897	Parcubacteria bacterium GW2011_GWB1_56_8	1618888 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034290	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_53_7	1618650	7/30/2015	707	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_53_7	1618650 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034283	Streptomyces sp. CNQ-509	444103	7/30/2015	6367	Streptomyces sp. CNQ-509	444103 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000034303	Parcubacteria bacterium GW2011_GWF2_43_11	1618967	7/30/2015	539	Parcubacteria bacterium GW2011_GWF2_43_11	1618967 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034294	Parcubacteria bacterium GW2011_GWA2_33_14	1618807	7/30/2015	673	Parcubacteria bacterium GW2011_GWA2_33_14	1618807 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034304	Microgenomates bacterium GW2011_GWC1_41_8	1618519	7/30/2015	1100	Microgenomates bacterium GW2011_GWC1_41_8	1618519 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034292	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_40_9	1618408	7/30/2015	340	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_40_9	1618408 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034302	candidate division WS6 bacterium GW2011_GWC1_33_20	1619089	7/30/2015	666	candidate division WS6 bacterium GW2011_GWC1_33_20	1619089 74243 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034301	Parcubacteria (Nomurabacteria) bacterium GW2011_GWF2_40_12	1618776	7/30/2015	760	Parcubacteria (Nomurabacteria) bacterium GW2011_GWF2_40_12	1618776 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034313	Parcubacteria bacterium GW2011_GWA1_60_11	1618805	7/30/2015	237	Parcubacteria bacterium GW2011_GWA1_60_11	1618805 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034320	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_42_18	1618442	7/30/2015	1324	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_42_18	1618442 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034324	Microgenomates (Daviesbacteria) bacterium GW2011_GWF2_38_6	1618432	7/30/2015	952	Microgenomates (Daviesbacteria) bacterium GW2011_GWF2_38_6	1618432 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034323	Microgenomates bacterium GW2011_GWC1_46_16	1618527	7/30/2015	779	Microgenomates bacterium GW2011_GWC1_46_16	1618527 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034329	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_45_5	1618581	7/30/2015	755	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_45_5	1618581 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034328	Parcubacteria bacterium GW2011_GWA2_49_9	1618852	7/30/2015	983	Parcubacteria bacterium GW2011_GWA2_49_9	1618852 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034333	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_37_8	1619036	7/30/2015	847	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_37_8	1619036 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034319	Parcubacteria bacterium GW2011_GWF2_39_13b	1618962	7/30/2015	440	Parcubacteria bacterium GW2011_GWF2_39_13b	1618962 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034316	Berkelbacteria bacterium GW2011_GWA2_35_9	1618333	7/30/2015	680	Berkelbacteria bacterium GW2011_GWA2_35_9	1618333 1618330 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034318	Microgenomates bacterium GW2011_GWA2_46_7	1618502	7/30/2015	671	Microgenomates bacterium GW2011_GWA2_46_7	1618502 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034347	Parcubacteria bacterium GW2011_GWB1_45_7	1618878	7/30/2015	359	Parcubacteria bacterium GW2011_GWB1_45_7	1618878 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034349	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_32_13	1618475	7/30/2015	593	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_32_13	1618475 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034342	Parcubacteria bacterium GW2011_GWA2_42_18	1618821	7/30/2015	606	Parcubacteria bacterium GW2011_GWA2_42_18	1618821 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034344	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_36_23	1618480	7/30/2015	552	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_36_23	1618480 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034358	Parcubacteria bacterium GW2011_GWD2_43_10	1618945	7/30/2015	802	Parcubacteria bacterium GW2011_GWD2_43_10	1618945 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034371	Microgenomates (Roizmanbacteria) bacterium GW2011_GWC2_41_7	1618487	7/30/2015	1049	Microgenomates (Roizmanbacteria) bacterium GW2011_GWC2_41_7	1618487 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034375	Parcubacteria bacterium GW2011_GWA2_42_28	1618822	7/30/2015	524	Parcubacteria bacterium GW2011_GWA2_42_28	1618822 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034380	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA1_41_6	1619020	7/30/2015	323	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA1_41_6	1619020 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034379	Microgenomates bacterium GW2011_GWB1_40_9	1618504	7/30/2015	568	Microgenomates bacterium GW2011_GWB1_40_9	1618504 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034388	Parcubacteria bacterium GW2011_GWA2_47_12	1618841	7/30/2015	770	Parcubacteria bacterium GW2011_GWA2_47_12	1618841 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034392	Altererythrobacter atlanticus	1267766	7/30/2015	3276	Altererythrobacter atlanticus	1267766 361177 335929 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000034406	Microgenomates (Shapirobacteria) bacterium GW2011_GWE2_38_30	1618490	7/30/2015	902	Microgenomates (Shapirobacteria) bacterium GW2011_GWE2_38_30	1618490 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034403	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA1_48_10	1619022	7/30/2015	328	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA1_48_10	1619022 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034417	Parcubacteria bacterium GW2011_GWA2_56_21	1618859	7/30/2015	422	Parcubacteria bacterium GW2011_GWA2_56_21	1618859 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034415	Peregrinibacteria bacterium GW2011_GWA2_44_7	1619057	7/30/2015	1347	Peregrinibacteria bacterium GW2011_GWA2_44_7	1619057 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034426	Parcubacteria bacterium GW2011_GWA1_48_11b	1618795	7/30/2015	647	Parcubacteria bacterium GW2011_GWA1_48_11b	1618795 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034410	Sedimenticola sp. SIP-G1	1543721	7/30/2015	3407	Sedimenticola sp. SIP-G1	1543721 349742 118884 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034416	Mycobacterium arupense	342002	7/30/2015	3776	Mycobacterium arupense	342002 1073531 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000034427	Parcubacteria bacterium GW2011_GWA2_47_9	1618849	7/30/2015	815	Parcubacteria bacterium GW2011_GWA2_47_9	1618849 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034423	Parcubacteria bacterium GW2011_GWA1_51_12	1618799	7/30/2015	797	Parcubacteria bacterium GW2011_GWA1_51_12	1618799 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034431	Parcubacteria (Falkowbacteria) bacterium GW2011_GWF2_43_32	1618643	7/30/2015	794	Parcubacteria (Falkowbacteria) bacterium GW2011_GWF2_43_32	1618643 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034439	Parcubacteria bacterium GW2011_GWA2_44_12	1618829	7/30/2015	813	Parcubacteria bacterium GW2011_GWA2_44_12	1618829 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032614	Burkholderia fungorum	134537	7/27/2015	8142	Burkholderia fungorum	134537 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000034432	Microgenomates (Pacebacteria) bacterium GW2011_GWA1_46_10	1618469	7/30/2015	922	Microgenomates (Pacebacteria) bacterium GW2011_GWA1_46_10	1618469 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032611	Martelella endophytica	1486262	7/27/2015	4020	Martelella endophytica	1486262 293088 255475 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000034442	Parcubacteria bacterium GW2011_GWB1_50_9	1618884	7/30/2015	578	Parcubacteria bacterium GW2011_GWB1_50_9	1618884 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034446	Parcubacteria bacterium GW2011_GWC1_38_6	1618898	7/30/2015	599	Parcubacteria bacterium GW2011_GWC1_38_6	1618898 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034445	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWC2_52_8b	1618676	7/30/2015	1092	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWC2_52_8b	1618676 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034449	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_42_27	1619049	7/30/2015	1154	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_42_27	1619049 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034456	Parcubacteria bacterium GW2011_GWA2_51_10	1618855	7/30/2015	796	Parcubacteria bacterium GW2011_GWA2_51_10	1618855 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034452	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_40_7	1618744	7/30/2015	587	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_40_7	1618744 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034453	candidate division TM6 bacterium GW2011_GWE2_42_60	1619076	7/30/2015	939	candidate division TM6 bacterium GW2011_GWE2_42_60	1619076 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034457	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_35_19	1618478	7/30/2015	1198	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_35_19	1618478 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032633	Paenibacillus beijingensis	1126833	7/27/2015	4723	Paenibacillus beijingensis	1126833 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000032634	Burkholderia ubonensis MSMB22	1249668	7/27/2015	6236	Burkholderia ubonensis MSMB22	1249668 101571 32008 119060 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000034472	Parcubacteria bacterium GW2011_GWA2_47_21	1618843	7/30/2015	519	Parcubacteria bacterium GW2011_GWA2_47_21	1618843 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034469	Parcubacteria bacterium GW2011_GWA2_46_7	1618837	7/30/2015	459	Parcubacteria bacterium GW2011_GWA2_46_7	1618837 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034471	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_37_7	1618481	7/30/2015	1069	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_37_7	1618481 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034475	Parcubacteria bacterium GW2011_GWA2_45_14	1618832	7/30/2015	1230	Parcubacteria bacterium GW2011_GWA2_45_14	1618832 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034480	Parcubacteria bacterium GW2011_GWA2_46_9	1618838	7/30/2015	1036	Parcubacteria bacterium GW2011_GWA2_46_9	1618838 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034489	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_40_24	1618406	7/30/2015	280	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_40_24	1618406 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034487	Berkelbacteria bacterium GW2011_GWA2_46_7	1618335	7/30/2015	460	Berkelbacteria bacterium GW2011_GWA2_46_7	1618335 1618330 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034492	Microgenomates (Daviesbacteria) bacterium GW2011_GWB1_36_5	1618426	7/30/2015	1231	Microgenomates (Daviesbacteria) bacterium GW2011_GWB1_36_5	1618426 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034499	Parcubacteria bacterium GW2011_GWC1_34_10	1618891	7/30/2015	537	Parcubacteria bacterium GW2011_GWC1_34_10	1618891 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034498	Berkelbacteria bacterium GW2011_GWB1_38_5	1618336	7/30/2015	613	Berkelbacteria bacterium GW2011_GWB1_38_5	1618336 1618330 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034508	Berkelbacteria bacterium GW2011_GWA1_36_9	1618331	7/30/2015	920	Berkelbacteria bacterium GW2011_GWA1_36_9	1618331 1618330 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034504	candidate division WWE3 bacterium GW2011_GWC2_44_9	1619125	7/30/2015	756	candidate division WWE3 bacterium GW2011_GWC2_44_9	1619125 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034493	Microgenomates (Curtissbacteria) bacterium GW2011_GWA2_41_24	1618411	7/30/2015	1085	Microgenomates (Curtissbacteria) bacterium GW2011_GWA2_41_24	1618411 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034512	Parcubacteria bacterium GW2011_GWB1_45_9	1618879	7/30/2015	622	Parcubacteria bacterium GW2011_GWB1_45_9	1618879 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034507	candidate division WWE3 bacterium GW2011_GWC1_41_7	1619119	7/30/2015	968	candidate division WWE3 bacterium GW2011_GWC1_41_7	1619119 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034502	Microgenomates (Amesbacteria) bacterium GW2011_GWC1_47_15	1618364	7/30/2015	1026	Microgenomates (Amesbacteria) bacterium GW2011_GWC1_47_15	1618364 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034505	Parcubacteria bacterium GW2011_GWA1_47_11	1618792	7/30/2015	696	Parcubacteria bacterium GW2011_GWA1_47_11	1618792 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034518	Parcubacteria bacterium GW2011_GWC1_42_11	1618905	7/30/2015	742	Parcubacteria bacterium GW2011_GWC1_42_11	1618905 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034509	Microgenomates (Levybacteria) bacterium GW2011_GWC1_40_19	1618466	7/30/2015	822	Microgenomates (Levybacteria) bacterium GW2011_GWC1_40_19	1618466 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034516	Parcubacteria (Kuenenbacteria) bacterium GW2011_GWA2_42_15	1618677	7/30/2015	832	Parcubacteria (Kuenenbacteria) bacterium GW2011_GWA2_42_15	1618677 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034522	Microgenomates bacterium GW2011_GWC1_44_9	1618525	7/30/2015	858	Microgenomates bacterium GW2011_GWC1_44_9	1618525 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034526	Parcubacteria bacterium GW2011_GWC1_43_11b	1618908	7/30/2015	744	Parcubacteria bacterium GW2011_GWC1_43_11b	1618908 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034538	Microgenomates bacterium GW2011_GWF1_44_10	1618537	7/30/2015	1089	Microgenomates bacterium GW2011_GWF1_44_10	1618537 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034535	Microgenomates bacterium GW2011_GWC1_39_7	1618515	7/30/2015	635	Microgenomates bacterium GW2011_GWC1_39_7	1618515 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034534	Parcubacteria bacterium GW2011_GWA2_40_23	1618816	7/30/2015	1221	Parcubacteria bacterium GW2011_GWA2_40_23	1618816 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034531	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_40_16	1618405	7/30/2015	1037	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_40_16	1618405 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034536	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_35_8	1618479	7/30/2015	633	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_35_8	1618479 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034541	Microgenomates (Levybacteria) bacterium GW2011_GWA2_40_8	1618459	7/30/2015	759	Microgenomates (Levybacteria) bacterium GW2011_GWA2_40_8	1618459 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034539	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWC2_39_8	1618450	7/30/2015	1544	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWC2_39_8	1618450 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034546	Parcubacteria bacterium GW2011_GWA2_47_7	1618846	7/30/2015	995	Parcubacteria bacterium GW2011_GWA2_47_7	1618846 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034543	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_43_11	1618436	7/30/2015	1511	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_43_11	1618436 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034562	Microgenomates (Woesebacteria) bacterium GW2011_GWA2_40_7b	1618563	7/30/2015	692	Microgenomates (Woesebacteria) bacterium GW2011_GWA2_40_7b	1618563 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034567	Parcubacteria bacterium GW2011_GWA2_31_28	1618806	7/30/2015	526	Parcubacteria bacterium GW2011_GWA2_31_28	1618806 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034569	Parcubacteria (Azambacteria) bacterium GW2011_GWC1_46_13	1618619	7/30/2015	648	Parcubacteria (Azambacteria) bacterium GW2011_GWC1_46_13	1618619 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034581	candidate division CPR3 bacterium GW2011_GWF2_35_18	1618350	7/30/2015	1062	candidate division CPR3 bacterium GW2011_GWF2_35_18	1618350 1618340 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034580	Parcubacteria bacterium GW2011_GWC2_38_7	1618920	7/30/2015	863	Parcubacteria bacterium GW2011_GWC2_38_7	1618920 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034588	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWB1_49_7	1618448	7/30/2015	1156	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWB1_49_7	1618448 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034591	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_37_7	1618545	7/30/2015	852	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_37_7	1618545 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034584	Microgenomates bacterium GW2011_GWC2_46_7	1618532	7/30/2015	496	Microgenomates bacterium GW2011_GWC2_46_7	1618532 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034589	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWC2_49_12	1618675	7/30/2015	690	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWC2_49_12	1618675 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034595	Parcubacteria (Azambacteria) bacterium GW2011_GWA1_44_9	1618610	7/30/2015	730	Parcubacteria (Azambacteria) bacterium GW2011_GWA1_44_9	1618610 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034600	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWC1_48_8	1618666	7/30/2015	630	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWC1_48_8	1618666 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034605	Parcubacteria (Moranbacteria) bacterium GW2011_GWF1_34_10	1618715	7/30/2015	1233	Parcubacteria (Moranbacteria) bacterium GW2011_GWF1_34_10	1618715 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034608	Parcubacteria bacterium GW2011_GWA2_49_16	1618851	7/30/2015	615	Parcubacteria bacterium GW2011_GWA2_49_16	1618851 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034612	Parcubacteria bacterium GW2011_GWA1_36_12	1618782	7/30/2015	904	Parcubacteria bacterium GW2011_GWA1_36_12	1618782 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034618	Microgenomates bacterium GW2011_GWA2_44_7	1618500	7/30/2015	1296	Microgenomates bacterium GW2011_GWA2_44_7	1618500 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034620	candidate division TM6 bacterium GW2011_GWF2_43_17	1619085	7/30/2015	387	candidate division TM6 bacterium GW2011_GWF2_43_17	1619085 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034626	Parcubacteria bacterium GW2011_GWA2_38_13	1618811	7/30/2015	1020	Parcubacteria bacterium GW2011_GWA2_38_13	1618811 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034625	candidate division TM6 bacterium GW2011_GWF2_38_10	1619084	7/30/2015	911	candidate division TM6 bacterium GW2011_GWF2_38_10	1619084 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034602	Parcubacteria bacterium GW2011_GWF2_50_9	1618975	7/30/2015	1121	Parcubacteria bacterium GW2011_GWF2_50_9	1618975 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034604	Microgenomates (Collierbacteria) bacterium GW2011_GWB1_44_35	1618383	7/30/2015	300	Microgenomates (Collierbacteria) bacterium GW2011_GWB1_44_35	1618383 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034610	Parcubacteria bacterium GW2011_GWA1_38_7	1618783	7/30/2015	843	Parcubacteria bacterium GW2011_GWA1_38_7	1618783 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034611	Microgenomates (Woesebacteria) bacterium GW2011_GWC1_43_10b	1618585	7/30/2015	346	Microgenomates (Woesebacteria) bacterium GW2011_GWC1_43_10b	1618585 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034624	Microgenomates (Levybacteria) bacterium GW2011_GWA1_39_32	1618454	7/30/2015	840	Microgenomates (Levybacteria) bacterium GW2011_GWA1_39_32	1618454 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034628	Parcubacteria bacterium GW2011_GWC1_43_11	1618907	7/30/2015	698	Parcubacteria bacterium GW2011_GWC1_43_11	1618907 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034634	candidate division TM6 bacterium GW2011_GWF2_33_332	1619080	7/30/2015	1552	candidate division TM6 bacterium GW2011_GWF2_33_332	1619080 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034632	Parcubacteria bacterium GW2011_GWC1_39_8	1618901	7/30/2015	426	Parcubacteria bacterium GW2011_GWC1_39_8	1618901 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034647	Microgenomates bacterium GW2011_GWF2_47_9	1618541	7/30/2015	780	Microgenomates bacterium GW2011_GWF2_47_9	1618541 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034639	Parcubacteria bacterium GW2011_GWC1_45_13	1618914	7/30/2015	815	Parcubacteria bacterium GW2011_GWC1_45_13	1618914 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034654	Parcubacteria bacterium GW2011_GWC1_45_14	1618915	7/30/2015	954	Parcubacteria bacterium GW2011_GWC1_45_14	1618915 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034661	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_48_13	1618439	7/30/2015	616	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA1_48_13	1618439 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034653	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_45_8	1618559	7/30/2015	235	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_45_8	1618559 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034665	Parcubacteria (Wolfebacteria) bacterium GW2011_GWC2_39_22	1619013	7/30/2015	1009	Parcubacteria (Wolfebacteria) bacterium GW2011_GWC2_39_22	1619013 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034666	Parcubacteria bacterium GW2011_GWA2_44_13	1618830	7/30/2015	900	Parcubacteria bacterium GW2011_GWA2_44_13	1618830 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034674	Peregrinibacteria bacterium GW2011_GWF2_43_17	1619068	7/30/2015	1132	Peregrinibacteria bacterium GW2011_GWF2_43_17	1619068 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034678	candidate division WWE3 bacterium GW2011_GWF2_42_42	1619142	7/30/2015	790	candidate division WWE3 bacterium GW2011_GWF2_42_42	1619142 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034675	Parcubacteria bacterium GW2011_GWE2_38_18	1618949	7/30/2015	615	Parcubacteria bacterium GW2011_GWE2_38_18	1618949 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034676	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_41_13b	1618555	7/30/2015	825	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_41_13b	1618555 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034686	Parcubacteria bacterium GW2011_GWC1_40_13	1618903	7/30/2015	639	Parcubacteria bacterium GW2011_GWC1_40_13	1618903 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034682	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWB1_47_6b	1618655	7/30/2015	761	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWB1_47_6b	1618655 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034687	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_40_101	1618575	7/30/2015	336	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_40_101	1618575 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034688	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_34_18	1618477	7/30/2015	482	Microgenomates (Roizmanbacteria) bacterium GW2011_GWA2_34_18	1618477 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034703	Parcubacteria bacterium GW2011_GWC2_45_7	1618932	7/30/2015	871	Parcubacteria bacterium GW2011_GWC2_45_7	1618932 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034708	Candidatus Saccharibacteria bacterium GW2011_GWA2_46_10	1619069	7/30/2015	747	Candidatus Saccharibacteria bacterium GW2011_GWA2_46_10	1619069 95818 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034705	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_46_218	1619001	7/30/2015	1025	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_46_218	1619001 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034706	Parcubacteria (Azambacteria) bacterium GW2011_GWA2_39_10	1618611	7/30/2015	338	Parcubacteria (Azambacteria) bacterium GW2011_GWA2_39_10	1618611 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034696	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_45_21	1618649	7/30/2015	676	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_45_21	1618649 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034711	Parcubacteria (Uhrbacteria) bacterium GW2011_GWA2_53_10	1618980	7/30/2015	542	Parcubacteria (Uhrbacteria) bacterium GW2011_GWA2_53_10	1618980 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034700	Parcubacteria bacterium GW2011_GWA2_45_15	1618833	7/30/2015	469	Parcubacteria bacterium GW2011_GWA2_45_15	1618833 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034722	archaeon Loki	1538547	7/30/2015	5378	archaeon Loki	1538547 1655637 1655434 2157 131567	Archaea	
UP000034723	Geoglobus ahangari	113653	7/30/2015	1973	Geoglobus ahangari	113653 190818 2232 2231 183980 28890 2157 131567	Archaea	
UP000034718	Microgenomates bacterium GW2011_GWA1_48_10	1618496	7/30/2015	1016	Microgenomates bacterium GW2011_GWA1_48_10	1618496 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034727	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWA2_45_9	1618663	7/30/2015	577	Parcubacteria (Jorgensenbacteria) bacterium GW2011_GWA2_45_9	1618663 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034721	Parcubacteria bacterium GW2011_GWA1_53_13	1618800	7/30/2015	563	Parcubacteria bacterium GW2011_GWA1_53_13	1618800 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034714	Parcubacteria bacterium GW2011_GWA2_43_11	1618825	7/30/2015	972	Parcubacteria bacterium GW2011_GWA2_43_11	1618825 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034730	Parcubacteria bacterium GW2011_GWC1_35_8	1618893	7/30/2015	447	Parcubacteria bacterium GW2011_GWC1_35_8	1618893 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034739	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_47_9	1618445	7/30/2015	1273	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_47_9	1618445 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034729	Microgenomates bacterium GW2011_GWC1_49_7	1618530	7/30/2015	468	Microgenomates bacterium GW2011_GWC1_49_7	1618530 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034735	Microgenomates (Daviesbacteria) bacterium GW2011_GWA2_38_17	1618421	7/30/2015	526	Microgenomates (Daviesbacteria) bacterium GW2011_GWA2_38_17	1618421 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034734	Parcubacteria bacterium GW2011_GWB1_41_4	1618867	7/30/2015	503	Parcubacteria bacterium GW2011_GWB1_41_4	1618867 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034736	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_44_13b	1618647	7/30/2015	759	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWA2_44_13b	1618647 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034737	Peregrinibacteria bacterium GW2011_GWA2_47_7	1619058	7/30/2015	709	Peregrinibacteria bacterium GW2011_GWA2_47_7	1619058 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034740	Parcubacteria (Adlerbacteria) bacterium GW2011_GWA1_54_10	1618605	7/30/2015	648	Parcubacteria (Adlerbacteria) bacterium GW2011_GWA1_54_10	1618605 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034744	Parcubacteria (Moranbacteria) bacterium GW2011_GWE2_47_10	1618714	7/30/2015	1031	Parcubacteria (Moranbacteria) bacterium GW2011_GWE2_47_10	1618714 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034745	Parcubacteria bacterium GW2011_GWA1_45_10	1618789	7/30/2015	493	Parcubacteria bacterium GW2011_GWA1_45_10	1618789 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034751	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_43_7	1618747	7/30/2015	816	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_43_7	1618747 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034749	Parcubacteria (Nomurabacteria) bacterium GW2011_GWA2_40_9	1618734	7/30/2015	669	Parcubacteria (Nomurabacteria) bacterium GW2011_GWA2_40_9	1618734 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034746	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_41_16	1618997	7/30/2015	1271	Parcubacteria (Uhrbacteria) bacterium GW2011_GWF2_41_16	1618997 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034748	candidate division TM6 bacterium GW2011_GWE2_41_16	1619075	7/30/2015	854	candidate division TM6 bacterium GW2011_GWE2_41_16	1619075 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034765	Peregrinibacteria bacterium GW2011_GWC2_33_13	1619061	7/30/2015	1292	Peregrinibacteria bacterium GW2011_GWC2_33_13	1619061 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034764	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWD2_39_48	1619031	7/30/2015	554	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWD2_39_48	1619031 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034753	Microgenomates (Daviesbacteria) bacterium GW2011_GWB1_41_5	1618429	7/30/2015	1228	Microgenomates (Daviesbacteria) bacterium GW2011_GWB1_41_5	1618429 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034766	candidate division TM6 bacterium GW2011_GWF2_32_72	1619079	7/30/2015	881	candidate division TM6 bacterium GW2011_GWF2_32_72	1619079 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034773	Parcubacteria bacterium GW2011_GWC1_38_22	1618897	7/30/2015	933	Parcubacteria bacterium GW2011_GWC1_38_22	1618897 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034772	Microgenomates (Beckwithbacteria) bacterium GW2011_GWC2_47_9	1618373	7/30/2015	402	Microgenomates (Beckwithbacteria) bacterium GW2011_GWC2_47_9	1618373 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034777	Parcubacteria bacterium GW2011_GWA2_47_10	1618839	7/30/2015	1441	Parcubacteria bacterium GW2011_GWA2_47_10	1618839 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034752	bacterium GW2011_GWA1_44_22	1620410	7/30/2015	335	bacterium GW2011_GWA1_44_22	1620410 49928 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034774	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_39_10	1618572	7/30/2015	1172	Microgenomates (Woesebacteria) bacterium GW2011_GWB1_39_10	1618572 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034781	Microgenomates bacterium GW2011_GWA1_45_10	1618493	7/30/2015	523	Microgenomates bacterium GW2011_GWA1_45_10	1618493 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034785	Microgenomates (Daviesbacteria) bacterium GW2011_GWA2_42_7	1618425	7/30/2015	866	Microgenomates (Daviesbacteria) bacterium GW2011_GWA2_42_7	1618425 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034759	Parcubacteria bacterium GW2011_GWC1_35_21	1618892	7/30/2015	629	Parcubacteria bacterium GW2011_GWC1_35_21	1618892 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034789	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWA2_58_9	1618672	7/30/2015	655	Parcubacteria (Kaiserbacteria) bacterium GW2011_GWA2_58_9	1618672 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034790	Candidatus Saccharibacteria bacterium GW2011_GWC2_48_9	1619071	7/30/2015	1172	Candidatus Saccharibacteria bacterium GW2011_GWC2_48_9	1619071 95818 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034796	Parcubacteria bacterium GW2011_GWC2_42_6	1618928	7/30/2015	485	Parcubacteria bacterium GW2011_GWC2_42_6	1618928 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034793	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_39_8	1618552	7/30/2015	1159	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_39_8	1618552 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034788	Microgenomates bacterium GW2011_GWF1_38_5	1618536	7/30/2015	516	Microgenomates bacterium GW2011_GWF1_38_5	1618536 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034794	Microgenomates (Collierbacteria) bacterium GW2011_GWA2_46_26	1618381	7/30/2015	1173	Microgenomates (Collierbacteria) bacterium GW2011_GWA2_46_26	1618381 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034803	Microgenomates (Woesebacteria) bacterium GW2011_GWC2_31_9	1618586	7/30/2015	921	Microgenomates (Woesebacteria) bacterium GW2011_GWC2_31_9	1618586 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034799	candidate division WS6 bacterium GW2011_GWF2_39_15	1619100	7/30/2015	883	candidate division WS6 bacterium GW2011_GWF2_39_15	1619100 74243 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034809	Microgenomates bacterium GW2011_GWC1_43_13	1618521	7/30/2015	764	Microgenomates bacterium GW2011_GWC1_43_13	1618521 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034813	Parcubacteria bacterium GW2011_GWA2_40_37	1618817	7/30/2015	840	Parcubacteria bacterium GW2011_GWA2_40_37	1618817 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034816	candidate division WS6 bacterium GW2011_GWF1_35_23	1619097	7/30/2015	380	candidate division WS6 bacterium GW2011_GWF1_35_23	1619097 74243 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034815	Parcubacteria bacterium GW2011_GWB1_48_6	1618881	7/30/2015	242	Parcubacteria bacterium GW2011_GWB1_48_6	1618881 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034811	Parcubacteria bacterium GW2011_GWC2_44_17	1618929	7/30/2015	1065	Parcubacteria bacterium GW2011_GWC2_44_17	1618929 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034810	Parcubacteria (Wolfebacteria) bacterium GW2011_GWC1_43_10	1619011	7/30/2015	680	Parcubacteria (Wolfebacteria) bacterium GW2011_GWC1_43_10	1619011 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034801	Parcubacteria bacterium GW2011_GWA1_56_13	1618803	7/30/2015	759	Parcubacteria bacterium GW2011_GWA1_56_13	1618803 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034818	Peregrinibacteria bacterium GW2011_GWF2_39_17	1619067	7/30/2015	1127	Peregrinibacteria bacterium GW2011_GWF2_39_17	1619067 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034814	Parcubacteria bacterium GW2011_GWA2_43_9b	1618828	7/30/2015	860	Parcubacteria bacterium GW2011_GWA2_43_9b	1618828 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034826	Microgenomates (Woesebacteria) bacterium GW2011_GWA2_44_33	1618564	7/30/2015	945	Microgenomates (Woesebacteria) bacterium GW2011_GWA2_44_33	1618564 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034824	Microgenomates (Levybacteria) bacterium GW2011_GWA2_40_16	1618458	7/30/2015	854	Microgenomates (Levybacteria) bacterium GW2011_GWA2_40_16	1618458 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034837	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_42_32	1619039	7/30/2015	1429	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_42_32	1619039 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034836	Parcubacteria bacterium GW2011_GWC2_39_11	1618921	7/30/2015	682	Parcubacteria bacterium GW2011_GWC2_39_11	1618921 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034839	Parcubacteria (Moranbacteria) bacterium GW2011_GWF2_35_39	1618721	7/30/2015	1019	Parcubacteria (Moranbacteria) bacterium GW2011_GWF2_35_39	1618721 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034845	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA1_39_13	1619019	7/30/2015	338	Parcubacteria (Yanofskybacteria) bacterium GW2011_GWA1_39_13	1619019 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034843	Parcubacteria bacterium GW2011_GWD2_38_11	1618941	7/30/2015	903	Parcubacteria bacterium GW2011_GWD2_38_11	1618941 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034847	Microgenomates bacterium GW2011_GWC2_45_8	1618531	7/30/2015	575	Microgenomates bacterium GW2011_GWC2_45_8	1618531 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034849	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_37_14	1619046	7/30/2015	1012	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_37_14	1619046 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034855	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_40_10	1619037	7/30/2015	343	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWA2_40_10	1619037 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034846	Parcubacteria (Uhrbacteria) bacterium GW2011_GWD2_52_7	1618989	7/30/2015	920	Parcubacteria (Uhrbacteria) bacterium GW2011_GWD2_52_7	1618989 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034841	Ceratocystis fimbriata f. sp. platani	88771	7/30/2015	5620	Ceratocystis platani	88771 5157 1028423 5592 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000034853	Microgenomates (Amesbacteria) bacterium GW2011_GWC1_46_24	1618363	7/30/2015	1072	Microgenomates (Amesbacteria) bacterium GW2011_GWC1_46_24	1618363 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034852	candidate division WS6 bacterium GW2011_GWA2_37_6	1619087	7/30/2015	743	candidate division WS6 bacterium GW2011_GWA2_37_6	1619087 74243 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034854	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_41_11	1618409	7/30/2015	922	Microgenomates (Curtissbacteria) bacterium GW2011_GWA1_41_11	1618409 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034858	Peregrinibacteria bacterium GW2011_GWC2_54_8	1619063	7/30/2015	1238	Peregrinibacteria bacterium GW2011_GWC2_54_8	1619063 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034862	candidate division TM6 bacterium GW2011_GWF2_30_66	1619078	7/30/2015	932	candidate division TM6 bacterium GW2011_GWF2_30_66	1619078 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034869	Parcubacteria bacterium GW2011_GWA2_43_13	1618826	7/30/2015	883	Parcubacteria bacterium GW2011_GWA2_43_13	1618826 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034875	candidate division CPR1 bacterium GW2011_GWA2_42_17	1618341	7/30/2015	698	candidate division CPR1 bacterium GW2011_GWA2_42_17	1618341 1618338 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034867	Parcubacteria (Moranbacteria) bacterium GW2011_GWA2_39_41	1618695	7/30/2015	605	Parcubacteria (Moranbacteria) bacterium GW2011_GWA2_39_41	1618695 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034879	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_47_6	1618749	7/30/2015	581	Parcubacteria (Nomurabacteria) bacterium GW2011_GWB1_47_6	1618749 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034883	Sandaracinus amylolyticus	927083	7/30/2015	8941	Sandaracinus amylolyticus	927083 1055688 1055686 80812 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000026398	Bordetella hinzii 5132	1331257	8/3/2015	4707	Bordetella hinzii 5132	1331257 103855 517 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000034885	Microgenomates bacterium GW2011_GWA2_46_16	1618501	7/30/2015	720	Microgenomates bacterium GW2011_GWA2_46_16	1618501 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034891	Parcubacteria bacterium GW2011_GWA2_44_15	1618831	7/30/2015	277	Parcubacteria bacterium GW2011_GWA2_44_15	1618831 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034892	Parcubacteria bacterium GW2011_GWA2_40_14	1618814	7/30/2015	685	Parcubacteria bacterium GW2011_GWA2_40_14	1618814 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034889	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWC2_44_8	1618657	7/30/2015	526	Parcubacteria (Giovannonibacteria) bacterium GW2011_GWC2_44_8	1618657 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034873	candidate division WWE3 bacterium GW2011_GWC1_47_10	1619122	7/30/2015	538	candidate division WWE3 bacterium GW2011_GWC1_47_10	1619122 422282 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034896	Parcubacteria bacterium GW2011_GWF2_44_8	1618971	7/30/2015	583	Parcubacteria bacterium GW2011_GWF2_44_8	1618971 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034877	Microgenomates (Amesbacteria) bacterium GW2011_GWC1_48_10	1618365	7/30/2015	986	Microgenomates (Amesbacteria) bacterium GW2011_GWC1_48_10	1618365 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034894	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_43_14	1618443	7/30/2015	1699	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWA2_43_14	1618443 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria

UP000034881	Microgenomates (Daviesbacteria) bacterium GW2011_GWC2_40_12	1618431	7/30/2015	1309	Microgenomates (Daviesbacteria) bacterium GW2011_GWC2_40_12	1618431 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034897	Microgenomates (Levybacteria) bacterium GW2011_GWA1_39_34	1618455	7/30/2015	339	Microgenomates (Levybacteria) bacterium GW2011_GWA1_39_34	1618455 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032722	Mycoplasma meleagridis	29561	7/27/2015	571	Mycoplasma meleagridis	29561 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000034893	Microgenomates (Curtissbacteria) bacterium GW2011_GWC2_38_9	1618414	7/30/2015	606	Microgenomates (Curtissbacteria) bacterium GW2011_GWC2_38_9	1618414 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032721	Xenorhabdus doucetiae	351671	8/5/2015	3749	Xenorhabdus doucetiae	351671 626 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034912	Parcubacteria bacterium GW2011_GWC1_36_9	1618895	7/30/2015	645	Parcubacteria bacterium GW2011_GWC1_36_9	1618895 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032733	Magnetospira sp. QH-2	1288970	7/27/2015	3700	Magnetospira sp. QH-2	1288970 1182780 41295 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000032726	Muricauda lutaonensis	516051	7/27/2015	2882	Muricauda lutaonensis	516051 111500 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000032737	Acholeplasma brassicae	61635	7/27/2015	1671	Acholeplasma brassicae	61635 2147 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000034905	Parcubacteria bacterium GW2011_GWA2_51_12	1618856	7/30/2015	589	Parcubacteria bacterium GW2011_GWA2_51_12	1618856 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034919	Parcubacteria bacterium GW2011_GWB1_43_6	1618872	7/30/2015	621	Parcubacteria bacterium GW2011_GWB1_43_6	1618872 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034916	Parcubacteria (OD1-vii) bacterium GW2011_GWA2_38_13b	1618780	7/30/2015	1022	Parcubacteria (OD1-vii) bacterium GW2011_GWA2_38_13b	1618780 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034914	Parcubacteria bacterium GW2011_GWA2_47_8	1618847	7/30/2015	738	Parcubacteria bacterium GW2011_GWA2_47_8	1618847 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032735	Xenorhabdus poinarii	40577	8/5/2015	3557	Xenorhabdus poinarii	40577 626 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000032740	Acholeplasma palmae	38986	7/27/2015	1433	Acholeplasma palmae	38986 2147 2146 186329 31969 544448 2 131567	Bacteria	Tenericutes
UP000032743	Paracoccus sp. 361	1603292	7/30/2015	3463	Paracoccus sp. 361	1603292 265 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000034928	Microgenomates (Levybacteria) bacterium GW2011_GWA1_39_11	1618453	7/30/2015	899	Microgenomates (Levybacteria) bacterium GW2011_GWA1_39_11	1618453 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000032749	Oleispira antarctica RB-8	698738	7/27/2015	3895	Oleispira antarctica RB-8	698738 188908 188907 135620 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000034935	Parcubacteria bacterium GW2011_GWB1_40_14	1618865	7/30/2015	963	Parcubacteria bacterium GW2011_GWB1_40_14	1618865 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034927	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_34_16	1619045	7/30/2015	363	Parcubacteria (Magasanikbacteria) bacterium GW2011_GWC2_34_16	1619045 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034940	Peregrinibacteria bacterium GW2011_GWA2_54_9	1619059	7/30/2015	1125	Peregrinibacteria bacterium GW2011_GWA2_54_9	1619059 1619053 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034934	Parcubacteria (Nomurabacteria) bacterium GW2011_GWF1_31_48	1618767	7/30/2015	778	Parcubacteria (Nomurabacteria) bacterium GW2011_GWF1_31_48	1618767 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034942	Microgenomates (Woesebacteria) bacterium GW2011_GWD2_40_19	1618595	7/30/2015	796	Microgenomates (Woesebacteria) bacterium GW2011_GWD2_40_19	1618595 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034945	Parcubacteria (Moranbacteria) bacterium GW2011_GWE1_35_17	1618707	7/30/2015	1299	Parcubacteria (Moranbacteria) bacterium GW2011_GWE1_35_17	1618707 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034938	candidate division TM6 bacterium GW2011_GWF2_36_6	1619082	7/30/2015	580	candidate division TM6 bacterium GW2011_GWF2_36_6	1619082 1104668 95901 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034948	Microgenomates bacterium GW2011_GWC1_38_12	1618512	7/30/2015	1187	Microgenomates bacterium GW2011_GWC1_38_12	1618512 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034953	Microgenomates bacterium GW2011_GWA2_40_6	1618499	7/30/2015	643	Microgenomates bacterium GW2011_GWA2_40_6	1618499 1046980 67820 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034946	Parcubacteria bacterium GW2011_GWA2_39_18	1618813	7/30/2015	561	Parcubacteria bacterium GW2011_GWA2_39_18	1618813 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034952	Parcubacteria (Nomurabacteria) bacterium GW2011_GWE1_35_16	1618761	7/30/2015	826	Parcubacteria (Nomurabacteria) bacterium GW2011_GWE1_35_16	1618761 1046984 221216 2323 2 131567	Bacteria	Unclassified Bacteria
UP000034982	Tannerella sp. oral taxon BU063 isolate Cell 1/3	1411022	7/30/2015	2311	Tannerella sp. oral taxon BU063 isolate Cell 1/3	1411022 712710 195950 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000026918	Streptomyces albulus	68570	8/7/2015	8069	Streptomyces albulus	68570 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000026912	Brugia malayi (Filarial nematode worm)	6279	8/2/2015	17067	Brugia malayi	6279 6278 6296 6295 6274 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000026960	Oryza barthii	65489	7/27/2015	40212	Oryza barthii	65489 4527 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000026962	Oryza punctata (Red rice)	4537	7/27/2015	38428	Oryza punctata	4537 4527 1648021 147380 147367 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	

UP000027084	Peptococcaceae bacterium SCADC1_2_3	1487582	7/27/2015	2187	Peptococcaceae bacterium SCADC1_2_3	1487582 208050 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000027093	Nitrososphaera viennensis EN76	926571	7/27/2015	3117	Nitrososphaera viennensis EN76	926571 1034015 497726 1033997 1033996 1643678 651137 2157 131567	Archaea	
UP000027088	Mycoplasma californicum	2113	7/27/2015	610	Mycoplasma californicum	2113 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000027142	Bacillus lehensis G1	1246626	7/27/2015	4016	Bacillus lehensis G1	1246626 300825 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000027148	endosymbiont of Llaveia axin axin	1415657	7/27/2015	243	endosymbiont of Llaveia axin axin	1415657 117744 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000027145	Leuconostoc pseudomesenteroides PS12	1339247	7/27/2015	1935	Leuconostoc pseudomesenteroides PS12	1339247 33968 1243 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000027135	Zootermopsis nevadensis (Dampwood termite)	136037	7/27/2015	14539	Zootermopsis nevadensis	136037 7502 127821 127820 7501 7499 6970 33341 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000027238	Colletotrichum sublineola (Sorghum anthracnose fungus)	1173701	7/27/2015	12697	Colletotrichum sublineola	1173701 5455 681950 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000027249	Halomonas campaniensis	213554	7/27/2015	3550	Halomonas campaniensis	213554 2745 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000010096	halophilic archaeon DL31	756883	7/27/2015	3413	halophilic archaeon DL31	756883 93506 29294 2157 131567	Archaea	
UP000010097	Candidatus Portiera aleyrodidarum BT-B-HRs	1206109	7/27/2015	273	Candidatus Portiera aleyrodidarum BT-B-HRs	1206109 91844 235572 114399 114403 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000010111	Megasphaera elsdenii DSM 20460	1064535	7/27/2015	2194	Megasphaera elsdenii DSM 20460	1064535 907 906 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000010101	Anabaena sp. 90	46234	7/27/2015	4476	Anabaena sp. 90	46234 1163 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000010099	Prevotella intermedia (strain 17)	246198	7/30/2015	2252	Prevotella intermedia 17	246198 28131 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000032803	Legionella hackeliae	449	7/27/2015	3214	Legionella hackeliae	449 445 444 118969 1236 1224 2 131567	Bacteria	Proteobacteria
UP000032810	Candidatus Portiera aleyrodidarum	91844	7/27/2015	278	Candidatus Portiera aleyrodidarum	91844 235572 114399 114403 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000032809	Defluviitoga tunisiensis	1006576	7/27/2015	1820	Defluviitoga tunisiensis	1006576 1511648 1643949 1643947 188708 200918 2 131567	Bacteria	Thermotogae
UP000032870	Acinetobacter sp. HR7	1509403	7/27/2015	2934	Acinetobacter sp. HR7	1509403 469 468 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000344	Vaccinia virus (strain Western Reserve) (VACV) (Vaccinia virus (strain WR))	10254	7/30/2015	217	Vaccinia virus WR	10254 10245 10242 10241 10240 35237 10239	Vruses	
UP000001662	Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	610130	7/30/2015	4133	[Clostridium] saccharolyticum WM1	610130 84030 1506553 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000000272	Thermosediminibacter oceani (strain ATCC BAA-1034 / DSM 16646 / JW/IW-1228P)	555079	7/30/2015	2151	Thermosediminibacter oceani DSM 16646	555079 291990 291988 543371 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000009047	Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	644282	7/30/2015	3268	Desulfarculus baarsii DSM 2075	644282 453230 453229 453228 453227 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000000276	Corynebacterium pseudotuberculosis (strain C231)	681645	8/7/2015	2090	Corynebacterium pseudotuberculosis C231	681645 1719 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000339	Salmonella phage ViI	867696	7/27/2015	208	Salmonella phage ViI	867696 1298971 10662 28883 35237 10239	Vruses	
UP000002318	Spirochaeta smaragdinae (strain DSM 11293 / JCM 15392 / SEBR 4228)	573413	7/30/2015	4211	Spirochaeta smaragdinae DSM 11293	573413 55206 146 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000001661	Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	574087	7/30/2015	2276	Acetohalobium arabaticum DSM 5501	574087 28187 28186 53434 53433 186801 1239 2 131567	Bacteria	Firmicutes
UP000010290	Providencia sneebia DSM 19967	1141660	7/27/2015	3113	Providencia sneebia DSM 19967	1141660 516075 586 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000346	Acidilobus saccharovorans (strain DSM 16705 / JCM 18335 / VKM B-2471 / 345-15)	666510	7/30/2015	1499	Acidilobus saccharovorans 345-15	666510 242703 105850 871007 871006 183924 28889 2157 131567	Archaea	
UP000000394	Indian citrus ringspot virus (isolate Kinnow mandarin/India/K1/1996) (ICRSV)	651357	7/30/2015	6	Indian citrus ringspot virus K1	651357 104664 249199 675064 675063 35278 439488 10239	Vruses	
UP000000677	Potato virus M (strain Russian) (PVM)	12168	7/30/2015	6	Potato virus M (strain Russian)	12168 12167 12163 675068 675063 35278 439488 10239	Vruses	
UP000006933	Citrus leaf blotch virus (isolate Nagami kumquat/France/SRA-153/1984) (CLBV)	686981	7/30/2015	3	Citrus leaf blotch virus FRA/SRA-153	686981 129141 699166 675068 675063 35278 439488 10239	Vruses	
UP000000678	Apple stem pitting virus (isolate PA66) (ASPV)	651356	7/30/2015	5	Apple stem pitting virus PA66	651356 35350 129725 675068 675063 35278 439488 10239	Vruses	
UP000000398	Botrytis virus F (isolate Botrytis cinerea/New Zealand/Howitt/2001) (BotV-F)	686946	7/30/2015	2	Botrytis virus F NZL/Howitt	686946 129395 675062 675061 675063 35278 439488 10239	Vruses	
UP000000399	Grapevine fleck virus (isolate Italy/MT48) (GFkV)	652668	7/30/2015	4	Grapevine fleck virus isolate MT48	652668 103722 249185 249184 675063 35278 439488 10239	Vruses	
UP000000343	Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9)	1198114	7/30/2015	4514	Granulicella tundricola MP5ACTX9	1198114 940615 940557 204434 204433 204432 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000008689	Lolium latent virus (isolate Lolium/USA/US1/-) (LoLV)	686945	7/30/2015	6	Lolium latent virus	686945 365150 675076 675064 675063 35278 439488 10239	Vruses	
UP000002677	gamma proteobacterium HdN1	83406	7/27/2015	3683	gamma proteobacterium HdN1	83406 33811 118884 1236 1224 2 131567	Bacteria	Proteobacteria
UP000001663	Shallot virus X (ShVX)	31770	7/27/2015	6	Shallot virus X	31770 140568 675064 675063 35278 439488 10239	Vruses	
UP000000680	White bream virus (isolate Blicca bjoerkna L./Germany/DF24/00) (WBV)	766180	7/30/2015	5	White bream virus (strain DF24/00)	766180 405554 694018 694017 11118 76804 35278 439488 10239	Vruses	
UP000000400	Maize rayado fino virus (isolate Costa Rica/Guapiles) (MRFV)	652669	7/30/2015	2	Maize rayado fino virus isolate Costa Rica	652669 59749 12051 249184 675063 35278 439488 10239	Vruses	
UP000000396	Apple stem grooving virus (strain P-209) (ASGV)	36402	7/30/2015	2	Apple stem grooving virus (strain P-209)	36402 28347 12174 675068 675063 35278 439488 10239	Vruses	

UP000000679	Grapevine virus A (isolate Is 151) (GVA)	651358	7/30/2015	5	Grapevine virus A isolate Is 151	651358 35288 184751 675068 675063 35278 439488 10239	Vruses	
UP000001664	Botrytis virus X (isolate Botrytis cinerea/New Zealand/Howitt/2006) (BOTV-X)	686947	7/30/2015	5	Botrytis virus X NZL/Howitt	686947 174142 675065 675064 675063 35278 439488 10239	Vruses	
UP000000401	Turnip yellow mosaic virus	12154	7/27/2015	3	Turnip yellow mosaic virus	12154 12148 249184 675063 35278 439488 10239	Vruses	
UP000010320	Psychromonas sp. CNPT3	314282	7/27/2015	2578	Psychromonas sp. CNPT3	314282 67572 267894 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000403	Heterosigma akashiwo RNA virus (strain SOG263) (HaRNAV)	239720	7/30/2015	1	Heterosigma akashiwo RNA virus SOG263	239720 324900 324902 324901 464095 35278 439488 10239	Vruses	
UP000000404	Duck hepatitis A virus (strain Duck/Taiwan/03D/2003) (DHAV)	693992	7/30/2015	1	Duck hepatitis A virus Taiwan/03D	693992 691956 691955 12058 464095 35278 439488 10239	Vruses	
UP000000676	Turkey astrovirus 1 (TAstV-1)	364370	7/27/2015	3	Turkey astrovirus 1	364370 1239437 249589 39733 35278 439488 10239	Vruses	
UP000000410	Tomato ringspot virus (isolate raspberry) (ToRSV)	12281	7/30/2015	4	Tomato ringspot virus (isolate raspberry)	12281 12280 167160 12270 675075 675072 464095 35278 439488 10239	Vruses	
UP000000825	Tomato torrado virus (isolate Solanum lycopersicum/Spain/PRIToTV0301/-) (ToTV)	686948	7/30/2015	3	Tomato torrado virus ESP/PRIToTV0301	686948 370833 675073 675072 464095 35278 439488 10239	Vruses	
UP000000681	Infectious flacherie virus (isolate Silkworm) (IFV) (Bombyx mori infectious flacherie virus)	649896	7/30/2015	1	Infectious flacherie virus isolate silkworm	649896 12742 232799 699189 464095 35278 439488 10239	Vruses	
UP000000682	Foot-and-mouth disease virus (isolate Swine/Taiwan/OTai/1997 serotype O) (FMDV)	649897	7/30/2015	1	Foot-and-mouth disease virus O/swine/1997	649897 12118 12110 12109 12058 464095 35278 439488 10239	Vruses	
UP000000395	Sclerotinia sclerotiorum debilitation-associated virus (isolate Sclerotinia/China/Xie/-) (SsDRV)	686987	7/30/2015	1	Sclerotinia sclerotiorum debilitation-associated virus CHN/Xie	686987 213034 675066 675064 675063 35278 439488 10239	Vruses	
UP000000407	Porcine sapelovirus (strain V13) (PSV) (Porcine enterovirus 8)	1002921	7/30/2015	1	Porcine sapelovirus 1	1002921 686984 686982 12058 464095 35278 439488 10239	Vruses	
UP000000670	Human parechovirus 2 (strain Williamson) (HPeV-2) (Echovirus 23)	122962	7/30/2015	1	Echovirus 23 strain Williamson	122962 39085 195054 138954 12058 464095 35278 439488 10239	Vruses	
UP000006923	Cherry rasp leaf virus (isolate Potato/United States) (CRLV)	650137	7/30/2015	2	Cherry rasp leaf virus isolate potato	650137 202566 310684 675072 464095 35278 439488 10239	Vruses	
UP000006824	Mushroom bacilliform virus (isolate Australia/AUS LF-1) (MBV)	650482	7/30/2015	4	Mushroom bacilliform virus LF-1/AUS	650482 32625 39742 39741 35278 439488 10239	Vruses	
UP000000406	Aichi virus (strain Human/A846/88/1989) (AiV) (Aichi virus (strain A846/88))	650132	7/30/2015	1	Aichi virus A846/88	650132 1313215 72149 194960 12058 464095 35278 439488 10239	Vruses	
UP000000409	Broad bean wilt virus 1 (strain Spinach/United States/ATCC PV-132/1963) (BBWV-1)	649895	7/30/2015	2	Broad bean wilt virus 1 ATCC PV132	649895 50817 12269 675075 675072 464095 35278 439488 10239	Vruses	
UP000001649	Brome mosaic virus (BMV)	12302	7/27/2015	4	Brome mosaic virus	12302 12300 39740 35278 439488 10239	Vruses	
UP000010367	Oscillatoria acuminata PCC 6304	56110	7/27/2015	5755	Oscillatoria acuminata PCC 6304	56110 118323 1158 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000000408	Porcine teschovirus 1 (isolate Pig/United Kingdom/F65/1967) (PTV-1) (Porcine teschovirus 1 (isolate F65))	650136	7/30/2015	1	Porcine teschovirus 1 isolate F65	650136 85506 118140 118139 12058 464095 35278 439488 10239	Vruses	
UP000000672	Seneca Valley virus (isolate -/United States/SSV-001/2002) (SVV)	686944	7/30/2015	1	Seneca Valley virus USA/SSV-001	686944 390157 586425 12058 464095 35278 439488 10239	Vruses	
UP000008687	Potato virus X (strain X3) (PVX)	12185	7/30/2015	5	Potato virus X (strain X3)	12185 12183 12176 675064 675063 35278 439488 10239	Vruses	
UP000000826	Norwalk virus (strain GI/Human/United States/Norwalk/1968) (Hu/NV/NV/1968/US)	524364	7/30/2015	3	Norovirus Hu/1968/US	524364 150080 11983 142786 11974 35278 439488 10239	Vruses	
UP000002319	Encephalomyocarditis virus (strain Rueckert) (EMCV)	650129	7/30/2015	2	Encephalomyocarditis virus strain Rueckert	650129 12104 12103 12058 464095 35278 439488 10239	Vruses	
UP000010366	Chamaesiphon minutus PCC 6605	1173020	7/27/2015	5815	Chamaesiphon minutus PCC 6605	1173020 1173032 217161 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000000412	Olive latent virus 2 (isolate Italy) (OLV-2)	650489	7/30/2015	4	Olive latent virus 2 isolate Italy	650489 33773 154322 39740 35278 439488 10239	Vruses	
UP000002502	Cucumber mosaic virus (strain FNY) (CMV)	12307	7/30/2015	5	Cucumber mosaic virus (strain FNY)	12307 12305 12304 39740 35278 439488 10239	Vruses	
UP000000675	Satsuma dwarf virus (isolate Satsuma mandarin/Japan/S-58/1977) (SDV)	650481	7/30/2015	2	Satsuma dwarf virus S-58	650481 47416 215920 675072 464095 35278 439488 10239	Vruses	
UP000000405	Equine rhinitis B virus 1 (strain Equine/Switzerland/P1436/71/1971) (ERBV-1) (Equine rhinovirus type 2)	650131	7/30/2015	1	Equine rhinitis B virus 1 strain P1436/71	650131 47001 312185 194961 12058 464095 35278 439488 10239	Vruses	
UP000000402	Gill-associated virus (isolate Giant tiger prawn/Australia) (GAV)	649894	7/30/2015	5	Gill-associated virus isolate Australia	649894 96491 199703 199704 76804 35278 439488 10239	Vruses	
UP000001650	Human astrovirus-1 (HAstV-1)	12456	7/27/2015	3	Human astrovirus 1	12456 1239565 249588 39733 35278 439488 10239	Vruses	
UP000000411	Pelargonium zonate spot virus (isolate Tomato/Italy/1982) (PZSV) (Pelargonium zonate spot virus (isolate Tomato))	650488	7/30/2015	4	Pelargonium zonate spot virus isolate tomato	650488 116056 413970 39740 35278 439488 10239	Vruses	
UP000010378	Nostoc sp. (strain ATCC 29411 / PCC 7524)	28072	7/30/2015	5398	Nostoc sp. PCC 7524	28072 1177 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000000413	Rabbit hemorrhagic disease virus (strain Rabbit/Germany/FRG/1989) (Ra/LV/RHDV/GH/1989/GE) (RHDV-FRG)	314536	7/30/2015	2	Rabbit hemorrhagic disease virus-FRG	314536 11976 95339 11974 35278 439488 10239	Vruses	
UP000010380	Rivularia sp. PCC 7116	373994	7/27/2015	6617	Rivularia sp. PCC 7116	373994 373984 1185 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000000668	Bovine enteric calicivirus Newbury agent-1 (isolate Bovine/UK/Newbury1/1976) (BEC)	331642	7/30/2015	2	Newbury agent 1	331642 696856 696855 11974 35278 439488 10239	Vruses	
UP000010388	Cyanobium gracile (strain ATCC 27147 / PCC 6307)	292564	7/30/2015	3261	Cyanobium gracile PCC 6307	292564 59930 167375 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria

UP000010384	Chroococcidiopsis thermalis PCC 7203	251229	7/27/2015	5740	Chroococcidiopsis thermalis PCC 7203	251229 54299 54298 52604 1117 2 131567	Bacteria	Cyanobacteria
UP000010382	Pleurocapsa sp. PCC 7327	118163	7/27/2015	4255	Pleurocapsa sp. PCC 7327	118163 54308 44474 52604 1117 2 131567	Bacteria	Cyanobacteria
UP000010390	Calothrix sp. PCC 7507	99598	7/27/2015	5924	Calothrix sp. PCC 7507	99598 1186 1185 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000010383	Geitlerinema sp. PCC 7407	1173025	7/27/2015	3813	Geitlerinema sp. PCC 7407	1173025 63132 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010381	Nostoc sp. PCC 7107	317936	7/27/2015	5185	Nostoc sp. PCC 7107	317936 1177 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000010385	Synechococcus sp. PCC 7502	1173263	7/27/2015	3310	Synechococcus sp. PCC 7502	1173263 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010389	Leptolyngbya sp. PCC 7376	111781	7/27/2015	4153	Leptolyngbya sp. PCC 7376	111781 47251 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000006919	Ruminococcus albus (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7)	697329	7/30/2015	3775	Ruminococcus albus 7 = DSM 20455	697329 1264 1263 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000010379	Synechococcus sp. (strain ATCC 27167 / PCC 6312)	195253	7/30/2015	3541	Synechococcus sp. PCC 6312	195253 1129 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010386	Pseudanabaena sp. PCC 7367	82654	7/27/2015	3824	Pseudanabaena sp. PCC 7367	82654 1152 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010422	Pneumocystis jiroveci (strain SE8) (Pneumocystis pneumonia agent)	1209962	7/30/2015	3419	Pneumocystis jirovecii SE8	1209962 42068 4753 44281 37987 147553 451866 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000010469	Caldisphaera lagunensis (strain DSM 15908 / JCM 11604 / IC-154)	1056495	7/30/2015	1477	Caldisphaera lagunensis DSM 15908	1056495 200415 200414 255472 871006 183924 28889 2157 131567	Archaea	
UP000010475	Cylindrospermum stagnale PCC 7417	56107	7/27/2015	6200	Cylindrospermum stagnale PCC 7417	56107 142864 56106 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000010483	Cyanobacterium stanieri (strain ATCC 29140 / PCC 7202)	292563	7/30/2015	2831	Cyanobacterium stanieri PCC 7202	292563 102235 102234 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010481	Halothece sp. (strain PCC 7418) (Synechococcus sp. (strain PCC 7418))	65093	7/30/2015	3701	Halothece sp. PCC 7418	65093 76023 92682 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010472	Crinalium epipsammum PCC 9333	1173022	7/27/2015	4697	Crinalium epipsammum PCC 9333	1173022 241425 241421 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010476	Gloeocapsa sp. PCC 7428	1173026	7/27/2015	5003	Gloeocapsa sp. PCC 7428	1173026 102231 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010480	Cyanobacterium aponinum (strain PCC 10605)	755178	7/30/2015	3415	Cyanobacterium aponinum PCC 10605	755178 379064 102234 1118 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010467	Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	937777	7/30/2015	4164	Deinococcus peraridilitoris DSM 19664	937777 432329 1298 183710 118964 188787 1297 2 131567	Bacteria	Deinococcus-Thermus
UP000010468	Natronobacterium gregoryi (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2)	797304	7/30/2015	3624	Natronobacterium gregoryi SP2	797304 44930 2256 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000010466	Mycoplasma cynos (strain C142)	1246955	7/30/2015	871	Mycoplasma cynos C142	1246955 171284 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000010473	Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	111780	7/30/2015	4751	Stanieria cyanosphaera PCC 7437	111780 102116 102115 52604 1117 2 131567	Bacteria	Cyanobacteria
UP000010474	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	272123	7/30/2015	5797	Anabaena cylindrica PCC 7122	272123 1165 1163 1162 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000010471	Microcoleus sp. PCC 7113	1173027	7/27/2015	6397	Microcoleus sp. PCC 7113	1173027 44471 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010477	Calothrix sp. PCC 6303	1170562	7/27/2015	5484	Calothrix sp. PCC 6303	1170562 32054 1186 1185 1161 1117 2 131567	Bacteria	Cyanobacteria
UP000010478	Oscillatoria nigro-viridis PCC 7112	179408	7/27/2015	6276	Oscillatoria nigro-viridis PCC 7112	179408 482564 1158 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000010556	Myotis davidii (David's myotis)	225400	7/27/2015	15446	Myotis davidii	225400 9434 9431 30560 9397 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000010552	Pteropus alecto (Black flying fox)	9402	7/27/2015	19520	Pteropus alecto	9402 9401 77225 9398 30559 9397 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000010796	Echinicola vietnamensis (strain DSM 17526 / LMG 23754 / KMM 6221)	926556	7/30/2015	4509	Echinicola vietnamensis DSM 17526	926556 390884 390846 563798 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000010797	Desulfitobacterium dichloroeliminans (strain LMG P-21439 / DCA1)	871963	7/30/2015	3294	Desulfitobacterium dichloroeliminans LMG P-21439	871963 233055 36853 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000010795	Thermobacillus composti (strain DSM 18247 / JCM 13945 / KWC4)	717605	7/30/2015	3802	Thermobacillus composti KWC4	717605 377615 76632 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000010798	Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	886293	7/27/2015	7126	Singulisphaera acidiphila DSM 18658	886293 466153 466152 126 112 203683 203682 2 131567	Bacteria	Planctomycetes
UP000010799	Liberibacter crescens (strain BT-1)	1215343	7/30/2015	1376	Liberibacter crescens BT-1	1215343 1273132 34019 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000010802	Tepidanaerobacter acetatoxydans (strain DSM 21804 / JCM 16047 / Re1)	1209989	7/27/2015	2640	Tepidanaerobacter acetatoxydans Re1	1209989 499229 499228 186814 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000010816	Thioflavicoccus mobilis 8321	765912	7/27/2015	3528	Thioflavicoccus mobilis	765912 80679 156885 1046 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000010824	Methanoregula formicica (strain DSM 22288 / NBRC 105244 / SMSP)	593750	7/30/2015	2815	Methanoregula formicica SMSP	593750 882104 395331 1198451 2191 224756 28890 2157 131567	Archaea	
UP000010843	Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	797303	7/30/2015	4138	Natrinema pellirubrum DSM 15624	797303 69525 88723 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000010821	Helicobacter heilmannii ASB1.4	1216962	7/27/2015	1814	Helicobacter heilmannii ASB1.4	1216962 35817 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000010847	Desulfitobacterium metallireducens DSM 15288	871968	7/27/2015	3029	Desulfitobacterium metallireducens DSM 15288	871968 142877 36853 186807 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000010862	Prevotella dentalis (strain ATCC 49559 / DSM 3688 / JCM 13448 / NCTC 12043 / ES 2772) (Mitsuokella dentalis)	908937	7/30/2015	2494	Prevotella dentalis DSM 3688	908937 52227 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group

UP000010809	Thioalkalivibrio nitratireducens (strain DSM 14787 / UNIQEM 213 / ALEN2)	1255043	7/30/2015	3762	Thioalkalivibrio nitratireducens DSM 14787	1255043 186931 106633 72276 135613 1236 1224 2 131567	Bacteria	Proteobacteria
UP000010866	Methanomethylovorans hollandica (strain DSM 15978 / NBRC 107637 / DMS1)	867904	7/30/2015	2551	Methanomethylovorans hollandica DSM 15978	867904 101192 101191 2206 94695 224756 28890 2157 131567	Archaea	
UP000010844	Mycobacterium smegmatis JS623	710686	7/27/2015	6935	Mycobacterium smegmatis JS623	710686 1772 1763 1762 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000010846	Halovivax ruber (strain DSM 18193 / JCM 13892 / XH-70)	797302	7/30/2015	3099	Halovivax ruber XH-70	797302 387341 332951 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000010880	Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	748449	7/30/2015	2452	Halobacteroides halobius DSM 5150	748449 42422 42417 53434 53433 186801 1239 2 131567	Bacteria	Firmicutes
UP000010878	Natronococcus occultus SP4	694430	7/27/2015	4153	Natronococcus occultus SP4	694430 29288 29287 1644061 1644060 183963 28890 2157 131567	Archaea	
UP000006707	Grapevine leafroll-associated virus 3 (isolate United States/NY1) (GLRaV-3) (Grapevine leafroll-associated closterovirus (isolate 109))	651354	7/30/2015	13	Grapevine leafroll-associated virus 3 isolate NY1	651354 55951 217160 69973 35278 439488 10239	Vruses	
UP000001099	Lettuce infectious yellows virus (isolate United States/92) (LIYV)	651355	7/30/2015	9	Lettuce infectious yellows virus isolate 92	651355 31713 67753 69973 35278 439488 10239	Vruses	
UP000001098	Feline calicivirus (strain Cat/United States/Urbana/1960) (FCV)	292349	7/30/2015	3	Feline calicivirus (strain Urbana)	292349 11978 95337 11974 35278 439488 10239	Vruses	
UP000001103	Ourmia melon virus (isolate Melon/Iran/VE9) (OuMV)	652838	7/30/2015	3	Ourmia melon virus VE9	652838 186786 186783 35278 439488 10239	Vruses	
UP000006705	Hepatitis E virus genotype 1 (isolate Human/China/HeBei/1987) (HEV)	652674	7/30/2015	3	Hepatitis E virus isolate Hetian	652674 12461 186677 291484 35278 439488 10239	Vruses	
UP000006703	Blackberry virus Y (isolate Blackberry plant/USA:Arkansas/C3ARK/2005) (BVY)	686949	7/30/2015	1	Blackberry virus Y USA/C3ARK	686949 323118 675844 39729 35278 439488 10239	Vruses	
UP000001102	Raspberry bushy dwarf virus (isolate Malling Jewel raspberry/R15) (RBDV)	652675	7/30/2015	3	Raspberry bushy dwarf virus isolate R15	652675 12451 39760 35278 439488 10239	Vruses	
UP000000568	Ryegrass mosaic virus (isolate Denmark/Danish) (RGMV)	652106	7/30/2015	1	Ryegrass mosaic virus isolate Danish	652106 40666 39730 39729 35278 439488 10239	Vruses	
UP000006710	Sindbis virus (SINV)	11034	7/27/2015	3	Sindbis virus	11034 177874 11019 11018 35278 439488 10239	Vruses	
UP000001104	Saccharomyces 20S RNA narnavirus (ScNV-20S)	186772	7/27/2015	1	Saccharomyces 20S RNA narnavirus	186772 186767 186766 35278 439488 10239	Vruses	
UP000007084	Sweet potato mild mottle virus (isolate Salazar) (SPMMV)	652105	7/30/2015	1	Sweet potato mild mottle virus isolate Salazar	652105 41459 137757 39729 35278 439488 10239	Vruses	
UP000006704	Barley yellow mosaic virus (isolate China/Yancheng/1998) (BaYMV)	652104	7/30/2015	2	Barley yellow mosaic virus isolate Yancheng	652104 12465 39731 39729 35278 439488 10239	Vruses	
UP000011002	Enterobacteriaceae bacterium (strain FGI 57)	693444	7/30/2015	4320	Enterobacteriaceae bacterium strain FGI 57	693444 36866 191675 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000569	Chikungunya virus (strain S27-African prototype) (CHIKV)	371094	7/30/2015	2	Chikungunya virus strain S27-African prototype	371094 37124 177875 11019 11018 35278 439488 10239	Vruses	
UP000001100	Beet necrotic yellow vein virus (isolate Japan/S) (BNYVV)	652670	7/30/2015	9	Beet necrotic yellow vein virus S	652670 31721 143901 1513233 35278 439488 10239	Vruses	
UP000000570	Semliki forest virus (SFV)	11033	7/27/2015	2	Semliki Forest virus	11033 177875 11019 11018 35278 439488 10239	Vruses	
UP000000414	Striped jack nervous necrosis virus (SjNNV)	35297	7/27/2015	3	Striped Jack nervous necrosis virus	35297 143919 12283 35278 439488 10239	Vruses	
UP000001665	Panicum mosaic virus (strain United States/Kansas 109S) (PMV)	652599	7/30/2015	5	Panicum mosaic virus strain Kansas 109S	652599 40279 186844 39738 35278 439488 10239	Vruses	
UP000001105	Cryphonectria parasitica mitovirus 1 (strain American chestnut tree/New Jersey/NB631) (CMV1) (Cryphonectria mitovirus 1)	186769	7/30/2015	1	Cryphonectria parasitica mitovirus 1-NB631	186769 343865 186768 186766 35278 439488 10239	Vruses	
UP000006709	Carnation mottle virus (isolate China/Shanghai) (CarMV)	652111	7/30/2015	4	Carnation mottle virus isolate Shanghai	652111 11986 11985 39738 35278 439488 10239	Vruses	
UP000001666	Tomato bushy stunt virus (strain Cherry) (TBSV)	12147	7/30/2015	4	Tomato bushy stunt virus (STRAIN CHERRY)	12147 12145 12141 39738 35278 439488 10239	Vruses	
UP000009270	Soil-borne wheat mosaic virus (strain United States/Nebraska/1981) (SBWMV)	652673	7/30/2015	5	Soil-borne wheat mosaic virus strain Nebraska	652673 28375 12291 675071 35278 439488 10239	Vruses	
UP000001667	Barley stripe mosaic virus (BSMV)	12327	7/27/2015	7	Barley stripe mosaic virus	12327 12326 675071 35278 439488 10239	Vruses	
UP000006711	Helicoverpa armigera stunt virus (HaSV)	37206	7/27/2015	3	Helicoverpa armigera stunt virus	37206 85651 1283207 35278 439488 10239	Vruses	
UP000001668	Peanut clump virus (isolate 87/TGTA2) (PCV)	652837	7/30/2015	7	Peanut clump virus 87/TGTA2	652837 28355 119492 675071 35278 439488 10239	Vruses	
UP000000571	Rubella virus (strain Therien) (RUBV)	11045	7/30/2015	2	Rubella virus strain Therien	11045 11041 11040 11018 35278 439488 10239	Vruses	
UP000000831	Nudaurelia capensis beta virus (isolate Pine emperor moth/South Africa) (NbetaV)	652108	7/30/2015	2	Nudaurelia capensis beta virus isolate South Africa	652108 85652 85650 1283207 35278 439488 10239	Vruses	
UP000001101	Citrus leprosis virus C (isolate Citrus sinesis/Brazil/Cordeiropolis/2003) (CiLV-C)	686950	7/30/2015	6	Citrus leprosis virus C BRA/Cordeiropolis	686950 347219 675070 35278 439488 10239	Vruses	
UP000000573	Oat chlorotic stunt virus (isolate United Kingdom) (OCSV)	652110	7/30/2015	3	Oat chlorotic stunt virus isolate United Kingdom	652110 146762 146761 39738 35278 439488 10239	Vruses	
UP000001671	Southern bean mosaic virus (isolate Bean/United States/Arkansas) (SBMV)	652938	7/30/2015	4	Southern bean mosaic virus isolate Arkansas	652938 12139 12137 35278 439488 10239	Vruses	
UP000007085	Oryza sativa endornavirus (isolate Japan/1995) (OsEV)	654933	7/30/2015	1	Oryza sativa endornavirus (isolate Japan)	654933 362693 310748 564644 35325 10239	Vruses	
UP000001673	Atkinsonella hypoxylon virus (isolate 2H) (AhV)	647331	7/30/2015	2	Atkinsonella hypoxylon virus isolate 2H	647331 12429 10239	Vruses	

UP000006715	Potato mop-top virus (isolate Potato/Sweden/Sw) (PMTV)	652839	7/30/2015	7	Potato mop-top virus Sw	652839 37128 186886 675071 35278 439488 10239	Vruses	
UP000006720	Rice gall dwarf virus (RGDV)	10986	7/27/2015	12	Rice gall dwarf virus	10986 10985 689832 10880 35325 10239	Vruses	
UP000001670	Poinsettia latent virus (isolate Euphorbia pulcherrima/Germany/Siepen/2005) (PnLV) (Poinsettia cryptic virus)	686943	7/30/2015	4	Poinsettia latent virus isolate Germany/Siepen	686943 305785 645516 35278 439488 10239	Vruses	
UP000000572	Pothos latent virus (isolate Pigeonpea/India) (PoLV)	652109	7/30/2015	4	Pothos latent virus isolate pigeonpea	652109 44562 186457 39738 35278 439488 10239	Vruses	
UP000001669	Tobacco rattle virus (isolate PpK20) (TRV)	652939	7/30/2015	6	Tobacco rattle virus PpK20	652939 12295 12293 675071 35278 439488 10239	Vruses	
UP000000351	Saccharomyces cerevisiae virus L-A (ScV-L-A) (ScVL1)	11008	7/27/2015	2	Saccharomyces cerevisiae virus L-A	11008 11007 11006 35325 10239	Vruses	
UP000000713	Aquareovirus C (isolate Golden shiner/USA/GSRV/1977) (AQRV-C)	185783	7/30/2015	12	Golden shiner reovirus	185783 185782 10979 689831 10880 35325 10239	Vruses	
UP000000352	Helminthosporium victoriae virus-190S (Hv190SV)	45237	7/27/2015	2	Helminthosporium victoriae virus 190S	45237 674981 11006 35325 10239	Vruses	
UP000000349	Micromonas pusilla reovirus (isolate Netherlands/2005) (MpRV)	649596	7/30/2015	11	Micromonas pusilla reovirus (isolate Netherlands)	649596 338781 699182 689832 10880 35325 10239	Vruses	
UP000006714	Penicillium chrysogenum virus (isolate Caston/2003) (PcV)	654932	7/30/2015	4	Penicillium chrysogenum virus (isolate Caston)	654932 158372 11014 249310 35325 10239	Vruses	
UP000006716	Human coronavirus 229E (HCoV-229E)	11137	7/27/2015	8	Human coronavirus 229E	11137 693996 693995 11118 76804 35278 439488 10239	Vruses	
UP000000835	Feline coronavirus (strain FIPV WSU-79/1146) (FCoV)	33734	7/30/2015	10	Feline infectious peritonitis virus (strain 79-1146)	33734 11135 12663 693997 693996 693995 11118 76804 35278 439488 10239	Vruses	
UP000006717	Avian infectious bronchitis virus (strain Beaudette) (IBV)	11122	7/30/2015	10	Avian infectious bronchitis virus (strain Beaudette)	11122 11120 694014 694013 693995 11118 76804 35278 439488 10239	Vruses	
UP000006921	Cryptosporidium parvum virus 1 (strain KSU-1)	766191	7/30/2015	2	Cryptosporidium parvum virus 1 (strain KSU-1)	766191 675060 675059 11012 35325 10239	Vruses	
UP000000356	Poliovirus type 1 (strain Mahoney)	12081	7/30/2015	1	Human poliovirus 1 Mahoney	12081 12080 138950 12059 12058 464095 35278 439488 10239	Vruses	
UP000000353	Equine arteritis virus (strain Bucyrus) (EAV)	299386	7/30/2015	9	Equine arteritis virus	299386 11047 11046 76803 76804 35278 439488 10239	Vruses	
UP000000348	Rice ragged stunt virus (isolate Thailand) (RRSV)	649603	7/30/2015	11	Rice ragged stunt virus (isolate Thailand)	649603 42475 10992 689831 10880 35325 10239	Vruses	
UP000000355	Breda virus 1 (BRV-1)	360393	7/27/2015	6	Breda virus serotype 1	360393 46473 74501 11155 694017 11118 76804 35278 439488 10239	Vruses	
UP000006721	Leishmania RNA virus 1 - 1 (isolate Leishmania guyanensis) (LRV-1-1)	58103	7/30/2015	3	Leishmania RNA virus 1 - 1	58103 1678905 39755 11006 35325 10239	Vruses	
UP000001675	Colorado tick fever virus (strain USA/Florio N-7180) (CTFV)	648168	7/30/2015	13	Colorado tick fever virus Florio N-7180	648168 46839 10911 689831 10880 35325 10239	Vruses	
UP000000359	Beet yellows virus (isolate Ukraine) (BYV) (Sugar beet yellows virus)	478555	7/30/2015	8	Beet yellows virus isolate Ukraine	478555 12161 12160 69973 35278 439488 10239	Vruses	
UP000000357	Avian encephalomyelitis virus (strain Calnek vaccine) (AEV)	475778	7/30/2015	1	Avian encephalomyelitis virus strain Calnek	475778 70796 689759 12058 464095 35278 439488 10239	Vruses	
UP000000575	Tobacco necrosis virus (strain A) (TNV-A)	12055	7/30/2015	5	Tobacco necrosis virus A	12055 1299309 39738 35278 439488 10239	Vruses	
UP000001676	Aedes pseudoscutellaris reovirus (isolate France) (ApRV)	648170	7/30/2015	9	Aedes pseudoscutellaris reovirus isolate France	648170 341721 699180 689831 10880 35325 10239	Vruses	
UP000000358	Alfalfa mosaic virus (strain 425 / isolate Leiden)	12322	7/30/2015	4	Alfalfa mosaic virus (strain 425 / isolate Leiden)	12322 12321 12320 39740 35278 439488 10239	Vruses	
UP000006719	Cryphonectria parasitica mycoreovirus 1 (strain 9B21) (CpMYRV-1)	230407	7/30/2015	11	Cryphonectria parasitica mycoreovirus-1 (9B21)	230407 311228 311227 689831 10880 35325 10239	Vruses	
UP000001674	Aquareovirus G (isolate American grass carp/USA/PB01-155/-) (AQRV-G)	648234	7/30/2015	12	American grass carp reovirus PB01-155	648234 465447 519014 10979 689831 10880 35325 10239	Vruses	
UP000000520	Potato virus Y (strain N) (PVY)	12219	7/30/2015	2	Potato virus Y strain N	12219 12216 12195 39729 35278 439488 10239	Vruses	
UP000006724	Human hepatitis A virus genotype IB (isolate HM175) (HHAV) (Human hepatitis A virus (isolate Human/Australia/HM175/1976))	12098	7/30/2015	1	Human hepatitis A virus Hu/Australia/HM175/1976	12098 208726 12092 12091 12058 464095 35278 439488 10239	Vruses	
UP000000354	Human SARS coronavirus (SARS-CoV) (Severe acute respiratory syndrome coronavirus)	227859	7/27/2015	15	SARS coronavirus	227859 694009 694002 693995 11118 76804 35278 439488 10239	Vruses	
UP000000350	Giardia lamblia virus (isolate Wang) (GLV)	649893	7/30/2015	2	Giardia lamblia virus isolate Wang	649893 29255 11011 11006 35325 10239	Vruses	
UP000001672	White clover cryptic virus 1 (isolate Boccardo/2004) (WCCV-1)	654934	7/30/2015	2	White clover cryptic virus 1 (isolate Boccardo)	654934 292052 1511808 11012 35325 10239	Vruses	
UP000001677	Fiji disease virus (isolate Sugarcane) (FDV)	648172	7/30/2015	12	Fiji disease virus isolate Sugarcane	648172 77698 73144 10988 689831 10880 35325 10239	Vruses	
UP000002317	Bovine viral diarrhea virus (isolate NADL) (BVDV) (Mucosal disease virus)	11100	7/30/2015	1	Bovine viral diarrhea virus 1-NADL	11100 11099 11095 11050 35278 439488 10239	Vruses	
UP000006723	Potato leafroll virus (strain Potato/Scotland/strain 1/1984) (PLrV)	12046	8/2/2015	9	Potato leafroll virus (STRAIN 1)	12046 12045 119164 119163 35278 439488 10239	Vruses	
UP000002500	Dengue virus type 1 (strain Nauru/West Pac/1974) (DENV-1)	11059	7/30/2015	1	Dengue virus 1 Nauru/West Pac/1974	11059 11053 12637 11052 11051 11050 35278 439488 10239	Vruses	
UP000000832	Banna virus (strain Indonesia/JKT-6423/1980) (BAV)	649604	7/30/2015	12	Banna virus strain JKT-	649604 77763 208294 689832 10880 35325 10239	Vruses	
UP000000522	Tobacco mosaic virus (strain vulgare) (TMV) (Tobacco mosaic virus (strain U1))	12243	8/2/2015	3	Tobacco mosaic virus (vulgare)	12243 12242 12234 675071 35278 439488 10239	Vruses	
UP000006722	Barley yellow dwarf virus (isolate PAV) (BYDV)	12040	7/30/2015	6	Barley yellow dwarf virus-PAV	12040 12036 119163 35278 439488 10239	Vruses	

UP000000519	Pea enation mosaic virus-1 (strain WSG) (PEMV-1)	693989	7/30/2015	5	Pea enation mosaic virus-1 strain WSG	693989 193121 12289 119163 35278 439488 10239	Vruses	
UP000000360	Yellow fever virus (strain 17D vaccine) (YFV)	11090	7/30/2015	1	Yellow fever virus 17D	11090 11089 40005 11051 11050 35278 439488 10239	Vruses	
UP000006712	Lymantria dispar cypovirus 1 (isolate Rao) (LdCPV-1)	648169	7/30/2015	10	Lymantria dispar cypovirus 1 isolate Rao	648169 165803 205895 10981 689831 10880 35325 10239	Vruses	
UP000006727	Physcomitrella patens subsp. patens (Moss)	3218	7/30/2015	34837	Physcomitrella patens	3218 3217 3216 3215 114656 3214 404260 3208 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000007086	Rice tungro spherical virus (strain A) (RTSV) (Rice tungro spherical waikavirus)	337081	7/30/2015	1	Rice tungro spherical virus (isolate A)	337081 35287 12050 675072 464095 35278 439488 10239	Vruses	
UP000027395	Planktothrix agardhii NIVA-CYA 126/8	388467	7/27/2015	4187	Planktothrix agardhii NIVA-CYA 126/8	388467 1160 54304 1150 1301283 1117 2 131567	Bacteria	Cyanobacteria
UP000027425	Desulfonatronum thiodismutans	159290	7/27/2015	2828	Desulfonatronum thiodismutans	159290 66848 224380 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000007103	Parsnip yellow fleck virus (isolate P-121) (PYFV)	33762	7/30/2015	1	Parsnip yellow fleck virus (isolate P-121)	33762 12777 12057 675072 464095 35278 439488 10239	Vruses	
UP000000518	Hepatitis C virus genotype 1a (isolate H) (HCV)	11108	7/30/2015	2	Hepatitis C virus (isolate H)	11108 31646 41856 11103 11102 11050 35278 439488 10239	Vruses	
UP000000521	Brome streak virus (strain 11-Cal) (BStV) (Brome streak mosaic rymovirus)	117138	7/30/2015	1	Brome streak virus (strain 11-Cal)	117138 42631 156207 39729 35278 439488 10239	Vruses	
UP000011058	Fibrella aestuarina BUZ 2	1166018	7/27/2015	5627	Fibrella aestuarina BUZ 2	1166018 651143 861914 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000011074	Streptomyces rimosus subsp. rimosus ATCC 10970	1265868	7/27/2015	8409	Streptomyces rimosus subsp. rimosus ATCC 10970	1265868 132474 1927 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000011064	Pseudogymnoascus destructans (strain ATCC MYA-4855 / 20631-21) (Bat white-nose syndrome fungus) (Geomyces destructans)	658429	7/30/2015	9122	Pseudogymnoascus destructans 20631-21	658429 655981 78156 34379 221903 147548 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000027604	Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	1349767	7/27/2015	5488	Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	1349767 55508 29580 75682 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000027583	Asaia platycodi SF2.1	1382230	7/27/2015	3273	Asaia platycodi SF2.1	1382230 610243 91914 433 204441 28211 1224 2 131567	Bacteria	Proteobacteria
UP000027616	Mucinivorans hirudinis	1433126	7/27/2015	2816	Mucinivorans hirudinis	1433126 1611681 171550 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000011081	Vavraia culicis (isolate floridensis) (Microsporidian parasite)	948595	7/30/2015	2768	Vavraia culicis subsp. floridensis	948595 103449 35235 35232 6036 6029 4751 33154 2759 131567	eukaryotes	
UP000011082	Vittaforma corneae (strain ATCC 50505) (Microsporidian parasite) (Nosema corneum)	993615	7/30/2015	2236	Vittaforma corneae ATCC 50505	993615 42399 42398 27974 6032 6029 4751 33154 2759 131567	eukaryotes	
UP000027602	Bacillus methanolicus MGA3	796606	7/27/2015	3271	Bacillus methanolicus	796606 1471 1386 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000011096	Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	1213859	7/30/2015	15380	Colletotrichum gloeosporioides Nara gc5	1213859 474922 5455 681950 1028384 222543 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000011115	Solanum tuberosum (Potato)	4113	8/2/2015	53104	Solanum tuberosum	4113 4107 424574 424551 4070 4069 91888 71274 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000011116	Hordeum vulgare var. distichum (Domesticated barley)	112509	8/2/2015	52397	Hordeum vulgare subsp. vulgare	112509 4513 4512 1648017 147389 1648038 147368 359160 4479 38820 4734 1437197 4447 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000027980	Terribacillus aidingensis	586416	7/27/2015	3230	Terribacillus aidingensis	586416 459532 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000027982	Fimbriimonas ginsengisoli Gsoil 348	661478	7/27/2015	4817	Fimbriimonas ginsengisoli Gsoil 348	661478 1005039 1005038 1663426 1663425 1663419 67819 2 131567	Bacteria	Armatimonadetes
UP000027983	Pelosinus sp. UFO1	484770	7/27/2015	4754	Pelosinus sp. UFO1	484770 365348 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000027986	Dermacoccus nishinomiyaensis	1274	7/27/2015	2255	Dermacoccus nishinomiyaensis	1274 57495 145357 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000027985	Virgibacillus sp. SK37	403957	7/27/2015	3815	Virgibacillus sp. SK37	403957 84406 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000035682	Strongyloides ratti (Parasitic roundworm)	34506	7/27/2015	9956	Strongyloides ratti	34506 6247 6246 55746 6236 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000011126	Mycoplasma mycoides subsp. capri str. GM12	436113	7/27/2015	372	Mycoplasma mycoides subsp. capri str. GM12	436113 44100 40477 2102 656088 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000011124	Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	546271	7/30/2015	2243	Selenomonas sputigena ATCC 35185	546271 69823 970 31977 909929 909932 1239 2 131567	Bacteria	Firmicutes
UP000028183	endosymbiont of Acanthamoeba sp. UWC8	86106	7/27/2015	1511	endosymbiont of Acanthamoeba sp. UWC8	86106 204454 44746 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000028181	Rhizobium galegae	399	7/27/2015	6146	Neorhizobium galegae	399 1525371 227290 82115 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000011131	Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	1278073	7/30/2015	8043	Myxococcus stipitatus DSM 14675	1278073 83455 32 31 80811 29 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000001304	Ignisphaera aggregans (strain DSM 17230 / JCM 13409 / AQ1.S1)	583356	7/30/2015	1929	Ignisphaera aggregans DSM 17230	583356 334771 334767 2272 114380 183924 28889 2157 131567	Archaea	
UP000001303	Zinderia insecticola (strain CARI)	871271	7/30/2015	206	Candidatus Zinderia insecticola CARI	871271 884215 884214 75682 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000001299	Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) (Clostridium proteoclasticum)	515622	7/30/2015	3799	Butyrivibrio proteoclasticus B316	515622 43305 830 186803 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000002240	Xenotropic MuLV-related virus (isolate VP62) (XMRV)	373193	7/30/2015	3	Xenotropic MuLV-related virus VP62	373193 438045 1038067 99182 353769 153135 327045 11632 35268 10239	Vruses	
UP000002241	Human immunodeficiency virus type 1 group M subtype B (isolate HXB2) (HIV-1)	11706	8/2/2015	9	HIV-1 M:B_HXB2R	11706 505185 388795 11676 11652 11646 327045 11632 35268 10239	Vruses	

UP000002501	Cauliflower mosaic virus (strain Strasbourg) (CaMV)	10648	7/30/2015	6	Cauliflower mosaic virus (STRAIN STRASBOURG)	10648 10641 10639 186534 35268 10239	Vruses	
UP000001061	Human T-cell leukemia virus 1 (isolate Caribbea HS-35 subtype A) (HTLV-1)	11927	7/30/2015	9	Human T-cell lymphotrophic virus type 1 (Caribbean isolate)	11927 402042 11908 194440 153136 327045 11632 35268 10239	Vruses	
UP000002238	Avian leukosis virus RSA (RSV-SRA) (Rous sarcoma virus (strain Schmidt-Ruppin A))	269446	7/27/2015	4	Rous sarcoma virus (strain Schmidt-Ruppin A)	269446 11889 11886 153057 327045 11632 35268 10239	Vruses	
UP000002242	Human immunodeficiency virus type 2 subtype A (isolate BEN) (HIV-2)	11714	7/30/2015	9	Human immunodeficiency virus type 2 (ISOLATE BEN)	11714 388908 11709 11652 11646 327045 11632 35268 10239	Vruses	
UP000002243	Commelina yellow mottle virus (CoYMV)	10653	7/27/2015	3	Commelina yellow mottle virus	10653 10652 186534 35268 10239	Vruses	
UP000008029	Human T-cell leukemia virus 3 (strain 2026ND) (HTLV-3)	402036	7/30/2015	6	HTLV-3 strain 2026ND	402036 28332 194443 153136 327045 11632 35268 10239	Vruses	
UP000002245	Petunia vein clearing virus (isolate Shepherd) (PVCV)	492094	7/30/2015	1	Petunia vein clearing virus isolate Shepherd	492094 59504 186845 186534 35268 10239	Vruses	
UP000009098	Duck hepatitis B virus (isolate Shanghai/DHBVQCA34) (DHBV)	644639	7/30/2015	4	Duck hepatitis B virus isolate DHBVQCA34	644639 12639 10437 10404 35268 10239	Vruses	
UP000002244	Cassava vein mosaic virus (CsVMV)	38062	7/27/2015	5	Cassava vein mosaic virus	38062 186533 186534 35268 10239	Vruses	
UP000001063	Simian foamy virus (isolate chimpanzee) (SFVcpz)	298339	7/30/2015	5	Pan troglodytes foamy virus	298339 11642 11640 327046 11632 35268 10239	Vruses	
UP000002239	Rice dwarf virus (isolate Fujian) (RDV)	142804	7/30/2015	13	Rice dwarf virus (isolate Fujian)	142804 10991 10985 689832 10880 35325 10239	Vruses	
UP000001065	Soybean chlorotic mottle virus	10651	7/27/2015	9	Soybean chlorotic mottle virus	10651 187214 186534 35268 10239	Vruses	
UP000002246	Rice tungro bacilliform virus (isolate Philippines) (RTBV)	10655	7/30/2015	4	Rice tungro bacilliform virus (isolate Philippines)	10655 10654 187212 186534 35268 10239	Vruses	
UP000007803	Sulfurimonas autotrophica (strain ATCC BAA-671 / DSM 16294 / JCM 11897 / OK10)	563040	7/30/2015	2155	Sulfurimonas autotrophica DSM 16294	563040 202747 202746 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000008707	Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9)	768066	7/30/2015	3469	Halomonas elongata DSM 2581	768066 2746 2745 28256 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008703	Streptomyces violaceusniger Tu 4113	653045	7/27/2015	8941	Streptomyces violaceusniger Tu 4113	653045 68280 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000006859	Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	198628	7/30/2015	4532	Dickeya dadantii 3937	198628 204038 204037 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000028481	Thermodesulfobacterium commune DSM 2178	289377	7/27/2015	1430	Thermodesulfobacterium commune DSM 2178	289377 1741 1740 188711 188710 67799 200940 2 131567	Bacteria	Thermodesulfobacteria
UP000028504	Corynebacterium atypicum	191610	7/27/2015	1533	Corynebacterium atypicum	191610 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000011174	Candidatus Uzinura diaspidicola str. ASNER	1133592	7/27/2015	227	Candidatus Uzinura diaspidicola str. ASNER	1133592 670956 670955 313602 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000011185	Trachipleistophora hominis (Microsporidian parasite)	72359	7/27/2015	3212	Trachipleistophora hominis	72359 72358 35232 6036 6029 4751 33154 2759 131567	eukaryotes	
UP000028680	Planktomarina temperata RCA23	666509	7/27/2015	3024	Planktomarina temperata RCA23	666509 1284658 1284657 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000011173	Nonlabens dokdonensis (strain DSM 17205 / KCTC 12402 / DSW-6) (Donghaeana dokdonensis)	592029	7/30/2015	3613	Nonlabens dokdonensis DSW-6	592029 328515 363408 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000028780	Corynebacterium imitans	156978	7/27/2015	2011	Corynebacterium imitans	156978 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000011220	Clostridium stercorarium subsp. stercorarium (strain ATCC 35414 / DSM 8532 / NCIMB 11754)	1121335	7/30/2015	2669	[Clostridium] stercorarium subsp. stercorarium DSM 8532	1121335 160845 1510 1508657 541000 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000028868	Halobacillus karajensis	195088	8/4/2015	3959	Halobacillus karajensis	195088 45667 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000028875	Virgibacillus sp. Vm-5	1462526	8/4/2015	4389	Virgibacillus sp. Vm-5	1462526 84406 186817 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000028760	Poecilia formosa (Amazon molly) (Limia formosa)	48698	7/27/2015	30440	Poecilia formosa	48698 8080 586240 8079 8087 28738 1489913 1489908 1489872 123369 123368 123367 123366 123365 1489388 186625 1489341 32443 41665 186623 7898 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000028924	Auxenochlorella protothecoides (Green microalga) (Chlorella protothecoides)	3075	7/27/2015	7001	Auxenochlorella protothecoides	3075 191392 35461 35460 75966 3041 33090 2759 131567	eukaryotes	
UP000028926	Candidatus Paracaedibacter acanthamoebae	91604	7/27/2015	1803	Candidatus Paracaedibacter acanthamoebae	91604 1521255 255531 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000028921	Sulfitobacter sp. CB2047	1525218	7/27/2015	3563	Sulfitobacter sp. CB2047	1525218 60136 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000028933	Elizabethkingia anophelis NUHP1	1338011	7/27/2015	4061	Elizabethkingia anophelis NUHP1	1338011 1117645 308865 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000028931	Pseudomonas alkylphenolia	237609	7/27/2015	5119	Pseudomonas alkylphenolia	237609 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000028939	Corynebacterium ureicelerivorans	401472	7/27/2015	1837	Corynebacterium ureicelerivorans	401472 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000028936	Rickettsiales bacterium Ac37b	1528098	7/27/2015	1659	Rickettsiales bacterium Ac37b	1528098 1699067 210592 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000028946	Candidatus Caedibacter acanthamoebae	244581	7/27/2015	1629	Candidatus Caedibacter acanthamoebae	244581 28905 255531 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000028945	Basilea psittacipulmonis DSM 24701	1072685	7/27/2015	1452	Basilea psittacipulmonis DSM 24701	1072685 1472345 1472344 506 80840 28216 1224 2 131567	Bacteria	Proteobacteria
UP000028761	Papio anubis (Olive baboon)	9555	7/27/2015	20931	Papio anubis	9555 9554 9528 9527 314294 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	

UP000028992	Sphingobacterium sp. ML3W	1538644	7/27/2015	4058	Sphingobacterium sp. ML3W	1538644 28453 84566 200666 117747 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000011243	Atlantic salmon paramyxovirus (isolate -/Norway/Yrkje371/1995) (ASPV)	1283346	7/30/2015	9		#REF!	Vruses	
UP000011237	Burkholderia phage BcepMu (isolate -/United States/Summer/2002) (Bacteriophage BcepMu)	1283335	7/30/2015	53	Burkholderia phage BcepMu USA/Summer/2002	1283335 264729 1198139 10662 28883 35237 10239	Vruses	
UP000011235	Burkholderia phage Bcep781 (isolate -/United States/Beer/1978) (Bacteriophage Bcep781)	1283334	7/30/2015	66	Burkholderia phage Bcep781	209052 1198138 10662 28883 35237 10239	Vruses	
UP000011244	Fer-de-Lance paramyxovirus (strain ATCC VR-895) (FLDV) (Fer-de-Lance virus)	1283347	7/30/2015	8	Fer-de-Lance paramyxovirus	122203 1283308 11159 11158 11157 35301 439488 10239	Vruses	
UP000011238	Ranid herpesvirus 1 (strain McKinnell) (RaHV-1)	1283342	7/30/2015	132	Ranid herpesvirus 1	85655 692605 548682 548681 35237 10239	Vruses	
UP000011239	Anguillid herpesvirus 1 (isolate Anguilla anguilla/Netherlands/500138/1998) (AngHV-1) (European eel herpesvirus)	1283343	7/30/2015	129	Anguillid herpesvirus 1	150286 692606 548682 548681 35237 10239	Vruses	
UP000028990	Fukomys damarensis (Damaraland mole rat) (Cryptomys damarensis)	885580	7/27/2015	20405	Fukomys damarensis	885580 423606 10167 33550 9989 314147 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000029079	Weissella ceti	759620	7/27/2015	1338	Weissella ceti	759620 46255 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000029120	Arabis alpina (Alpine rock-cress)	50452	7/30/2015	23245	Arabis alpina	50452 50451 981070 3700 3699 91836 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000006565	Methanolacinia petrolearia (strain DSM 11571 / OCM 486 / SEBR 4847) (Methanoplanus petrolearius)	679926	7/30/2015	2779	Methanolacinia petrolearia DSM 11571	679926 54120 230355 2194 2191 224756 28890 2157 131567	Archaea	
UP000029247	Corynebacterium sp. ATCC 6931	1487956	7/27/2015	2105	Corynebacterium sp. ATCC 6931	1487956 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000002254	Canis familiaris (Dog) (Canis lupus familiaris)	9615	8/9/2015	25497	Canis lupus familiaris	9615 9612 9611 9608 379584 33554 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000011265	Tobacco vein clearing virus (isolate Nicotiana edwardsonii/United States/Lockhart/2000) (TVCV)	1289468	7/30/2015	4	Tobacco vein clearing virus	107324 186533 186534 35268 10239	Vruses	
UP000011263	Heterocapsa circularisquama RNA virus 01 (strain 34) (HcRNAV01)	1289474	7/30/2015	2			Vruses	
UP000011264	Torque teno sus virus k2 (isolate Pig/New Zealand/38E05/2007) (TTSuVk2)	1239832	7/30/2015	4	Torque teno sus virus k2b	1239832 1218488 1218487 687329 29258 10239	Vruses	
UP000011271	Aeropyrum pernix bacilliform virus 1 (isolate -/Japan/Tanaka/2005) (APBV1)	1289471	7/30/2015	14	Aeropyrum pernix bacilliform virus 1	700542 1232738 1232737 686617 10239	Vruses	
UP000011272	Trichomonas vaginalis virus 1 (TVV1)	674953	7/27/2015	2	Trichomonas vaginalis virus	674953 674952 11006 35325 10239	Vruses	
UP000011260	Rhizosolenia setigera RNA virus 01 (isolate RsRNAV06) (RsetRNAV01) (Rhizosolenia setigera RNA virus)	1289384	7/30/2015	2	Rhizosolenia setigera RNA virus 01	359987 674962 1231622 464095 35278 439488 10239	Vruses	
UP000011261	Aurantiochytrium single-stranded RNA virus 01 (isolate -/Japan/AuRNAV01/2000) (AuRNAV01) (Schizochytrium single-stranded RNA virus)	1289385	7/30/2015	1	Aurantiochytrium single-stranded RNA virus 01	674971 674970 1231622 464095 35278 439488 10239	Vruses	
UP000011269	Euprosterna elaeasa virus (isolate Euprosterna elaeasa/-/Zeddam/-) (EvV)	1289470	7/30/2015	2	Euprosterna elaeasa virus	186165 1283211 1283210 35278 439488 10239	Vruses	
UP000011262	Potato virus T (isolate Chenopodium amaranticolor/Peru/ /1992) (PVT)	1289386	7/30/2015	3	Potato virus T	36403 1232754 675068 675063 35278 439488 10239	Vruses	
UP000011276	Rosellinia necatrix megabirnavirus 1 (isolate -/Japan/W779/2001) (RnMBV1)	658904	7/30/2015	2	Rosellinia necatrix megabirnavirus 1/W779	658904 1285598 1285597 1285596 686617 10239	Vruses	
UP000011300	Nile crocodilepox virus (isolate Crocodylus niloticus/Zimbabwe/Ume/2001) (CRV)	1289473	7/30/2015	172	Nile crocodilepox virus Zimbabwe/Ume/2001	1289473 1285600 1285599 10241 10240 35237 10239	Vruses	
UP000011274	Musca hytrovirus(isolate Musca domestica/United States/Boucias/-) (MHV)	523909	7/30/2015	108	Musca domestica salivary gland hypertrophy virus	523909 1285595 1285593 1285590 686617 10239	Vruses	
UP000011277	Torque teno zalophus virus 1 (ZcTTV)	1218490	7/27/2015	3	Torque teno zalophus virus	1218490 1218489 687329 29258 10239	Vruses	
UP000011266	Providence virus (isolate Helicoverpa zea/United States/vFLM1/-) (PRVFL)	1289469	7/30/2015	4	Providence virus	213633 1283209 1283208 35278 439488 10239	Vruses	
UP000011301	Glossina hytrovirus (isolate Glossina pallidipes/Ethiopia/Seibersdorf/-) (GHV)	379529	7/30/2015	160	Glossina pallidipes salivary gland hypertrophy virus	379529 1285594 1285591 1285590 686617 10239	Vruses	
UP000029408	Mollicutes bacterium HR1	1541959	8/4/2015	1811	Mollicutes bacterium HR1	1541959 1609545 39945 31969 544448 2 131567	Bacteria	Tenericutes
UP000029431	Paenibacillus larvae subsp. larvae DSM 25430	697284	8/8/2015	3693	Paenibacillus larvae subsp. larvae DSM 25430	697284 147375 1464 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000011518	Tupaia chinensis (Chinese tree shrew)	246437	7/27/2015	20824	Tupaia chinensis	246437 9394 9393 9392 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000029487	Paenibacillus sp. FSL R7-0331	1536773	7/27/2015	5436	Paenibacillus sp. FSL R7-0331	1536773 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000011547	Candidatus Kinetoplastibacterium desouzaii TCC079E	1208919	8/4/2015	742	Candidatus Kinetoplastibacterium desouzaii TCC079E	1208919 994692 33055 119066 28216 1224 2 131567	Bacteria	Proteobacteria
UP000029494	Lactobacillus sp. wkB8	1545702	7/27/2015	1772	Lactobacillus sp. wkB8	1545702 1578 33958 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000029482	Streptomyces glaucescens	1907	7/27/2015	6550	Streptomyces glaucescens	1907 1883 2062 85011 1760 201174 2 131567	Bacteria	Actinobacteria
UP000029498	Pluralibacter gergoviae (Enterobacter gergoviae)	61647	8/5/2015	4672	Pluralibacter gergoviae	61647 1330546 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria

UP000029501	Paenibacillus odorifer	189426	7/27/2015	5426	Paenibacillus odorifer	189426 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000029500	Paenibacillus graminis	189425	8/8/2015	5576	Paenibacillus graminis	189425 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000029499	Pseudomonas rhizosphaerae	216142	7/27/2015	3893	Pseudomonas	216142 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000029507	Paenibacillus stellifer	169760	7/27/2015	4417	Paenibacillus stellifer	169760 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000029493	Pseudomonas cremoricolorata	157783	7/27/2015	4020	Pseudomonas cremoricolorata	157783 286 135621 72274 1236 1224 2 131567	Bacteria	Proteobacteria
UP000029516	Cedecea neteri	158822	7/27/2015	4399	Cedecea neteri	158822 158483 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000029556	Prevotella buccalis DNF00853	1401074	7/27/2015	2225	Prevotella buccalis DNF00853	1401074 28127 838 171552 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000011658	Candidatus Kinetoplastibacterium galatii TCC219	1208921	8/4/2015	727	Candidatus Kinetoplastibacterium galatii TCC219	1208921 994695 33055 119066 28216 1224 2 131567	Bacteria	Proteobacteria
UP000011668	Thanatephorus cucumeris (strain AG1-IA) (Rice sheath blight fungus) (Rhizoctonia solani)	983506	7/30/2015	10482	Rhizoctonia solani AG-1 IA	983506 456999 1322061 34425 5250 36064 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000029660	Vibrio coralliilyticus	190893	7/27/2015	4908	Vibrio coralliilyticus	190893 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000029665	Pycnoporus cinnabarinus (Cinnabar-red polypore) (Trametes cinnabarina)	5643	7/27/2015	10180	Trametes cinnabarina	5643 5324 83233 5303 355688 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000029742	Salivirus A (isolate Human/Nigeria/NG-J1/2007) (SV-A)	651733	7/30/2015	1	Salivirus NG-J1	651733 1330524 688449 12058 464095 35278 439488 10239	Vruses	
UP000029741	Alphamesonivirus 1 (isolate Aedes harrisoni/Cote d'Ivoire/C79/2004) (CAVV) (Cavally virus (isolate C79))	1552985	7/30/2015	7	Alphamesonivirus 1	1312874 1312873 1312872 76804 35278 439488 10239	Vruses	
UP000029755	Aquamavirus A (isolate Phoca hispida/Canada/HO.02.21/2002) (SePV-1) (Seal picornavirus type 1 (isolate HO.02.21))	1554492	7/30/2015	1	Aquamavirus A	1330066 1330065 12058 464095 35278 439488 10239	Vruses	
UP000029748	Mischivirus A (isolate Miniopterus schreibersii/China/MsPV-1/2010) (MscPV1)	1195365	7/30/2015	1	Miniopterus schreibersii picornavirus 1	1195365 1511779 1511778 12058 464095 35278 439488 10239	Vruses	
UP000029754	Avisivirus A (isolate Turkey/USA/USA-IN1/2010) (TuASV)	1554484	7/30/2015	1	Avisivirus A	1511772 1511771 12058 464095 35278 439488 10239	Vruses	
UP000029746	Oscivirus A1 (isolate Oriental magpie robin/Hong Kong/10717/2010) (OsV-A1)	1554480	7/30/2015	1	Oscivirus A1	871700 1511781 1511780 12058 464095 35278 439488 10239	Vruses	
UP000029751	Gallivirus A (isolate Turkey/Hungary/M176/2011) (GV-A1) (Turkey gallivirus (isolate M176))	1560035	7/30/2015	1	Gallivirus A	1511776 1511775 12058 464095 35278 439488 10239	Vruses	
UP000029745	Pasivirus A1 isolate (isolate Swine/France/Pasivirus 1/2010) (SPaV1) (Swine pasivirus 1)	1554498	7/30/2015	1			Vruses	
UP000029743	Rosavirus A2 (isolate Human/Gambia/GA7403/2008) (RoV-A2)	1554474	7/30/2015	1	Rosavirus A2	1511807 1511805 1511804 12058 464095 35278 439488 10239	Vruses	
UP000029744	Passerivirus A1 (isolate Turdus pallidus/Hong Kong/00356/2007) (PasV-A1)	1554479	7/30/2015	1	Passerivirus A1	871699 1511803 1511802 12058 464095 35278 439488 10239	Vruses	
UP000029750	Hunnivirus A (isolate Sheep/Hungary/OHUV1/2009) (HuV-A2) (Ovine hungarovirus OHUV1)	1168173	7/30/2015	1	Ovine hungarovirus OHUV1/2009/HUN	1168173 1431474 1431460 1431456 12058 464095 35278 439488 10239	Vruses	
UP000029752	Cadicivirus A (isolate Dog/Hong Kong/209/2008) (CaPdV 1) (Canine picodicistrovirus (isolate 209))	1554482	7/30/2015	2	Cadicivirus A	1330068 1330067 12058 464095 35278 439488 10239	Vruses	
UP000029758	Furcraea necrotic streak virus (isolate/Colombia/Furcraea/Cauca/2004) (FNSV)	1554495	7/30/2015	5	Furcraea necrotic streak virus	676234 1299310 39738 35278 439488 10239	Vruses	
UP000029753	Cosavirus A (isolate Human/Pakistan/0553/-) (HCoSV-A)	1554483	7/30/2015	1	Cosavirus A	1330491 586418 12058 464095 35278 439488 10239	Vruses	
UP000029769	Spring viraemia of carp virus (strain ATCC VR-1390) (SVCV)	1559360	7/30/2015	5	Spring viraemia of carp virus	696863 1513299 11270 11157 35301 439488 10239	Vruses	
UP000029766	Galinsoga mosaic virus (GaMV)	60714	7/27/2015	5	Galinsoga mosaic virus	60714 1299312 39738 35278 439488 10239	Vruses	
UP000029759	Maize necrotic streak virus (MNeSV)	137556	7/27/2015	5	Maize necrotic streak virus	137556 1299313 39738 35278 439488 10239	Vruses	
UP000029747	Mosavirus A2 (isolate Coracias garrulus/Hungary/SZAL6-MoV/2011) (MoV-A2)	1554481	7/30/2015	1	Mosavirus A2	1481453 1481452 1481451 12058 464095 35278 439488 10239	Vruses	
UP000029765	Nyamanini virus (isolate Tick/Thailand/39/1968) (NYMV)	1557032	7/30/2015	6	Nyamanini virus	644610 1513295 1513294 11157 35301 439488 10239	Vruses	
UP000029762	Infectious hypodermal and hematopoietic necrosis virus (IHHNV) (Decapod penstyldensovirus 1)	1513224	7/27/2015	3	Decapod penstyldensovirus 1	1513224 1513223 40120 10780 29258 10239	Vruses	
UP000029767	Perch rhabdovirus (isolate Perch/France/PRV/1981) (PRV)	1559359	7/30/2015	5	Perch rhabdovirus	1256869 1298653 11270 11157 35301 439488 10239	Vruses	
UP000029777	Abalone herpesvirus (isolate Abalone/Australia/Victoria/2009) (AbHV)	1241371	7/30/2015	112	Abalone herpesvirus Victoria/AUS/2009	1241371 860343 548681 35237 10239	Vruses	
UP000029781	Cafeteria roenbergensis virus (strain BV-PW1) (CroV)	693272	7/30/2015	544	Cafeteria roenbergensis virus BV-PW1	693272 1513235 1513234 549779 35237 10239	Vruses	
UP000029782	Southern tomato virus (STV)	591166	7/27/2015	2	Southern tomato virus	591166 1511861 1511860 35325 10239	Vruses	
UP000029779	Helicoverpa zea nudivirus 2 (HzNV-2)	1128424	7/27/2015	113	Helicoverpa zea nudivirus 2	1128424 29250 1511854 1511852 35237 10239	Vruses	
UP000029780	Marseillevirus marseillevirus (GBM)	694581	7/30/2015	428	Marseillevirus	694581 1513458 944644 35237 10239	Vruses	
UP000029764	Eidolon helvum parvovirus 1 (isolate Bat/Ghana/-/2009) (Eh-BtPV-1)	1560037	7/30/2015	4	Eidolon helvum parvovirus 1	1131483 1511912 1511911 40119 10780 29258 10239	Vruses	
UP000011713	Hyaloperonospora arabidopsidis (strain Emoy2) (Downy mildew agent) (Peronospora arabidopsidis)	559515	7/30/2015	13836	Hyaloperonospora arabidopsidis Emoy2	559515 272952 184462 4777 4776 4762 33634 2759 131567	eukaryotes	
UP000029760	Hibiscus green spot virus (isolate Citrus volkameriana /USA/WAI 1-1/2009) (HGSV-2)	1554497	7/30/2015	8	Hibiscus green spot virus	1100890 1549608 1513277 35278 439488 10239	Vruses	

UP000029756	Grapevine leafroll-associated virus 7 (isolate Grapevine/Albania/AA42/-) (GLRaV-7)	1554493	7/30/2015	10	Grapevine leafroll-associated virus 7	217615 1513308 69973 35278 439488 10239	Vruses	
UP000029761	Fenneropenaeus chinensis hepatopancreatic densovirus (isolate Shrimp/China/HB/2008) (FcDNV)	1556324	7/30/2015	3	Fenneropenaeus chinensis hepatopancreatic densovirus	797418 1513202 1513201 40120 10780 29258 10239	Vruses	
UP000029773	Beet curly top Iran virus (isolate Sugar beet/Iran/Kerman/-) (BCTIV)	1559363	7/30/2015	5	Beet curly top Iran virus	391228 1298630 10811 29258 10239	Vruses	
UP000011721	Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	1167006	7/30/2015	3514	Desulfocapsa sulfexigens DSM 10523	1167006 65555 53318 213121 213118 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000029749	Megrivirus A (isolate Turkey/USA/124/2008) (Turkey hepatitis virus 2993D (isolate 124))	980964	7/30/2015	1	Turkey hepatitis virus 2993D	980964 1330070 1330069 12058 464095 35278 439488 10239	Vruses	
UP000029763	Galliform aveparvovirus 1 (isolate Chicken/Hungary/ABU-P1/-/-) (ChPV)	717641	7/30/2015	4	Chicken parvovirus ABU-P1	717641 1511865 1511864 40119 10780 29258 10239	Vruses	
UP000011715	Magnaporthiopsis poae (strain ATCC 64411 / 73-15) (Kentucky bluegrass fungus) (Magnaporthe poae)	644358	7/30/2015	11303	Magnaporthiopsis poae ATCC 64411	644358 148304 1491576 81093 639021 222544 147550 715989 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000029774	Eragrostis curvula streak virus (isolate Eragrostis curvula/South Africa/g382/2008) (ECSV)	1559364	7/30/2015	3	Eragrostis curvula streak virus	638358 1298632 10811 29258 10239	Vruses	
UP000029776	Lloviu cuevavirus (isolate Bat/Spain/Asturias-Bat86/2003) (LLOV)	1559366	7/30/2015	9	Lloviu cuevavirus	1513237 1513236 11266 11157 35301 439488 10239	Vruses	
UP000029775	Turnip curly top virus (isolate Turnip/South Africa/B11/2006) (TCTV)	1559365	7/30/2015	6	Turnip curly top virus	859650 1298631 10811 29258 10239	Vruses	
UP000029771	Tupaia virus (isolate Tupaia/Thailand/-/1986) (TUPV)	1560034	7/30/2015	7	Tupaia virus isolate Tupaia/Thailand/-/1986	1560034 318558 1513300 11270 11157 35301 439488 10239	Vruses	
UP000029757	Pegivirus A (isolate Saguinus labiatus/-/GBV-A-lab/1996) (SPgVlab)	1554494	7/30/2015	1	Pegivirus A	1307800 1307799 11050 35278 439488 10239	Vruses	
UP000011723	Corynebacterium halotolerans YIM 70093 = DSM 44683	1121362	7/27/2015	2853	Corynebacterium halotolerans YIM 70093 = DSM 44683	1121362 225326 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000029768	Drosophila melanogaster sigma virus (isolate Drosophila/USA/AP30/2005) (DMelSV)	666363	7/30/2015	6	Drosophila melanogaster sigmavirus AP30	666363 1094373 1308858 11270 11157 35301 439488 10239	Vruses	
UP000029770	Tibrogargan virus (strain CS132) (TIBV)	1559361	7/30/2015	9	Tibrogargan virus strain CS132	1559361 318844 1299306 11270 11157 35301 439488 10239	Vruses	
UP000011729	Bartonella australis (strain Aust/NH1)	1094489	7/30/2015	1260	Bartonella australis Aust/NH1	1094489 388640 773 772 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000011724	Desulfovibrio piezophilus (strain DSM 21447 / JCM 15486 / C1TLV30)	1322246	7/30/2015	3342	Desulfovibrio piezophilus C1TLV30	1322246 879567 872 194924 213115 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000029829	Thalassobacter sp. 16PALIMAR09	1225651	7/27/2015	3345	Thalassobacter sp. 16PALIMAR09	1225651 266808 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000011728	Clostridium saccharoperbutylacetonicum N1-4(HMT)	931276	8/14/2015	5810	Clostridium saccharoperbutylacetonicum N1-4(HMT)	931276 1335640 36745 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000011712	Felis catus (Cat) (Felis silvestris catus)	9685	8/2/2015	20363	Felis catus	9685 9682 338152 9681 379583 33554 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000029855	Listeriaceae bacterium FSL A5-0209	1497679	7/27/2015	3332	Listeriaceae bacterium FSL A5-0209	1497679 1081735 186820 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000029858	Paracoccus sp. 5503	1525717	8/4/2015	2948	Paracoccus sp. 5503	1545044 265 31989 204455 28211 1224 2 131567	Bacteria	Proteobacteria
UP000029857	Helicobacter bilis	37372	8/4/2015	1969	Helicobacter bilis	37372 209 72293 213849 29547 68525 1224 2 131567	Bacteria	Proteobacteria
UP000029867	Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)	4909	7/27/2015	6873	Pichia kudriavzevii	4909 4919 1156497 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008281	Caenorhabditis remanei (Caenorhabditis vulgaris)	31234	7/30/2015	31252	Caenorhabditis remanei	31234 6237 55885 6243 55879 6236 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000029914	Corynebacterium doosanense CAU 212 = DSM 45436	558173	7/27/2015	2476	Corynebacterium doosanense CAU 212 = DSM 45436	558173 1121358 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000008076	Entamoeba dispar (strain ATCC PRA-260 / SAW760)	370354	7/30/2015	8606	Entamoeba dispar SAW760	370354 46681 5758 33084 555406 554915 2759 131567	eukaryotes	
UP000008743	Capsaspora owczarzaki (strain ATCC 30864)	595528	7/30/2015	9794	Capsaspora owczarzaki ATCC 30864	595528 192875 192874 127916 42461 33154 2759 131567	eukaryotes	
UP000011765	Thermodesulfobium narugense DSM 14796	747365	7/27/2015	1797	Thermodesulfobium narugense DSM 14796	747365 184064 227388 227387 68295 186801 1239 2 131567	Bacteria	Firmicutes
UP000029940	Rosellinia necatrix quadrivirus 1 (isolate Rosellinia necatrix/Japan/W1075/1997) (RnQV1)	1559369	7/30/2015	4	Rosellinia necatrix quadrivirus 1	1000373 1299297 1299296 35325 10239	Vruses	
UP000011750	Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	51351	8/2/2015	40809	Brassica rapa subsp. pekinensis	51351 3711 3705 981071 3700 3699 91836 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000009168	Tetrahymena thermophila (strain SB210)	312017	8/2/2015	26976	Tetrahymena thermophila SB210	312017 5911 5890 291294 37093 31277 6020 431838 5878 33630 2759 131567	eukaryotes	
UP000001307	Oikopleura dioica (Tunicate)	34765	7/27/2015	17050	Oikopleura dioica	34765 34763 41302 30302 7712 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000011757	Marinobacter sp. BSs20148	490759	8/4/2015	3885	Marinobacter sp. BSs20148	490759 2742 72275 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000011761	Baudoinia compniacensis (strain UAMH 10762) (Angels' share fungus)	717646	7/30/2015	10508	Baudoinia panamericana UAMH 10762	717646 1709381 483074 668547 134362 451867 147541 715962 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000009169	Trichophyton equinum (strain ATCC MYA-4606 / CBS 127.97) (Horse ringworm fungus)	559882	7/30/2015	8676	Trichophyton equinum CBS 127.97	559882 63418 5550 34384 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	

UP000008311	Ricinus communis (Castor bean)	3988	7/30/2015	31219	Ricinus communis	3988 3987 235880 235629 3977 3646 91835 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000008694	Arabidopsis lyrata subsp. lyrata (Lyre-leaved rock-cress)	81972	7/30/2015	32113	Arabidopsis lyrata subsp. lyrata	81972 59689 3701 980083 3700 3699 91836 71275 1437201 91827 71240 1437183 3398 58024 78536 58023 3193 131221 35493 33090 2759 131567	eukaryotes	
UP000029986	Hafnia alvei FB1	1453496	8/4/2015	4059	Hafnia alvei FB1	1453496 569 568 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000011777	Candida maltosa (strain Xu316) (Yeast)	1245528	7/30/2015	5976	Candida maltosa Xu316	1245528 5479 1535326 1535325 766764 4892 4891 147537 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008912	Ailuropoda melanoleuca (Giant panda)	9646	7/27/2015	21139	Ailuropoda melanoleuca	9646 9645 9632 379584 33554 314145 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001072	Melampsora larici-populina (strain 98AG31 / pathotype 3-4-7) (Poplar leaf rust fungus)	747676	7/30/2015	16237	Melampsora larici-populina 98AG31	747676 203908 5260 5259 5258 162484 29000 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000001064	Dictyostelium purpureum (Slime mold)	5786	7/30/2015	12347	Dictyostelium purpureum	5786 5782 33083 142796 554915 2759 131567	eukaryotes	
UP000006671	Naegleria gruberi (Amoeba)	5762	7/30/2015	15636	Naegleria gruberi	5762 5761 5765 41165 5752 2759 131567	eukaryotes	
UP000011785	Oryctes rhinoceros nudivirus (isolate Oryctes rhinoceros/Malaysia/Ma07/2007) (OrNV)	1046081	7/30/2015	138	Oryctes rhinoceros nudivirus	92521 1511853 1511852 35237 10239	Vruses	
UP000008312	Blastocystis hominis	12968	7/30/2015	5820	Blastocystis hominis	12968 12967 33634 2759 131567	eukaryotes	
UP000008744	Drosophila persimilis (Fruit fly)	7234	7/30/2015	16754	Drosophila persimilis	7234 32358 32355 32341 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000011786	Thrush coronavirus HKU12 (isolate Grey-backed thrush/Hong Kong/HKU12-600/2007) (ThCoV-HKU12) (Thrush coronavirus HKU12-600)	572290	7/30/2015	9	Thrush coronavirus HKU12-600	572290 1297662 1159901 693995 11118 76804 35278 439488 10239	Vruses	
UP000007071	Maize chlorotic mottle virus (isolate United States/Kansas/1987) (MCMV)	882210	7/30/2015	4	Maize chlorotic mottle virus Kansas/1987	882210 12138 39739 39738 35278 439488 10239	Vruses	
UP000007241	Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) (Frog chytrid fungus)	684364	7/30/2015	8610	Batrachochytrium dendrobatidis JAM81	684364 109871 100474 1142503 451442 451435 4761 4751 33154 2759 131567	eukaryotes	
UP000007755	Acromyrmex echinatior (Panamanian leafcutter ant) (Acromyrmex octospinosus echinatior)	103372	7/27/2015	13962	Acromyrmex echinatior	103372 64782 143999 34695 36668 34725 7434 7400 7399 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002473	Lassa virus (strain Mouse/Sierra Leone/Josiah/1976) (LASV)	11622	7/30/2015	4	Lassa virus Josiah	11622 11620 1653394 11617 35301 439488 10239	Vruses	
UP000007797	Dictyostelium fasciculatum (strain SH3) (Slime mold)	1054147	7/30/2015	12152	Dictyostelium fasciculatum SH3	1054147 261658 5782 33083 142796 554915 2759 131567	eukaryotes	
UP000002327	Vesicular stomatitis Indiana virus (strain San Juan) (VSIV)	11285	8/2/2015	6	Vesicular stomatitis Indiana virus strain San Juan	11285 11277 11271 11270 11157 35301 439488 10239	Vruses	
UP000000311	Camponotus floridanus (Florida carpenter ant)	104421	7/27/2015	14787	Camponotus floridanus	104421 13390 72773 7479 36668 34725 7434 7400 7399 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002474	Lymphocytic choriomeningitis virus (strain Armstrong) (LCMV)	11624	7/30/2015	4	Lymphocytic choriomeningitis virus (strain Armstrong)	11624 11623 1653394 11617 35301 439488 10239	Vruses	
UP000007799	Salpingoeca rosetta (strain ATCC 50818 / BSB-021)	946362	7/30/2015	11698	Salpingoeca rosetta	946362 86017 81529 28009 33154 2759 131567	eukaryotes	
UP000007795	Tobacco streak virus (strain WC) (TSV)	12318	7/30/2015	5	Tobacco streak virus (strain WC)	12318 12317 64948 12316 39740 35278 439488 10239	Vruses	
UP000002472	Human respiratory syncytial virus B (strain B1)	79692	7/30/2015	11	Human respiratory syncytial virus B1	79692 208895 11250 11245 11244 11158 11157 35301 439488 10239	Vruses	
UP000002476	Bunyamwera virus (BUNV)	35304	7/27/2015	4	Bunyamwera virus	35304 11572 11571 35301 439488 10239	Vruses	
UP000007661	Vesicular exanthema of swine virus serotype A48 (isolate Swine/United States/A48/1948) (VESV)	85617	7/30/2015	3	Vesicular exanthema of swine virus A48	85617 35612 95337 11974 35278 439488 10239	Vruses	
UP000030061	Paenibacillus sp. MAEPY2	1395587	7/27/2015	6163	Paenibacillus sp. MAEPY2	1395587 44249 186822 1385 91061 1239 2 131567	Bacteria	Firmicutes
UP000029965	Chlorocebus sabaeus (Green monkey) (Cercopithecus sabaeus)	60711	7/27/2015	19239	Chlorocebus sabaeus	60711 392815 9528 9527 314294 9526 314293 376913 9443 314146 1437010 9347 32525 40674 32524 32523 1338369 8287 117571 117570 7776 7742 89593 7711 33511 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000002477	Rift valley fever virus (strain ZH-548 M12) (RVFV)	11589	7/30/2015	4	Rift valley fever virus (STRAIN ZH-548 M12)	11589 11588 11584 11571 35301 439488 10239	Vruses	
UP000007798	Drosophila willistoni (Fruit fly)	7260	7/30/2015	15447	Drosophila willistoni	7260 32367 32365 32341 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006675	Hepatitis delta virus genotype I (isolate D380) (HDV)	31762	7/30/2015	2	Hepatitis delta virus (ISOLATE D380)	31762 12475 39759 10239	Vruses	
UP000002331	Mumps virus (strain Miyahara vaccine) (MuV)	11171	7/30/2015	8	Mumps virus Miyahara vaccine	11171 11161 39744 11159 11158 11157 35301 439488 10239	Vruses	
UP000006678	Mirafiori lettuce virus (isolate Lettuce/Netherlands/LS301-O) (MiLV) (Mirafiori lettuce big-vein virus)	652964	7/30/2015	7	Mirafiori lettuce virus LS301-O	652964 200255 88129 568247 35301 439488 10239	Vruses	
UP000002328	Newcastle disease virus (strain Chicken/United States/B1/48) (NDV)	652953	7/30/2015	8	Newcastle disease virus B1/48	652953 11176 260963 11159 11158 11157 35301 439488 10239	Vruses	

UP000007049	Sapporo virus (isolate GI/Human/Germany/pJG-Sap01) (Hu/Dresden/pJG-Sap01/DE)	291175	7/30/2015	3	Sapovirus Hu/Dresden/pJG-Sap01/DE	291175 280756 95342 95341 11974 35278 439488 10239	Vruses	
UP000006844	Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	401053	7/30/2015	4177	Terriglobus saanensis SP1PR4	401053 870903 392733 204434 204433 204432 57723 131550 2 131567	Bacteria	Fibrobacteres/Acidobacteria group
UP000006676	European mountain ash ringspot-associated virus (isolate Sorbus aucuparia) (EMARAV)	267407	7/30/2015	4	European mountain ash ringspot-associated virus	267407 675845 674978 439488 10239	Vruses	
UP000001460	Cryptosporidium muris (strain RN66)	441375	7/30/2015	3930	Cryptosporidium muris RN66	441375 5808 5806 35082 423054 75739 5796 1280412 5794 33630 2759 131567	eukaryotes	
UP000002471	Avian metapneumovirus (isolate Canada goose/Minnesota/15a/2001) (AMPV)	652954	7/30/2015	9	Avian metapneumovirus 15a	652954 38525 162387 11244 11158 11157 35301 439488 10239	Vruses	
UP000000305	Daphnia pulex (Water flea)	6669	7/27/2015	30137	Daphnia pulex	6669 6668 77658 116561 6665 84337 116557 6658 6657 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000001070	Drosophila grimshawi (Fruit fly) (Idiomyia grimshawi)	7222	7/30/2015	14754	Drosophila grimshawi	7222 32378 48302 48301 48384 504493 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006679	Influenza A virus (strain A/Goose/Guangdong/1/1996 H5N1 genotype Gs/Gd)	93838	7/30/2015	12	Influenza A virus (A/goose/Guangdong/1/1996(H5N1))	93838 102793 11320 197911 11308 35301 439488 10239	Vruses	
UP000030066	Candidatus Mycoplasma girerdii	1318617	7/27/2015	572	Candidatus Mycoplasma girerdii	1318617 2093 2092 2085 31969 544448 2 131567	Bacteria	Tenericutes
UP000007040	Loa loa (Eye worm) (Filaria loa)	7209	7/27/2015	15314	Loa loa	7209 7208 6296 6295 6274 119089 6231 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007800	Perkinsus marinus (strain ATCC 50983 / TXsc)	423536	7/30/2015	23114	Perkinsus marinus ATCC 50983	423536 31276 28000 27999 27998 27997 33630 2759 131567	eukaryotes	
UP000008154	Lettuce big-vein associated virus (isolate Japan/Kagawa) (LBVaV)	652962	7/30/2015	6	Lettuce big-vein associated virus isolate Kagawa	652962 311413 140295 35301 439488 10239	Vruses	
UP000006677	Rice stripe virus (isolate T) (RSV)	36394	7/30/2015	7	Rice stripe virus (isolate T)	36394 12331 12329 35301 439488 10239	Vruses	
UP000008973	Thogoto virus (isolate SiAr 126) (Tho)	126796	7/30/2015	7	Thogoto virus (isolate SiAr 126)	126796 11569 35323 11308 35301 439488 10239	Vruses	
UP000001058	Volvox carteri (Green alga)	3067	7/30/2015	14335	Volvox carteri	3067 3066 3065 3042 3166 3041 33090 2759 131567	eukaryotes	
UP000008158	Influenza B virus (strain B/Lee/1940)	518987	7/30/2015	11	Influenza B virus (B/Lee/1940)	518987 11520 197912 11308 35301 439488 10239	Vruses	
UP000008286	Influenza C virus (strain C/Ann Arbor/1/1950)	11553	7/30/2015	8	Influenza C virus (C/Ann Arbor/1/50)	11553 11552 197913 11308 35301 439488 10239	Vruses	
UP000001292	Drosophila sechellia (Fruit fly)	7238	7/30/2015	16138	Drosophila sechellia	7238 32351 32346 32341 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000007801	Drosophila ananassae (Fruit fly)	7217	7/30/2015	14968	Drosophila ananassae	7217 545632 32347 32346 32341 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006674	Tomato spotted wilt virus (strain Brazilian Br-01) (TSWV)	36413	7/30/2015	5	Tomato spotted wilt virus (strain Brazilian BR-01)	36413 11613 11611 11571 35301 439488 10239	Vruses	
UP000008864	Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) (Athlete's foot fungus)	559305	7/30/2015	10005	Trichophyton rubrum CBS 118892	559305 5551 5550 34384 33183 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000008237	Harpegnathos saltator (Jerdon's jumping ant)	610380	7/30/2015	15029	Harpegnathos saltator	610380 604375 141711 43085 36668 34725 7434 7400 7399 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000006681	Vulcanisaeta distributa (strain DSM 14429 / JCM 11212 / NBRC 100878 / IC-017)	572478	7/30/2015	2493	Vulcanisaeta distributa DSM 14429	572478 164451 164450 2267 2266 183924 28889 2157 131567	Archaea	
UP000008472	Aedes albopictus densovirus (isolate Boublik/1994) (AalDNV)	648330	7/30/2015	3	Aedes albopictus densovirus Boublik/1994	648330 35338 1513193 136466 40120 10780 29258 10239	Vruses	
UP000008469	Adeno-associated virus 2 (isolate Srivastava/1982) (AAV-2)	648242	8/2/2015	6	Adeno-associated virus 2 Srivastava/1982	648242 10804 1511891 10803 40119 10780 29258 10239	Vruses	
UP000030071	Vibrio tubiashii ATCC 19109	1051646	7/30/2015	4914	Vibrio tubiashii ATCC	1051646 29498 662 641 135623 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006683	Ferrimonas balearica (strain DSM 9799 / CCM 4581 / PAT)	550540	7/30/2015	3781	Ferrimonas balearica DSM 9799	550540 44012 44011 267892 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008294	Junonia coenia densovirus (isolate pBRJ/1990) (JcDNV)	648250	7/30/2015	4	Junonia coenia densovirus pBRJ/1990	648250 12524 1513188 10806 40120 10780 29258 10239	Vruses	
UP000008470	Aleutian mink disease parvovirus (strain G) (ADV)	10783	7/30/2015	4	Aleutian mink disease parvovirus (STRAIN G)	10783 28314 1511862 310911 40119 10780 29258 10239	Vruses	
UP000006930	Human herpesvirus 6B (strain Z29) (HHV-6 variant B) (Human B lymphotropic virus)	36351	7/30/2015	97	Human herpesvirus 6 strain Z29	36351 32604 40272 10357 10292 548681 35237 10239	Vruses	
UP000030104	Penicillium italicum	40296	7/27/2015	9993	Penicillium italicum	40296 5073 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000009247	Frog adenovirus 1 (strain ATCC VR-896) (FrAdV-1)	114102	7/30/2015	23	Frog adenovirus 1	114102 298331 129876 10508 35237 10239	Vruses	
UP000030103	Porphyromonas macacae	28115	7/27/2015	1843	Porphyromonas macacae	28115 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group

UP000006364	Acidianus filamentous virus 2 (isolate Italy/Pozzuoli) (AFV-2)	654910	7/30/2015	52	Acidianus filamentous virus 2 (isolate Pozzuoli)	654910 300186 564646 10477 1511857 35237 10239	Vruses	
UP000009251	Human papillomavirus type 16	333760	7/27/2015	8	Human papillomavirus type 16	333760 337041 333750 151340 35237 10239	Vruses	
UP000009249	Cydia pomonella granulosis virus (isolate Mexico/1963) (CpGV) (Cydia pomonella granulovirus)	654905	7/30/2015	143	Cydia pomonella granulosis virus (isolate Mexican)	654905 28289 558017 10442 35237 10239	Vruses	
UP000008785	Bovine papillomavirus type 5	40537	7/27/2015	6	Epsilonpapillomavirus 1	40537 325459 151340 35237 10239	Vruses	
UP000009252	Human papillomavirus type 5	333923	7/27/2015	8	Human papillomavirus type	333923 337051 333922 151340 35237 10239	Vruses	
UP000008167	Human adenovirus C serotype 2 (HAdV-2) (Human adenovirus 2)	10515	8/2/2015	45	Human adenovirus 2	10515 129951 10509 10508 35237 10239	Vruses	
UP000009253	Human papillomavirus type 4	10617	7/27/2015	7	Human papillomavirus type	10617 333926 325455 151340 35237 10239	Vruses	
UP000008788	Canine oral papillomavirus (strain Y62) (COPV)	766192	7/30/2015	7	Canine oral papillomavirus (strain Y62)	766192 35258 325462 151340 35237 10239	Vruses	
UP000009250	Thermoproteus tenax virus 1 (strain KRA1) (TTV1)	10480	7/30/2015	37	Thermoproteus tenax virus 1 (STRAIN KRA1)	10480 10479 341939 10477 1511857 35237 10239	Vruses	
UP000009060	European elk papillomavirus (EEPV)	10565	7/27/2015	15	Deltapapillomavirus 1	10565 325454 151340 35237 10239	Vruses	
UP000008786	Fringilla coelebs papillomavirus (isolate Chaffinch/Netherlands/Dutch) (FcPV)	654914	7/30/2015	6	Fringilla coelebs papillomavirus (Dutch isolate)	654914 197771 325458 151340 35237 10239	Vruses	
UP000006367	Human papillomavirus type 41	10589	7/27/2015	11	Human papillomavirus type 41	10589 334205 475861 151340 35237 10239	Vruses	
UP000008790	Psittacus erithacus timneh papillomavirus (isolate African grey parrot) (PePV)	654917	7/30/2015	6	Psittacus erithacus timneh papillomavirus (isolate African grey parrot)	654917 197772 334213 151340 35237 10239	Vruses	
UP000006369	Bovine papillomavirus type 3	10561	7/27/2015	8	Xipapillomavirus 1	10561 333921 151340 35237 10239	Vruses	
UP000008789	Phocoena spinipinnis papillomavirus (isolate Burmeister's porpoise/Peru/PsPV1) (PsPV)	654916	7/30/2015	8	Phocoena spinipinnis papillomavirus (isolate Peru)	654916 82676 325461 151340 35237 10239	Vruses	
UP000006372	Human papillomavirus type 1a	10583	8/2/2015	8	Human papillomavirus type	10583 334203 334202 151340 35237 10239	Vruses	
UP000008791	Equus caballus papillomavirus 1 (strain Olson) (EcPV-1)	654918	7/30/2015	7	Equus caballus papillomavirus - 1 (strain Olson)	654918 333920 333919 333918 151340 35237 10239	Vruses	
UP000030116	Porphyromonas sp. COT-290 OH860	1515615	7/27/2015	1618	Porphyromonas sp. COT-290 OH860	1515615 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000030125	Porphyromonas cangingivalis	36874	7/27/2015	1769	Porphyromonas cangingivalis	36874 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000011816	Sphingomonas sp. MM-1	745310	7/27/2015	4252	Sphingomonas sp. MM-1	745310 13687 41297 204457 28211 1224 2 131567	Bacteria	Proteobacteria
UP000008787	Cottontail rabbit papillomavirus (strain Kansas) (CRPV) (Papillomavirus sylvilagi)	31553	7/30/2015	8	Papillomavirus sylvilagi (STRAIN KANSAS)	31553 10623 325457 151340 35237 10239	Vruses	
UP000011835	Bifidobacterium thermophilum RBL67	1254439	7/27/2015	1838	Bifidobacterium thermophilum RBL67	1254439 33905 1678 31953 85004 1760 201174 2 131567	Bacteria	Actinobacteria
UP000030126	Porphyromonas sp. COT-108 OH1349	1537504	7/27/2015	1734	Porphyromonas sp. COT-108 OH1349	1537504 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000006518	Campoletis sonorensis ichnovirus (strain Texas A&M) (CsIV)	654920	7/30/2015	5	Campoletis sonorensis ichnovirus (strain Texas A&M)	654920 10484 10483 10482 35237 10239	Vruses	
UP000011834	Morganella morganii subsp. morganii KT	1124991	7/27/2015	3510	Morganella morganii subsp. morganii KT	1124991 180434 582 581 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008168	Microplitis demolitor bracovirus (isolate Webb) (MdBV)	654919	7/30/2015	53	Microplitis demolitor bracovirus (isolate Webb)	654919 53988 10485 10482 35237 10239	Vruses	
UP000009192	Drosophila mojavensis (Fruit fly)	7230	7/30/2015	14525	Drosophila mojavensis	7230 198037 32324 32321 32281 7215 186285 46879 46877 43845 7214 43746 43741 43738 480117 480118 43733 7203 7147 33392 33340 7496 85512 50557 6960 197562 197563 6656 88770 1206794 33317 33213 6072 33208 33154 2759 131567	eukaryotes	
UP000030149	Flavobacterium enshiense DK69	1107311	7/27/2015	2848	Flavobacterium enshiense DK69	1107311 1341165 237 49546 200644 117743 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000030143	Penicillium expansum (Blue mold rot fungus)	27334	7/27/2015	11060	Penicillium expansum	27334 5073 1131492 5042 451871 147545 716546 147538 716545 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000007705	Simian virus 40 (SV40)	10633	7/27/2015	6	Simian virus 40	10633 10624 151341 35237 10239	Vruses	
UP000011846	Bibersteinia trehalosi USDA-ARS-USMARC-192	1171377	7/27/2015	2244	Bibersteinia trehalosi USDA-ARS-USMARC-192	1171377 47735 476528 712 135625 1236 1224 2 131567	Bacteria	Proteobacteria
UP000030139	Porphyromonas crevioricanis	393921	7/27/2015	1583	Porphyromonas crevioricanis	393921 836 171551 171549 200643 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000862	Paramecium bursaria Chlorella virus 1 (PBCV-1)	10506	7/27/2015	794	Paramecium bursaria Chlorella virus 1	10506 181083 10501 35237 10239	Vruses	
UP000000863	Emiliania huxleyi virus 86 (isolate United Kingdom/English Channel/1999) (EhV-86)	654925	7/30/2015	472	Emiliania huxleyi virus 86 (isolate United Kingdom)	654925 181082 346673 10501 35237 10239	Vruses	
UP000000868	Rabbit fibroma virus (strain Kasza) (RFV) (Shope fibroma virus (strain Kasza))	10272	7/30/2015	153	Rabbit fibroma virus (strain Kasza)	10272 10271 10270 10241 10240 35237 10239	Vruses	
UP000000866	Deerpox virus (strain Mule deer/United States/W-848-83/1983) (DPV)	305674	7/30/2015	165	Deerpox virus W-848-83	305674 573057 573055 10241 10240 35237 10239	Vruses	
UP000000864	Ectocarpus siliculosus virus 1 (isolate New Zealand/Kaikoura/1988) (EsV-1)	654926	7/30/2015	231	Ectocarpus siliculosus virus 1 (isolate Kaikoura)	654926 37665 181085 10501 35237 10239	Vruses	

UP000000485	Cellvibrio gilvus (strain ATCC 13127 / NRRL B-14078)	593907	8/2/2015	3153	Cellulomonas gilvus ATCC 13127	593907 11 1707 85016 85006 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000870	Orf virus (strain Goat/Texas/SA00/2000) (OV-SA00) (Orf virus-San Angelo 2000)	647330	7/30/2015	129	Orf virus strain SA00	647330 10258 10257 10241 10240 35237 10239	Vruses	
UP000011859	Rhodanobacter denitrificans	666685	7/27/2015	3773	Rhodanobacter denitrificans	666685 75309 32033 135614 1236 1224 2 131567	Bacteria	Proteobacteria
UP000011864	Paraglaciecola psychrophila 170	1129794	8/4/2015	5601	Paraglaciecola psychrophila 170	1129794 326544 1621534 72275 135622 1236 1224 2 131567	Bacteria	Proteobacteria
UP000006622	Methanosalsum zhilinae (strain DSM 4017 / NBRC 107636 / OCM 62 / WeN5) (Methanohalophilus zhilinae)	679901	7/30/2015	1972	Methanosalsum zhilinae DSM 4017	679901 39669 196136 2206 94695 224756 28890 2157 131567	Archaea	
UP000011863	Ilumatobacter coccineus YM16-304	1313172	7/27/2015	4290	Ilumatobacter coccineus YM16-304	1313172 467094 682522 84994 84993 84992 201174 2 131567	Bacteria	Actinobacteria
UP000000869	Molluscum contagiosum virus subtype 1 (MOCV) (MCVI)	10280	7/27/2015	163	Molluscum contagiosum virus subtype 1	10280 10279 10278 10241 10240 35237 10239	Vruses	
UP000000872	Amsacta moorei entomopoxvirus (AmEPV)	28321	7/27/2015	278	Amsacta moorei entomopoxvirus 'L'	28321 10286 10284 10240 35237 10239	Vruses	
UP000000492	Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	662755	7/30/2015	2160	Corynebacterium resistens DSM 45100	662755 258224 1716 1653 85007 1760 201174 2 131567	Bacteria	Actinobacteria
UP000000867	Myxoma virus (strain Lausanne) (MYXV)	31530	7/30/2015	158	Myxoma virus (strain Lausanne)	31530 10273 10270 10241 10240 35237 10239	Vruses	
UP000011867	Natronomonas moolapensis (strain DSM 18674 / JCM 14361 / 8.8.11)	268739	7/30/2015	2723	Natronomonas moolapensis 8.8.11	268739 416273 63743 2236 2235 183963 28890 2157 131567	Archaea	
UP000000493	Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	761193	7/30/2015	5750	Runella slithyformis DSM 19594	761193 106 105 89373 768507 768503 976 68336 2 131567	Bacteria	Bacteroidetes/Chlorobi group
UP000000494	Hyphomicrobium sp. (strain MC1)	717785	7/30/2015	4889	Hyphomicrobium sp. MC1	717785 81 45401 356 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000871	Swinepox virus (strain Swine/Nebraska/17077-99/1999) (SWPV)	300880	7/30/2015	146	Swinepox virus (strain 17077-99)	300880 10276 10275 10241 10240 35237 10239	Vruses	
UP000000495	Parachlamydia acanthamoebae (strain UV7)	765952	7/30/2015	2784	Parachlamydia acanthamoebae UV-7	765952 83552 83551 92713 51291 204429 204428 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000006621	Flexistipes sinusarabici (strain DSM 4947 / MAS 10)	717231	7/30/2015	2185	Flexistipes sinusarabici DSM 4947	717231 2352 2351 191394 191393 68337 200930 2 131567	Bacteria	Deferribacteres
UP000000496	Simkania negevensis (strain ATCC VR-1471 / Z)	331113	7/30/2015	2516	Simkania negevensis Z	331113 83561 34093 92712 51291 204429 204428 51290 2 131567	Bacteria	Chlamydiae/Verrucomicrobia group
UP000009254	Human T-cell leukemia virus 2 (HTLV-2)	11909	7/27/2015	6	Human T-lymphotropic virus 2	11909 194441 153136 327045 11632 35268 10239	Vruses	
UP000008063	Serpula lacrymans var. lacrymans (strain S7.3) (Dry rot fungus)	936435	7/30/2015	14339	Serpula lacrymans var. lacrymans S7.3	936435 341189 85982 80744 389951 227334 68889 452333 155619 5302 5204 451864 4751 33154 2759 131567	eukaryotes	
UP000011866	Thalassolituus oleivorans MIL-1	1298593	7/27/2015	3634	Thalassolituus oleivorans MIL-1	1298593 187493 187492 135620 135619 1236 1224 2 131567	Bacteria	Proteobacteria
UP000008937	Clostridium sp. (strain SY8519)	1042156	7/30/2015	2601	Clostridium sp. SY8519	1042156 1485 31979 186802 186801 1239 2 131567	Bacteria	Firmicutes
UP000008930	Weissella koreensis (strain KACC 15510)	1045854	7/30/2015	1346	Weissella koreensis KACC 15510	1045854 165096 46255 81850 186826 91061 1239 2 131567	Bacteria	Firmicutes
UP000008929	Eggerthella sp. (strain YY7918)	502558	7/30/2015	2674	Eggerthella sp. YY7918	502558 84111 1643826 1643822 84998 201174 2 131567	Bacteria	Actinobacteria
UP000000501	Nitrosomonas sp. (strain Is79A3)	261292	7/30/2015	3273	Nitrosomonas sp. Is79A3	261292 914 206379 32003 28216 1224 2 131567	Bacteria	Proteobacteria
UP000006639	Midichloria mitochondrii (strain IricVA)	696127	7/30/2015	1181	Candidatus Midichloria mitochondrii IricVA	696127 234827 411566 1328881 766 28211 1224 2 131567	Bacteria	Proteobacteria
UP000000504	Moranella endobia (strain PCIT)	903503	7/30/2015	405	Candidatus Moranella endobia PCIT	903503 1048758 1048757 543 91347 1236 1224 2 131567	Bacteria	Proteobacteria
UP000000503	Treponema caldarium (strain ATCC 51460 / DSM 7334 / H1) (Spirochaeta caldaria)	744872	7/30/2015	2754	Treponema caldarium DSM 7334	744872 215591 157 137 136 203692 203691 2 131567	Bacteria	Spirochaetes
UP000009255	Influenza A virus (strain A/Puerto Rico/8/1934 H1N1)	211044	7/30/2015	12	Influenza A virus (A/Puerto Rico/8/1934(H1N1))	211044 114727 11320 197911 11308 35301 439488 10239	Vruses	
UP000011958	Pneumocystis murina (strain B123) (Pneumocystis carinii f. sp. muris)	1069680	7/30/2015	3776	Pneumocystis murina B123	1069680 263815 4753 44281 37987 147553 451866 4890 451864 4751 33154 2759 131567	eukaryotes	
UP000012040	Bdellovibrio exovorus JSS	1184267	7/27/2015	2618	Bdellovibrio exovorus JSS	1184267 453816 958 213483 213481 28221 68525 1224 2 131567	Bacteria	Proteobacteria
UP000011976	Pseudozyma antarctica (strain T-34) (Yeast) (Candida antarctica)	1151754	7/30/2015	6640	Pseudozyma antarctica T-34	1151754 84753 63298 85578 5268 5267 5257 452284 5204 451864 4751 33154 2759 131567	eukaryotes	

Sheet 2

	Number of reference proteomes with HMMER detected target protein			
Bacteria group/phylum	Total number of reference proteomes	KdpA	KdpD	TrkH
Proteobacteria	608	245	245	397
Firmicutes	483	99	105	408
Unclassified Bacteria	366	2	2	12
Actinobacteria	223	119	123	104
Bacteroidetes/Chlorobi group	184	53	54	144
Tenericutes	59	0	1	45
Cyanobacteria	59	35	33	57
Spirochaetes	27	2	3	25
Deinococcus-Thermus	15	6	7	14
Chlamydiae/Verrucomicrobia	13	3	4	7
Thermotogae	10	0	1	10
Chloroflexi	10	2	2	8
Fibrobacteres/Acidobacteria	9	7	6	1
Aquificae	8	2	2	4
Fusobacteria	8	1	0	8
Planctomycetes	7	3	3	5
Synergistetes	7	0	0	6
Nitrospirae	6	3	3	1
Deferribacteres	4	0	0	4
Thermodesulfobacteria	3	0	0	1
Armatimonadetes	2	2	2	0
Gemmatimonadetes	2	1	1	0
Elusimicrobia	2	0	0	0
Caldiserica	1	0	0	1
Dictyoglomi	1	0	0	1
Chrysiogenetes	1	0	0	1

Sheet 3

	All KdpD proteins retrieved from the RFP																		
Annotation on prediction	**HMMER search output**																		
	Whole protein prediction			**KdpD domain prediction**					**Uniprot entry name**	**Protein name**	**Gene name**	**Organism (and Synonym)**	**length**	**Taxonomic lineage (ALL)**	**Organism ID**	**Protein sequence**	**Whole protein domain architecture predicted by CDD: [domain start~~domain name (E-value)~~domain end] (unpredicted domain labled as "X")**	**KdpD group**	
	E-value	**score**	**bias**	**E-value**	**score**	**bias**	**exp**	**KdpD domain**											
	2.5E-176	591.9	0.3	1.6E-85	295.2	0	2.2	2	C8WRB1_ALIAD	Osmosensitive K channel His kinase sensor	Aaci_0254	Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	754	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Alicyclobacillus, Alicyclobacillus acidocaldarius, Alicyclobacillus acidocaldarius (Bacillus acidocaldarius), Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	521098	>tr|C8WRB1|C8WRB1_ALIAD Osmosensitive K channel His kinase sensor OS=Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) GN=Aaci_0254 PE=4 SV=1 MTGGEVIRPTGGSGRRGRLRVFIGAAPGVGKTYTMLREARRLREEGTDVVIGWV ETHGRPATEKLLEGLEVIPPRVLKVGQATFEEPDLDAIVARRPEVCVIDELAHTNPP GAMHEKRYEDVMYLLDRGISVMTAFNIQHLESVRDEVQQQLGIRVREVVPEWFLR EADEVTVIDVTPETLRQRLRDGEIYPPEKVDAALQNFFRVDRLAWLRQMSLRAVA DDVDERLEHSYERRAIPGPVGAKEVVLVCVSHPDRAATLIERGRRRMAMRMKGDL HVVYAAETDEDRMTERARAEVDELRRLAEFHGAEWVLEPKRDRPVGEVILRVAR RVNATQVVLGQPRKGASPRRLMAWHHPVQYLLKHLQYVDLRVVGWRPLSPAAR EQRNWASERVVRERKLPGKLTLYIGAAPGVGKTYRMLQDAHDWKVRGIDVVIGLI ETHGRPETEAQIGDLERIPKRRIEYGGKVYEEPDLAAILARRPQVVLMDELAHTNA PGSMFKKRYQDILYLLEHGVDVVSAVNVQHLESLKDRVEHITGATIRERVPDWFV KLASEVKLIDVSPETLVERLLEGKIYPPEKVEQALSNFFQLAHLAALREIALREVADV VDGRLAPPPPADPERILVCVNYRPHSEALIRRGWRIADRLQAKLYVLVVQTEFPLS SQSERDFAAVRDLAEQFGAEFLLRPALHKSVGQVIVETAESESVSQIVMGQPLNR GLGARFAHRPITYVLNRAEFVDLHIVAYAGRWSQPSA	21~~KdpD (7.46611E-97) ~~224,247~~Usp (7.8134E-35) ~~373,400~~KdpD (6.11315E-106) ~~607,621~~Usp (5.65694E-34) ~~744	non-kinase	KdpD;Usp;KdpD;Usp
	3.9E-172	578.2	2.3	1.9E-89	308.1	0	2.8	2	U5QMZ5_9CYAN	Sensor protein KdpD (EC 2.7.13.3)	kdpDGKIL_2723	Gloeobacter kilaueensis JS1	753	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter kilaueensis, Gloeobacter kilaueensis JS1	1183438	>tr|U5QMZ5|U5QMZ5_9CYAN Sensor protein KdpD OS=Gloeobacter kilaueensis JS1 GN=kdpD PE=4 SV=1 MIRQSDEQPDPETLLRTLLEFSPGRFKLYLGYAPGVGKTLRMLQEAQLLVCRGVD LVVGIVETHGRPETARLLEGLEVVDPRRALHQGVTLEELDLEAVLARRPATVIIDEL AHTNAPGSSHTRRYEDVEALLAAGISVISTMNIQHLESVAETAGRLIGFAVHERVP ARIVQAADEIQLVDTSPEKLLERLAQGKVDARFQAGGQFFRSSTLVYLRELALRTV AGLVDDAILVRQGSGVAGPAGVRERLLVAVSTNPSSARLIRRGARIAERFDGELFV VYVDAGNTPSAEQQRTLAEHRQLCERAGGNFVVLQGHNISQALVGFALEKHITQV ILGESMRTPVEQLLRGSVINDLLRSTSNLDVLVVGETESVGPLPPPASPPVPSHTC FLPAALERQTRGCGRHKIYLGAAPGVGKTCAMLQEAHDLSAAGVDVVCGLIETHG RAETAALITGLEVIPRRQLTYRGRAFSEFDREAVLARRPAIVLLDELAHTNLPGLGT ARRYQDVEILLAAGIDVISTLNIQHLESLNTLVERTTGVRVRETVPDLVVECADEVV LIDLTTDELQRRLREGKIYAPAKIEQALSHFFRAENLIALRELALREVADDCTARKFD TATPTEERVLVCTNLRSNAQQLIRRGARIARRLGAALVVTYIQTTGSALSEAEKRQ LDGVRRLSAELGGSFIELSASNVAERIVSLAHEQAATLLVLGESRRSHLEKLLHGSV IEQVLRRTRNLDTLIVGNFEHE	24~~KdpD (1.40005E-88) ~~228,249~~Usp (9.2622E-38) ~~370,405~~KdpD (2.02942E-110) ~~610,626~~Usp (4.61773E-23) ~~748	non-kinase	KdpD;Usp;KdpD;Usp

	1.5E-169	569.8	2.8	1E-88	305.6	0.3	2.3	2	Q7NN44_GLOVI	Potassium-transporting P-type ATPase D chain	kdpD gll0570	Gloeobacter violaceus (strain PCC 7421)	754	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter violaceus, Gloeobacter violaceus (strain PCC 7421)	251221	>tr|Q7NN44|Q7NN44_GLOVI Potassium-transporting P-type ATPase D chain OS=Gloeobacter violaceus (strain PCC 7421) GN=kdpD PE=4 SV=1 MFRPNEDCPDPQSLLHELMQLSRGRLKLYLGYTPGVGKTVRMLQEARRLRRRGV DLVVGWVETHGRPDTEALLADLEVMAPRQVAYQGVIIPELDLEAILQRRPATVLID ELAHTNAPGSRHRKRYEDVEVLLDAGVSVMSAMNIQHLESVAEAAGRLIGAVVHE TVPDRLLRSAEEVQLVDASPEAVLERLQRGDAARYIPPGSPFLRRSTLVYLRELAL RAVAEVVDADILSGKNGVAGPAGVRERVLAAVSTNPASARLIRRGARIAERLDAEL FVAYVETGRPLAPPEAQTLQEHRAATEAAAGEFVQLQNRDVAGALIDFALQKNIT QVIVGESLRSPAEELVRGSVINTLLRTTSNIDVLIVGEAESSMVGPLTPVAAQPPFA VGCLLVGADSRRAHGCGRHKIYLGAAPGVGKTFAMLQEAHHLHASGIDVVCGVIE THGRAETAALIENLEVVPKRAIGYQGRTFLELDVEAVLRRRPAVVLVDELAHTNIAG AGNTKRFQDVEVLLGAGIDVVSTLNIQHLESLNTLVERTTGVKVRETLPDLVVEAA DEVVLVDLPTGELTQRLREGKIYAQAKVEQALANFFRPENLSALRELALREVADDC TTRKLEEAAHGPGGRVLVCINLRPNAEQLIRRGARIASRLSAPLVVAHIGAHDDGP TARAVERLGELTRQLGGEFIERPAAANQVPEQIDALAHEQGVTLLVMGESRRSR WEKLLHGCVIEQVVRRVRNLDVLIVGDLEHE	23~~KdpD (1.16945E-86) ~~228,248~~Usp (1.76104E-37) ~~369,406~~KdpD (4.06369E-107) ~~611,628~~Usp (6.55657E-34) ~~749	non-kinase	KdpD;Usp;KdpD;Usp
	1.7E-160	540.2	3.4	1.8E-91	314.7	0.5	2.2	2	A0A089ML71_9BACL	Histidine kinase	PODO_02720	Paenibacillus odorifer	774	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus odorifer	189426	>tr|A0A089ML71|A0A089ML71_9BACL Histidine kinase OS=Paenibacillus odorifer GN=PODO_02720 PE=4 SV=1 MGTYRRKTPEELLLSIYELHRGRLKIYIGPVSGSGKTYQMLREGQALKAQGIDVVIC AVSTNQSPETRDQLGDLERIPSIHWFQKEIEKKDLDVEAIVARNPEVVLTDGLAHH NREGAERSTRLEDIKYLLGCGISVITTVNVYELEGAADLARKWTGIEVEYSLPAEVL TLADDIVLIDVTPEKILQRLSEGHLGKKQRTSLFNKGNLSKLRELALRMVAEDVNGS LEKHREEQGLLGASGIAEKVLVSAQYYWNGSIHIIRRGQQIAKRLNGDLAVVSFWK QGLTPSKEAATFKRSLWKLTEKIGASMEEISFRSKREIPGLLVKYAIQHNITRIVMG HSKQTAWQELWKGSIANSLLKQIRGVDVFFVADRAEREGERVLPTRQSRNERKA DAYHRLSSQEVKDKIDAIRGGTFKVYIGAAPGVGKTYKMLREGNDLLKRGIDVVIG LLETHGRKETLEQIGELEILPRLSIDYRGTVLEEMDTAAIIKRNPEVVLVDELAHTNM PGSKHKKRYMDVMELLDAGISVISTVNVQHLESLNDAVEQITGVRVRETFPDSILQ RADEVELIDVSPKTLQERMKDGKIYAMTKVDQALGAFFKIGNLIALRELALREIADD VDERLEAWERVGSLRGPWRRQEVIYVCITLGDHAERLIRRGFRIAYRLKACWYVT YVQEYKQSGPSYDKRINDLKELTERLGGTFKMIPNVLPARVSSLLLERSQALQSTQ IIIGQSQRSWVRKWLRGDVTKQILRSARNVDVLVVANLMREEP	20~~KdpD (1.28141E-58) ~~224,246~~Usp (2.55185E-17) ~~371,412~~KdpD (5.21805E-117) ~~621,644~~Usp (4.75109E-27) ~~767	non-kinase	KdpD;Usp;KdpD;Usp
	4E-160	538.9	3.6	3E-92	317.2	0.3	2.2	2	V9VZT0_9BACL	Sensor protein KdpD (EC 2.7.13.3)	kdpD ERIC2_c03150	Paenibacillus larvae subsp. larvae DSM 25430	769	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus larvae, Paenibacillus larvae subsp. larvae, Paenibacillus larvae subsp. larvae DSM 25430	697284	>tr|V9VZT0|V9VZT0_9BACL Sensor protein KdpD OS=Paenibacillus larvae subsp. larvae DSM 25430 GN=kdpD PE=4 SV=1 MEEFRRKTPEEILQSISDINRGRLKIYLGAVSGSGKTYHMLREAQSLKENGIDVVLC AVSTLNRPETARQASGLETIPSIDWTKDGVIQQDLNLVALVERNPEVVLVDGLAHR NRQGALFPTRLGDISFLLEKGISVITTVNVYELEGVRELARKLAGVEVKTTVPSGTL EMADEVRLIDVTPETILKRLEEGNLPGQKEHHLFLKGNIGVLRELALRLVAEDVNGS LEKYRKSKGLSGPSGAGERILVSTQYHWNGSIYVRRGQQIANRLNGDLYVICFQH TGKPLSKEQAAFKRSLKKLVDKIGAVFVELPFPGRRKLADSLLDYAMKNSVTRIVL GHSKHTRIQELWQGSIINDILRKMTRTDLFVVADRAERDGERILPAKRKVGTKKAE LYRRHSKQEMQKEIEKIRRGVFKVYIGAAPGVGKTYTMLREGNDLARKGIDVIVGL LETHGRRETAEQLGNLGMIPRRKIDYRGTTLEEMDTDAIIERAPDVVLVDELAHTN VPGSRHNKRFEDVLDILNAGISVITTVNVQHLESLNDAVEQITGVRVRETVPDSILW MADEVELIDVPPQTLRQRMKEGRIYSMEKVEQALGHFFKIGNLIALRELALREIADD VDERLESWERKESLRGPWRREETIFVCVKLNDHAERIIRRGFRIAFRLKARWHVA YLHHGSGMEDEARLKELKGLTERLGGSFEVITGQGKKDPADLLLAKANEYNSTQM ILGKSCSPSWRDRWQGSLVKRLLRGARHMDVLVVTEYER	20~~KdpD (5.10518E-60) ~~224,246~~Usp (1.71023E-14) ~~371,412~~KdpD (2.318E-114) ~~621,644~~Usp (4.54747E-26) ~~765	non-kinase	KdpD;Usp;KdpD;Usp
	1.8E-159	536.8	8.4	3E-91	313.9	1.1	2.3	2	A0A089ME28_9BACL	Histidine kinase	PGRAT_25535	Paenibacillus graminis	785	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus graminis	189425	>tr|A0A089ME28|A0A089ME28_9BACL Histidine kinase OS=Paenibacillus graminis GN=PGRAT_25535 PE=4 SV=1 MENFKRKSPEEILLSISKLHRGRLKIFIGAVSGSGKTYHMLREGTALQQQGIDVVIC AVSTLQRPETIEQIGELERIPSIHWVQDGTEKKDLNMEALILRNPEVVLVDGLAHRN RPGAEHKTRLEDIHFLLGHGISVMTTVNVYELEGVRELAQKYMGIEVEETVSAHTL ELADEIRLIDVTPETLLQRVSEGHVRNSKTATLFRRGTLGVLRELALRLVAEGVNDS LEKHREQMGMLGPSGAAERILVSTQYHWNGSIYVRRGQQVAKRLNGELIIITFTN QKRPLTKEQAAFKESLVKLVQKVGAEFEELPFHSRRRLPDRLIQYALEHNVTRIML GHSRQSRWQEFWQGSVVNDILRKSRNMDIFMVADRAEHHGERILPAKLAVPADN PLYHRLSSREVDEKIGRIKRGRFKVFIGAAPGVGKTYTMLREGNHLLKKGVDVVIG LLETHGRQETGQQVAELPLIERAKIKYSETVLEEMDTGAILRRNPELVLVDELAHTN VPGSKYKKRYEDVMEILNAGISVISTVNVQHLESLNDAVAQITGVRVRETVPDSILR LADEVELIDVAPQALQARMKDGKIYAREKIDQALDNFFKMGNLIALRELSLREIADD VDERLEAGERVSSLRGPWNKQEVIFVCVKLSQSAGKLIRRGFRTAFRLKADWIVA YVHSAKELTGDEEKMKASIENLTIRLGGKFEMISSSGPSSRLAEVIQAKADEHHAT QLIIGQCDRPPWKRLWEGTIIKKLLRTARHMDILIVANYDPHIKRDTLPEAAAHE	20~~KdpD (1.36979E-58) ~~224,246~~Usp (9.72001E-21) ~~371,411~~KdpD (3.84259E-112) ~~620,643~~Usp (7.47441E-24) ~~767	non-kinase	KdpD;Usp;KdpD;Usp

	7.8E-159	534.7	7.7	1.7E-93	321.3	0.8	2.3	2	D3EAK7_GEOS4	Osmosensitive K channel His kinase sensor	GYMC10_0435	Geobacillus sp. (strain Y412MC10)	775	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Geobacillus sp. (strain Y412MC10)	481743	>tr|D3EAK7|D3EAK7_GEOS4 Osmosensitive K channel His kinase sensor OS=Geobacillus sp. (strain Y412MC10) GN=GYMC10_0435 PE=4 SV=1 MDPFRRKSPEELLRSISKLHQGRLKVYIGAVSGSGKTYHMLREGQTLRLQGIDVVI CAVSTMQRPETVEQVRDLERVPSIHWMEDGVEKKDLDLDLLVQRNPEVVLVDGL AHRNRKGARHAARLDDIRFLLSRGISVITTVNVYELADVQDIASKLTGIKASHTVPA DTLESADEVVLIDVTPETMLERAQGGLLGDGSLWKQGNLAVLRELTLRLVAEGVS HSLERYRKEQGLVGPSGADERILVSTQYHWNGSIYMRRGQQIAKRLNGELLAVTF VKPEVELTKEQAAFKRSMVKLAVRIGAKLEELPLRSRRELADMLVQYALEHHVTRI VLGHSKQTRMQELWQGSIIQDLLKKTRGIDIFMVADRAEHDGERIIPARLHPLRLPS ESFHRLNEQELDQKIEQVKRGRFKVYIGAAPGVGKTYAMLREGNDLLKKGLTVLV GLLETHGRKDTLSQVGNLEALPRKRVDYRGSRLEEMDTDEILRRRPDVVLVDELA HTNVPGSKRKKRYEDVQDILSAGISVITTVNVQHLESLNDAVEQITGVRVRETIPDH ILQSADEVQLVDVTPESLRQRMKDGNIYAKEKIHQALSHFFKTGNLIALRELALREIA DDVDERLESWQRSGSLRGPWRREEIIYVVVGRGPQAERLIRRGFRIAHRLKAAW YVAFPLERHDSLSHDEEQRLTALQTLTERLGGTFTMLPLPIKRGPACACSGRLVAA ADEVKATQFIIGQPQMAGWKLFARRKWIRRLLRSSRHMDVLVVADYDPRV	20~~KdpD (1.28074E-54) ~~221,243~~Usp (8.19054E-17) ~~368,409~~KdpD (6.98031E-113) ~~618,641~~Usp (4.20678E-20) ~~769	non-kinase	KdpD;Usp;KdpD;Usp
	1E-158	534.3	8.7	4E-90	310.2	1.1	2.3	2	H6NGY0_9BACL	Potassium-transporting p-type ATPase d chain	PM3016_1497	Paenibacillus mucilaginosus 3016	772	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus mucilaginosus, Paenibacillus mucilaginosus 3016	1116391	>tr|H6NGY0|H6NGY0_9BACL Potassium-transporting p-type ATPase d chain OS=Paenibacillus mucilaginosus 3016 GN=PM3016_1497 PE=4 SV=1 MDEFRRKTPEEILKSISELQRGRLKIYVGPFSGSGKTYHMLQEGNSLKQRGIDVVI CAVSTMQRKETIEQIGCLERVPSIHWVKDGVEKKDLNIEALLARNPEVVLVDGLAH RNRMEARFRTRLQDIQHLLKQGISVITTVNVYELEGYTELAQRLTGIEVDETVPADT LELADEIRLIDVTPESILARLSEGAMEATHTSLSKRDNLGKLRELALRLVAEDVNESL EEHREALGLNGPSGASERILVSTQYHWNGSIYIRRGEQIARRLNGDMLVVTFVDP KKPLSKEQTAFKRSIVKLTEKLEVSFDELPFVRRRAMPRQLVDYAIDNKVTRIVLGH SKQTTWQEWWRGSVVNTLMKLARHVDLFYMADSAEQKGERILPTSITKKADANI YKRLSGSEVKERIIRIKRGTFKIYIGAAPGVGKTYTMLKEGNILLKKGIDVVIGLLETH GRKETFEQIGDLTTIPRQVSDYRGTRLEEMNMEAIIRLNPEVVLVDELAHTNVPGS KNKKRYEDILEILEAGISVISTMNVQHVESLNDAVEQLTGVRVRETVPDRILRLADE VQLIDVAPNALQQRLRDGKIYARNKVEQALNHFFKTGNLIALRELALREIADDVDER LEAWERRDSLRGPWRREEVIFVCVTLSPRAESLIRRGFRIAHRLKADWVVHYIAVK ADLPEEQQKRIMDLRELTQRLGGIFNMQVMERRRQVAVKLLEQANVNKSTQLIIG QSQMKFWERMLYGNTVKTILKYGRHMDVLVVSGFVPKER	20~~KdpD (1.1717E-58) ~~223,245~~Usp (2.99918E-16) ~~366,410~~KdpD (6.43534E-107) ~~619,642~~Usp (2.02956E-25) ~~765	non-kinase	KdpD;Usp;KdpD;Usp
	1.2E-158	534.1	2.5	5.7E-89	306.5	0.3	2.3	2	C6D694_PAESJ	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Pjdr2_5993	Paenibacillus sp. (strain JDR-2)	775	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. (strain JDR-2)	324057	>tr|C6D694|C6D694_PAESJ Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Paenibacillus sp. (strain JDR-2) GN=Pjdr2_5993 PE=4 SV=1 MNDSYRRKTPEELLKAITKLHHGRLKIYIGAVSGAGKTYHMLREGQQLRKQGIDVV TCAVSTMQRPETMEQLAELERIPSIRWEKDGSQRKDLDLAAIKARNPEVVLVDGL AHRNRPDSLLPTRLDDIRHLLECGISVITTLNVYELNGVSDLAYQLTGIEAEHTVPD DILELADEVRLIDVSPETILTRLNEGHLRNASSPHLLLRGNLGKLRELALRLMAEDV NDSLEDHRRQQGLVGPSGAAERILVAAQYHWNGSIHIRRGQQVARRLNGELLVV SFVKADKAMTKEATAFKRSIIKLTQKIGAGFEELAVPHLHRRHLSEQMARYAMDHG VTRIVLGHSKHTPLQELLHGSVVNGILRYARRIDVFFVADRTEAEGERILPAKHRTT PEPIYKRLSPAQQQQTTDRLKRGTFKVYIGAAPGVGKTYTMLREGNVLLRKGIDV VIGLLETHGRKETLEQIGDLEEIPKAAIPYKGTQLKEMDVSAILSRFPEVVLIDELAH TNVPGSHYKKRYEDVLAILDAGISVISTVNVQHLESLNDAVEQITGVKVRETVPDR MLRLADEVELIDVSPKALQERMRQGKIYPMNKVEESLGAFFQLGNLIALRELALREI ADDVDERLESWERTGALRGPWRRQEVIFVAITDLAQGERLIRRGFRIAYRLKAEW HVMAVHNGKTEQAAVDRRMKELQQLTEQLGGMFVRKEMKQTRDIPAFLLTHANA RKSTQLIVAQEKSSWLARLFRPSIMKKLLQGGRNMDVMVVSCLPSQEQ	21~~KdpD (2.57283E-57) ~~225,247~~Usp (1.79906E-14) ~~374,413~~KdpD (4.75319E-107) ~~622,645~~Usp (3.94183E-19) ~~768	non-kinase	KdpD;Usp;KdpD;Usp
	3.6E-158	532.6	6.2	1.2E-89	308.7	1.1	2.3	2	E3EDL7_PAEPS	Histidine kinase	kdpD1 PPSC2_06480	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	775	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus polymyxa (Bacillus polymyxa), Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	886882	>tr|E3EDL7|E3EDL7_PAEPS Histidine kinase OS=Paenibacillus polymyxa (strain SC2) GN=kdpD1 PE=4 SV=1 MESFKRKSPEEILDSINKLHRGRLKIYIGAVSGSGKTYHMLQEGQSLQHEGIDVVIC AVSTLQRRETVEQVGSLERVPSIHWMKDGEEQKDLNVEALVARNPEVVLVDHLA HHNRKDASFPTRLEDIRYLLEMGISVITTVNVYELEGITEWVYQLTGFEAEYTVPVD TLELADEIRLIDATPEMILERLAKGYMHTPNPEMFHRGNLGKLRELALRLVAEDVND SLERHREELGLHGASGAAERILVPVQYHWNGSIYVRRGEQVAKRLGGDMLVVSF VSSKRKLSKESAAFKRSIEQLADKIGSTFEEIPLFSRRRLPRQLIHYAVTHNVTRIVM GHSRQTPWQELVKGSLVNGILKRMKNMDLLLIADRAEQEGERILPTMRQEEGDTD PYHRLSVEEVQAEEAKILRGKLKVYIGAAPGVGKTYTMLREGNDLLESGIDVVIGLL ETHGRAETLAQVGSLEMISRQSIERHGAHLEEMDTEAILRRNPEVVLVDELAHTNV PGSLRSKRYEDVLAILEQGISVISTMNVQHLESLNDAVEQITGIRVRETVPDHMMRL ADEVQLVDVAPKSLQQRMREGKIYAPAKVEQALSHFFKLGNLIALRELALRELADD VDERLESWDRHESLRGPWRREEVIFVGVTLSENAERLIRRGFRIAFRLKAVWIVTY VHIGERIPERLNPRLEQLKLLTHRLGGTFEIRLVSSKREIADILIAPVEGYSGTQLIVG QSSRSSCWGKTAVVPRILRQARHMDVLIVADYDPDIKLETDY	20~~KdpD (3.10657E-53) ~~223,245~~Usp (4.51981E-15) ~~370,411~~KdpD (1.0726E-110) ~~619,642~~Usp (5.54451E-18) ~~763	non-kinase	KdpD;Usp;KdpD;Usp

	3.9E-158	532.4	13.2	4.2E-91	313.4	1.4	3.2	2	A0A0D3VH18_9BACL	Histidine kinase	UB51_10565	Paenibacillus sp. IHBB 10380	773	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. IHBB 10380	1566358	>tr|A0A0D3VH18|A0A0D3VH18_9BACL Histidine kinase OS=Paenibacillus sp. IHBB 10380 GN=UB51_10565 PE=4 SV=1 MDNFRRKKPEEILQSISKLHQGRLKVYIGSVSGSGKTYHMLREGQSLKSQGIDVVI CAVSTMQRAETIEQIGDLERVPSIHWWKNGIEKKDLDLDALIERNPEVVLVDGLAH RNREDAPLSTRLEDIQRLISHGMSVITTVNVYELEDVRSVAQKLTKIEVAETVPTDT LNLADEVVLIDVTPEKMLTRVAEGKLSLDDKEIFKRGNLAILRELTLRLVAEGVNDSL EKYREEWGLIGPSGAGERILVSTQYHWNGSIYMRRGQQIAKRLNGDLLVVTFVNK DKELTREAAAFKRSQLKLANRIGAEFEELPLCARRELPRVLVHYALENNVTRILLGH SKQTRWQELWHGSIVHDMLKKTRNVDIFIVADRAEHDGERILPTKISKPEEDKELF RRLSSQELDQKIEQIKRGTFQVYIGAAPGVGKTFTMLREGNHLLKKGIDVCVGLLE THGRNDTQAQVNLLEILPRKVIEYRGTQLAEMDTAEIIRRNPEVVLVDELAHTNVP GSQYKKRYEDVLEILAAGISVITTVNVQHLESLNDAVEQITGVRVRETIPDHILRLAD EVQLIDVTPQSLQQRMKDGKIYNMKKVHQALNNFFRTGNLIALRELALREIADDVD ERLEAWERNNSLRGPWRRKEVIYVCINNTLHAERLIRRGFRIANRLKAIWYVTFVQ LEHADSTAVMTEQLEALKKLTERLGGKFEIQTTRRRKHIPDVLVSKANEYQATQMI VGQSKTKLWKEVWQGSIIKKLLRATRHLDVLVVADFEPLN	20~~KdpD (5.00442E-59) ~~223,245~~Usp (3.59779E-19) ~~370,411~~KdpD (1.77021E-109) ~~620,643~~Usp (2.09691E-26) ~~767	non-kinase	KdpD;Usp;KdpD;Usp
	1E-156	527.8	8.7	1E-88	305.6	2.2	2.3	2	A0A0A2UAK1_9BACL	Histidine kinase	P364_0106835	Paenibacillus sp. MAEPY2	779	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. MAEPY2	1395587	>tr|A0A0A2UAK1|A0A0A2UAK1_9BACL Histidine kinase OS=Paenibacillus sp. MAEPY2 GN=P364_0106835 PE=4 SV=1 MEDSFKRKSPEDILKMITKLQQGTLKIYIGPVSGSGKTYHMLREGNTLRQQGIDVVI CAVSTMRRPETVEQLGELERIPSIHWSRGKDGMEMKDLNLDALLARNPEVVLVDG LAHRNRKGARHATRLEDIQYLLRHNISVITTVNVYELEGYTELARQLTGIAAEHTVP ADTLELADEVKLIDVTPETVLSRLAEGHLRGHEGEAVFRQGNLGILRELALRLVAE GVNESLREHREEMGITVTTGIMERILVSTQYHWNGSIYIRRGQQIAKRLNGDLQAV TFRNMKQPLTKEAIVFRRSMIKLVEKFGGRFEELPVVHRRKMPSTLAQYAVQHQIT RIVMGHSRHTRWQELWQGSFVNSLLRRMRGVDLFLLADRAQQEGERVLPARLP EMEAPTYRRLSEQEMKEQIGQIRRGKFKVYIGAAPGVGKTYMMLREGNDLLRKGI DVQIGLLETHNRAETVEQIGQLSVIPREQRTYQEVQLEEMDTEAILRLCPEVVLVD ELAHTNIPGSMRQKRYEDVLLLLEAGISVITTVNVQHLESLNDAVEHITGIRVRETVP DQILQMADEVQLIDVAPQALRQRMREGKIYAAAKVNQALEHFFRIGNLIALRELALR ELADDVDERLESQEPKSALRGPWRRQEAVFVCVSCDEHADRLIRRGFRTAYRLK AVWHVHHVYVGKVMSDEARCQLEELEQLTVRLGGKFYIHHCLRLRDVPGILAGKA SEEKATQLVVGQAKRVWWLNGYRGKGSVVSRLVRLSRHIDVLIVADYDYDQSGM	21~~KdpD (3.12895E-57) ~~227,249~~Usp (1.84461E-18) ~~374,413~~KdpD (2.69567E-105) ~~622,645~~Usp (3.65951E-23) ~~770	non-kinase	KdpD;Usp;KdpD;Usp
	3.7E-155	522.7	0.1	6.8E-83	286.6	0.4	2.1	2	I0INM1_LEPFC	Putative osmosensitive K+ channel signal transduction histidine kinase, sensor subunit	kdpDLFE_1179	Leptospirillum ferrooxidans (strain C2-3)	740	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Leptospirillum, Leptospirillum sp. Group I, Leptospirillum ferrooxidans, Leptospirillum ferrooxidans (strain C2-3)	1162668	>tr|I0INM1|I0INM1_LEPFC Putative osmosensitive K+ channel signal transduction histidine kinase, sensor subunit OS=Leptospirillum ferrooxidans (strain C2-3) GN=kdpD PE=4 SV=1 MNEKLEDFSRFDPFLGTILKMGKGRLKIYLGWAPGTGKTRRALLDLNAMKERGVD VVIGWIEENLRPDVFRLSEMFETIPPVGIHIGSESFPEMDLEFILKRRPSTVFVDELA HGNVLGSRHQNRWEDIEEILDAGISVVTTLNSMHVQDLSEAAGGILGYPVQEIVPV DFIKRADEVVVVDLPPSELTIRIREGNVFPKEQIERALKGAFRESNLIKLRGMTLEF MAKVLDSQLTRQGGKKGVYERITVLVSEHTPSLERLVGYAGNLSRRMGGELLVLH LRKISFLGKRSPPDQEILSRFQQEARGAGGKFSILWTRNPGWTLWRFIQRTKTTR LVMGHAGTQSPWRKSLVRSVLRYFSRIDVEIHLIPTLGQPHPVESAPESDSFLPVS SGMKGRLTLFLGAAAGIGKTYRMLQEAQDRKTSGTDVVVGYLETHRRQETQQMA EGLRVIPRKMISYHGLVLGEMDVDEILRLKPELVLVDELAHSNPPGFLNKKRYQDV LLFLEAGIHVFTTLNVQHLESLNDLIEFQTGIRVHETVPDSTVLLASEIVLVDLTAEAL QSRLMEGKVYPLQKVEEALRNFFTKNNLTALRELAMQCVLGGGRGRVIRSGRGG RILAGVSDRPEDAALIRRGAVLSDRLNLELCVLSVRREPGEGLYSKMLLDLTQSFG GIFLSEVSGKKWNEHFVERCHDINPSLVLLGQSAWRPGFESTAEIIARNLNQFPLLI IPLDIRDHVVEK	21~~KdpD (1.25331E-70) ~~224,247~~Usp (0.000038151) ~~371,396~~KdpD (2.30841E-103) ~~598,616~~Usp (0.000000000110241) ~~730	non-kinase	KdpD;Usp;KdpD;Usp
	4.6E-154	519.1	7.4	1.6E-90	311.5	1.8	2.3	2	X4ZZ42_9BACL	Potassium-transporting ATPase subunit D	PSAB_12625	Paenibacillus sabinae T27	776	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	1268072	>tr|X4ZZ42|X4ZZ42_9BACL Potassium-transporting ATPase subunit D OS=Paenibacillus sabinae T27 GN=PSAB_12625 PE=4 SV=1 MPPYKRKTPEEILYSIYRLHRGRLKIIIGSVSGSGKTYHMLQEGRLLKERGIDVVCC AVSTMQRTETVQQLEELDRIPSLHWLKGGKEQKDLPLETLLKRNPEVLLVDGLAH RNRKGAQFATRLEDIRFLMENGISVITTVNVYELEGVGESIFKMTGIRAENTVPMD TLELADEVRLIDVSPETILKRIEEGVLGDVTHPALSRRGNLAVLRELSLRLVAEGVN ESLEKHREEHGLVGPSGATERILVSAQYHWNGSLYVRRGQQIAKRLNGELIVVTF VKSDKPLTKEQQTFKQSIIKLVKRVDARFEELQMARLRKLPSELVRYAIQNNVTRIV MGHSKKSSWQEKWQGSIANRVLRKTRNIDVFLMADRAEQEGERILPIKRPKRQE EPFHRLTSQEIQKKIETIRHGTLKVYIGAAPGVGKTYKMLQEGNLLLGKGIDVVIGLL ETHGRKETREQIGKLTAIPRAKIQYQSTFLEEMDTEAIIARHPEVVLVDELAHTNVP GSQSRKRYEDVIRLLENGISVITTVNVQHLESLNDAVAQLTGVRVRETVPDAILKMA NEVELIDVTPQMLQERMREGKIYAAEKVNQALESFFKMGNLIALRELALREIADDV DERLEAWDRDAALRGSWSRQEVIFVCVDTGPRAERLIRRGFRIAHRLKAEWYVH YVHCGVGQTPEELKRLDTLRLLTERLGGKMEVTEATGSADIHRHLLARMNELRTT QLIIGQSHKPLWRTLFKETFIHYLLRNARHMDMLIVADFDPNVSEPAR	20~~KdpD (3.41229E-53) ~~224,246~~Usp (7.19502E-18) ~~371,410~~KdpD (1.06712E-105) ~~619,642~~Usp (1.27313E-27) ~~765	non-kinase	KdpD;Usp;KdpD;Usp

	2.2E-153	516.9	6.9	8E-94	322.3	0.7	2.3	2	C0ZJR1_BREBN	Sensor protein (EC 2.7.13.3)	kdpD BBR47_03850	Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	776	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus brevis (Bacillus brevis), Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	358681	>tr|C0ZJR1|C0ZJR1_BREBN Sensor protein OS=Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599) GN=kdpD PE=4 SV=1 MVEQFRRKSPEEILQSISRMHRGRLKIILGAVSGAGKTYHLLMEGQTLKKKGIDVV VAGSVEATHPKLAQKREGLEQIEPIIWYSLGEAKHDLDVAAIIERDPEVVLVDGLAH RNRSDAPRPTRLDDVQFLLNNNISVIATVNIYELAGMKEMAERLTKAEVRIDQCVP EDTLAMADEVKLLDVTPEAILKRLQEDDRNPTRTKHPLFRRDNLHMLRELALRFVA TGVNEDLEDYREKHGMVGASGATEKVLVSAQYHWNGSILVRRGQQVAKRLGGE LLVVCFLPLSKKLTKEEATFKRSIGKLVDKVGGTFEEQMLAREKDVANELVAYAME NNVTRIVMGQSKRTRWDEIWYGSIVHKILRQTKNIDILIVADRSERDGERVMPTKR EQAVTVNPYRRLSDEEMQQEIGKIKRGTLKVYVGAAPGVGKTYTMLREGNELAEN GIDVVIGLLETHGRKETIEQVGGLPLIPRKRIPYKNVTLEEMDTDEIIRRNPEVVLVD ELAHTNVPGSAYEKRYHDVEKILAAGISVISTMNIQHLESLNDSVEQITGIRVRETVP DHILHQADEVELIDISPKALRQRMREGNIYAMEKVEQSLTNFFKTGNLIALRELALR EVADDVDERLEAWERRTLRGPWRQQEVIFVCVNLRADSERLIRRGFRIAYRLKAS WHVAYVQDHPSLTEEEETQLAKLKALTERLGGRFERYEAPSRRKVFTKLVWHMN EKGTTQVVIGQSARTRWKEILEGSVIQRLLREVRHMDVLVVADHAPDMM	20~~KdpD (5.81109E-46) ~~225,250~~Usp (3.51347E-20) ~~375,415~~KdpD (1.85055E-114) ~~624,646~~Usp (1.3597E-32) ~~769	non-kinase	KdpD;Usp;KdpD;Usp
	2.7E-152	513.4	4.5	1E-88	305.7	1.3	2.3	2	F5LL22_9BACL	Universal stress family protein	HMPREF9413_0622	Paenibacillus sp. HGF7	784	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. HGF7	944559	>tr|F5LL22|F5LL22_9BACL Universal stress family protein OS=Paenibacillus sp. HGF7 GN=HMPREF9413_0622 PE=4 SV=1 MDNFRRKTPEEILLSISEIHRGRLKIYIGAVSGSGKTYHMLREGQTLREQGIDVVLC AVSMEGRPETMEQAGGLERVESIEWMKDGVRQQDLPLDDLAARNPEVVLTDGL AHRNRPGALYPTRLEDIKFLLSKGISVLATVNVYELEGVRELARKMTGIVVEHTVPA DTLELADEVRLIDATPETILNRLEEGGMRGCQWYERKVLERGNIGVLRELALRLVA EGVNESLEKHRGEMGMTGPSGADERILVSAQYHWNGSIYVRRGQQIADRLSGDL FVVSFTAPGKALSKDAATFRRSIIKLVEKVGGTFEELPFPGRRKLAQALIRYGIDRK VTRIVLGHSKHSRWQEFWQGSVLNDAVSRLQGIDLFVVADRAERDGERILPVKRK SDARPPVELYRRPSPQEMERQIRKARRGRFKVYIGAAPGVGKTYSMLREGNDLL RKNIDVVIGLLELHGRKETADQVGDLELIPRKISTYRGTELQEMDTEAVIRRMPDLV LVDELAHTNVPQSVNKKRYEDILEILNAGISVISTVNVQHLESLNDSVEQLTGVRVR ETVPDSILRLADEVELIDVTPQTLRQRMKEGKIYGMDKVDQALGHFFKTVNLIALRE LALREIADDVDERLEAWERVGSLRGPWRREEVIFVCVKLNQHAERIIRRGFRIAYR LKARWHVAYIRSGSAVGDEEARIAALQTLTERLGGRFEVLGAAGRRRTADGLLAR ALELSATQLIIGQARESLWERLFHGSIVKRIMRGARSMDVLVVAESESARVRRGRQ SRG	20~~KdpD (4.38902E-53) ~~226,248~~Usp (2.82796E-16) ~~373,414~~KdpD (2.8619E-108) ~~624,647~~Usp (1.54678E-26) ~~769	non-kinase	KdpD;Usp;KdpD;Usp
	2.8E-152	513.3	8.2	1.3E-90	311.9	1.7	2.3	2	A0A089LVB4_9BACL	Histidine kinase	PSTEL_14245	Paenibacillus stellifer	777	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus stellifer	169760	>tr|A0A089LVB4|A0A089LVB4_9BACL Histidine kinase OS=Paenibacillus stellifer GN=PSTEL_14245 PE=4 SV=1 MAPYKRKTPDEILESISRLQRGRLKIIIGSVSGSGKTYHMLQEGRQLKQQGIDVVY SAVSTMKRAETVQQLQDLESVPSIHWWRDGIEQKDLPVEVLLERNPEVLLVDGLA HRNRKGARFRTRLEDIRFLMNNGISVITTVNVYELEGAGEAIFQKTGIRSEVTVPLD TLELADEVRLIDVSPETILTRIEEGVLGQSAHPALSRRGNLAVLREAALRLVAEGVN ESLEKHRDENGLIGPSGAIERILVSAQYHWNGSLYVRRGQQIAKRLNGELMVVTF VKPGKPLSKEQITFKQSITKLVKRVDARFEELPLINIRQMPTLLVRYAIRNKVTRIVM GHSNKSRWQEKWQGSIANRVLRKTRNIDVFLMADRAEREGERILPIKPGAKSPEE PFHRLTRQEMQKKIEKIRHGTLKVYIGASPGVGKTYKMLQEGNLLLNKGIDVMIGLL ETHGRKETQEQIGRLPVIPRAKIAYTSAVLEEMDTEAIIARHPEVVLVDELAHTNVP GSRNRKRYEDVINLLENGISVITTVNVQHLESLNDAVAQLTGVRVRETVPDAILKMA NEVELIDVTPQMLQERMREGKIYAADKVNQALESFFKIGNLIALRELALRELADDVD ERLEAWDRDSAFRGAWSRQEVIFVCVDMDARAERLIRRGFRIAHRLKAEWYVHY VHCGAELTQEKRKRLDALRLLTERLGGNMEITEVKGRVDINRQLLGRMNALHTTQ LIIGQSRKPLWLSWFKESLVHYLLRNARHMDMLIVADFDPNVTEPAR	20~~KdpD (9.24133E-52) ~~224,246~~Usp (1.50538E-17) ~~371,411~~KdpD (6.73824E-109) ~~620,643~~Usp (3.46385E-28) ~~766	non-kinase	KdpD;Usp;KdpD;Usp
	7.6E-150	505.4	8.4	2.4E-90	311	1.7	2.4	2	A0A075QZZ7_BRELA	Sensor protein KdpD (EC 2.7.13.3)	kdpD BRLA_c003560	Brevibacillus laterosporus LMG 15441	790	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus laterosporus (Bacillus laterosporus), Brevibacillus laterosporus LMG 15441	1042163	>tr|A0A075QZZ7|A0A075QZZ7_BRELA Sensor protein KdpD OS=Brevibacillus laterosporus LMG 15441 GN=kdpD PE=4 SV=1 MDDFRRKTPEEILRSISEIHKGRLQIILGAVSGSGKTYHMLLEGQRLRKKGLDVVIG VIHSRAINQGKNYEKLEGFDVMPAIVWDEKGMLKEDLDVEGIVRRDPEVVLVDELA HRNRPEAVRRTRIEDVRYLLEHNISVITTLNIYELEGMKGIAQRLTGVPVRVADCVA DETLAEADEVKLLDVPPEVILKRLQEGRILPHSSGQGEALSKLTSKHQCLYRHDNL AVLRELALRFVAGEVNDDLDRYREQQGMLGPSGASERILVTVQYHWNGSILIRRG QQVAKRLGAELLIACFRNNKRMMSKEEETFKRSMVTLAQKVGASFEEVSLSKDSD VAKEMVQYALQHNITRIVMGQSKRSRWEEIVHGSIINKILRKSKNTDVLIVADRSAT SGGRVLPAKRHRGFVPHPFHRLSTEEMEKEIKRIKRGKLKIFVGAAPGVGKTYTML REANELLHSGIDVVIGLLETHGRKETHEQIGKLTIIPRKVMLYKNVYLEEMDTEAIIR RNPEVVLVDELAHTNVPTSRFLKRYEDVEHILQAGISVISTMNIQHVESLTDSVEQI TGIRIRETVPDRILHDADEIELVDISPKALQERMKEGNIYALDKVEQSLNHFFQLGNL IALRELALREVADDVDERLESWERKGALRGPWRKQETIFVCVNLREDSGRLIRRG FRIAYRLKADWYVAYVQDHNPLTPDELDLLDKLRYLTERMGGSFEIYQVQERRHIF RELVMQMDRKNVTQVIIGHSARTRWEEIKTGSVVQKLLRQIRHMDVLVVADHNPV TQ	20~~KdpD (5.51897E-54) ~~241,263~~Usp (8.43389E-24) ~~388,428~~KdpD (1.58711E-110) ~~637,660~~Usp (1.30528E-29) ~~783	non-kinase	KdpD;Usp;KdpD;Usp

	1.6E-149	504.3	6.8	8.3E-90	309.2	1.2	2.5	2	A0A089L2I9_9BACL	Histidine kinase	R70331_28055	Paenibacillus sp. FSL R7-0331	779	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. FSL R7-0331	1536773	>tr|A0A089L2I9|A0A089L2I9_9BACL Histidine kinase OS=Paenibacillus sp. FSL R7-0331 GN=R70331_28055 PE=4 SV=1 MAPYKRKTPEEILDSISRLHAGRLKIIIGSVSGSGKTYQMLHEGKLLKQQGIDVVISA VSTMQRADTIEQSLDLERVPSIRWQKDGKEQKDLPLTALIERNPEVVLVDGLAHR NRSGARFPTRLEDIRYLMEQGISIITTINVYELAGVAMIIYEKTGLRAEETVPLHTLEL ADEVRLIDVSPETILNRISEGILGDQLHPALSHHGNLGVLREISLRLVAEGVNDSLEK YRAEQGLIGPSGATERILVSAQYHWNGSLYVRRGQQIAKRLNGDLQVVTFIVSNQ KLTKDQQVFRRSIQKLVKKVDARFEEILLPHRRKLPSMLVRYATQNKVTRIIMGHS NKNRWQEFWQGSIGNRVLGRTRNIDVFLMADRAEQEGERILPVKAKPKGAEESF HRLSSTEIKQRIETIRRGTFKVYIGAAPGVGKTYKMLQEGNILLKKGIDVVIGLLETH GRKETIRQVGELSVLPRARISYQSTGLEEMDTDAIIERHPEVVLVDELAHTNVPGS RTKKRFEDVLRLLDSGISVITTVNVQHLESLNDSVEQLTGVRVRETVPDAVLQMAD EVELIDVTPTMLQERMRAGKIYAFALEKVNQALASFFKIGNLIALRELALRELADDVDE RLEAWDRDGSLRGSWGRREVIFVCVDLGPRSERLIRRGFRIAYRLKAEWFVHYV HCGAQKTQQEQKRLDALRHLTERLGGRMEAAETNGRRRVHRGLLTRMNEVQTT QLIVGYSRKPLWYRLFKESAVHYLLRNARHMDMLIVADFDPDMVDVDKVQ	20~~KdpD (1.65654E-48) ~~224,246~~Usp (3.5476E-16) ~~371,411~~KdpD (1.30241E-109) ~~620,643~~Usp (2.54387E-25) ~~766	non-kinase	KdpD;Usp;KdpD;Usp
	2.3E-147	497.2	0	2.5E-83	288	0	2.6	2	J9ZAA5_LEPFM	Putative osmosensitive K+ channel signal transduction histidine kinase, sensor subunit (KdpD)	kdpD2 LFML04_0561	Leptospirillum ferriphilum (strain ML-04)	741	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Leptospirillum, Leptospirillum sp. Group III, Leptospirillum ferriphilum, Leptospirillum ferriphilum (strain ML-04)	1048260	>tr|J9ZAA5|J9ZAA5_LEPFM Putative osmosensitive K+ channel signal transduction histidine kinase, sensor subunit (KdpD) OS=Leptospirillum ferriphilum (strain ML-04) GN=kdpD2 PE=4 SV=1 MSAPKKEDLSARKVLHTLLSMGPGRLKVYLGWAPGVGKSRRALLDLATLKKRGIV PVIGWLEDKGREEIRILAGEFRSVPPREVVVAGKSFREMDVEAILRESPPIVFVDEL ARDNPPVSGRLSRWEEVGRLLESGISVVTTLNAMHVHELAPTVSRLLERPVEVTL PLDFLRKADEIVVVDIPPAELRERIRKGLVFPPEQIDRALKGPYREPNLVRLRELTLD FAARVLDAQLVRQGGKKGVYERVLVLVSDHPEAFKSLLGYGGALSRRLGGELLVL HLRKISLLGKRPPLDRTVLEEMQQAVRENGGKMSVLWTRNFAWTLWRFIQKTGT TRLIMGHAGRVRPWRKSLVRNVLRYFPRIDVEILLLPSLVDLPPVPEPGGGEIPVP EREEGGGTFTLFLGAAAGIGKTYRMLAEAQHLLREGVNLVVGYLETHRRPETEKM ATGLPFLPRIPVYYHGLVLEEMDLDGILARRPRLVLVDELAHSNPPGFRNPKRYQD VFEILSAGIDVFSTLNVQHLETLNDLIEFQTGIRVHETVPDSVLMRVDSLVLVDLTPE ALQARLMEGNVYPPEKVQEALDNFFTKSNLTALRELAMRQVAETARFRLMIRGRG GILLVGVSDRLEDGALIRRGATLSERLGLSMVVLSITSGHTVPRWRNELESLTRTL SGTFSEESSDRWEEFFVERCRALRPGLVLLGQSAWRPGMESTAEKIARNLTDTP LLIIPLNIREHRKEVFG	24~~KdpD (7.4817E-57) ~~228,247~~Usp (0.0000714438) ~~368,394~~KdpD (1.80584E-106) ~~602,617~~Usp (0.00470996) ~~729	non-kinase	KdpD;Usp;KdpD;Usp
	9.1E-135	456.1	0	5.6E-90	309.8	0.4	2.2	2	C9R8E9_AMMDK	Osmosensitive K channel His kinase sensor	Adeg_1482	Ammonifex degensii (strain DSM 10501 / KC4)	731	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Moorella group, Ammonifex, Ammonifex degensii, Ammonifex degensii (strain DSM 10501 / KC4)	429009	>tr|C9R8E9|C9R8E9_AMMDK Osmosensitive K channel His kinase sensor OS=Ammonifex degensii (strain DSM 10501 / KC4) GN=Adeg_1482 PE=4 SV=1 MGVNGGRLKLLVGIISWPGNTVALLQEGQELLSQGRDVVIGILKYSDPEIEALSRTL RSIPPLGERLNLPEILAQRPEVVLVDDAGALYPEDSPYQARWQEVEEILAAGIDVV ATVHALELEGFKEFLPFPLTSPLSLSEGIIPASFLDRASEVELVDVTPEELSRQGISL PPGFDPRSRLGPYLAAANFAAFRRAVLKRLADEVDEQLFRPGVETRAKAARERILL AVSTQRNLERLLRRSLLLAERLQASLMVVHLRVPGRHQEPFPWDYVERMLASVG GTWMEEEVGDESEVPARLSEIIAANHITRLVVGHSARSRWEELVKGSVLNELLRR NRHINVLVVAPASETKEGEAEAAPGGAVPDLRLPLKGKLKIYLGPIAGVGKTYRML RDAHELKEKGVDVVVGYVETHGRAETEAQIGDLEVLPRKQVVYRGKTFTELDLEG VLRRRPQVVLIDELAHTNVPGVKNAKRYQDVLEILAAGIDVYTTLNVQHLESLNDVI EEITGVKVRETLPDWVLALADEIILVDLASSLLLKRLEQGKIYPLPKVEQALRHFFRP ENIIALRELALRQLAHYLGEKQARLAPERKERILVAVNLKPYAERLVRRGLRLAVAQ HAELMVVHCDVTGGKLSPEATSIRNYLKRLCDSIGISYYEQKVLSDRDVALVLANL CRAKGITQMVLGHSQRSRWQEFWKGSVISQLLRFLRTVDLHLVPVNSGSWAAEV AV	4~~KdpD (2.63127E-26) ~~164,251~~Usp (0.0000000000483919) ~~346,372~~KdpD (6.77887E-115) ~~577,594~~Usp (6.12816E-28) ~~719	non-kinase	KdpD;Usp;KdpD;Usp
	9.3E-100	341.7	0.1	2E-99	340.9	0.1	1.4	1	D7BWQ6_STRBB	Histidine kinase (EC 2.7.13.3)	SBI_00291	Streptomyces bingchenggensis (strain BCW-1)	849	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7BWQ6|D7BWQ6_STRBB Histidine kinase OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_00291 PE=4 SV=1 MARGKFRIYLGAAPGVGKTYSMLSEAHRRVERGTDCVVAFVEHHHRPRTEVMLH GLEQMPRKELEYRGGTFTEMDVDAVLARRPQVVLVDELAHTNVPGSRNAKRWQ DVEELLAAGIDVISTVNIQHLESLGDVVESITGIRQQETVPDEVVRRADQVELVDMS PEALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLTEYR SEHKVRAIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVMAVYIARSDGL ASTSNSPKELAVQRTLVEDLGGTFHHVVGDDVSAGLLDFARAVNATQIVLGVSRR KGWQYVFGPGVGATVARESGPDLDVHLITHDEAGKGRGLPVARGARLGRTRIIG GWLAGVLGPALLTLLLNGVVPEMGLANDMLLFLAMTVAAALLGGLLPALASAVVG SLLLNWFFTPPVHTLTIADPKNIVAIAVFIGVAVSVASVVVDLAARRTHQASRLRAES EILSFLTGNVLRGETSLDALLERVRETFGMESVALLERHSDVDPWTCAGSVGADP AQCPEDADVDVPVSEHMALALSGRVLPAADRRVLAAFAAQAAVVLDRQRLQGEA DQAKDLAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSEDVAWSEEDQAELLEA IEEGADRLDLLVGNLLDMSRLQTGTVTPVIREADLDEVVPMALGGVPEGSVELDIP ETLPMVHVDKGLLERAVANVVENAVKHSPPDRRVLVSASAMADRVEVRVVDRGP GVPDEAKDRIFEPFQRYGDSPRGTGVGLGLAVARGFVEAQGGTLHAEDTPGGGL TMVLSVRTAPERRPEQPSLPAAATS	1~~KdpD (1.38596E-124) ~~211,233~~Usp (2.31972E-32) ~~358,434~~DUF4118 (0.00594439) ~~468,X,614~~HisKA (2.85978E-15) ~~680,729~~HATPase_c (1.56018E-26) ~~830	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.2E-99	341.4	0.1	2E-99	340.4	0.1	1.6	1	K4R5Q9_9ACTN	Histidine kinase (EC 2.7.13.3)	kdpD3 BN159_7227	Streptomyces davawensis JCM 4913	844	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces davawensis, Streptomyces davawensis JCM 4913	1214101	>tr|K4R5Q9|K4R5Q9_9ACTN Histidine kinase OS=Streptomyces davawensis JCM 4913 GN=kdpD3 PE=4 SV=1 MGRGRLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLH GLEQLPRKELAYRGTTFTEMDVDAVLARRPQVVLVDELAHTNIPGSRNSKRWRD VEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSP QALRRRMAHGNVYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLREYR GEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGL TAASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLAFARGVNATQIVLGVSRRKS WQYVFGPGVGATVARESGPDLDVHLITHDEVGKGRGGLPVPRGARLGRLRILWG WAVGGLGPVLLTFLLTSVTPEVGLANDMLLFLTLTVAAALLGGLLPALASAVVGSL LLNWYFTPPVHTFTIADPTNIVAIAIFVGVAVSVASVVDLAARRTHQAARLRTESEIL SFLAGNVLRGETSLEALLERVRETFGMESAALLERASEVDPWTCAGSVGPRPCT NPEGADVDVPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLREEADQ ARALAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDEAELLAGIEE GADRLDHLVGNLLDMSRLQTGTVSAIVREIDLDEVVPMALGGVPEDSVELDIPETL PMVNVDKGLLERAVANVVENAVKYSPTGTSVLVSASAIADRVEVRVVDRGPGVPD EAKERVFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLHAEDTPGGGLTMV LSLPRAQGSRPEARTPAA	1~~KdpD (5.4682E-124) ~~211,233~~Usp (1.60443E-31) ~~356,X,613~~HisKA (2.66755E-14) ~~679,728~~HATPase_c (1.92467E-26) ~~829	kinase	KdpD;Usp;X;HisKA;HATPase_c
	3.6E-99	339.8	0.1	6E-99	339.1	0.1	1.4	1	A0A0F4JNS4_9ACTN	Histidine kinase	VR44_08850	Streptomyces katrae	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces katrae	68223	>tr|A0A0F4JNS4|A0A0F4JNS4_9ACTN Histidine kinase OS=Streptomyces katrae GN=VR44_08850 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVGFVEHHNRPRTEVMLH GLELIERRELDYRGSTFTEMDVDAILARRPAVVLVDELAHTNVPGSRNAKRWQDV EELLQAGIDVVSTVNIQHLESLGDVVETITGVRQRETVPDEVARRADQIELVDMSP QALRRRMAHGNVYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYR GEHNIRSTWQARERIVVGITGGPEGRTLIRRAARLAEKGAGGEVLAVYIAASDGLT SASPKELAVQRTLVEDLGGTFHHVIGDNVPDALLEFARGVNATQIVLGVSRRRSW QSVFSPGVSATVARESGPDLDVHIVTHDEAAKGRRGLPVARGARLSRSRIIWGW AAGIAGPAVLAVLLSQFVPELGLANDMLLFLTFTVAAALLGGLLPALASAAFGSLLL NYYFTPPLHEFTVSDPKNIVAIAIFVGVAVSVASVVDLAARRTHQAARLRAESEILS FLAGSVLRGEDSLDALLERLRETFAMQSVVLLERTSEVEPWTTAASVGTGPISRP EDADVDLPIGDNMALALAGRVLPAEDRRVLGAFAAQAAVVLDRQRLVDEAEKSRR LAEANRIRTALLAAVSHDLRTPLAGIKASVTSLRSDDVEWSEEDKAELLEGIEDGAD RLAALIGNLLDMSRLNTGTVVPLIRETDLDEVVPMALGGVPEDSVGLDIPETLPMV AVDRGLLERAVANIVENAVKYSPHGQPVNVSASALGNRVELRVVDRGPGVPDEA KNRIFEPFQRHGDAPRGAGVGLGLAVARGFTEAIGGTLAAEDTPGGGLTMVLTLP VAGDGPPVSPEMPTSAVT	1~~KdpD (5.46546E-124) ~~211,233~~Usp (1.36508E-32) ~~356,X,613~~HisKA (0.000000000000143033) ~~679,728~~HATPase_c (1.19484E-25) ~~829	kinase	KdpD;Usp;X;HisKA;HATPase_c
	4E-99	339.6	0.1	7E-99	339	0.1	1.3	1	A0A0C5FSD5_9ACTN	Histidine kinase (EC 2.7.13.3)	TU94_02380	Streptomyces cyaneogriseus subsp. noncyanogenus	857	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cyaneogriseus, Streptomyces cyaneogriseus subsp. noncyanogenus	477245	>tr|A0A0C5FSD5|A0A0C5FSD5_9ACTN Histidine kinase OS=Streptomyces cyaneogriseus subsp. noncyanogenus GN=TU94_02380 PE=4 SV=1 MARGKLRIYLGAAPGVGKTCAMLSEAHRRAERGTDCVVAFVEHHHRPRTEVMLH GLEQIPRKEIEYRDTAFTEMDVDAVLARRPRVALVDELAHTNVPGSRNAKRWQDV EELLAAGIDVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQ ALRRRMAHGNIYRPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNQYRSE HQVFRIWGSRERIVVGLTGGPEGHTLIRRAVRLAEKGAGGEVMAVYIARSDGLTS ASPGELAVQRRLVEDLGGTFHQVVGDDVPAALLDFARGVNATQIVLGVSRRKSW QYVFGPGVGATVARDSGPDLDVHFVTHDAVGKGRGLPAAARGARLGRARVVWG WLVGVLGPALLTWMLTGAAVDVGLANDMLLLLTLTVAAALLGGLAPALASALVGS LLLNWYFTPPVRTLTIADPKNIVAIAVFVGVAVSVASVVDLAARRTHQAARLRAESE ILSFLAGNVLRGETSLEALLERVRETFGMESAALLERTGETEPWTSAGSAGPRPA RIPEEADVDVPVGDHMTLALSGGVLPAADRRVLAAFAAQAAVVLDRRRLRREADR ARELAEGNRMRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDQAELLAAIE EGADRLDHLVGNLLDMSRLQTGTVTPIIRETDLDEVVPMALGGVPEGSVELDIPET LPMVHVDRGLLERAVANIVENAVKYSPPGEKVLVSASALAGRVEVRVVDRGPGVP DAAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAETIGGTLDTEDTPGGGLTMVL AVPTAARQRPDRPAAAATRGQEPPGAAGRP	1~~KdpD (9.21165E-124) ~~211,233~~Usp (4.36398E-30) ~~356,426~~DUF4118 (0.000200969) ~~466,X,613~~HisKA (5.80874E-16) ~~679,728~~HATPase_c (4.45246E-24) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.5E-99	339.5	0.1	6E-99	339.1	0.1	1.2	1	A0A0F4JBL3_9ACTN	Histidine kinase (Fragment)	VR44_18800	Streptomyces katrae	310	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces katrae	68223	>tr|A0A0F4JBL3|A0A0F4JBL3_9ACTN Histidine kinase (Fragment) OS=Streptomyces katrae GN=VR44_18800 PE=4 SV=1 MGRGRLRIYLGAAPGVGKTYAMLSEGHRRVERGGDVVVGFVEHHGRPRTEVML HGLEQVPRRELVHRGASFTEMDVDAVLARRPAVALVDELAHTNVPGSRNAKRW QDVEELLRAGIDVVTTVNIQHLESLGDVVETITGVRQRETVPDEVVRRADQVELVD MSPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRADEYLQ QYRGEHGIRSTWQARERIVVGLTGGPEGRTLIRRASRMAAKSSGSEILAVYIARSD GLTSASPKELAVQRTLVEDLGGTFHHVIGDNVPEALLA	1~~KdpD (7.16031E-130) ~~210,233~~Usp (1.28169E-14) ~~310	non-kinase	KdpD;Usp
	1.2E-98	338.1	0.1	1.9E-98	337.4	0.1	1.4	1	V6KLU9_STRRC	Histidine kinase (EC 2.7.13.3)	M878_19640	Streptomyces roseochromogenus subsp. oscitans DS 12.976	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	1352936	>tr|V6KLU9|V6KLU9_STRRC Histidine kinase OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_19640 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRIERGTDCVVAFVEHHHRPRTEVMLH GLEQVPRRELEYRGTVFTEMDVDAVLARRPQVALVDELPHTNIPGSRNAKRWQD VEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSP QALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNEYRR EHRVSTIWGSRERIVVGLTGGPEGRTLIRRASRLAEKGAGGEVLAVYISRSDGLTS ASPKELAVQRTLVEDLGGTFHHVVGDDIPVALLDFARGVNATQIVLGVSRRRSWQ YAFGPGVGATVARDSGPDLDVHLITHDEVGKGRGLPVARGARLGRPRVIWGWV VGVLGPVPLTWLLTGAAPDVGLANDMLLYLTLTVAAALLGGLFPALASAVVGSLLL NWYFTPPVHTWTIADPKNIVAIAVFFGVAASVASVVDQAARRTHQAARLRAESEIL SFLAGHVLRGETTLEALLERVRETFGMESVALLERTGETAPWTCAGSVGPEPARI PEDADVDVPVGDHMALSLRGRVLPAADRRVLAAFAAQAAVVLDRQRLQREADRA GELAEGNRIRTALLAAVSHDLRTPLAGIKAAVTSLRSDDVEWSERDQADLLEAIEE GADRLDHLVGNLLDMSRLQTGTVTPIIRESDLDEVVPMALGGVPEDSVELDIPETL PMVYVDRGLLERAVANVVENAVKYSPPGEPVLVSASALADRVEVRVVDRGPGVP DEAKDRIFEPFQRYGDAPRGVGVGLGLAVARGFAEAVGGTLLAEDTPGGGLTMV LAVPTAPERERPGGLVVSGG	1~~KdpD (5.19781E-124) ~~211,233~~Usp (5.11039E-30) ~~356,381~~DUF4118 (0.00000000268333) ~~482,X,612~~HisKA (9.45605E-15) ~~678,727~~HATPase_c (2.63844E-24) ~~826	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.7E-98	337.6	0.1	2.7E-98	336.9	0.1	1.3	1	B1VXM4_STRGG	Histidine kinase (EC 2.7.13.3)	SGR_1661	Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces griseus group, Streptomyces griseus subgroup, Streptomyces griseus, Streptomyces griseus subsp. griseus, Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	455632	>tr|B1VXM4|B1VXM4_STRGG Histidine kinase OS=Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350) GN=SGR_1661 PE=4 SV=1 MGRGTLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLH GLELLPRRELEYRGTVFTEMDVDAVLERAPAVALVDELAHTNVPGSRNAKRWQD VEELLKAGIDVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSP QALRRRMAHGNIYRPDKMDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYR GEHNIRTTWQARERIVVGLTGGPEGRTLIRRASRMAAKGSGSEILAVYIARSDGLT SASPKELAVQRTLVEDLGGTFHHVIGDDIPAALLEFARGVNATQIVLGSSRRKTWQ YIYGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPMARGARLGRARILWGWLV GVVGPVLLAVVLRSMEDAPGLANDVLLFLFLTVAAALLGGVRPALASAAVGSMLLN YWFTPPTHTLTVQDPENLVAIVIFFAVAVAVSSVVDLAARRTHQAARLRAESEILSF LAGSVLRGETALDALLDRVRETFAMESVALLERSSDVEPWTCAGYVGPAPVTRPE DADVDMPVGDNMALALSGRVLPAEDRRVLGAFAAQAAVVLDRQRLVGEAEQAR RLAEGNRIRTALLAAVSHDLRTPLASIKAAVSSLRSDDVAWSEEDEAELLEGIEDG ADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVDLDIPETLP MVAVDPGLLERVVANIVENAVKYNPGQEPVAVAASALGGRVELRVVDRGRGVPD EAKERIFEPFQRYGDAPRGAGVGLGLAVSRGFAEAMGGTLDAEDTPGGGLTMVL TLTAAPGGVRTETELPARATS	1~~KdpD (2.29705E-123) ~~211,233~~Usp (4.50791E-31) ~~356,381~~DUF4118 (0.000000030185) ~~466,X,612~~HisKA (3.18897E-14) ~~678,727~~HATPase_c (4.74353E-27) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2E-98	337.4	0.1	3.1E-98	336.7	0.1	1.3	1	V4IUF9_9ACTN	Histidine kinase (EC 2.7.13.3)	B590_07920	Streptomyces sp. PVA 94-07	841	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. PVA 94-07	1223307	>tr|V4IUF9|V4IUF9_9ACTN Histidine kinase OS=Streptomyces sp. PVA 94-07 GN=B590_07920 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRAERGTDVVVGLVEHHRRPRTEALLR GLEVVPRRTCAYRGGSFTEMDVDAVLERAPAVVLVDELAHTNVPGSRHDKRWQ DVEELLAAGVDVVSTVNIQHLASLGDVVESITGVRQRETVPDEVVRRADEIELVDM APQALRRRMAHGNIYQPEKLDAALAHYFRPGNLTALRELALLWTADRVDEHLRRY RGEHRIRATWPARERIVVGLTGGPEGSTLIRRAARLAEKGAGGEVLAVHIAASEGL RAASPRELARQRALVEEVGGTFHHVIGDDVPSALLEFARGADATQVVLGASRRRS WQYLLGPGVSATVARDSGPDLDVHIVTHDAVARGRGLPAARGARLGRARVAWG WAVGLGGPLLLTLLLGGVLPDVGLTNDMLLFLAATVAAALLGGMLPALASAAVGS VLLNYFFTPPLREPVVADPRNMVALVIFVGVAVSVASVVDLAARRTHQAARLRAEA EILSFLAGSVLRGEDSLDALLARLRETFAMDAAALLERGGDGAPWSRVAAAGENP PGRPEDASVDIPVGDDLALVLSGRALPAEDRRVLSAFAAQAAVALDRQRLVGQAG EARRLAESERFRTALLAAVSHDLRTPLTGIKASVSSLRSAEVEWSPEDRGALLEGI EDGADRLDALIGNLLDMSRLTTGTVVPLLRETGLDEVVPRALAGVPEGSVVLDVPE SLPLVTVDRGLLERVVANLVENAVKYSPGDRPVLISAGSLRERVELRVVDRGPGV PHASKEQIFEPFQRLGDAPRGAGVGLGLAVARGFTEAIRATLTAEDTPGGGLTMV LGLPRADAGEASGQRA	1~~KdpD (1.6433E-119) ~~211,233~~Usp (7.04247E-28) ~~356,X,612~~HisKA (0.000000000000473485) ~~678,727~~HATPase_c (6.61189E-22) ~~826	kinase	KdpD;Usp;X;HisKA;HATPase_c
	2.8E-98	336.9	0.1	5.9E-98	335.8	0	1.6	1	G8X3F8_STREN	Histidine kinase (EC 2.7.13.3)	SCATT_46380	Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	874	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cattleya, Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	1003195	>tr|G8X3F8|G8X3F8_STREN Histidine kinase OS=Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057) GN=SCATT_46380 PE=4 SV=1 MAFLRFAGFALRTLGDAGPFRRYEDGAMARGRLRIYLGAAPGVGKTYAMLSEGH RRLERGTDLVVGFVETHNRPRTEVMLHGLEQIPRRTLTYRGSRFTEMDVDAVLAR RPEVALVDELPHTNVPGSRNAKRWQDVEELLEAGVDVISTVNIQHLESLGDVVESI TGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYQPDKIDAALANYFRP GNLTALRELALLWTADRVDEYLQQYRAEHRISSTWQARERIVVGLTGGPEGRTLI RRAARLAAKGSGSEILAVYVARSDGLASGSPKELTVQRTLVEDLGGSFHHVVGDD VPTALLDFARGVNATQIVLGTSRRKAWQYVLGPGVGATVARESGPDLDVHIVTHE EAAKGRGLPVARGARLGRARIALGWLVGCGGPALLTPLLLAFTPGLGLANDMLLY LATTVAAALVGGMLPALASAAVGSLLINYFFAPPVHRFTIADPHNIVAIVIFVAVAVS VASVVDLAARRTHQAARLRAEAEILSLLAGNVLRGETSLDALLERVRETFAMDSVA LLERNDEYAPWTRAGGVGPTPCGRPDAADVAVPVGDRMSLALSGRVLPAEDRR LLSAFAAQAAVLLDRRRLVGEAEQARELAEGNRIRTALLAAVSHDLRTPLAAIKAAV SSLRSDDVAWSPEDEADLLEAIEEGADKLDHLVGNLLDMSRLQTGTVTPLMQEVD LDEVVPMALGGVPPDSVALDIPETLPMVLADPGLLERLVANVVENAVKYSGDAER VLVAASALRDRVELRIADRGPGVPDTAKERIFEPFQRYGDAPRGAGVGLGLAVAR GFAEAMGGTLVADDTPGGGLTMVLTLRAAGALDPSAPELPAEVTS	28~~KdpD (6.4028E-123) ~~238,260~~Usp (6.96805E-30) ~~383,438~~DUF4118 (0.000048136) ~~492,X,639~~HisKA (0.000000000000113289) ~~705,754~~HATPase_c (3.46044E-25) ~~855	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3E-98	336.8	0.3	5.8E-98	335.9	0.2	1.5	1	K4R0W2_9ACTN	Histidine kinase (EC 2.7.13.3)	kdpD1 BN159_2584	Streptomyces davawensis JCM 4913	849	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces davawensis, Streptomyces davawensis JCM 4913	1214101	>tr|K4R0W2|K4R0W2_9ACTN Histidine kinase OS=Streptomyces davawensis JCM 4913 GN=kdpD1 PE=4 SV=1 MGRGRLRIYLGAAPGVGKTYAMLSEAHRRAERGTDCVVALVEHHDRPRTEVMLH GLEQLPRKQLAYRGTAFTEMDVDAVLARRPEVALVDELAHTNVLGSRNAKRWKD VEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSP QALRRRMAHGNVYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLRTYR GEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGL TAASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLAFARGVNATQIVLGSSRRKT WQYVFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVARGARLGRSRIVWG WLAGIGGPALLTLLLTNVDADLGLTNNMLLFLTLTVAAALLGGLLPALASAAFGSLL LNWFFTPPVNRLTIADPKNILALVIFVGVAVSVASVVDLAARRTHQAARLRAESEIL SFLAGDVLRGETSLEALLERVRETFGMESAALLERASEVEPWTCAGRVGLGPTVE RPEDADVDMPAGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLREEADQ ARALAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDEAELLAGIEE GADRLDHLVGNLLDMSRLQTGTVSAIVREIDLDEVVPMALGGVPEDSVELDVPETL PMVAVDPGLLERSVANIVENAVKYSPPGMPVLVSASSIADRVEVRVVDRGPGVPD DAKERIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLTAEDTPGGGLTMVL TLRAAAGPLFRPAFPEPERQAT	1~~KdpD (1.75849E-121) ~~211,233~~Usp (4.77426E-32) ~~356,X,613~~HisKA (7.03885E-14) ~~679,728~~HATPase_c (6.25304E-26) ~~829	kinase	KdpD;Usp;X;HisKA;HATPase_c

	3E-98	336.8	0.1	5.6E-98	335.9	0.1	1.5	1	B5I2H9_9ACTN	Histidine kinase (EC 2.7.13.3)	SSEG_09855	Streptomyces sviceus ATCC 29083	851	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sviceus, Streptomyces sviceus ATCC 29083	463191	>tr|B5I2H9|B5I2H9_9ACTN Histidine kinase OS=Streptomyces sviceus ATCC 29083 GN=SSEG_09855 PE=4 SV=1 MGRGRLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVGFVEHHGRPRTEVML RGLEEMPRREIEYRDSVFTEMDVDAVLRRAPAVALVDELAHTNIPGSRNARRWQ DVEELLAAGIDVVSTVNIQHLESLGDVVEAITGVRQRETVPDEVVRRADQIELVDM SPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLKQY RSEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDG LTSASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGVNATQVVLGSSRRK TWQYVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARSARLGRARILWG WLVGLAAPVLLTLLLTTVDLGLANDMLLFLAVVVAAALLGGLFPALASAAVGSLLLN YFYTPPLHRWTIADPKNIVAIVIFVGVGISVASVVDLAARRTHQAARLRAESEILSFL AGNVLRGETRLEELLERVRETFGMESAALLERAGDVEPWTCAGRAGLGPAVERP EDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLQEEADQSR ALAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSHDVAWSEEDQAELLEGIEEG ADRLDHLVGNLLDMSRLQTGTVTAIVREIDLDEVVPMALGGVPDGSVELDVPETLP MVAVDPGLLERSVANLVENAVKYSPPGTPVRVSASAIADRVEVRVVDRGPGVPD EAKERIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMNGTLNAEDTPGGGLTMVL TLRAADTHAQLLVDPFEEAEPERQAT	1~~KdpD (2.10711E-123) ~~211,233~~Usp (3.50986E-31) ~~356,425~~DUF4118 (0.000682158) ~~480,X,611~~HisKA (3.34852E-15) ~~677,726~~HATPase_c (3.0061E-26) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.4E-98	336.6	0.2	5.9E-98	335.8	0.2	1.4	1	S5VP11_STRCU	Histidine kinase (EC 2.7.13.3)	B446_27470	Streptomyces collinus Tu 365	858	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces collinus, Streptomyces collinus Tu 365	1214242	>tr|S5VP11|S5VP11_STRCU Histidine kinase OS=Streptomyces collinus Tu 365 GN=B446_27470 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVGHVEHHDRPRTEVMLH GLEQVPRRRLEHRGAAFAEMDVDAVLHRAPAVALVDELAHTNVPGSRNAKRWQ DVEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDM SPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNAY RSEHQVSRIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYISRSDG LTSASPKELAVQRTLVEDLGGTFHHVVGDDIPASLLDFARGVNATQIVLGSSRRKA WQYVFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVARGGRLGRTRIVSG WLVGLAGPAIFAVLLNTVDLGLANDMLLFLAVTVAAALLGGLLPALASAAFGSLLLN YFYTPPLHRLTVADPKNIVAIAIFFGVGMSVASVVDLAARRTHQAARLRAESEILSF LAGNVLRGETGLDELLERVRETFAMESAALLERAGDVEPWTCAGRAGFGPPLGR PEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVALDRRRLQEEADQA KELAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSEDVAWSEEDRAELLEGIEE GADRLDHLVGNLLDMSRLHTGTVTPLIREIDVDEVVPMALFGVPEDSVELDVPETL PMVAVDPGLLERSVANLVENAVKYSPARHRVLVSASALVDRVEVRVVDRGPGVP DEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGSLNAEDTPGGGLTM VLSLRAAGTRPEHLPAGEPGTSAGEPGTEPERQAS	1~~KdpD (2.36248E-124) ~~211,233~~Usp (1.85027E-31) ~~356,430~~DUF4118 (0.000129294) ~~480,X,611~~HisKA (7.53991E-15) ~~677,726~~HATPase_c (7.3468E-19) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.9E-98	336.4	0.2	6.3E-98	335.7	0.1	1.3	1	A0A0D4DJP8_9ACTN	Histidine kinase (EC 2.7.13.3)	T261_2153	Streptomyces lydicus A02	851	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	1403539	>tr|A0A0D4DJP8|A0A0D4DJP8_9ACTN Histidine kinase OS=Streptomyces lydicus A02 GN=T261_2153 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDLVVGFVEHHGRPRTEVMLH GLEHIARRDLEYRGTSFTEMDVDAVLERRPAVALVDELAHTNVPGSRNGKRWQDI EELLEAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSPQ ALRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYRAE HSIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEVLAVYIARSDGLTS ASPKELAVQRTLVEDLGGTFHHVIGDDIPVALLEFARGVNATQIVLGSSRRKAWQY VFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRARIVAGWLVG VAGPVLLSLLLTSVVNGPGLANDVLLFLFLTVVAALLGGQLPALASAAVGSLLLNFY FTPPTHTLTISDPKNIVAIVIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLAG SVLRGETTLDALLERVRETFGMETVVLLERAGDVDPWTCAGRAGGTGTGAPPAR PEDADVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLVGEAERA RELAEGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVAWSEEDEKELLAGIEAG ADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVTLDIPEELPI VAVDPGLLERSVANLVENAVKYSPDGETVLVSASALGDRVEVRIADRGPGVPDSA KDRIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLAAEDTPGGGMTMVLTL RAAPGGPPVRPDVPAEAVT	1~~KdpD (2.5183E-122) ~~211,233~~Usp (2.17746E-31) ~~356,402~~DUF4118 (0.000000054122) ~~466,X,616~~HisKA (0.000000000000201231) ~~682,731~~HATPase_c (5.96416E-25) ~~832	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	5.1E-98	336	0.1	8.9E-98	335.2	0	1.4	1	A0A0F5W4Y7_9ACTN	Histidine kinase	TN53_04920	Streptomyces sp. WM6386	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	1415558	>tr|A0A0F5W4Y7|A0A0F5W4Y7_9ACTN Histidine kinase OS=Streptomyces sp. WM6386 GN=TN53_04920 PE=4 SV=1 MGRGRLRIYLGAAPGVGKTYAMLSEGHRRIERGTDCVVAFVEHHGRPRTEVMLH GLEQIPRRELAYRGSAFTEMDVDAVLHRAPAVALVDELAHTNVPGSRNAKRWQD VEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMS PQALRRRMAHGNIYRSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLKQYR SEHQVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLT AASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGANATQIILGSSRRKTWQ YVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRARIIWGWAV GVVGPPVLAVLLNTVDLGLANDMLLFLTVTVAAALLGGVAPALASAAVGSLLLNYF YTPPLHHWTIADPKNIVAIAIFVGVGVSVSSVVDLAARRTHQAARLRAESEILSFLA GNVLRGETSLEELLERVRETFAMESAALLERVSDVEPWTCAGRAGLGRPVERPE DADVDVPVGDHMALTLTGRVLPAEDRRVLAAFAAQAAVALDRRRLQEEADQART LAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDQAELLEGIEEGA DRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEDSVELDIPETLPM VAVDPGLLERSVANLVENAVKYSPTGEAVLVSASAIADRVEVRVVDRGPGVPEEA KERIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMSGTLNAEDTPGGGLTMVLTL RAAGSQPEPQLLVQPERQVT	1~~KdpD (6.38632E-123) ~~211,233~~Usp (1.00491E-31) ~~356,381~~DUF4118 (0.0000212091) ~~463,X,611~~HisKA (5.17576E-15) ~~677,726~~HATPase_c (7.09831E-25) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	5.7E-98	335.9	0.6	9.4E-98	335.2	0.4	1.4	1	A0A059W4G8_STRA9	Histidine kinase (EC 2.7.13.3)	DC74_5947	Streptomyces albulus	851	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	68570	>tr|A0A059W4G8|A0A059W4G8_STRA9 Histidine kinase OS=Streptomyces albulus GN=DC74_5947 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDVVVAFVEHHGRPRTEVMLH GLEQVQRRELEYRGSTFTEMDVDAVLERKPAVALVDELAHTNVPGSRNGKRWQ DVEELLEAGITVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMS PQAIRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYR AEHSIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEVLAVYIARSDGL TSASPKELADQRTLVEDLGGTFHHVIGDDIPGALLEFARGVNATQIVLGSSRRKTW QYVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRSRIIAGWLV GVAGPVSLSLFLTKLSNGPGLANDVLLFLFLTVLAALLGGQLPALASAAVGSLLLNF YFTPPTHTLTVSDPKNIVAIAIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLA GSVLRGETTLDALLERVRETFGMDTVALLERRSDVDPWTCAGRAGGGDNTPPLA RPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRQRLVGEAER ARELAEGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVAWSEEDEAELLEGIEA GADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVTLDIPEEL PMVAVDPGLLERSVANLVENAVKYSPDGEVVLVSASALGDRVELRVADRGPGVP DSAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAVGGTLAAEDTPGGGMTM VLTMPAAAGLPPVRPDLPAQATT	1~~KdpD (1.31877E-123) ~~211,233~~Usp (8.22103E-33) ~~356,420~~DUF4118 (0.00000851277) ~~466,X,616~~HisKA (0.000000000000167677) ~~682,731~~HATPase_c (3.83192E-24) ~~831	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	6.1E-98	335.8	0.6	1E-97	335	0.4	1.4	1	A7IKC2_XANP2	Histidine kinase (EC 2.7.13.3)	Xaut_3236	Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	900	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Xanthobacter, Xanthobacter autotrophicus, Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	78245	>tr|A7IKC2|A7IKC2_XANP2 Histidine kinase OS=Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2) GN=Xaut_3236 PE=4 SV=1 MPDDRAAPVRPSPDALLAAAEQETRGRLKIFLGAAPGVGKTYEMLASGHARRND GADVVIGVVETHGRRETEALVAGLEVIPRRRSIPYKGRMIEEMDLDAILARRPALVLV DELAHTNAPESRHAKRYMDVEELLAAGIDVYTTLNIQHVESLNDVVAQITRVRVRE TVPDAIIDRADDIEVIDITPGDLLQRLKEGKVYVPETARRAVENYFSPGNLTALRELA LRRTAERVDEQLLSHMRAHAISGPWAAGERVLVCLSEDPRSAALVRYTKRLADRL RAPWVALYVETERALRLDTAERDRIADFLRLAERMGGEAVTIPGGTRIADDVLSYA RSANVTHIVIGKSDRSRWFEILHGSVVHDLVRRSGNISVHVIAGDKETPAPGRSGA AVPTARRETWPYLASLVIVALATLVGFGLQKVLALQNIALVFLTAVLVSAVRFGLAP ALVASGAAMLAFNFFFIPPLYTFTITDPENVVALFFFLVVAIIASNLTARVRAQALAA RARAKTAEDLYLFSKKLAGAGTLDDLLWATAFQIASMLNVRVVIVLPDGDTLAVKA AYPPEDAIDAADLAAARWAFENNRWAGRGADTLPGAKRLFMPMQTGRGAVGVI GIDRDKEGPLLTPEQRRLMDALADQAALAVERVNLVADVEKAKLDAATDRLRTALL TSISHDLKTPLASIMGAAGTLRSFFSALTEEARSDLLSTVEEEAERLNRFIANLLDM TRLESGAIVPNAGLCDVSEVVGSALDRARSILRHHRLEIDLAPDLPMLSIDPVLFEQ ALFNLLDNAAKYAPEGALVRIEGWSDGAFVTLRVLDEGPGIAEEDRERVFDKFYR VRKGDQVRAGTGLGLGISRGFLEAMGGTLTADGRPDRRGAAFTIRMPVPPQARA LKALP	25~~KdpD (1.52261E-122) ~~233,255~~Usp (1.51442E-43) ~~379,403~~DUF4118 (1.24455E-19) ~~497,529~~GAF (0.0000837882) ~~648,665~~HisKA (0.00000000000889613) ~~731,784~~HATPase_c (5.96041E-24) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.3E-98	335.7	0	1.3E-97	334.8	0	1.5	1	G8QN97_DECSP	Histidine kinase (EC 2.7.13.3)	Dsui_0272	Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	898	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azospira, Azospira oryzae, Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	640081	>tr|G8QN97|G8QN97_DECSP Histidine kinase OS=Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) GN=Dsui_0272 PE=4 SV=1 MSDPLQRPDPDALLARLEAEEIQARRGRLKIFFGASPGVGKTYAMLAAARTLQSQ GVDVAVGVVETHGRRETAELVQGLELLPSRQVEHRGRRLQEFDLDGALQRAPDL VLVDELAHSNAPGSRHPKRWQDVEELLAAGIDVFTTVNVQHLESLNDVVGRITGA RVWETVPDRLFDAADEVVLVDLPPEELLTRLKAGKVYVPQQAERAMANFFRKGN LLALRELALRRTADRVDDDVRAYRRDQSVSTVWPTRESLLVCIGPGPGSERLVRS AARLATQLEVPWHALYVETPRYQRLPEGERGRVLKSLRLAQELGAETANRPGQD AAAAAIQYAREHNLGKVLLGRELPGDWRRWLPWRTSLARRLARQAPDLDVMQV ASDGVDGEAPPLPDGPARPAAVNVRGYGLAAAAVAAVTLVATPLHGALDLANIVM LFLLAVLFAAVKLGRNPAILAAFLSVAAFDFFFVSPRLSFAVSDVQYLLTFSVMLAV ALITAQLTAGLRFQVDVAQSRERRSDALYEMARELSAALTVEQIDDITRRFVQQGF QARALLLVPGQQERLSLPEGLPADLPVDLGIAQWAADHGEAAGHSTDTLPSAPM RYLPLKAPMRTRGVLAVLPREQPWLPSPEQERLLETCATLVAIAVERVHYIEVAQE ALVQMESERLRNGLLAALSHDLRTPLTALVGLADSLSLGGALPPAQAELAQAIRGE AMRTSALVHNLLDMARLQSGQVTLKKEWQPLEEVVGAALQARASVLAQHRVRVVD LPADLPLLEFDAVLMERVFCNLIENAAKYTPPGSLIEIGARREAERVLVSVSDNGPG LPPGKEAGLFEKFTRGQDESAIPGVGLGLAIVRAIVDAHKGKVWAENRSDGPGAR FVFTLPLGQPPALPTELL	24~~KdpD (4.74322E-115) ~~234,257~~Usp (5.27777E-38) ~~381,432~~DUF4118 (9.68767E-19) ~~506,532~~GAF (2.22936E-15) ~~649,666~~HisKA (0.00000000000149603) ~~730,783~~HATPase_c (9.15842E-30) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	6.3E-98	335.7	2.1	1.1E-97	334.9	0.5	2	1	K0F3U7_9NOCA	Histidine kinase (EC 2.7.13.3)	O3I_031400	Nocardia brasiliensis ATCC 700358	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia brasiliensis, Nocardia brasiliensis ATCC 700358	1133849	>tr|K0F3U7|K0F3U7_9NOCA Histidine kinase OS=Nocardia brasiliensis ATCC 700358 GN=O3I_031400 PE=4 SV=1 MKRGQLRIYLGAAPGVGKTYAMLGEAHRRLERGRDVVAAVVETHGRAKTAALLE GIERIPARTVRYRGAELPELDVEAVLRRRPTVALVDELAHTNAPGSKHEKRWQDV EELLDAGIDVISTVNVQHLESLNDVVEQITGIQQKETVPDAVVRGADQVELVDLTPE ALRRRLSHGNVYAADKVDAALRNYFRPGNLTALRELALLWLADQVDAALAKYRAD HKITELWEARERVVVAVTGGPESETVVRRASRIASKASAELVLVHVVRGDGLAGV STARLARLRELAASLDASLHTVTGDDVPTALLEFAREVNATQLVLGTSRRSRWAR MLDEGIGSTVVQQSGKIDVHMVTHEEAHRGLRRSSFMPRQPIRAWLAAVLVPMA VCGIGIVFLDGYLQLGGLSAVFFIGVVAVALLGGVVPAAFSALLSGLLLNWFFADPR YSLTISEPDNFVTVVVLLFVAVAVAALVDVAAKQTLQARRASQEAELLTMFAGAVL HGADLPNLLEQVRETYGQRAVSMLCGEQVVAEVGADPPQRATDADTTIQAGDAT SLLLLAGRPLAAGDRPVLNAVANQAAGLVRQSRLAEEASAAAALLEADRLRRALLS AVSHDLRTPLAGAKAAVSSLRSDDIEFSAEDTSELLETIEESVDQLTALVGNLLDSS RLAVGVVKPQLRQVYMDEVVHRALVSVGMGARGLRRAAMDRVKVEVGDVSVRA DSGLLERVVANLIDNALRHATRDMAFTQPAGSGDYHPPPVRVTAEREGDRVSIAV VDTGPGVPPGAEEQLFEPFQRLGDRDNTTGVGLGLSVVRGFVEAMGGTVHAEP TPGGGLTMIVDLPAAANGASSS	1~~KdpD (2.28119E-124) ~~211,233~~Usp (1.58734E-34) ~~354,375~~DUF4118 (0.0000000340636) ~~453,X,600~~HisKA (0.00000000000150051) ~~666,723~~HATPase_c (4.35012E-28) ~~838	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	6.9E-98	335.6	0.9	1.2E-97	334.8	0.6	1.4	1	W5WJG4_9PSEU	Histidine kinase (EC 2.7.13.3)	KALB_7344	Kutzneria albida DSM 43870	850	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Kutzneria, Kutzneria albida, Kutzneria albida DSM 43870	1449976	>tr|W5WJG4|W5WJG4_9PSEU Histidine kinase OS=Kutzneria albida DSM 43870 GN=KALB_7344 PE=4 SV=1 MRPDRRRRGELRIYLGAAPGVGKTFAMLGEARRRAERGTDVVVGLVETHDRAKT AELLDGLEVLPRKHISHRGLDFQEMDLDAVLARAPEVVLVDELAHTNVPGSRNDK RWQDIEELLDAGIEVLSTVNVQHLESLNDVVERITGVTQRETVPDQVVRNAEQIEL VDITPEALRRRLAHGNVYPARKIDAALGNYFRVGNLTALRELALLWVADQVDVALQ RYRSEQQITETWETRERVVVSVTGGPESETLVRRARRIATRAGAELLVLHVLRGD GLAGVPADTVARYRRLAEDVGATFHTVVGDDVPTALLDFARGVNATQLVLGTSRR SRVARLFEEGIGATVVQESGPIDVHMVTHGEARRALRWRLSRSPLTPSRQVLGW LLALLVPSLATLLGVLLRGTVTVSTDLVDYFLATVVVALIGGVGPAVAAAVLSAGLL NFFFTPPLYSLTVAEGENIVTLVAMVVVAVMVALVVDRAARRAEQAARARTEAALL ASYARTVLTSPYPLVRLLEKVRENFGLTSVALLEKRHGTWDRVACVGPRPCDEPD EADIDVPVTPEVHLALRGRALAAADQRALEAAAGQALLALRQQRMAAQTADAQR RAETTELRTALLSAVGHDLRTPLTSIKAAASSLRDPELRLSTEDTGELLATVEESAD RLAGLVDNLLDSSRLATGAVQPLLRPVGYYEVVAKALSGIDDRRSVQVDVDERLP QVLADVGLLERVVANVIDNALRHGRAGTRVNGDEPPVAVRASAHAAQVELRVVD HGRGLPKGAGEALFAPFQRLGDRDATSGVGLGLSVAKGFTEAMGGSISAEDTPG GGLTLVISLPVSTGAVPEEAQGS	7~~KdpD (8.24272E-121) ~~216,238~~Usp (9.2784E-26) ~~359,385~~DUF4118 (0.00000000201052) ~~463,X,613~~HisKA (0.00000000000105614) ~~678,728~~HATPase_c (7.17314E-23) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	7.2E-98	335.5	1.1	1.5E-97	334.5	0.8	1.6	1	U5VZI3_9ACTN	Histidine kinase (EC 2.7.13.3)	AFR_13825	Actinoplanes friuliensis DSM 7358	824	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	1246995	>tr|U5VZI3|U5VZI3_9ACTN Histidine kinase OS=Actinoplanes friuliensis DSM 7358 GN=AFR_13825 PE=4 SV=1 MARGELRIFLGAAPGVGKTYTMLEEAHRRVERGTDVVVAFVETHGRKHTQAMLA DLETVPRCTVEYRGAEFTEMNLDAVLARRPEIAVVDELAHTNVPGSRNAKRWQD VQELLDAGIDVLTTVNVQHLESLNDVVARITGVEQRETVPDAVVRAAEQVELVDMT PEALRRRMAHGNIYRPEKIDAALGNYFRTGNLTALRELALLWLADKVEDQLGKYR ADNNIDTTWETRERVVVALTGGAEGDTLIRRAARIAARDKGADLMAVHVTRNDGL TGADPAALSRQRVLVESLGGTYHQVVGADVPRALLDFARAVNATQIVLGVSSRGK LAQLFAAGVGVTTTAMSGSIDVHLVTHERAAQGRRAQRLPAALSRRRRVAGFAAT IAGLPALTALLHVGPSLSLTNDILVFLVAVVGVSLIGGLWPALLAAIAGSLLLNYFFTS PIGRFTIAEVDNLLALAIFVVVALAVSWVVDTAARKTRQAAEAGADAQTLATVAGS VLRGDRPLIALLDRLRETFALQSVTLLEDGAVVANVGDTACTVAGEADAEVKVNDH LKMLLRGRPLEASARRIVEAFAAQAAVALRQERLSAEAASARPLAEADRMRTALLA AVSHDLRTPLASAKAAVAGLRSADVDFDDNDRGELLATADESLDRLDRLVANLLD MSRLQAGALGVIPIDVGVEDIVPRALDDLGPDGRTVAVHIPDDVPLVHADPGLLERI VVNLVANALRYSPAGQPPVVTASALGDIVEVRVIDHGPGIPEDRWNDVFLPFQRL GDRDNHTGVGLGLALSRGLTEAMGGTLTPEETPAGGLTMILALPAS	1~~KdpD (4.09767E-121) ~~211,233~~Usp (2.19735E-19) ~~355,382~~DUF4118 (0.0000000000576864) ~~479,X,603~~HisKA (0.00000000000374965) ~~669,720~~HATPase_c (7.00154E-23) ~~821	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	7.2E-98	335.5	0.5	1.2E-97	334.8	0.3	1.4	1	A0A0A8EGX6_9ACTN	Histidine kinase (EC 2.7.13.3)	GZL_02853	Streptomyces sp. 769	851	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	1262452	>tr|A0A0A8EGX6|A0A0A8EGX6_9ACTN Histidine kinase OS=Streptomyces sp. 769 GN=GZL_02853 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDVVVAFVEHHGRPRTEVMLH GLEQVQRRELEYRGSTFTEMDVDAVLERKPAVALVDELAHTNVPGSRNGKRWQ DVEELLEAGITVISTVNIQHLESLGDVVESITGVRQRETVPDEIVRRADQIELVDMSP QAIRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRA EHSIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEVLAVYIARSDGLT SASPKELAVQRTLVEDLGGTFHHHVIGDDIPGALLEFARGVNATQIVLGSSRRKTW QYMFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRSRIIAGWLI GVGGPVLLSLLLTRLSNGPGLANDVLLFLFLTVVAALLGGQLPALASAAVGSLLLNF YFTPPTHTLTVNDPKNIVAIAIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLA GSVLRGETTLDALLERVRETFGMDAVVLLERRSEVEPWTCAGRAGGEGGVSPLA RPEDADVDVPVGDHMALALTGRVLPAEDRRVLSAFAAQAAVVLDRQRLVGEAER ARELAEGNRIRTALLAAVSHDLRTPLAGIKASVTSLRSDDVAWSEEDEAELLEGIEA GADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVTLDIPEEL PMVAVDPGLLERSVANLVENAVKYSPDGEAVLVAASALGDRVELRIADRGPGVPD SAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAIGGTLAAEDTPGGGMTMVL TLPTAAGVPPVRPDLPAQATT	1~~KdpD (6.9447E-123) ~~211,233~~Usp (1.35226E-32) ~~356,402~~DUF4118 (0.000000264815) ~~466,X,616~~HisKA (0.000000000000162916) ~~682,731~~HATPase_c (7.47401E-24) ~~832	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.3E-98	335.3	0.8	1.8E-97	334.3	0.5	1.6	1	Q89FC5_BRADU	Histidine kinase (EC 2.7.13.3)	bll6776	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	907	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium diazoefficiens, Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	224911	>tr|Q89FC5|Q89FC5_BRADU Histidine kinase OS=Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110) GN=bll6776 PE=4 SV=1 MVRERRDSEQRPSPEALLEAARREESASGKLKIFVGAAPGVGKTYEMLQSAHAK RKAGIDVVVGFVETHGRAETEALVRGLEVVPRKRLDYRGQTIEEMDLDAVIARRP QIALVDELAHTNAAGSRHPKRYLDVEELLSHGIDVYTAVNIQHTESLNDVVAQITHV RVRETVPDSVFDRADAIELIDLTPDDLIQRLREGKVYVPRQAERALEHYFSPGNLT ALRELALRRTAERVDEQLLTHMQANAIAGPWAAGERILVCVSEDPRAAGLVRYTK RLADRLHAPFTAISIETRRSLQLSDDERDRLADTLRLAEALGGEALTIPAVGRRIAD DVVNFAQGNNVTQIVIGKSTRSRWFEITRGSVVHDLVRRAGNITVHVIAGDDVPGE AAPKTAVQTAARTEPFDPLPYLKALGIVLIGLGAAELIQPRFGIENVDLVLLTAVVAV AVRYGLWPSLLATVAASLSYNFFFLPPIYTFTITDPTNVAAFVLFMVVAMIVSNVAA RVRTQADTAIGRIRTTEQLYAFSRKLAGTATLDDVLWATAYQIALMLKVRVVLLLPE DGLLTVKSGYPPEDQLDQADLAAANWAWSNDRPAGRGSDTLPGAKRLFLPMRT GRGPIGVIGIDNDRTGPLLTPDQRRLLDALVDQGALAIERVLLVEDMDRVKRTVES ERLRSALLTSISHDLKTPLASVLGAASTMRDLAGALSDTEKRDLLATVIDESERLNR FIANLLDMTKLESGAIVPNTALHDLSEIVGSALRRAAKILTAHKVELVLAADLPMLQL DAVLFEQVLFNLLDNAAKYSPAETTISIKSQRERDQVVLQIADEGSGIPPDEVESVF DKFYRVQKGDHVRPGTGLGLAISRGFVEAMHGTISAANRSDRSGAVLTIRLPVPA QTHALDTAA	29~~KdpD (3.94257E-122) ~~236,258~~Usp (1.60415E-44) ~~383,410~~DUF4118 (1.0032E-17) ~~510,536~~GAF (0.0000000000119586) ~~655,672~~HisKA (0.0000000000170594) ~~738,791~~HATPase_c (7.93415E-26) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	8.4E-98	335.3	0.1	1.3E-97	334.7	0	1.3	1	F2R822_STRVP	Histidine kinase (EC 2.7.13.3)	SVEN_5545	Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces venezuelae, Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	953739	>tr|F2R822|F2R822_STRVP Histidine kinase OS=Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745) GN=SVEN_5545 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEGHRRVERGTDCVVAFVEHHGRPRTEVMLH GLEQVPRRTLEYRATTFTEMDIDAVLARRPAVALVDELAHTNVPGSRNPKRWQD VAELLAAGIDVISTVNIQHLESLGDVVEAITGVRQRETVPDEVVRRADQIELVDMSP EALRRRMAHGNVYTSDKVDAALSNYFRPGNLTALRELALLWTADRVDEYLQQYR GEHNIRSTWQARERIVVGLTGGPEGRTLIRRATRLAEKGAGGEVLAVYIARSDGLT AASPKELAVQRTLVEDLGGTFHHVIGDDIPSALLEFARGVNATQIVLGSSRRRTWQ YVFGPGVGQTVARDSGPDLDVHIVTHGEVAKGRGLPVSRGARLGRSRIIGGWLA GVAGPLLLALLLTHVDADLGLANDMLLFLALTVAAALLGGFLPALASAAVGSLLLN WFFTPPIHRLTVADPKNIVAIAVFLGVAMSVASVVDLAARRTHQAARLRAESEVLS YLAGSVLRGETSLDALLERVRETFSMESVALLERQDEVEPWTRAASVGPHPAVR PEDADVDMPVGDHLALALSGRVLPAEDRRVLGAFAAQAAVVLDRQRLVGEAEEA RKLAEGNKIRTSLLAAVSHDLRTPLAGIKASVSSLRSDDVEWSEQDRAELLEGIEA GADRLDHLVGNLLDMSRLQTGTVMPLIRTVDLDEVVPMALGGVPDGSAELDIPET LPMVEVDKGLLERAVANIVENAVKYSPDGVPVAVAASTLGDRVELRVVDRGPGVP DEAKDGIFEPFQRFGDAPRGSGVGLGLAVARGFVEAMGGTLGAEDTPGGGLTM VLTLKASRTGAPAPPDLPAHAVT	1~~KdpD (2.50139E-123) ~~211,233~~Usp (6.73761E-32) ~~356,425~~DUF4118 (0.000000121355) ~~482,X,612~~HisKA (6.88013E-14) ~~678,727~~HATPase_c (4.74353E-27) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.8E-98	335.3	0.6	1.3E-97	334.7	0.4	1.3	1	A6X5I1_OCHA4	Histidine kinase (EC 2.7.13.3)	Oant_3779	Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	912	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Ochrobactrum, Ochrobactrum anthropi, Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	439375	>tr|A6X5I1|A6X5I1_OCHA4 Histidine kinase OS=Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168) GN=Oant_3779 PE=4 SV=1 MICRPSFQELYLTSDPLRFGENRPSPDALLEQAERETRGRLKIFLGAAPGVGKTYE MLMSGRARRADGIDVVIGVVETHGRVETEALTEGLEIIPRAQVAYRGHLLDEMDID AVLARKPQLVLVDELAHTNAPGSRHPKRYQDVEEILARGIDVYTTLNIQHVESLND VVAQITRIRVRETVPDSIIDRADDIELIDLTPNDLIKRLNEGKIYLPKTAKRAIHNYFSS GNLTALRELALRRTAQRVDEQLLSHMRAHAIEGPWAAGDRILVAVDERPRSISLVR YARRLADRLRAPWAAIHIETARSAGLTEEAKDRLATALRLAEQLGGETIIIPGQSVA EDIVRYASTHNFTQIVAGKSIKSRWREMIDGSIARELVRLSGAIDIHITAGVDYENGE TPRKVKTASQKATPDITPYLIGMVMTGIALVTGLLLDQFLDVRSIALVFVVGVLGVA VTLGLWPALFASVLSAFAYNFFFLSPLYTLSIADPESVVALVFFLFVSFIASNLASRV QRQAAAARQRARMTEDLYLFSKKLAGTGSLDDVLWATAFQIASMLKVRVVMLLPE GNSITVRGGYPPDDTLDDADIAAAHWTWEHDLPAGRGANTLPGAKRLYLPLKTAR TSVGVIGLDNDRMGPILTPEQQRLFEALADQAAIAIERVQLVGDVERAKLAAEADK LRSALLTSISHDLKTPLAAILGAATTLRDYSSSLPDTDRSDLVATVVDQSERLNRFIA NLLDMTRIEAGAMKPNLSLHYVGDLIGAALNRAAKILVHHQVNIAVPADLPMVQLD AVLFEQVLFNLFDNAAKYAPENTPITIKAHAAPSRITLEISDRGPGIPPGDLERVFDT FYRVRKGDHVQAGTGLGLSIARGFIEAMGGSIRAGNRHEGTGAVFTIALPVPADE VDKNS	38~~KdpD (1.38656E-124) ~~246,268~~Usp (1.98789E-45) ~~389,460~~DUF4118 (0.00000000852311) ~~512,543~~GAF (0.000000000000137389) ~~662,679~~HisKA (0.0000000000261673) ~~745,798~~HATPase_c (9.71094E-27) ~~901	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.8E-98	335.3	0.1	1.6E-97	334.4	0.1	1.5	1	A0A0F7NCT0_9ACTN	Histidine kinase	AA958_26985	Streptomyces sp. CNQ-509	853	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. CNQ-509	444103	>tr|A0A0F7NCT0|A0A0F7NCT0_9ACTN Histidine kinase OS=Streptomyces sp. CNQ-509 GN=AA958_26985 PE=4 SV=1 MTRGKLRIYLGAAPGVGKTYAMLSEAHRRLERGTDVVVGFVEHHDRPRAEVLLH GLEQIPRRELDYRGTRFTEMDVDAVLARRPTVVLVDEMAHTNVPGSRNEKRWQD IKELLSAGIDVISTVNIQHLESLGDVVENITGVRQRETVPDAVVRKAGQIELVDMSP EALRRRMAHGNIYDPGKIDAALSNYFRPGNLTALRELALLWVADRVDDYLREYRS EHDIRDTWQARERIVVGITGGPEGRTLIRRGARLATKGAGGEIMAVYISRSDGLTP LNTAPPEELAVQRTLVEDLGGTFHHVIGDDVPDALLEFARGVNATQIVLGSSRRKA WQYAFGPGVGATVARESGPDLDVHIVTHGEVAKGRGLPLARGARLGRGRIAAG WLVGLAGPVLLTAVMLRLDSTLGLANEVLLFLFATVLAALLGGTLPALASAGAGSL LLNYYFTPPVETFTIADARNIVALVVFFAVAVAVASVVDLAARRTSQAARLRAESEV MSLLAGSVLRGEGSLESLLDRVRETFGMESVSLFERQRGEDGWTCVGRVGASA GAPAGPDDADADMPVGDDMTLALTGRKLPAADRRVLGAFAAQAAVVLERQRLAA EAVEARKLAEGNRIRTALLAAVSHDLRTPLAAIKAAVTSLRSDDVAWSEEDEAELL TAIEEGADRLDALVGNLLDMSRLQTGTVTPLLREVDLDEVVPKALAGVPEGSVTLG IPETLPMVTVDAGLLERSVANVVENAVKYSPPGTPVLVQASALGDRVELRVVDRG PGVPDSGKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEALGGTLVAEDTPGGG LTMVLTLRAAPGRGTPAPAELPAQATT	3~~KdpD (6.52155E-122) ~~211,233~~Usp (2.46324E-31) ~~359,386~~DUF4118 (0.0000190536) ~~467,X,617~~HisKA (6.95436E-14) ~~683,732~~HATPase_c (4.90523E-24) ~~833	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1E-97	335	0.5	1.6E-97	334.4	0.3	1.3	1	B5GUP4_STRC2	Sensor protein (EC 2.7.13.3) (Turgor pressure sensor)	SCLAV_4779 SSCG_03029	Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces clavuligerus, Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	443255	>tr|B5GUP4|B5GUP4_STRCL Sensor protein OS=Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602) GN=SCLAV_4779 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLH GLEQIHRRELEYRDAVFTEMDVDAVLERRPAVALVDELAHTNVPGSRNAKRWQD VEELLAAGIDVISTVNIQHFESLGDVVESITGVRQRETVPDEVVRRADQIELVDMTP QALRRRMAHGNIYKSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYR GEHNIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGLT SASPKELNLQRTLVEDLGGTFHHVIGDDIPASLLEFARGVNGTQIVLGSSRRKAW QYIFGPGVGATVARDSGPDLDVHIVTHDEAGKGRGLPVARGARLGRSRIIAGWLV GVAAPVLLSLLLTGLDDSLGLANDVLLFLFLTVLAALLGGLLPALASAAVGSLLLNFY FTPPVRTLTVYDPKNIVAIVIFFAVAVAVASVVDLAARRTHQAARLRAESEILSFLAG SVLRGETTLDALLQRVRETFGMESVALLERRSDVDPWTTAGSVGPRSVVRPEDA DVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLVGQAEEARTLA EGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSEEDEAELLEGIEAGADR LDHLVGNLLDMSRLQTGTVTPLIRVTDLDEVVPMALVSVPDESVELDIPESLPMVA VDRGLLERAVANIVENAVKYSPAGTPVSVSASALGDRVEVRVADRGPGVPDDEK ERIFEPFQRYGDAPRGAGVGLGLAVARGFTEAMGGTLSAEDTPGGGMTMVLTLK AAPGVEPVSADLPARITS	1~~KdpD (2.15483E-123) ~~211,233~~Usp (1.7517E-29) ~~356,X,612~~HisKA (2.81428E-14) ~~678,727~~HATPase_c (8.96409E-29) ~~828	kinase	KdpD;Usp;X;HisKA;HATPase_c
	1E-97	335	0.2	1.7E-97	334.4	0.2	1.3	1	E4NB97_KITSK	Histidine kinase (EC 2.7.13.3)	kdpD1 KSE_26670	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	877	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Kitasatospora, Kitasatospora setae, Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	452652	>tr|E4NB97|E4NB97_KITSK Histidine kinase OS=Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) GN=kdpD1 PE=4 SV=1 MVHTARGRLRIYLGAAPGVGKTYAMLAEAHRRIERGADVAVGFVETHGRARTAEL LTGLETVPRRTMTHRGAEFTELDLDAVLARDPAVALVDELAHTNVPGARNAKRW QDVEELLAAGIDVVSTVNIQHLESLGDVVEGITGVRQRETVPDEVVRRADQIELVD MSPQALRRRLAHGNVYAPEKVDAALAHYFRPGNLTALRELALLWTADRVDEYLQ RYRAEQGIQGTWQARERIVVGLTGGPEGATLVRRAARIAARNSAGELLAVHISRS DGLSGSSPQALIEQRALVESLGGSFHTVLGDDPAAGLLDFARGVNATQIVIGTSRR KVWQYVYGPGVGYTVTRDSGDIDVHMVNHEHAARGRGRIPIRRVTDLGRTRTVA GWVIGVAGPPLLALLLTRLGGPGLSTDMLLFLALTVCAALVGGLFPAIASALVSSSA LNYYFAPPIHTFTIAQPENIVAVAIFAAVGIAVATVVDVAARRSHVAARAQAEAQTL SALAGTVLRGAPTGEGVLTALLEQVRETFQQEAVALLERTDAHGPWQAAAAVGP RPPAGPEQADADVPVGERLALVLRGRVLPAADRRMLGAFANQAAVLLERRRLAG EAAAARREAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRAEDVEWDEEDEAELL AGIESGADRLDHLINNLLDMSRLQTGTVTPLLRPTDLDEVVPFALGGVPPGSVRLD VPESLPMVRADAGLLERVLANLVENAVKYGPPGSPVLVKADLLERSGRVELRVVD RGPGVPEEARERIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGAVTAEDTP GGGLTMVVALPAAPSGPHPDERTERTERTEHAERAEQGGRTERDERKAGPA	5~~KdpD (3.0703E-122) ~~214,236~~Usp (4.9536E-22) ~~358,413~~DUF4118 (0.000000533705) ~~472,X,618~~HisKA (0.00000000000160649) ~~684,733~~HATPase_c (2.80406E-26) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.1E-97	335	0.1	1.9E-97	334.2	0.1	1.4	1	H2K2C9_STRHJ	Histidine kinase (EC 2.7.13.3)	SHJG_6969	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	852	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	1133850	>tr|H2K2C9|H2K2C9_STRHJ Histidine kinase OS=Streptomyces hygroscopicus subsp. jinggangensis (strain 5008) GN=SHJG_6969 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVALVESHGRPRTEVMLH GLEQVPRRQLEYRGAVFGEMDVEAVLRRAPAVALVDELAHTNIPGSRNTKRWQD VEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADDIELVDMS PQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDAYLNAYR SEHRVSTIWGSRERIVVGLTGGPEGRTLIRRATRLAEKGAGGEVMAVYIARSDGL SSASPKELAIQRTLVEDLGGTFHQVVGDDVPAALLDFARGVNATQIVLGSSRRKA WQYVFGPGVGATVARDSGPDLDVHIVTHEEVAKGRGLPVARGGRLGRARIIWG WAVGLAGPAVLAVLLNTVDLGLANDMLLFLAVTVAAALLGGLLPALASAAFGSLLL NYFYTPPLHRLTVADPKNIVAIAIFFGVGMAVASVVDLAARRTHQAARLRAESEILS FLAGNVLRGETSLEELLERVRETFAMESAALLERASDVAPWTCAGRAGFGPPLER PEDADVDVPVGDHMALALSGRVLPAADRRVLAAFAAQAAVVLDRRRLKEEADRA RTLAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDQAELLEGIEE GADRLDHLVGNLLDMSRLQTGTVTPLIREIDVDEVVPMALGGVPEDSVELDVPETL PMVAVDPGLLERSVANLVENAVKYSPHGRRVLVAASAIADRVEVRVVDRGPGVP DEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLTAEDTPGGGLTMV LSLRAAGPRPEPLPAGESRTEPERQATW	1~~KdpD (2.8211E-124) ~~211,233~~Usp (5.14819E-31) ~~356,430~~DUF4118 (0.000225917) ~~480,X,611~~HisKA (2.90354E-15) ~~677,726~~HATPase_c (3.28916E-26) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.1E-97	334.9	1.1	1.7E-97	334.3	0.8	1.3	1	D9T8N8_MICAI	Histidine kinase (EC 2.7.13.3)	Micau_0598	Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Micromonospora, Micromonospora aurantiaca, Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	644283	>tr|D9T8N8|D9T8N8_MICAI Histidine kinase OS=Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442) GN=Micau_0598 PE=4 SV=1 MGRGELRIYLGAAPGVGKTYAVLEEAQRRAERGTDVVIGLVETHGRRHTAEMVG DLEVVPRRSMTYRGVEFTEMDLDAVLARRPEVVVVDELAHTNVPGSRHEKRWQ DVQELLDAGISVLSTVNVQHLESLNDVVAQITGTTQRETVPDQVVRAAEQVELVD MTPEALRRRMAHGNIYRPDKIDAALGNYFRVGNLTALRELALLWLADKVDEQLDA YRAQQGISDTWEARERVVVALTGGPEGETLIRRAARIAARSKGADLLAVHVARSD GLAGADPAQLARQRVLVESLGGTYHQVLGTDIPAALLDFARGVNATQLVLGASRR GRFAQVFSRGVGVTTTALSGPIDVHLVTHPEAGRGRRGTSVPAALSRRRRLIGYA LAVLGMPLLTLVLRTLPDLTLTNDILLFLAGVVGVALVGGLWPALVAALGGSLLLNW FFTPPYRTLTIAEADNLLALGVFVGVAIAVSWVVDVAARRTREAARASADAQTLAT VAGSVLRGERPLPALLDRLRETFGLRAVSVLELTDEAGGRPARARGADAWRVVA SVGERPPGSPGAGETVVPVDDRLSVVLAGRRLEAADRRVVEAFAAQAAVALRQE RLAEEAATARPLAAADRMRTALLAAVSHDLRTPLASAKAAVSSLRSHDVEFDADD REELLATADESLDRLGRLVANLLDMSRLQAGALGVSATAIGLEDAVPLALDELGPA AAEVTTDIPADLPAALADPGLLERVLVNIVANALRHSPPGRPPAITGSAHAGQVELR VIDTGPGIPEDQWEHVFLPFQRLGDRDNQTGVGLGLALSRGLAEAMGGSITPETT PGGGLTMVLRLPAATQPEGPQE	1~~KdpD (3.08596E-119) ~~211,233~~Usp (2.1901E-20) ~~355,424~~DUF4118 (0.000117754) ~~475,X,619~~HisKA (0.000000000000745247) ~~685,736~~HATPase_c (6.74021E-26) ~~837	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.2E-97	334.8	0.3	2.1E-97	334	0.2	1.4	1	C9Z0G1_STRSW	Histidine kinase (EC 2.7.13.3)	SCAB_24001	Streptomyces scabiei (strain 87.22)	880	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces scabiei, Streptomyces scabiei (strain 87.22)	680198	>tr|C9Z0G1|C9Z0G1_STRSW Histidine kinase OS=Streptomyces scabiei (strain 87.22) GN=SCAB_24001 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRIERGTDCVVAVVEHHGRPRTEVMLH GLEQIPRRELAHRDAVFTEMDVDAVLARRPRVALVDELAHTNVPGSRNDRRWQD VQELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMS PQALRRRMAHGNVYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNAY RSEHQVSRIWGSRERIVVGLTGGREGRTLIRRAARLAEKGAGGEVMAVYIARSDG LTSASPKELAAQRTLVEDLGGTFHHVVGDDIPAALLAFARGGNATQIVLGVSRRKS WQYVFGPGVGATVARNSGPDLDVHLITHDEAGKGRGLPVARGARLGRVRMIWG WLVGTAGPLLLALVLVASSTDLGLANDMLLFLSLTVAAALLGGLLPALAAAVLGSLL LNWFFTPPVHTLTVDDPTNIVAIVVFIGVAVAVASVVDLAARRTHQAARLRAESEIL SFLAGSVLRGETSLEALLERVRETFGMESVALLERGSDVEPWTCAGSVGPRRVD RPEAADVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRRRLQQEAGR ARELAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSPEDEAELLAGIEE GADRLDHLVGNLLDMSRLQTGTVSTLIREIDLDEVVPMALGGVPEGSVGLEIPESL PMVAVDPGLLERAVANIVENAVKYSPPGTPAQVSASALGGRVEVRVTDRGPGVP DEAKERIFAPFQRHGDAPRGTGVGLGLAVARGFAEAMGGTLDAEDTPGGGLTMV LTVRAVQKAPGPDTPPPSGTGPALHTSTGADAAPTGGTAADAPVGTAASAERRG I	1~~KdpD (4.36767E-125) ~~211,233~~Usp (4.03425E-30) ~~356,X,612~~HisKA (1.29262E-14) ~~678,727~~HATPase_c (1.19151E-26) ~~828	kinase	KdpD;Usp;X;HisKA;HATPase_c
	1.3E-97	334.7	0.5	2.1E-97	334.1	0.3	1.3	1	L8EQ10_STRRM	Histidine kinase (EC 2.7.13.3)	SRIM_19057	Streptomyces rimosus subsp. rimosus ATCC 10970	855	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rimosus, Streptomyces rimosus subsp. rimosus, Streptomyces rimosus subsp. rimosus ATCC 10970	1265868	>tr|L8EQ10|L8EQ10_STRRM Histidine kinase OS=Streptomyces rimosus subsp. rimosus ATCC 10970 GN=SRIM_19057 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYSMLSEAHRRVERGTDVVVAFVEHHDRPRTEVMLH GLEQIERVELEYRGSVFTEMDVDAVLRRDPAVALVDELAHTNVPGSRNAKRWQD VEELLEAGIDVISTVNVQHLESLGDVVESITGVRQRETVPDEIVRRADQIELVDMSP EAIRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRA EHSVSKIWAGRERIVVGLTGGPEGRTLIRRASRMAAKGSGSEVLAVYIARSDGLT SASPKELAVQRTLVEDLGGTFHHVIGDDIPNALLEFARGVNATQIVLGSSRRKAW QYVFGPGVGATVARDSGPDLDVHIVTHDEVAKGRGLPVARGARLGRARIIAGWLL GVAGPVLLSLLLAALDNGPGLANDVLLFLFLTVAAALIGGLLPALAAAAVGSLLLNFY FTPPTHSITIADPKNIVAIVIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLAGS VLRGETTLDALLERVRETFGMESVALLERTGDVAPWTCAGRVGGTAEGDPKAKP LMRPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRQRLVGEA ERARELAEGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVAWSEDDEAELLAGI EAGADRLDHLVGNLLDMSRLQTGTVTPLIRDIDLDEVVPMALGGVPEGSVTLDIPE ELPIVAVDPGLLERCVANLVENGVKYSPDGERVLVSASALGDRVELRIADRGPGVP DSAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLAAEDTPGGGMTM VLTLRAAAGRPPVRPDLPAQATT	1~~KdpD (1.49188E-122) ~~211,233~~Usp (1.08924E-30) ~~356,402~~DUF4118 (0.0049151) ~~466,X,620~~HisKA (0.000000000000363911) ~~686,735~~HATPase_c (5.41491E-25) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.3E-97	334.7	0.2	2.2E-97	334	0.1	1.4	1	A1UKX9_MYCSK	Histidine kinase (EC 2.7.13.3)	Mkms_4295	Mycobacterium sp. (strain KMS)	836	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. (strain KMS)	189918	>tr|A1UKX9|A1UKX9_MYCSK Histidine kinase OS=Mycobacterium sp. (strain KMS) GN=Mkms_4295 PE=4 SV=1 MTVANGPKRGELRIYLGAAPGVGKTYAMLGEAHRRLARGTDVVAAVVETHGRAK TAELLDGIEVLPPRHVTYRGGRFPELDVDAVLARRPEVVLVDELAHTNTPGSRNAK RWQDVEALLAAGITVISTVNVQHLESLNDVVTQITGIEQRETVPDEVVRSADQVEL VDITPEALRRRLSHGNVYAPERIDAALSNYFRRGNLTALRELALLWLADQVDAALA KYRADNRITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVVRGD GLTGVSAPEMGRVRELAASLGATLHTVTGDDVPTALLDFARERNATQLVLGTSRR SRWARILDEGIGAAVVQRSGKIDVHMVTHDEAHRSPTASPRTRRAASWLAALAVP AAICALTVLLLDPLLGVAGESAVFFVGVLLVALLGGVAPAALSAVLSGLLLNYFLINP RHTFTIAEPDSALTIVVMLAVAVAVAALVDGAASRRREARHAAREAELLALFAGAV LRGADLTVLLERVRETYGQRAVSLLREKAGVVACVGADPCVDVNTADTAIEVGDD EFWLLLAGRKLAARDRRVLSAVAGQAAGLVRQRELTEEAGRAEAIARADELRRSL LSAVSHDLRTPLAAAKAAVSSLRSDEVDFSADDRAELLATVEESVDQLTALVANLL DSSRLAAGVVRPQLSAVYLEEAVQRALLGISRGATGSGDIGIDRVEVDVDGCVVA ADSGLLERVLANLIDNALRYAPDGPVRVTAGRVGERVLIAVTDTGPGIPPGGQDRV FGAFQRLGDQDTTSGVGLGLSVARGFVEAMGGTVTANDTPGGGLTVEIDLAAPQ EAHA	7~~KdpD (1.03504E-121) ~~217,239~~Usp (7.29206E-35) ~~360,410~~DUF4118 (0.0000035244) ~~460,X,605~~HisKA (0.00000000000978673) ~~671,728~~HATPase_c (1.57177E-28) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.4E-97	334.6	0.2	2.2E-97	333.9	0.1	1.3	1	A0A0F4JBV1_9ACTN	Histidine kinase	VR45_25750	Streptomyces sp. NRRL S-495	861	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-495	1609133	>tr|A0A0F4JBV1|A0A0F4JBV1_9ACTN Histidine kinase OS=Streptomyces sp. NRRL S-495 GN=VR45_25750 PE=4 SV=1 MGRGRLRIYLGAAPGVGKTYAMLAEAHRRLERGTDVVVAFVEDHGRRHTAARVA GLELVPRRELTHRGAVFTELDLDALLARRPQVALVDELAHTNVPGCRNEKRWQD VEELLAAGIDVVSTVNIQHLESLGDVVEGITGVRQRETVPDEVVRRADQIELVDMS PQALRRRLAHGNVYAPEKVDAALANYFRPGNLTALRELALLWTADRVDEYLQKYR AEQGIKGTWQARERIVVGLTGGPEGATLIRRAARIAARGSGGELLAVHISRSDGLA GSGSGSSQTLIEQRALVEGLGGSYHAVLGDDPAAGLLEFARGVNATQIVLGTSRR PAWQYIYGPGVSGTVTRESGDIDVHIVTHEHEAKGRGRIPIRRVTDLGRTRTVAG WLIGVAGPPLLALLLINVDGLGLTTDMLLFLSLTVCAALVGGLYPAVASALVSSSAL NYYFAPPIHTFTIDEPQNILAVAIFTAVGIAVASVVVDLAARRTHQAARSQTEAQTLSA LAGTVLRGAPSGDGVLTALLEQVRETFQQESAALLERPDPLGAWHPVATAGPRP PERPETADVDPVPGENLALALRGRVLPGEDRRLLGAFAAQAAVVLERRRLAGEAA AARREAEGNRIRTALLAAVSHDLRTPLAGIKASVVSSLRSADVEWDEADEAELLAGI EAGADRLDHLINNLLDMSRLQTGTVTPLIQETDLDEVVPFALGGVPPGAVRLDVPE TLPMILADGGLLERSLANLIENAVKYSPEGVKVLVKAGALRPPGEPGRVELRIVDR GPGVPEDAKERIFAPFQRYGDAPRGAGVGLGLAVARGFVEAMNGSVTAEDTPG GGLTMVVTLPAAERVPGPGDAPGPELPAAPA	1~~KdpD (4.76402E-125) ~~211,233~~Usp (5.18766E-20) ~~358,404~~DUF4118 (0.0000000672132) ~~484,X,618~~HisKA (1.98352E-14) ~~684,733~~HATPase_c (9.18432E-25) ~~839	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.5E-97	334.5	0.5	3.1E-97	333.5	0.3	1.5	1	A0A0A1H5J5_9BURK	Histidine kinase (EC 2.7.13.3)	E1O_24670	Burkholderiales bacterium GJ-E10	917	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, unclassified Burkholderiales (miscellaneous), Burkholderiales bacterium GJ-E10	1469502	>tr|A0A0A1H5J5|A0A0A1H5J5_9BURK Histidine kinase OS=Burkholderiales bacterium GJ-E10 GN=E1O_24670 PE=4 SV=1 MADQRPDPDALLARIQNEAERAARGRLKLFFGASAGVGKTYAMLSAARRQRDQG VDVVIGVVETHGRSETEALTLGLERIPLREIAYRDRTFAEFDLDAALQRKPALILVDE LAHSNVEGSRHPKRWQDVEELLAAGIDVYTTINVQHLETLNDVVSGITGVRVRETV PDRVFDRADEVVLVDLTPDELLQRLKDGKVYISRQAESAVRNFFRKGNLIALRELA LRRTADRVDGEMLQYRRDRAVAPVWQTRDSLLACVTAGADDDRVVRTAGRIASR LEIPWHAIYVETPERTRIGDAARQAVMKALKLAQSMGAETATLADHDEVAATVRY ARDHNLSRMIVGHSGPLRRWLPRGWSARTGLSRAGLPIWHRSFADRLAGSAPDL EVTIVSAVDPASAGSRSPAREDRFVFEAGSLPAYAGAAAVCAGAALISAPLQSIFTL PNIVMLFLLAVVLVALRFGRGPAVLASFLSVLEFDFFYVPPKFSFAVSDVQYLLTFA VMLAVGLIAGQLTAGLKYQARVANRREGRVRGLYEMARDLSGALLPDQIAEICER FLDRELHAQATLLLADDQEKVVLPRDDGDRADSVPLEPGIAQWALDHGEAAGMG TNTLPATPALYLPLKAPMRMRGVLVVRPREAARLQGPEQSRLLDTVARLAAIALER VHYVDVAQRVSLQMESERLRNSLLSAISHDLRTPLAALVGLADSLQWSGGTPVQ QKAIVERMREQTQRMRSLVENLLDMARLQAGQVALNRQWNAIEEVVERALRAMA HALAAHVVRVQLPADLPMLEMDAALMERVFDNLLENAGKFTPPGSVIDIGARAEP ERVVLWVEDNGPGVPRGKEEAIFSKFERGHVESATPGVGLGLAICRAIVEAHGGII RAENRPGGGARFWIELPRGNPPDVPAESVDLQ	22~~KdpD (7.61416E-124) ~~232,255~~Usp (5.60216E-29) ~~393,433~~DUF4118 (8.69707E-21) ~~520,547~~GAF (2.52212E-16) ~~666,683~~HisKA (0.000000000000162152) ~~747,800~~HATPase_c (4.0514E-29) ~~901	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.7E-97	334.3	0.6	2.8E-97	333.6	0.4	1.4	1	C8XB10_NAKMY	Osmosensitive K channel His kinase sensor	Namu_5030	Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	815	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Nakamurellales, Nakamurellaceae, Nakamurella, Nakamurella multipartita, Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	479431	>tr|C8XB10|C8XB10_NAKMY Osmosensitive K channel His kinase sensor OS=Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) GN=Namu_5030 PE=4 SV=1 MGTRGQLRVYLGAAPGVGKTYKMLEEAHRRLERGTDVVVGVVEGHERPLTEALL VGLEVIPRQVRPYRGARFAEMDLDAVLARRPQVVLVDELAHTNVPGSRHGKRWQ DVEELLDAGITVITTVNIQHLESLNDVVQEITGVVQRETVPDEIVRRADQIELVDMTP EALRRRMAHGNIYRPDKVDAALHNYFRVGNLTALRELGLLWLADKVDDQLDRYRA DHHITDTWEARERVVVALSGGPEGDTLIRRAARIADRTKGTDLIAVTIIRSDGLAGP GPAHLARQRALVESLGGTYHQVVGADIPTALLDFARGVNATQLVLGASRRGRFA QLFARGVGVTTTAGSGAIDVHLVTHEKAQSGRRPPRPSWAGALTRRRRVLGFVL ALVGMPLLSLALIGLRGQLSLPSDILALLLGVVGVALVGGLLPALVAAFLGFGLLNY YFVPPLHQFTVAEAENLLALLAFLLVAVAVSVVVDLAARRTGQASRAQAEAATLST LAGSVLRGERPLPALLEQVRETFGQDSVTLLERHPDTVAGPDLRRDQRAWSVAA WVGESPSTAPAQGVEVAVNDEVSLVLRGPALAAADQRIVEAFGAEAAVALRQQR LSEQAAAVVRLTEVDRLRTALLTAVGHDFRTPLAAATAAVTSLRSSDVTFGPQDR DELLATAEESLARLSRLVENLLDMSRLQAGALAMHLQPIGVAELVPIAVDDLGEAG RAVQVRDADDVPDVTADAALLERVLANVIANAVRHSPRTGRRWSPSASTTGGSR CASSTTARVLPRRTTTGCSCRSSGSATATTPAASVWAWRCPAD	2~~KdpD (1.96103E-114) ~~212,234~~Usp (1.76203E-29) ~~356,X,622~~HisKA (0.000000000672718) ~~688,X	dysfunctional kinase	KdpD;Usp;X;HisKA;X;
	1.8E-97	334.2	0.1	3.2E-97	333.4	0.1	1.4	1	D7C8J1_STRBB	Histidine kinase (EC 2.7.13.3)	kdpDSBI_03259	Streptomyces bingchenggensis (strain BCW-1)	857	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7C8J1|D7C8J1_STRBB Histidine kinase OS=Streptomyces bingchenggensis (strain BCW-1) GN=kdpD PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYGMLSEGHRRVERGTDLVVGFVEHHGRPRTQVML RGLEEVPRREMEYREARFTEMDVDAVLARRPAVVLVDELAHTNVPGSRNAKRW QDVEELLRAGIDVVTNLNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVD MSPQALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWTADRVDEYLQ QYRSEHSIRSTWQARERIVVGITGGPEGRTLIRRAARMAAKGSGSEVLAVYVARS DGLTSASPKELAVQRTLVEDLGGTFHHVIGEDVPRALLDFARGVNATQIVLGSSRR KTWQYIFGPGVGVTVARDSGPDLDVHIVTHDEVAKGRGLPVARGARLGRTRLIAG WLTGVAGPVLLTLLLTHSGGALATDGGPGFANEVLLFLFLTVVAALLGGLLPALAS AAVGSLLLNYYFTPPTHTLTIADPQNILAIAVFVAVAVCVASVVDLAARRTHQAARL RAESEVLSFLAGSVLRGETSLEALLERVRETFGMDSVALLERESDVAPWTCAGSV GGNGGAPLPERPEDADVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLD RQRLALEAERARDLAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSPE DEAELLEGIEQGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALVGVPE TCVSLEIPEELPMVAVDPGLLERSVANIVENAVKYSPDGLPVLVSASALGDRVELR VADRGPGVPDSAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFVEAMGGRLAAE DTPGGGMTMVLTLRAAGGREPVGSPLPAQVTS	1~~KdpD (7.91125E-123) ~~211,233~~Usp (9.6955E-32) ~~356,X,622~~HisKA (8.94945E-15) ~~688,737~~HATPase_c (2.16676E-25) ~~838	kinase	KdpD;Usp;X;HisKA;HATPase_c
	1.9E-97	334.1	0.2	3.3E-97	333.4	0.1	1.4	1	V6KSM8_STRRC	Histidine kinase (EC 2.7.13.3)	M878_10520	Streptomyces roseochromogenus subsp. oscitans DS 12.976	860	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	1352936	>tr|V6KSM8|V6KSM8_STRRC Histidine kinase OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_10520 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLAEAHRRVERGTDCVVAYVEHYDRPRTEVMLH GLELVPRKRLEYREAVFTEMDVDAVLRRAPAVALVDELAHTNVPGSRNAKRWQD VEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSP EALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNAYRS EHRVSKIWGSRERIVVGLTGGPEGRTLIRRASRLAEKGAGGEVLAVYISRSDGLTS ASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGVNATQIVLGSSRRKAWQ YVLGPGVGATVARESGPDLDVHIVTHEEAAKGRGLPVARGARLGRARIISGWLVG LGGPVALAVLLNAVDVGLANDMLLFLAVTVAAALLGGLLPALASVAFGSLLLNYYYT PPLHQWTIADPKNIVAIAIFLCVAVSVASVVDLAARRTHQAARLRAESEILSFLAGN VLRGETSLEELLERVRETFAMESAALLERAGDVEPWTCAGRAGFGRPLERPEDA DVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAIALDRRRLQEEADQARALAE GNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDRAELLEGIEEGADRL DHLVGNLLDMSRLQTGTVTPIIREIDVDEVVPMALGGVPEDSVELDIPETLPIVEVD PGLLERSVANLVENAVKYSPRGRPVLVSASAIADRVEVRIVDRGPGVPDEAKDRIF EPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLSLRAAG ARPEPLPAGEHTAEPPVGEDIAEPERQTL	1~~KdpD (1.18718E-121) ~~211,233~~Usp (7.00039E-31) ~~356,X,611~~HisKA (1.46959E-14) ~~677,726~~HATPase_c (1.33143E-25) ~~827	kinase	KdpD;Usp;X;HisKA;HATPase_c

	2.4E-97	333.8	2.2	5.9E-97	332.5	0.5	2.1	1	H6R5W2_NOCCG	Histidine kinase (EC 2.7.13.3)	kdpD NOCYR_3889	Nocardia cyriacigeorgica (strain GUH-2)	865	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia cyriacigeorgica, Nocardia cyriacigeorgica (strain GUH-2)	1127134	>tr|H6R5W2|H6R5W2_NOCCG Histidine kinase OS=Nocardia cyriacigeorgica (strain GUH-2) GN=kdpD PE=4 SV=1 MKRGHLRIYLGAAPGVGKTYAMLGEAHRRLERGRDVVAAVVETHGRAKTAALLD GIERIPPKVIEYRGTAFQELDVAAVLRREPAVVLVDELAHTNAPGSKNEKRWQDIE ELLDAGIDVISTVNVQHLESLNDVVEQITGIQQRETVPDAVVRAAEQIELVDITPEAL RRRMSHGNVYAADKVDAALRNYFRPGNLTALRELALLWLADQVDAALAKYRADH RITDLWEARERVVVAVTGGPESETIVRRARRIATKSSAELVVVHVVRGDGLAGVS TARLTRLRELAAGLDASLHTVTGEDVPAALLEFAREVNATQLVLGTSRRSRWARIF DEGIGSAVVQQSGKIDVHMVTHEEANRRRSWPSLRRPVWAWVAALVVPVLVCAI GAWFLDGALELGGLSAMFFVAVVLVSLLGGVLPAAISALLSGVLLNWFFAEPRYSL TVAEPDSIFTIAVLLIVAVAMAALVDRAAARSRQARKASRQAELLTVFAGAVLHGAD LPKLLEQVRETYGMRAVALVAGEDVLAAVGAEPPCRPGDADTTIEAGDTVHRLLL AGHPLDPGDRPVLTAVANQAVGLVRQARLAEEAGAAAALLEADRLRRALLSAVSH DLRTPLAGAKAAVSSLRSDDVEFSPEDTAELLETVEESVDQLTALVGNLLDSSRLA VGVVSPQLRQVYLDEVVHRALVGVGMGARGLRRAAMDRVEVDVDALSVRADGG LLERVLANLIDNALRHSTPGTPIRITAERDGGKVAIAVVDIGPGIPAGAEEQLFEPFQ RLGDRDNSTGVGLGLSVVRGFVEAMGGTVHAEPTPGGGLTMLVELPAGADAAP PRDSDESGEGPATMDSAGSSRGDDPAQGPDRAGVT	1~~KdpD (4.1814E-122) ~~211,233~~Usp (1.47277E-33) ~~354,389~~DUF4118 (0.0000000000882306) ~~469,X,598~~HisKA (0.00000000000101332) ~~664,721~~HATPase_c (3.03138E-28) ~~822	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.1E-97	333.5	0.4	2.9E-96	330.3	0.1	2.1	1	W0LHX2_9ENTR	Histidine kinase (EC 2.7.13.3)	Z042_19825	Serratia multitudinisentens RB-25	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia multitudinisentens, Serratia multitudinisentens RB-25	1441930	>tr|W0LHX2|W0LHX2_9ENTR Histidine kinase OS=Serratia multitudinisentens RB-25 GN=Z042_19825 PE=4 SV=1 MVDDERPNPDSLLALANEKPRGKLKVFFGACAGVGKTYAMLQEAQRQRAQGLD VLVGVVETHGRGETAALLAGLTVLPQKRIQHRGRLLHEFDLDAALARHPALILMDE LAHSNASGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGGVTGVRVRE TVPDHVFDEATEVVLVDLPPDDLRQRLNEGKVYLPGQAERAIEHFFRKGNLIALRE LALRRTADRVDDQMRAFRDSQGREKVWHTRDSILLCVGHGSGNEKLVRIAARLA ARLGCHWHAVYVETPKLHRLPEHQRRAILRALRLAQELGAETATLADPFEEQAVL RYAREHNLGKIIIGRRSEQRWKIRGSFADRLGHLGPDLDLVIVALENDTPLPLSKEH DSRTFTEKWRFQLRGYAVAVALCAMITLLSQWLLPGFDSANLVMVYLLGVAIVALF FGRWPSVLAAVINVASFDLFFVQPEWSFAVSDMQYLLTFAVMLTVGITIGNLTAGV RYQARVARYREQRARHLYEMSHGLSQALNHDDIAKTSRHFLSSSFQAKTALLLPQ EDGSLRQMAGEDGGLLSVDEAIARWSYSKGTPAGAGTDTLPGVPYQLLPLSTPK QTFGLLAIEPSNLRQLMVPEQQRLLQTFAVLIASALERLHLAHSAEKAKLDAEREQL RNSLLAALSHDLRTPLTVLFGQAEILTLDLAAEGSSHAPQASQIRQQVLSTTRLVNN LLDMARIQSGGFHLRKEWQSLEEIVGASLHMLEPLLVQHQIKVELPSEMVLINCDG NLLERVFTNLLENANKYAGTEAIIGIRARAVPEWLEVEIWDNGPGIPTEQLQLIFDK FSRGNKESAIPGVGLGLAICRAIIEVHGGRIWAENGAHGGASFRFMLPLETPPALE GEGFDL	21~~KdpD (1.08473E-118) ~~229,252~~Usp (7.51325E-39) ~~372,401~~DUF4118 (1.87035E-20) ~~500,526~~GAF (3.06957E-17) ~~644,661~~HisKA (0.000000000337651) ~~726,779~~HATPase_c (3.84237E-31) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.1E-97	333.5	0.6	4.9E-97	332.8	0.4	1.3	1	I0H1T1_ACTM4	Histidine kinase (EC 2.7.13.3)	AMIS_17480	Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	832	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes missouriensis, Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	512565	>tr|I0H1T1|I0H1T1_ACTM4 Histidine kinase OS=Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431) GN=AMIS_17480 PE=4 SV=1 MARGELRIYLGAAPGVGKTYTMLEEAHRRGERGTDVVIALVETHGRKHTTAMTAG LEVVPRREVTYRGAAFAEMDLDAVLARRPELAVVDELAHSNVPGSRHAKRWQDV RELLEAGISVLTTVNVQHLESLNDVVARITGVPQRETVPDAVVRAAEQVELVDMTP EALRRRMAHGNIYRPEKVDAALGNYFRTGNLTALRELALLWLADKVEQQLGQYRA DHDIDSTWETRERVVVALTGGPEGDTLIRRAARIAARSKGADLLAVHVARSDGLA GANPAELARQRVLAESLGGTYHQVVGADVPRALLDFARGVNATQIVLGASSRGR FAQLFAAGVGVTTIARSGSIDVHLVTHELAGRGRRRGPLPPALSRKRRIIGFGVALL GLPLLTVALEAGPPLPLIDDILLFLVAVVGVALIGGLWPALLAAVGGSLLLNWFFTAP VGRFTIAEGQNLLALAIFVLVAVAVSWVVDTAARTTRQAARASAEAQTLAAVAGG VLRGERPLTALLDRLRETFALDSVTLVEKGPGGTGTVVASVGDPVCVSPGAADGE VTADGDLMILLRGRTLEASDRRIVEAFAAQAAVALRQERLAAEAATAKPLAEADRL RTALLAAVSHDLRTPLASAKAAVASLRSSEVEFDDEDRAELLATADESLERLDRLV ANLLDMSRLQAGALGVVPIEVGAEEVVPRALDDCGPEGRKVAVRVPEDLPLLRAD PGLLERVLVNLVANALRHSPPDAPPMITGSTHGDMVELRVIDHGPGIPADRWDDV FLPFQRLGDRDNHTGVGLGLALSRGLTEAMGGTLTPGETPGGGLTMVLALPVAR LC	1~~KdpD (4.21641E-120) ~~211,233~~Usp (6.96153E-22) ~~355,383~~DUF4118 (0.000000000214841) ~~478,X,608~~HisKA (0.000000000000342697) ~~674,725~~HATPase_c (3.95475E-22) ~~826	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.6E-97	333.3	0.2	6.1E-97	332.5	0.1	1.4	1	V6KFF6_STRNV	Histidine kinase (EC 2.7.13.3)	M877_09270	Streptomyces niveus NCIMB 11891	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces niveus (Streptomyces spheroides), Streptomyces niveus NCIMB 11891	1352941	>tr|V6KFF6|V6KFF6_STRNV Histidine kinase OS=Streptomyces niveus NCIMB 11891 GN=M877_09270 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHNRPRTEVMLK GLEQIHRRELPHRGTVFTEMDVDAVIERRPAVALVDELAHTNVPGSRNSKRWQD VEELLQAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEMVRRADQIELVDMS PQALRRRMAHGNIYQPDKVNAALSHYFRPGNLTALRELALLWTADRVDEYLQQY RGEHNIRSTWQARERIAVGLTGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGL TSASPKELTLQRTLVEDLGGTFHHVIGDDVPSALLEFARGVNATQIVLGSSRRKS WQYIFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVARGARLGRSRILSGW LAGVVAPVLLTLLLTALDDTLGLANDVLLFLFLTVLAALLGGLRPALASAAVGSVLLN FYFTPPTHTLTIQDPRNIVAIVIFFAVAVSVASVVDIAARRTHQAARLRAESEILSFLA GSVLRGETTLDALLERVRETFSMESVALLERTSDVDPWTRAGSVGPRPVDRPEA ADVDMPVGDHMALALSGRVLPAEDRRVLSAFAAQAAVVLDRQRLVGEAEGARRL AEGNRIRTALLAAVSHDLRTPLAAIKAAVTSLRSDDVEWSDEDHAELLEGIENGAD RLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALLGVPEGSVVLDIPESLPMVA VDPGLLERAVANIVENAVKYSPDGTRVNVSASSLGARVQVRVVDRGSGVPDEAK ERIFEPFQRHGDAPRGAGVGLGLAVARGFVDAMDGTLTAEDTPGGGLTMVLDLT AVPGLAPAGPELPAEVSS	1~~KdpD (3.04533E-121) ~~211,233~~Usp (1.20566E-30) ~~356,420~~DUF4118 (0.00000381449) ~~466,X,612~~HisKA (2.68217E-14) ~~678,727~~HATPase_c (3.00348E-26) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.7E-97	333.2	0.3	6E-97	332.5	0.2	1.4	1	Q82KK7_STRAW	Histidine kinase (EC 2.7.13.3)	kdpD SAV_2396	Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	851	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces avermitilis, Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	227882	>tr|Q82KK7|Q82KK7_STRAW Histidine kinase OS=Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680) GN=kdpD PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHGRPRTEVMLH GLEQVARRELAYRDTVFAEMDVDAVLRRAPAVALVDELAHTNVPGSRNAKRWQD VEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEMVRRADQIELVDMS PQALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDAYLTEYR SEHRVSAIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVMAVYIARSDGL TSASPKELAVQRTLVEDLGGTFHHVVGDDIPSALLDFSRGVNATQIVLGSSRRKA WQYMFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVARGARLGRSRIIWG WLVGVAGPVVLALLLNTVDLGLANDMLLFLALTVAAALLGGLLPALASAAFGSLLLN YYYTPPLHRLTIADPKNIIAIAIFVGVAVSVASVVDLAARRTHQAARLRAESEILSFLA GSVLRGETSLDALLERVRETFGMESVALLERESDVAPWTCAGSVGVRPLVDRPE DADVDMPVGDHMALALSGRVLPASDRRVLAAFAAQAAVVLDRQRLQREADQART LAEGNSIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDRAELLEGIEDGA DRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEDSVVLDIPESLPM VAVDPGLLERSVANLVENAVKYSPSDESVLVAASALANRVELRVVDRGPGVPDEA KDRIFAPFQRYGDAPRGVGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLTV GAAVDSPAGRPGLAHATAERQTRC	1~~KdpD (3.05015E-122) ~~211,233~~Usp (6.96116E-32) ~~356,X,611~~HisKA (0.000000000000042042) ~~677,726~~HATPase_c (4.18087E-24) ~~827	kinase	KdpD;Usp;X;HisKA;HATPase_c
	5E-97	332.8	0.4	1E-96	331.8	0.3	1.6	1	F3ZIK4_9ACTN	Histidine kinase (EC 2.7.13.3)	STTU_1469	Streptomyces sp. Tu6071	885	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. Tu6071	355249	>tr|F3ZIK4|F3ZIK4_9ACTN Histidine kinase OS=Streptomyces sp. Tu6071 GN=STTU_1469 PE=4 SV=1 MARGKLRIYLGSAPGVGKTYAMLAEAHRRLERGTDVVVGYVEHHARPRTEVLLT GLEELPRAHHTHRDAAFTEMDVDAVLRRAPAVVLVDELAHTNVPGARNAKRWQD VEELLAAGIDVVSTVNIQHLESLGDVVESITGVTQRETVPDEVVRRADQIELVDMS PQALRRRLAHGNVYAPDKVDAALANYFRPGNLTALRELALLWTADRVDEYLQQY RGEHNIESTWQARERIVVGITGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGL TAASPKELAVQRTLVEDLGGTFHHVIGDDIPAALLDFAKGVNATQIVLGSSRRRSW QYALGPGVGMTVARESGPDLDVHIVTHEAAAKGRGLPVARGARLGRSRILTGWL VGVGGPVLLALVLRSLDEGPGLANDVLLFLFLTVGAALLGGLVPALASAAVGSLLL NFWFTPPTHTFTISDPSNIVAIVIFFSVAVAVSVVDLAARRTHQAARLRAESEILSF LAGDVLRGETTLDALLDRVRETFAMHSVALLEREGDREPWTPAGSVGPQPAARP EDADVDMPVGDHMALALSGRVLPAADRRVLAAFAAQSAVVLDRERLQRQARQAR TLAEGNRIRTALLAAVSHDLRTPLAAIKAAVTSLRAEDVAWSEEDRDALQEAIENG ADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGLPPDALVDLDVPETL PMVAVDAGLLERAVGNVVENAVKYSPSRTPVLVAASTLGERVELRVVDRGPGVP DEAKDRIFEPFQRHGDAPRGSGVGLGLAVARGFTEALGGTLSAEDTPGGGLTMV LTLPVARRRPKENSAEAADEGSGPPEDRPGPVPPEDDPPRAARPQPSSPDRPDR KAARS	1~~KdpD (1.23715E-119) ~~211,233~~Usp (3.20446E-31) ~~356,391~~DUF4118 (0.000000000409708) ~~466,X,612~~HisKA (0.000000000000491331) ~~678,728~~HATPase_c (1.88454E-26) ~~829	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	5.4E-97	332.7	0.5	1.1E-96	331.7	0.3	1.5	1	A0A059MKD5_9NOCA	Histidine kinase (EC 2.7.13.3)	N505_0124930	Rhodococcus sp. BCP1	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. BCP1	931223	>tr|A0A059MKD5|A0A059MKD5_9NOCA Histidine kinase OS=Rhodococcus sp. BCP1 GN=N505_0124930 PE=4 SV=1 MTGTARTAAPEASRRGRLRIYLGAAPGAGKTFAMLGEAHRRIARGGDVVVAIVNT HGRARTAEQLAGLETVPPRRIGYRDAVFEELDLDAVLARRPAVALVDELAHTNVP GSRHAKRWQDVEELLDAGIDVLSTVNIQHLESLNDVVEQITGVVQRETVPDDVVR RADQVELVDITPQALQRRLAHGNVYAPEKVDAALRNYFREGNLTALREIALLWLAD QVDLALAKYRGEHAITDTWEARERVVVAVTGGPESETLVRRASRIAAKASAELMV VHVVRGDGLTGVSAPQMGKVRTLAASLGASLHSVVGDDVPTTLLDFAREVNATQ LVLGTSRRPRWARILDEGIGAAVVRDSGKIDVHMVTHEHTARGPRMALLGRHERR LQSWIAAFVIPVVATGVMALIDHFTGFEGQHTLYFVVVLAVALFGGIGPAIVAALLS ALLLNFFFTEPRYSFTIAEPANFVTTVVLLVVAVAVAALVDAAAARAREARLASQEA ELLALFAGAVLRGADLPRLLEKVRETYAQHGVSLVRTDREPAQVLGTAGSAPPTS MQAADTVCEVDDSAYALLLGGPQLRARDRRILTAVAGQAAGLVRQQELAAEAAR ASALAETDRLRRLLLSAVSHDLRTPLAAVKAAVSSLRSTDVEFSPEDTAELLATIEE STDQLTGLVSNLLDSSRLAAGVITPVLQPVYLDEVVHRAMVTLSSGGSDTARNVR ERIEVDVDDTVVAADSGLLERVLANLLDNALRYAPTGPIRVGAGTSGDRTTVTIAD CGPGLAPGDTGNVFAAFPRAGDHRSSRGAGLGLTVARGFAEAMGGTVTATETP GGGTTMVVELAAAPARVPR	13~~KdpD (2.54674E-121) ~~223,245~~Usp (9.77689E-34) ~~366,389~~DUF4118 (0.0000210512) ~~467,X,616~~HisKA (0.000000000000461332) ~~682,739~~HATPase_c (7.91696E-25) ~~839	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	5.4E-97	332.7	0.1	9.5E-97	331.9	0.1	1.4	1	A0A0B5DGU4_9ACTN	Histidine kinase (EC 2.7.13.3)	SNOD_25015	Streptomyces nodosus	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces nodosus	40318	>tr|A0A0B5DGU4|A0A0B5DGU4_9ACTN Histidine kinase OS=Streptomyces nodosus GN=SNOD_25015 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCAVAFVEHHDRPRTEVMLH GLEQIPRKELVHRGSVFTEMDVDAVLHRAPAVALVDELAHTNVPGSRNAKRWQD VEELLAAGINVVSTVNIQHLESLGDVVESITGIRQRETVPDEVVRRADQIELVDMSP QALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLTEYRS QHKVSTIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTS ASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGVNATQIILGSSRRKAWQ YVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRTRIVAGWLT GVLGPVVLALLLNSVRLGLANDMLLFLTLTVAAALLGGLFPALASAAFGSLLLNYYY TPPLHRLTIADPKNIVAIAIFVGVAVSVASVVDLAARRTHQAARLRAESEILSFLAGS VLRGETSLEALLERVRETFGMESAALLERTSEVDPWTCAGSVGLSAPVARPDDA DVDVPAGDHMALALSGRVLPASDRRVLAAFAAQAAVVLDRQRLQQEAEQARALA EGNRIRTALLAAVSHDLRTPLAGIKASVTSLRSDDVEWSEEDRAELLAAIEEGADR LDHLVGNLLDMSRLQTGTVTPLIREVDLDEVVPMALGGVPEDSVELDIPESLPIVAV DAGLLERAVANLVENAVKYSSLGTPVLVSASALADRVEVRVVDRGPGVPDDAKER IFEPFQRHGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLTLRAV QGRQDPARLAEAERQTT	1~~KdpD (1.13503E-122) ~~211,233~~Usp (1.10782E-31) ~~356,391~~DUF4118 (0.0000297384) ~~463,X,611~~HisKA (0.000000000000101041) ~~677,726~~HATPase_c (5.12702E-27) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	6E-97	332.5	2.4	8.6E-97	332	1.7	1.2	1	I3VXZ5_THESW	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Tsac_2388	Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	379	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family III. Incertae Sedis, Thermoanaerobacterium, Thermoanaerobacterium saccharolyticum, Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	1094508	>tr|I3VXZ5|I3VXZ5_THESW Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485) GN=Tsac_2388 PE=4 SV=1 MNDSFKRLTPEEALEIANKSQRGKLKIFLGYAPGVGKTYAMLDEANRRLKRGQDV VIGVVETYGRKETEAMIGDLEIIPKKEIIYKGTVQYEMDLDAILKRKPQVVLVDELAH TNVPGSKHNKRYEDVEEILQNGINVLSTLNIQHLESLNDTVKQITGITVRETIPDTIV NNADEIEVIDVTPDALQNRLKRGEVYNLDKVDQALKNFFRKGNLNALRELALRQSA DEVDEDLEQYMKEHGIQENWETNEKIMVCISFNPLVKKLIRRGARRAHRFKCEWI VVYVECTNIFAKKPTKKDMEVLESHFKLAKQLGAEVVVLRGKSVSEELLKFAKERH ITQIIMGHSNRRKWETLLRGSTVQKLINSAKNIEIHVIPYN	20~~KdpD (2.14748E-127) ~~230,252~~Usp (3.59439E-47) ~~377	non-kinase	KdpD;Usp
	6.1E-97	332.5	0.3	1.1E-96	331.7	0.2	1.4	1	O54137_STRCO	Histidine kinase (EC 2.7.13.3)	SCO5871	Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albidoflavus group, Streptomyces coelicolor, Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	100226	>tr|O54137|O54137_STRCO Histidine kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) GN=SCO5871 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVALVEHHGRARTEVMLR GLEQVPRREAEYRGAAFTELDLDAVLARAPRVALVDELAHTNVPGVRNAKRWQD VEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMS PQALRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRADEYLQQY RSEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDG LTSASPKELAVQRTLVEDLGGTFHHVLGEDIPAALLDFARGVNATQIVLGSSRRKA WQYVFGPGVGATVARESGSDLDVHIVTHEEVAKGRGLPVARGARLGRSRIVWG WFAGLGGPVLLTLLLSTVHLGLANDVLLYLALTVAAALLGGLYPALASAAVGSLLLN WYFTPPVNRITIADPRNMLALAIFVGVALSVASVVDVAARRTHQAARLRAESEILSF LAGDVLRGETSLETLLERVRETFGMESAALLEREGDVAPWTCAGRAGSGPPVDR PEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLREEADRA RTLAEGNRIRTALLAAVSHDLRTPLAGIKAAVTSLRSDDVAWSEEDRAELLEGIEE GADRLDHLVGNLLDMSRLQTGTVTPLIREIDVDEVAPMALGGVPEGSAELDIPETL PMVAVDAGLLERALANLVENAVKYSPDDRTVLVAASALADRVEVRVVDRGPGVP DEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTM VLTLRAVGSSAPTSRPATAERQAAL	1~~KdpD (2.50743E-123) ~~210,233~~Usp (2.1904E-30) ~~356,423~~DUF4118 (0.00000653967) ~~480,X,611~~HisKA (4.42981E-14) ~~677,726~~HATPase_c (2.00265E-27) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	6.3E-97	332.5	0.7	9.6E-97	331.9	0.5	1.3	1	A1TED5_MYCVP	Histidine kinase (EC 2.7.13.3)	Mvan_4762	Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	850	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium vanbaalenii, Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	350058	>tr|A1TED5|A1TED5_MYCVP Histidine kinase OS=Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1) GN=Mvan_4762 PE=4 SV=1 MDDESVAASPHKAKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDVVAAVVE THGRKKTAELFEGIEIVPPKLIAYRGSDFAELDVEAVLRRNPQVVLVDELAHTNTPG SKNTKRWQDIEELLDAGITVITTVNVQHLESLNDVVTQITGIEQQEKVPDEVVRAAD QVELVDITPEALRRRLAHGNVYAPERVDAALSNYFRRGNLTALRELALLWLADQV DSALEKYRADNKITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVH VVQGDGLSGVSGPQMGKVRELAASIGATLHTVVGDGAGGVPAALLDFAREMNAT QLVLGTSRRSRWARIFDEGIGATVVQKSGRIDVHMVTHEQAGGESLWARVSPRQ RHAVSWLAALAVPGAICAATVLLLDRFLGIGGESAMFFIGVLVVALLGGVAPAALS AVLSGVLLNFFLVEPRHTFTISEPDSAITIVVLLVVAVAVAALVDGAANRTRESRRA AREAELLALFAGAVLRGADLNTLLERVREAYSQQSVTLVRGEAHGGGVVGCAGS EPCVTVETADTAIEVGSKDDPEEFWLLLAGRRLDARDRRVLGAVANQAAGLARQ RELAEEAGRAEAIARADELRRSLLSAVSHDLRTPLAAAKAAVSSLRSEDVGFSPED TAELLATVEESIDQLSGLVGNLLDSSRLAAGVVRPELQPVYLEEAVPRALLGISRGS TGLRAGLDRVKVEVGDTVVMADSGLLERVLANVIDNALRYAPDGPVRVTAGRVAD RVLIAVADEGPGVARGAETELFAPFQRLGDQDTSSGVGLGLSVARGFVEAMGGTI SATDTPGGGMTVEIDLAAPR	13~~KdpD (1.49548E-120) ~~223,245~~Usp (7.55268E-31) ~~369,392~~DUF4118 (0.0000000384976) ~~472,X,624~~HisKA (0.00000000000277994) ~~690,746~~HATPase_c (5.63078E-24) ~~846	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	6.5E-97	332.4	0.3	1.3E-96	331.5	0.2	1.5	1	Q20XR7_RHOPB	Histidine kinase (EC 2.7.13.3)	RPC_4547	Rhodopseudomonas palustris (strain BisB18)	907	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Rhodopseudomonas, Rhodopseudomonas palustris, Rhodopseudomonas palustris (strain BisB18)	316056	>tr|Q20XR7|Q20XR7_RHOPB Histidine kinase OS=Rhodopseudomonas palustris (strain BisB18) GN=RPC_4547 PE=4 SV=1 MADHRRNADQRPSPDALLDAARREDDGRGRLKIFVGAAPGVGKTFEMLQSAHAK RKAGVDVVVGVVETHGRSETEALLAGLEVIPRRRLDYKDHVLDEMDLDALIARRP RLALVDELAHSNAPGSRHPKRYLDVEELLSHGIDVYTAVNIQHIESLNDVVAQITHV RVRETVPDSIFDRADAIELVDLTPDDLIQRLREGKVYVPKQAERALEHYFSPGNLT ALRELALRRTAERVDEQLLNHMQANAIAGPWAAGERILVCINEDTRSAGLVRYTR RLADRLHAPWSAICVETRSAQRLTEVERDRLADTLRLAEALGGEGMTIPGSGRHV ADDVISFAHNNNVTQIVVGKSTRSLWVELLRGSVVHDLIRRAGNISVHVIAGEELAA DPVARKTVKTLERNDSFDPRPYLMAVLMVAAALGLAILIEPTFGVVNVDLVFLTAVV SVAVRYGLLPSLLASVTASLCYNFFFLPPFYTFTIAEPTNIAAFLFFMLIALLVSNLAG RVRSQAVSAIGRVRTTESLYAFSRKLAGTAALDDVLWATAYQAALMLHVRVVLLL PEDGRIVVKAGYPPEDQLDDADLAAANWAWSNDRPAGRGSETLPGAKRLFLPM RTGRGPIGVIGIDDDRSGPLLTPDQRRLLDALVDQGALAIERVQLVEDMDRVKRSA ESDRLRQALLTSISHDLKTPLAAVLGAASTLRDLSPKLSDAQRAELIGSIVEESERL NRFIANLLDMTRLEAGAVVPNAALHDLGDVVGSALRRAATILAHHNVQLDLEAELP MLQIDAVLFEQAIFNLLDNAAKYAPLGTTITVRAARHGDAVLLQIIDEGEGIPPEDLE TVFDKFYRVRKSDQVRAGTGLGLAISRGFIEAMQGSMTAANRSDRSGAVLSIRLP VPPARAALDTAA	27~~KdpD (1.97186E-114) ~~236,258~~Usp (1.50911E-41) ~~383,410~~DUF4118 (2.88526E-18) ~~510,537~~GAF (0.00000000000333186) ~~655,672~~HisKA (0.0000000000399009) ~~738,791~~HATPase_c (1.28756E-25) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.5E-97	332.4	0.6	1E-96	331.8	0.4	1.3	1	B0KD64_THEP3	Osmosensitive K+ channel signal transduction histidine kinase, sensor domain	Teth39_0496	Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	379	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Thermoanaerobacter, Thermoanaerobacter pseudethanolicus, Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	340099	>tr|B0KD64|B0KD64_THEP3 Osmosensitive K+ channel signal transduction histidine kinase, sensor domain OS=Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) GN=Teth39_0496 PE=4 SV=1 MSEGFRRLTPEEALEIIKKQQRGKLKIFLGYAPGVGKTYAMLNEGNRRLKRGQDV VIGYVETHGRKETEAQIGNLEIIPRKKIEYHGMILEEMDTDAIIARKPEVVLIDELAHT NAPGSKHKKRYEDVEEILRHGINVITTLNIQHLESLNDVIQQITGVAVRETIPDSIVD NADEIVAVDLTPDALLNRLKRGDIYPVSKVDECLSNFFRKGNLNALRELMLRLTAEE VDIELEEYMKEHGITDTWETNEKIMVCITPNPLSKKLIRRGARRARRFKCDWVVVY VNCTHFLAPKLTEKDKEVLESHFMLAKQLGAEVYTLTGKSVSDELLKFAKQMHITQ IIIGHSQRSRLQTFFRGSTVIKLIKKAKNIEIHVIPYK	21~~KdpD (2.78624E-133) ~~230,252~~Usp (2.78451E-40) ~~377	non-kinase	KdpD;Usp
	6.6E-97	332.4	0.2	1.1E-96	331.6	0.2	1.4	1	B2JE24_BURP8	Histidine kinase (EC 2.7.13.3)	Bphy_2054	Burkholderia phymatum (strain DSM 17167 / STM815)	949	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia phymatum, Burkholderia phymatum (strain DSM 17167 / STM815)	391038	>tr|B2JE24|B2JE24_BURP8 Histidine kinase OS=Burkholderia phymatum (strain DSM 17167 / STM815) GN=Bphy_2054 PE=4 SV=1 MPRPDPDELLDKLQREEEKRQRGKLKIFFGASAGVGKTYAMLQAARRRMEEGID VVVGIAETHGRGETAALLEGLDVLPLARIEYRARSLAEFDLDAALERKPQLILVDEL AHSNVPGARHAKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETV PDRVFDRADEVTLVDLPAEELLDRMRDGKVYMPQQAERAVRNFFRKGNLIALREL ALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPLLVRAAARLAAS LKADWIAVYVETPKLQRLSDARRERTLDALKLAAELGAETATLAGADAVTTLVGYA RVRNVSKLVAGGSSATGVTRWLRRPFGERLAERASDLDLTLIRASSDEAGPAGTT RERIADAEGRAWRDALIAARDRRSPPRSYAWAVAICAGVTLIASQLIDRIDLTNLVM LYLLGVIFTAVKLGRGPGVMLSFLSVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLL TSLVIGHLTSSLRREARVARRREQRTGAMYAMARELAAALTTEQIVGIGSRHVSEV FRARVAVLLPDSADQVKQKIDDPDTTIMLDSASLDVDVGQWVYDQQKPAGHGTD TLPAARALYLPLRAPMRTRGVLAVVMEDERELDVPEQQRMLDAFAAQIALALERV HYVDIARDALVSMESERLRNSLLSAISHDLRTPLTAIVGFSSMLAAQRDARTDAQG ELVDAIHEEALRMTGIVTNLLDMARLQAGSLKLNRQWSLLEETVGSALRDCRRTLA RHPVTVSLPADLPLLQLDAVLMERLFANLFENAAKYVPPDTPLMIGAQCIEENGTP FVRVTVDDTGPGLPPGMEARIFEKFTRGEKESAKPGIGLGLAICRAIAEAHGGKIG AANRIAADGRVEGARFWFTLPIDTPPPVPDVSDLPDEAAAEPDPEPHRRQQADTH PHTHS	21~~KdpD (3.04068E-123) ~~230,252~~Usp (8.16192E-28) ~~374,416~~DUF4118 (1.12355E-19) ~~512,541~~GAF (2.51224E-17) ~~664,681~~HisKA (3.81537E-14) ~~746,799~~HATPase_c (3.93794E-22) ~~909	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7E-97	332.3	1.1	1.4E-96	331.3	0.8	1.5	1	R4LLR9_9ACTN	Histidine kinase (EC 2.7.13.3)	L083_3149	Actinoplanes sp. N902-109	827	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	649831	>tr|R4LLR9|R4LLR9_9ACTN Histidine kinase OS=Actinoplanes sp. N902-109 GN=L083_3149 PE=4 SV=1 MARGELRIHLGAAPGVGKTYTMLEEAHRRAERGTDVVIGLVETHGRKHTEAMIGE LEVIPRTQLRYRGAGFTEMDLDAVLARRPELAVVDELAHSNVPGARNAKRWQDV QELLAAGIDVLTTVNVQHLESLNDVVAQITGVEQRETVPDAVVRAAEQVELVDMT PEALRRRMAHGNIYQPEKIDAALGNYFRAGNLTALRELALLWLADKVEDQLDKYR ADHKIDTRWETRERVVVALTGGREGGTLIRRAARIAARNKGADLLAVHIARNDGLN GADPAALSRQRVLVESLGGSYHQVVGADVPQALLDFARAVNATQIVLGASSRGRL AQLFTAGVGVTTTALSGTIDVHLVPHERAGAGRRAGRVPAALSRRRRVAGLVTVL AGLPVLTALLSIGAGLTLANDILVFLAAVVAVSLIGGLWPALIAAVAGSMLLNYFFTP PVRRFTIAEGENLLALGIFVVVALAVSWVVDTAARKTRQAAQAGADAQTLATVAG SVLRGDRPLIALMERLAEIFALRSVTLLDKGVVVAGVGDNPCVDAGESDVEVKVDD DLVVLLCGRPLAASDRRIVEAFAAQAAVALRQERLSAEAATAKPLAEADRMRTALL AAVSHDLRTPLASAKASVASLRSGDVDFDEQDRAELLETADVSLDRLIRLVTNLLD MSRLQTGALGVSATAIGAEEIVPRALDDLGPAGRTVALHIPDDLPLLSADPGLLERV LVNLSANALRHSPPGHPPMITASTLGSTVEIRVVDRGPGIPEDRWEDVFAPFQRL GDRDNHTGVGLGLALSRGLTEAMGGTLTPEATPGGGLTMTVSLPTAEPR	1~~KdpD (5.08749E-119) ~~211,233~~Usp (8.2928E-19) ~~355,385~~DUF4118 (0.000000010335) ~~479,X,603~~HisKA (0.00000000000189101) ~~669,720~~HATPase_c (7.61255E-22) ~~821	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	7.3E-97	332.3	0.1	1.3E-96	331.5	0.1	1.4	1	G2P2E4_STRVO	Histidine kinase (EC 2.7.13.3)	Strvi_2184	Streptomyces violaceusniger Tu 4113	870	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces violaceusniger, Streptomyces violaceusniger Tu 4113	653045	>tr|G2P2E4|G2P2E4_STRVO Histidine kinase OS=Streptomyces violaceusniger Tu 4113 GN=Strvi_2184 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEGHRRVERGADLVVGFVEHHGRRRTQVMM HGLEEVPRRELEYRGSTFTEMEVDAVLARRPAIALVDELAHTNVPGSRNEKRWQ DVEELLRAGIDVVSTVNIQHLESLGDVVESITGVRQRETLPDEVVRRADQIELIDMS PQALRRRMAHGNIYAPDKVDAALSNYFRPGNLTALRELALLWTADRVDEYLQQYR DEHSIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGLT SASPKELAVQRTLVEDLGGTFHHVIGEDIPGALLEFARGVNATQIVLGSSRRKTWQ YVFGPGVGTMVARDSGPDLDVHIVTHDEVAKGRGLPVARGARLGRSRLIAGWVV GVAGPALLTLLLTGTGATLASEAGPGFANQVLLFLFLNVLAALLGGMVPALASAAV GSLLLNYYFTPPTHTLTIADPENIVAIAIFVAVAVCVASVVDLAARRTHQAARLRAES EILSFLAGSVLRGETSLEALLERVRETFAMDSVALLERESDVAPWTCAGSVGSHD GTPAPERPEDAEVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRL AQQAGQARELAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSEEDEA ELLEGIEDGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALVGVPMAKV TLDIPEELPMVAVDPGLLERGVANIVENAVKYSPPDHPVLVSASALGDRVELRVAD GGPGVPDSEKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMDGRLTAEDTP GGGMTMVLTLRVAAGRPPADPGLPVQVGSTSGTTTRKGRPAT	1~~KdpD (2.12538E-123) ~~211,233~~Usp (3.9968E-30) ~~356,426~~DUF4118 (0.00000758081) ~~471,X,622~~HisKA (1.63107E-14) ~~688,737~~HATPase_c (6.92415E-26) ~~838	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	7.6E-97	332.2	0.3	1.7E-96	331.1	0.2	1.6	1	Q5YZH6_NOCFA	Histidine kinase (EC 2.7.13.3)	kdpDNFA_15690	Nocardia farcinica (strain IFM 10152)	828	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia farcinica, Nocardia farcinica (strain IFM 10152)	247156	>tr|Q5YZH6|Q5YZH6_NOCFA Histidine kinase OS=Nocardia farcinica (strain IFM 10152) GN=kdpD PE=4 SV=1 MSTSDAPAPRRGRLRIYLGAAPGAGKTYAMLGEAQRRIARGGDVVVAIVNTHGRP RTEEQLAGLEVVPPRRITYRGVEFEELDLDAVLARRPAVALVDELAHTNVPGSRHA KRWQDVAELLAAGIDVLSTVNIQHLESLADVVEQITGVAQRERIPDAVVRRAEQIEL VDITPQALRRRLAHGNVYAPEKVDAALRNYFREGNLTALREIALLWLADQVDLALA KYRGEHAITDTWEARERVVVAVTGGPESETLVRRASRIAAKAGADLLVVHVVRGD GLTTPEMGAVRELAAGLGADVHSVVGDDVPATLLDFARQVNATQLVVGTSRRSR WARILDEGIGAAVVRDSGKIDVHMVTHEHRVRGPRPALLGRHDRRPAAWLAAFLI PVAATAVMAAIVRLTGTAGLNALFFVAVLAVALFGGVGPAIVAALLSGLLLNYFFTE PLYSLTIAEPANFVTTVVLLVVAVAVAALVDTAAARAREAGSAAREAELLALFAGAV LRGADVPALLEKVRETYAQRGVSLVRLDGDRVEVLGTAGAEPPSTPAAADTRGD VEDSPYALLLAGPRLRPRDRRVLTAVAGQAAGLVRQRELAAEAARAAMLAETDRL RRLLLSAVSHDLRTPLAAVKAAAAGLRSTDVEFSPEDTAELLATIEESTDQLTRLVT NLLDSSRLAAGVVTPEPRPVYVDEVVHSALLSLGVDAGERLTLELGDTLVRADATL LERVLANLLDNALRYAPDGPIRVCATNSGERTTVTVADHGPGLDSGVTAFPRTGD QRTGGAGLGLVVARGFVEAMGGTLTAAETPGGGTTMIIDLPAVSTEAPA	9~~KdpD (3.08015E-118) ~~219,241~~Usp (1.47463E-32) ~~359,381~~DUF4118 (0.000000847973) ~~458,X,609~~HisKA (0.00000000248205) ~~675,725~~HATPase_c (2.68741E-20) ~~819	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	8.8E-97	332	0.4	1.2E-96	331.6	0.3	1.2	1	R4M6T0_MYCTX	Sensor protein	J113_07245	Mycobacterium tuberculosis CAS/NITR204	334	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex, Mycobacterium tuberculosis, Mycobacterium tuberculosis CAS, Mycobacterium tuberculosis CAS/NITR204	1310114	>tr|R4M6T0|R4M6T0_MYCTX Sensor protein OS=Mycobacterium tuberculosis CAS/NITR204 GN=J113_07245 PE=4 SV=1 MIEHVTTKRGQLRIYLGAAPGVGKTYAMLGEAHRRLERGTDVVAAVVETHGRNKT AKLLEGIEMIPPRYVEYRGARFPELDVEAVLRRHPQVVLVDELAHTNTPGSKNPKR WQDVQEILDAGITVISTVNIQHLEGLNDVVEQITGIEQKEKIPDEIVRAADQVELVDI TPEALRRRLAHGNVYAAERVDAALSNYFRTGNLTALREIALLWLADQVDAALEKY RADKKITATWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVIRGDGL AGVSAPQLGRPRLDKPRCDQPALVLRRHAAGLRPRDERHAARRRHIAAIAMGTPV	8~~KdpD (5.12193E-127) ~~217,239~~Usp (0.0000000144775) ~~279	non-kinase	KdpD;Usp
	8.9E-97	332	0.1	1.4E-96	331.3	0.1	1.3	1	D3P2B3_AZOS1	Histidine kinase (EC 2.7.13.3)	kdpD AZL_b02700	Azospirillum sp. (strain B510)	912	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum sp. (strain B510)	137722	>tr|D3P2B3|D3P2B3_AZOS1 Histidine kinase OS=Azospirillum sp. (strain B510) GN=kdpD PE=4 SV=1 MAEPDSDERPSPDALLEEANRERRGRLKIFLGAAPGVGKTYAMLEDAHARRRDG TDLVVGVVETHGRHDTEALLDGLDILPRRRIDYRGRPFQEMDLDAILARRPRLVLV DELAHTNIPGSRHLKRWQDVEEILDAGIDVCSTLNVQHLESLNDVVERIAGIKVRET LPDSVLHRADEIALIDLPPQELIRRLQEGKVYVPEQAKRAADHFFSAGTLTALREMA LRQAAERVDAQMLRYMRAHAIAGPWPTRERILVCIGDGPQALRLVRTAKRAAERR DAPWVVLYVDTHRNHALSEEDKDGIAQALRLAAQLGGETAVVPGERAAAEILAFA RARNVSQIIVGRAHPRRRLRALHQSVTTDLLARNEDFDVLVVAGEDERPARSLET RAPSVVFDWLAYVVATLTVASATAIGLAIDVWLPLPNISVAYLVGVLLVAIRHGLAP SIYASVLSFLTFNFLFTEPKYTFAITDAQNIMTVFFFLVAAVITSNLAARVRAQVETT RLSARRTANLYDFNRRISAAVGLDDVLWAVVHHVASTMNGHSLVLLPREGRLEVA AGYPPEDTLDEKSMAAARWSWENGKTAGRGSTTLPAADWLFLPLRTGRGPMGV LGVQMTGEQQLLSPEQGRLLDTLADQAAVAIERTALVADIETARVAAETERLRSAL LSSLSHDLRTPLVSILGASSSLTSYGETLAPPERMELVQTIQEEAERLNRFVQNLLD MTRIGSGALKPRTDWVDLADVIGAALERAKRMLGDRPVRLELEPGLPLLRLDPVLT GQVFFNLIDNACKYSPDGSPILLQASRAGGEVLIELCDQGAGIPEADRERIFDMFY RVEAGDAQTAGTGLGLAICRGIVEAHGGTIRALPGRHGVGTCIAILLPVPAGPEIAD IEGDSARGEDSGTPDSGR	22~~KdpD (1.71494E-123) ~~232,254~~Usp (1.20723E-39) ~~377,400~~DUF4118 (1.84251E-20) ~~500,527~~GAF (1.01171E-14) ~~645,674~~HisKA (0.00000000504122) ~~728,783~~HATPase_c (1.1709E-24) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	9.3E-97	331.9	0.1	1.5E-96	331.2	0.1	1.3	1	V6KFS0_STRNV	Histidine kinase (EC 2.7.13.3)	M877_08465	Streptomyces niveus NCIMB 11891	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces niveus (Streptomyces spheroides), Streptomyces niveus NCIMB 11891	1352941	>tr|V6KFS0|V6KFS0_STRNV Histidine kinase OS=Streptomyces niveus NCIMB 11891 GN=M877_08465 PE=4 SV=1 MRRGKLRIYLGAAPGVGKTYAMLAEAQRRVERGTDCVVGFVEHHHRPRTEVMLH GLEQIGRLEIPYRGTVFTEMDVDAVLARRPAVALVDELAHTNVPGSRNSKRWRDV EELLQAGIDVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMDP QALRRRMAHGNIYQPDKLDAALSNYFRPGNLTALRELALLWTADRVDEYLQQYR GEHNIRSTWQARERIVVGLTGGPEGRTLVRRAVRLAEKGAGGEVLAVYIARSDGL TSASPKELTAQRILVEDLGGTFHHVIGDDVPSSLLEFARGVNATQVVLGSSRRKT WQYVFGPGVGQTVTRDSGPDLDVHIVTHGEVARGRGLPVARGARLGRARIVGG WLTGVVGPVLLTLLLDGLAPDVGLANDMLLFLTLTVAAALLGGLVPALASAAFGSL LLNYYFTPPLHEFTISDPKNIVAIVIFFGVAVSVASVVDIAARRTHQAARLRAESEILS FLAGSVLRGETTLDALLERVRETFAMESVALLERESDIAPWTCAGSVGPAERVER PEDADVDLPIGDHMALALAGRVLPAEDRRVLSAFAAQAAVVLDRQRLLGEAGQAR ELAEGNRIRTALLAAVSHDLRTPLAGIKAAVTSLRSHDVEWSEDDHRELLAGIEEG ADRLDNLIGNLLDMSRLQTGTVSTLIRETELDEVVPMALGGVPEGSVVLDIPESLP MVAVDPGLLERAVANIVENAVKYSPDNAPVFVSASAIADRVEVRVVDRGPGVPDD AKDRIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLTAEDTPGGGFTTVLT LRTAAGHPPTRPDLPPTVTS	1~~KdpD (1.7925E-121) ~~211,233~~Usp (2.30761E-28) ~~356,403~~DUF4118 (0.000000430472) ~~466,X,613~~HisKA (1.90074E-14) ~~679,728~~HATPase_c (2.49735E-25) ~~829	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	9.6E-97	331.9	0.4	1.5E-96	331.3	0.3	1.3	1	F8AWU8_FRADG	Histidine kinase (EC 2.7.13.3)	Fsym Dg_3009	Frankia symbiont subsp. Datisca glomerata	889	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia symbiont subsp. Datisca glomerata	656024	>tr|F8AWU8|F8AWU8_FRADG Histidine kinase OS=Frankia symbiont subsp. Datisca glomerata GN=FsymDg_3009 PE=4 SV=1 MDVVSRGTLRVYLGAAPGVGKTFAALDEAHRRRDRGTDVVVGFVETHGRPRTAA LLDGLEVVPRQEISYRGSTFTEMDVDAVLARRPAVAVVDELAHTNVPGSRNAKR WQDVQELLDAGIDVISNVNIQHMESLNDVVETITGVAQRETVPDEVVRQADQVEL VDMAPEALRRRMAHGNIYAPEKIDAALSNYFRVGNLTALREIALLWVADKVDEQLD RYRAEHGISGTWETRERVVVALTGGPEGDTLIRRAVRIADRGKGADLLAVHVARS DGLTGANPRALARQRALVEDLGGTYHHVIGDDVPAALLDFARAENATQLVLGASR RGRFAQVLSPGIGVTTTKLSGSIDVHMVTHEEAGRGWRLPRRAHGLRPRRRLIAT AMAAIVLPLLTIGLANSRGSLNVTTDVLVYLLAVVITALVGGFWPALLAAVASSLLLN YYFFAAHHRWTIAERNNVFALVAFVLVGIMVSRVVDLAARRYTQAVRASAEAATLS VLAGSVLRGEDALPALLERVRETFGMTAATLLERTDDSRQSGPGTRNERNGQNA RSGGGVGVARTATAADADRPLLPGGRGWRAVHSVGLDPCTRPEEGDVDVPVGD NLALVLRGRPLPAADRRILAAFAVQAALALEQRRLAEAAAEAGPLAEADRVRTALL AAVSHDLRSPLASARAAVTSLRSRDVTWTPDEQAELLATADESMDRLTRLVDNLL DMSRLQAGVLSVFPRQTGLDDVVPHALDELGLPGRTVEIQVPDGLPDIYADPALLE RIVVNLAANALRHSPAGTHPVITASALEDRVELRVIDRGPGIPVENRDRVFQPFQR LGDRDNTTGVGLGLALSRGLAEAMGGSLVTDDTPGGGLTMVLTLPAAWSVQHPV PAAPPSG	6~~KdpD (3.36588E-122) ~~214,236~~Usp (1.33975E-29) ~~358,380~~DUF4118 (0.000000000021637) ~~483,X,654~~HisKA (0.000000000000582112) ~~720,771~~HATPase_c (1.71719E-25) ~~872	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1E-96	331.8	0.2	1.8E-96	331	0.1	1.4	1	B8I9I9_METNO	Histidine kinase (EC 2.7.13.3)	Mnod_0197	Methylobacterium nodulans (strain ORS2060 / LMG 21967)	907	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium nodulans, Methylobacterium nodulans (strain ORS2060 / LMG 21967)	460265	>tr|B8I9I9|B8I9I9_METNO Histidine kinase OS=Methylobacterium nodulans (strain ORS2060 / LMG 21967) GN=Mnod_0197 PE=4 SV=1 MSEPRRDPTRPSPDALLAAARREEGRRGRLKVFLGAAPGVGKTYEMLTIGRARR KAGADVVVGIVETHGRAETEVLLEGFEVIPRRRVPYRGTLLEEMDLDALLARRPAL ALVDELAHTNAPGSRHPKRYQDVEELLDAGIDVLTTLNIQHVESLNDVVASITRIRV RETVPDSILDRADDIEVVDLNPDDLIQRLKDGKVYVPQNAERALKHYFSRGNLTAL RELALRCTADRVDDELLSHMRANAIAGPWGAGERVLVCVGEDPRAAGLVRYAKR LADRLHAPWTALTVEGPRSPSLSEAERDRIADTLRLADRLGGDTVTIPGGRRIAED ILAYARSANVNHVVVGKSDRSWLFELMHGSVVHDLVRRSGTISVHVVAGEAAEAA PVPRKTVATMAATPAWGPRPYAVALLAVAAALGVALLGQPYVGVENSNLFLLSSV VAVAVRYGLGPSLLAVVAASLSYNFFFLPPVYTFTIADPTNVAAFVLFTVVAVLVSN LAARSQRVAAVAQARARATERLYGFSRKLASCGTLDDVLWATCAQVAAMLKVRV VLLLPEQDGLAVRAGYPPEDMLDDADVAAAKWAFDNDRSAGRGADTLPGAKRLF LPMRTGRGTIGVIGLDADGTGPILTPEGRRLLDALADQGALAIERVRLVEDLDRAE RAAETDRLRQALLTSMSHDLRTPLASVLGAATTLRDLDEALAPEAKRDLLATIIAES ERLNRFIANLLDMTRLEAGAVAPNLAPHDIGETVGTALRRTEAMLAGHRVAIDVPA DLPALRLDPVLFEQVLVNLLDNAAKYAPEGSTVTIRGWREGSLVRLQVLDEGEGL PEAEIERVFDKFYRVRKGDRVRAGTGLGLSIARGFVEAMGGALVAANRPDRPGA AFTLTLPVPAKDRDAAPEIAA	30~~KdpD (5.33967E-118) ~~235,257~~Usp (4.62757E-40) ~~378,434~~DUF4118 (0.000000000000493868) ~~504,534~~GAF (0.00000000000478361) ~~653,670~~HisKA (0.000000000000995726) ~~736,789~~HATPase_c (6.34984E-26) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1E-96	331.8	0.4	2.2E-96	330.7	0.3	1.6	1	G8RR39_MYCRN	Histidine kinase (EC 2.7.13.3)	Mycrh N_3443	Mycobacterium rhodesiae (strain NBB3)	840	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium rhodesiae, Mycobacterium rhodesiae (strain NBB3)	710685	>tr|G8RR39|G8RR39_MYCRN Histidine kinase OS=Mycobacterium rhodesiae (strain NBB3) GN=MycrhN_3443 PE=4 SV=1 MTDRPGSQRKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDVVAAVVETHGR KKTADLIEGIETVPPKLVEYRGKQFPELDVEAVLRRAPQVVLVDELAHTNTPGSTN PKRWQDVEELLAAGITVISTVNVQHLESLNDVVTQITGIEQQEKVPDEIVRAADQIE LVDITPEALRRRLAHGNVYAPERVDAALSNYFRRGNLTALRELALLWLADQVDAAL ERYREENQITATWEARERVVVAVTGGAESETLVRRASRIASKSSAELLVVHVVRG DGLSGVSAPQMGRVRELAVSLGATLHTVVGDSVGGVPAALLDFARDENATQLVI GTSRRSRWARIFDEGIGASVVQQSGPIDVHMVTHPEARKESLWSRISPRQRHLTS WLAAAVVPSAVCALLVLLLDPFLGVGGESALFFIGVLVVALLGGVAPATLSAVLSG VLLNYFLIEPRHTFTIAEPDNAITTVVLLAVAAAVSVLVDNAAKRARAERRASQEAE LLALFAGSVLRGADLETLLERVRETYAQRAVSMLRVNAGIVACVGDNPCVDVDSA DTAIEVGDDEFWMLMAGRKLPARDRRVLTAVAKQAAGLVTQRELAEEAGKAEAIS QADELRRSLLSAVSHDLRTPLAAAKAAVSSLRSDDIDFSAEDTSELLATIEESIDQLT ALVGNLLDSSRLAAGVLRPELGPVYLEETVQRALLGISKGTTGFRRHGLDRVKVEV GDTVAKADSGLLERVLANLVDNALRYAPDSPIRVTAGQVGNRVLIAVVDEGPGIPR DNEDRLFAPFQRLGDQDTSIGVGLGLSVARGFVEAMGGTISATDTPGGGLTVEID LAAAS	10~~KdpD (2.17877E-121) ~~219,241~~Usp (2.02045E-31) ~~365,388~~DUF4118 (0.0000022622) ~~467,X,613~~HisKA (0.00000000000193514) ~~679,736~~HATPase_c (3.72045E-27) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.1E-96	331.7	0.2	2E-96	330.9	0.1	1.4	1	Q142K6_BURXL	Histidine kinase (EC 2.7.13.3)	Bxe_A3249	Burkholderia xenovorans (strain LB400)	944	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia xenovorans, Burkholderia xenovorans (strain LB400)	266265	>tr|Q142K6|Q142K6_BURXL Histidine kinase OS=Burkholderia xenovorans (strain LB400) GN=Bxe_A3249 PE=4 SV=1 MNRPDPDELLDKLQRDEEKRQRGRLKIFFGASAGVGKTYAMLQAARRRHDEGAD VVVGIAETHGRSETAALLEGLDVLPLAQIEYRGRKLGEFDLDAALARKPQLILVDEL AHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETV PDRVFDSADEVTLVDLPAEELLDRMRDGKVYLPQQAERAVRNFFRKGNLIALREL ALRRTADRVDAQMREYRADRSIRRIWQARERLLVCVGPGPEAAPMLVRAAARLAA SLKADWIAVYVETPALQRLPDARRERTLNALKLAAELGAETATLAGADAATALIGY AQARNVSKLVAGASARTGAERWLRRPLSERIAEKAGDLDLTLIRASSGRDGGEHR HLLNTTANAWREALSAARERRSPPRAYAFALAICAAITLLASQLSDHIDLTNLVMLY LLGVIFAAVKLGRGPGVVLSFMSVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLLTS LVISHLTSSLRREASVARRREQRTGAMYAMARELAAALTTEQIVGIGSRHVSEVFG ARVAILLPDSVDQVKQKIEDPDAAVTLEGEMLDSDVGQWVYDQQKPAGHGTDTL PAAAALYLPLKAPMRTRGVLAVVTRNEGELDVPEQQRMLDAFAAQIALALERVHY VDIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAQSPDAQPNAELVEA IHEEALRMTGIVTNLLDMARLQAGSLQLNQQWTLLEETVGAALRACKRVLANHPV QVKLPADLPLLHLDAVLMERLFSNLFENAAKYTAPATPLTIGAQRLDTDGKSFVRV TVDDNGPGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEAHGGTIGALNR VSANGHVEGARFWFTLPVETPPEAPDALEDEGADALTHVDTDSESTPNPFAKPS HD	21~~KdpD (8.66115E-123) ~~230,252~~Usp (1.9741E-30) ~~374,412~~DUF4118 (6.56566E-20) ~~512,538~~GAF (2.89995E-17) ~~661,678~~HisKA (0.000000000000534028) ~~741,794~~HATPase_c (7.64922E-23) ~~904	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.2E-96	331.6	0.3	2.6E-96	330.4	0.1	1.7	1	E3I288_RHOVT	Histidine kinase (EC 2.7.13.3)	Rvan_3284	Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	905	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Rhodomicrobium, Rhodomicrobium vannielii, Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	648757	>tr|E3I288|E3I288_RHOVT Histidine kinase OS=Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299) GN=Rvan_3284 PE=4 SV=1 MADARETNRPSPDALLELARNENRGRLKIFLGAAPGVGKTYEMLLSARAKCTEGA DVVVGVVETHGRPETAALLAGYEIVPRRPVTYKGRIIEEMDLDAVLARRPQVALVD ELAHTNAPGSRHPKRYMDVEELLAAGIDVYTTLNIQHVDSLNDVVAQITRIRVQET VPDSVLDKADDIEVIDLAPDELIQRLREGKVYVPEQARRALQHYFSPGNLTALRELA LRRTAQRVDEQLLTHMKAHAIEGPWAAGDRVLVCISEDPRSAGLVRYTKRLADRL RAPWTALYIETLRSQDLSIAERDRIADTLRLAERLGGVAATLPGRGRVADDVMDFA RSNNVTQIVIGKSERSRWFEALYGSVVHDLVRRSANISVHVIAGDALNKETIPRKTV RTATSSDASALGYVAAIVATAGAVLAARLAQPYLGAETIPLMFLMGVLGIAYYFGL GASLFAAIAAMLSYNFFFIPPLYTFTIADPINISALFFFLFTALAVSNLTARVRRQAEL ARNRAAITSALYAFSKNLASNATFDDLLWAAVSQIATSLKADVVILLPETSGQLNVA AAFPPGDMIEDSDVGAAKWSLDNGFAAGRGADTLPGARRLFLPLRTGRGVIGVV GLGPGLRSDILLTPDERRLLDALMDQTAVAIERIKLAKEMDDARVAAEAERLRGALL TSLSHDLRTPLASILGAANSLREYDELFDAQAKSDLVLTIEEEAQRMSRFVANLLD MMRLESGAVKLRREPVDVTEILGAAVRRTAPLLKHCTVEFDIERDLPLLNLDPVLM EQVFVNLLDNAGKYAPPGSTITLRARTVGSSVRICVMDEGPGIPEDKLSLVFEKFH RADNGDRQRAGTGLGLAICRGFVEAMGGAISAANRSDRTGAILAISFPASSTVRLP HERSVT	22~~KdpD (6.34138E-124) ~~232,254~~Usp (4.72062E-45) ~~378,405~~DUF4118 (1.59839E-17) ~~504,530~~GAF (0.00000000000040164) ~~651,668~~HisKA (0.000000000022221) ~~734,787~~HATPase_c (5.58176E-25) ~~890	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.3E-96	331.5	0.9	2E-96	330.9	0.6	1.3	1	G8AUY1_AZOBR	Histidine kinase (EC 2.7.13.3)	kdpD_p230081	Azospirillum brasilense Sp245	919	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum brasilense, Azospirillum brasilense Sp245	1064539	>tr|G8AUY1|G8AUY1_AZOBR Histidine kinase OS=Azospirillum brasilense Sp245 GN=kdpD PE=4 SV=1 MPNDRTAAAARPSPEALLRAAAREGRGRLKLFLGAAPGVGKTYEMLLTAQAKRR DGVDVVVGVVETHGRRETEALLAGLTVLPRLKVEYKGRRLDEMDLDAILARRPAIV LVDELAHTNAPGSRHAKRYLDVEEILAAGIDVYTTMNIQHVESLNDVVARITRVRVR ETVPDSILDRADDIEVIDITPDDLIQRLKDGKVYVPRTAERAIRHYFSPGNLTALREL ALRRTAQRVDDQLLTHMQAHAIAGPWAAGERLLVCVNEDPACAAVVRYARRQAE RLRAHWTALHVETPRSLRLSEAERDRIADALRLVEKLGGEAVTIPGGDVAGTVVE YARTNNVAHIVIAKSHRGPWAELLRSSVAFRLIRQAGGISVHVIADDAEEPIPPKTV RTAAPRRPALSWWPYAAATGYVALALGIGEVLQQVLDVSNVALVFLTAVLTSAVT GGLGPSLYACVASILAFNYFFLNPLYTFSIADPENIVALFFFAVVAVIASNLTARVRA QAVTARLRAKTTEDLYGFSRKLAGVVTMDDLLWATAHQIAAMLKVHVVLLLPEGG TVSVRAGYPPEDELREADLAAAVWAWENNRPAGRGSDTLPGAKWLFLPLRTGR GPVGVVGIDTDTARTGKPGALLTPDQRRLLDALTDQAALAIERVTLAEDVDRARLA AETERLRSALLTSISHDLRTPLASILGSATSLTAYGAGMDEASRRDLAATIQEEAER LNRFIANLLDMTRLESGAIRPRTGPVDLAETVGSALGRAGRILAGHRVDVDLAADL PMLEADDVLFEQVLFNLLDNAAKYAPTGSLIQVGASREGDRVRIEVRDEGDGIPAA DVERIFDKFYRVQAQDRQRAGTGLGLAICRGFVEAMGGTIAAGNRKDRSGAVFTL TMPAAAALPDLEGPDLEGPGLEEEGTP	24~~KdpD (1.98001E-110) ~~234,256~~Usp (1.0769E-43) ~~379,405~~DUF4118 (2.43082E-16) ~~505,531~~GAF (0.000000000000116308) ~~655,672~~HisKA (0.0000000000129215) ~~738,791~~HATPase_c (8.16951E-28) ~~893	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.3E-96	331.4	1.4	1.9E-96	330.9	0.3	1.8	1	G8M761_9BURK	Histidine kinase (EC 2.7.13.3)	BYI23_A008920	Burkholderia sp. YI23	925	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. YI23	1097668	>tr|G8M761|G8M761_9BURK Histidine kinase OS=Burkholderia sp. YI23 GN=BYI23_A008920 PE=4 SV=1 MPRPTPDELLDKLHREEEKRHRGTLKVFFGASAGVGKTFAMLQAARRRRDEGVD VVIGIVETHGRKETLALLEGLETLPPARIEYKHRVITEFDLDAALQRKPQLILVDELA HSNVQGSRHLKRWQDVQELLDANIDVYTTVNVQHLESLNDIVGRITGIRVWETVP DRVFDLADEVTLVDLPPEELLDRLREGKVYLPQQAEHAVRNFFRKGNLIALRELAL RRTADRVDAQMREYRADQSIERIWRARERLIACIGPGPESATLVRAAARLAAALKA DWLAVYVETPKLQRLSDDIRKRTLDALKLASELGAETVTLDGADAAATLIDYAHMR NVSKLVAGASGKAGWRRRFERTVSERIIGQGSDIDVTLVSTGTRDANRRTLAEAF GTWRDGAHSSPRAYGYALAIGAGITLVAQGLAARQIAITNLVMLYLLGVIFAAVKLG RGPGVMLSFLSVAAFDFFFVAPELSFSVTDTQYLLTFVVMLLTSLTISHLTSSLRRE ARIASQRERRTGAMYAMTKELAAALMTEQIIEIGTRHVAEVFQSKVAILLPDAADKV RQKVGEPNPDVTLDAACLDLDIAQWVYDQQKPAGRGTDTLPASQALYLPLKAPM RTRGVLALSTGREAELAVPEQRRMIETFASQIALALERVHYVEIAQDALVNMESER LRNSLLSAISHDLRTPLTSIVGFASVLEEQAREAGGGEQASQELVHAIHEEALRMS GLVVNLLEMARLQAGAIRLNRQWSMLEETVGAALATSRRVLAGRAVQAHVPANL PLLRLDAVLMERLFANLLENAAKYTPPGTPIRIGAALEHDGDARFVRVCIDDEGPGL PSGMQHRLFDKFTRGEKESAQPGIGLGLAICRAIVETHGGQIGAENRADANGRIE GARFWFTLPANDAAPEDVPPDEDVESKAAGDV	21~~KdpD (6.20217E-124) ~~230,252~~Usp (5.23638E-29) ~~375,403~~DUF4118 (8.42113E-17) ~~504,531~~GAF (1.7134E-17) ~~653,670~~HisKA (0.00000000000455676) ~~738,791~~HATPase_c (1.94523E-23) ~~901	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.4E-96	331.3	1.3	2.2E-96	330.7	0.9	1.3	1	A0A0F0HCB2_NOCAE	Histidine kinase	UK23_07235	Lechevalieria aerocolonigenes (Nocardia aerocolonigenes) (Saccharothrix aerocolonigenes)	829	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Lechevalieria, Lechevalieria aerocolonigenes (Nocardia aerocolonigenes) (Saccharothrix aerocolonigenes)	68170	>tr|A0A0F0HCB2|A0A0F0HCB2_NOCAE Histidine kinase OS=Lechevalieria aerocolonigenes GN=UK23_07235 PE=4 SV=1 MSAKPRRGELRIFLGAAPGVGKTFSMLGEAHRRRERGTDVVIGFVETHGRAKTA QLVEGLEIVQRRHCTHRGVELTEMDVDAVLARAPEVAVVDELAHTNVPGSRNAKR WQDVEELLEAGIDVLSTVNVQHLESLNDVVQRITGVPQQETVPDEVVRKADQMQ LVDLTPEALRRRLAHGDVYAANKIDAALGNYFRVGNLTALRELALLWVADQVDVAL LRYRAEQQITDTWETRERVVVAITGGKESETLIRRARRIATRAGGDLLVVHVLRGD GLAGADPHSLQKYRKLTEDLGATFHTVVGDDVPTALLEFSRGVNATQLVVGTSRR SRFARVFSAGIGSTVVQESGAIDVHMVTHPATTSGWRGRFASSPLRPSRLALGW FLAVVGPALVTAAGASMRGSLNFSTNVIVYLLVTLVVAIVGGLGPAITAALLNALLLN FFFTEPFYTFTIDAQQNVLTFFAMIIVGVSTALVVNYAARRATQAARARTEATLLAS YARTVLTNPFPLARLLEKVKENFGLQSVALLERVDGEWERVACVGVSPCDEPDEA DVDVAVTPDVHLALRGRSLPASDRRVLEAAAGQALLALRQQRMAEQALETQRQA SRTELRTALLSAVGHDLRTPLTSIKASVGSLRDPELKLSGSDTAELLEAVEESADRL TGLVDNLLDSSRLATGAVEPQFRAVGYYEAVARALSGLSGDIEVDVPESLPPVRA DVGLLERVIANVVGNALRYAGAVALRASAHGSEVELRVVDHGRGLPRGTADQVF APFQRLGDRTPGGVGLGLSVAKGFTEAMGGTISMEDTPGGGLTVVISLPVEEKVS	5~~KdpD (4.47596E-123) ~~215,237~~Usp (7.80667E-26) ~~358,384~~DUF4118 (0.00000051048) ~~479,X,612~~HisKA (0.00000000000436772) ~~677,725~~HATPase_c (1.32946E-22) ~~822	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.5E-96	331.2	0.2	2.7E-96	330.4	0.1	1.4	1	V5XI24_MYCNE	Histidine kinase (EC 2.7.13.3)	D174_21895	Mycobacterium neoaurum VKM Ac-1815D	838	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	700508	>tr|V5XI24|V5XI24_MYCNE Histidine kinase OS=Mycobacterium neoaurum VKM Ac-1815D GN=D174_21895 PE=4 SV=1 MTDRPKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDLVAAVVETHGRSKTA ELLEGIEIIPPRLVEYRGATFGELDVDAVLARRPQVVLVDELAHTNTPGSANPKRW QDIEQLLAAGITVITTVNVQHLESLNDVVAQITGIEQQEKVPDEVVRAADQIELVDIT PEALRRRLSHGNVYAPDRIDAALSNYFRRGNLTALRELALLWLADQVDAALAKYR SDNKITATWEARERVVVAVTGDKESETLVRRASRIASKSSAELMIVHVVRGDGLA GVSAPMMGTVRDLAASLGASVHTVVGDDVPAALLDFAREMNATQLVVGTSRRTR WARILDEGIGAAVVQNSGTIDVHMVTHEQTGRATARSGNRNWRQHAASWLAAV VVPTALAAVAVLWLDRYLGVSGESALFFVGVLAVALLGGVAPAALSAVLSGLLINY FLAEPRYTFTISEPDSAITIAVLLMVAVAVAALVDSAAKRAREARRASQEAELLAHF AGSVLRGADPTALLERVREVYSQTAVSLLRERDGETHVVACAGKQPCVDVDSAD TAIEVGDDEFWLLMSGRKLPAKDRRVLGAVAKQAAGLVRQRELISEAGRAEAVAR ADELRRSLLSAVSHDLRTPLAAAKASVSSLRSSDIDFSPEDTAELLATVEESVDQLT ALVGNLLDSSRLAAGVVKPELRRVYLEEAVQRALLGISRSSKDSGWDRVKVDVGD AVALADPGLLERVLVNVIDNALRYGGDNPVRVNAGRVGERVLITVADEGPGIPRG AEEQLFAPFQRLGDQDNSTGVGLGLSVASGFVTAMGGTISATDTPGGGLTVVIEL AAPQEGPQP	5~~KdpD (1.15881E-122) ~~215,237~~Usp (1.29367E-32) ~~358,381~~DUF4118 (0.000000390734) ~~464,X,609~~HisKA (0.00000000000314337) ~~675,729~~HATPase_c (1.44929E-24) ~~829	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.5E-96	331.2	0.6	1.5E-96	331.2	0.4	2	1	V9XNV1_9NOCA	Histidine kinase (EC 2.7.13.3)	Y013_25420	Rhodococcus pyridinivorans SB3094	843	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus pyridinivorans, Rhodococcus pyridinivorans SB3094	1435356	>tr|V9XNV1|V9XNV1_9NOCA Histidine kinase OS=Rhodococcus pyridinivorans SB3094 GN=Y013_25420 PE=4 SV=1 MTSTAPNTSRPLRRGRLRIYLGAAPGAGKTFAMLGEAHRRLVRGTDVVVAIVDTH GRARTAEQLAGLEIVPPRRRTYRGTEFEELDLDAVLARRPAVALVDELAHTNAPG SRHPKRWQDVEELLDAGIDVLSTVNIQHLESLNDVVEQITGVVQRETVPDDVVRR AEQVELVDITPQALQRRLAHGNVYAAEKIDAALRNYFREGNLTALREIALLWLADQ VDVALAKYRGDHAITATWEARERVVAAVTGGPESETLVRRASRIAGRAGAELMVV HVVRGDGLTGVSAPQMTKVRTVAESVGASVHSVVGDDVPTTLLDFAREVNATQL VIGTSRRSRWARILDEGISSAVVRDSGRIDVHMVTHEHTSRAPKMALLGRHDHRL QSWIAAILIPFVATALMAGVDRLSGVAGQNALFFVVILVVALFGGVGPAIVAALLSG LLLNFFFTEPRYSFTIAEPDNFVTTIVLLVVAVAVAALVDAASARAREARLASQEAEL LASFAGAVLRGADLPQLLEKVRETYSQDGVSLLRSDRNSPKLLGTAGTAPPMSQH AADTACEVDDSAYALLLAGPQLRARDRRILTAVAGQAAALVRQQELAAEASHASS LAETDRLRRLLLSAVSHDLRTPLAAIKASASSLRSTDIEFSPEDTAELLATIEESTDQ LTALVSNLLDSSRLAAGVITPVVTPVYLDEVIHRALLTLTNGESELSRTIRERIHIDVG EATVAADGALLERVVANLLDNALRYAPTGPIRVESITSDGRTVLTIADTGPGLHHKD TDTFPRAGDHRATGGAGLGLTVARGFVEVMGGNLTTTDTPGGGTTMVVDLAAAP VEVRP	13~~KdpD (4.60305E-120) ~~222,244~~Usp (8.31841E-33) ~~365,388~~DUF4118 (0.000000000610547) ~~466,X,615~~HisKA (0.000000000000280297) ~~681,738~~HATPase_c (3.18853E-17) ~~818	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.7E-96	331.1	0.2	2.9E-96	330.3	0.1	1.4	1	Q6N5H3_RHOPA	Histidine kinase (EC 2.7.13.3)	kdpD RPA3001	Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	907	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Rhodopseudomonas, Rhodopseudomonas palustris, Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	258594	>tr|Q6N5H3|Q6N5H3_RHOPA Histidine kinase OS=Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009) GN=kdpD PE=4 SV=1 MPDPRVEPPSRPSPDALLEQARRQEPGTGRLKVFLGAAPGVGKTYAMLQSAHAR AKAGVDVVIGYAETHGRAETEALLAGLETVPRRRIPYKGQVLEEMDLDAVLARRP QLAIVDELAHSNAPGSRHPKRYLDVLELLANGIDVYTAVNIQHIESLNDVVAQITTV RVRETVPDSAFERADAIELVDLTPDDLIQRLKEGKVYVPKQAERALEHYFSPGNLT ALRELALRRTAERVDEQLLSHMQANAIPGPWAAGERVLVCVSHDQRSQGLVRYT KRLADRLRAPWTAINIETRRSLSLTEQQRDRLADTLRLAEALGGEALAIPGGDRSL AHDILAFARANNITQIVVGKAPRSFWYEALRGSTVHELVRGSGNISIHVMTGTAVSI EESQTGSLRPAEGTEPFNPWPYPMALVLVGIGLGVAKLIEPFFSIENVDLVFLTAV VGVAVRYGLGPSLLASVVASLCYNFFFLPPVYTFTITDPTNIVAFFFFMLIAILVSNL AGRVRAQATAAAQRVRTTESLYAFSRKLAGTAALDDVLWATAYQIALMLKVRVVL LLPEQGRIAVKAGYPPEDQLDPADLAAANWAWENDRVAGRGSDTLPGAKRLFLP MRTGRGPIGVIGIDDDRAGALLTPDQRRLLDALTDQGALAIERVHLVEDMDRVKRD AESDRLRQALLTSISHDLKTPLAAVLGAATTMRDLASHLSDAQRTELIGTIVEESER LNRFIANLLDMTKLESGAVVPNSAAHDLGELVGATLRRATSILAQHTVKLDLGHDL PLIEVDPVLFEQALFNLLDNAAKYAPAGSAIQLRAAQSGGQVELQVRDEGEGIPPA ELETVFDKFYRVRKGDHIRPGTGLGLAIARGFIEAMGGRLSAGNRSDRSGAAMTI RLPIASRGDALISAA	29~~KdpD (5.65846E-123) ~~236,258~~Usp (1.45799E-43) ~~383,414~~DUF4118 (7.13981E-16) ~~504,537~~GAF (0.000000000000976868) ~~655,672~~HisKA (0.0000000000996812) ~~738,791~~HATPase_c (1.54813E-24) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.8E-96	331	0.3	3.1E-96	330.2	0.2	1.4	1	C5APB1_METEA	Histidine kinase (EC 2.7.13.3)	kdpD MexAM1_META1p0132	Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	905	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium extorquens group, Methylobacterium extorquens (Methylobacterium dichloromethanicum) (Protomonas extorquens), Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	272630	>tr|C5APB1|C5APB1_METEA Histidine kinase OS=Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1) GN=kdpD PE=4 SV=1 MPGTGRDPNRPSPDALLEAARREERTRGRLKVFLGAAPGVGKTYEMLTIGRARLT AGADVVVGVVETHGRAETEALLEGFETIPRRAVPYRGTVLEEMDLDALLARRPAL ALVDELAHTNAPGSRHPKRYQDVEELLDAGIDVLTTLNIQHVESLNDVVASITRIRV RETVPDSILDRADDIEVVDLNPDDLIERLKAGKVVYVPANAERALKHYFSRGNLTALR ELALRRTADRVDDELLSHMRANAIPGPWAAGERVLVCVSEDPRSAGLVRYAKRLA DRLHAPWTALVVEGPRAASLSEAARDRVAEALRLADRLGGDAVTLPGGRRIADDI LAYARAANVNHIVVGKATRSWIFELVNGSVVHDLVRRSGNISVHVVPGEAAPAET ASRRAVATAAPPATFDARSYALALLVTGAGLGLALLLEPSTGVENADLMLLTAVVA VAVRWGLGPSLAAVVAASLSYNFFFLPPVYTFTIADPTNVAAFLLFTLVAVLVSNLA ARARLSAVVSQGRAKATERLFGFSRKLAACGTLDDVLWATSAQVAAMLRVRVVL LLPDAQTVAVRAGYPPEDMLDEADLAAAQWAFDNERPAGRGADTLPGAKRLFLP MRTGRGTIGVIGLDADGTGPILTPEGRRLLDALADMGALALERVRLVEDLDRAERA AETDRLARALLTSISHDLRTPLASVLGAASTLRDLEGALPVESKAELLTTIIEESERL NRFIVNLLDMTRLEAGAVAPNLAPQDVAETIDTALRRTQKILAGHRVAVEIAPDLPT LRLDPVLFEQVLVNLLDNAAKYAPEGSTVTLRARQDGRTVRIEVLDEGFGLPEADV ERVFDKFYRVRKSDRVRAGTGLGLAISRGFVEAMGGTVTAGNRRDRLGAAFTVM LPVPARTTPRDIAA	27~~KdpD (3.04116E-115) ~~235,257~~Usp (3.55982E-40) ~~381,434~~DUF4118 (0.00000000000252316) ~~506,534~~GAF (0.0000000000855798) ~~653,674~~HisKA (0.0000000000454645) ~~736,789~~HATPase_c (9.04499E-26) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.9E-96	330.9	0	2.9E-96	330.3	0	1.3	1	C7Q1T4_CATAD	Histidine kinase (EC 2.7.13.3)	Caci_6794	Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897)	891	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Catenulisporales, Catenulisporaceae, Catenulispora, Catenulispora acidiphila, Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897)	479433	>tr|C7Q1T4|C7Q1T4_CATAD Histidine kinase OS=Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897) GN=Caci_6794 PE=4 SV=1 MSARGNLRVYLGAAPGVGKTYHMLDEAQRRAERGGDVVVGFVETHGRPHTQA MVDGLEIVPRRRMEYRGSDFEEMDIDAVLARQPSVVLIDELAHTNIPGSRNTKRW QDVEELLAAGIDVIASVNIQHLVSLNDVVQKITGVPQRETVPDEVVRSADQIELIDM APEALRRRMAHGNIYQPEKIDAALSNYFRPGNLGALRELALLWVAGRVDEALQRY RDQHGIDKVWETRERIVVALTGGPEGATLIRRGARIAQRVGAKGSDLLAVHVARS DGLTGASPALLAEQRALVESLGGTFHSVVGDDIPNALLQFARAENATQLVIGVSRR GRLERFLGGYGIGETVVQQSGDIDVHMVTHERSAADQSRWMWARRVLRQPETG PRWWGPVAGLIVPILLTLVLANVRSGLNLTNQVLVFLAGVVAVARLGGLLSAFFAS LTASLLLNYYFIRPFYRLTINDPQNILALVVFALVALIVASVVDFASRQERRAGKASA EAETLSELARSVLRGDEAIGALLGRFRETFGMESVALLERVEPGSPVLPDETDDPD AWRIVAATSAGGEMPCRTPGEGNVVVHAGPDAMLVLRGRALPAADQHVLTAFAA QAAVALERSRLARQAAEAVPLAAADKMRTALLAAVSHDLRTPLAAAKLSVASLRDT TVQWSEEDRADLLSGAEESLDRLSRLVENLLDMSRLQAGALNLRLEDVAIEDVAA MALDSLGIEGSLVEFGDLSGVSEVLADPVLLERAVANLIANALKHGSLNRPVLLAAS ELAGRVELRVTDRGPGVRPEDWERIFTPFQRLGDRDNTTGVGLGLALSRGLVEA MGGALTPEETPGGGMTMVVSLPAAGMAGNEDDSGDGTGNGSGDGEHDVEVTA ALAAAEEPAR	2~~KdpD (1.2415E-118) ~~212,234~~Usp (1.78287E-33) ~~359,389~~DUF4118 (0.00000000168356) ~~488,X,632~~HisKA (0.000000000000707417) ~~698,749~~HATPase_c (2.92252E-22) ~~850	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.9E-96	330.9	1.1	3.2E-96	330.2	0.8	1.4	1	F8JAZ5_HYPSM	Histidine kinase (EC 2.7.13.3)	kdpD HYPMC_3099	Hyphomicrobium sp. (strain MC1)	907	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium sp. (strain MC1)	717785	>tr|F8JAZ5|F8JAZ5_HYPSM Histidine kinase OS=Hyphomicrobium sp. (strain MC1) GN=kdpD PE=4 SV=1 MAEENRTPDHRPSPEALLEVLKREERQKGRLKIFLGAAPGVGKTYEMLRTARAKV KEGADVVVGVVETHGRKETKALLRGLDVVPPRQVEYKGRTLEELDIDAVIARRPEI ALIDELAHTNAPMSRHPKRYLDVEELLDEGIDVFTTINIQHIDSLNDVVAQITGIRVR ETVPDSILARADDVELVDITPEDLIQRLKEGKVYVPDQARRALENFFSPVKLTALRE LALRRTAERVDEQLVTQLRAKAMSGPWAACERVLVCVNEDVRSSGLVRYAKRAA DRLHAQWTAVTIETRRSLRFSEGERNRIAEAMRLAELLGGETLTMPGSSKSIADDII SYARAHNVTQIIVGKSDRPRWFEILNGSVVHDLVRQSGNISVHVISGEQLPAEPAT AQTVRTARDQPQHRPLNYFITFIAMAAALGVAWVLRPWIGVESVDLIFLTAIVGVA AKLGIGPSLVASVAGALLYNYFFLPPLFTFTIADAKNVAAFLCFVVVAIVVSNIAARM RSQTVIAMNRASTTESLYGFSRKLAGTGTLDDVLWATVFQIASMLKVRVVLLLPEN GSIAVKAGYPPEDMLDPSDIAAATWAWTNDRPAGRGSDTLPGSPRLFLPLRTAR GIVGVVGIDSDRPGPLLTPDQRRLFDALVNQGALAIERVHLVEDVERAKRSIETERL RAALLTSLSHDLKTPLAAILGAATTMRDLGDKFDAEAQSELLATIIDESERLNRFIAN LLDMTKLEAGAIVAKTEIQDVGEIVDAALKRARKILSRHKVQANLPSEPLKVDADPV LLEQVLFNLLDNAAKYAPENTLIEVGAWNDHGLVVIQIRDEGPGIPDRDVEKIFDKF YRANKADHVRAGTGLGLPISRGFIEIMGGTITAGNRPDRSGALLTVTLPASARSET LENAA	27~~KdpD (1.36501E-123) ~~236,258~~Usp (2.57614E-42) ~~383,410~~DUF4118 (9.78214E-16) ~~510,536~~GAF (3.56799E-14) ~~655,672~~HisKA (0.00000000000231245) ~~738,791~~HATPase_c (3.10067E-26) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.1E-96	330.8	0	3.5E-96	330	0	1.4	1	A0A0B5EJU1_9ACTN	Histidine kinase (EC 2.7.13.3)	SLNWT_1393	Streptomyces albus	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albus	1888	>tr|A0A0B5EJU1|A0A0B5EJU1_9ACTN Histidine kinase OS=Streptomyces albus GN=SLNWT_1393 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAYAEPHERPRTEILLHG LEQLPRRELCHRGAAFTEMDVDAALERRPAVALVDELAHTNIPGSRNAKRWQDV EELLAAGIDVVSTVNIQHLESLGDVVESITGVRQQETVPDEVVRHADQIELVDMSP QALRRRMAHGNIYQPDRVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYR GEHDIRSTWQARERIVVGLTGGPEGRTLIRRASRMAAKGSGSEILAVYIARSDGLT AASPKELAVQRTLVEDLGGTFHHVIGDDIPSALLEFARGVNATQIVLGSSRRKAWQ YVFGPGVGMTVARDSGPDLDVHIVTHEEAAKGRGLPVTRGARLGRPRLIAGWIIG VAGPALLALLLHEFDSDLGLANDVLLFLSLTVAAALLGGLLPALASAAVGSLLLNWY FTPPVRRITIADPSNIVALVVFIAVAVAVASVVVDLAARRTHQAARLRAESEILSFLAG SVLRGETTLDALLERVRETFAMDSVALLERESDVAPWTSAGSVGPNPCVRPEDA DVDMPVRDTMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLQSEAEQARALA EGNRIRTALLAAVSHDLRTPLSAIKAAVSSLRSDDIAWSEQDQADLLEGIEDGADRL DHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVALDIPESLPMVAV DPGLLERAVANVVENAVKYSTGASRVLVAASALGDRVELRVVDRGPGVPEEAKD RIFEPFQRHGDAPRGAGVGLGLAVARGFAEAMGGTLAAEDTPGGGLTMVLTLRA PAPRPPAAAEPSGRAAR	1~~KdpD (4.07308E-122) ~~211,233~~Usp (2.78521E-30) ~~356,X,612~~HisKA (4.09453E-14) ~~678,727~~HATPase_c (7.06519E-27) ~~828	kinase	KdpD;Usp;X;HisKA;HATPase_c

	2.1E-96	330.8	0.5	4E-96	329.8	0.3	1.5	1	R5AGZ3_9CLOT	Histidine kinase (EC 2.7.13.3)	BN452_00246	Clostridium sp. CAG:1013	888	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:1013	1262769	>tr|R5AGZ3|R5AGZ3_9CLOT Histidine kinase OS=Clostridium sp. CAG:1013 GN=BN452_00246 PE=4 SV=1 MEVAFNGHIENQRQGSLKIFFGYAAGVGKTYAMLEAAHQAQKQGIDIVVGYVERH TRPDTLALLEGLEQLPNREIEYKGIKLKEFDLDAALKRHPQIMLVDELAHSNAAGCR HAKRYQDVEELLRAGIDVYTTVNVQHLESLNDLVASITQVAVSERIPDSVFDSADQ VELVDIEPDDLIARLQSGKVYRKNQASRALNHFFTRDNLAALREIALRRTADRLSRN AQKSGNETVAKAGEHILICLSSSPSNAKVIRTAARMAEAFHSGFTALFVETPETKEL KGESLKRLRDNLRLAEQLGAQIATVYGDDPAVQIAEYAKVSGITKIVLGRTNHQSKI FLRSKTLADKLTKLAGDIDIYIIPDAQPFYKRKFNLLRKEEQKFRWIDLLKVVLITLLT TIISFGFYATGLREANIIIVYILGVLITAIWTHGHLYGALASLLSVISFNFFFTVPRFTLE ATDPDYPVTFLIMLTASIISSSLATRVKKQARQSAQKAYYMELLMNSSQKMQQGR DEQEIIALAAEQIRALLDRPVLYSLAMKGKELEFQVCPQSETNKMIGAMTAEEIGVA DWVVKNNKHAGATTNTLSHAQNLYLSVRGNQEVMGVIGIPSKYYPPLEVFEKNLLI SLLNECGLILERRRLRAEKQAIEMETQRERLRSNLLRAISHDLRTPLTSISGNAGVL MEKSILLDEDKKQEIYSSIYDDSMWLVNLTENLLSITRIENGTMHLQMNAELIDDVF REAISHIDRKASEHELSVELADDLLMAKMDVRLIVQVIINIVNNAIKYTPEGSHICLSA QKEKKMVRIRISDDGPGISDEAKQHLFDMFYTADIGKADSRRGLGLGLSLCKSIVD AHGGELSVSDNKPHGAVFSFTLPLEEVNFDHV	13~~KdpD (9.67315E-124) ~~222, 240~~Usp (9.26068E-36) ~~363,388~~DUF4118 (1.05129E-16) ~~489,X,656~~HisKA (0.000000000715072) ~~722,775~~HATPase_c (3.41519E-28) ~~878	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.5E-96	330.5	0.1	4.6E-96	329.6	0.1	1.5	1	R6BNL0_9CLOT	Histidine kinase (EC 2.7.13.3)	BN513_00389	Clostridium sp. CAG:169	900	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:169	1262778	>tr|R6BNL0|R6BNL0_9CLOT Histidine kinase OS=Clostridium sp. CAG:169 GN=BN513_00389 PE=4 SV=1 MSENNLMADKLLKAIQEEERDKTRGHLKIFFGYAAGVGKTYAMLKAAHEAKQRGI DVIAGYIEPHARPKTAALLHGLEVLPSKSVPYNGITLREFDIDAALQRKPQLILVDEL AHTNADGSRHAKRYQDIKELLYAGIDVYTTVNVQHIESLNDMVASITGVFVRERIPD SIFDQADQVELVDIEPQELIERLKEGNVYRESQAKRAVNNFFTVENLTALREIALRR CADRVNILTENSRIKSHGDYHTDEHILVCLSSSPSNAKLIRTAARMANAFRSDFTAL FVETPAFSAMKVEDKKRLQDNVHLARQLGAKIETVYGDDIPLQVAEFARLSGVSKI VIGRSVAAKKHLFSKPTLTEKLIAYAPNLDVYIIPDTTSAPVSYYAKKAKGIRHLVYS PADLAKSIGILLAASGIGFLFQKLGFAEANIITVYVLGVLLTSAITTHWIYSLISSIVSVL LFNFLFTVPRFSLEAYDQGYPVTFIIMFLAALLTGSLATQLKNHAKQSAQAAYRTKV LFDTNQILQQEKNQEDIISATSRQLVKLLGRGIVFYPVENGLLGEARTFSPDGNVLD NSCLSVNEQGVAKWVLKNNKHAGATTDTLSDAKCLYLAVRIMDRVYGVVGIVIGQ QPLDAFENSILLSILGECAMSLENEKNAREKEEAAILARNEQLRANLLRAISHDLRT PLTSISGNASNLLSNGKSFDEDTKLQLYTDIYDDSMWLINLVENLLAVTRIEEGRLNI RASANLIDEVIAEALHHVNRKSVEHCITVEHEEDFILAKIDARLIVQVIINIVDNAIKYT PKGSHIQIKTRKQDEHVIVTVADDGEGIPDELKPKVFDMFYSGANKIADSRRSLGL GLSLCKSIIHAHGGTISVSDNIPHGTVFTFTLPAEEAQIHE	24~~KdpD (6.98954E-125) ~~232,252~~Usp (1.73157E-35) ~~375,402~~DUF4118 (0.000000000000050691) ~~503,529~~GAF (0.00014528) ~~652,669~~HisKA (0.0000000017785) ~~735,788~~HATPase_c (1.46829E-29) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.5E-96	330.5	0.6	4.1E-96	329.8	0.4	1.4	1	A0A0D5EL36_9BURK	Histidine kinase (EC 2.7.13.3)	BW23_2577	Burkholderia ubonensis MSMB22	951	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	1249668	>tr|A0A0D5EL36|A0A0D5EL36_9BURK Histidine kinase OS=Burkholderia ubonensis MSMB22 GN=BW23_2577 PE=4 SV=1 MNRPDPDQLLDKLQRDEEKQRRGQLKIFFGASAGVGKTYAMLQAARQRRQEGV DVVVGIVETHGRSETAALLDGLDVLPLAKLDYRGRALAEFDLDAALARKPELILVDE LAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWET VPDRVFDAADEVTLVDLPAEELLERMRDGKVYLAQQAERAVRNFFRKGNLIALRE LALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPTLVRAAARLAA SLKADWIAVYVETPRLQRLPDAQRERTLNALKLAAELGAETATLAGGDAVAALIGY AKVRNVSKVVAGGSRKTGLARWFARPFGEKLAERAGDVDLMLIRASASDEVRAA PLDARARDWRDAFARLGGHRSPPRHYAYAAAICAAITMVATVVSERLDLTNLVML YLLGVVFSAVRLGRGPGVLQSFLSVAAFDFFFVPPRMSFSVSDTQYLLTFFGMLL TSLVISHLTSTLTREASIAQRRERRTGAIYAMARELAAALTIEQIVEIGSRHVSEVFR ARVAILLPDSADKVQQKIEEPDAAVTLTGPDLDNDVGQWVYDQQKPAGHGTDTL PATAALYLPLKAPMRTRGVLAIVSTDPRELEEPEQQRMLDAFAAQIALAIERVHYVE IARDALVSMESERLRNSLLSAISHDLRTPLTTIVGFSSMLANARAAATRGDATAAPR HGPREDELVEAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGAALA ACRRVLARHPARVALPADLPLLQMDAVLMERLFTNLFENAAKYTPADTPLEIGAQC VTEDGQPFVRVHVDDHGPGLPPGMETRIFDKFTRGEKESATPGIGLGLAICRAIVE AHGGRIGALNRIGPDGRVTGARFWFTLPVDTPPAAPAVSDDEADALRALPFAPSS SEPPRDHE	21~~KdpD (6.06801E-122) ~~230,252~~Usp (2.38127E-33) ~~374,422~~DUF4118 (6.34598E-19) ~~510,536~~GAF (2.23256E-18) ~~659,676~~HisKA (0.0000000000173651) ~~752,805~~HATPase_c (3.91477E-22) ~~915	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.6E-96	330.5	0.3	3.8E-96	329.9	0.2	1.2	1	F4CT89_PSEUX	Histidine kinase (EC 2.7.13.3)	Psed_4144	Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	857	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Pseudonocardia, Pseudonocardia dioxanivorans, Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	675635	>tr|F4CT89|F4CT89_PSEUX Histidine kinase OS=Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190) GN=Psed_4144 PE=4 SV=1 MMAVGQGVERVGRAGELRIYLGAAPGVGKTFAMLGEARRRCERGTDVVVGLVE THGRPRTAELLEGLEVLPRREVVRGGNVLTELDVEAVLARRPDVVLVDELAHTNA PGSRHAKRWQDVEEILAAGIDVLSTVNVQHLESLNDVVQRITGVRQRETVPDGFV RRAEQIELVDITPEALRRRLAHGNVYAAEKVDAALANYFQPGNLIALRELALLWVA DEVDVALQRYRSDKHIRETWETRERVVVALTGGPESETVLRRAARIAKRAGQADL LAVHVLRGDGLAGAPVGAAARLRTLADDVGASFHTVVGDSGASGVTDSLLEFAR GVNATQLVLGTSRRSRLARLFDPGIGARVVQESGSIDVHMVTHDAAGSALRLPTL RSNVPGGRRMLGWVLCVLAPVAATALGVALRGIVGLSTDVVLFFLATVVAALVGG LGPALVAAVLGVLMLNFFLTPPLYSLTIGETENVVTLVAMLLVAVLVALVVDRAARR AEQAARARTEAALLASFARTVLTRADPLPRLLEKVREAFGLRCVALLERGDGAAG WARIAVSGPAECGRPEDAEVDVAVEAGLHLVGTGRSLPAHDRRLLEVVGGQALV ALRSQRAAADAVAAQRRAEANETRSGLLSAVGHDLRTPLTSIKASAGSLRDPSLPL SDADRAELAATIEESADRLTGLVDNLLDSSRLAAGAVTPLLEPLGYAEVVARALLGL PGAERIDLDVAEDLPDVCADAGLLERVVANLLDNALRHGDGAAVAVRGSAYADRV ELRVVDAGPGVPPRQRDRLFTPFQRLGDRGTGTGLGLSVARGLTEVMGGTLTAE DTPGGGLTVVVSLPAVALRSSGSTAPGSTAH	12~~KdpD (5.88155E-121) ~~222,244~~Usp (5.29401E-20) ~~370,396~~DUF4118 (0.0000000100383) ~~474,X,625~~HisKA (0.000000000000943728) ~~691,741~~HATPase_c (2.01265E-24) ~~839	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.6E-96	330.4	0.2	6.2E-96	329.2	0.1	1.7	1	Q7CJR5_YERPE	Sensor for high-affinity potassium transport system (Two-component regulatory protein sensor kinase KdpD) (EC 2.7.3.-)	kdpD kdpD 1 y1262 YP_2492 YPO2689	Yersinia pestis	908	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia pseudotuberculosis complex, Yersinia pestis	632	>tr|Q7CJR5|Q7CJR5_YERPE Sensor for high-affinity potassium transport system OS=Yersinia pestis GN=kdpD PE=4 SV=1 MVDAEPTRPNPDSLLAVANEKPRGRLKVFFGACAGVGKTYAMLQEAQRLRAQGL DVLVGVVETHGRSETAALLEGLTALPLKRIHHRNRQIREFDLDAALARRPALILMDE LAHSNANGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGGVTGIRVRET VPDHMFDEASEVVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIALREL ALRRTADRVDDQMRAFRDTQGRERVWHTRDAILLCIGHHAGNEKLVRTAARLAA RLGCIWHAVYVETPRLHGLPEAKRRAILRTLKLAQELGAETATLSDPSEEQAVLRY AREHNLGKIIIGRRTEQHWKLRGSFADRLGKLGPDLDLVIIALDADPPTNVAKEPDS RPFTEKWRMQLRGCVAAIALCALITVLSLWLIPRFDQANLVMVYLLGVVIIALFYGR WPSVLAAVINVASFDLFFVQPHWSLAVTDVQYLLTFGVMLIVGIVVGNLTAGVRYQ AKIARYREQRARHLYEMSRSLSRALTPEDIAKTSRHFLSSSFQAKTSLLLPQEEGH LQPIMPDDGGILSVDDAIAHWSFNQGAPAGAGTDTLPGVPYQLLPLTAAQQTYGV LAIEPANLRQLMVPEQQRLLQTFTSLIANALERLHLARSAELAKLDAEREQLRNSLL AALSHDLRTPLTVLFGQAEILTLDLAAEGSRHAPQANQIRQQVLSTTRLVNNLLDM ARIQSGGFNLRKEWQSLEEIIGSALYMLETTLSQHQIRVELPDEMVLINCDASLLER VFINLLENAHKYAGHAALLGIRAEVQGEWLNVDVWDNGPGVTIGQENLIFDKFSR GNKESAIPGVGLGLAICRAIIDVHGGRIWVEKRQEGGASFRFVLPLEKVPEIDADNI DTNNIDTENNDIS	23~~KdpD (9.32591E-124) ~~231,254~~Usp (1.98006E-39) ~~374,404~~DUF4118 (3.16208E-24) ~~502,528~~GAF (2.81733E-15) ~~646,663~~HisKA (0.000000000129128) ~~728,781~~HATPase_c (3.52491E-26) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.6E-96	330.4	0.4	4.4E-96	329.7	0.3	1.4	1	D5MJR3_9BACT	Histidine kinase (EC 2.7.13.3)	kdpD DAMO_0414	Candidatus Methylomirabilis oxyfera	900	cellular organisms, Bacteria, unclassified Bacteria, candidate division NC10, Candidatus Methylomirabilis, Candidatus Methylomirabilis oxyfera	671143	>tr|D5MJR3|D5MJR3_9BACT Histidine kinase OS=Candidatus Methylomirabilis oxyfera GN=kdpD PE=4 SV=1 MTVMSEHRPDPEALLARVKEEAAREKRGKLKVFLGAAAGVGKTYAMLEAAREQR AEGVDVVAGLVETHGRPETEALLQGLEILASHRLEYRGTTLKEFDLDTALTRHPTVI LVDELAHTNAPGSRHTKRWQDVMELLGAGIHVYTTLNVQHLESLNDIVTRITGTVV RETIPDSVLEQADEIELIDLPPDDLLQRLKEGKIYVPELAKEAIGNFFRKGNLTALRE LALRRTADRVDAQMRAYMSDQAIPTTWPVTERLIVLVGPSPHSAQTVRGAKRMA AALRAEWIAVYVETEAYARLSETDRRRVAENLRLAEQLGAEVVTLSGSQTNESAA VLRYANERNVTKIILGKPTRSLWRRIVAGSIVDALVRGSGDIDIYVISGTGIPHAPVA RVERAPEPDWSAYGRAATVVALCTAVAWLMYPYFELSNLIMVYLLGVTGVAARS GPGPSVLASILSVAVFDFFFVVPHFTFRVADAQYLVTFAVMLVVALVISGFTVRIRI QAESARQRERRTAALYALSRELASARGVEHVLRAAGRHIADVFGGQVAVLLPDPS GHLGLQVGPSAQFEVTPSERGVAQWVYEHGQTAGCGTSTLPGAKVLYLPLVAS QGILGVLGLLPADPHSLEAPEQLHQLETFANQTALALERTQLAAAAQEAQVRAEA EKLRSSLLSSVSHDLRTPLATITGAASSLLEGDKILDDQTQQDLLESLLEEAERLNR LVNNLLEMTRMESGTLQVRKEWHVLEEVVGAALGRLTKLLCDRPVTTSLPADLPL VPIDDVLIEQVLINLLDNAIKHTPPDGGPLEITVRAHNSMVTVEVADRGPGLPPGDEE RVFEKFYRGYGLTSRGTGLGLAICRGIVEAHGGRIRAENRPGGGVAFRFTIPLTGT PPELEGIDV	25~~KdpD (2.81586E-123) ~~235,257~~Usp (3.8415E-41) ~~382,411~~DUF4118 (0.00000000000012724) ~~502,531~~GAF (1.48595E-14) ~~650,679~~HisKA (0.0000192606) ~~733,786~~HATPase_c (2.26518E-32) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.7E-96	330.4	0.3	6E-96	329.3	0.1	1.7	1	W8TZ56_YEREN	Histidine kinase (EC 2.7.13.3)	kdpDLC20_01655	Yersinia enterocolitica LC20	899	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia enterocolitica, Yersinia enterocolitica LC20	1443113	>tr|W8TZ56|W8TZ56_YEREN Histidine kinase OS=Yersinia enterocolitica LC20 GN=kdpD PE=4 SV=1 MVDAEPTRPNPDSLLAVANEKSRGRLKVFFGACAGVGKTYAMLQEAQRLRAQGL DVLVGVVETHGRSETAALLAGLAILPPKRIHHRNRQVREFDLDAALARHPALILMDE LAHSNAHGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGGVTGIRVRET VPDHMFDEATEVVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIALREL ALRRTADRVDDQMRAFRDTQGRERVWHTRDAILLCIGHNSGNEKLVRTAARLAA RLGCIWHAVYVETPRLHRLPEAKRRAILRSLKLAQELGAETATLSEPCEEQAILRYA REHNLGKIIIGRRTEKHWKLRGSFADRLGKLGPDLDLVIIALEGDTPSSVVKETDSR TFTEKWRMQLRGCAAAIGLCALITILSQWLIPGFDQANLVMVYLLGVVIIALFYGRW PSVLAAFINVASFDLFFVQPHWSLAVTDVQYLLTFAVMLIVGIVVGNLTAGVRYQA RIARYREQRARHLYEMSRGLSRALTAADIAKTSRHFLSSSFQAKTDLLLPQEDGRL QQITTDEGGALSVDEAIARWSFDRGAPAGAGTDTLPGVPYQLLPLTASQQTYGVL AIEPANLRQLMVPEQQRLLQTFTSLIANALERLHLARSAELAKLDAEREQLRNSLLA ALSHDLRTPLTVLFGQAEILTLDLAAEGSRHAPQANQIRQQVLSTTRLVNNLLDMA RIQSGGFNLRKEWQSLEEIVGSALHMLETTLSHHQIRVELPGDMVLINCDGSLLER VFINLLENAHKYAGYDALLGIRATVQGEWLNVEVWDNGPGVTAGQEQLIFDKFSR GNKESAIPGVGLGLAICRAIIDVHGGRIWVEKGQDGGASFHFTLPLEKPPEIDGENI DTEK	21~~KdpD (1.49408E-118) ~~231,254~~Usp (1.57471E-39) ~~374,404~~DUF4118 (1.36081E-23) ~~502,531~~GAF (1.37984E-15) ~~646,663~~HisKA (0.0000000000886711) ~~728,781~~HATPase_c (2.98522E-26) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.7E-96	330.4	2.5	5.9E-96	329.3	1.7	1.6	1	C6W8N7_ACTMD	Histidine kinase (EC 2.7.13.3)	Amir_3228	Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	854	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Actinosynnema, Actinosynnema mirum, Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	446462	>tr|C6W8N7|C6W8N7_ACTMD Histidine kinase OS=Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971) GN=Amir_3228 PE=4 SV=1 MDKRKRGELRIYLGAAPGVGKTFAMLGEAHRRRERGADVVVALVETHGRERTAT MVDGLEVLPRKEVQHRGTTITEMDVDAVLARAPEIAVVDELAHTNAPGSRNAKRW QDVEELLDAGIDVLSTLNIQHLESLNDVVRRITRVEQRETIPDEVVRRAEQVELVDL TPEALRRRLAHGNVYAAHKIDAALGNYFRVGNLTALRELALLWVADQVDVALQRY RTEQRITDTWEARERVVVAVTGGAESETLIRRARRIAARAGAELLVVHTMRGDGL AGSAPESIAVLRKLTEDVGATFHMVVGDDVPAALLEFARGVNATQLVLGTSRRTR LARVFDEGIGAAVIGQSGSIDVHMVTHDESRRAPRWKVDRNPLTASRQVLGWSL ALLLPVLVTGIGMALQEELDFSTDLVGFFLATVVVALVGGLGPAVVAALVGAVLLN YFFTPPFYSLTIATPENMLTLVVMVTVAVLVALVVDRAARLAAQAARARTEAALLAS YARTVLTSPHPLVRLLEKVRENFGMESVAMLERVDGRWRRVACVGPRPCDEPDE ADADVPVTADVHLSLRGRPLPAADQRALETAAGQALLALRQQRMAVETADAQRR AATTELRTAILSAVGHDLRTPLTSIKAAIGSLRDPALALSEEDTGELLEAVEVSADRL AGLIDNLLDSSRLATGAVAPLLRPVTYDEVVAQALSGLDERAAVSVEVPEDLPPVL ADSGLLERVVANVVDNALRHGRMAPRRVVDVDGDGVITEHEPEVVVRASAHDDR VELRVVDHGSGVPEKSARAVFTPFQRLGDRDSTPGVGLGLSVAKGFVDAMGGAI SAEDTPGGGLTMVISLPVADAWAADA	5~~KdpD (5.1185E-120) ~~214,236~~Usp (1.12953E-21) ~~357,383~~DUF4118 (0.00931463) ~~460,X,611~~HisKA (0.000000000128028) ~~676,726~~HATPase_c (3.33817E-24) ~~844	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.8E-96	330.4	0.1	2E-95	327.6	0	2.2	1	A0A0F5MTF9_9MYCO	Histidine kinase	WR43_16135	Mycobacterium arupense	842	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium terrae complex, Mycobacterium arupense	342002	>tr|A0A0F5MTF9|A0A0F5MTF9_9MYCO Histidine kinase OS=Mycobacterium arupense GN=WR43_16135 PE=4 SV=1 MNSGDAPSRRGELRIYLGAAPGVGKTYAMLGEAHRRMERGTDVVAAVVETHGR KKTAELLAGIEILPPRWIDYRGKSFPELDVAAVLARRPQVVLVDELAHTNTPGSAN PKRWQDVEQLLAAGITVISTLNVQHLDSLNDVVAQITGVEQQETVPDSFVRQASQI ELVDIDPEALRRRLAHGNVYAPEKVDAALSNYFRSGNLTALRELALLWVADQVDA ALAKYRADKKITATWEARERVVVAVTGGPESETLVRRASRIASKSSAELLTLHVLR GDGLAQLPTARIGKIRELATSLGGSLHVVVGDDVPSALLDFAREVNATQLVIGTSR RSRWARLVDEGIGARVVRLSGTIDVHIVTHEESRQGFRRSAIAPRQRLVLRWLAA LLVPSVVCLVTALWMDPFLHTGGESALFFVSVLVVALLGGVAPAVLSAVVSGLLLN YFLTDPRHSFTIAETDSAITEIVLLLVAVAVAVLVDRAAERSREAGRASQEAELLALF AGSVLRGADLATLLERVRETYALRSVSILRERPDGAGPTLVASAGLDPCTTVESAD TAIDVGDDEFWMLAAGRQLAGRDRRVLSAVAKQAAGLVRQGELTTEANRAEAVM RADELRRSLLSAVSHDLRTPLAAAKAAVSSLRAEDVGFSPQDTAELLATVEESVD QLTALVGNLLDSSRLAAGAVQPELRRVYLEEAVERALVSIGRGETGFRRSGIDRVN VEVGDAVVLADAGLLDRVLANLLDNALRYAPDSPVRVSACRAADRVLIDVADQGR GLPPGGERLFEPFQRVGDQDNTTGMGLGLSVARGFVEAMGGTIRATETPGGGL TMVVDLAAPPPT	8~~KdpD (2.40109E-118) ~~218,240~~Usp (1.0658E-33) ~~361,383~~DUF4118 (0.0000292653) ~~463,X,614~~HisKA (0.0000000000236068) ~~680,737~~HATPase_c (1.27119E-25) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2.8E-96	330.4	0.4	2.8E-96	330.4	0.3	1.6	1	G2NR18_STREK	Histidine kinase (EC 2.7.13.3)	SACTE_5033	Streptomyces sp. (strain SirexAA-E / ActE)	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. (strain SirexAA-E / ActE)	862751	>tr|G2NR18|G2NR18_STREK Histidine kinase OS=Streptomyces sp. (strain SirexAA-E / ActE) GN=SACTE_5033 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVLLH GLEQIRRRDIEHRSAVFSEMDVDAVLERAPAVALVDELAHTNVPGSRNAKRWQD VEELLRAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVARRADQIELVDMSP QALRRRMAHGNVYQSDQVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYR GEHDISTPWQARERIVVGLTGGPEGRTLIRRASRMAAKGSGSEIMAVYIARSDGL TSASPKELAGQRTLVEDLGGTFHHVIGDDIPSALLAFARGVNATQVVLGSSRRKA WQYVYGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPIARGARLGRTRILWGW AVGVGGPAVLALLLRGMENGPGLANDVLLFLFMTVAAALLGGLAPALASAAVGSL LLNYWFTPPTHTLTVQDPENFVAIVIFFAVAVAVASVVVDLAARRTHQAARLRAESEI LSALAGSVLRGETALDALLDRVRETFGMESVALLERQSEVEPWTRAGSVGPAPV ARPDDADVDMPVGDHMALALSGRVLPAEDRRVLGAFAAQAAVVLDRQRLVDEAE AARRLAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSDEDEAEFLAGI EDGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVELDIPE TLPMVAVDPGLLERAVANIVENAVKYSPDEARVTVAASALGARVELRVADRGRGV PDEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAESMGGTLGAEDTPGGGLT MVLTLKAVPGRVRDGPGAPEPAAR	1~~KdpD (7.2878E-121) ~~211,233~~Usp (1.03601E-29) ~~356,392~~DUF4118 (0.0000300039) ~~458,X,612~~HisKA (2.48358E-14) ~~678,727~~HATPase_c (6.27793E-28) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.1E-96	330.2	0.3	1.6E-95	327.8	0.1	2	1	C5BG89_EDWI9	Histidine kinase (EC 2.7.13.3)	NT01EI_2891	Edwardsiella ictaluri (strain 93-146)	902	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Edwardsiella, Edwardsiella ictaluri, Edwardsiella ictaluri (strain 93-146)	634503	>tr|C5BG89|C5BG89_EDWI9 Histidine kinase OS=Edwardsiella ictaluri (strain 93-146) GN=NT01EI_2891 PE=4 SV=1 MVDDEQRPDPDTLLAQVGEPARGRLKVFFGACAGVGKTYAMLQEAQRLRAQGL DVAIGVVETHGRSETAALLDGLELLAQKRIQHRGRQIREFDLDRALARAPALILMDE LAHTNAPGSRHPKRWQDVEELLAAGIDVLTTVNVQHLESLNDVVGSVTGVQVRE TLPDRLFDAASEVVLVDLPPDDLRQRLKEGKVYIPGQAERAIEHFFRKGNLIALREL ALRRTADRVDDQMRAFRSGPGGSRVWHTRDALLLCIGQYADNDKLVRTAARLAG RLGCVWHAVYVETPHLHRLPENERRAILRSMRLAQELGAETATLSDTAPEHAILRY AREHNLGKILLGRRQREARRLRWPGASFVDRLARLGPDLDLLIVAVEDRPSGPRE NDPRPFGEKWRVQIQGFLVAAALCAVISLCGKLIQPTFDQVNLVMVYLLGVVVVAL FFGRWPSVFAACISVASFDLFFVQPQWSFAVSDVQYLVTFGVMLIVGILIGNLTAG MRYQARVARYREQRARHMYEMSKALGNALNHDAVVRSACASLNHSFGARTTLLL PDGDGLLRPRHGDEAGVTNVDLAIAQWCLDRRQPAGAGTDTLPGVPYQLLPLSS AQNTFGVLAIEPANLRQLMVPEQQRLLQTYTVMIANALERLHLAHSAAAARLEAER EQLRNSLLAALSHDLRTPLTVLFGQAEILTLDLASERSVHAPQAEEIRQQILNTSRL VNNLLDMARIQSGGFRLRKAWQSLEEIVGSAIHTLEPMLVGHPLALSLPADLPLVN CDGALIERVLQNLLENAGKYAGNTASIAILARVGADGLEVEVSDSGPGIAAEQRPHI FNKFTRGDKESAIPGVGLGLAICRAIIDIHGGRIWVESPPQGGAHFHFTLPLETVPE IDPETDKEMTDNP	20~~KdpD (3.29698E-125) ~~230,253~~Usp (4.58022E-35) ~~376,403~~DUF4118 (6.96322E-22) ~~502,572~~GAF (0.00000000016635) ~~646,664~~HisKA (0.000000000298677) ~~728,781~~HATPase_c (9.40899E-31) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.2E-96	330.2	0.4	5.2E-96	329.5	0.3	1.3	1	A9HGJ6_GLUDA	Histidine kinase (EC 2.7.13.3)	kdpDGDI1566	Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5)	894	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Gluconacetobacter, Gluconacetobacter diazotrophicus (Acetobacter diazotrophicus), Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5)	272568	>tr|A9HGJ6|A9HGJ6_GLUDA Histidine kinase OS=Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5) GN=kdpD PE=4 SV=1 MMEDRTDRPDPDALLRQAAHDMGGTRGRLKIFVGAAPGVGKTFEMLTTAHRLIR DGVDVVVGVVETHGRSETAALLDGLEVVPRRVVAYRGQTLTEMDLDAILARQPRL VLVDELAHTNAPGSRHPKRWMDVEELLAAGMDVFTTVNIQHLESLNDIVAGITRIR VRETVPDTVIDRADEIELIDLTPADLLQRLREGKVYTAPAASRAMRNYFSPGNLTAL RELALRQTARQVDAQLIDHMRSNAISGPWAAGERILVCLTLQDVDGSLLRYGRRL AERFHAPWTVLHVETSREAGETIRQRTASQMHLAQSMGAETITIPGQDVATETLA WARSHNVTQIVAGRPARRPWTSWMTPWTWTSVTRILADRAGDIPVHVVGATNG HEGAEEKPEKRPLAFGPYIAATGIVAGALVLSLVLRHGMEVQNVSLTFLTAVLGVA LGFGLWPSLYASVMAVLSFNFFFLPPLYTFVIAAPDNIAALAFFSITAVTASHLGNR VRAQAIVARHRAEITESLYEFSRKLTGVTSMDELLWTTCQQIATMLDRQVVILLPQ DDKLIIRASDPPEKSLDSADLAAATWAWRHDRSAGRGSDNLPGARRLFVPLRTAR GPIGVIGLDSDGPGLLLGQEQQRLVDALGDQAALAIERIILSHDLDQARLHAETERL RGALLSSISHDLRTPLSSILGAASSLDSYDALLDKKDRKELLTTIREEAERLSRFVAN LLDMTRLEAGALTPARQPCDLGEVAGSALARASVILRHHRVSLKVAPDLPVPLDD VLVEQALFNILDNAAKYTPEGSMVMIEIAQKGGSLRLRLTDEGPGLPADNPNQIFD KFTRIQFADRQRPGTGLGLAIAKGFVETAGGSITAENRPDRTGAVFTLSFPIVAEV SG	24~~KdpD (6.11271E-115) ~~234,256~~Usp (1.084E-33) ~~381,402~~DUF4118 (1.71413E-16) ~~502,528~~GAF (0.00000000000233829) ~~647,664~~HisKA (4.70611E-14) ~~730,784~~HATPase_c (5.03955E-24) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.2E-96	330.2	0.4	4.4E-96	329.7	0.3	1.2	1	Q8R869_CALS4	Osmosensitive K+ channel His kinase sensor domain protein	KdpD2 TTE2155	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	380	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	273068	>tr|Q8R869|Q8R869_CALS4 Osmosensitive K+ channel His kinase sensor domain protein OS=Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) GN=KdpD2 PE=4 SV=1 MSGGYRRLTPEEALEIVKKEQRGKLKIFLGYAPGVGKTYAMLNEGNRRLKRGQDV VIGYVETHGRKDTEAQIGNLEIIPRKKIEYHGMILEEMDVDAIIARKPEVVLIDELAHT NAPGSKHKKRYEDVQEILEHGINVLTTLNIQHIESLNDIIQQITGIAVRETVPDSIIDNA DEIVAVDLTPDALINRLKRGDVYPLSKLDECLSNFFRKGNLSALRELMLRLTAEEVD LELEEYMKEHGIEDTWETNEKIMVCITPNPLSKKLIRRGARRARRFKCDWVVVYV DCTHFLAPKLTEKDKEVLESHFMLAKQLGAEVYTLRGKSVSDELLKFAKKMHITQII IGHSQRSWLQTLFRGSTVIKLIKKAKNIEIHVIPYTK	20~~KdpD (6.7387E-135) ~~230,252~~Usp (4.42212E-41) ~~377	non-kinase	KdpD;Usp
	3.3E-96	330.1	0.8	3.3E-96	330.1	0.6	1.8	1	B8ET99_METSB	Histidine kinase (EC 2.7.13.3)	Msil_2823	Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	901	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Methylocella, Methylocella silvestris, Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	395965	>tr|B8ET99|B8ET99_METSB Histidine kinase OS=Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906) GN=Msil_2823 PE=4 SV=1 MSERRDFDKRPSPDALLGAAEQETRGRLKVFFGAVPGVGKTYEMLTAAHARKAE GVDVVIGVVESHGRPETEALIRGLEIVPLRQIAYKGRTIGEVDLDAILKRRPQLVLM DELAHTNAPESRHPKRYLDVEELLNAGIDVYTTLNVQHLESLNDVVAQITRVRVQE KIPDSILDRADEIELIDLTPKDLIQRLHEGKVYAQDTAGRALENYFSIGNLTALRELAL RRTAQRVDEQLLTHMQAHAISGPWAAGERILVCVNDSPNAIGLVRYGRRVAERLR APWAAINIETGASVRLDQAARDRLAETLRQAERLGAEAIVLPGRTITEEILRYAAET NVTHIVIARSQRPRWQELLQGSVTHSLIRGAGDISVHVIAPREAATQPAKTADPKG GAAPSLGWKQALAVIGLVGLATAVGAVLRQYLDVHNVALVFLMGVLTSAVSFGLW PALFASIVSMLSFNFFFLRPLYTFTIADPESVVALVFFFIVAVIASNLTASVRSQAVV ARKRAKTTEDLYLFSRKLAGVGALDDVLWAAAFQIASMLSVRVVILLPAADGSLEV RAGYPPEDQVEPADIAAARWAFESNRPAGRGADTLPGAQRLFLPMWTGRGSIG VVGLDSDREGALLTPESRRLLDALIDQTALAIERVNLVEDLDRARLVSETDRLRSAL LTSISHDLRTPLASIMGAAGALSDFAGQLTDESKRELTDTIQEEAERLNRFIANLLD MTRLESGAVHPNAAPHDLSDVVGAVLKRARKILAAHRVEVALAPDLPMLDIDAVLF EQALFNLLDNAAKYAPAGSLIRLQAVKDDGFVVLQILDEGPGIPAADVERIFDKFTR AQKGDQVGAGTGLGLAVCRGFIEAMHGTIAAGNRSDTHGAVFTIRLPALEPASGE LSA	25~~KdpD (1.16729E-120) ~~233,255~~Usp (2.73528E-41) ~~378,406~~DUF4118 (4.78966E-18) ~~504,531~~GAF (0.000000000000388034) ~~650,667~~HisKA (0.000000000000234191) ~~733,786~~HATPase_c (1.44054E-25) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.4E-96	330.1	0.2	6E-96	329.3	0.1	1.4	1	A0A0D5V8M9_9BURK	Histidine kinase (EC 2.7.13.3)	OI25_467	Burkholderia fungorum	944	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia fungorum	134537	>tr|A0A0D5V8M9|A0A0D5V8M9_9BURK Histidine kinase OS=Burkholderia fungorum GN=OI25_467 PE=4 SV=1 MNRPDPDELLDKLQRDEEKRQRGRLKIFFGASAGVGKTYAMLQAARRRADEGTD VVVGIAETHGRGETAALLEGLDVLPLAMIEYRGRKLGEFDLDAALARKPQLILVDEL AHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETV PDRVFDRADEVTLVDLPAEELLDRMRDGKVYLPQQAERAVRNFFRKGNLIALREL ALRRTADRVDAQMREYRADRSIERIWQARERLLVCVGPGPEAPMLVRAAARLAA SLKADWIAVYVETPALQRLPDARRERTLNALKLAAELGAETATLAGTDAVAALIGY AQARNVSKLVAGASARSGFQRWVRRPLGERIAERAGDLDLTLIRASSERDGGEQ RRLLNTTANAWREALSAARERRSPPRAYGIALTICAAITLLSSQLIDHIDLTNLVMLY LLGVIFTAVKLGRGPGVVLSFMSVAAFDFFFVPPRMSLSVSDTQYLLTFLGMLLTS LVISHLTSSLRREASVARRREQRTGAMYAMARELAAALTTEQIVGIGSRHVSEVFG ARVAILLPDSADQVKQKIEDPDAAITLEGEMLDSDVGQWVYDQQKPAGHGTDTLP AAAALYLPLKAPMRTRGVLAVVMRDERELDVPEQQRMLDAFAAQIALALERVHYV DIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAQSREAHPGAQPGDD LVEAIHEEALRMTGIVTNLLDMARLQAGSLQLNQQWTLLEETVGAALRACKRVLA NHPVQVKLPADLPLLHLDAVLMERLFSNLFENAAKYTPPDTPLTIGAQRLDADGKS FVRVAVDDNGPGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEAHGGTIG ALNRMSPDGRVEGARFWFTLPVETPPEAPDALEDEGADALPDRDPTSNLLSKPS HE	134537	21~~KdpD (7.73995E-122) ~~230,252~~Usp (1.07462E-31) ~~374,415~~DUF4118 (1.10304E-19) ~~512,538~~GAF (5.76711E-18) ~~661,678~~HisKA (0.00000000000222345) ~~745,798~~HATPase_c (1.76987E-22) ~~908	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.6E-96	330	2.1	1.3E-95	328.2	0.2	2.2	1	E9T4H6_RHOHA	Histidine kinase (EC 2.7.13.3)	HMPREF0724_13396	Rhodococcus equi ATCC 33707	857	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus hoagii (Corynebacterium equii), Rhodococcus equi ATCC 33707	525370	>tr|E9T4H6|E9T4H6_RHOHA Histidine kinase OS=Rhodococcus equi ATCC 33707 GN=HMPREF0724_13396 PE=4 SV=1 MRSPRVNDGVVSSPEQHRAPRRGELRIYLGAAPGVGKTYAMLGEAHRRLERGG DVVAAVVETHGRARTAEQAAGLELIPPKFVEYRGTAMPELDVEAVLARRPAVVLV DELAHTNTPGSRNEKRWQDVYELLDAGIDVLSTLNVQHLESLNDVVQQITGVTQQ ETVPDAVVRAASQVELVDITPEALRRRLSHGNVYSAEKVDAALGNYFRRGNLTAL RELALLWVADQVDAALAKYRAENKITDTWEARERVVVAVTGGPESETLVRRASRI AGKASAELMVVHVVRGDGIEGVSAAEMGKVRKLATSIGASLHSVVGDDVPTTLLE FAREVNATQLVIGTSRRSRWARILDEGIGAAIVQQSGKIDVHMVTHDEAATRHRIS FLGRGERRAVSWLAAVVVPSIAAALMGLIDRVAGVGGQNALFFVVVLVVSLLGGV GPAILSALISGLLLNYFFTAPLYSFTIAQPDNFITTVVLLVVAVAVAILVDAAAKRSRE ARRASQEAELLALFAGSVLRGADLPALLEKVRETYSQTGVSVVRRGEGVVSAAGA SAPSTVDEAGTVCEVSDGEYALLLAGEELGARDRKVLYAVANQAVGLIRQRQLAE EASKAQALAEADRLRRSLLSAVSHDLRTPLAAVKAAVSSLRSDDVEFSPEDTAELL ATVEESTDQLTALVGNLLDSSRLAAGVVKPTLRRVYLEEVVHRALVGAGFGGPGS ARRVRDQVKVEVGDAAVMADAGLLERVIANLVDNALRYAPDEPVRIGAARAGDH MTITVADTGPGLARGTHEQVFDAFQRLGDRDNTVGVGLGLSVVKGFVEAMGGTV GVTDTPGGGLTMIVELDAAPAGAGEVEGAR	525370	20~~KdpD (1.07133E-119) ~~230,252~~Usp (3.35176E-33) ~~373,X,620~~HisKA (0.0000000000013584) ~~686,743~~HATPase_c (3.40198E-27) ~~843	kinase	KdpD;Usp;X;HisKA;HATPase_c
	3.8E-96	329.9	0.4	6E-96	329.3	0.3	1.3	1	B5H8P9_STRPR	Histidine kinase (EC 2.7.13.3)	SSDG_01621	Streptomyces pristinaespiralis ATCC 25486	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pristinaespiralis, Streptomyces pristinaespiralis ATCC 25486	457429	>tr|B5H8P9|B5H8P9_STRPR Histidine kinase OS=Streptomyces pristinaespiralis ATCC 25486 GN=SSDG_01621 PE=4 SV=1 MGRGKLRIYLGAAPGVGKTYAMLSEAHRRAERGTDCVVALVETHERPRTARLLD GLEQIERREITHRGAVLTEMDIDAVLERRPAVALVDELAHTNVPGSRNSKRWQDV EELLAAGTDVISTVNIQHLESLGDVVETITGVRQLETVPDEVVRRADQIELVDMAPQ ALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWLADRVDEYLQQYRG EHNIRSTWQARERIVVGLTGGPEGGTLIRRAARLAEKGAGGEVLAVYIARSDGLTS ASPKELAVQRTLVEDVGGTFHHVIGDDVPSALLEFARGVNATQIVLGSSRRKAWQ YLFGPGVGATVARDSGPDLDVHIVTHDEAGKGRGLPGARGTRLGRSRIAGGWLV GVAGPALLTALLTSLENGPGLANNVLLFLFLTVIAALLGGLLPALASAAVGSLVLNYF FTSPTHTLDIAEPRNLVAIVIFFAVGVAVASVVDLAARRTHQAARLKAESEILSFLAG SVLRGQTALDALLERVRETFAMESVALLERESDVDPWTCTASVGPRPATRPDDA DVDMPVGDRMAMALSGRVLPAEDRRVLAAFATQAAVVVDRQRLVGEAEQAREL AEGNRIRTALLAAVSHDLRTPLAGIKAAVTSLRSDDVAWSEEDEAELLAGIEEGAD RLDHLVGNLLDMSRLQTGTVTPLIRETSLDEVIPLALVGVPAESVELDIPESLPMVA VDRGLLERAVANIVENAVKYSPDAVCVTVAASSLGQRVELRIVDRGAGVPDEAKE RIFEPFQRYGDAPRGAGVGLGLAVARGFMEAMGGTLTAEDTPGGGMTMVLTLTA VPGHGTTPAGLTAEATS	457429	1~~KdpD (2.38412E-121) ~~211,233~~Usp (7.40869E-31) ~~356,X,612~~HisKA (0.000000000000152707) ~~678,727~~HATPase_c (1.24116E-26) ~~828	kinase	KdpD;Usp;X;HisKA;HATPase_c

	4.1E-96	329.8	0	7.1E-96	329	0	1.4	1	A0A0D4DG89_9ACTN	Histidine kinase (EC 2.7.13.3)	T261_1308	Streptomyces lydicus A02	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	1403539	>tr|A0A0D4DG89|A0A0D4DG89_9ACTN Histidine kinase OS=Streptomyces lydicus A02 GN=T261_1308 PE=4 SV=1 MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLH GLEQVPRKELEYRGTSFTEMDVDAVLERAPAVALVDELPHTNIPGSRNAKRWQDI EELLAAGIHVISTCNIQHLESLGDIVESITGIRQKETVPDEVVRRADQIELVDMSPHA LRRRMAHGNIYKPHKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYRSEH QVSKIWGSRERIVVGLTGGSEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTSG SPKELAVQRTLIEDLGGTFHHVMGEDIPSALLEFSRGVNATQIVLGTSRRKAWQYI FGPGVGATVARDSGPDLDVHIVTHEEAAKGRGLPVARGARLGRPRIIWGWLTGV AGPALLTLPLMYVGAGLGFANDVLLFLTLTVAAALLGGLLPALASAVVGSLLLNWF FTPPVGRLTIADPKNILALVIFLLVAASVASVVDVAARRTHQAARLRAESEILSFLAG SVLRGETTLDALLERVRETFAMDAVALLERETETAPWTCSGSVGDASPLSRPEDA DVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLKSQADHARKLA EGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVEWSDEDRAELLAGIEEGADR LDHLVGNLLDMSRVQTGTVTPLIREIDLDEVVPMALGGVPEDSVVLDIPEALPMVA VDPGLLERSVANIVENAVKYSPDGETVLVSASTLGDRVEVRVADRGPGVPDDAKD RIFEPFQRYGDAPRGAGVGLGLAVARGFAEAIGATLTAEDTPGGGMTMVLTVPTA AGHLPAQPDLPAAVTS	1~~KdpD (6.52106E-122) ~~211,233~~Usp (2.85697E-29) ~~356,432~~DUF4118 (0.000123084) ~~482,X,613~~HisKA (0.000000000000040627) ~~679,728~~HATPase_c (1.45786E-24) ~~829	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.1E-96	329.8	0.4	9.8E-96	328.6	0.3	1.7	1	KDPD_MYCTU (P9WGL3)	Sensor protein KdpD (EC 2.7.13.3)	kdpD Rv1028c MTCY10G2.21	Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)	860	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex, Mycobacterium tuberculosis, Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)	83332	>sp|P9WGL3|KDPD_MYCTU Sensor protein KdpD OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=kdpD PE=1 SV=1 MTLLFADLCAIFTPYRWMIEHVTTKRGQLRIYLGAAPGVGKTYAMLGEAHRRLER GTDVVAAVVETHGRNKTAKLLEGIEMIPPRYVEYRGARFPELDVEAVLRRHPQVV LVDELAHTNTPGSKNPKRWQDVQEILDAGITVISTVNIQHLEGLNDVVEQITGIEQK EKIPDEIVRAADQVELVDITPEALRRRLAHGNVYAAERVDAALSNYFRTGNLTALRE IALLWLADQVDAALEKYRADKKITATWEARERVVVAVTGGPESETLVRRASRIASK SSAELMVVHVIRGDGLAGVSAPQLGRVRELATSLGATMHTVVGDDVPTALLDFAR EMNATQLVVGTSRRSRWARLFDEGIGARTVQEPGGIDVHMVTHPAASRASGWS RVSPRERHIASWLAALVVPSVICAITVAWLDRFMGIGGESALFFIGVLIVALLGGVA PAALSALLSGMLLNYFLTEPRYTWTIAEPDAAVTEFVLLAMAVAVAVLVDGAASRT REARRASQEAELLALFAGSVLRGADLATLLQRVRETYSQRAVTMLRVRQGASTG ETVACVGTNPCRDVDSADTAIEVGDDEFWMLMAGRKLAARDRRVLTAVATQAAG LVKQRELAEEAGQAEAIARADELRRSLLSAVSHDLRTPLAAAKVAVSSLRTEDVAF SPEDTAELLATIEESIDQLTALVANLLDSSRLAAGVIRPQLRRAYLEEAVQRALVSIG KGATGFYRSGIDRVKVDVGDAVAMADAGLLERVLANLIDNALRYAPDCVVRVNAG RVRERVLINVIDEGPGVPRGTEEQLFAPFQRPGDHDNTTGVGLGMSVARGFVEA MGGTISATDTPGGGLTVVIDLAAPEDRP	25~~KdpD (3.75162E-124) ~~234,256~~Usp (3.34914E-37) ~~377,400~~DUF4118 (0.0000221883) ~~479,X,630~~HisKA (0.0000000000055797) ~~696,753~~HATPase_c (8.44034E-26) ~~853	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.2E-96	329.8	0.1	6.5E-96	329.2	0	1.3	1	Q2J7V2_FRASC	Histidine kinase (EC 2.7.13.3)	Francci3_3283	Frankia sp. (strain CcI3)	854	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain CcI3)	106370	>tr|Q2J7V2|Q2J7V2_FRASC Histidine kinase OS=Frankia sp. (strain CcI3) GN=Francci3_3283 PE=4 SV=1 MASGRLRIYLGAAPGVGKTYDMLCEAQRRKARGTDVVVGLVETHGRPRTAALLD GLEIMPRRTVSYRGATFTEMDVDAILARAPAVVLVDELAHTTVPGCRNAKRWQDV HELLNAGIDVLSTLNIQHLESLNDVVERITGVPQRETVPDAVVRAAEQVELVDMTP EALRRRMVHGNIYGPDKVDAALGNYFRVGNLTALRELALLWLADKVDEQLDHYRT EHQISGIWETRERVVVALTGGPEGDTLIRRAARIADRAKGADLLAVHVTRSDGLAG ASPAHLARQRVLVESLGGSYHQVVGDDIPIALLEFARAENATQLVLGASRRGRLA HMIDPGIGVTTTKLSGPIDVHLVTHEEVGKGRLLPRRARGLTLRRRLAGVLAAVVLL PLLTLALTHQRTGLNLTSNVLGFLIVVVAVALVGGLLPALLAAVGGLLLNYYFIQPV HRFIVAESNNVLALLAFLAVAVMVSSVVDLAARRTSQAVRATAEAEMLSTLAGSVL RGEQALPALLTQVRETFGLTSVALLERAAEGGQNGARKADRHGWRVVDSAGPD PCLRPDEADTEVPVSENLTLVLRGRPLPAADRRVLTAFAAQAAVALEQRRLAQVA AEAGPLAEADRTRRALLTAVSHDLRSPLATASAAVANLRGNEVEWSAEEQAELLA TAEEALDHLARLVENLLDMSRLQAGRLSVFPAPVGLDDVIPGVLRDLGPAARDVA VTVPDDLPLVYADPALLERVIANLLSNAARYSPPGQPPLITASALHDRIQLRVIDRG PGLPAEDRDQAFTPFQRLGDTDNASGIGLGLALSRGLTEAMGGTLTPEDTPGGG LTMVVALPVATVGDSTQPADGAA	4~~KdpD (2.67594E-120) ~~211,233~~Usp (3.04034E-21) ~~355,X,620~~HisKA (0.0000000000308812) ~~686,737~~HATPase_c (1.27374E-25) ~~838	kinase	KdpD;Usp;X;HisKA;HATPase_c

	4.2E-96	329.8	0.3	8E-96	328.9	0.2	1.5	1	A0A0F0HN07_9PSEU	Histidine kinase	UK12_20160	Saccharothrix sp. ST-888	862	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix sp. ST-888	1427391	>tr|A0A0F0HN07|A0A0F0HN07_9PSEU Histidine kinase OS=Saccharothrix sp. ST-888 GN=UK12_20160 PE=4 SV=1 MARGRLRIYLGAAPGVGKTYAMLAEAHRRHDRGTEVVVGFVEHHNRRLTAELIDG LESVPRRELIHRGAVFTEMDVDAILARRPAVALVDELAHTNIPGCRNAKRWQDVE ELLAAGIDVVSTVNIQHLESLGDVVEGITGVRQRETVPDAVVRRADQIELVDMSPQ ALRRRLAHGNVYAPEKIDAARANYFRLGNLTALRELALLWTADRVDEYLQRYREE QGIERTWQARERIVVGLTGGPEGATLIRRAARIAARGSGGEVLAVHISRSDGLAG SGSPHALIEQRALVESLGGSFHTVLGDDPAAALLDFARGVNATQIVLGSSRRRAW QYIYGPGVSATVTRDSGDIDVHIVTHEHAAKGRGRIPIRRVTDLGRTRTVAGWLIG VAGPPLLAVFLTQVHGLGLSTDMLLFLSLTVCAALIGGLFPAIASALVGSTALNYYF TPPVHTFNISEPENIMAVGIFTAVGIAVASVVDLAARRTHQAARSQAEAQTLSALA GTVLRGAPSGDSLLTVLLDQVRETFQQDSAALLERAGEHAPWRIAASAGPRPPPER PEDGDVDVPVGAELALVLRGRVLPAEDRRLLGAFAAQAAAVLLERRRLAGEAAAAR REAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRTEDVEWDEADEAELLAGIEAG ADRLDHLINNLLDMSRLQTGTVTPLIHEIDLDEVVPFALGGVPLEAVKLDVPETLPMI HADAGLLERSLANLIENAVKYSPDGVKVLVKADALHPPGTPGRVELRVVDRGPGV PEAAKERIFAPFQRYGDAPRGAGVGLGLAVARGFVEAMGGTVAAEDTPGGGLTM VVTLPAVDLPDVNFPEQPPLPPNRKAEPE	1~~KdpD (4.09078E-121) ~~211,233~~Usp (2.24079E-22) ~~356,385~~DUF4118 (0.000000002399) ~~482,X,616~~HisKA (1.65525E-14) ~~682,731~~HATPase_c (5.2607E-24) ~~837	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.3E-96	329.8	0.4	8E-96	328.9	0.3	1.5	1	Q98GX8_RHILO	Histidine kinase (EC 2.7.13.3)	mll3127	Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	907	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium, Rhizobium loti (Mesorhizobium loti), Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	266835	>tr|Q98GX8|Q98GX8_RHILO Histidine kinase OS=Rhizobium loti (strain MAFF303099) GN=mll3127 PE=4 SV=1 MPDDRSNENRPSPDALLEHAEREGRGRLRIFLGAAPGVGKTYEMLMSGRARLAD GIDVVIGVVETHGRRETQALVEGYEVIPRRKVDYKGRVLEEMDIDAILARRPALVLV DELAHTNAPGSRHPKRYLDVQEILARGIDVYTTLNIQHVESLNDVVAQITRVRVRET VPDSIIDQADDVEIIDLTPDDLIKRLEEGKVYFPNTAQRAIENYFSSGNLTALRELAL RRTAQRVDEQLLNHMQSHAIQGPWAAGERVLVCVDARPGGAARIRYARRLADRL RAPWTALHVDTPRSAGMSEEDKDRLAALMRLAEQLGAEVTTIPGQSVAQDIVRHA TANNFTHIVVGRPTRSRWRELIEGSLTYDLIRNAGDISVHVISGTERDAEAASRRVK AAAEQKQFQIWPYLLATTYVAGSLALSAVLDQFLDVRNLAIVFLLAVLTSAVAGGL WPALYACFLSALAFNYFFLEPRYTLTIRDPESIVALAVFLAVAVIASNLAARMQRQA VAARSRARATEDIYLFSKKLAGAGTLDDVLWATAFQIASMLKLRVVLLLPEDGTITV KAGYPPDDTLAEADIAAARWAWEHNRAAGRGADTLPGAKRLYLPLRTGRTAIGVI GLDNDKQGPLLTPEQQRLLDALADQAAVAIERIQLVADVDRAKLAAEADRLRSALL TSISHDLKTPLSAIMGAAGTLKEFAPDLPEQDRAELLSTVIDESERLNRFIANLLDMT KIESGAMEPNYALHYVGDIVGTALNRARKITSEHKIEVDIPPDLPMLKLDPVLFEQV LFNLLDNASKYSPPGSTIRLQGWADNGSVIVQIMDEGPGIPSHDLERVFDTFYRVR KGDQVRAGTGLGLSICRGFVESMGGTISAANRTDRPGAAFTIRMPVPTEAPDRGE ETSMDRPS	23~~KdpD (2.69126E-122) ~~233,255~~Usp (8.50241E-48) ~~378,404~~DUF4118 (1.53422E-16) ~~502,530~~GAF (1.66533E-16) ~~649,666~~HisKA (0.00000000000178578) ~~732,785~~HATPase_c (1.2963E-26) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.4E-96	329.7	0.6	7.1E-96	329	0.4	1.3	1	A4Z015_BRASO	Histidine kinase (EC 2.7.13.3)	kdpD BRADO5827	Bradyrhizobium sp. (strain ORS278)	905	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium sp. (strain ORS278)	114615	>tr|A4Z015|A4Z015_BRASO Histidine kinase OS=Bradyrhizobium sp. (strain ORS278) GN=kdpD PE=4 SV=1 MAHQRRDPDQRPSPEALLEAARREESPAGKLKIFVGAAPGVGKTYEMLSSAHAK LKAGIDVVIGFVETHGRVETDALVRGLEVIPRKRIGYKDQVIEEMDLDAVIARRPKL AIVDELAHTNAAGSRHPKRYLDVEELLSHGIDVYTAVNVQHIESLNDVVAQITHVRV RETVPDSILDRADAIELIDLTPDDLIQRLKEGKVYVPKQAERALEHYFSPGNLTALR ELALRRTAERVDEQLLNHMQANAIAGPWAAGERILVCVSEDPRAAGLVRYTKRLA DRVHAPWTAVTIETRRNLQLSDKQRDRLADTLRLAESLGGEALTIPSAGRRIADDLI GFAQANNVTQIIIGKSQRSRLFEIIRGSVVHDLVRRAGNISIHVIPGEETPGETGTSV QTRARSEPLQAKPYIMALLITAVGLGLAELIQPFFGIENVDLVFLTAVVGVAARYGL WPSLLASLMASLCYNFFFLPPIYTFTITDPTNVAAFFFFMLIALLVSNVASRVRVQA DSATQRIRTTEQLYAFSRKLAGTATLDDVLWATAYQAALMLKVRVVLLLPQDGKLI VMAGYPPEDQLDDADLAAASWAWSNDRAAGRGSDTLPGAKRLFLPMRTGRGLI GVIGIDDDRSGPLLTPDQRRLLDALVDQGALAIERVLLVEDMDKVKRTMEQDRLRS ALLTSISHDLKTPLASVLGAASTMRDLATRLSDKEKLDLLATVIDESERLNRFIANLL DMTKLESGAIKPNTAPHDLGEIVGSALRRASKILAGHKISLELAADLPMLELDAVLF EQVLFNLLDNAAKYAPADTTIELRSRRDGAWVVLDVRDEGDGIPPDEVEHVFDKF YRVQKGDQVRPGTGLGLAISRGFVEAMQGRMTAGNRADRSGAVLTIRLPVPPQA KTLETAA	29~~KdpD (1.87078E-121) ~~236,258~~Usp (5.58343E-45) ~~383,408~~DUF4118 (7.35903E-19) ~~508,534~~GAF (0.00000000000311252) ~~653,670~~HisKA (0.0000000000903436) ~~736,789~~HATPase_c (1.14859E-26) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4.4E-96	329.7	0.1	6.6E-96	329.1	0.1	1.3	1	Q605R4_METCA	Histidine kinase (EC 2.7.13.3)	kdpD MCA2214	Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	910	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylococcus, Methylococcus capsulatus, Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	243233	>tr|Q605R4|Q605R4_METCA Histidine kinase OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) GN=kdpD PE=4 SV=1 MAAERPDPDALLARVEREQARARRGRLKIFFGAAAGVGKTYAMLEAARERRAEGI DVVVGLVETHGRKETEALLEGLEMLPVRTVEYRGTVVGEFDLDGALKRRPSVILV DELAHTNTAGSRHPKRWQDVEELLRAGIDVYTTLNVQHLESLNDDVGQISGIRVW ETVPDTVFEAADEVELIDLPPDELLVRLKEGKVYLPQQAELAAENFFRKGNLIALRE LALRQTAARVDAQMQDYREDHTIREVWQVGERILVCIGPNPMAERLIRAGKRLAA SLKAEWLVVYVETPALQRLPAERRDAVLRMLRLAEQLGAETVTLSAPDMSEAIIDL ARERNVTKIVMGKPRRRGWKRWLLGSVVDTIIAEAHNINVYLLGSPPGEDRGQES LQAPQPGLSAKPDRGGGAEYRGYLGAATATFLCTLTAKAMFGRFELTNLVMVYLL GVIFVATRYGRGPSILASILGVLAFDFFFVVPYHTFSVADTQYLFTFAVMFSVALVT ANLMANVRSQAKVASHRERRATVLYAMSKELAASRSEAEIVRIAVRQIETEFGGRA VLLFPDESGRIGYPVSPLAEEFLPGIDMSVAQWVFDHDEMAGRGTNTLPGASGV YIPLTGAEKTIGVLVMKPVNLRRVFLPEQQKLLQTFVNLIVQAIERVRLAEQARINQ VRMESERLRNSLLSSISHDLRTPLATIVGSASTLVEGDYALEPEDRRELCRAIYDES RRMASLVNNILDMAWFDAGVVKLHLQWHVLEEIVGTVLTRLKKQLERRPVTVRLP RDAPFVYVDSVMLEQVLANLMENAIRYTPENSPIEIAAEATPFTMTITVSDHGPGIP KGQEELIFEKFYRVHREGPQSGVGLGLAICRAIVEAHGGYIRARNRAGGGAVFTIV LPLRESPPRIEPEAEPAE	22~~KdpD (5.26949E-124) ~~232,254~~Usp (9.88461E-51) ~~377,411~~DUF4118 (2.68387E-19) ~~510,536~~GAF (0.000000000000478912) ~~656,673~~HisKA (0.00000000000010215) ~~738,792~~HATPase_c (9.38647E-32) ~~893	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.5E-96	329.7	0.1	8.2E-96	328.8	0.1	1.5	1	A0A0A1FTM0_9MYCO	Histidine kinase (EC 2.7.13.3)	G155_23795	Mycobacterium sp. VKM Ac-1817D	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. VKM Ac-1817D	1273687	>tr|A0A0A1FTM0|A0A0A1FTM0_9MYCO Histidine kinase OS=Mycobacterium sp. VKM Ac-1817D GN=G155_23795 PE=4 SV=1 MSTPSSSPAKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDLVAAVVETHGR RKTAELLEGIETIPPRYVEYRGGRFPELDVAAVLARNPQVVLVDELAHTNTPGSKN PKRWQDVEELLAAGITVISTVNVQHLESLNDVVTQITGIEQQEKVPDEVVRAADQI ELVDITPEALRRRLSHGNVYAPERVDAALSNYFRRGNLTALRELALLWLADQVDAA LAKYRADNKITDTWEARERVVVAVTGGAESETLVRRASRIASKSSAELMVVHVVR GDGLSGVSAPQMGKVRELAASLGATVHTVVGDDVPAALLDFARERNATQLVLGT SRRSRWARIFEEGIGPAVVQQSGKIDVHMVTHDQARRGFGWATATPRQRHIAS WLAAVVVPSAICLLIVGVLDPILGVSGESALFFIGVLVVALLGGVAPAALSALLSGLL LNYFLVAPRHTFTISEPDSAVTVVVLLLVAVAVAALVDGAASRAREARKASQEAEL LTLFAGSVLRGADLTTLLERLRETYSQRAVSLLREQNGTAEIVACVGTKPCAEVDT ADTAIEVGDDEFWLLMAGRKLAARDRRVLSAVAKQAAGLVKQRELTEEASKAAAI AQADELRRSLLSAVSHDLRTPLAAAKAAASSLRSEDIDFSAEDTAELLATIEESVDA LTALVGNLLDSSRLSAGVVRPELRRVYLEETVQRALLGISKGTTGFTREGLDRVKV EVGDAVAMADAGLLERVLANLIDNALRYAPEGPIRVSAGQVADRVLIAVIDEGPGM PRGAEEQLFAPFQRLGDHNTTIGVGLGLSVARGFVEAMGGTISATDTPGGGLTVE IDLAAPPKDDAL	9~~KdpD (6.54684E-122) ~~219,241~~Usp (1.75443E-35) ~~362,X,613~~HisKA (0.00000000990324) ~~679,736~~HATPase_c (2.18882E-27) ~~836	kinase	KdpD;Usp;X;HisKA;HATPase_c
	4.6E-96	329.7	0	8.2E-96	328.8	0	1.4	1	B3EAQ0_GEOLS	Histidine kinase (EC 2.7.13.3)	Glov_3227	Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	890	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter lovleyi, Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	398767	>tr|B3EAQ0|B3EAQ0_GEOLS Histidine kinase OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) GN=Glov_3227 PE=4 SV=1 MTIPDTTIRPTPEAMLKLAQAEEAQSGQGRLKVFLGYAAGVGKTYAMLEAARERK RDGRDVVVGYVESHGRSETDALLDGLELIPRRELSYAGVLLPEMDLDAILTRKPQI VLVDELAHCNVPGSRHEKRWQDVEELLAAGIDVYTTVNIQHFESLNDVVAQITGIT VRETVPDRLLDIAFEIKLIDLPPEDLLQRLHEGKVYIPDQAAKAIEKFFRPGNLMALR ELSLRRTAARVDDQMRAYMETQSIPGPWPTAERLLVCVSGSPFSEQLIRATRRLA EELKAPWHTVYIETPGSDRQTRENRERIWQDLRFAESLGAQVATLTATSVPDAVV EYAVRHNVTRIVVGKPSRSRWQELLHPPIVDQIIRRSISSDVFVVRISSDGRQGGA QQQVKHPHHAHPFGYPAAALLVAAATLLCGLVSRFLEPTNLVMVYLLAVVVAAVR LGRRPAMLTAFLGVLAFDFFFVPPHITFVVADTQYLITFAGLLVVGLVISSLVARSQ ERADVIRVREIQTASLYYLSRDLAAAADISKVLKSVIRNVEEALNAKAVMLLPEGER LELQAASDGLILDSKEQAVADWAFRNRQPAGRGTDTLISAELLYLPLQTPASQLGV LGIRMEDELDYRSTESRRLLDAFATQAAMAIERVQFSHQAEQAQILQARENLERAL LNSISHDLRTPLVTVTGVLASLRDDGMHLNDQARDELLDTAAGEAERLNRFVGNLL DMTRIEAGAIRLNSELCDIQDLVGCAMAAIKQRVGGRTIRIRLPDDLPMVPMDLVL MTQVLVNLLDNSLKYSPAESSIEISARLERGWLLLEIADQGPGVPEQDLKRVFDKF YRIPVPEGVGGTGLGLSICKGIVEAHNGSIRAINKSGGGLMMVIRLPLSR	26~~KdpD (1.98443E-120) ~~236,258~~Usp (5.05909E-43) ~~380,430~~DUF4118 (9.45088E-19) ~~505,531~~GAF (0.000000000016542) ~~649,666~~HisKA (0.00000000624432) ~~732,787~~HATPase_c (2.20769E-30) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4.6E-96	329.7	0.6	9.9E-96	328.6	0.4	1.6	1	R4T157_AMYOR	Histidine kinase (EC 2.7.13.3)	kdpD AORI_5977	Amycolatopsis orientalis HCCB10007	861	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis orientalis (Nocardia orientalis), Amycolatopsis orientalis HCCB10007	1156913	>tr|R4T157|R4T157_AMYOR Histidine kinase OS=Amycolatopsis orientalis HCCB10007 GN=kdpD PE=4 SV=1 MDENTTKPRRGELRIYLGAAPGVGKTYAMLGEARRRLDRGTDVVIGLVETHGRKK TAELVEGLETVPRRRSAHREHEFEEMDLDALLARAPEVAVVDELAHTNVPGSRNE KRWQDIDELLDAGIDVLSTVNVQHLQSLNDVVERITGVTQQETVPDEVVRRAEQL ELVDITPEALRRRLAHGNVYPAERIDAALGNYFRPGNLTALRELALLWVADQVDVA LQRYRAEQKITDTWEARERVVVSITGGPESETLIRRASRIANRAGAELQVLHILRG DGLAGMGPTAVGKYRKLTEEVGATFHTVVGDDVPTALLDFAQGVNATQLVVGTS RRSRVARLFDEGIGAAVVQRSGPIDVHMVTHAEAGGRLRARFNRSPLPSTRRLAG WALAFVLPVLSTLLGVLLKEQLDFSTDMVAYMLATVLVALVGGLGPALLAAVLSAG LLNFFFTPPLYTLTVHEPRNVITLIAMVLVAILVAAVVDTAARRATQAARARTEAALL ASYARTVLTHTNPIERLLEKVRENFGMTSVTLLEKRDGKWKRVANAGTDPCADPD QADADIAVTADVHLTLRGRALPASDRGVLEAVAGQALLALRQQRTAKAAIRAERKA EATELRTALLSAVGHDLRTPLTSIKAAIGSLRATDISLSEEDTDELFEAIEESADRLA GLIDNLLDSSRLATGAVRPHLRPVGYDEVVSHALSNVDNSASVVVAIDSRLPSVCA DPGLLERVVANVIDNALRHGASGEPVSARASTHSEYVELRIIDHGRGLKKGTADSA FAPFQRLGGDRDSVPGVGLGLSVAKGFTEAMGGRIRAEDTPGGGLTVVISLPAYV GQDPEKSLLAFDDEGLENEEEERVR	8~~KdpD (1.50294E-121) ~~218,240~~Usp (5.50508E-31) ~~361,387~~DUF4118 (5.97688E-16) ~~481,X,615~~HisKA (0.0000000000236125) ~~680,730~~HATPase_c (7.69372E-22) ~~832	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.8E-96	329.6	0.2	1.1E-95	328.4	0.1	1.7	1	L0J3C9_MYCSM	Histidine kinase (EC 2.7.13.3)	Mycsm_05135	Mycobacterium smegmatis JS623	885	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis JS623	710686	>tr|L0J3C9|L0J3C9_MYCSM Histidine kinase OS=Mycobacterium smegmatis JS623 GN=Mycsm_05135 PE=4 SV=1 MTSHDQPLAPGPSDADDPPTLPASGSDLLPVRASSDADALTHRTDYKKKRGELRI YLGAAPGVGKTFAMLGEAHRRLERGTDLVAAVVETHGRKKTADMLAGIEAIPPKYI EYRGTKFPELDVEAVLKRQPEVVLVDELAHTNTPGSKNPKRWQDVEELLDAGITVI STVNVQHLESLNDVVAQITGIEQQEKVPDEIVRAADQVELVDITPEALRRRLAHGN VYAPERIDAALSNYFRRGNLTALRELALLWLADQVDAALEKYREENKITQTWEARE RVVVAVTGGSESETLVRRASRIASKSSAELMVVHVVRGDGLSGVSAPQMGKVRE LVLSLGATLHTVVGDDVPSALLDFAREINATQLVLGTSRRSRWARIFDEGIGATVV QDSGTIDVHMVTHPEASRGSWWSRVSPRQQHLASWVAALVVPSAICALIVALLD PYLKISGESALFFVGVLVVALLGGVAPAALSAVLSGLLLNYFLIEPRYTLTIAEPDNAI TSFVLLVVAVAVAALVDSAAKRTREARHASQEAELLALFSGSVLRGADLETLLERV RETYSQRAVSMLRVLDGDSEGEIVACVGDDPCVDVDSADTAIEVGDDEFWMLMA GRKLPARDRRVLTAVAKQAAGLVKQRELTEEASKAEAIAQADELRRSLLSAVSHDL RTPLAAAKAAVSSLRSSDIDFSAEDTAELLATIEESIDQLTALVGNLLDSSRLAAGVL RPELQRVYLEETVQRALLAISKGITGFRRQGLDRVKVDVDDAVVMADSGLLERVL ANLIDNALRYAPDSPIRVTAGQVGERVLIAVIDEGPGIPRGTEEQLFAPFQRLGDHD TSIGVGLGLSVARGFVEAMGGTISATDTPGGGLTIEIDLAAPQDGVA	48~~KdpD (2.04736E-123) ~~258,280~~Usp (1.85505E-33) ~~401,424~~DUF4118 (0.000000641491) ~~503,X,654~~HisKA (0.00000000000312127) ~~720,777~~HATPase_c (4.75317E-27) ~~877	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	5E-96	329.5	1.3	8.8E-96	328.7	0.9	1.4	1	C3KRJ3_RHISN	Histidine kinase (EC 2.7.13.3)	kdpD NGR_b12490	Rhizobium sp. (strain NGR234)	901	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Sinorhizobium fredii group, Rhizobium fredii (Sinorhizobium fredii), Rhizobium sp. (strain NGR234)	394	>tr|C3KRJ3|C3KRJ3_RHISN Histidine kinase OS=Rhizobium sp. (strain NGR234) GN=kdpD PE=4 SV=1 MPGDRPDVDTRPSPDALLENAEREARGRLKIFLGAAPGVGKTYEMLVSGRARKS EGVDVVIGIVETHGRQETQALVDGLEAIARRNVEYRGHVLDEMDLDAILARRPQLV LVDELAHTNVEGSRHSKRYLDVEEILAKGIDVYSTLNVQHIESLNDIVAQITRIRVRE TVPDSIIDRADDVEIIDLTPDDLIKRLHEGKVYLPTTAKRAIANYFSPGNLTALRELAL RRTAERVDDQLVSHMQAHAIPGPWAAGDRVLVCIDHGSRGAALVRYAKRQADRL RAPWSAIHVETTGSINLPDADKDRLASHLRLAEQLGGEAITIPGQSVARDILRHAAA HNFTHVVTGKPNKPRWRELIEGSVSHDLIRHAGEISVHVVSGAARAASAARGVKT APPPKQVKLQAYLLSTLYVSIALAFSALLDQVLDVRNLALVLLIGVLTSAVTAGLGPA LYACFVSALAFNFFFLEPRYTFTIRDPESVLALVFFLVVAVTASNLTARVQRQAAAA RQRARTTEDLYLFAKKLASTGTLDDVLWATAHQIASMLKVRVVILLPESGSIAVKA GYPPDDTLVDADIAAARWAWENDRPAGRGADTLPGAKRLYLPLRTGRAAIGVVG LDNDRQGPLLTPEQQRLFDALADQAALAIERVQLVADVDRARLAAEADRLRSALLT SISHDLKTPLAAIMGSAGTLRDYSGAMPEEDRTDLLSTVVDESERLNRFIANLLDM TRIESGATEPNASLHDVGDVVGTALRRAAKMLARHKTAIDAPGDLPMLKLDPVLFE QVLFNLLDNAAKYAPPGSTVRIRAWVDDNSVALQVMDEGPGIPSGDLERVFDSFY RVRKGDHVRAGTGLGLSICRGFIEAMGGTIAAGNRTDRSGAVFTITMPIPVGAPNV EDLT	24~~KdpD (1.45837E-120) ~~234,256~~Usp (6.51996E-42) ~~377,404~~DUF4118 (9.49864E-14) ~~498,530~~GAF (0.000000000677602) ~~649,666~~HisKA (0.00000000000342396) ~~732,785~~HATPase_c (2.42336E-26) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5.2E-96	329.5	0.3	5.2E-96	329.5	0.2	1.7	1	B1M7D3_METRJ	Histidine kinase (EC 2.7.13.3)	Mrad2831_0205	Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	905	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium radiotolerans, Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	426355	>tr|B1M7D3|B1M7D3_METRJ Histidine kinase OS=Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831) GN=Mrad2831_0205 PE=4 SV=1 MPETGRDPTRPSPDALLEAARREERTRGRLKVFLGAAPGVGKTYEMLTIGRARLK AGIDVVVGVVETHGRAETEALLDGFETIPRRRSVPYHGTVLQEMDLDALLARRPALA LVDELAHTNAPGSRHPKRYQDVEELLDAGIDVLTTLNIQHVESLNDVVASITRIRVR ETVPDGVLDRADDIEVVDLNPDDLIQRLKDGKVYVPTHAERALKHYFSRGNLTALR ELALRRTADRVDDELLGHMRANAIAGPWAAGERVLVCVNEDPRSSGLVRYAKRL ADRLHAPWTALSIEGARAAALSEAERDRIAEALRLADRLGGDAVTLPGGRRIADDV LDYARSANVNHIVVGKAHRSWLFELLNGSVVHDLVRRSGAISVHVVPGEAVPDET PPRRAVAVTAPRPGFDARPYAIALAAIAAGLGAAIVAEPYAGVENADLFLLTAVVAV AVRWGLGPALAAVVAASLAYNFFFLPPVYTLTIADPTNVAAFLLFTLVAVLVSNLAS RARRVAVVSQGRARATERLFGFSRKLAACGTLDDVLWATCAQVAAMLKVRVVLL LPDGQAVTVRAGYPPEDMLDEADLAAAQWAFDNDRPAGRGADTLPGAKRLFLP MRTGRGTIGVIGLDSDGTGPILSPEGRRLLDALADMGALAIERVRLVEDLDRAERA AETDRLRQALLTSISHDLRTPLASVLGAASTLRDLDAALPAEAKAELLATIIEESERL NRFIANLLDMTRLEAGAVAPNLSAQDVAETVDTALRRTQKILADHRVAVEVEADLP ALALDPVLFEQVLVNLLDNAAKYAPEGSTVTVRARRAGDRVRIAVLDEGDGLPDA DVERVFDKFYRVRKGDRVRAGTGLGLAISRGFVEAMGGTVTAENRRDRGGACFT VSLPVPARNAPRDIAA	27~~KdpD (4.82554E-119) ~~235,257~~Usp (1.33485E-38) ~~381,431~~DUF4118 (0.0000000554893) ~~507,534~~GAF (0.00000000000407333) ~~653,670~~HisKA (0.0000000000016489) ~~736,789~~HATPase_c (3.02216E-28) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5.6E-96	329.4	0.3	8.9E-96	328.7	0.2	1.3	1	B4E5Q8_BURCJ	Histidine kinase (EC 2.7.13.3)	kdpDBCAL2380	Burkholderia cenocepacia (strain J2315))	947	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia cenocepacia, Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) (Burkholderia cepacia (strain J2315))	216591	>tr|B4E5Q8|B4E5Q8_BURCJ Histidine kinase OS=Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) GN=kdpD PE=4 SV=1 MNRPDPDQLLDKLQRDEEKQRRGQLKIFFGASAGVGKTYAMLQAARQRRQDGV DVVVGIVETHGRSETAALLDGLDVLPPARIDYRGRTLAEFDLDGALARAPQLILVDE LAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWET VPDRVFDAADEVTLVDLPAEELLERMRDGKVYLAQQAERAVRNFFRKGNLIALRE LALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPTLVRAAARLAA SLKADWIAVYVETPRLQRLPDARRQRTLDALKLAAELGAETATLAGADAVAALIGY AKVRNVSKLVAGGSPKVGLARRFARPFGEQLAERAGDVDLMLIRASASDEARAAP LDARARDWRDAFAQFGTHRSPPRHYAYAAAICAAITVVASVVSGRLDLTNLVMLY LLGVVFSAVRLGRGPGVLQSFLSVAAFDFFFVPPRMSFSVSDTQYLLTFFGMLLT SLVISHLTSTLTRQASVAQRRERRTGAIYAMARELGAALTTEQIVEIGSRHVGEVFR ARVAFLLPDSADQVRQKIEEPDAAVTLTGAELDSDVGQWVYDQQKPAGRGTDTL PATAALYLPLKAPMRTRGVLAVASREPRELEVPEQQRMLDAFAAQIALALERVHY VEIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLANGRAAAQAGDAAA AARLAQREGELVDAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGA ALAACRRVLARHPARVALPADLPLLQMDAVLMERLFTNLFENAAKYTPPDTSLDIG AERVTDDGQPFVRVHVDDHGPGLPAGMETRIFDKFTRGEKESATPGIGLGLAICR AIVEAHGGKIGALNRTAPDGHVTGARFWFTLPVDTPPAAPAVSDDEPDLPGASPP SESLPDHE	21~~KdpD (2.62463E-113) ~~230,252~~Usp (6.16622E-32) ~~374,422~~DUF4118 (2.73463E-19) ~~510,536~~GAF (2.2816E-18) ~~659,676~~HisKA (0.0000000000771902) ~~752,805~~HATPase_c (1.49668E-21) ~~915	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	6.2E-96	329.2	0	1.1E-95	328.4	0	1.4	1	C4LDL9_TOLAT	Histidine kinase (EC 2.7.13.3)	Tola_1195	Tolumonas auensis (strain DSM 9187 / TA4)	897	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Tolumonas, Tolumonas auensis, Tolumonas auensis (strain DSM 9187 / TA4)	595494	>tr|C4LDL9|C4LDL9_TOLAT Histidine kinase OS=Tolumonas auensis (strain DSM 9187 / TA4) GN=Tola_1195 PE=4 SV=1 MPLDNDDQRPDPDELLAEVRSPRGRLKIFFGACAGVGKTYAMLQEAKRLRAEGL DVLVGVVETHGRSETAALLEGLTPLPLKQVHYRKHTFHEFDIDGALSRAPALVLVD ELAHSNMPGSRHPKRWQDVEELLAAGIDVLTTLNVQHLESLNDIVGSITGIRVRET VPDRLYEEADEIVLVDLPPDDLRRRLDEGKVYLPQQAERAIEHFFRKENLIALRELA LRCTADRVDDQMQAYRHSGEPVWHTRDAILVCIGPGSGNEKLVRVAARLASRLG CVWHAVYVETPRLHRLPEQERRSILSTLHFAQELGAETSTLPAQDEADAILYYARE HNLGKILIGRHQKKPWYRWGQSRFAHRLGTKGPDLDLLIVSLTDTEHAASTLLPAD IRHKDEKWQREATGIGAALLSCIVITFLSTILVSYLAPLNIVMLYLLGVVFVALQYGR MSASIAAILNVASFDFFFIAPHFSFAVSDVQYLLTFAVMLLVGLLIGQLTAWARYQA RVARYREERARHLFEMAKELSSALTAEDIAHISAHFLNRSFRANSMLLLPDDQKILH CVGKKPLQVDHAIAQWCFDHNAHAGMGTDTLPAAAQRYVPLITPLQTLGVLMLEP ANLRLLMIPEQQRLLDTYALLISVALERLKFARVAETAKLQSETERLRNALLAALSH DLRTPLTVLFAQAEILMQSLALEQSPHIQQANAIRTQVLGTTRLVNNLLDMARLESE GVHLRKEWQSLQEIAGSALATLNIPLTGHPLNINIPPDLPLLHCDGVLIERVLVNLLE NGCKYAGDGITIGIDVTESKDFLQVTVWNLGPELPVGKEKLIFEKFARGEKESSIP GIGLGLAICRAIVETHGGKIWAENRVGGGVNFHHFTLPLQPLPELEPELVNNNE	23~~KdpD (7.10733E-125) ~~231,252~~Usp (2.2779E-41) ~~374,407~~DUF4118 (2.23453E-21) ~~503,531~~GAF (0.0000000000041742) ~~644,661~~HisKA (0.00000000419789) ~~726,779~~HATPase_c (6.71829E-25) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.2E-96	329.2	0	1.6E-95	327.9	0	1.8	1	Q741U1_MYCPA	Histidine kinase (EC 2.7.13.3)	kdpD MAP_0996c	Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	858	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium avium complex (MAC), Mycobacterium avium, Mycobacterium paratuberculosis, Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	262316	>tr|Q741U1|Q741U1_MYCPA Histidine kinase OS=Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10) GN=kdpD PE=4 SV=1 MMVDVTDVRDHHPKRGELRIYLGAAPGVGKTYSMLGEAHRRLERGTDLVAGVVE THGRAKTAELLEGIEIIPPRYIEYRGGRFPELDVPAVLARHPQVVLVDELAHTNTPG SKNPKRWQDVEELLDAGITVISTVNVQHLESLNDVVAQITGIEQKETVPDSVVRQA SQVELIDITPEALRRRLSHGNVYAPDRIDAALSNYFRRGNLTALRELVLLWLADQV DTALAKYRAENKITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVH VIRGDGLAGLSESRMAKIRELASSLDASLHTIVGDEVPAALLEFAREMNATQLVIGT SRRSRWARLFEEGIGPRIVELSGKIDVHLVTHEESKRGFRASSLAPRERRVASWL AALIVPSVICAVTVTWLDPYLDTGGESALFFVGVLLVGLLGGIAPAALSAVLSGLLL NYYLIAPRHSFTIAEPNSAITELVLLLIAVAVAVLVDFAAKRTREARRASQEAELLTLF AGSVLRGADLETLLERVRETYAQRSVSMLRESEDARAGGTKTQVVACVGRDPCV SVDAADTAIEVGGPDSSEFQMLLAGRKLSARDRRVLSAVARQAAGLIRQRELAEE ASRTEAIVRADELRRSLLSAVSHDLRTPLAAAKVAVSSLRAEDVAFSPTDTAELLAT IEESIDQLTALVGNLLDSSRLAAGAIHPDLRRVYLEEAVQRALVSIGKGATGFFRSAI DRVKVDVGDAMVMADAGLLERVLANLIDNALRYAPNCVVRVNAGQVGDRVLISVI DEGPGIPHGAEEQIFEAFQRLGDHDNTTGVGLGMSVARGFVEAMGGTITATDTP GGGLTVMVDMAAPQSEGAA	13~~KdpD (2.84277E-122) ~~223,245~~Usp (1.14912E-33) ~~366,X,626~~HisKA (0.0000000000390949) ~~692,749~~HATPase_c (4.46982E-26) ~~847	kinase	KdpD;Usp;X;HisKA;HATPase_c
	6.5E-96	329.2	0.2	9.5E-96	328.6	0.1	1.3	1	D2Q286_KRIFD	Histidine kinase (EC 2.7.13.3)	Kfla_6791	Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	854	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Kribbella, Kribbella flavida, Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	479435	>tr|D2Q286|D2Q286_KRIFD Histidine kinase OS=Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399) GN=Kfla_6791 PE=4 SV=1 MGGMAGRGRLRIYLGAAPGVGKTYKMLGEAQRRRERGTDVVVGFVETHGREHT AAMLDGLEVVPRRLVDHRGASFTELDLDALLARRPQVALVDELAHTNVPGSRNAK RWQDVDELLGAGIDVISTVNIQHLESINDVVEKITGVPQRETVPDRVVRAAHQIELV DMAPEALRRRMAHGNVYAADKVDAALGNYFRIGNLSALRELALLWLADRVDAGL QQYREQHQIDTTWEARERVVVALTGGPEGETLIRRAARIAARSAGGDLLAVHVTR SDGLTGADPGRLAQQRQLVESLGGSYHQVVGDDVPAALLTFARAENATQLVLGG SRRTFLSTLLTGPGIGATTIRESGDIDVHIVTHAEMGRGRLPQAQGSLSRRRLAYG FALAVLLPPVLALALGLGGDTLNLTSNVLAFLFAVVVVALVGGLWPALLTAVAGTV VLNFFFTPPTRAFTIAEPNNALALGIFVAVAALVSSVVDRAARRTRQAARAAAEAET LATLAGTVLRGETALQALLERVREAFGMTSACLMERVDSDELTETWRPLASAGTP TCRRPEEGDAEIPGRDGLVLVLQGRSLAADERRLVGAFAAHAAALVDRVRLSEAA AEAKPLAEADKLRTALLRAVGHDLRSPLASAKASVTSLRSSDVDWSPAERDELLA TADESLDRLSRLVDNLLDLSRLQAGVLPVFTRPTALDEILPGVLAELGPAEVTIDLP GTLPLVDADPALLERVVANLLTNAIRYSPPGREPLLTGSVLGDVVEIRVVDRGPGL PAEDRDRVFAPFQRLGDTDNTTGVGLGLALARGLAEAMGGSLRPEDTPGGGLTM VVSMPSATMAEDAPVPGRLERGGTR	5~~KdpD (3.75779E-122) ~~215,237~~Usp (6.41215E-23) ~~360,421~~DUF4118 (0.000340319) ~~479,X,617~~HisKA (0.0000000000537323) ~~683,732~~HATPase_c (7.88241E-25) ~~832	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	6.6E-96	329.1	1.3	1.2E-95	328.3	0.9	1.4	1	A4FMI4_SACEN	Histidine kinase (EC 2.7.13.3)	kdpD SACE_6086	Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	879	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharopolyspora, Saccharopolyspora erythraea (Streptomyces erythraeus), Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	405948	>tr|A4FMI4|A4FMI4_SACEN Histidine kinase OS=Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338) GN=kdpD PE=4 SV=1 MAGKSARRGELRIYLGAAPGVGKTYAMLGEAHRRAARGTDVVVGLVETHAREKT AALLDGLEVVPRRRIAHRGVEVTEMDLDAVLARRPEVAVVDELAHTNAPGSRNEK RWQDIDELLDAGINVLSTVNVQHLESLNDVVEAITGVRQQETVPDEVVRRAGQIEL ADITPEALRRRMAHGNVYSADRVDAALGNYFRTGNLTALRELALLWLADQVDVAL RRYRAERKITDTWEARERVVVSITGGPESETLIRRARRIAARAGAELQVVHVLRGD GLAGASPGNLARARRLADGVGASFHTVVGDDVPEALLEFARGADATQLVVGTSR RSRWARLLDEGIGAAVVQKSGSIDVHMVTHPEAGGRRLFKNIARNPLSSARQLW GWVLALALPSAVTALAYFSGAMALSADVVGYFLATVVVALVGGMAPAITAALLSG GLLNFFLTPPLYSLTIAEPQNVVTLLAMLFVGLLVAILVDRAARLAERAAHARTEAAL LASYARTVLTHPDPLPRLLEKVVENFGLTSAALLERQEGDWHVAASTGPRPCTRP GESDVDIEVNPDVHLVLKGPGDRALPAADRTVLEGAAGQALVALRQQRMAAEAR EAQRRADATELRTALLSAVGHDLRTPLASIKASVSSLRAPDLRLSEEDTTELLTGVE ESADRLTALVDNLLDSSRLATGAIVPRLDPVGYDEIVFRALAGLDGRQHVDIDTDE SLPDVLADAGLLERVVANVVQNALKYGRPEGGRIGVRASAHASWVELRVVDHGP GLPEGAAETVFAPFERLGDRGGRGDQGETGVGLGLSVAKGFMEAMQGSIRAED TPGGGLTIVLSLPAASPAVGDGVGSAGDGAVVHGGGAAPGAVVPADVDEQGRR	6~~KdpD (1.27886E-121) ~~216,238~~Usp (5.84955E-25) ~~359,386~~DUF4118 (0.000000000000405423) ~~479,X,616~~HisKA (0.0000000000221626) ~~681,731~~HATPase_c (8.05383E-25) ~~838	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	7.1E-96	329	0.7	1.1E-95	328.4	0.5	1.3	1	A4JGG6_BURVG	Histidine kinase (EC 2.7.13.3)	Bcep1808_2370	Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))	997	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia vietnamiensis, Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))	269482	>tr|A4JGG6|A4JGG6_BURVG Histidine kinase OS=Burkholderia vietnamiensis (strain G4 / LMG 22486) GN=Bcep1808_2370 PE=4 SV=1 MNRPDPDQLLDKLQRDAAKQRRGQLKVFFGASAGVGKTYAMLQAARQRKQDGV DVVVGIVETHGRSETAALLDGLDVLPLAHIEYRGRTLAEFDLDGALARAPQLILVDE LAHSNVQGARHLKRWQDVHELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWET VPDRVFDAADEVTLVDLPAEELLERMRDGKVYLAQQAERAVRNFFRKGNLIALRE LALRRTADRVDAQMREYRADRSIQRIWQARERLLVCIGPGPEAPTLVRAAARLAA SLKADWIAVYVETPRLQRLPDARRQRTLDALKLAAELGAETATLAGDDAVAALIGY AKVRNVSKIVAGGSPKVGVVRRFARPFGEQLAERAGDVDLMLIRASASDEVRAAP LDARARDWRDAFAQFGTRRSPPRHYLYAAAICAAITGLASVVSGRLDLTNLVMLYL LGVVFSAVRLGRGPGVLQSFLSVAAFDFFFVPPRMSFSVSDTQYLLTFFGMLLTS LVISHLTSTLTRQASIAQRRERRTGAIYAMARELGAALTTEQIVEIGSRHVSEVFRA RVAFLLPDSADQVRQKIEDPDAAVTLTGAELDSDVGQWVYDQQKPAGRGTDTLP ATAALYLPLKAPMRTRGVLAVVSREPHELEVPEQQRMLDAFAAQIALALERVHYV EIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLANGRAAAEGASASLAS PASPESSASPVSSAAPAAPAAPTTPTTPTTPTTPAPPSPLDAAAAQRLAQRERELV DAIHDEALRMTGIVTNLLDMARLQAGSLQIKRQWSLLEETVGAALAACKRVLARHP ARVSLPADLPLLQMDAVLMERLFTNLFENAAKYTPADAPIEIGAERVSDDGQPFVR VYVDDHGPGLPHGMETRIFDKFTRGEKESATPGIGLGLAICRAIVEAHGGKIGALN RTAPDGRVTGARFWFTLPVDTPPAVPAAPDDDIDDDIDAPGASFPSEPLPDHD	21~~KdpD (4.53325E-113) ~~230,252~~Usp (2.79606E-32) ~~374,410~~DUF4118 (4.66414E-22) ~~510,536~~GAF (1.03045E-17) ~~659,676~~HisKA (0.000013224) ~~798,851~~HATPase_c (2.62652E-22) ~~961	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	7.2E-96	329	0.3	1.1E-95	328.4	0.2	1.3	1	Q2SZS1_BURTA	Two-component system, sensor kinase protein KdpD (EC 2.7.3.-) (Universal stress family protein)	kdpD BTH_I1024 DR63_2806	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	1035	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, pseudomallei group, Burkholderia thailandensis, Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	271848	>tr|Q2SZS1|Q2SZS1_BURTA Two-component system, sensor kinase protein KdpD OS=Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301) GN=kdpD PE=4 SV=1 MNRPDPDQLLDKIQREEEKQQRGKLKIFFGASAGVGKTYAMLLAARARKQEGVD VVVGIVETHGRSETASLLDGLDVLPLMQIEYRGRTIGEFDLDAALARKPQLVLVDEL AHSNVPGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWETV PDRVFDVADEVTLVDLPAEELLSRLREGKVYMAQQAERAVRNFFRKGNLIALREL ALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPTLVRAAARLAAS LKADWLAVYVETPRLARLPDALRQRTLNALKLAAELGAETATLTGADAVAALIGYA QVRNASKIVAGGSSKTGFLRRFSRPFGERLAERAGDVDLMLIRASAGEDARTPLD AGARAWRDTLSSVVDGRSPPRNYGYAAAICALITGVANLLQGHLDLTNLVMLYLL GVVFSAVRLGRGPGVVQSFLSVAAFDYFFVPPRMSFSVTDTQYLLTFFGMLLTSL VISHLTSSLTRGATIAQRRERRTSAMYAMARELGAALTAEQIVEIGSRHVSEVFRA RVAILLPDSGDKIQQKIENPDEAVTITGAALDIDVGQWVYDQQKPAGHGTDTLPAA TALYLPLKAPMRTRGVLAVVTKDPGELEVPEQQRMLDAFAAQIALAVERVHYVEIA RDALVNMESERLRNSLLSAISHDLRTPLTAIVGLSSMLANARGGGSSAREDELVES IHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGAALAACKRVLARHPA RVRLPADLPLLQTDAVLMERLFANLFENAAKYTPLDTPIEIGAERIVDDSRPFVRVF VDDHGPGLPAGMEARIFEKFTRGEKESATPGIGLGLAICRAIVDAHGGKIGALNRL GPDGKVEGARFWFTLPVDTPPPEPGAGDDAPDDEAGEAGAAGAAAGGADEAAA GGPSAGEPPAGAGSRSVFGDRFAAARAAGEFDAEERTAGERESGGRTAGDRAP DAAADPARPASGQAAAASSAPRRAEGAPSPVSNEHPHAHE	21~~KdpD (1.52988E-122) ~~230,252~~Usp (2.92886E-30) ~~374,409~~DUF4118 (7.61905E-21) ~~508,537~~GAF (1.18882E-16) ~~658,675~~HisKA (6.51991E-14) ~~741,794~~HATPase_c (2.88073E-22) ~~904	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	7.6E-96	328.9	0.3	1.3E-95	328.2	0.2	1.4	1	E1T3S2_BURSG	Histidine kinase (EC 2.7.13.3)	BC1003_2353	Burkholderia sp. (strain CCGE1003)	957	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. (strain CCGE1003)	640512	>tr|E1T3S2|E1T3S2_BURSG Histidine kinase OS=Burkholderia sp. (strain CCGE1003) GN=BC1003_2353 PE=4 SV=1 MNRPDPDELLDKLQRDEQKRQRGKLKIFFGASAGVGKTYAMLQAARRRRDEGAD VLVGIAETHGRGETAALLEGLELLPLAQIEYRGRKLGEFDLDAALARKPQLILVDEL AHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETV PDRVFDRADEVTLVDLPAEELLDRMRDGKVYLAQQAERAVRNFFRKGNLIALREL ALRRTADRVDAQMHEYRADRSIERIWQARERLLVCVGPGPEAPTLVRAAARLAAS LKADWIAVYVETPALQRLPDARRERTLNALKLAAELGAETATLAGTDAVAALTGYA QARNVSKLVAGASTRTGIARWLRRPLGERLAEQGSHADITLIGLSSAGGSGEQRR LLDTTANAWRDALSAARERRSPARAYAFALAICAGITAVASQLLARIDLTNLVMLYL LGVIFAAAKLGRGPGVLLSFLSVAAFDFFFVPPRLSLSVSDTQYLLTFFGMLLTSLVI SHLTSSLRREARVARRREQRTGAMYAMARELAAALTAEQIVGIGSRHVSEVFGAR VAILLPDSADRVRQKIEDADAAITLEGELLDTDVGQWTYDHQKPAGHGTDTLPAAA ALYLPLKAPMRTRGVLAVVLRDERELSVPEQQRMLDAFAAQIALALERVHYVDIAR DALVSMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAQSREQAGDARRDDELVEA IHEEALRMTGIVTNLLDMARLQAGSLQLNRQWTLLEETVGAALRACRRVLAGHPV RVELPADLPLLHLDAVLMERLFSNLFENAAKYTPPGTPLTIGAQRVDEDGKSFVRV SVDDNGPGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEAHGGSIGAINR VSAQGAGPLAAAGAGGRVEGARFWFTLPVDTPPDVTHAADALEEESADNLRPDP PPTEPARPAHE	21~~KdpD (8.20815E-113) ~~230,252~~Usp (5.91381E-30) ~~375,412~~DUF4118 (1.84092E-18) ~~509,540~~GAF (2.45705E-18) ~~661,678~~HisKA (0.000000000000640732) ~~745,798~~HATPase_c (6.09437E-21) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.9E-96	328.9	0	1.2E-95	328.3	0	1.3	1	Q8ZQW4_SALTY	Histidine kinase (EC 2.7.13.3)	kdpD STM0703	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella typhimurium, Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	99287	>tr|Q8ZQW4|Q8ZQW4_SALTY Histidine kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=kdpD PE=4 SV=1 MNDEPLRPDPDRLLEQTPPPHRGKLKIFFGACAGVGKTWAMLAQAQRLRAQGLD VVIGVVETHGRKETAALLDGLTILPPKRHSHRGRQIREFDLDAALARRPALILMDEL AHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETV PDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIAGQAERAIEHFFRKGNLIALRELAL RRTADRVDDQMRAWRAHPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRL GSVWHAVYVETPTLHRLPEKQRRAILSALRLAQELGAETATLSDPAEEKAVVRYA REHNLGKIVMGRPASRRWWRRDAFADRLARRAPDLDQVIVALEEPPARALAQTP DNRPFKEKWRGQIQGCLVAVALCAITTLIAMQWLVTFDAANLVMLYLLGVVVIALL YGRWPSVVATVINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGV RYQARVARYREQRTRHLYEMSKALAVGRSEHDIAATSERFIASTFQARSQILLPDA NGKLLPLTHQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSADKT YGLAIVEPGNLRQLMVPEQQRLLETFTLLVANALERLTLTASEEQARLASERESIRN ALLAALSHDLRTPLTVLFGQAEILTLDLASAGSPHARQASEIRQHILNTTRLVNNLLD MARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLLHPITLSLPQQLTLIHVDGPLFE RVLINLLENAVKYAGPQASIGIDAAVKDDRLQLDVWDNGPGIPAGQEQKIFDKFAR GNKESAVPGVGLGLAICHAIVEVHGGTLTAYNRPQGGACFRVTLPQGKPPELDDF HEDM	20~~KdpD (2.60408E-127) ~~230,253~~Usp (8.68063E-43) ~~373,403~~DUF4118 (1.02757E-20) ~~501,530~~GAF (2.81335E-14) ~~644,661~~HisKA (0.00000000225602) ~~726,778~~HATPase_c (1.22562E-31) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.1E-96	328.8	0.3	1.3E-95	328.2	0.2	1.3	1	A0A0F2TI26_9ACTN	Histidine kinase	VM95_06620	Streptomyces rubellomurinus	851	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rubellomurinus	359131	>tr|A0A0F2TI26|A0A0F2TI26_9ACTN Histidine kinase OS=Streptomyces rubellomurinus GN=VM95_06620 PE=4 SV=1 MARDLTPGTGTRRGRLRVYLGSAPGVGKTYRMLDEARRRQERGADVLVGYIECH GRRHTEAMIDGLEVQPRVHRSYRDAEFEEMDLDGVLARRPSVVLVDELAHTNIPG GRHAKRWQDVEEILAAGIDVITTVNIQHLESLNDVVQKITGIPQRETVPDEVVRRAD QIELVDMAPQALRRRMAHGNVYKAEKVDAALSNYFRVGNLTALRELALLWVAGR VDEGLRDYRASHNIDRVWETRERVVVALTGGPEGETLIRRAARIADRTAGGDLLA VHVSRSDGLAGASSGALAQQRLLVETLGGSYHVVVGDDIPTALLAFARAHDATQL VLGTSRRGRITRFLTGPGIGETTVDASEDIDVHMVTHEFTGRGRLPSLGRRHSRR RTVVGYLAGLALPWLLTAVLSQAHATINLTTDALIFQLGVVIVALLGGATSALLAAFI ASVLLNYYFIPPVHSLTIGETNNIVALVVFAAIALAVSTVVDHAGKLTTRAARATAEA ETLSTLAGSVLRGADALPALLEKSRTAFGMRTVTLLSRTGEVLAHSEADHPDDGS GEHETTEVPVGADALLVLTGRRLPAADQRVLTAFAAHVAAALERDRLAVVAAEVE PIKAADRMRTALLAAVSHDLRTPLAAALASVGSLRSPDVEFSPEDQAELLATADES LVKLTRLVDNLLDMSRLQAGALTLHLTETHLDEILPRALDSLPDPDAPVQPLDLDTT PPVLADPPLLERVLANVITNALRHNAPGAPVLVTASHHADLVEIRVIDRGPGIAPED RDRVFLPFQRLGDTDNTTGVGLGLALSRGLAEAMGGSLEVEDTPGGGTTMLLTL PAATTTDFGEEPAHHE	12~~KdpD (9.10268E-118) ~~221,243~~Usp (1.59309E-29) ~~366,387~~DUF4118 (0.0000000126596) ~~485,X,617~~HisKA (0.00000000000895252) ~~683,734~~HATPase_c (5.8517E-29) ~~835	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.7E-96	328.7	1.6	1.3E-95	328.1	0.7	1.6	1	G7ZDP0_AZOL4	Histidine kinase (EC 2.7.13.3)	kdpD AZOL_p20517	Azospirillum lipoferum (strain 4B)	917	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum lipoferum (strain 4B)	862719	>tr|G7ZDP0|G7ZDP0_AZOL4 Histidine kinase OS=Azospirillum lipoferum (strain 4B) GN=kdpD PE=4 SV=1 MTDDQGGRNQRPSPDALLRQAEREGRGRLKIFLGAAPGVGKTFAMLLTAQAKRR DGADLVVGVVETHGRADTEALVAGLEIVPRRIVRHKGHALAEMDLDAILARRPKIVL VDELAHTNAPGSRHAKRYLDVQELLDAGIDVYSTLNIQHVESLNDVVAKITRVRVR ETVPDSVIDRADDIEVIDLTPEDLIQRLKEGKVYVPRTAEQAIRHYFSPGNLTALREL ALRRTADRVDDQLLTHMQAHAISGPWAAGERLLVCIDQDANCGALVRYARRQAE RLRARWGAIHVETSRDLRLSEAERDRIADTLRLVERLGGEAVTIPGRDVADAVVEY ARANNITHLVIAKSGRPRWSELLHGSVAHSLIRRAGDISVHVIAAANPGANPGDTV PPKTVRTETDGRWSFHGLPYLAATGYVAAALGLGHLLHLALGLSNIALVFLTAVLA SAVTGGLGPSLYACIASVLSFNYFFLPPLYTFTISDPENIVALLVFAVVAAIASNLTA RVRAQALTARQRAKTTEDLYRFSRKLAGVVTMDDLLWATAYQIAAMLKAHVVLLM PDGDGQADRLTVRAGYPPEDVLEEADLAAAMWSWQNNKPAGRGADTLPGARW LFLPMRTGRGPVALVGVDTGGGDRSRKSGLLSPDQRRLLDALGDQAALAIERVM LAEDVDRAKLAAETERLRSALLTSISHDLRTPLASILGSATSLTRYGSTLDEAGRLD LATNIQEEAERLNRFIANLLDMTRLESGAVRPRSGPVDLSELVGSALERTGRILAG HHVEVDLAPDLPMVDLDPVLFEQVLFNLLDNAAKYAPAGSRVTVRARRLGDAVEV RLMDEGDGIPPADVDRIFDKFYRVHAQDRQRAGTGLGLAICRGFVEAMGGAIAAG NRSDRSGAVFTLTIPAAADLPALEDSSL	24~~KdpD (2.16574E-121) ~~234,256~~Usp (4.23018E-43) ~~379,435~~DUF4118 (2.25885E-15) ~~510,536~~GAF (0.00000000000542964) ~~664,681~~HisKA (0.0000000000420856) ~~747,800~~HATPase_c (3.01098E-27) ~~903	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	8.8E-96	328.7	0.5	1.3E-95	328.1	0.3	1.3	1	A0A0B4XAK7_9RHIZ	Histidine kinase (EC 2.7.13.3)	kdpD RGR602_PC00988	Rhizobium gallicum bv. gallicum R602	902	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium gallicum, Rhizobium gallicum bv. gallicum, Rhizobium gallicum bv. gallicum R602	1418105	>tr|A0A0B4XAK7|A0A0B4XAK7_9RHIZ Histidine kinase OS=Rhizobium gallicum bv. gallicum R602 GN=kdpD PE=4 SV=1 MPDDRSDQAARPSPDALLVKARAETRGRLKIFLGAAPGVGKTYEMLVSGRAKLAD GVDVVVGVVETHGRKETQALLDGFSTIPRAKVQYKGHTLEEMDLDAILARKPDLVL VDELAHTNAEGSRHPKRYLDVKELLDRGIDVYTTLNIQHVESLNDVVSQITRIRVRE TVPDSVIDLADDIEIIDLTPDDLIKRLHHDGKVYVPKTAERALSNYFTPGNLTALRELAL RKTAQRVDDQLVSHMQAHAISGPWAAGERVLVSIDQHPRSASLVRYATRMASRL RAPWSAVYIETNQSVSLTEEQRDTIAATLRLAERLGGEALTLPGAGVAEELLRHAS ANNVTHIVVGSPVKAPWRQWFQHSPVDELIRRAGGISVHVISGNEKGGNAGRGV KPAPALPAFNIKAYVLATIYVAAALAFSTVLDQVLDVRNLALVFLMAVLTSAVLHGL RPALYSCILGALAFNFFFLPPRFTLTIRDPESVVAFFFFIGVAVIASNLTATVQRQAA AARQRARTTEDLYLFSRKLASTGTLDDVLWATAFQIASMLKVRVVLLLPEGGTIAV KAGYPPDDTLDDADIAAARWAWEHNHAAGRGADTLPGAKRLYVPLRTGRTAVGV IGLDSDRRDGPLFTPEQQRLLDALADQAALAIERIQLVADVDRAKLAAEADRLRSAL LTSISHDLKTPLAAILGAAGTLRDYFGSMPVEDRNDLLATIIDESERLNRFIANLLDM TKIESGAMEPNDGLHYPGDIAGSALRRAAKILEGHEAQMIMPADLPMVRVDPVLFE QALFNLLDNAAKYAPEGSAIRIEGFVDAGNVVIQIADEGPGIPPPDLTRVFDTFYRV RKRDQVRAGTGLGLSICRGFIEAMGGTIDAGNRKDRCGAVFTIRLPEADDIPKLDE LK	26~~KdpD (1.09535E-110) ~~234,256~~Usp (1.91647E-43) ~~379,404~~DUF4118 (1.85888E-16) ~~499,530~~GAF (0.00000000560502) ~~650,667~~HisKA (0.000000000000823456) ~~733,786~~HATPase_c (3.88757E-27) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.9E-96	328.7	0.3	3.8E-95	326.7	0.1	1.9	1	A8GB59_SERP5	Histidine kinase (EC 2.7.13.3)	Spro_1245	Serratia proteamaculans (strain 568)	897	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia proteamaculans, Serratia proteamaculans (strain 568)	399741	>tr|A8GB59|A8GB59_SERP5 Histidine kinase OS=Serratia proteamaculans (strain 568) GN=Spro_1245 PE=4 SV=1 MVEEEQQRPDPDSLLALANEKPRGRLKVFFGACAGVGKTYAMLQEAQRLRAQGL NVLVGVVETHGRSETAALLGGLDLLAQKRIQYRGRMVQEFDLDAALARHPALILM DELAHSNAHGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGGVTGVRV RETVPDHVFDEATEVVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIAL RELALRRTADRVDDQMRAFRDTQGRERVWHTRDSILLCVGHNSGNEKLVRIAAR LAARLGCHWHAVYVETPKLHRLPESQRRAILRALRLAQELGAETATLSEPDEERA VLRYAREHNLGKIIIGRRSEQRWKLRGSFADRLGKLGPDLDLVIVALENDSPPQPG KEHDSRNFGEKWRMQLRGCAVAVALCALITLLSQWLLPGFDQANLVMVYLLGVAI VALFFGRWPSVLAAVINVASFDLFFVQPEWSFAVSDMQYLLTFGVMLTVGITIGNL TAGVRYQARVARYREQRARHLYEISRGLSQALTTEDIAKTSRHFLSSSFQAKTVLL LPQEDGKLQQMVGETGGLLSVDEAIARWSFDKGMPAGAGTDTLPGVPYQLLPLA TSKQTFGLLAIEPSNLRQLMVPEQQRLLQTFAVLIASALERLHLARSAEEAKLDAER EQLRNSLLAALSHDLRTPLTVLFGQAEILTLDLAAEGSNHATQASQIRQQVLSTTRL VNNLLDMARIQSGGFNLRKEWQSLEEIVGASLHMLEPLMTQHQIKVELPAELVLVN CDGSLLERVFTNLLENANKYAGYDATIGIRAHTLPEWLEVEVWDDGPGIPEGKMQ LIFDKFSRGNKESAIPGVGLGLAICRAIIEVHGGRIWAENGANGGASFRFVLPLEKP PEIDSEAFDL	23~~KdpD (1.04268E-108) ~~231,254~~Usp (1.15088E-40) ~~374,404~~DUF4118 (4.3445E-21) ~~502,528~~GAF (3.2978E-16) ~~646,663~~HisKA (0.000000000437894) ~~728,781~~HATPase_c (8.2579E-31) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	9E-96	328.7	0.1	2.7E-95	327.2	0	1.8	1	A0A090ADE5_9GAMM	Histidine kinase (EC 2.7.13.3)	THII_1571	Thioploca ingrica	909	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Thiotrichaceae, Thioploca, Thioploca ingrica	40754	>tr|A0A090ADE5|A0A090ADE5_9GAMM Histidine kinase OS=Thioploca ingrica GN=THII_1571 PE=4 SV=1 MDDKRPDPDELLNKIQQEEAKQQRGRLKIFFGGCAGVGKTFAMLSAAGAQRQQ GIDVVAGVVETHGRSETAQLLADLEVLPPKLIEYRDRQLPEFDLDGALARKPSLILI DELAHSNVAGSRHPKRWQDVEELLTAGISVYTTVNVQHLESLNDIVGQITGIRVW ETVPDHVFEKADEITLVDLTPDELLQRLKEGKVYLPQQAEHAIQHFFRKGNLIALRE LALRRTADRVDAQMRDYRADRSIHPVWQAKERLMVCIGSSLEGDQLVRSAARLA TGLRADWLAVYVETPGLQRLPANHRDRILKTLKLAQELGAETAVLSGSELASTLMS YARSHNVTKWVVGKSSRSSLARLWRTSLADELANRSQDIDVYVVSHTLASETAAT LPAANAISLEFEENSERQPQGYVWAIAAGIGVTFIAAGLSNFLDLANVIMLYLLAVVL VTVRFGRGAGVFASILSVVIFDFFFVPPKLSLTIADTQYLFTFVVMLVISLIISHLTASL RYQARVASYRERRASALYALSKELSSALTVAQIIEISTEHLRGMFQAQIALLLPDSR EKVRQPVAEMQENPRFSLFDPGIAQWVYDNQQPAGLGTNTLPANPVLYLPLRAP MRTRGVLAMAQANSRQIFQPEQQRLLDTFAAQIALALERVHYVEIAQDVLVSMEA ERLRNSLLSAISHDLRTPLTAIVGLSSTLSTQPELPVQTRQELANALYEEALRINGLV TNLLDMARLQSGGLKLNQQWQPIEEVIGSALRASERLLSKHQIATDLPPDLPLLLF DAVLIERVLCNLLENAAKYTPAESCITLHGRVNADEFQFSVIDNGPGLTAGMEEKIF DKFTRGEKKYSQAGVGLGLAICKAIVEAHGGKITAENVQPTGAKFTFTLPLGQSPP LPETELTDDES	23~~KdpD (8.38758E-125) ~~232,254~~Usp (1.65276E-42) ~~377,409~~DUF4118 (4.83184E-23) ~~508,534~~GAF (6.87003E-20) ~~655,672~~HisKA (0.0000000000164704) ~~737,790~~HATPase_c (2.87823E-30) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	9.3E-96	328.6	0.2	1.6E-95	327.9	0.1	1.4	1	F2LE20_BURGS	Histidine kinase (EC 2.7.13.3)	bgla_1g29620	Burkholderia gladioli (strain BSR3)	996	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia gladioli (Pseudomonas marginata) (Phytomonas marginata), Burkholderia gladioli (strain BSR3)	999541	>tr|F2LE20|F2LE20_BURGS Histidine kinase OS=Burkholderia gladioli (strain BSR3) GN=bgla_1g29620 PE=4 SV=1 MNRPDPDQLLDKIQREEERQQRGRLKIFFGASAGVGKTYAMLQAARARADEGVD VLVGIVETHGRRETAALVEGLELPPPLAVSHRGRELAEFDLDAALARRPQLVLVDE LAHSNLPGSRHLKRWQDVHELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWET VPDRVFDAADEVTLVDLPAEELLERMRDGKVYMAQQAERAVRNFFRKGNLIALRE LALRRTADRVDAQMREYRADRSIARIWQARERLLVCVGAGPEAPTLVRAAARLAA GLKADWIAVYVETPRSQRLDDARRRRPLDALKLAAELGAETVTLAGADPVAALIGY AQVRNVSKLVAGGSPRTGLLRRLARPFGERLAERAGDLDLMLLRTSAQDDPRHG ESDAGVRAWREAFSRLAGERSPPRHYVTAALICAALTGVAAIAQARLDLTNLVML YLLGVVFSAVRLGRGPGVMQSFLSVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLL TSLVISHLTSSLTRSAGVAERRERRTGAMYAMARELAAALAAEQIVEIGSRHVAEV FRARVAMLLPDGADQVRQKIENPDEAVTLTGASLDTDVGQWVYDQQKPAGRGT DTLPAALARYLPLKAPMRTRGVLAVVTQDSRELDAPEQQRMLDAFAAQIALALER VHYVEIARDALVSMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAGMHADAARAK AGAKAAADPVALPAAAGAHEAAAGDQPTDREHELVEAIHDEALRMTGIVTNLLDM ARLQAGSLQLKRQWSLLEETVGAALAACKRVLARHPVQVRLPADLPLLQTDAVLM ERLFANLFENAAKYTPPGTGLTIGAEAVEEDGKPFVRVSVDDHGPGLRAGMEARI FDKFTRGEKESATPGIGLGLAICRAIVDAHGGRIGARNRLAPDGSVAGASFWFTLP VDAPPPVPDVDEADAIDEAEDVDAIDAPRRDDHAAGSRHVPGAAEAGAPLSPSPK NVDHE	21~~KdpD (3.30506E-120) ~~230,252~~Usp (1.24581E-29) ~~374,410~~DUF4118 (2.64271E-20) ~~509,539~~GAF (1.87408E-15) ~~659,676~~HisKA (0.00000000857314) ~~772,825~~HATPase_c (6.41867E-22) ~~935	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1E-95	328.5	0	1.5E-95	327.9	0	1.3	1	B5R668_SALG2	Histidine kinase (EC 2.7.13.3)	kdpDSG0700	Salmonella gallinarum (strain 287/91 / NCTC 13346)	900	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella gallinarum, Salmonella gallinarum (strain 287/91 / NCTC 13346)	550538	>tr|B5R668|B5R668_SALG2 Histidine kinase OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=kdpD PE=4 SV=1 MNDEPLRPDPDRLLEQTPPPHRGKLKIFFGACAGVGKTWAMLAQAQRLRAQGLD VVIGVVETHGREETAALLDGLTILPPKRHSHRGRQIREFDLDAALARRPALILMDEL AHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETV PDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIAGQAERAIEHFFRKGNLIALRELAL RRTADRVDDQMRAWRAHPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRL GSVWHAVYVETPTLHRLPEKQRRAILSALRLAQELGAETATLSDPAEEKAVVRYA REHNLGKIVMGRPASRRWWRRDAFADRLARRAPDLDQVIVALEEPPARALAQTP DNRPFKEKWRGQIQGCLVAVALCAITTLIAMQWLVTFDAANLVMLYLLGVVVIALL YGRWPSVVATVINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGV RYQARVARYREQRTRHLYEMSKALAVGRSEHDIAATSERFIASTFQARSQILLPDA NGKLLPLTHQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSADKT YGLAIVEPGNLRQLMVPEQQRLLETFTLLVANALERLTLTASEEQARLASERESIRN ALLAALSHDLRTPLTVLFGQAEILTLDLASAGSPHARQASEIRQHILNTTRLVNNLLD MARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLLHPITLSLPQQLTLIHVDGPLFE SVLINLLENAVKYAGPQASIGIDAAVKDDRLQLDVWDNGPGIPAGQEQKIFDKFAR GNKESAVPGVGLGLGLGLAICHAIVEVHGGTLTAYNRPQGGACFRVTLPQGKP PELDDFHEDM	20~~KdpD (5.97384E-127) ~~230,253~~Usp (8.48231E-43) ~~373,403~~DUF4118 (9.35386E-21) ~~501,530~~GAF (2.89573E-14) ~~644,661~~HisKA (0.00000000227628) ~~726,778~~HATPase_c (4.57784E-23) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1E-95	328.5	0.1	1.8E-95	327.7	0.1	1.4	1	D3PV90_STANL	Histidine kinase (EC 2.7.13.3)	Snas_1437	Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	854	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Glycomycetales, Glycomycetaceae, Stackebrandtia, Stackebrandtia nassauensis, Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	446470	>tr|D3PV90|D3PV90_STANL Histidine kinase OS=Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21) GN=Snas_1437 PE=4 SV=1 MKRGHLRIYLGAAPGVGKTYAALEEARRRVARGTDVVVGFVETHGRRSTAALLD GLEVLPRHSVGYRGTAFEEFDVDAVLRRRPEVAVVDELAHTNVPGSRNQKRWQ DIDELLDAGINVISTVNIQHLESLNDVVTKITGVPQQETVPDEVVRRAEQVELADLT PEALRRRMTHGNVYPPEKIDAALSNYFRVGNLTALRELALLWLADKVEDQLSKYR SDKDIKDTWESKERVVVALSGDAEGDTLIRRAKRIAARSGGADLRAVYVASGDGL AGARNAKNLARQRLLVESMGGTFHQVIGDDIPTALLDFARGVNATQLVLGASRRG RFAQILSTGVGVTTTAKSGSIDVHLVTHDRVAKVKRPTSPAPLSRQRRITGFTATIL GLPALVAALLPLRDDLNATSIMLIMLTAVMGIALTGGMWPAVLAAVGGFLLVNFFFL PPLYTFAIGDQEHLLALCVFVFVGFVGATVVNILAARTRQAGRASAEAQTLSILAGS VLRGEDALPALMNQMLDTFGLTSVTLLERRRDGVGPDERHDPADWTMVACAGT PCASPGEAETDIPIDDKLSLALKGRTLDAADRRIVEAFAMQAAVALKQERLAAEAA TARPLAAADKMRTALLAAVSHDLRTPLASAKAAVAGLRGNGDMFSAADRDELLLT ADESLDRLDRLVSNLLDMSRLQAGALGAHTIPIGLEEVVPTALDELGEAGREVRLD VAGDLPEVAADPGLLERIIVNVVGNALRHSPPGTPPLVKAGAHDDIVELRVIDHGP GVPDVDQEQLFTPFQRLGDRDNASGVGLGLALSRGLAEAMSGTLTAENTPGGGL TMVLSLPQAGVNIDMESNPRQEES	1~~KdpD (1.4442E-120) ~~211,233~~Usp (2.52908E-27) ~~356,385~~DUF4118 (0.000000000134531) ~~480,X,618~~HisKA (0.00000000000329391) ~~684,735~~HATPase_c (2.30145E-25) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.1E-95	328.5	0.6	1.6E-95	327.9	0.4	1.3	1	A0A068SL95_RHIGA	Histidine kinase (EC 2.7.13.3)	RG540_CH02720	Rhizobium galegae	901	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Neorhizobium, Rhizobium galegae	399	>tr|A0A068SL95|A0A068SL95_RHIGA Histidine kinase OS=Rhizobium galegae GN=RG540_CH02720 PE=4 SV=1 MPDDSRESENRPSPDALLEHAEREARGRLKIFLGAAPGVGKTYEMLMSGRARKV DGLDVVIGVVETHGRQETEALVEGFEIVPRKAIDYRGQQLDEMDLDAILARRPALV LVDELAHTNAAGSRHPKRYMDVQEILGQGIDVYSTLNIQHVESLNDVVAQITRVRV RETVPDSIIDRADDVEIIDITPDDLIKRLNDGKVYVPQTARRAIENYFSPGNLTALREL ALRRTAQRVDEQLLNHMQAHAISGPWAAGDRVLVCLDHGRNGASLVRYARRQA DRLRAPWAALHLETPQSVNLPEQDKDRLAANMRLAEQLGGETVTLPALQPSREII AYANANNFTHIVVGRPARPRWRQILQGSVTYDLIRYAGDISVHVISGDTKEGEPKR GLKAAQLPKAFRFKPYVKSTIFVALAIIAGAALDQTLDVRNLALVFLMAVLAAAVRG GLGPGLFASVAGALSFNFFFLEPRYTFTVRDPESLVALFFYLGVAVVASNLTAAVQ RQAAAARQRARTTEDLYLFSKKLAGTGTLDDVLWATAFQIASMLKVRVVILLPENG SIAVKAGYPPDDDTLVDADIAAAKWAWEHNRPAGRAADTLPGAKRLYLPMRTGRE AVGVIGLDNDKQGPLLTPEQQRLFDALTDQAALAIERIQLVSDVDKAKLAAETDRL RTALLTSISHDLKTPLAAIMGSAGTLKDFGADIPEEARAELLTSVVDESERLNRFISN LLDMTRIGSGAMEPNYAFHFAGDIVGTALSRAAKIVSAHKLNVGIPADMPMLKVDP VLFEQVLFNLIDNAAKYAPEDTVIDIRGWQDGGSILISVMDEGPGIPPDDLERIFDS FYRVRKGDHVRAGTGLGLSICRGFIEAMGGTIRASNRSDRPGAIFTIRMPVPAETP ILGEQE	24~~KdpD (7.47799E-121) ~~234,256~~Usp (1.30578E-44) ~~379,404~~DUF4118 (0.000000000000296186) ~~497,530~~GAF (4.08986E-16) ~~649,666~~HisKA (0.00000000000187352) ~~732,785~~HATPase_c (1.60674E-29) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.1E-95	328.4	0	1.5E-95	327.9	0	1.2	1	A8KYG2_FRASN	Histidine kinase (EC 2.7.13.3)	Franean1_0599	Frankia sp. (strain EAN1pec)	938	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain EAN1pec)	298653	>tr|A8KYG2|A8KYG2_FRASN Histidine kinase OS=Frankia sp. (strain EAN1pec) GN=Franean1_0599 PE=4 SV=1 MRNAGRGRAGAFRRPPRRPHHGWVPRGTLRIYLGAAPGVGKTYAALDEAHRRS ERGTDVVIGFVETHGRPRTAAMLHDLEIVPRRTLTYRGGSFTEMDLDAVLARRPK VAFVDELAHTNVPGSRHAKRWHDVQELLAAGIDVISTVNVQHLESLNDVVGTITGV PQRETVPDDVVRRADQVELVDMAPEALRRRMAHGNVYGPEKVDAALANYFRVG NLTALRELALLWLAGKVDDQLDRYRADHGIGGTWETRERVVVALTGGPEGDTLIR RACRIAARGKGADLLAVHVARSDGLTGADPSALARQRALVESLGGSYHQVIGDDV PTALLEFARAENATQLVLGASRRGRLARILSPGIGATTTTRSGSIDVHMVTHPEAW GHRPAPAGGVDAAAHRPARPGWPGWRLPRGRTALEPRRRIIAAGLTLVLVPALT AGLAASRGTFNLTTEMLAYLLIVVTVALVGGFGPALLCAIASSLLLNYYFTAPVRAW TIADGDNALALLGFVLVASLVSRVVSTSARRYEQAVRASAEAATLSVLAGSVLRGE DALPALLARARETFGMTSVTLLERTDDDQVGVEWSPVATIAGTGPDGASVDGAS GAGPGTSQAGAGGPTGGRADPDGDGDGSEIVDIPVREDLRLVLTGRSLPAADRR ILTAFAAQAAVALDQHRLREAAAEAAPIAAADKVRTALLTAVSHDLRTPLAAAKAAV SCLRGYDITLTDDEEAELLATADESLDKLTRLVENLLDMSRLQAGALSVFPRAVGL DDIVPPALDEIGPAANRIGVRVPDDLPDVRADPVLLERVIVNLVTNALRYAPADTPP VITASALGDRVELRVVDSGPGIPVRQRDNVFQPFQRLGDRDNTTGVGLGLALSRG LAEAMGGALTPDETPGGGLTMVLSLPAALNPTAVTNPITAPLDVPTGPAADDRAG	26~~KdpD (2.43516E-117) ~~234,256~~Usp (4.85796E-31) ~~378,422~~DUF4118 (0.00000000251662) ~~525,X,690~~HisKA (0.0000000000105701) ~~756,807~~HATPase_c (5.71126E-26) ~~908	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.1E-95	328.4	0.5	2.3E-95	327.3	0.4	1.6	1	G0FV52_AMYMS	Histidine kinase (EC 2.7.13.3)	RAM_09620	Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis mediterranei (Nocardia mediterranei), Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	713604	>tr|G0FV52|G0FV52_AMYMS Histidine kinase OS=Amycolatopsis mediterranei (strain S699) GN=RAM_09620 PE=4 SV=1 MTTENGPAKPRRGELRIYLGAAPGVGKTFAMLGEARRRLDRGTDVVVGLVETHG REKTAVLLEGLEIVPRRHAEHRGRAFDEMDVDAILARAPEVAVIDELAHTNVPGSR NAKRWQDVEELLTAGIDVLSTVNVQHLQSLNDVVERITGVTQQETVPDEVVRRAE QLELVDITPEALRRRLAHGNVYPAERIDAALGNYFRPGNLTALRELALLWVADQVD VALQRYRAEQRITDTWEARERVVASITGGPESETLIRRASRIATRAGAELQVVHILR GDGLAGISPAAMARCRKLAEEVGATFHTVVGDDVPGALLDFARGVNATQLVLGTS RRSRVARLFDEGIGAAVVRRSGPIDVHMVTHSEAGGRLRTGLTASPLGLSRLVTG SVLGVVLPVLVTLVGVFVPTGLDFATDVIAYVLVTVVVALVGGLGPALVAAVLGAG LLNFFFTPPLYTLNVHTPQNLVTLIAMVVVAVLVALVVDQAARRAAQAARARTEAA LLASYARTVLTHANPIERLLAKVRENFALTSVTLLEKQDGVWQCVATAGEHPCAD PDEADADIAVTADVHLTLRGRALPAADRRVLEAVAGQALLALRQQRTAAAAARAE RKAEATELRTTLLSAVGHDLRTPLTSIKASIGSLRAADLELSEEDTAELMEAIELSAD RLAGLIDNLLDSSRLATGAVRPHLRPVGYDEVVAHALSTVDGSDDVVVAVDDQLP SVLADPGLLERVVANVLDNALRHGGAPVSARASAHSGQVELRIVDHGKGLRKGAA DSAFAPFQRLGGDRDTTPGVGLGLSVAKGFTEAMGGTIRAEDTPGGGLTVVVSL PAFSVEFEQEGVR	10~~KdpD (1.74823E-122) ~~220,242~~Usp (1.35597E-34) ~~363,431~~DUF4118 (0.0000173857) ~~471,X,617~~HisKA (0.0000000000463093) ~~682,732~~HATPase_c (9.85484E-21) ~~832	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.2E-95	328.3	0.2	1.8E-95	327.7	0.1	1.3	1	W6RZV1_9RHIZ	Histidine kinase (EC 2.7.13.3)	kdpDLPU83_4162	Rhizobium sp. LPU83	905	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium sp. LPU83	348824	>tr|W6RZV1|W6RZV1_9RHIZ Histidine kinase OS=Rhizobium sp. LPU83 GN=kdpD PE=4 SV=1 MTRMPEDNRDKVGRPSPDALLEKARQETRGRLKIFLGAAPGVGKTYEMLESGRA KISDGVDVVIGIVETHGRKETQALVDGFEVIPRVKIDYKGRPLEEMDIDAILARHPSL VLVDELAHTNAEGSRHPKRYLDVKELLDGGIDVYSTLNIQHVESLNDVVSQITRIRV RETVPDSIIDMADDVEIIDLTPDDLIKRLHDGKVYVPKTAERALTNYFTPGNLTALRE LALRKTAQRVDDQLLTHMQAHAIPGPWAAGERVLVSVDQHPRSTSLVRYASRMA ARLRAPWAAVYVETNRSINLTEADRDTIAATLRLAEQLGGEAITIPGREVSEELVRH AAANNVTHIVIGAPSKPSWRDWLHRSIADDLIRKSGNISVHVISGSEKEGTSTRGV NAAPSSPAFNIQAYLSATTYVAIALIVGVVLDQVLDVRNLALVFLMAVLTSAVIHGLR PALYTCILSALSFNFFFLPPRYTLTISDPESVLALFFFLGVAVIASNLTATVQRQAAA ARQRARTTEDLYLFSKKLAGTGTLDDVLWATAFQLASMLKVRVVLLLPEEGTIAVK AGYPPDDTLDEADIAAARWAWEHNHAAGRGADTLPGAKRLYVPLRTGRAAVGVI GLDNDRRDGRLLMPEQQRLLDALADQAALAIERIQLVADVDRARLAAEADRLRSAL LTSISHDLKTPLAAILGAAGTLRDYLDSMSQEDRVDLLSTVIDESERLNRFIANLLDM TKIESGAMEPNYALHYPGDIAGSALRRAEKILAHHKTVVTIPADLPMVRVDPVLFEQ VLFNLLDNAAKYAPQGSSIRIDGWADGYNVMIQVSDKGPGIPPADVDRVFDTFYR VRKGDQVRAGTGLGLSICRGFVEAMGGTITAANRSDRSGAVFTIRLPKPNEIQKLD ELQ	29~~KdpD (8.36929E-119) ~~237,259~~Usp (1.18289E-41) ~~382,407~~DUF4118 (6.46568E-17) ~~502,533~~GAF (0.00000013287) ~~653,670~~HisKA (0.0000000000029283) ~~736,789~~HATPase_c (1.16693E-28) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.3E-95	328.1	0.7	2.9E-95	327	0.5	1.6	1	B2HPR8_MYCMM	Histidine kinase (EC 2.7.13.3)	kdpDMMAR_0634	Mycobacterium marinum (strain ATCC BAA-535 / M)	839	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium marinum, Mycobacterium marinum (strain ATCC BAA-535 / M)	216594	>tr|B2HPR8|B2HPR8_MYCMM Histidine kinase OS=Mycobacterium marinum (strain ATCC BAA-535 / M) GN=kdpD PE=4 SV=1 MTPDYPRKRGELRIYLGAAPGVGKTFAMLGEAQRRLERGTDVVAAVVETHGRKR TAELLEGIERIPPKFIEYRGSRFAELDVEAVLRRQPQVVLVDELAHTNTPGSKNPKR WQDVEELLDAGITVISTVNVQHLESLNDVVAQITGIEQQEKVPDEIVRAAEQVELV DITPEALRRRLAHGNVYAAERVDAALANYFRTGNLTALRELALLWLADQVDAALEK YRADKKITATWEARERVVVAVTGGPESETLVRRAFRIASKASAELMVVHLARGDG LSGVAAPQMGKVRELAASLGATVHTVVGDDVPTALLDFAREMNATQLVLGTSRR SRWARVLDEGIGATVVQQSGPIDVHMVTHQEAGRPARWSWLWPREHHLVSWL AAVVVPSLICALTVAWLDRFLAVGGESALFVIGVLVVALLGGVAPAALSAVLSGLLL NYFLIEPRYTFTIADPDNAVTTLVLLVVAVAVAALVDNAAKRSREAGRASREAELLA LFAGSVLRGADLEALLEKVRETYSQRAVSILRIEAGTSQGAIVSCVGEDPCVDVDT ADTAIDVGDDEFWMLMAGRKLLARDRRVLTAVAKQAAGLIKQRELADEAGKAQAI EQADQLRRALLSAVSHDLRTPLAAAKAAVSSLRSDDVDFSADDMGELLATIEESVD QLTALVGNLLDSSRLAAGVVRPQLRRVYLEETVQRALLGISRGATGYGRSGLDRV KVEVGGAVAIADAGLLERVLANLIDNGLRYAPDSPVRVYAGRVGDRVLINVADEGP GIPRGAEEQMFAPFQRLGDRDNRIGVGLGLSVAKGFVEAMGGTISATDTPGGGL TVVVDLAAA	8~~KdpD (1.47146E-119) ~~217,239~~Usp (1.04886E-34) ~~360,383~~DUF4118 (0.000000326348) ~~459,X,613~~HisKA (0.00000000000109733) ~~679,736~~HATPase_c (1.48738E-25) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.3E-95	328.1	0.2	2.4E-95	327.3	0.1	1.4	1	D2B156_STRRD	Histidine kinase (EC 2.7.13.3)	Sros_0436	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	851	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	479432	>tr|D2B156|D2B156_STRRD Histidine kinase OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_0436 PE=4 SV=1 MPRGRLRVYLGAAPGVGKTFAMLGEGHRRLARGRDVVVGLVETHGRPRTAELID GMEVVPRRTVIHREAAFTELDVDAVIARAPRIALIDELAHTNVPGSRNAKRWQDVE EILDAGIDVVSTVNIQHLESLNDVVRQITGVPQRETVPDEVVRRADQVELVDMSPE ALRRRLAHGNVYAPEKVDAALSNYFRVGNLTALRELALLWVAGKVDEQLDRYRAE HGIEGTWEARERVVVALTGGPEGDTLIRRAARIAARSKGADLLAVHVTRADGLAG GDPVNLARQRVLAESLGGTYHQVVGDDVPRALLDFARGVNATQLVLGASRRGRF AQILSRGVGVTTTALSGSIDVHMITHGEAQKGRRPPPSRAALTRTRRLAGWAVAG AGLPTLTGVLLPFRETLTLPSEILFFLLVVVGVALIGGMWPAVTAAVGGSLLLNYFF TPPVHTLTIYDPENLFALVVFVLVAIMVSGIVDVAARRTREAARASADAEVLSTLAG HVLRGESALPSLLARLRETFALTSVTLLERIDGPVPDDQSDPEAWRIVATAGATPC TCPGTADADVVIDEQLVLAVRGRLLEASDRRVLEAFAAEAAVALRQERLRREADLA GPLAETDRMRTALLAAVSHDLRTPLASARLAVESLRGTEIEWSAEDREELLATADE SLVKLDRLVANLLDMSRLQAGVLGLALQPVALEEVIPRSIDDLGPLRDRVEGDVSV DLPEVVADPVLLERILVNVMSNAVRYSPAGRKALVAGSRHGDYVEIRVVDRGPGIP AEAHDRVFMPFQRLGDRDNHTGVGLGLALSRGLAEAMGGTLTPEETPGGGLTMI LTLPVSSRADGLPAVERA	3~~KdpD (2.20801E-121) ~~211,233~~Usp (4.93433E-20) ~~355,381~~DUF4118 (0.00000000000504974) ~~476,X,618~~HisKA (0.0000000000042847) ~~684,735~~HATPase_c (3.30158E-25) ~~836	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.4E-95	328	0.1	2.6E-95	327.2	0.1	1.4	1	V5U9D6_9BURK	Histidine kinase (EC 2.7.13.3)	X636_00780	Pandoraea sp. RB-44	967	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Pandoraea, Pandoraea sp. RB-44	1380774	>tr|V5U9D6|V5U9D6_9BURK Histidine kinase OS=Pandoraea sp. RB-44 GN=X636_00780 PE=4 SV=1 MERPDPDELLDKLHRDEAREQRGRLKIFFGASAGVGKTFAMLQAARKLREEGTD VVVGVLETHGREETASLLEDLEVLPQQSVEYRGRVLREFDLDGMLARKPAVALID ELAHTNVPGGRHPKRWQDVQELLGAGIDVYTTLNVQHLERLNDVVGQITGIRVW ETVPDRVFDLADEVKLVDLPPDELLERMREGKVYLPAQAERAVRNFFRKGNLIALR ELALRRTADRVDAQMREYRADQSIGHVWQARERLLVAIGPGPEGVTLVRAAARL AASLRADWLAVHVETPAILKQSPERREGTYATLKLAQELGAETLTLDGAHAAATLL AYAQMRNVSKLVVGASGARRWWTAHTPLHEQLVRLARGVEVVLIAPAAGDASAD RRVVRGDWRDWVDTAVPELGIVGGPWRAYAWAAAVCGAVSLAAAELTSFLDLA NIAMLYLLGVIAVAMRLGRGPGVLASFLSVVAFDFFFVPPKMSLSVSDTQYLLTFA VMLTVALVISHLTTSLRFQARLATWRERRTGAVYAMARELAAALTTTQILEIGARH VREVFQARVALLLPDSQGSVRQPVENVQVETMPAHIDTDVAQWVYDRQQAAGR GTDTLPASDAYYLPLRAPMRTRGVLVVAAQPNADGALGSPEQHRLLDTFAAQIAL ALERVHYVEIAQDALVTMESERLRNSLLSAISHDLRTPLTSIVGFASMLCRNAQTP GPLRAELVDAIHEEAQRMTGLVTNLLDMAKLQAGGVQLNRQWQMLEEVVGTSLR ACRRVLAAHAVTTRLPADLPLLRFDAVLLERLFANLLENAAKYSPPGSHIEIAARVR GDMVEVSVSDDGPGLPAGTEGRIFEKFMRGEKESSKPGIGLGLAICRAIVEAHGG RIHADNVPQGHGARFTFTLPVETPPEAPLGPLAPLAPLAAMRGDAALPGQDDDRA SPSGREGLDEDAAGHHDDAHPTREPGTNATREHE	20~~KdpD (4.44561E-123) ~~230,252~~Usp (2.11988E-21) ~~374,411~~DUF4118 (2.62975E-22) ~~511,540~~GAF (6.35048E-16) ~~660,677~~HisKA (2.04134E-14) ~~742,795~~HATPase_c (5.55783E-31) ~~897	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.5E-95	328	0.2	3E-95	327	0.1	1.6	1	A0A097R090_HAFAL	Histidine kinase (EC 2.7.13.3)	AT03_06750	Hafnia alvei FB1	901	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Hafnia, Hafnia alvei, Hafnia alvei FB1	1453496	>tr|A0A097R090|A0A097R090_HAFAL Histidine kinase OS=Hafnia alvei FB1 GN=AT03_06750 PE=4 SV=1 MLDDEELRRPDPDTLLAQVCEKPRGKLKVFFGACAGVGKTYAMLQEAQRLRAQG LDVLVGVVETHGRAETAAQLEGLDILPLKRIHHRGRQVREFALDQALARHPALILM DELAHSNAAGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGSVTGIRVR ETVPDRIFDDASEIVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIALRE LALRRTADRVDEQMREFRNSQDKERVWHTRDAILLCIGHNVDNDKLVRTASRLAA RLGCIWHAVYVETPRLHRLPENQRRAILRSVKLAQELGAETTTLSDPNEEKAILRY AREHNLGKIIIGRRNKKERRWWWHESFADRLAKLGPDLDLIIVAVEDKPRTTSKES DSRPFSEKWRIQIRGCLVAIALCALITLLARMIFPNFDQANIVMVYLLGVVIVALFYG RWPSVLSAVVSVASFDLFFIQPQWSFAVTDVQYLVTFGVMLTVGIVIGNLTAGVR YQARVARYREQRARHMYELSKALSNAITNEDIARSGSYFLNSSFNARTSVLIPSDD TPLVQVTPPQEGVSGVDFAIAHWCFDKQQPAGAGTDTLPGVPYQLLPLSTSQQT FGVLAIEPMNMRQLMVPEQQRLLQTYAVMIASALERLHLAQTAASARMDTEREQL RNSLLAALSHDLRTPLTVLFGQAEILTLDLAAEKSPHAQQANQIRQQILNTTRLVNN LLDMARIQSGGFNLRKEWQSLEEIVGSAVNTLEPMLNSHPLTIDLPADLPLVNCDG SLIERVIQNLLENAGKYAGLESPLAIRAKASEDWLEVEIEDRGNGIPAEQLQLIFNKF TRGDKESAIPGVGLGLAICRAIIEVHGGKIWAENIAQGGACFHFTLPLEAPPDIEDE LEHPSS	24~~KdpD (9.76017E-127) ~~232,255~~Usp (1.42236E-40) ~~377,406~~DUF4118 (1.10642E-24) ~~504,532~~GAF (0.00000000000810885) ~~648,665~~HisKA (0.000000000032355) ~~730,783~~HATPase_c (5.57482E-29) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.6E-95	327.9	0.2	2.5E-95	327.3	0.1	1.3	1	Q63VS0_BURPS	Histidine kinase (EC 2.7.13.3)	kdpD BPSL1174	Burkholderia pseudomallei (strain K96243)	993	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, pseudomallei group, Burkholderia pseudomallei (Pseudomonas pseudomallei), Burkholderia pseudomallei (strain K96243)	272560	>tr|Q63VS0|Q63VS0_BURPS Histidine kinase OS=Burkholderia pseudomallei (strain K96243) GN=kdpD PE=4 SV=1 MNRPDPDQLLDKIQREEEKQQRGRLKIFFGASAGVGKTYAMLLAARARKQEGVD VVVGIVETHGRSETAALLDGLDVLPLMQIEYRGRTIGEFDLDAALARRPRLVLVDEL AHSNVPGARHLKRWQDVYELLDAGIDVYTSVNVQHLESLNDVVGAITGIRVWETV PDRVFDAADEVTLVDLPAEELLSRLREGKVYMAQQAERAVRNFFRKGNLIALREL ALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGAEAPTLVRAAARLAAS LKADWLAVYVETPRLARLPDALRQRTLNALKLAAELGAETATLTGADAVAALIGYA QVRNASKIVAGGSSKTGFLRRFSRPFGEQLAERAGDLDLMLIRASASEDARAPLD ARARAWRDAFSSVVDGRSPPRHYGYAAAICALITGAANLLQGHLDLTNLVMLYLL GVVFSAVRLGRGPGVVQSFLSVAAFDYFFVPPRMSFSVTDTQYLLTFFGMLLTSL VISHLTSSLTRGAAIAQRRERRTSAMYAMARELAAALTAEQIVEIGSRHVSEVFRA RVAMLLPDSGDKVRQKIENPDEAVTITGAALDIDVGQWVYDQQKPAGHGTDTLPA AAALYLPLKAPMRTRGVLAVVTKDPGELEVPEQRRMLDAFAAQIALAVERVHYVEI ARDALVNMESERLRNSLLSAISHDLRTPLTAIVGLSSMLANARGATREGSPAREDE LVDAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGAALAACKRVLAR HPARVRLPADLPLLQTDAVLMERLFANLFENAAKYTPLDTPIEIGAERIVDDGRPFV RVFVDDHGPGLPAGMEARIFEKFTRGEKESATPGIGLGLAICRAIVDAHGGKIGAL NRLGPDGRVEGARFWFTLPVDTPPPEPGAGDEAPDDDAGAAADASGMRDAGRA AGRRIAGERVAGERAFAAAARPVPGQAAAADAPRRDGGAPPLSNEPPHAHE	21~~KdpD (8.35063E-121) ~~230,252~~Usp (3.79273E-28) ~~374,409~~DUF4118 (2.34333E-20) ~~508,537~~GAF (2.79686E-16) ~~658,675~~HisKA (0.000000000000473468) ~~744,797~~HATPase_c (1.58082E-22) ~~907	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.6E-95	327.9	0.4	7.7E-95	325.7	0.1	2	1	F8GKK6_NITSI	Histidine kinase (EC 2.7.13.3)	Nit79A3_1973	Nitrosomonas sp. (strain Is79A3)	889	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas sp. (strain Is79A3)	261292	>tr|F8GKK6|F8GKK6_NITSI Histidine kinase OS=Nitrosomonas sp. (strain Is79A3) GN=Nit79A3_1973 PE=4 SV=1 MTDERPDPDHLLAEIKKEEIAAQRGKLKIFIGACAGVGKTYTMLNAAQQRLAEGID VVIGVVETHGRSDTIKLLEKLTLLPLHEIKYREKSLLEFDIDAALQRAPQLIIIDELAHT NIEGSRHAKRWQDVDELLASGIDVYTTLNVQHLESLNDVVGSITGIRIWETVPDRF FDSADDVTLVDLPPDELLERLREGKVYVPEQVEHAAKNFFRKGNLIALRELALRRT ADRVDSQMRAYRADHAIANVWQTRERIIACIGPGPLGNKLVRSAARLAKELKADW HAVYVETPALQRLSKIDRQRILDHLTLAEELGAETATLAGSDLIATLIAYAQSRNASK LVVGRPVDLPWFQHWRPRFIDALARFAPDIDIYVVVGNEKPTRIKNREIKPGTIKW WNYAWATIACGVTTILAAGLLHIFDLSNVVMILLLTVVGISIKFGRGPGAWAAALSV MLFDFFFVPPRFSFSVSDVQYLFTFALMLLVALTIGQLAAKLRFEATIANLRERRAQ ALAALSKELSGALTVEQVVEIANRNVSGTFNSAVALLLPSSQEKTKVAGTSSSQPT TDIAVAQWVYDHQLPAGFGTHTLSAAVSHYLPLKAPMRTRGVLVLEAKDLLFLNE PEEKRLLDTFAAQIALALERVHYVEVAQDALVSIEGERLRNSLLSAISHDLRTPLTAL VGLASTLTDTNLPENSQKELALAIRNEAQQMTELVTNLLDMARLQAGGVKLKKDW QSIEEIVGSACMQLHRVMTTKKLIISIPANLPLCECDPILIQRVIVNLLDNADKFTPPG STISVCATAGIDELAIVIEDNGPGLPLGQETKVFDKFARGETESNKPGVGLGLALCK AIVEAHGGKISAENRVDGGARFTLTLPLGIAPIPEELL	22~~KdpD (7.27575E-118) ~~232,254~~Usp (9.558E-42) ~~376,399~~DUF4118 (7.56348E-19) ~~497,525~~GAF (0.00000000000249658) ~~642,659~~HisKA (1.14742E-14) ~~723,776~~HATPase_c (6.31311E-29) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.7E-95	327.8	0.4	3.2E-95	326.9	0.3	1.5	1	J7Q9H9_METSZ	Histidine kinase (EC 2.7.13.3)	BN69_2486	Methylocystis sp. (strain SC2)	899	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylocystaceae, Methylocystis, Methylocystis sp. (strain SC2)	187303	>tr|J7Q9H9|J7Q9H9_METSZ Histidine kinase OS=Methylocystis sp. (strain SC2) GN=BN69_2486 PE=4 SV=1 MARDDGDFDRRPDPDALLALSDKESKGKLRVFLGAAPGVGKTYAMLARAQTAKA EGVDVVVGVAETHGRAETQALLNGLETLPRRKCDYRGRIIEEFDIDAALARKPQLIL VDELAHTNAPDSRHPKRWQDVEELLDVGIDIWTTLNVQHLESLADVVSRVTGVAV RETVPDRVLQNAADVILVDITPEELLQRLKDGKVYVPETARRATQNFFTPRNLTAL RELALRRTAERVDDQMVDFLRQGAIEGPWATSERLLVCVGRDANSEAVVRAGAR LATALNATWIALYVERGGQDEDSAEVVRSVDQALRLAERLGAEIARTPGDDLAGE ALSFARRENITQIVLGRSRARPFSRLLRRSLTDEILRRSTDIAVHVVVQEDGPPQSR QAWKLPTLSQTWLGFGGAAVSVMMTVLVGHGLERWLGLVNPSVVFLLPVVLCA VWLGMWSAIIAAVLSFLACDFFFFSPRYELTISQPQEFLTLVVALVVAVITGMLASK MRTYAQNMRQRSQAVQSLFEFSRKLSTITTLDDILWASTLQIQKAGEASSVIMLIP EEGGLKVSAAWPPVDRMDAGELAAARWALEKSEPAGWRTDTLPNVRFQFRPLA TARGVVAVCGIEPKTPEEPLSAAAESTISSLLEQTAIAIDRSMLVGESVKAAALEEN EKLRTILLSALSHDLRTPLTSITGAVTSLRELGEKLPPEDRKDLLLSIEEEAGRLSRFI ANMLDMSRIESGALAPRSDLVDVAEVIRSVLERAKRSFPGKETSISIAPDLPPIRGD ANLLGQVLFNLIDNAHKYGGPAGAIVHARREGGDVVITVTDEGPGVKTADIERIFEK FYRSGRVDGRKAGTGLGLSICRGLVRAMGGTIVAQSPAARRRGTRLIMRFPAAGE SRRGVAA	24~~KdpD (8.75768E-123) ~~234,256~~Usp (1.76971E-38) ~~378,406~~DUF4118 (0.00000000155291) ~~500,528~~GAF (0.00000258669) ~~648,665~~HisKA (0.0000000000086311) ~~731,784~~HATPase_c (2.2824E-25) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.7E-95	327.8	1.3	2.5E-95	327.2	0.9	1.2	1	Q7CTB1_AGRFC	Histidine kinase (EC 2.7.13.3)	kdpDAtu3787	Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	900	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Agrobacterium fabrum, Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	176299	>tr|Q7CTB1|Q7CTB1_AGRFC Histidine kinase OS=Agrobacterium fabrum (strain C58 / ATCC 33970) GN=kdpD PE=4 SV=1 MPDDISDMPSRPSPDALLENAQREARGRLKIFLGAAPGVGKTYEMLMSGRAKLAD GVDTVIGVVETHGRRETEALVEGLSVVPRKRIDYRGQVLEEMDIDAILARRPALVL VDELAHTNAAGSRHPKRYMDVQEILAQGINVYTTLNIQHVESLNDVVAQITRIRVRE TVPDSIIDRADDVEIIDITPDDLIKRLQDGKVYLPRTARRAIENYFSRGNLTALRELAL RRTAQRVDEQLLNHMQSHAISGPWAAGDRVLVCLDHGRNGPGLVRYARRQADR LRAPWTALHLDTPRSQQLSEAEKDRLAGTMRLAQQLGGETVTLPALDLTREIIAYA NANNFTHIIIGRPRKSWWQRIFQRSLTHDLIDHAGDISVHVISGDKNEEKPGQAVK LAPARSPQSFRSYLNSTLFVGLAIIVGIVLDQTLDVQNLALVFLMAVLAAAVRGGLG PALYASLLGALAFNFFFLEPRYTLTVSSPDSLVALLFYFGVALVASNLTVAVQRQAA SARSRARTTEDLYLFSKKLAGTGTLDDVLWAAAYQMASMLKVRVVLLMPENGAIA VKAGYPPDDTLVDADIAAAQWAWEHNKAAGRGADTLPGAKRLYLPLRTGSGAVG VVGLDDDRSGPLLTPEQQRLFDALADQAALAVERIQLASDVDRARLAAETDRLRT ALLTSISHDLKTPLAAILGSAGTLKDFADDIPPDARAELLSTIVEESERLNRFISNLLD MTRIGSGAMEPNYGLHFLGDMVGTALSRAAKIVVRHEVVLDIPSDLPMLKVDPVLF EQVLFNLIDNAAKYAPEHTTIAIRGWRQGKNIFLSVADEGPGIPPDDLERVFDSFYR VRKVDHVQAGTGLGLSICKGFIEAMGGSIRAENRADRGGAQFTIGLPVAVDTPVL DHD	24~~KdpD (3.9992E-122) ~~234,256~~Usp (5.81186E-48) ~~379,405~~DUF4118 (6.25228E-19) ~~504,530~~GAF (0.00000000706499) ~~649,666~~HisKA (0.000000000000384966) ~~732,785~~HATPase_c (2.87113E-28) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.7E-95	327.8	2.9	2.8E-95	327.1	2	1.3	1	Q5KUV6_GEOKA	K+-transporting ATPase d chain	GK3245	Geobacillus kaustophilus (strain HTA426)	374	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Geobacillus, Geobacillus kaustophilus, Geobacillus kaustophilus (strain HTA426)	235909	>tr|Q5KUV6|Q5KUV6_GEOKA K+-transporting ATPase d chain OS=Geobacillus kaustophilus (strain HTA426) GN=GK3245 PE=4 SV=1 MNHKYRRMTPEEILKKIENMKKGRLKIYIGAAPGVGKTFHMLRDAHDVREKGIDIVI GIVETHGRAETEAEIKDLEIIPRKKIHYKGKEFAELDVDAVIRRNPDVVIVDELAHTN APGSKNKKRYQDVQEILQAGIHVWTAMNIQHLESVHDIVEQVTGVQVNERVPDFM LREADEIEVIDITPEALRERIKEGKVYGKEKIDQALNHFFRKGNLVALRELTLREVAD DIEMRLEKEREEQGIEEPTGIHEKILVCVNYRPNAEKLIRRGWRIAQRLNAELYILHI KQKRQSPERTIAEWEKMAKQFGATFLVREAASRRVAHQIVDVCREYKITQIVMGM SARTRWEEIWKGSLINVIMQQLKHVDVLVVSDR	20~~KdpD (5.47856E-121) ~~230,252~~Usp (1.31718E-38) ~~372	non-kinase	KdpD;Usp
	1.7E-95	327.8	0.1	3.9E-95	326.6	0.1	1.6	1	U5WM98_MYCKA	Histidine kinase (EC 2.7.13.3)	MKAN_08405	Mycobacterium kansasii ATCC 12478	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium kansasii, Mycobacterium kansasii ATCC 12478	557599	>tr|U5WM98|U5WM98_MYCKA Histidine kinase OS=Mycobacterium kansasii ATCC 12478 GN=MKAN_08405 PE=4 SV=1 MSAVDPPRKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDLVAAVVETHGRM KTAALLDGIEIIPPHYVEYRGTTFPELDVPAVLARHPQVVLVDELAHTNTPGSKNHK RWQDVEELLDAGITVISTVNIQHLESLNDVVAQITGIEQKETLPDSVVRQAAQVELI DITPEALRRRLSHGNVYASDKIDAALSNYFRRGNLTALRELALLWLADQVDTALAK YRAENQITDLWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVIRGDG LAGLSEARMSKIRELAGSLDASLHTVVGDDVADALLDFAREINATQLVIGTSRRTR WARLFEEGIGQAIVERSGKIDVHLVTHEESRRGLRTTPIAPRERRVASWLAAVIVP SLICAITVAVLDRYLDTSGESALFFVGVLVVALLGGVAPAVLSAVLSSLLLNYYLTDP RHTFTIAEPSAAVTEAVLLLVAVAVAVLVDGAAKRAREARRASQEAELLTLFAGSV LRGADLETLLERVRETYSQRAVSMLREYADEDRTRSEVVASVGKEPCATVDSADT AIEVGDDEFWMLMAGKKLSARDRRVLNAVARQAAGLVRQREMAEEASRTEAIVR ADELRRSLLSAVSHDLRTPLAAAKVAVSSLRAQDIAFSPADTAELLATIEESIDALTA LVGNLLDSSRLAAGVLRPDLQRVYLEEEVQRALVSIGKGATGFYRSAIDRVKVDVG GAVVMADAGLLERVLANLIDNALRYAPDCVVRVNAGRVGDRVLINVIDEGPGVPP GSQGQIFEPFQRLGDNDNTTGVGLGMSVARGFVEAMGGTVAAGDTPGGGLTVV VDLAAPPEDGDL	9~~KdpD (7.82852E-120) ~~218,240~~Usp (9.00212E-35) ~~361,X,616~~HisKA (0.0000000000537096) ~~682,739~~HATPase_c (9.84087E-26) ~~839	kinase	KdpD;Usp;X;HisKA;HATPase_c

	2E-95	327.5	0.1	4E-95	326.6	0.1	1.5	1	I3Y596_THIV6	Histidine kinase (EC 2.7.13.3)	Thivi_0076	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	907	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiocystis, Thiocystis violascens, Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	765911	>tr|I3Y596|I3Y596_THIV6 Histidine kinase OS=Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) GN=Thivi_0076 PE=4 SV=1 MSDGRPDPDALLERIKEDEQRAARGRLKVFFGASAGVGKTYAMLSAARAQAEQG VDLVVGVIETHGRRETEALLTGLERLPLKELEYRGRVLREFDLDGALARHPSLILID ELAHSNLTGSRHPKRWQDVEELLSAGIDVYSTVNVQHLETLNDVVGGITGIRVWE TVPDHVFDAADEVVLVDLAPDELLQRLKEGKVYLPHQAERAIQNFFRKGNLIALRE LALRRTADRVDRQMLDYRRDQSVAPVWQTRESVLACIGPGESAERIIRRAARIAA RDDVPWHALYVETPSLQRRSRAQRQCILKRLKLAQELGAETATLSGGDPVEVVIG YARSHNLFRILLGRDHPRRWRPWYRSFADRIGGQAPELEVMLVAHDEARPPSPD QDRTDESWLERLKAPWRSYAMSLLICATAAVATAPLHSMFDLANIAMLFLLAVVVV AARYGLGPSVMASFLNVAAFDFLHVSPRFSFSISDIQYLLTFVVMLGVGLVIAQLTT GMKYQARVASRRERRARALYELSRDLSGALLPEQIAQIGQRFAESEFGARSVIML ANDSERFSALVLPAPGELPVDVGIGKWAFDHGAEAGCGTDTLPGSPLLYLPLQAP MRVRGVLALEPRDPRQIMVPEQRRLLDTFARLIAIALERVHYVEVAQTTTLQMESE RLRNAFLAAISHDLRTPLTALVGLADALAMTRPPPTAEQAELAAAMREEALRMSSL VNNLLDMARLQSGSVRLNRQWQPLEEVVGSALGAVHSIIAGHRVRVDLPGDLPLL EFDAVLIERVLVNLLENAAKYTPPGSRIGIGAAPATPDRIEIWVEDNGPGLPVGKEE AVFQTFERGQTAGATPGIGLGLALCRAIMEAHGGTIRAERRPAGGARFVFSLPRG TPPVVETADEASPVEASPR	22~~KdpD (6.89278E-126) ~~232,255~~Usp (1.31103E-24) ~~376,405~~DUF4118 (1.20513E-18) ~~504,531~~GAF (3.55443E-18) ~~648,665~~HisKA (1.2578E-15) ~~730,783~~HATPase_c (2.89319E-28) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.3E-95	327.4	0.3	3.9E-95	326.6	0.2	1.4	1	E8TDR5_MESCW	Histidine kinase (EC 2.7.13.3)	Mesci_1804	Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)	909	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium, Mesorhizobium ciceri, Mesorhizobium ciceri biovar biserrulae, Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)	765698	>tr|E8TDR5|E8TDR5_MESCW Histidine kinase OS=Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271) GN=Mesci_1804 PE=4 SV=1 MPDDRSSDTRPSPDALLDHAEREGRGRLRIFLGAAPGVGKTYEMLMSGRARLAD GVDVVIGVVETHGRKETLALVEGYEVIPRRKVDYKGRILDEMDIDAILARRPALVLV DELAHTNAPGSRHPKRYLDVQEILTHGIDVYTTLNIQHVESLNDVVAQITKVRVRET VPDSIIDQADDVEIIDLTPDDLIKRLEEGKVYFPNTAQRAIENYFSPGNLTALRELAL RRTAQRVDDQLLIHMQAHAIPGPWAAGERVLVCLDARPGGAARVRYARRLADRL RAPWTALHVDSTRSASMPEDDKDRLATNLRLAQQLGAEVTTIPGQNVAQDIVRYA TANNFTHIVVGRPTRSRWRELIEGSLTYDLIRNAGDISVHVISGSERGTEAASRSV KAADEQRQFEIRPYLKATAFVIGSLAFAVLLDQFLDVRNLAIILLIGVLASAVTGGLW PALYACFVSALAFNYFFLEPRYTLTIRDPESIVALGVFLVVAVIASNLTARVQRQAV AARSRARATEDIYLFSKKLAGAGTLDDVLWATAFQIASMLKLRVVLLLPEDGTITVK AGYPPDDTLAEADIAAARWAWEHNRAAGRGADTLPGAKRLYLPLRTGRTAIGVV GLDNDKQGPLLTPEQQRLLDALADQAAVAIERIQLVADVDRAKLAAEADRLRSALL TSISHDLKTPLAAIMGAAGTLRDFSAALPEPDRAELLSTVLDESERLNRFIANLLDM TKIESGAMEPNYAFHYVGDIVGSALQRARKIIGEHKIETDIPRDLPMLKVDPVLFEQ ALFNLLDNAAKYAPAGSTIRVQGWTDNGSVLLQIMDEGPGIPPGDLERIFDTFYRV RKRDQIRAGTGLGLSICRGFIEAMGGTITAANRTDGSGAVFTIKMPKPANPPNFDA SNTDDVGDLA	23~~KdpD (2.4857E-114) ~~233,255~~Usp (4.12845E-47) ~~378,404~~DUF4118 (9.01356E-17) ~~502,530~~GAF (1.89017E-16) ~~649,666~~HisKA (0.0000000000012691) ~~732,785~~HATPase_c (5.51704E-28) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.3E-95	327.3	0	3.6E-95	326.7	0	1.3	1	A0A089UJW6_9ENTR	Histidine kinase (EC 2.7.13.3)	LH23_11605	Cedecea neteri	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cedecea, Cedecea neteri	158822	>tr|A0A089UJW6|A0A089UJW6_9ENTR Histidine kinase OS=Cedecea neteri GN=LH23_11605 PE=4 SV=1 MTEEPLRPNPDKLLEKVNRQPRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGLD VLVGVVETHGRKETAELLKGLTIQPPRRIHHRGRLVQEFDLDAALARSPALILMDEL AHTNAPGSRHPKRWQDVEELLEAGIDVLTSVNVQHLESLNDVVGGVTGIQVRETV PDPIFDAADEVVLVDLPPDDLRQRLHEGKVYISGQAERAIEHFFRKGNLIALRELAL RRTADRVDDQMRAWRDNQGQEKVWHTRDAILLCIGHSNGNEKLVRTAARLAAKL GSIWHAVYVETPQLHRLPEHQRRTILSALRLAQELGAETATLADPNEEKAVLRYAR EHNLGKIIIGRHTTRRWWHRTSFADRLAKRAPDLDLLIVALDEKPLPSPARAPDTR TLSEKWRIQLRGCAVAVVLCAFITFIANQWLVAFDAANLVMIYLLGVVMVALFYGR WPSVLATVINVISFDLFFIAPRGTLAVSDVQYLLTFGVMLTVGLVIGNLTAGVRYQA RIARYREQRTRHLYEMSKALADDRTPQDVAATSVQFINNTFQARSLLLLPDDHGKL SRIAAEGEPAQWDEAIARWSFDKGQPAGAGTDTLPGVPYRILPLSTTERTLGLLV VEPENLRQLMIPEQQRLLETFTLLVATALDRLLLTASEEQARLSSEREQIRNSLLAA LSHDLRTPLTVLFGQAEILTLDLASEGSKHAPQANEIRQHVLNTTRLVNNLLDMARI QSGGFNLRKEWLTLEEVVGSALKMLEPGLGGRHIALNLPDPLMLIEVDGPLFERVL INLLENAVKYAGYKANIGIKATSTADKLDLEVWDSGPGVPAGKELLIFDKFARGNK ESAIPGVGLGLAICRAIVEVHGGTIYALNRPEGGASFHVVLPLSPPPELPEMIEVL	22~~KdpD (2.7805E-125) ~~230,253~~Usp (1.44838E-39) ~~373,403~~DUF4118 (2.64488E-20) ~~501,527~~GAF (2.49708E-16) ~~644,661~~HisKA (0.0000000219598) ~~726,779~~HATPase_c (1.32769E-25) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.3E-95	327.3	0.2	3.8E-95	326.6	0.1	1.3	1	B6JA61_OLICO	Histidine kinase (EC 2.7.13.3)	kdpDOCA5_c03360	Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	901	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Oligotropha, Oligotropha carboxidovorans (Pseudomonas carboxydovorans), Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	504832	>tr|B6JA61|B6JA61_OLICO Histidine kinase OS=Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5) GN=kdpD PE=4 SV=1 MSDDPIREHSRPSPDALLESAQRETRGHLKIFLGAAPGVGKTYEMLMSGRAQRA DGVDVVIGVVETHGRAETEALVDGFEIVPRRTVPYRGHVLDEMDIDAILARKPALV LVDELAHTNAPGSRHPKRYLDVEELLANGIDVYSTLNIQHVESLNDVVAQITRIRVR ETVPDSIIDRADDIEIIDITPGDLIKRLNEGKVYLPKTAKRATQNYFSPSNLTALRELA LRRTAQRVDDQLVTHMQAHAITGPWSAGERVLVCINERPGATALVRYGRRQADR LRAPWAAVHVETSKDARLSEHQKDKIASALRLAEQLGAEAVTLPGENVAQEILTYA STNNYTHVIVGMPTSPRWRELFAGSVSHDLIRAKTDVSVHVISPGNGEDTRRPAT VSARSKKRPDVGHYLWSTLYVAVALGLGTALSRFLDVRNIALVFLMAVLASAMGG GLWPALFASVLSALAFNFFFLDPLYTLVIGDPESVVAFAFFLVVAVIASNLASRVQR QAVTARERAKTTEGLYQFSKKLAGAGTLGDVLWATVYQIASMLHVRVVALLPENG RIAVQAGYPPDDTLDDADIAAAHWAWEHDKPAGRGADTLPGAKRLYLPLKTGRT QVGVIGLDNDKQGPVLTPAEQRLFDSLADQAALAIERIQLVADVDNARLAAEADKL RSALLTSLSHDLKTPLASILGSAGALRDYSTSLTDSGRVELLTTIVEEAERLNRFIAN LLDMTRLESGAAAVSLTPLFIGDSVGSALRRAEKILACHRVDLAVPPDLPMVRLDP VLFEQVLFNLLDNARKYAPAGSLILIRAWAEEDHVVLQIVDEGPGIPSDDLTRIFDS FHRVRKKDHVQAGTGLGLSICKGFVEAMGGTIFATNRADRPGAIFTLRFSIGPEPS PMEGRI	26~~KdpD (2.64966E-112) ~~234,256~~Usp (1.61787E-39) ~~379,404~~DUF4118 (3.06211E-20) ~~504,530~~GAF (1.65672E-15) ~~649,666~~HisKA (0.0000000000573943) ~~732,785~~HATPase_c (8.45486E-28) ~~888	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.4E-95	327.3	0.7	4E-95	326.6	0.5	1.4	1	A6W6R8_KINRD	Histidine kinase (EC 2.7.13.3)	Krad_1019	Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	858	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Kineosporiales, Kineosporiaceae, Kineococcus, Kineococcus radiotolerans, Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	266940	>tr|A6W6R8|A6W6R8_KINRD Histidine kinase OS=Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216) GN=Krad_1019 PE=4 SV=1 MPQTGRVEPRRDEKRRGRLRVFLGAAPGVGKTFAALDEAHRRRRRGTDVVVGL VECHGRERTEALLAGLEVLPRRTVEHRGLAVAELDVEAVLRRRPEVVVVDELAHT NAPGSKHPKRWQDVEEILAAGVDVVSTVNIQHLESLNDVVEHITGIEQRETVPDAV LRSADQVQLVDMTPEALQRRISHGNVYAGDRVDAALSNYFRTGNLTALRELALLW LADRVDEGLERYRAQQGIDATWPARERVVVALTGGAEGATLVRRAARLAGRGAG GELHAVHVARGDGLLRTSPVRLAEQRELVETLGGTYHQVVGDDVATSLLEFARG VNASQIVVGASRHRRLASLFRRSVGDGVVRGAGAVDVLVVTHEEQARRSGLPRP ARAALSGTRRVLGWLVALLGPLLVTGVLLAIPHQDLSTDLMVFLVVVVGAALAGGV LPALAAALVAGLAVNWFFTEPLHRFTIAQPANAVALAVFLLVALAVSSTVDTAARRT RDAARSRAESEALSVLTRTALLAADPLAEALRHTRETFAVDSVTLLERSDVRAPW AVAAATGAPVCTRPADADAEVVLDDLTCLVLRGRLLGAGDRRVLEVFATQIAAVR QKQRLRAEAAQVRRLEEGEAVRGALLTAVSHDLRTPLATLKASLDSLRAKDIDLPE EIRDELLAEVGNSADRLQGLIDDLLDLTRVRSGTVEPLLVVVDLEDVVAGAVRDVG PGRVVVDLPPGLPPVSTDPGLLQRVVANLVQNAVRHGGTRVEVVASSSTDDARR VVRLLVVDHGPGLPDAAKERAFTPFQRLGDRSTAGLGLGLAVARGLAEAVGGRL EAQDTPGGGLTMVLDLPPAGHAQALVPAPGGSPA	14~~KdpD (1.66616E-117) ~~224,246~~Usp (1.40852E-31) ~~368,395~~DUF4118 (0.0000229276) ~~484,X,623~~HisKA (0.0000000000103566) ~~689,738~~HATPase_c (1.56429E-20) ~~840	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.5E-95	327.3	0.8	3.7E-95	326.7	0.6	1.3	1	Q2RV86_RHORT	Histidine kinase (EC 2.7.13.3)	Rru_A1158	Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	897	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum rubrum, Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	269796	>tr|Q2RV86|Q2RV86_RHORT Histidine kinase OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1) GN=Rru_A1158 PE=4 SV=1 MAPADRENRPSPDALLAEAHREGRGKLKIFLGAAPGVGKTYAMLEAARERARDG VDVAVAVVETHGRRETEALVHGLDVVPKRTLEYRGRDFEEMDLDGVLARRPALAL VDELAHTNISGSRHLKRWQDVQELLDVGIDVYTTLNVQHLESLNDVVERISGVRVR ETLPDSVLQQADEIKLIDLAPEDLLKRLEEGKVYVPDQARRAANAFFSRGNLTALR EMALRQAAERVDAQMISYMHAHAIQGPWPARERLMACIGDDLAAESVVRLAARS AERRQAPWIAVYIETARHLSLSEEVKDRIARALRLAEELGGEATTVQGDDVVAEVL SFAKARNITQIIIGRPRRHRQRWFGGGDTAKALLARAEAFNVTVIGRENASPSPIAR IRRDMPKDWLGYGLATLAVALATGFSVLIDMWMPVPNISVAYLMAVLLVAMRLGL APSIFASLLSFLIYSFLFTEPRLTLAITDSHNILTMVFFLVAAVIVSNLGSRLREQVQA TRLSARRTGTLYDFSRKIAAAATQDDVLWAVVHHVASTIHGQSLILLPENDRLAIKA GYPPEDTLDDKAAAAAEWAWTHGTRAGAGSATLPTSPWLFLPLKTVRGPVGVM GVQMAGAGIPPPSEARLLETLADQAAVAIERTALVADIEAARVAGERDRLRTALLS SLSHDLRTPLVSIMGSASALVNYQDTLSDDAERELALTIQDEAERLNRFVQNLLDM TKLGAGALKPRIDWADFRDIVGGALERAKRLIGQRKVRIDLSDDFPLLCVDSVLME QVVFNLIDNACKYTPPGSAITVWGRPRRDKVVVEICDQGPGIPEADREQVFDMFY RVKAQDAQIAGTGLGLAICRGLVEAHGGTIAAEPGINDCGTCIVITLPLLVEPELLGA EEKV	22~~KdpD (1.43916E-114) ~~232,254~~Usp (2.01334E-40) ~~377,400~~DUF4118 (6.33756E-19) ~~499,525~~GAF (0.0000000000139044) ~~643,660~~HisKA (0.0000000000157104) ~~726,779~~HATPase_c (3.74927E-26) ~~881	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.5E-95	327.2	0.2	4.2E-95	326.5	0.1	1.4	1	A0A0F4JR63_9ACTN	Histidine kinase	VR45_11645	Streptomyces sp. NRRL S-495	890	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-495	1609133	>tr|A0A0F4JR63|A0A0F4JR63_9ACTN Histidine kinase OS=Streptomyces sp. NRRL S-495 GN=VR45_11645 PE=4 SV=1 MARDLTPGTGHRRGRLRVYLGSAPGVGKTYRMLDEARRRQDRGADVVVGWIEC HGRRHTEAMLDGLEVVPGVHRAYRETDFEEMDLDGVLRRKPTVVLVDELAHTNIP GGRHGKRWQDVDELLDAGIDVITTVNIQHLESLNDVVQKITGIPQRETVPDEVVRR ADQIELVDMAPQALRRRMAHGNVYKAEKVDAALSNYFRVGNLTALRELALLWVA GRVDEGLRDYRASHNIDRVWETRERVVVALTGGPEGETLVRRAARIADRTAGGD LLAVHVTRSDGLAGASSGALAQQRQLVESLGGSYHVVVGDDIPTSLLAFARAHDA TQLVLGTSRRGRTARFLTGPGIGETTVDASEDIDVHMVTHEFTGRGRLPALGRRH SRRRTVAGFLAGPIVPSLLTLVLSQFHDTVNLTTDALIFQLGVVVVALLGGATSALL ASLVASVLLNYFFIPPVHAFTIGETNNIIALVVFAAVALTVSTVVDHATRLTARAARA TAEAETLSTLAGSVLRGADALPALLEKSRTAFGMSSVALLGRTGGEVLASCDTAA EVKDAADGDRADNGGAAPDHTLVTTEVPVGADAVLVLTGRRLPAADQRVLTAFA AHVAAALERDRLAVVAAEVEPIKAADRMRTALLAAVSHDLRTPLAAALASVGSLRS PDVEFSPEDQAELLATADESLVKLTRLVDNLLDMSRLQAGALTLHLAETHLDEILPR ALDSLADPYAPVQPLDLETVPPVLADPPLLERVLANVITNALRHNAPGAPVLVAAS HHAGRVELRVIDRGPGIAPEDRDRVFLPFQRLGDTDNTTGVGLGLALSRGLAEAM DGSLEVEDTPGGGTTMLLTLPAAPARPLPAGPVPVPADPLPADPLPAGPMPAQH PGEAPV	11~~KdpD (9.09957E-116) ~~221,243~~Usp (1.09605E-30) ~~366,392~~DUF4118 (0.000000000861322) ~~485,X,632~~HisKA (0.00000000000238385) ~~698,749~~HATPase_c (2.43989E-27) ~~849	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.7E-95	327.1	1.7	3.8E-95	326.6	1.2	1.2	1	Q8R8I8_CALS4	Osmosensitive K+ channel His kinase sensor domain protein	KdpDTTE2009	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	365	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	273068	>tr|Q8R8I8|Q8R8I8_CALS4 Osmosensitive K+ channel His kinase sensor domain protein OS=Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) GN=KdpD PE=4 SV=1 MREIERANKGRLKIYLGAAPGVGKTYHMLQDANEMKKRGIDVVIGFVETYGRKDT EEQIGDLEIIPLKEINYKGVILKEMDLEAIIKRKPQVVVVDELAHTNAPGSKNEKRYQ DVLELIDNGISVMTAVNIQHFESLNDYVNRMTNVKVRETIPDKILELADEIEVVDVSP ETLIERLKNGKIYSPDKIETALNNFFRVGNLAALRELTLREVANEVDDRLLEYRNKK KVVGLKGAQEKILVCVNLRFNAEYLIRRGYRLAKMLKADLFVLHVYNDDELKDHKN LKKLDEITMLCNKLEAKFYMVKSNDPAKAIIKFAEENAITQIVVGQSVRRRIDEIIRGS IVRRIMKGTKFIDVLVVADPRG	7~~KdpD (3.07006E-128) ~~217,239~~Usp (2.79724E-42) ~~361	non-kinase	KdpD;Usp

	2.8E-95	327.1	0.2	4.6E-95	326.4	0.1	1.4	1	F4F4Z0_VERMA	Histidine kinase (EC 2.7.13.3)	VAB18032_21895	Verrucosispora maris (strain AB-18-032)	850	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Verrucosispora, Verrucosispora maris, Verrucosispora maris (strain AB-18-032)	263358	>tr|F4F4Z0|F4F4Z0_VERMA Histidine kinase OS=Verrucosispora maris (strain AB-18-032) GN=VAB18032_21895 PE=4 SV=1 MPRGELRIYLGAAPGVGKTYAMLEEAQRRAERGIDVVIALVETHGRPHTAAMIGDL EVIARRTATYRGGTFQEMDLDAVLARHPAVAVVDELAHTNVPGSRHAKRWQDIQ ELLDAGISVLSTVNIQHLESLNDVVAQITGTTQRETVPDQIVRAAAQVELVDMTPEA LRRRMAHGNIYPPDKIDAALGNYFRVGNLTALRELALLWLAGTVDEQLDAYRAQQ GISATWEARERVVVALTGGPEGATLIRRAARIAARSKGTDLLAVHVARNDGLAGA DPAHLARQRVLVESLGGTYHQVLGSDIPAALLDFARGVNATQLVLGASRRGRFAQ VLSRGVGVTTTALSGPIDVHLVTHPEAGRGRRTAGVPALSRRRRLLGFTLAVLGM PVLTASLKALPDLTLTSDILLFLAAVVGVALVGGLWPALLAALGGSLLLNWFFTPPF ATLTIAGADNLLALAVFVGVAVAVSGVVDMAARRTRDAARASAEAQTLATVAGSV LRGQRPLTALLDRLRETFALRAVSVLELVDAADGRPDRAREEAAWRLVASVGDAP ATSPGAGETAVPVDDRLTVVLCGRRLAASDRRVVEAFAAQAAVALRQQRLAAQA AAARPLAAADRMRTALLAAVSHDLRTPLASAKAAVSSLRSHDVEFDAADRDELLAT ADESLDRLGRLVANLLDMSRLQAGALGVHAVAIGVEDVVPRALDELGPPAAGVRT DIPADLPAATADPGLLERVLVNIVANALRHSPPHRPPLVTASAHAGLVELRIIDHGP GIPADQWEHVFQPFQRLGDRDNTAGVGLGLALSRGLAEAMGGSITPETTPGGGL TMVLRLPAAASVTAMEEPPA	3~~KdpD (4.06331E-117) ~~211,233~~Usp (3.28198E-19) ~~355,X,618~~HisKA (0.00000000000187698) ~~684,735~~HATPase_c (2.66848E-26) ~~836	kinase	KdpD;Usp;X;HisKA;HATPase_c
	3.9E-95	326.6	0.1	8.7E-95	325.5	0.1	1.6	1	A0A0F5K0K5_9BURK	Sensor protein KdpD	WM40_09820	Burkholderia andropogonis	944	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia andropogonis	28092	>tr|A0A0F5K0K5|A0A0F5K0K5_9BURK Sensor protein KdpD OS=Burkholderia andropogonis GN=WM40_09820 PE=4 SV=1 MTERPDPDELLSRIQRDEARQQRGKLKIFFGASAGVGKTYAMLQAAHRLADEGLD VVAGVVETHGRRETIALLSGLEVLPAAYFEQRGRRLAEFDLDAALARRPALILIDEL AHSNVAGARHAKRWQDVQELLDAGIDVYTTVNVQHLETLNDIVGQITGIRVWETV PDRIFDLADEVTLVDLPPEELLERLRDGKVYMPAQAERAIENFFRKGNLIALRELAL RRTADRVDAQMREYRADQSIERLWRARERLIVCVGPGPDSAAMVRTASRLASSL KADWLAVYVDTPRLHRLADVERKPTFEALKLAGELGAETVVLDGANAAESLAAYA LMRNVSKVLVGKSSRGRLRALLQPPFAACLAQAAPQVELTLIAPSSDVRHADKRA RRPLLRRGESSGDPRSPLSAYVIATIIAAAITAVVTLSLSQANLSNLVMLYLLGVVFA AVKLGRGPGAYLSFLSVFLFDFFCVDPRFSFAIADTQYLLTFVVMLTTSLTISHLTS SLRRQARAASARERRTAAMYAMVKELGAALTEGQIIEIATRHTHEVFGARVAVLLP DSEDQVRQKIDHPDPMTALPEESLAIDVAQWVYDRQQPAGAGTNTLPASTAYYL PLKAPMRTRGVMALVSNRNTQWASPEQNRLLETFASQIALALERVHYVEIAQDAL VSMESERLRNSLLATISHDLRTPLTAILGLAATLAAQLRESTSSRNDQGIDLANTIH GEAQHMVSLVSNLLDMARLQGGIKLDLQWLMLEEAVGAALALCRRILDGRPVTVT IASDVPMIRLDAVLMERVFVNLFENVCKYATPGTTIGIVGTVVHDGARRFVKVAVN DIGPGLVPGTEGKIFDKFTRGVKESATRGVGLGLAICRAIVEAHGGQMQARNRISA TGERIGASFSLTLPADVQPPAIEEMGEDDMRDEECSGRLIAADAKRGDGEHE	22~~KdpD (2.08458E-122) ~~231,253~~Usp (1.56852E-33) ~~376,432~~DUF4118 (0.00000000000034506) ~~505,537~~GAF (1.1766E-18) ~~657,674~~HisKA (0.00000000000130107) ~~743,795~~HATPase_c (5.00623E-16) ~~905	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.9E-95	326.6	0.1	6.4E-95	325.9	0.1	1.3	1	E4NDZ4_KITSK	Histidine kinase (EC 2.7.13.3)	kdpD2 KSE_36210	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	857	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Kitasatospora, Kitasatospora setae, Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	452652	>tr|E4NDZ4|E4NDZ4_KITSK Histidine kinase OS=Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) GN=kdpD2 PE=4 SV=1 MPADPRPRPHPEDRRPGRLRVYLGAAPGVGKTYRMLDEAHRRRERGTDVVVG WLDTHDRPRTARLLDGLEQLPRATREYRGAEFAELDLDGLLARRPELALVDELAH TNVPGGRHAKRWQDVEELLAAGIDVVTTVNIQHLESLNDVVQKITGVPQRETVPD EVVRRADQIELVDMAPQALRRRLAHGNVYRAEQVDAALAHYFRIGNLTALRELALL WLAGRVDEGLRDYRAAHRIDRVWETRERVVVALTGGPEGVTLIRRAARISDRAA GGELLAVHVSRSDGLAGASPGRLAEQRRLVESLGGSYHSVVGDDIPEALLAFARA RDATQLVLGTSRRGRLNRFLTGPGIGETTVDRSEDIDVHMVTHAFTGRGRLPPLG RRHSRRRTRSGYAAGLAVPVMLTAALSQAHHALNLTTDALILQLGVVAVALLGGA VSALLASLAASLLLNYYFIPPVHTFTIGEANNFIALAVFAAVALCVSTVVDHAGRQTA RAARATAEAETLSTLAGSVLRGADAVPALLERTRTSFGLDTVTLLDRATGRALDAV ESPVESPAESPAESPDTTATADPVHTTDLPVGPDALLRLTGRRLPDTDQRVLAAF GAHLAAALERDRLATAAAEVEPIRAADRMRTALLAAVSHDLRTPLAAALASVGSLR SPDVDFSAEDRAELLTLADESLHRLTRLVDNLLDLSRLQAGALTPHLRPTHLDEVL PAALDALATPDAPVRSAVTEAVPPVLADPPLLERVLANVLANALRHNPPGAPVLVT ASAHADRVEIRVVDRGPGIPPEDRDRVFLPFQRLGDTDNTTGTGLGLALSRGLAE AMGGTLTAEDTPGGGTTMLLTLRAAETP	15~~KdpD (1.40408E-115) ~~224,246~~Usp (3.29128E-30) ~~369,X,633~~HisKA (0.00000000000321699) ~~699,750~~HATPase_c (2.30218E-31) ~~851	kinase	KdpD;Usp;X;HisKA;HATPase_c

	3.9E-95	326.6	0.2	6.9E-95	325.8	0.1	1.4	1	A9AXU7_HERA2	Histidine kinase (EC 2.7.13.3)	Haur_2273	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	895	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Herpetosiphonales, Herpetosiphonaceae, Herpetosiphon, Herpetosiphon aurantiacus (Herpetosiphon giganteus), Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	316274	>tr|A9AXU7|A9AXU7_HERA2 Histidine kinase OS=Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785) GN=Haur_2273 PE=4 SV=1 MEHQRPNPDQLLERIQSANQQAQRGRLKVFFGAAAGVGKTYAMLQAAQQRRAE GIDVLVGYIETHGRAETDALLVGLPQLPALQVEYRGTSLREFDLDAALERKPSLILV DELAHSNAPNLRHAKRWQDINELLHAGIDVYTTVNVQHLESLNDLVAQVTGVIVRE TVPDAVLESADEVELIDLPPDELLGRLNEGKIYIASQAAQAARNFFRKGNLIALREL ALRRTADRVDAQMQRYRHDHAIPTTWPTRERLLVGVGPSPLSERLVRATRRMAN DLKAEWLVVYVETPKHLRLSEADRDRVTATLRLAESLGAQIVTLGGINPGEEMLRY ARQRNVSKIVVGKPAQPRWRELLFGSIVDQLIRQSGEIDVYVISGEHDDTHKPNAK PSLQPHSPKINYVKSSGVVLACTMVCYGIFPHLELSNLIMLYLLGVTWVAARYGRG PAISASILSVAAFDFFFVQPYLTFAVSDVQYILTFMVMLIVALTISTLTVQIQAQAETA RQRERRTAALYAMTREFASIRGLDNLLQTAAQHISSVFEGQTAILLPNPKGQLRPIV GQQWPFISDQRELITAQWVYDHQQKAGMHSDTLPSAQAMYLPLIATRGVVGVLA LQPEQPRRLLDPSHVHLLETFANQTTVAIERAHLAEEAQAASVQIETERMRNSLLS SVSHDLRTPLAAISGAASTLLDQTNQLDQHIQHELIQTIADEGQRLNRLLSNLLDMT RLEAGAVQVHKEWQALEEVLGTALARLAPQIDQRSISIELPNQAFVPFDSILIEQVL VNLLENSLKYSPSSSPIEIRAVERIGLIEVQIADHGPGIPPSALETIFEKFFRVQAKRS ASSGVGLGLTICRGIIEAHGGTIWAENRPAGGAIFAFTLPIEGQPPQIRGE	22~~KdpD (5.6864E-124) ~~232,254~~Usp (9.06379E-45) ~~377,400~~DUF4118 (1.02681E-19) ~~494,527~~GAF (4.89745E-15) ~~646,663~~HisKA (0.0000000372216) ~~715,781~~HATPase_c (8.08471E-30) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.9E-95	326.6	0.3	6.5E-95	325.9	0.2	1.4	1	A0A0F0HJ10_9PSEU	Histidine kinase	UK12_27900	Saccharothrix sp. ST-888	853	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix sp. ST-888	1427391	>tr|A0A0F0HJ10|A0A0F0HJ10_9PSEU Histidine kinase OS=Saccharothrix sp. ST-888 GN=UK12_27900 PE=4 SV=1 MSRDLTPGTLTRRGKLRVYLGSAPGVGKTYRMLDEARRRQERGADVVVGYIECH GRRHTENMLAGLDIVPRLTRTYRDTEFQEMDLEGVLARRPTVVLVDELAHTNIPG GRNAKRWQDIDELLDAGIDVITTVNIQHLESLNDVVQKITGIPQRETVPDEVVRRAD QIELVDMAPQALRRRMAHGNVYKAEKVDAALSNYFRVGNLTALRELALLWVAGR VDEGLRDYRASHNIDRVWETRERVVVALTGGPEGETLIRRAARIADRTAGGELLA VHVTKSDGLAGASPGALAQQRQLVETLGGSYHVVVGDDIPTALLAFARGRDATQL VLGTSRRGRITRLLTGPGIGETTVDASEDIDVHMVTHEFTGRGRLPSLGRRHSRN RTIAGYVAGLVVPSLLTAVLSQFHTQVNLTTDALIFQLGVVAVALLGGAVSALLASL VASLLLNYFFIPPTHTFTIGETNNVIALLVFAMVALTVSTVVDHATRLTSRAARATAE AETLSTLAGSVLRGADAVPALLEKSRTAFAMATVALLDRSSGEVLARSDADAEGT SGEAVTEIAVGADAVMILTGRRLPAADQRVLTAFAAHVAAALERDRLASVAAEVEP IKAADRMRTALLAAVSHDLRTPLAAALASIGSLRSPDVEFSPEDEAELLTMADESLV KLTRLVDNLLDMSRLQAGALTLHLVPTHLEEVLPRALDSLSDPDAPVQPLGLDSAP PVLADPPLLERVLANVITNALRHNAPGAPVLVAASSLPQPPAGGTPLNRVEIRVIDR GPGIAPEDRDRVFLPFQRLGDTDNTTGVGLGLALSRGLAEAMGGTLEVEDTPGG GTTMLLTLPAAGTGEPTP	12~~KdpD (1.84018E-117) ~~221,243~~Usp (7.95736E-30) ~~366,391~~DUF4118 (0.000823939) ~~489,X,616~~HisKA (0.0000000000721137) ~~682,733~~HATPase_c (7.9752E-26) ~~843	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.1E-95	326.6	0.1	6.3E-95	325.9	0	1.3	1	A7MQV1_CROS8	Histidine kinase (EC 2.7.13.3)	ESA_02644	Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cronobacter, Cronobacter sakazakii (Enterobacter sakazakii), Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	290339	>tr|A7MQV1|A7MQV1_CROS8 Histidine kinase OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=ESA_02644 PE=4 SV=1 MTEEPMRPDPDRLLIQTQGRTRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGLDI LVGVVETHGRQETAALLKGLAIQPLKRIHHRGRVVQEFDLDAALARNPALILMDEL AHSNAPGSRHPKRWQDVDELLDAGIDVFTTVNVQHLESLNDVVGGVTGIQVRET VPDPIFDAADEIVLVDLPPDDLRQRLHEGKVYIAGQAERAIEHFFRKGNLIALRELAL RRTADRVDDQMRAWRDRQGQEKVWHTRDAILLCIGQGAGNEKLVRTAARLAAR LGSVWHAVYVETPRLHQLPETSRRAILSALHLAQELGAETATLADPVEEKAVLRYA REYNLGKIVIGRRNKRRWWSQDTFAERLARHAPDLDLLIVALDDKPTATAKAAD NRPFMEKWRVQLRGCAVAVALCALITLVAHQWLIAFDAANLVMVYLLGVVLVALF YGRWPSVVATVINVVSFDLFFIAPRGTLAVSDVQYLLTFAVMLSVGLIIGNLTAGVR YQARIARYREQRTRHLYEMSKALAVGRSARDIAATSQQFITSTFHARGLLLLPDEH GKLQAPQPLAEITPWDEAIARWSFDKGLPAGAGTDTLPGVPYQILPLRTAGKTLG LVIVEPGNLRQLMIPEQQRLLETFTLLVASALERLFLTESEEQARLASEREQLRNSL LAALSHDLRTPLTVLFGQAEILTLDLAAEGSNHAPQASEIRQHVLNTTRLVNNLLDM ARIQSGGFNLREEWLTVEEVVGSALKMLEPGLGGRHIELSLSDPLTLIHVDGPLFE RVLINLLENAAKYAGPRAQTGVRTSWRDDRLDLEVWDNGPGIPAGQEQAIFAKFA RGNKESAIPGVGLGLAICQAIVEVHGGEIYARNRPEGGASFHVLLPNETPPELDIHE VM	22~~KdpD (4.27246E-126) ~~230,253~~Usp (4.61098E-37) ~~373,403~~DUF4118 (1.79613E-20) ~~501,529~~GAF (2.65919E-14) ~~644,661~~HisKA (0.0000000277971) ~~726,779~~HATPase_c (4.16095E-27) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4.2E-95	326.5	0	4.9E-95	326.3	0	1	1	K8W5U1_9ENTR	Sensor protein KdpD	OO7_12934	Providencia sneebia DSM 19967	266	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia sneebia, Providencia sneebia DSM 19967	1141660	>tr|K8W5U1|K8W5U1_9ENTR Sensor protein KdpD OS=Providencia sneebia DSM 19967 GN=OO7_12934 PE=4 SV=1 MNNQDPERPNPDELLLKANVDGRGKLKIFFGSCAGVGKTYAMLQEAQRLRAQGL DVLIGVVETHEREDTAALLEGLSILPPRRIHHRGRRLQGFDIDAAIARYPAIILMDEL AFSNPAGSRHPKRWQDVEELLDAGIDVLTTINVQHIESLNDVVGSITGIRVRETVP DHIFDDADEVVLVDLPPDDLRQRLKDGKVYIPGQAERAIEHFFRKGNLIALRELALR RTADRVDGQMREFRDGKGQAPVWHTRDGLLLCIGDMQEMKN	22~~KdpD (1.48834E-128) ~~231	non-kinase	KdpD
	4.2E-95	326.5	0	6.4E-95	325.9	0	1.3	1	Q8X9G1_ECO57	Sensor for high-affinity potassium transport system	kdpD ECs0723 Z0842	Escherichia coli O157:H7	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli O157:H7	83334	>tr|Q8X9G1|Q8X9G1_ECO57 Sensor for high-affinity potassium transport system OS=Escherichia coli O157:H7 GN=kdpD PE=4 SV=1 MNNEPLRPDPDRLLEQTAAPHRGKLKVFFGACAGVGKTWAMLAEAQRLRAQGL DIVVGVVETHGRKDTAAMLEGLAVLPPKRLAYRGRHISEFDLDAALARRPALILMD ELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRE TVPDPFFDAADDVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRK LALRRTADRVDEQMRAWRGHPGEEKVWHTRDAILLCIGHNTGSEKLVRAAARLA SRLGSVWHAVYVETPALHRLPEKKRRAILSALRLAQELGAETATLSDPAEEKAVVR YAREHNLGKIILGRPASRRWWRRETFADRLARIAPDLDQVLVALDEPPARTINNAP DSRSFKDKWRVQIQGCVVAAALCAVITLIAMQWLMAFDAANLVMLYLLGVVVVAL FYGRWPSVVATVINVVSFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAG VRYQARVARYREQRTRHLYEMSKALAVGRSPQDIAATSEQFIASTFHARSQVLLP DDNGKLQPLTHPQGMTPWDDAIAQWSFDKGLPAGAGTDTLPGVPYQILPLKSGE KTYGLVVVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEEQARMASEREQ IRNALLAALSHDLRTPLTVLFGQAEILTLDLASEGSPHARQASEIRQHVLNTTRLVN NLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLSSPINLSLPEPLTLIHVDG PLFERVLINLLENAVKYAGAQAEIGIDAHVEGENLQLDVWDNGPGLPPGQEQTIFD KFARGNKESAVPGVGLGLAICRAIVDVHGGTITAFNRPEGGACFRVTLPQQTAPE LEEFHEDM	20~~KdpD (3.97046E-129) ~~230,253~~Usp (8.59003E-42) ~~373,403~~DUF4118 (6.10853E-21) ~~501,527~~GAF (2.92186E-17) ~~644,661~~HisKA (0.000000000260724) ~~726,778~~HATPase_c (1.21374E-31) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.2E-95	326.5	0.4	7E-95	325.8	0.3	1.4	1	Q0RF14_FRAAA	Histidine kinase (EC 2.7.13.3)	kdpD FRAAL5304	Frankia alni (strain ACN14a)	880	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia alni, Frankia alni (strain ACN14a)	326424	>tr|Q0RF14|Q0RF14_FRAAA Histidine kinase OS=Frankia alni (strain ACN14a) GN=kdpD PE=4 SV=1 MKKRPVRTFRCFPPRPDGRTMGGVPRGTLRIYLGAAPGVGKTYAALDEARRRRD RGTDVVVGLVETHARHHTAAMLDGLEVIPRRFAEHRGATFTEMDLDAVLARRPAV AVVDELAHTNVPGSRHAKRWQDVQELLDAGIDVISTVNVQHLESLNDVVETITGV AQRETVPDAVVRAASQVELVDMAPEALRRRMAHGNIYAADKVDAALANYFRPGN LTALRELALLWLAGKVDDQLDRYRAEHHIGGTWETRERVVVALTGGPEGETLIRR AARIASRTKGAELLAVHVARSDGLTGADPAALAGQRVLVDSLGGSFHQVIGDDVP TALLDFARAENATQLVLGASRRGRLARILTPGIGVTTTNQSGPIDVHMVTHAEAGT GWRLPRVRSGLTPRRRLVATALTLALVPALTAALVQGRGTLNLATEMLGYLIVVVS VALIGGFWPALLCALASSLLLNYYFTPPLHHWSVAEGNNALALAGFVLVATMVSR VVDLSARRYGQAARAAAEATTLSMLAGSVLRGEDALPALLDRARETFAMTSATLL ERDGDGWRAVLSVGPDPCSRPEDGAVDVPVGDTLALTLTGRPLPAADRRILAAF AAQAAVALDQRRLAEAAARAVPIAQADRVRAALLTAVSHDLRTPLAAAKAAVTGLH STEAVLSRDERDELLATAEESLDRLTRLVENLLDMSRLQAGALSVFPRPIGLDDVV PHALDELGPPARAIAIRIPDDLPTIDADPALLERVLVNLVGNALRHAPAGRPPVITAS SLADRVELRVVDHGPGIPADHRDQVFRPFQRLGDRDNTTGVGLGLALSRGLTEA MNGTLTPEDTPGGGLTMVVSLPAAEPPPSLTALDDAELGPATRSPASVDDLA	26~~KdpD (2.81445E-120) ~~234,256~~Usp (5.7719E-31) ~~378,400~~DUF4118 (0.000413138) ~~503,X,631~~HisKA (0.00000000000295131) ~~697,748~~HATPase_c (3.94163E-27) ~~849	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.3E-95	326.5	0.1	7.4E-95	325.7	0.1	1.4	1	R6P495_9CLOT	Histidine kinase (EC 2.7.13.3)	BN578_00327	Clostridium leptum CAG:27	898	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium leptum CAG:27	1263068	>tr|R6P495|R6P495_9CLOT Histidine kinase OS=Clostridium leptum CAG:27 GN=BN578_00327 PE=4 SV=1 METQRPSPEELLYHIHQQQDQSTHGKLKIFFGYAAGVGKTYTMLEAAHQAQKEG RDVVVGYVERHVRPETLALLDGLEQMPCKEVPYKGVMLKEFDLDEALARKPQLIL VDELAHSNAPGCRHAKRYQDVEELLRAGIDVYTTVNVQHLESLNDLVASITGVSVS ERIPDRIFDSADQVELVDIEPADLIIRLQAGKVYREGQAQRALNHFFSEENLTALREI ALRRTADRLNRTAQKRGSETAARAGEHILICLSSAPSNAKVIRTAARMAEAFHSGF TALFVETPETKELKGDNLKRLRDHLRLAEQMGAQIATVYGDDPAVQIAEYARVSG VTKIVLGRTNHRSLLFFKGKSLADRLTDLAGNLEIYIIPDTQPLYKKRIAFHKNDEPW FRWQDLVKTLVITLLSTLVGFAFFAAGLRDANIIIIYILGVLVTAIWTHGHVYGAIGSL LSVVAFNFFFTVPRFTLEATAPDYPVTFLIMLIASVISSTLATRVKKQARQSAQKAY YTELLMSSSQKLQQGKNEQEIIQLAAEQVSILLERPVLYALAKGKGELQFQVTPAE RREELLKSMTIEERGVADWVVKNNKRAGATTNTLSHAQNLYLAVRGLQGVMGVV GIPSKYYPVPEVFEKNLMVSILNECGLILERRRFREEKQAIELETQQERLRSNLLRAI SHDLRTPLTSISGNAGVLMEKSIVLDEEKKQELYRSIYDDSMWLVNLTENLLSITRI ENGTMHLQMGAELMDDVFQEALAHVDRQSKDHHISVELPDDLLLAKMDVRLIVQV IINIVNNAIKYTPAGSHIILRAEKQGAKVAVSISDDGPGISDEAKIHLFDMFYTASQGK PDNRRGLGLGLNLCRSIVTAHGGEITVTDNIPHGSIFTFTLPLEEVELNNV	25~~KdpD (3.05563E-120) ~~232,250~~Usp (1.56126E-34) ~~373,398~~DUF4118 (1.43963E-16) ~~499,X,666~~HisKA (0.000000000208726) ~~732,785~~HATPase_c (6.75769E-27) ~~888	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.6E-95	326.4	0.2	8.1E-95	325.6	0.2	1.4	1	Q39SW3_GEOMG	Histidine kinase (EC 2.7.13.3)	kdpD Gmet_2436	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	888	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter metallireducens, Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	269799	>tr|Q39SW3|Q39SW3_GEOMG Histidine kinase OS=Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) GN=kdpD PE=4 SV=1 MTDINDERRPSPEALLRLAQKEEAQAEQGRLKIFLGYAAGVGKTYAMLEAARQRK GEGRDVVAAYVESHGRAETDALLEGVEIIPPARIEYQGVTLREVDVDAVLARKPQL ALVDELAHTNAPGSRHEKRWQDVEELLAAGINVYTTVNVQHFESLNDVVVQITGIA VRETVPDSLLDQATEIRLVDIPPEDLLQRLREGKVYVPEQAAFATEKFFRPGNLIAL RELSLRRAASRVDEEMRAYMESRAIPGPWPATERLLVSVSGSPYSERLIRTTRRL ADELKAPWFTVYVETPGGGRQEQENRKRVWKDLRLAESLGAHVATLTATSAADA IIDYARSHNVTQIVVGKPAKPRWRELLRLPLVDQIIRLSGAIDVHVVSFEPAGAKKG PVIPRQRRPISLTGYMASLALVAATTLVCLLGRPFLAPTNMVMIYLLAVVLAALRLG LKPAILTAFLGVLAFDFFFVPPRLTFAVADTQYLITFVALFTVGVVISTLVSKARERA EAVREREVQTAALYYLSRDLAAAADIETLVQAVVRNIGESLAAGSTVLLPKGDRLE VAAASKGLKPDVKEMAVADWAFRNRQPAGQGTETLVSAGLLYLPLQTSGNILGVL GIRLKNVADYRSTQPRRLLDAFVTQTAMALERVQLSRQAEQTQILQARETLERALL NSISHDLRTPLVSITGALDTLREKVHTLANEARMELLDTAWEEAERLNRFVGNLLD MTRLEAGALKVKKELCDVQDLVGCALAALERRIGGRQVDVHLPPDLPLVRMDMVL MTQVLANLLDNALKYSPPESGIEISVRVNDGRLEMEVADHGPGIPEQDLKRVFDKF YRIPIPEGSRGTGLGLSICKGIVEAHGGAIRAENRARGGLRVIVTLTIK	26~~KdpD (8.03267E-120) ~~236,258~~Usp (3.08242E-47) ~~381,405~~DUF4118 (1.29882E-22) ~~504,530~~GAF (0.000000002768) ~~648,665~~HisKA (0.00000000096013) ~~731,786~~HATPase_c (9.08781E-33) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5E-95	326.3	0.4	1.1E-94	325.1	0	1.8	1	A0R398_MYCS2	Histidine kinase (EC 2.7.13.3)	MSMEG_5395	Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	839	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	246196	>tr|A0R398|A0R398_MYCS2 Histidine kinase OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=MSMEG_5395 PE=4 SV=1 MTTRASNASKRGELRIYLGAAPGVGKTYAMLGEAHRRLDRGTDLVAAVVETHGR KNTAELLAGIEVIPPRYIEYRGGRFPELDVPAVLDRKPQVVLVDELAHTNTPGSKN AKRWQDVDELLNAGITVISTVNVQHLDSLNDVVAAITGIEQQETVPDEVVRSADQI ELVDITPEALRRRLSHGNVYAPERIDAALSNYFRRGNLTALRELALLWLADQVDAA LAKYRADNKITALWETRERVVVAVTGGTESETLVRRAFRIASKSSAELMVVHVVH GDGLTGISAAQMGKVRELAVSLGATVHTVVGDDVPTALLDFARDINATQLVLGTS RRSRWARMFDEGIGATVVQQSQKIDVHMVTHEAAKRGFRWSSTSPRQRHAAS WAAALMVPSLICAFSVAILDPFLDVGGKSALFFVGVLVVALLGGVAPAALSAVLSG LLLNYFLTSPRHTFTMSDPDSALTIVVLLAVAVAVAALVDGAAKRAREARHASREA ELLALFAGSVLRGADLTALLERVRETYAQRAVSLLRETSDGATIVDCVGQDPCDRV AAADTAVEAGDEFWLLLSGRELPARDRRVLGAVANQAAGLVRQRELTEEAAKAN AIAKADELSRSLLSAVSHDLRTPLAAAKAAASSLRSCDIDFSAEDTAELLATIEESVD ALTALVGNLLDSSRLAAGVIHPELRPVYLEETVQRALLGIRRGPTGYGRSAVDRVK VEVGDSVALADGGLLERVLANLIDNALRYAPDGLIRVTAGRVANKVLIAVVDEGPGI PRGAEDALFAPFQPRLGDTNTTTGVGLGLSVAKGFVEAMGGTISAGDTPGGGLTV EIELAVPA	9~~KdpD (5.7279E-121) ~~219,241~~Usp (1.37285E-33) ~~362,385~~DUF4118 (0.000000190821) ~~465,X,616~~HisKA (0.000000524543) ~~678,735~~HATPase_c (1.32538E-26) ~~835	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	5.5E-95	326.1	0	8.3E-95	325.5	0	1.3	1	KDPD_ECOLI	Sensor protein KdpD (EC 2.7.13.3)	kdpD b0695 JW0683	Escherichia coli (strain K12)	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli (strain K12)	83333	>sp|P21865|KDPD_ECOLI Sensor protein KdpD OS=Escherichia coli (strain K12) GN=kdpD PE=1 SV=2 MNNEPLRPDPDRLLEQTAAPHRGKLKVFFGACAGVGKTWAMLAEAQRLRAQGL DIVVGVVETHGRKDTAAMLEGLAVLPLKRQAYRGRHISEFDLDAALARRPALILMD ELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRE TVPDPFFDAADDVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRE LALRRTADRVDEQMRAWRGHPGEEKVWHTRDAILLCIGHNTGSEKLVRAAARLA SRLGSVWHAVYVETPALHRLPEKKRRAILSALRLAQELGAETATLSDPAEEKAVVR YAREHNLGKIILGRPASRRWWRRETFADRLARIAPDLDQVLVALDEPPARTINNAP DNRSFKDKWRVQIQGCVVAAALCAVITLIAMQWLMAFDAANLVMLYLLGVVVVAL FYGRWPSVVATVINVVSFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAG VRYQARVARYREQRTRHLYEMSKALAVGRSPQDIAATSEQFIASTFHARSQVLLP DDNGKLQPLTHPQGMTPWDDAIAQWSFDKGLPAGAGTDTLPGVPYQILPLKSGE KTYGLVVVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEEQARMASEREQ IRNALLAALSHDLRTPLTVLFGQAEILTLDLASEGSPHARQASEIRQHVLNTTRLVN NLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLSSPINLSLPEPLTLIHVDG PLFERVLINLLENAVKYAGAQAEIGIDAHVEGENLQLDVWDNGPGLPPGQEQTIFD KFARGNKESAVPGVGLGLAICRAIVDVHGGTITAFNRPEGGACFRVTLPQQTAPE LEEFHEDM	20~~KdpD (1.73015E-129) ~~230,253~~Usp (9.20189E-42) ~~373,403~~DUF4118 (5.76547E-21) ~~501,527~~GAF (3.21301E-17) ~~644,661~~HisKA (0.000000000276051) ~~726,778~~HATPase_c (1.27434E-31) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5.8E-95	326	0.3	9.2E-95	325.4	0.2	1.3	1	A0A0D5LMW2_9RHIZ	Histidine kinase (EC 2.7.13.3)	TM49_04465	Martelella endophytica	906	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	1486262	>tr|A0A0D5LMW2|A0A0D5LMW2_9RHIZ Histidine kinase OS=Martelella endophytica GN=TM49_04465 PE=4 SV=1 MGSEESTRDTTRPSPDALLEKAEQETRGRLKIFLGAAPGVGKTYEMLLSGRARKS DGDDVVIGVVETHGRKETEALVRGFEIIPRTKIEYKGRILEEMDLDAVLERGPALVL VDELAHTNAPGSRHPKRYLDVLELLDHGIDVYTTLNIQHLESLNDVVAQITRIRVRE TLPDSILQKADDVEIIDITPDDLIKRLNEGKVYVPRTAKRAIENYFSPRNLTALRELAL RQTAQRVDQQLLSQMRQSAIEGPWPAGERILVCVNEDPCSSGLVRYAKRLADRL HAPWVALHVEGRRTQSLDDDGRDRIAAALRLAQSLEGDAVTVPGGGGRVAADIV AYARANNITHIVIGKSERSRWFEILHGSVVHELVRHAGDISVDVVAGSKPGGVPAS RASVAVAEPRSRPDWKAYLKATMVVAMAVGFGLALWPWLGVEHIALIFLTGVVTV AVWFGLLPSLYASVLSAACYNFFFTNPYHTFLISRPREIVSVVFFTIVAVIVSNVAAR ARAQTIAAKARARTTEALYSFSRKLAGASTLDDVLWASAHQMASMLKARIIILLPEN GTVAVRAGVPPDDTLVDADIAAARWALEHNRPAGRGADTLPGAARLYVPLTTGET PVGVVGLDSDRQGPLLTPEEQRLLDALADQAAVAIERIQLVADVDKARLAAEADKL RSALLASISHDLKTPLAAILGAAGNLRDYSAALSEQDRNDMLSTIVDESERLNRFIA NLLDMSRIETGAMEPNASLQYLDDMVGSALRRAQKMLSRHHVRTELPADLPMLK VDPVLFEQVIFNLLDNAAKYAPPQTAIRMRAWKDGNWVMIQILDEGPGIPPADLER VFDSFHRARKRDHVLAGTGLGLSICRGFVEAMGGTITSANRTDRSGAVFTIRMPT PANPPRVGDAS	27~~KdpD (3.2409E-120) ~~235,257~~Usp (1.82051E-43) ~~382,409~~DUF4118 (2.53559E-17) ~~509,535~~GAF (6.16221E-18) ~~654,671~~HisKA (0.000000000000231603) ~~737,790~~HATPase_c (1.17887E-27) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	6.6E-95	325.9	0	1.3E-94	325	0	1.5	1	A0A024HIT0_PSEKB	Histidine kinase (EC 2.7.13.3)	kdpD5 PKB_3065	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	901	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas knackmussii, Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	1301098	>tr|A0A024HIT0|A0A024HIT0_PSEKB Histidine kinase OS=Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13) GN=kdpD5 PE=4 SV=1 MSDTQRPDPDQLLAQIRQDEAQQQRGRLKIFFGACAGVGKTYAMLSAARAALAQ GTQVLVGVVETHGRAETEALLQGLERLPLRQVEYKGRRLGEFDLDGALARHPPLI LIDELAHSNVAGSRHPKRWQDVEELLAAGIHVWSTMNVQHLESLNDIVGSITGIRV WETVPDRIFDGADEVVMVDLPPDDLLQRLKEGKVYLAHQAERAVRNFFRKGNLIA LRELALRRTADRVDSEMLEYRGRILSQPVWGTRGSLLVGVGINEQDEKTVRSSAR LASQLDVPWHAVYVETPRLQRLPEARRQRTLRTLKLAQELGAEIAVLAGQDEAEV LVKYARQHNLSKVVLGRRGGSRSWRWRAGLADRIAAQGADLDLLQIALPATRGG RTEEAPRGPGSPPYLPGYLMAVLAVGAITLVATPLTEVFERTNIVMLFLLAVVAVAV RCGRGPAVLAAFLAVASFDFFFVPPRFTLAISGVQYLVTFAVMLVVALVIGQMAAG LTYQARVAQGGEDRMRGLYEMSRQLSAALMIEQVADIASQFLASELNARSALFVT DLQDRLRPPVPTDELAEVDAAVAQWCFDKEEPAGHGTDTLPAGPTLYLPLTAPM RVRGVLAIQPRENARLAIPEQRRLLDTCASLLAISLERIHYIEVAQSSTLQMESERM RNSLIGAISHDLRTPLTSLVGLAEALVQAQPPLGGAHLELANGIRELTLRMNNLLNN LLDMARLESGAVELKRAWQPLEETIGSALATCRLALGERQVEVALPADMPLVQVD AVLFERVLVNLLENAAKYTPPGTPIHIGAAARRKSFELWIDDWGPGVPPGREATIF NKFERGRKESAIPGMGLGLALCRTIIEAHGGSISASNRPGGGARFLITLPRGEPPQ VPVEDEPDDTQRQP	24~~KdpD (4.53937E-124) ~~233,256~~Usp (2.93452E-33) ~~377,403~~DUF4118 (0.00000000000106195) ~~501,528~~GAF (2.69668E-16) ~~644,661~~HisKA (0.00003422) ~~714,779~~HATPase_c (1.05668E-25) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.8E-95	325.8	0.3	1.7E-94	324.6	0	1.8	1	Q7NXN0_CHRVO	Histidine kinase (EC 2.7.13.3)	kdpD CV_1596	Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	895	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Chromobacterium group, Chromobacterium, Chromobacterium violaceum, Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	243365	>tr|Q7NXN0|Q7NXN0_CHRVO Histidine kinase OS=Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) GN=kdpD PE=4 SV=1 MTDQRPDPDALLDELKREALEAQRGRLKIFFGACAGVGKTYAMLAAARVKRQEG VRVLVGVVETHGRKETAEQLEGLDILPLSRIEYKGRALSEFDIDAALAAKPQLILIDE FAHSNAPGSRHPKRWQDVEELLAAGIDVYTTLNVQHLESLNDVVGQITGIIVRETL PDHVFDMADEVSLVDLPPDELLSRLAAGKVYLPHQAERAVKNFFRKGNLLALREL ALRRTADRVDAQMRAYRADQSIKPVWHARERLLVCVGPGPGTEKLVRSAKRLAA NLDADWIAVYVETPRLQRLPEEQRARILKGLKLAQELGAETTVLGGSSLAATLLAY ARTRNVSKLVVGKSNRGWAARLWEGSLVGELSRLSGDVDVYVVAHELEEEADQ RGKRVPSLLFSDSESGHAARGYLAAAAICFATTELNHLLVPYFALSNVIMVHLLAVV LIATRYGRGPGVLASFLSVAAFDFFFVPPQLSFAVSDTQYLLTFGVMLVVALIISQL TARFRFEATIATYRERRTRALYDLGRELASALTASQIIETAVGRLEPLFRAKVMLFIP NSEDRLRAATETGNDADAGVAQWVFDNQQPAGLGTNTLPSNAALYVPLKAPMR VRGVIALLPEDAVHPFLPEQQRLLETCAAQIALALERVHYVEVAQDAIVAMESERL RNSVLSVVSHDLRTPLTTMLGLANMLNAPTLPPGRQSEIAQSIQDEAIRMTKLVTN LLDMAKLQSGVKLNKEWQLLDEVVGSAVRACEHSLRHHKLELKLSRDLPVLEYDA VLIERVLVNLLENAGKYTPAGSRIELAARHDGDKVRITVTDDGPGLPASMEHRAFD KFTRGAPESTTPGVGLGLAICRAIIENHGGTIEAGNAQPHGARFSFTLPAGSPPEL PPEDA	22~~KdpD (6.65683E-112) ~~232,254~~Usp (2.71236E-45) ~~377,414~~DUF4118 (2.0082E-24) ~~505,536~~GAF (4.12424E-16) ~~648,665~~HisKA (3.30403E-14) ~~729,781~~HATPase_c (1.63047E-31) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	7.7E-95	325.6	0.5	1.5E-94	324.7	0.3	1.5	1	K0K8R8_SACES	Histidine kinase (EC 2.7.13.3)	kdpD BN6_59730	Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	897	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix espanaensis, Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	1179773	>tr|K0K8R8|K0K8R8_SACES Histidine kinase OS=Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764) GN=kdpD PE=4 SV=1 MPLARSVEPGARGGGQAPDAVVYAFLARLDGHAEVRRHGEHTVRVDGKRKRGE LRIYLGSAPGVGKTFAMLGEAHRRRERGTDVVVGLVETHGREKTARLLDGLEQLP RTAFGHRGVEFGEMDIDALLARAPEVAVVDELAHTNVPGSRNVKRWEDVEELLD AGIDVLSTVNVQHLESLNDVVQRITGVAQRETVPDEVVRRAEQVELVDITPEALRR RLAHGNVYAAHKIDAALGNYFRLGNLTALRELALLWVADQVDVALQRYRTEQHIT DTWETRERVVAAITGGNESETLIRRARRIAVRAGADLMVVHIMRGDGLTGASPQV VGKLRKITEDVGATFHTVVGDDVPTALLDFARGVNATQLVLGTSRRSRLARVFDE GIGAAVIQSSGPIDVHMVTHAESRRGPRWTVGRNPLTRGRVLLGWALAVLLPLAV TGLGVLSRDDLTFSTDLIGFFLVTVVVALVGGLGPAVGAALFGAGLLNFFFTPPYY SLAVATPENLITLLAMLTVAVLVALVVDRAARLAEQGARARTEAALLASYARTVLTS PYPLARLLEKVRENFGLESVALLERRGGEWERVACVGPRPCDEPDEADADVPVT SDVHLALRGRTLPAGDQRALEAAAGQALMALRQQRMAAETADAQRRAETTELRT ALLSAVGHDLRTPLTSIKAAIGSLRDDTLPLSPEDTEELLETVEVSADRLAGLIDNLL DSSRLATGAVRPVLRAVTFDEVVARALAGIDDRRLVSVDVGEQLPQVRADVGLLE RVVANVIDNALRHGRLSPRRLVDVDGDGAITADEPEVAVRASAYGDRVELRVVDH GRGLPKNTADAVFAPFQRLGDRDSTPGVGLGLSVAKGFVDAMGGTIVAEDTPGG GLTIVISLPVAEVAVA	50~~KdpD (3.3736E-118) ~~259,281~~Usp (3.48495E-22) ~~402,428~~DUF4118 (0.0000000000104288) ~~511,X,656~~HisKA (0.000000000000873546) ~~721,771~~HATPase_c (1.38623E-23) ~~889	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.3E-95	325.5	0.2	1.3E-94	324.9	0.1	1.3	1	C5AAP0_BURGB	Histidine kinase (EC 2.7.13.3)	bglu_1g26250	Burkholderia glumae (strain BGR1)	976	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia glumae (Pseudomonas glumae), Burkholderia glumae (strain BGR1)	626418	>tr|C5AAP0|C5AAP0_BURGB Histidine kinase OS=Burkholderia glumae (strain BGR1) GN=bglu_1g26250 PE=4 SV=1 MNRPDPDQLLDKLQREEEKQQRGRLKIFFGASAGVGKTYAMLRAARSRADEGVR VLVGIVETHGRRETAALLDGLDLLAPRVIEHRGRRLEEFDLDAALERRPQLVLVDEL AHSNLPGSRHLKRWQDVHELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWETV PDRVFDAADEVTLVDLPADELLERMRDGKVYLPQQAERAVRNFFRKGNLIALREL ALRRTADRVDAQMREYRADRSIARIWQARERLLVCVGPGPEAPTLVRAAARLAAG LKADWIAVYVETPRSQRLDDARRRRPLDALKLAAELGAETVTLAGGDAVAALIGYA QVRNVSKLVAGGSPRTGFARRLARPFGERLAERAGDLDLMLLRTSAQDEARRAP SDAGALAWRDAFLRLAGERSPPRHYAVAAAICAVLTGIASLAQTRLDLTNLVMLYL LGVVFSAVRLGRGPGVMQSFLSVAAFDFFFVPPQMSLSVSDTQYLLTFFGMLLTS LVISHLTSSLTRAAGLAERRERRTGAMYAMARELAAALTAEQIVEIGSRHVAEVFR ARVAMLLPDSADQVRQKIENPDEALTLTGAALDSDVGQWVYDQQKPAGRGTDTL PAAQARYLPLKAPMRTRGVLAVVTQDARELDMPEQQRMLDAFAAQIALALERVHY VEIARDALVSMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAGLHEAAGQGGAGA AGAAESAASRERELVEAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEET VGAALGACKRVLAHHPVQVRLPADLPLLQTDAVLMERLFANLFENAAKYTPAGAA LVIGAERIDEDGAPFVRVTVDDHGPGLRAGMEARIFDKFTRGEKESATPGIGLGLA ICRAIVDAHGGRIGARNRLAPDGSILGAQFWFTLPVDAPPPVPESDEAGEAHAER TAAAGSAPDEDGPGGAGQTRARVARAAFEPPLKPDHE	21~~KdpD (3.95153E-113) ~~230,252~~Usp (3.66143E-30) ~~374,410~~DUF4118 (1.21926E-20) ~~510,538~~GAF (2.85908E-15) ~~659,676~~HisKA (0.000000000118797) ~~755,808~~HATPase_c (3.89575E-21) ~~918	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	9.1E-95	325.4	0.4	9.1E-95	325.4	0.3	1.9	1	W5W977_9PSEU	Uncharacterized protein	KALB_4148	Kutzneria albida DSM 43870	736	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Kutzneria, Kutzneria albida, Kutzneria albida DSM 43870	1449976	>tr|W5W977|W5W977_9PSEU Uncharacterized protein OS=Kutzneria albida DSM 43870 GN=KALB_4148 PE=4 SV=1 MTRGRLRIYLGAAPGVGKTYAMLAEGHRRLDRGTDVVIGFVESHGRKLTIAMAEG LRTVPRRALTYRGVDLTEMDLAAVLARRPQVVLVDELAHTNVPGSVNEKRWQDV DQLLAAGIDVVSTLNIQHLESLNDVVEDITGIRQRETIADEVVRRADQIELVDMTPEA LRRRMVHGNVYPPDRVDTALTHYFRPGNLTALRELALLWVADRVEEGLQRYRAE HGIAGTWETRERVAVGLLGHLEDEVLIRRAARITARIPGSDLLAVHVVSVDGLTET DPAVLATLRELVEDLGGSYHQVLDEDVAEGLRRFTRSESITQLVLGAGHRGPLRS LLLGEGVGSRVIRLLGSVDVHVVTHGHAAGSPGRSTRWRWYGAAAIGGLLLAVA VALGPQSFLPAALTVLAVGIAAWQANSAARSRLVASALTTLAAGVPRGQVELPALL ELVRETVGLAAVSLLEPRPGSPDWYVIASAGDRPPERPDQADVRVPATGSVILAG RGRMRGTGDRQVLLACATQLAADLSHQRITEHAAELDERAAADRTRGTLLATATH DLQTALNQARDALAKLADQDGEHVAATSAAVERIGLLVADLLVLTRLRAGALDLYL RAVDVDEVIAAALEALGPGGPDIELRMAEDVPDVIADAATLIRAVTTLTARALRHSL PGRPPSIVVTTPPGHVEIQILDHDSAVDPATVASVALRVARGLIEAIGGQLRCARTE GGGLRVIVRLPSAR	3~~KdpD (2.63325E-117) ~~211,233~~Usp (5.13916E-17) ~~356,X,543~~HisKA (0.00575128) ~~602,649~~HATPase_c (0.0034758) ~~732	kinase	KdpD;Usp;X;HisKA;HATPase_c
	9.4E-95	325.4	0.6	1.6E-94	324.6	0.4	1.4	1	A0A0A1DR30_NOCSI	Histidine kinase (EC 2.7.13.3)	KR76_23675	Nocardioides simplex (Arthrobacter simplex)	833	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Pimelobacter, Nocardioides simplex (Arthrobacter simplex)	2045	>tr|A0A0A1DR30|A0A0A1DR30_NOCSI Histidine kinase OS=Nocardioides simplex GN=KR76_23675 PE=4 SV=1 MDRGRLRVYLGAAPGVGKTFAMLDEGHRRAERGTDVVVGYVETHGRPKTEQAL GDLEQVPRRRLGYKGAELEEMDLQAVLDRRPAVVLVDELAHTNVPGSVNEKRW QDVEALRDAGIEVVTTVNIQHLESLNDVTEAITGVRQRETVPDHVVRSADQIELVD VSPQALRRRMAHGNIYAADKIDAALSRYFREGNLTALRELALLWLADRVDEGLER YRAQHEIDSTWATRERVIVPVSGGPESLTLMRRAARIASRSAGGEWQALYVTRR DGLSGIAPDRLAQLRAKAEGLGGSFHTVVGDDPAEGILDFARAENATQVLIGASR RGRVSALLRPGVGERVVAASGDIDVHIVTHEHARRGGPSPLRPPASLGRRRRVA GLVFAVLGPVGFSLVLWASNDLHGLPTEAMTLMVVVVVTALIGGLLPAVLAALLSG VLLNLLFTPPFYTLTIDEPENAIAILLFVVVGIAVATVVDNAARRTAQAAKARAEADA LTVLSHSLLNASDDLAGLLTSACELFSARGAAVFRRRDDGTEEVLGACGTPPESV AAADMSADIDERTVLVLVGSRLPASERGLLNAYAAYAGVMAERRRATRAEVERLR LAEADRTRTALLAAVSHDLRSPLAAVKVAVSSLRSTDVQWSAQDEADLLETIEEAT DRLTALVTNLLDMSRIHTGSVRVALTETGLVRALDQAVAPLAGGARIEVRVDPDLE VLADPGLLDRVLANICENALKYTPDSARIRIDAVTDGDRVTLRIADTGPGVAAGDHA RLFVPFQRLGDVPDQDGVGLGLAVAAGLTEAMGGTIATEETPGGGLTFVLELPAA EEVQG	3~~KdpD (7.91414E-116) ~~211,233~~Usp (1.46767E-28) ~~355,X,609~~HisKA (0.0000000000025237) ~~675,724~~HATPase_c (6.86415E-26) ~~825	kinase	KdpD;Usp;X;HisKA;HATPase_c
	9.8E-95	325.3	0.4	4.5E-94	323.1	0	2.1	1	C6XCM9_METGS	Histidine kinase (EC 2.7.13.3)	Msip34_1057	Methylovorus glucosetrophus (strain SIP3-4)	906	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylovorus, Methylovorus glucosotrophus, Methylovorus glucosetrophus (strain SIP3-4)	582744	>tr|C6XCM9|C6XCM9_METGS Histidine kinase OS=Methylovorus glucosetrophus (strain SIP3-4) GN=Msip34_1057 PE=4 SV=1 MSHTRPDPDALLEKLQQEDARQQRGRLKIFFGSCAGVGKTFAMLTAAHARMQEG EDVLVGVIETHGRRDTESHLQGLPQLPLKSLSYRDKTLHEFDLDAALARRPGLLLV DELAHSNAEGSRHRKRWQDVEELCSAGIDVYTTLNVQHLESLNDVVGQITGIRVS ETVPDKVFDLADEVTLVDLPPEELLQRLQEGKVYMSQQAERARRHFFRKGNLIAL REMALRRTADRVDAQMREYRTDQSIQHVWQTHERILVGLGPGPEAEQLVRTAAR LAISMKAEWLAAYVETPALQKLGHAERQAILDNLRLAQTLGAATTATLSGDEVSTV LLDYARSRNVSRLVVGKPRRPLLMRLFIPSVTDQLAKEATDIDLHVVVRQPKPRHK PAPQHSLQMAANAHLSGLKKRGYLWALAISAATSVIAGMLLQYFELSNVIMLYLLG VMLISIRYGRGPGILSSILSVSAFDFFFVPPKLSFTVSDTQYLLTFGIMLSVALVISNL TSSLRYQAVIANYRERRSLALYEIGKELASTMTTQHIVEVSVHHIASLFQSRAAILLP DADDKLRAPEADAGHGHTLADVDLGIAQWTFDHQEHAGLGTNTLPSSPVLYVPLK APMRTRGVLAIVPENKAAIFLPEQRQLLDTFAAQIALALERKHYVEVARDALISMES ERLRNSLLSAISHDLRTPLTSLLGIADQLRQAPDMPSDRHAQLETLYDQAFRMQQL VVNLLDMARLQAGSVQLNSQWQVLEEVLGSALRAMQPVSQQHRIEVTLPPELPLL QFDAVLLERVFCNLLDNACKYSPPNTTIRISAQQHPGEVWVTVADEGWGLPAGM ETQIFQKFTRGKVESPQPGVGLGLSICKAIIQAHGGALWAEAQQPHGTRFIFSLPL GEPPAPPLAEETPA	23~~KdpD (9.47952E-121) ~~232,254~~Usp (5.54459E-41) ~~377,409~~DUF4118 (6.14071E-25) ~~508,534~~GAF (2.91814E-19) ~~655,672~~HisKA (0.00000000000154445) ~~736,789~~HATPase_c (1.21369E-27) ~~890	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1E-94	325.3	0.3	1.7E-94	324.5	0.2	1.4	1	D5W5H5_BURSC	Histidine kinase (EC 2.7.13.3)	BC1002_0922	Burkholderia sp. (strain CCGE1002)	951	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. (strain CCGE1002)	640511	>tr|D5W5H5|D5W5H5_BURSC Histidine kinase OS=Burkholderia sp. (strain CCGE1002) GN=BC1002_0922 PE=4 SV=1 MNRPDPDELLEKLQRDEEKRLRGRLKIFFGASAGVGKTYAMLQAARRRNEEGAD VLVGIAETHGRSETAALLAGLDVLPLAHIEYRGRKLGEFDLDAALARKPQLILVDEL AHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETV PDRVFDHADEVTLVDLPAEELLDRMRDGKVYMAQQAVRAVRNFFRKGNLIALREL ALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPALVRSAARLAA SLRADWLAVYVETPALQRLPDARRARTLNALKLAAELGAETATLAATDALDALIGY AQARNVSKLVAGASSRAGISRWLRRPLGERIAEKSGDLDLTLIRVTSERDSGEQR RLLNTTANAWREALSAARERRSPPRAYAFALAIGAAITMLSSQLIDRIDLTNLVMLY LLGVIFTAVKLGRGPGVVLSFASVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLLTS LVISHLTSSLRREASVARHREQRTGAMYEMARELAAALATEQIVGIGTRHLSEVFG ARVAILLPDSADQVKQKIEDPDPAITLEGDALDLDVGQWVYDQQKPAGHGTDTLP AAAALYLPLKAPMRTRGVLAVVVRDERELTVPEQRRMLDAFAAQIALALERVHYV DIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAQGRGGQGPTDPQSA AHRNDELVEAIHEEALRMTGIVTNLLDMARLQAGSLQLNQQWTLLEETVGAALRA CRRVLADHPVQVTLPADLPLLHLDAVLMERLFSNLFENAAKYTASGTPLAIGAQQI DAGGVPFVRVTIDDNGAGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEA HGGTIGALNRIAADGHVEGARFWFTLPVKTPPEAPETFDTLEDEDTPADTAADLN PLTRPAHE	22~~KdpD (1.72192E-117) ~~230,252~~Usp (4.54522E-28) ~~374,412~~DUF4118 (3.36527E-18) ~~512,539~~GAF (1.05209E-17) ~~661,678~~HisKA (0.0000000000163984) ~~751,804~~HATPase_c (1.60813E-20) ~~914	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.1E-94	325.1	0	1.7E-94	324.5	0	1.3	1	A9MK91_SALAR	Histidine kinase (EC 2.7.13.3)	SARI_02238	Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica subsp. arizonae, Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	41514	>tr|A9MK91|A9MK91_SALAR Histidine kinase OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=SARI_02238 PE=4 SV=1 MNDEPLRPDPDRLLEQTPPPHRGKLKIFFGACAGVGKTWAMLAQAQRLRAQGLD VVIGVVETHGRKETAALLDGLTILPPKRHSHRGRQIREFALDAALARRPALILMDEL AHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETV PDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIAGQAERAIEHFFRKGNLIALRELAL RRTADRVDDQMRAWRAHPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRL GSVWHAVYVETPTLHRLPEKQRRAILSALRLAQELGAETATLSDPAEEKAVVRYA REHNLGKIVMGRPASRRWWRRDAFADRLARRAPDLDQVIVALEEPPARALTQAP DNRSFKEKWRGQIQGCLVAVALCAITTLIAMQWLVAFDAANLVMLYLLGVVVIALF YGRWPSVVATVINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGV RYQARVARYREQRTRHLYEMSKALAVGRSEHDIAVTSEQFIASTFQARSQILLPDA HGKLLPLTHQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSADKT HGLAIVEPGNLRQLMVPEQQRLLETFTLLVANALERLTLTASEEQARLASERESIR NALLAALSHDLRTPLTVLFGQAEILTLDLASAGSPHARQASEIRQHILNTTRLVNNLL DMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLLHPITLSLPQQLTLIHVDGLLF ERVLINLLENAVKYAGPQASIGIDAAVKDDRLQLDVWDNGPGIPAGQEQTIFDKFA RGNKESAVPGVGLGLAICHAIVEVHGGTLTAYNRSQGGACFRVTLPQGKPPELDD FHEDM	20~~KdpD (4.65186E-126) ~~230,253~~Usp (1.23725E-42) ~~373,403~~DUF4118 (5.44168E-21) ~~501,537~~GAF (0.00000000000104032) ~~644,661~~HisKA (0.0000000255221) ~~726,778~~HATPase_c (2.36633E-30) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.1E-94	325.1	0	1.8E-94	324.4	0	1.3	1	I0DX86_PROSM	Histidine kinase (EC 2.7.13.3)	S70_15695	Providencia stuartii (strain MRSN 2154)	906	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia stuartii, Providencia stuartii (strain MRSN 2154)	1157951	>tr|I0DX86|I0DX86_PROSM Histidine kinase OS=Providencia stuartii (strain MRSN 2154) GN=S70_15695 PE=4 SV=1 MDNQDPVRPNPDELLAKANESGRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGL DVLVGVVETHEREETAALLDGLSQLPPRRLNHRGRRMSAFDIDAAIARHPAIILMD ELAFSNPAGSRHPKRWQDVEELLDAGIDVLTTINVQHIESLNDIVGSITGIHVRETV PDHIFDAADEIVLVDLPPDDLRQRLKEGKVYIPAQAERAIEHFFRKGNLIALRELALR RTADRVDDQMREFRDGKGHVPVWHTRDGLLLCIGHHNGNEKLVRAAARLAAKLG SVWHAIYVETPKLHRLPEGHRRAILKALRLAQDLGAETATLSDPYEEKAVLRYARE HNLGKILVGRRTKRRRWLDFGTHTNFAERLGALGPDLDLVIVALEERNDWVKEPE RKPFSEKWRSDVNGFLVAIAICTVITLFSRTFLLALDKANLVTLYLLSVVLVALFYGR RPSIFAALINVISFDLFFVQPHFSLAIMDMQYLVTFTVMLIVGVVVGNLTAGMRYQA RIARYREQRTRHLYEMTKELSRALTEQDIGKTGYHFINNAFQAKTCLLLPDENNQL SPLLCEGHSPMQIDQAIAKWSFEKRQPAGAGTDTLPSVPYQLQPITTADQTLAVL AIEPNNLRQLLIPEQQRMLQTFTGLIASALARLQLSKQAESAKLDIEREQLRNSLLA ALSHDLKTPLTVLFGQAEILTLNLSAENSPYTEQVNQMRQQILSTSRLVNNLLDMA RLQSGSIQPNFEWQSLQEITGSAVRTLDYTLHSHPLSIDIPANLLLYCDGNLIERVLI NLLENATKYSDKDTPMGICAQIEDNQVHIEVWDASNAIPDGQEKIIFDKFSRAQKE SAIPGVGLGLAICRAIIQLHDGNIWAENNKKGGASFHFVLPFKQLPDIEELDNYCES PSNTDH	21~~KdpD (3.23652E-126) ~~231,254~~Usp (2.09863E-26) ~~378,406~~DUF4118 (1.91295E-21) ~~504,530~~GAF (3.51258E-16) ~~648,665~~HisKA (0.0000000000486789) ~~730,782~~HATPase_c (1.9011E-21) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.3E-94	324.9	0.2	2.1E-94	324.2	0.1	1.4	1	N0B533_9RHIZ	Histidine kinase (EC 2.7.13.3)	HYPDE_28238	Hyphomicrobium denitrificans 1NES1	906	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium denitrificans, Hyphomicrobium denitrificans 1NES1	670307	>tr|N0B533|N0B533_9RHIZ Histidine kinase OS=Hyphomicrobium denitrificans 1NES1 GN=HYPDE_28238 PE=4 SV=1 MANTSRPEDTRRTSAKALLELAANERRGKLKVFLGMAPGVGKTYAMLSAARALK NEGLDVVVGVVETHGRSETAALLEGLEVLPRRTVPYRNRTLMEFDIDAAIARRPAL LLVDEFAHTNAPGLVHPKRYQDVEGVLQAGIDVWTTLNIQHLESLTDVVERIAGIT VRETIPDKVLERADEIVVVDLPPEELIRRLREGKVYLPDNARRAMDQFFQMGNLTA LRELALRRTADRVDEQMLSQLRRQGIEGPWPTAERLLVCVGNNELAETVVRAAA RMAAALKSDWIAIHIVQSEREQTDRGSIRKMEKAMRLADRLGATTVRLHAKDLTSE VLAYAKRNNITQIIVGRSRPRFFDRWIGRSFSTSLVAEAAGPSVTVVAPDTPSTPL HLASVLPEISEFWSGGLAAVVAVAGGVAAGKMLAQITRLPNLSMVFLFAVLICALR FGIFSAIAAAVLSFLAFNFFFIEPRYTLTVASPYELFGLLIFLVVAAATGSLAGRLREQ ANATRERAEATQALYEFSGKLSAATKIDDVLWLLAAQSAAVVKGKSIILLEQSHELS VVGSWPPEDTLGTADWAAARWAHRNGEPAGHLTETMPSAVYQFRPLVASTGSV GVLGVAPGDEEDALPSATASALQSFADQAAIAIERTRLVEQAAEAATAAESERLRG ALLSSISHDLRTPLASILGSATSLRQLGDRMRKQDRADLLATIEEESTRLSTFVSNLL DMTKLETGVLDIRRDWVDVADAVRGAVARAKKTFPTRRVETFIPAKLPLIRGDAAL LEQVMFNLLDNAHKYSPPESVTRVSITLATGGAVHIVVADEGIGIPSEALNKVFDKF YRAHIGDGRKPGTGLGLSICAGIIAAMGGTILAQSPIANGKGTEISILLPAAEDSATE QNAPKDVA	25~~KdpD (1.7473E-126) ~~235,257~~Usp (3.17615E-24) ~~380,432~~DUF4118 (0.000000000000316046) ~~503,530~~GAF (0.0000000565585) ~~648,666~~HisKA (0.00000000000700351) ~~731,784~~HATPase_c (1.13356E-24) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.3E-94	324.9	1.1	1.5E-94	324.7	0.1	1.6	1	B6IQY6_RHOCS	Histidine kinase (EC 2.7.13.3)	kdpDRC1_0433	Rhodospirillum centenum (strain ATCC 51521 / SW)	917	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum centenum (Rhodocista centenaria), Rhodospirillum centenum (strain ATCC 51521 / SW)	414684	>tr|B6IQY6|B6IQY6_RHOCS Histidine kinase OS=Rhodospirillum centenum (strain ATCC 51521 / SW) GN=kdpD PE=4 SV=1 MARPEDQDRPSPDALLEHARREQRGKLKIFLGAAPGVGKTYAMLEAAQSARRDG VALVVGIVETHGRAETERLVHGLEVVPRSRIDYRGRSFEEMDLDAILVRRPALVLV DELAHTNIPGSRHLKRWQDVEELLAAGIDVWSTLNVQHLDSLNDVIERIAGIKVRE TVPDSVLRGADEIEMIDLPPQELRKRLGEGKVYVPAQARMAVEKFFSVGNLTALR EMALRQAAERVDAQMLSYMRRNGIAGPWPTRDRILVAIGPEPNAATLVRSARRM ADRRQAPWTVAYVETHRHQTLSETRKAHVTEALRLAHQLGGETVVLPGDDIAGEL IGWARANNVSQIVLGRSRQRRRFGLTSTDDMLKRATAYDLLLVGGTEEKPEPSG QGAAGQALAGPAGSDRRGWRAYAWAGVALILATALSWGVFSVLPVANVSLVYLL AVLLIATRFGLVPSIVTAVLAFFAFNFFFTEPRQTFLVNTSEDLLTIGFFLVAAVFTG HLASRLRAQIELSRTSQRRTANLYDFARKVASAASEDDVLWAVVHHVAATLKAKA LVLLPLDGELAIRAGYPPEDRLDQRAAAAAQWAWSNGERAGRGSDTLPASEWLF LPLKTQRGTVGVLGVQGYEGGSRLSADQARLLDALVDQAALVLERTQLVRDIEAA QIAGEKEQLRAALLSSLSHDLRTPLVSILGSASSLLTLEHELDDDARRELARTIQEE AERMNRFVQNLLDMTKLGSGGLKPKTDWTDLADIVGRALARAKPLLKGRRIKVDL APDLPLLQLDPVLMEQVLFNLLDNAARYSPAQGAITVWARRRGDRVVAEVCDQG PGIPVADRDRVFDMFYRVAGGDQQTAGTGLGLAIAKGIVEAHGGSIGVLDGMHG VGACLVLRLPVPEEAPPAPAEMSAEVAVAVPAGGGPA	22~~KdpD (1.9841E-117) ~~232,254~~Usp (4.93477E-39) ~~374,405~~DUF4118 (6.72864E-16) ~~505,531~~GAF (0.000000000000146492) ~~650,667~~HisKA (0.000000000000120441) ~~733,786~~HATPase_c (1.47873E-25) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.3E-94	324.9	0.2	2.2E-94	324.1	0.1	1.4	1	C1A1E6_RHOE4	Histidine kinase (EC 2.7.13.3)	kdpDRER_37230	Rhodococcus erythropolis (strain PR4 / NBRC 100887)	846	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus erythropolis (Arthrobacter picolinophilus), Rhodococcus erythropolis (strain PR4 / NBRC 100887)	234621	>tr|C1A1E6|C1A1E6_RHOE4 Histidine kinase OS=Rhodococcus erythropolis (strain PR4 / NBRC 100887) GN=kdpD PE=4 SV=1 MSSSEKVGQSFGRARKRGELRIYLGAAPGVGKTFAMLGEAHRRRDRGCDVVAA VVETHGRARTAAQIGDLEIIPPKLVDYRGTRMPELDVEAVLARRPALVLVDELAHT NTPGSKNHKRWQDVQELLEAGIDVLSTVNVQHLESLNDVVAHITGVVQQETVPDA IVRSAAQVELVDITPEALRRRLSHGNVYSPERVDAALGNYFRRGNLTALRELALLW VADQVDAALAKYRAENKITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAE LMVVHVVRGDGLTGVSAPEMGKVRALAVGVGATLHTVVGDDVPSTLLEFAREEN ATQLVLGTSRRSRLARILDEGIGAAVVQQSGGIDVHMVTHEETTVRRRISLFGRSE YRLLSWIAAVVVPTAAAGLMGLIDRISGVQGENALFFVVVVLVALLGGVGPAMLSA LLSGLLLNYFFTDPRYSFTIAEPDNFITTVVLLIVAVAVALVDAAAKKAREAKRASE EAELLTLFAGSVLRGADLSTLLEKAREIYRQRGVSVVHHEDGVVAAVGAEPPARE ADADSVCEVNDGEYALMLSGPELSARDRRVLTVVAHQAVGMIRQDKLTVEASKA AALTEADQLRRALLSAVSHDLRTPLAGVKAAVSSLRSDDIEFSPEDTAELLATIEES ADQLTALVGNLLDSSRLAAGVVKPTLRAVYLDEVVHRALLGLGIGGRSDSRSHSVI VDVGTVAVQADQGLLERVIANLVDNALRYGGTTPVRVGAARVGDRTVITVADTGP GVPRGEAESMFEPFQRMGDRDNTGGVGLGLSVVRGFVDAMGGTVSATDTPGG GLTMMVELAGAGTNGSES	16~~KdpD (6.16064E-118) ~~225,247~~Usp (2.93088E-32) ~~368,X,615~~HisKA (0.000000000000080864) ~~681,736~~HATPase_c (3.97134E-27) ~~836	kinase	KdpD;Usp;X;HisKA;HATPase_c

	1.3E-94	324.9	0	2.3E-94	324.1	0	1.4	1	Q47H45_DECAR	Histidine kinase (EC 2.7.13.3)	Daro_1080	Dechloromonas aromatica (strain RCB)	902	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Dechloromonas, Dechloromonas aromatica, Dechloromonas aromatica (strain RCB)	159087	>tr|Q47H45|Q47H45_DECAR Histidine kinase OS=Dechloromonas aromatica (strain RCB) GN=Daro_1080 PE=4 SV=1 MADQRPDPDQLLNRVNAEEARSKRGKLKIFFGASAGVGKTYAMLGAARQQLLAG VDVVIGIVETHGRMETEVMADGLEYLPLRDIPYRDRLLKEFDLDGALARKPQLILMD ELAHSNVAGSRHAKRWQDIEELLAAGIDVYSTVNVQHLESLNDVVSGITGIRVWET VPDKVFDAADEIVLVDLPPDELLQRLQAGKVYLPNQAERAIRNFFRKGNLIALRELA LRRTADRVDDQMLQYRRDQLVSPVWQTRDSLLACIGTGAGGEKIVRTTARVANR LEAPWHAIYIETPALQRLSENSRHRILRNLKLAEELGAQTATLSGNDAEGVAVKYA RDHNLSKIFVGRDHPRPWRPWYRSFADRLGQRAPDLDVLQVARADIDREPGQAA RESIGDSIFDQWPAYAKAAAGCALAGVAAAALFPIVDLPNIVMVFLLAVVLVSVRY GRGPGVLASFLSVAIFDFFYVPPRFSFAVSDVQYLMTFAVMLAVGLITGQLTAGSK YQAKVATRREQRVRSLYEMSRDLSAALMPDQITEIGERFIVAELGAKAAFLLTDDN DRLQPALPSANGLPAVDMGIAQWAFDHAEAAGQGTNTLAASPILYLPLKAPMRQR GVLALEMRDTDRLLIPEQRRLLDTFASLIAIALERVHYVEVAQNTTVQMESERLRNS VLSAISHDLRTPMSVLVGLADSMFLTQPPPTGPQAEIAHSLKEEALRVSSQVNNLL DMAKLQSGRVELNRQWQPLEEVVVSALKTLERAFAEHQISVSLDENLPLVNIDSVL MERVIYNLLENTVKYTPPGSLVEIGANVTERMIEVWVEDNGPGLPEGKEEIIFKKFE RGQPESATRGVGLGLAICRAIVEAHGGEIYAVNRPQGGARFMFTLPRGNPPSLDA EEMPADEEAH	22~~KdpD (3.89419E-126) ~~232,255~~Usp (5.81856E-42) ~~376,428~~DUF4118 (3.68437E-22) ~~502,529~~GAF (4.1625E-19) ~~646,663~~HisKA (0.0000000019614) ~~728,781~~HATPase_c (1.23747E-27) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.4E-94	324.8	0.2	2.6E-94	323.9	0.1	1.5	1	A1VTB9_POLNA	Histidine kinase (EC 2.7.13.3)	Pnap_3601	Polaromonas naphthalenivorans (strain CJ2)	899	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Polaromonas, Polaromonas naphthalenivorans, Polaromonas naphthalenivorans (strain CJ2)	365044	>tr|A1VTB9|A1VTB9_POLNA Histidine kinase OS=Polaromonas naphthalenivorans (strain CJ2) GN=Pnap_3601 PE=4 SV=1 MNLPAGQRPDPDELLQRLQQQEAQRARGRLRIYFGASAGVGKTYAMLGAAQRE RKDGRDIVVGVIETHGRSETAELLAGLEQLPLREVAYRGRTLREFDLDAALARKPA VLLVDELAHSNVEGSRHPKRWQDVQELLDAGIDVWSAINVQHLESLNGTVGAITG IRVNETVPDTVLDAADEIILVDVTPDELTARLKAGKVYLPQQAERAAQNFFRKGNLI ALREIALRRTAEHVEDDVRSYRVEKSISPVWNTEGALLACIGPHEGAEQTVRTAAR LAGQLNVRWHAAYVETPRLQRLKEAERDRILAVIKLAGELGATTAVLAASDAAAEL VAQAQALNCATLVVGRPALPDWRTLWSGRSMTRRLARLAPTLDIVEVADARSSR RLAPAVPRSDDDAASAWHGSLPRYAWAVASSVAITLLATPLLNVFDLANIVMLFLL GTVLVALKLGRGPAALAAFLNVAAFDYFFVAPRLSLAVSDVQYLVTFAVMLVVGLL TGQLTAGLRFQARISSSRERRAQSLFELTRDLSAALMPSQVAELGEAAVQRDFGG QALVLTTDARDQLVLPVHAPPGFDASVADWAFRHAQAAGLATSTLSAQTWHYVP LKATMRVRGVLALQPARPRWLLIPEQLQQLDTLARQIAIALERVHYVDIAQQAVVE MESERLRNTLLAALSHDVRTPLTALIGLAESLQRSQPPLEPQQAGMAQAMAQQAR QLNALVSNLLDMARLQNGAVSLHRDWQSVEEVAGSAIRAAQPALNGRTVRTDIAP DLPLVEFDAALMERVLVNLLENAAKYGAPPFEIHARAAPDSLVLSVRDHGPGLPPA LRGREAELFEKFTRGQAESATPGVGLGLAICKAIVDAHRGKIVAGNAQGGGAQFTI TLPRGSPPEPAPE	26~~KdpD (2.27268E-120) ~~235,258~~Usp (2.98048E-24) ~~381,410~~DUF4118 (1.61027E-19) ~~510,537~~GAF (0.0000000000863724) ~~651,668~~HisKA (0.00000000603536) ~~733,786~~HATPase_c (3.07328E-26) ~~888	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.5E-94	324.7	1	2.4E-94	324	0.7	1.3	1	G2IMI9_9SPHN	Histidine kinase (EC 2.7.13.3)	kdpD SLG_31030	Sphingobium sp. SYK-6	891	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingobium, Sphingobium sp. SYK-6	627192	>tr|G2IMI9|G2IMI9_9SPHN Histidine kinase OS=Sphingobium sp. SYK-6 GN=kdpD PE=4 SV=1 MSSQPPPEDLRPNPEALLRQAAQEGRGRLKVFLGAAPGVGKTYEMLTEAVARKR EGTDVVIGVVETHGRAETEALVHGLEVIARRPVDYQGRTLSEMDVDAILARRPQLV LVDELAHTNAPGSRHDKRYQDVEELLAAGIEVYSTVNVQHLESLNDVVASFTRVR VRETLPDRVIENADIEVIDIPPDELIERLKQGKVYVPAEATRALGNYFSKSNLTALRE LALRRAAQAVDAEMLDYLRAHALAGNWAAGERIVVAVSEQSGAAELVRAAKRIAD ALRGPWTVVHIETPRSSQLGDADNARLAATLHLASQLGAQVATVPAETVVDGVIR FAAEARATQLIVGKSQRSRWFELRHGSVVDRLVRETPGITVHVLPMEEQAPVAAP TGRKKAQWGRPADYVISFGLIALVTLVGEVVFTAASIANVGLLFLLPVMIAASRYGL RLGIVCSLVASLAYNFFFIPPTHTFTIQDPQNILTVLVLLGVAVVSSQLAARARDQAL LAQRSAAQNSSLAGFARQLTAVSNAEELARLLCGEVGRLLGVHTLLLLPEEEELVL RAAVPPDARLETIELAASRWAFDHNQPAGRGSDTLTASEWLFHPLAAGGQVLGV FGIARPDAGTPIRSDRLPLLLSLLDQAALALERIALEGEMASITQLKERDRLRAALLS SVSHDLRTPLTTILGMLGELRPATDEQRRQLGEMRGEAERLNRFVDNLLDMVRIE TGALLQSVEPVDLAEAVVAAVHDMRAVLRGREVELDVSPDLPFVRVDPRLFHHCL INLIDNAVKYGSPDTPVTITARRSATGLALSVLDEGAGFPSGEERRIFETFARIEGS DRKGGTGLGLAIVKGFAEAMGIEVHAMNRPDRSGARFDLFMPEAILVKGARDE	24~~KdpD (5.27075E-120) ~~233,255~~Usp (4.44739E-39) ~~378,402~~DUF4118 (0.000000000000248037) ~~478,578~~GAF (0.00752079) ~~646,663~~HisKA (0.00000000000297571) ~~724,777~~HATPase_c (1.73547E-22) ~~875	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.5E-94	324.7	0	2.7E-94	323.9	0	1.4	1	E0SEX6_DICD3	Histidine kinase (EC 2.7.13.3)	kdpDDda3937_01552	Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	909	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Dickeya, Dickeya dadantii, Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	198628	>tr|E0SEX6|E0SEX6_DICD3 Histidine kinase OS=Dickeya dadantii (strain 3937) GN=kdpD PE=4 SV=1 MTDEEQRRPDPDSLLSQIEEQPRGKLKIFFGACAGVGKTYAMLQEAQRLKAQGL DVLVGVVETHGRSETAALVEGLPHLPMRKISHYGRHHHEFDLDAALARCPALILID ELAHSNIRGSRHPKRWQDVQELLDAGIDVFTTVNVQHLESLNDIVGGVTGIRVRET VPDPIFDDANEVVLVDLPPDDLRQRLNEGKVYLPMQAERAIENFFRKGNLLALREL ALRRMADRVDDQMRAMRASQGRERVWHTRDAILLCIGRGVGNEKLVRTAARLAA RLGSIWHAVYVETPRLHRLPEGERRAILRALKLAQDLGAETATLSDPSVERAVLRY ARDHNLGKIVIGRHTEQKLGWWRRTRFAEKLGKLGPDLDLVVVSVQDDAAPPPP KTPDIRGITDKWRLQFYGCGVAALLCTLITLLALWSPFSMLEPVNLVMLYLLAVVIIA LFYGRWPSVLAAFINVASFDLFFVVPKGTFAVADVQYLVTFAVMLTIGILVGNLTAG VRYQARVARYREQRVRHLYEMSKALNRSLSVQDIAKASHHFLRSTFQAKIAILLAE PVSSPTAELQQAALDEPDQLIVDQAIARWSYDHAAPAGAGTTTLPGVPYQLLPLA TPQLTFGVIALEPNNVRQLMIPEQQRMLETFTVLIANALERLHLVKSTENARLDAER EQLRNSLLAALSHDLRTPLTVLFGQAEILTLNLASEGSPYAPQASQIRQHILSTTRL VNNLLDMARIQSDGFNLRKEWQTLEELAGSALRQLENSLANNTIQLRLPQDMTLV YCDASLIERVLINLLENAIKYAGEQATITVSASPISSPASGDMLEVQVRDNGPGIPD GQEKVIFDKFARGHKESSIPGVGLGLAICRAIVEIHGGRIWATNADDGGAVFHFTL PLAPPPALEPEEMES	23~~KdpD (4.53979E-115) ~~231,254~~Usp (6.69166E-39) ~~376,408~~DUF4118 (8.89996E-21) ~~505,531~~GAF (4.87879E-14) ~~653,670~~HisKA (0.000000000827158) ~~735,788~~HATPase_c (2.4396E-30) ~~893	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.5E-94	324.7	0.1	3.9E-94	323.4	0.1	1.6	1	W5TT91_9NOCA	Histidine kinase (EC 2.7.13.3)	kdpDNONO_c56360	Nocardia nova SH22a	836	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia nova, Nocardia nova SH22a	1415166	>tr|W5TT91|W5TT91_9NOCA Histidine kinase OS=Nocardia nova SH22a GN=kdpD PE=4 SV=1 MKRGQLRIYLGAAPGVGKTYAMLGEAHRRLDRGRDVVAAVVETHGRSRTAELLE GIERIPPVMRSYRGATIAELDLDAVLRRAPAVALVDELAHTNAPGSKNEKRWQDV HALLDAGIDVISTVNVQHLDSLNDVVEQITGVVQRETVPDWVVRGADQVELVDITP EALRRRLSHGNVYAADKVDAALRNYFRPGNLTALRELALLWLADQVDAALAKYRA DHRITATWEARERVVVAVTGGPESETIVRRASRIATKSSAELMVVHVVRGDGLAG VSAQRLHRLRDLATGLGSSLHTVTGENVPAALLDFARGVNATQLVVGTSRRSRW ARIIDQGIGATVVQRSGSIDVHMVTHEEAQHGPRWSALVRRQRSAVSWAAALVV PTLITTLCYLWLDSRLDLAGESALYFIGVIAVALLGGVAPAALSAVLGGLLLNWFFT TPRHSLTIAEPDNFLTIVVMAAVAVAVAALVDISANRTREARTASREAELLTLFAGA VLHGADLPDLLERAREIYGQRAVSFTTDDEVIACVGDDPARTPGSADTAIGAGDEE HWLLLNGRALTPGDRRVLAAVAGQAAGLVRQRELAGQAQAAAGVMAADRLRRA LLSAVSHDLRTPLAAAKAAVSSLRSEDVQFSPADTAELLETIEESTDQLTALVGNLL DSSRLAAGAVEPQLRQVYLEEVVNRAIVGVGMGTRGVRQAVLDRVKVEVGDISV HADSGLLERVLANLIDNALRYSASGPQAPDTPVRVGAERDGDRVSITVVDYGPGV PTGLEDQMFEPFQRLGDRDNSTGVGLGLSVVRGFVEAMGGTVHAEPTPGGGLT MVIELPAEEAR	1~~KdpD (1.60921E-119) ~~211,233~~Usp (3.47738E-32) ~~354,377~~DUF4118 (0.0000000100141) ~~457,X,601~~HisKA (0.000000000000834469) ~~667,724~~HATPase_c (4.47318E-29) ~~830	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.8E-94	324.5	0.5	3E-94	323.7	0.4	1.4	1	R5RKN9_9FIRM	Universal stress family protein	BN747_02091	Firmicutes bacterium CAG:646	672	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	1262995	>tr|R5RKN9|R5RKN9_9FIRM Universal stress family protein OS=Firmicutes bacterium CAG:646 GN=BN747_02091 PE=4 SV=1 MEENRPDSEQLLKRLQYEEREKQKKNKGKLKIFLGYAAGSGKTYAMLEAAHEAQ KNGVDVVAGYIEPHARPDTQALVKGLEVIPPLFVKYKGVRLREFNLDAALERKPRL LLVDELAHTNARGCRNEKRYQDVKELLRAGIDVYTTINIQHLESLNDLVGNITRIEV RERIPDTIFDHADQVEVIDIEPDELIQRMKDGKIYKEQQAERALQNFFRKEKLAALR EIALRRTADRVNRIAQEERSLQENQDYHTGEHILVCISAAPSSARVIRTAARLAGAF HGELTALCVETPGMQEADEKTKTALRRHMELARLFGAKVVTVFGSDVAAQIAQYA VVGNVSKIVLGKTNHFSVRPWRRSEFLEKLTYLAPNIDVYIIPDMKQTGKYRPEKK RRRTPGDTWKKIIRDLFMITGVMGGATLLALGFRQMEFSEANTIMIYLLAVLLSSYI ANRKIYALYSSMLSVLLFNFFFTEPYYSLKAYDKGYPTTFLMLFIVGLFTGTMTRKL KQQNQESAKTAYRTEILLENSQKLRRCKSRRAVWDQVAVQVGKLLNLAILIYPVSE SGLVDQPLLFPRKGMTVEELEKCVNFREKGVVQWVVANHHRAGACTHTLPDAM AMYLPVQSEKEVKGVMGILLEERRPVDEFEYGLLIAMLNETGVKLQDPFVAEESKT S	32~~KdpD (2.09455E-119) ~~235,256~~Usp (2.53555E-33) ~~379,411~~DUF4118 (4.06471E-15) ~~509,539~~GAF (0.00198843) ~~661	non-kinase	KdpD;Usp;DUF4118;GAF

	1.8E-94	324.4	0.4	1.8E-94	324.4	0.2	2	1	B1MDK8_MYCA9	Histidine kinase (EC 2.7.13.3)	MAB_3251c	Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	835	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium chelonae group, Mycobacterium abscessus subgroup, Mycobacterium abscessus, Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	561007	>tr|B1MDK8|B1MDK8_MYCA9 Histidine kinase OS=Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543) GN=MAB_3251c PE=4 SV=1 MPDGLRARGTLRIYLGAAPGVGKTFAMLNEAHRRAGRGTDVVAAVVETHGRSKT AELLDGLELIPPKEMVHRGTAMYELDVDAVLERRPALVLIDEMAHTNVPGSRNPKR WQDIDEILDAGIDVLTTINVQHLESLNDVVEQITGIVQRETVPDAVVRRAEQVELVDI TPEALRRRMVHGNVYAPEKVGSALSNYFRTGNLTALRELALLWLADQVDAALAKY RSDNRITKTWEARERVVVAVTGGPESETLVRRASRIAAKSSAELLVVHVVRGDGL VGASTAVMTRVRRLANDIGASVQAVTGDDVPQTLLDFARGVNATQLVLGTSRRS RWARILDEGVAAAVIRDSGAIDVHMVTHGHTSGRLRSWSVPQDGRKRLIINWLAA ILVPPATALFIHFFDTAFGVGSKSALFLIAVLGVSLLGGVSTALVSAVISGLLLNFLFV APRYSFTIGETDNALTILMMMVTAVAVAALVDAAATRARQARRASREAELLALFAG GVLVNSDLSALLERVRTTYNQTAVSLLCAEGPAVASVGEDPPTRESEADSVFRVD DGAYALALNGPPVPSSDARVLQVVAGTAVGLVRSARLAEEASQASALAEADRLRR ALLSAVSHDLRTPLAAVKAAVSSLRSPDIEFSPEDTAELLATVEESADQLTALVGNL LDSSRLAAGVVKPRAVPVYVDEIAQRALLGATENDRKRVHLDLGGAVVRADPGLL ERVLANLVDNALRYSQGEVRVSHEEVDDRTLVIVADHGKGLEASKRGAAFDAFQR LGDRDNTVGVGLGLSVVKGFVEAMEGTVNATDTAGGGLTMIVDLPSAGSAPTGAI R	7~~KdpD (8.03994E-120) ~~216,238~~Usp (1.48217E-32) ~~359,383~~DUF4118 (0.00000114213) ~~466,X,608~~HisKA (0.00000000000158356) ~~674,724~~HATPase_c (2.11814E-21) ~~823	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2E-94	324.3	2	2E-94	324.3	0.1	1.9	1	Q74AA7_GEOSL	Histidine kinase (EC 2.7.13.3)	kdpD GSU2483	Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	899	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter sulfurreducens, Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	243231	>tr|Q74AA7|Q74AA7_GEOSL Histidine kinase OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) GN=kdpD PE=4 SV=2 MSDMDDERRPSPEAMLKLAQAEEAEAKRGKLKIFLGYAAGVGKTYAMLQAARER RHEGRDVVAAYVESHGRPETDALLEGLEILPAARIEYQGVMLPELDIDGVLARRPQ LALVDELAHTNAPGSRHEKRWQDVEELLAAGIDVFTTVNVQHFESLNDVVAQITGI AVRETVPDRLLDLAAEIRLVDIPPEDLLQRLREGKVYVPEQAAFAAEKFFRAGNLIA LRELSLRRAAVRVDEEMRAYMEARAIPGPWPAAERLLVSISGSPFSERLIRTTRRL ADELKAPWFTVYVETPGNGRHEQENRKRVWKDLRLAESLGAQVATVTATSVAEA LIDYARRHNVTRIVVGKPAKPRWREFLRLPLVDRIIRLSGAIDVHVVSYEPAEAGKG PVLPVRRGPISFSGYLASLALVVAASLACLLLRPFLAPTNMVMIYLLAVVLAALRLGL KPAILTAFLGVLAFDFFFIPPHLTFAVADTQYLITFVALFTVGVVISTLVSTVRERAEA VREREEQTASLYYLSRDLAAAADIETLVAAVIRNIGETLFARAAVLLPEGDRLRVAA ASKGLKPDVKEMAVADWAFRNRQTAGQGTETLASAGFLYLPLQTSGSVLGVLGV RLKNDADYRSTQVRRMLDAFTSQTAMALERVQLSRQAEQAQILQARENLERALLN SISHDLRTPLVAITGALDTLRDKVHTLADESRLELLDTAWEEAERLNRFVGNLLDM TRLESGAIKLKRELSDVQDLIGCALAALERRIGERGIDVRLAPDLPLVRIDMVLMTQ VLVNLLDNALKYSPPDSGVEITARVDGGRLRIEMADRGPGIPEQDLKRVFDKFYRI AVPEGAQGTGLGLSICKGIVEAHGGSIRAENRTGGGLRVIVTLPLAGGAKEGVSH GP	26~~KdpD (3.39061E-119) ~~236,258~~Usp (9.71227E-45) ~~381,405~~DUF4118 (1.06472E-22) ~~504,530~~GAF (0.00000000000253698) ~~648,665~~HisKA (0.00000000040703) ~~731,786~~HATPase_c (2.56594E-33) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.2E-94	324.2	0.9	3.3E-94	323.6	0.6	1.3	1	I4ETM6_MODMB	Histidine kinase (EC 2.7.13.3)	kdpD MODMU_1289	Modestobacter marinus (strain BC501)	841	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Geodermatophilales, Geodermatophilaceae, Modestobacter, Modestobacter multiseptatus, Modestobacter marinus (strain BC501)	1144889	>tr|I4ETM6|I4ETM6_MODMB Histidine kinase OS=Modestobacter marinus (strain BC501) GN=kdpD PE=4 SV=1 MGGMARGSLRIYLGAAPGVGKTFAVLGEAHRRLARGQDVVVGLVETHGRRRTLE QLEGLEVLPRLEVTHRGVTLTELDVDAVLARHPDLVVIDELAHTNAPGSRHAKRW QDVEELLAAGISVLTTVNVQHLASLTDVVEQITGIAQQETVPDEVVRRADQVELVD MSPEALRRRMAHGNVYPAERVDSAMGNFFRVGNLTALRELALLWLADRVDEGLR RYRSEHDIDHVWETRERVVVALTGGPEGETLVRRAARVARRNGNGVLMAVHVLH SDGLAGASPEALRAQRALVESLGGSYHQVVGDDVATALLQFARGADATQLVIGTS RRSRWARAVRGGIGGEVIARSGEIDVHIVTHAAAGSPGWRLPVLTTAVTWRRRW AGLALALGGVPLVTVLCLTAGSVLSLASVLLVFLLLVVAVALVGGLGPAVVAAVVG GLAENWFFTQPTGRLTVNQVDDVVALLGYLVVGVAVATVVDRSARRAVAAARSA AETEMLASLSRSVLAGDRALPSMLEQIREAFGLDEVTMVERTADGERTVGSCGQ AHGRTGDDVPITDTIALRLCGRPLDAGDRRVLVAFAEQAAVALQQGRLTAQAAEA DRLAAGNSMRTALLAAVSHDLRTPLAGIKAASSALRSTDLALTDDDRTELVATVDE SADRLTGLVDNLLDMSRLQSGAVAPTLDPTDLVAVLGTALTWLDGPQRARVVVHS PDGLPAALADPGLLERVVANLVGNATQHAPSGVVDVRAGVAAGRVELRVADRGP GVPEADRERVFAPFQRLGDAPGGQGVGLGLAVARGLTEAMGGTLTAEDTPGGG LTMVLSLAPAELPARRDAVGAA	4~~KdpD (5.18334E-119) ~~214,236~~Usp (1.05745E-24) ~~358,X,608~~HisKA (1.82313E-14) ~~674,726~~HATPase_c (9.11505E-26) ~~826	kinase	KdpD;Usp;X;HisKA;HATPase_c

	2.3E-94	324.1	0.4	3.6E-94	323.5	0.3	1.3	1	Q2K0Q3_RHIEC	Histidine kinase (EC 2.7.13.3)	kdpD RHE_PE00263	Rhizobium etli (strain CFN 42 / ATCC 51251)	902	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium etli, Rhizobium etli (strain CFN 42 / ATCC 51251)	347834	>tr|Q2K0Q3|Q2K0Q3_RHIEC Histidine kinase OS=Rhizobium etli (strain CFN 42 / ATCC 51251) GN=kdpD PE=4 SV=1 MPDDNRDQAGRPSPDALLEKARAEMRGRLKIFLGAAPGVGKTYEMLISGRAKIAD GHDVVIGVVETHGRKETEALVAGFEIIPRVEIDYKGRLLEEMDLDGILARRPDLVLV DELAHTNAEGSRHPKRYLDVKELLDRGIDVYTTLNIQHVESLNDVVSQITRVRVRE TVPDSIIDLADDVEIIDLTPDDLIKRLHDGKVYMPKTAERALTNYFTPGNLTALRELA LRKTAQRVDDQLLTHMQAHAIAGPWAAGERVLVSIDHHPRSASLVRYAARMASRL RAPWAAVYIETNRSINLSEAERDTIASTLRLAEQLGGEAITIPGREVAEELVRHASA NNVTHIVIGAPKKPTWRDWWGRSVTDELIRKTGEISVHVISGTEKDGTTARGIKAA AVAPQLDIRAYLLATVYVAIALGVSIVLDQVLDVRNLALVFLMAVLTSAVLHGLRPAL YSCILGALSFNFFFLPPRYTLTISDPESVLAFFFFLGVAIIASNLTATVQRQAAAARQ RARTTEDLYLFSKKLAGTGTLDDVLWATAFQLASMLKVRVVLLLPEEGSIAVKAGY PPDDTLDDADIAAAGWAWEHNHAAGRGADTLPGAKRLYVPLRTGRTAVGVIGLD SDRRDGPLLTPEQQRLLDALADQAALAIERVQLVADVDRARLAAEADRLRSALLTS ISHDLKTPLAAILGAAGTLRDYFASMPEEDRSDLLSTVVDESERLNRFIANLLDMTKI ESGAMEPNSALHYAGDIVGTALARAAKILEHHKTEMSIPAELPMVRVDPVLFEQVI FNLLDNAAKYAPEGSVIQIEGWADADNVVVQISDEGPGIPPADLARVFDTFYRVRK GDQVRAGTGLGLSICRGFIEAMGGTITAGNRRGRPGAVFTIRLPKPNDIPKLDELK	26~~KdpD (4.86902E-117) ~~234,256~~Usp (3.66035E-44) ~~379,404~~DUF4118 (1.39026E-17) ~~499,530~~GAF (0.0000000298134) ~~650,667~~HisKA (0.00000000000423276) ~~733,786~~HATPase_c (9.44449E-29) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.4E-94	324	0.2	3.9E-94	323.3	0.1	1.4	1	D5UVQ0_TSUPD	Histidine kinase (EC 2.7.13.3)	Tpau_3247	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	853	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Tsukamurellaceae, Tsukamurella, Tsukamurella paurometabola (Corynebacterium paurometabolum), Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	521096	>tr|D5UVQ0|D5UVQ0_TSUPD Histidine kinase OS=Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) GN=Tpau_3247 PE=4 SV=1 MPKGQLRVYLGAAPGVGKTYAMLTEGARRAARGTSVVVGYVETHGRPQTEAQV LGLDVIPRRRVDYRGAVLEEMDTDAVIAAHPTVALVDELAHTNAPGSRNDKRWQD IAQLLEAGITVITTVNIQHLESLGDVVESITGVRQRETIPDAVLRAADQVQLVDMTPE ALRRRMAHGNIYAPDKVDAALSHFFRVGNLTALRELALLWLADRVDEKLEQYRSA QGISTVWPTRDRTVVALTGGPEGATLLRRGARLAAKGAGGELKALYVARSDGLS GASPAALTQLRQLTESLGGTFQIVTGDDVAAAILQYAQSINAARIVLGQSRHRPVA SLLRRSVSDAVIDGSGDIDVNVVTHERAVSQRRRGLPRLDRSDSALLGTRRTIAG WVLALAGPPALTAVLANTRDYHSFATELMLYLMLTVAVALVGGIRPAVPAALLGSV LLNYYFAPPLYTFTVSSGENVFAVVMFVLTAIAVASVVSLAARQTARAARARAEAD VLSGLADTLLAADREGQAVLPALLDQAVATFSLRGASLLRREAPSDPWTVVAAEG DAPSTPEEATDSSLIGDTVALAVNGPPLSASEHGLLVAFAAHAAARLDREALSAAA SRARALAEGNRARTALLSAVSHDLRTPLAGIKAAVTSLRSDDVEWSEEDEAELLET IEESADRLDSLVGNLLDMSRLESDSLTLLTREVGIEEVLPAIWTALPDADLSFEFAD DAPTAYADPGLLERVLANLVENAVRHSDGKPVTVGVSGVHTPDTGDRLQVHVRD HGPGVPEAQREAMFAPFQRMGDAPAGNGVGLGLAVARGLTEAMGGTLTAEDTP GGGLTMIVDLPAAQPVSPEPKEMS	3~~KdpD (5.70516E-119) ~~211,233~~Usp (1.03339E-27) ~~355,383~~DUF4118 (0.0000000084761) ~~477,X,619~~HisKA (3.5952E-15) ~~685,734~~HATPase_c (7.82194E-26) ~~839	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.5E-94	324	0	4.2E-94	323.2	0	1.4	1	A0A090UEC1_9ENTR	Histidine kinase (EC 2.7.13.3)	kdpD CIFAM_08_00560	Citrobacter farmeri GTC 1319	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter farmeri, Citrobacter farmeri GTC 1319	1114922	>tr|A0A090UEC1|A0A090UEC1_9ENTR Histidine kinase OS=Citrobacter farmeri GTC 1319 GN=kdpD PE=4 SV=1 MVDDDVLRPDPDRLLEQAVSPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQGL DILIGVVETHGRKETAALLDGLSILPLRRQTRHGRHISEFDLDAALARRPALILMDEL AHSNAPGSRHPKRWQDIEELLDAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETV PDPFFDAADEVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRELAL RRTADRVDDQMRAWRGRPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRL GSVWHAVYVETPALHRLPEKQRRNILHALRLAQELGAETATLSDPSEDKAVVRYA REHNLGKIVLGRTTTRRWWHRDSFADRLAKRAPELDLMVVALDDPPVRTLTSMP DTRAFKDKWRVQIQGGLVAVALCALTTFIASQWLSAFDAANLVMLYLLGVVVIALF YGRWPSVFATFISVISFDLFFIAPRGTLAVSDVQYLLTFGVMLTVGLVVGNLTAGV RYQARVARYREQRTRHLYEMSKALAMGRSAQDIATTSEQFIASTFHARSQILLPD EEGKLTALTHQHGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLRSADK THGLVVVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEELARLASERESLR NALLAALSHDLRTPLTVLFGQTEILTLDLASEGSPHARQASEIRQHVLNTTRLVNNL LDMARIQSGGFNLKKEWLTLEEVVGSALKMLEPGLVHPVNLSLPAPLTLIHVDGPL FERVLINLLENAIKYAGPQAEIGIDAHVENDHLQLDVWDNGPGIPQGQEQRVFDKF ARGNKESAVPGVGLGLAICRAIVEVHGGAIAVYNRPQGGACFRVTLVQETPPELE DFHEDM	21~~KdpD (2.22426E-127) ~~231,254~~Usp (3.23078E-40) ~~374,404~~DUF4118 (6.35432E-22) ~~502,530~~GAF (2.01807E-15) ~~645,662~~HisKA (0.00000000190457) ~~727,779~~HATPase_c (6.0935E-32) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.6E-94	323.9	0.1	4.6E-94	323.1	0.1	1.4	1	A0A0F3K4W7_9NEIS	Sensor protein KdpD	VI06_17085	Aquitalea magnusonii	898	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Aquitalea, Aquitalea magnusonii	332411	>tr|A0A0F3K4W7|A0A0F3K4W7_9NEIS Sensor protein KdpD OS=Aquitalea magnusonii GN=VI06_17085 PE=4 SV=1 MTDTRPDPDALLDAIKQDELAAQRGRLKIFFGACAGVGKTFAMLSAARVRQQEGC KVLVGVVETHGRKETEAQLHGLEVLPLTQIEYKGRSLAEFDLDSALARQPQLILMD EFAHSNVPGSRHSKRWQDVEELLAAGIDVYTTLNVQHLESLNDVVGQITGIVVRE TLPDHVFDQAAEVALVDLPPDELLARLAAGKVYLAHQAERAVKNFFRKGNLLALRE LALRRTADRVDAQMRAYRADQSIKPVWHARERLLICVGHGPGTEKLVRSGKRLAA SLDADWIAVFVETPELQRLSESKRSRIMKGLKLAQELGAETTVLGGSDLAATLLAY ARTRNVSKLVVGKSSVRKLQRLWRRPLLEQLSRQANDVDVYVVAHELEDGQPQQ NDGFNSLLFGEASRQQQRHGYVAALLSCLLTTGLASLLTPFFELSNVVMVYLLAVV LVAVRFGRGPGVLASFLAVATFDFFFVPPRMSFSVSDTQYLLTFAVMFAVALIISQL AARLRFEANIATYRERRTRALYELGRELAAALTANQIIDIAVSRLQPLFNASIVLLTP NSQEQLRAENDSTAQADLGVAQWVYDKQQAAGLGTQTLPSNAMLYLPLKAPMR NRGVLAVLPEQLDQVFLPEQQRLLETCAAQIALALERVHYVEVAQDAIVAMESERL RNSVLSVISHDLRTPLTTLVGLSSLLAEGQVDARKQASIAQSIQEESLRMNHLVTNL LDMARLQSGVKLNKAWQLLDDVVGSALRACQRNLQGHQLEVALASDLPVLEYDA VLIERVLVNLLENAAKYTPPGSHITLLAQPEGATIRVCVQDDGPGLPSGLEQKLFDK FSRGNSESTTPGVGLGLAICRSIVEAHGGQITASNRQPHGAAFCFTLPVSQMPAL PGDEEIQP	22~~KdpD (5.96218E-111) ~~232,254~~Usp (4.79538E-42) ~~377,408~~DUF4118 (5.47561E-25) ~~505,535~~GAF (2.80587E-14) ~~648,665~~HisKA (0.000000000000935642) ~~729,781~~HATPase_c (2.10795E-30) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.8E-94	323.8	0.2	4.8E-94	323.1	0.2	1.4	1	A0A0D5AEG1_9NOCA	Histidine kinase (EC 2.7.13.3)	NY08_3522	Rhodococcus sp. B7740	817	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. B7740	1564114	>tr|A0A0D5AEG1|A0A0D5AEG1_9NOCA Histidine kinase OS=Rhodococcus sp. B7740 GN=NY08_3522 PE=4 SV=1 MADRGELRIYLGAAPGVGKTFAMLGEAHRLRSRGCDVVAAVVETHGRARTIDALD GIEVLPMATVHYRGSSAQELDLDAVLARQPQVVLVDELAHTNTPGSVHGKRWQD VEVLLDAGIDVISTLNVQHLESLNDVVQQITGVPQRETVPDSVVRAADEVELVDITP EALRSRLRHGNVYAAEKVDAALSNYFRGGNLTALRELALLWIADQVDAALVKYRK DNRITDTWEARERVVVAVTGGPESETLLRRASRIASKSSAELMVLHIVRGDGLMG VSAPQMGSVRKLAAGLGASVHSVVGDDVPSTLLDFARGVNATQLVIGTSRRSRA ARILDEGIGAAVVQNSGKIDVHMVTHAEQARRWGVQVDSGRRRILAWVAAVLVP CLAAAVLSTVGPDFDSSGESALFFMVVLCVALLGGVAPAALSALIAGFLLNYFFTTP RYSLTIAEPDNFVVTVVLLLVAVAVAALVDAAARRTRQARRATQEAELLTLFAGSVL RGADLTALLERARETYRQSGVALWDNQSGSIVGSAGAQAPVDRAGADTEVDAG DFTLLLVGERTHAHDRRVLAAVANQAAGMVRQGRLAEEASRANALAEADALRRA LLSAVSHDLRTPLSAVKAASSSLRSTDVQFSPEDTDELLATIDESADQLTALVSNLL DSSRLQAGVVQPSLRPVFVDDVLGGALVGADDRVRVEVGDVEVLADPGLLERVL ANLVNNSARYAPVGDITVSAAAHGEWASISVADHGPGIAEGAEDTMFDAFQRLGD RDNSVGVGLGLSVVRGFVRAMGGTVTASNTVGGGLTMTVELKAASR	4~~KdpD (1.1251E-117) ~~212,234~~Usp (4.31873E-30) ~~355,376~~DUF4118 (0.000082621) ~~453,X,600~~HisKA (0.00000000000019657) ~~666,712~~HATPase_c (4.5382E-26) ~~812	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.8E-94	323.8	1	3.7E-94	323.4	0.2	1.6	1	U2RI88_9FIRM	Histidine kinase (EC 2.7.13.3)	HMPREF1546_00027	Oscillibacter sp. KLE 1745	893	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	1226323	>tr|U2RI88|U2RI88_9FIRM Histidine kinase OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_00027 PE=4 SV=1 MEKTENSTPYSPRYGEAETGGTGRLKIFFGYAAGVGKTYAMLEAAHQAQKEGVD VVVGYVEPHARPDTLALLEGLEVLSCREVDYRGIRLREFDLDGALARRPQLILVDE LAHSNAPGCRHTKRYQDVEELLQAGINVYTTVNVQHLESLNDLVTSITGIVVNERIP DHVFDRANQVELVDIAPADLEKRLEEGKIYRQRQAKQALENFFTAENLTALREIAM RRTADQLNRTAVQEKKGKAARAGDHILICLSSAPSNAKVIRTAARMAEAFHSGFTA LFVQTPETKELSGENIKRLRSNLRLAEQLGAQIATVYGADPAEQIAEYARVSGITKI VMGRVNHRQHPWIGQKSLADRLIERTDLDVYIIPDRQPLYKKPLGKLRKSRVRFS WRDAVVTLLCLAISTAVGFAFDWAGFSESNIITIYILGVLVTAVSTSGHLYGAANSLL SVLAFNFFFTEPRFTLQADGPSYPVTFLIMLSSSIIASSLASRVKEQARMAAEKSYY TELLLGSSQKLQTIRTEWDCLRLTAEQLSRMFDRPVIYALNDADKELDFRIEPADE HTLLEKLSTEEIGVAKWVQKNNKHAGATTNTLPDSKWLFLSVRGTRGVMGIVGVP IAGYVVPDAFEKNLMVALLGECGLSQERIRLEEERNQIALQTQRESLQANLLRAVS HDLRTPLTNINGSVGILMGKDQTLKPEVREQLYTAIDDDTNWLINMTENLLAATQL ETDRTKLKTAPELLEDLFQSAVRQLDRRARDHHISVDLEDQTLMASMNAGMIQRVI INMMNNAIQYTPKDSHIILSGTRRKDWVEISVSDDGPGIPDEAKKHLFDLFYTAEQ GKPDSKRGLGLGLHLCQSIVNAHGGTITVSDHAPSGTTFRFTLPAVRTDGVK	20~~KdpD (1.57525E-122) ~~230,248~~Usp (3.68646E-36) ~~370,396~~DUF4118 (0.000000000914884) ~~479,X,662~~HisKA (0.000000175677) ~~724,781~~HATPase_c (1.42911E-28) ~~884	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2.9E-94	323.8	0.1	6.8E-94	322.6	0.1	1.7	1	C7RUE2_ACCPU	Histidine kinase (EC 2.7.13.3)	CAP2UW1_1684	Accumulibacter phosphatis (strain UW-1)	897	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, unclassified Betaproteobacteria, Candidatus Accumulibacter, Candidatus Accumulibacter phosphatis, Accumulibacter phosphatis (strain UW-1)	522306	>tr|C7RUE2|C7RUE2_ACCPU Histidine kinase OS=Accumulibacter phosphatis (strain UW-1) GN=CAP2UW1_1684 PE=4 SV=1 MTERPDPDRLLARVQEEEAKAARGKLKIFFGASAGVGKTYAMLGAARQQKELGT DVVIGVVETHGRKETEALLAGLERLPLRDIAHRDRMLKEFDLDGALARRPALILMD ELAHSNVAGSRHPKRWQDVHELLVAGIDVYSTVNVQHLETLNDVVSGIAGIRVWE TVPDRVFDAADEVVLVDLPPDELLQRLKEGKVYLPQQAERAIRNFFRKGNLIALRE LALRRTADRVDDEMLAYRRETSINTVWQTRDALLVCIGPGTGGERLVRTAARLAG RLEAPWHAVHVDTHTAGPEPELQRQRIVRALDLASSLGAETATLSADDAVATVVD YAREHNLSRVLVGRDHPRRWQPWYRSMVERVGHAAPDLDVVQVARNDDARTA VPSPTAPPTPGEWLAYFKATAICAVATALAAPLAGAIELTNIAMLFLLAVLIVAMRLG RGPAVLSAFLAVAAFDFFFVPPRFSFAVSDAQYLMTFGVMLIVALITGQLTARYKQ HAEVATQREARARGLYEMARDLSAALLPVQIAEACDRFLVVEFGARAALLLTDTRD HLQAAILAAKAAAGETPVVDEGVARWAFDHGEAAGLSTDTLPGSPLLYLPLKAPM RTRGVLAIAPRDPLRVQGPEARRQLETFASLVAIAVERMHYVDVAQTTLVQMESE SLRNSLLSAISHDLRTPLSVLVGLAESIRLTQPPPTDAQATIAATLKEEALRMSTKVN SLLDMARLQAGKVQLKRQWQPLEEVVGSALMATDVSLAAHSVHTALPDDLPLLEI DGVLIERVLCNLLDNAAKYTPAGTPVSIGAAARENEVEVWVDDSGPGLPRGREES IFEKFERGARESTTSGVGLGLAICRAIVEAHGGRIHAENRPRGGARFIFSLPRGVP PTVVEEGGAT	21~~KdpD (8.64417E-123) ~~231,254~~Usp (1.69802E-35) ~~375,398~~DUF4118 (5.64124E-27) ~~498,525~~GAF (4.96081E-15) ~~646,663~~HisKA (0.00000000015512) ~~728,781~~HATPase_c (3.73258E-30) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.9E-94	323.7	1.8	3.9E-94	323.3	1.3	1.2	1	K9U0M1_9CYAN	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Chro_3177	Chroococcidiopsis thermalis PCC 7203	367	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Chroococcidiopsis, Chroococcidiopsis thermalis, Chroococcidiopsis thermalis PCC 7203	251229	>tr|K9U0M1|K9U0M1_9CYAN Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Chroococcidiopsis thermalis PCC 7203 GN=Chro_3177 PE=4 SV=1 MAKKGKHKIFIGMAPGVGKTYRMLDEGHALKREGIDIVIGLLETHGRKETAQKAEG LEIVPRQHIMRSGMTLTEMDTEAIIKRSPQLVLVDELAHTNVPGSFHEKRYQDVEDI LRAGIDVYSTVNIQHLESLNDLVARITGIVVRERVPDRLLDEADEVVVVDVTPETLE ERLLEGKIYASNKIDQCLQNFFQRRNLIALRELALREVADNVEDDALELSARNNGN DLDGQYCNIHERVLVCVSTYPNSVQLLRRGARIAGYMNAPLYVVFVEDPDKFLTR EESLHVETCEKLCQEFGGTFIRVKNHDIAKAIADVACKYHVTQIVIGESQRSRWKIL LKGSLTQKLVRLLKNIDLHIIATDKKEPL	2~~KdpD (1.58093E-120) ~~212,238~~Usp (3.22796E-48) ~~360	non-kinase	KdpD;Usp

	3E-94	323.7	0	4.6E-94	323.1	0	1.3	1	D2TNK5_CITRI	Histidine kinase (EC 2.7.13.3)	kdpD ROD_07011	Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter rodentium, Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	637910	>tr|D2TNK5|D2TNK5_CITRI Histidine kinase OS=Citrobacter rodentium (strain ICC168) GN=kdpD PE=4 SV=1 MVNEEPLRPDPDRLLEQTAAPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQGL DVLVGVVETHGRQETAALLEGLVLLPLKRQAHRGRHISEFDLDAALARRPALILVD ELAHSNAPGSRHPRRWQDIEELLDAGIDVFTTVNVQHLESLNDVVSGVTGIQVRE TVPDPFFDAADEVVLVDLPPDDLHQRLKEGKVYFAGQAERAIERFFRKGNLIALRE LALRRTADRVDEQMRAWRARPGEDKVWHTRDAILLCIGHNTGSEKLVRAAARLA SRLGSVWHAVYVETPALHRLAEKQRRDILSALRLAQELGAETATLSDPCADKAAV RYAREHNLGKIVLGRPSSRRWWRKDNFAERLAKRAPELDVLIVALDEPPRRALPA VPDTRSVKDKWRVQIQGCLVAVALCAITTVIASQWLAAFDEANLVMLYLLGVVVVS LFYGRWPSVFATVISVISFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVVGNLTAG VRYQARVARYREQRARHLYEMSKALAMGRSEQDIAAISERFIASTFHARSQVLLP DEHGRLVPLTRQQGITPWDDAIARWSFDKGLPAGAGTDTLPAVPYQFMPLRCAE KTYGLVIVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEEQARLASERESL RNALLAALSHDLRTPLTVLFGQAEILTLDLASEGSAHAKQASEIRQQILNTTRLVNN LLDMARIQSGGFNLHKEWLTLEEVVGSALKMLEPGLLQPVNLSLPAPLTLIHVDGP LFERVLINLLENAIKYAGPQAEIGIDAQVTNNRLQLEVWDNGPGIPEGQQQFIFDKF ARGNKESAVPGVGLGLAICRAIVEVHGGTLTVRNRPQGGACFRVTLVQEPPPALE DFHEAM	21~~KdpD (3.49823E-120) ~~231,254~~Usp (7.15015E-40) ~~374,404~~DUF4118 (2.7511E-21) ~~502,528~~GAF (0.000000000000309992) ~~645,662~~HisKA (0.000000000480142) ~~727,779~~HATPase_c (2.0453E-33) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3E-94	323.7	0	4.7E-94	323.1	0	1.3	1	V6F0X5_9PROT	Histidine kinase (EC 2.7.13.3)	kdpD MGMSRv2__1827	Magnetospirillum gryphiswaldense MSR-1 v2	901	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum gryphiswaldense, Magnetospirillum gryphiswaldense MSR-1, Magnetospirillum gryphiswaldense MSR-1 v2	1430440	>tr|V6F0X5|V6F0X5_9PROT Histidine kinase OS=Magnetospirillum gryphiswaldense MSR-1 v2 GN=kdpD PE=4 SV=1 MNDDRHDRPSPDALLAEAQKESRGHLKIFLGAAPGVGKTYAMLETAHERRREGID VVAGIIETHDRRETEALLADLDILPPRLAEYRGRSFREMDLDGLLRRRPRIALVDEL AHSNIPGSRHLKRWQDVEELLAAGIDVYSTLNIQHLESINDIVEQISGVKVRETLPD SVLATADEIELIDLPPQDLIKRLEEGKVYVPEQARRAVHSFFSPGNLTALRELALRH AAERVDRQMVDYMRAHAIPGPWPARERILVCIDERVDAERLVRTAKRSAERRGA AWVAVTVETPAAHGLPEAAKDRIDAALRLAAQMGGDTVTLHGDDVGECVLSYAR EHNCTQIVVGRARKAGWLRRWSRSVTDDLISRAGDFTVVLVGGEDETRPKPARP AVNKTDDTWLHLGLGYAVALLATAAATGLGFVIHPWLPIANISVGYLLAVMIVAMK SGLRPGILASAASFLAFNFFFTEPRFTFAITDTQNIVTVVFFLIAAFIISNMAARLRDQ IRATRESARRTGNLYDFGRKISAAATQDDVLWAVVHHVSATIHGKSLVLLPGEAGL SIAAGYPPEDQIDDKSAGAADWAWSHGKIAGRGSATLPAAQWLFLPLKTGRGPV GVLGVQMTEDADLPSPGQMRLLETLADQAAVAIERTTMVADIETARVATERERLR AALLSSLSHDLRTPLVSIMGAASSLIAYDDKLDADGRRDLAQTIQDEAERLNRFVQ NLLDMTRLGSGALKPRVDWVDLRDVVTAAVKRTERLARRHAIKVDIAPDTPLLCLD AVLMEQVIFNLLDNACKYAPPGSPVKVWAKRTADHIAIEVADQGPGIPPEDREKVF DMFYRVRAADTQEAGTGLGLAICRGIVEAHGGTIKAEPGLHGAGTCIIIHLPPPPDL DLDGKGNP	21~~KdpD (1.23255E-121) ~~231,253~~Usp (1.09322E-39) ~~376,419~~DUF4118 (2.07931E-18) ~~503,529~~GAF (1.44705E-14) ~~648,665~~HisKA (0.0000000000005393) ~~731,784~~HATPase_c (7.98645E-29) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.2E-94	323.6	0.1	5E-94	323	0.1	1.3	1	A4G5J6_HERAR	Histidine kinase (EC 2.7.13.3)	kdpD HEAR1623	Herminiimonas arsenicoxydans	921	cellular organisms, Bacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herminiimonas, Herminiimonas arsenicoxydans	204773	>tr|A4G5J6|A4G5J6_HERAR Histidine kinase OS=Herminiimonas arsenicoxydans GN=kdpD PE=4 SV=1 MPPADYQRPDPDALLAHVQEQERRAERGKLRIYFGASAGVGKTYAMLSAARRMQ AEGHDVIVGIVETHGRNETAALLDGLEMLPRKEIAYRDKIISEFDIDAALVRRPALILV DELAHSNAPGSRHPKRWQDVHELLDAGIDVFTTVNVQHLETLNDVVGGITGIRVA ETLPDTVFDQADEVVLVDIPADDLLARLSTGKVYQPQQAERASRNFFRKGNLIALR ELALRRTADRIGDDVQAYRIEKSINGVWKTDSDLLVCVGPGTNCEHVIRSAAQLAG QLNAKWHAVYVETPQLQSLPPAHREHILKTLKLAQDLSATTAVLSGNTVANEIVNY ARSHNFSRIVLGRDHSKWPWQTSHLKLIAHHLPDIDLIEIGRIEGKGSSSSQNLSAR LSSGLDETPGGTKPRFMPYVWTVVACIFTALLATPLLPHLDLANIVMLFLLAEVLIAV RFGRGPAVLAAFLSVAVFDFFFVLPRFSFAVSDVQYLVTFSVLLVVGLIVGQLTSG LRFQARIAAHREGRARALYEFARELSSALQAEQIFEITQSFIQRTFRAKAVLLLPDD AARLRLPAQAADDIGSDAANGKNVAELDIGVAQWAFDRATPAGMGTDTLPASTYF YLPLVAPMRTRGVLAIQPGNRRWILIPEQRKQLDTFAALAAIALERVHYIEVAQDAL VRMESERLRNSLLSALSHDLRTPLTSLVGLSESLTMSKPPLTSSQQELAQALHDEA RRMSNLVSNLLDMARIQSGEVKFNLQWLQFEEVVGSALRASQSAIAHHEIKTRLA PDLPLVRFDAVLIERVLCNLIENAAKYTPAGSRIVIAAEISGRFLEVSVYDNGPGLPA GQEEAIFDKFTRGERESATPGVGLGLAICRAIVEAHQGTIRAAHSPDGGASINFTL PLGTPPAIDESEITTLDQRP	25~~KdpD (7.79129E-123) ~~235,258~~Usp (3.76172E-34) ~~377,411~~DUF4118 (1.59161E-22) ~~511,539~~GAF (8.32682E-19) ~~665,682~~HisKA (0.000000000000358193) ~~747,800~~HATPase_c (7.91806E-29) ~~901	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.2E-94	323.6	0.2	7.8E-94	322.4	0	1.8	1	Q8XU09_RALSO	Histidine kinase (EC 2.7.13.3)	kdpDRSc3385	Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	937	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia solanacearum (Pseudomonas solanacearum), Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	267608	>tr|Q8XU09|Q8XU09_RALSO Histidine kinase OS=Ralstonia solanacearum (strain GMI1000) GN=kdpD PE=4 SV=1 MDETRPNPDTLLAELQSGEEKAARGKLRIYFGASAGVGKTYAMLSAAKVARAEGI DVVVGLVETHGRAETAALVEGLEHLPPRQVEYRGRTLPEFDLDAALARKPALILVD ELAHSNVAGSRHPKRWQDIEDLLAAGIDVWTTVNVQHLDSLNEAVGSITGIRVWE TVPDAVFDSAAEVILVDLPADELLRRLAEGKVYLPEQARHAARNFFRKGNLIALREL ALRRTADRVDDDVQAYRRARRIENVWRTRETIVACLDPQGDGEQVIRSAARLAAQ LECDWHAVAVVMPHLRAADARAERLHALLKMAEDAGARIETLAGTNAVEAITGYV RRHNITKVVVGRPPARRWRSARAIVVALRLAIGLERRLPSGDFAEALARQCPEVD VIRAAADPARVQLPPRAASIGRVDVRDTAQRAAAEAEGTWLRPAYLAACVYVGAA TLLSSLVRPVFDLANIVMLFLAAVVAVAMRHGRGPAALASVLSVALFDFFFVPPRY SFAVSDVQYLLTFAVMLAVGLLVGQLTAGLREQAEAAVQREAAARALYEAARELS AALTLDQIVSIGGRFVNATFGGRCAFFFVGPDGRLGAAQVARPEGTPDAPSGMP NLDRVLADWTCQHGQPAGTGTHTLPSGSVLYLPLKAPMAIRGVLAVEPETFQVLA QPDNRRQIDACATLIAIAIAERVHYVEIAQDALLRIESERLRNSLLAAVSHDLRTPLTG LAGMAETLLRTQPPLSPLQAEAAEAIGEQAQRMRAMVTNLLDMARLQNHDVKLRL EWQSIEELVGAALKGTPLPTHAVVVDDLADLPLLRCDGPLMERVLSNLLENAGKF APAGTEVRISAGVVVHDAAHGDEMCVRVRDHGPGVPAGAERVIFEKFTRGDKESA TGGVGLGLAVCEAIVSAHGGRIWVETPADGGACFVVALPASDQPAMEDDIPA	22~~KdpD (7.13463E-126) ~~232,255~~Usp (3.82539E-30) ~~389,432~~DUF4118 (3.09553E-23) ~~532,558~~GAF (6.77085E-15) ~~684,701~~HisKA (3.84336E-15) ~~766,817~~HATPase_c (7.31882E-27) ~~923	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.5E-94	323.5	0	9.6E-94	322.1	0	1.7	1	H2IX79_RAHAC	Histidine kinase (EC 2.7.13.3)	Rahaq2_3200	Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	898	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Rahnella, Rahnella aquatilis, Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	745277	>tr|H2IX79|H2IX79_RAHAC Histidine kinase OS=Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65) GN=Rahaq2_3200 PE=4 SV=1 MTEDRPDPDSLLALANEKPRGQLKVFFGACAGVGKTFAMLQEAQRLRATGLDVL VGVVETHGRQETQALLPGLSLLPPKRIHHRGRQVQEFDLDAALARRPALILMDELA HSNAAGSRHPKRWQDVEELLDAGIDVFTTVNVQHLESLNDVVSGVTGIIIRETVPD RLFDDASEVVLVDLPPDSLRQRLKEGKVYIPGQAERAIEHFFRKGNLIALRELSLRR TADRVDDQMREYRDDQGVNRVWHIRDALLLCIGHGGGNEKLVRVASRLAARLGC VWHAVYVETPRLHRLPEGQRRAILHSLKLAQELGAETATLSDPQEEQAILRYARE HRLGKIMTGRRREKRWKFSTSFADKLAEIAPDLDLIVVGLEDAPPNTARKEQDSRT FADRFSRQLWGCALAVALCAVITMMSQWLLPTFDQANLVMVYLLGVVIVALFYGR WPSVLAAVINVVSFDLFFVQPRGSLAVTDAQYLVTFGVMLIVGILIGNLTAGVRYQ ARIARHREKRAQHLYEMSKGLSQSLTPEAIAQTSRHFISSSLNAKTAILLPQENGEL AQPAGEITSIVVDDAIARWSFDKKLPAGAGTDTLPGVPYQLLPLIASGESRGLLAVE PPNIRQLLVPEQQRLLQTFTVLIANALERLHLAASAETARLETEREQLRNSLLSALS HDLRTPLTVLFGQAEILTLDLASEGSKHAPQASQIRQQVLSTTRLVNNLLDMARIQS GGFNLRKEWQSVEEITGSALRMLEPVLVHDNIEIDLPKEMVLVNCDASLIERVLINL LENAHKYAGTGATIGIKATPLDEWLEMEVWDNGPGIPAGAEHSIFDKFARGNKES AIPGVGLGLAICRAIIEVHDGRIWAENGPDGGARFRFRLPLEALPEMESDMESDID EVS	20~~KdpD (6.11302E-115) ~~228,251~~Usp (8.19021E-36) ~~371,403~~DUF4118 (1.5826E-21) ~~499,525~~GAF (1.55738E-15) ~~642,659~~HisKA (0.000000000540644) ~~724,777~~HATPase_c (5.79819E-30) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.7E-94	323.4	0.7	7.3E-94	322.5	0.5	1.5	1	E4T7V3_PALPW	Histidine kinase (EC 2.7.13.3)	Palpr_2667	Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	886	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Paludibacter, Paludibacter propionicigenes, Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	694427	>tr|E4T7V3|E4T7V3_PALPW Histidine kinase OS=Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4) GN=Palpr_2667 PE=4 SV=1 MNDFEIDRPNPDELLAALAKEEEKNKRGKLKIFFGMCAGVGKTYTMLQAAHVEKK KGNDIVIGYVETHKRKETEALVHGFEIIPRKAIEYKSTSVEEMDLDAIIARHPQIVLVD ELAHTNAPGSRHNKRYQDVQELLENGINVFTTLNVQHLESRTDTVAQITGVIIRETL PDFIFETSDDIELVDITPDELLQRLSDGKVYTPERSKEAVNNFFRKGNITALREMSL RIVADRVDNQLHDYMQDKRIRGPWKSGLHFLVAIGVSPSSQGLLKWAKNLAYTM GANVEALYVETSQRLTPRDHEQLDANIELAKELGFKVRIVTNDDLVKAIINYAQKEN ITHIIVGKSRFSSLKSLLKLGNFVNRLIKYSGNIDVYILGSDTPVEDKINIKSTIPTFTS RSRQYLTVSLIVALTSVLSYLVRDIVGYQVVSVILLFMVSLLALFYGTGPVLFAATAS ALIWDYFFIPPQFTFLIQKPLDILLLVMFFIVALVNGTLTSRVRRQEKKIRVREERTH ALYQLTKDLNSVSGFDEVIKIAYDFINRYFKLECSIVVKNDVNQLEVMPKENSTIQLT ESEMSIIHWVEKNSMKAGNLTSTLPSNEFTYYPLIGSNSTLGVIVVKQTKVFTHGE EQFWESSLSQIIGKYERELLRNATRKTYMISESEKLYKTLFNSISHELRIPIAAIMGS SETLLEQQLPEQIQQELYSEINTASIRLNRLVENLLNMSRLESGRITPHPDWCDAH DLVNSVSESLQNELESFTFKIDIPDDLPLIYVDFGLIEQVLHNLVLNATQHSPKGSAI ELKIELADDNLFIKVTDRGHGFPEDELSSVFDKFYRGKDAKAGGTGLGLSIVKGFV EAHNGSVSAANGVNGGAVFTLKIPKKEKK	26~~KdpD (2.65945E-120) ~~235,257~~Usp (3.79093E-29) ~~379,403~~DUF4118 (1.65767E-16) ~~503,531~~GAF (0.000516883) ~~640,663~~HisKA (0.000000000000625423) ~~727,780~~HATPase_c (6.16469E-26) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.8E-94	323.4	0	8.5E-94	322.2	0	1.6	1	Q6D7I6_PECAS	Histidine kinase (EC 2.7.13.3)	kdpD ECA1339	Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	910	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pectobacterium, Pectobacterium atrosepticum (Erwinia carotovora subsp. atroseptica), Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	218491	>tr|Q6D7I6|Q6D7I6_PECAS Histidine kinase OS=Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) GN=kdpD PE=4 SV=1 MIDGEDRRPDPDSLLAQVGTPPRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGL DIIVGVVETHGRSETAALLDGLPQLPLKHLRHHGRHTVEFDLDAALARCPALILIDEL AHSNVNGSRHPKRWQDVQELLDAGIDVFTTVNVQHLESLNDVVGGVTGIRVRET VPDPIFDQASEVILVDLPPDDLRQRLNEGKVYLPLQAERAVENFFRKGNLIALRELA LRRMADRVDDQMRAMRAGQGREQVWHTRDAILLCIGHGTGNEKLVRTAARLAA RLGSAWHAVYVETPRLHRLPEPQRRAILRALKLAQDLGAETVTLSEPDEELAVLRY AREHNLGKIVIGRHVEQRFGWWWRTRFAERLGRLGPDLDLVVVAVQDDAPAAPI KTPDARGLVEKWRMQLFGCGLATLLCAFITLLASWSPFAMLEPVNLVMIYLLAVVI VALFFGRWPSVFAAVINVASFDLFFILPSGTFAVSDAQYLVTFAVMLGVGLLVGNL TAGVRYQARVARYREQRVRHLYEMSKALNRSLSSADIVEASQHFLSTTFQAKIAVL LADSLHHTSPDLPQPARDNQQLIVDNAIARWSFDHRAPAGAGTSTLPGVSYQILPL ATTQQIFGVLAIEPSNARQLMIPEQQRLLETFTVLIANALERLHLVQSTENARLDAE REQLRNSLLAALSHDLRTPLTVLFGQAEILTLNLASEGSPYAQQANQIRQHILNTTR LVNNLLDMARIQSDGFNLRKEWQTSEELIGSALQQLESALAKNTIQVNLPDEMVLV YCDAGLVERVFINLLENALKYAGEQATIVITAHVVPQTDTQENALEIIVMDNGPGIE HGQESIIFDKFSRGHKESSIPGVGLGLAICRAIVEIHGGRIWATHVESGGAAFHFTL PLSAPPDLEPEDIEEH	23~~KdpD (3.26839E-124) ~~231,254~~Usp (9.25612E-42) ~~376,407~~DUF4118 (6.28753E-20) ~~505,534~~GAF (3.64645E-15) ~~652,669~~HisKA (0.0000000030517) ~~734,788~~HATPase_c (7.2271E-27) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4E-94	323.3	0.4	6.4E-94	322.6	0.3	1.3	1	I3THQ2_TISMK	Histidine kinase (EC 2.7.13.3)	kdpD TMO_0451	Tistrella mobilis (strain KA081020-065)	915	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Tistrella, Tistrella mobilis, Tistrella mobilis (strain KA081020-065)	1110502	>tr|I3THQ2|I3THQ2_TISMK Histidine kinase OS=Tistrella mobilis (strain KA081020-065) GN=kdpD PE=4 SV=1 MTRDADRPAPEALIEDAKRERRGRLKIFLGAAPGVGKTYAMLEEAQRRRAEGTDV AVAVVETHGRAETEALLRGLEVIPRRILTHRGRSFPEMDLDAVLARRPALALVDEF AHTNIPGARHEKRFQDVAELIDAGIDVLTTLNVQHLESLNDIVQRITRIRVRETLPDD VLAMADEIELIDLPPDDLIRRLREGKVYLGDQARRAVLHFFSRGNLTALRELALRAA AERVDEEMIRYMRAHAVPGPWPARERLMVCIGTGAEAEAVVRAGRRMADRARL PWIAVHVETGTGAASAGDYTPQDRANRALRLAERLGAEVTVLPRPVHARRLADEL VALARERNVSRIVIGRAPRRPWWRRLGAGGGLAEALVSRATGFELTVIAAEAGTT AAAAEPGRLQAEAPGPHFGPRELALIGVSVAAAALVSTLVEMILPLPNVSLVFLIAV LVVAVRGGLWPSIAASVLSFFAYNFFFTVPHHTFQVSRTEDILTIVFFLIAAALTGNL AGRLRERVQAERQAARRVGNLYDFARKAAGAADVDDVAWAVVSHVARTLQCDA VLLLPEPDGGLRIGAGFPPEDRLTPANRAAAEWAWRHERPAGWSSDTLPASDW LFVPMKAARGPVGLVGVSFGGRDGRPKQLGPEQRRLLEAVVDQAALAVDRTLLA ADIERERLKGEADALRAALLSSISHDLRTPLVSIIGAASSLKSLGEALDPGARGELAD TIHDEARRLDAYVQNLLDMTRLGHGALALRRDWVDLAELAGRVRGRLARQLGGR QLDVVVPEGLPLLHVDAVLMEQVLVNLVDNAVKHGGPDGRITIAAALADRGRSIDI RVEDDGPGIPEADREAVFDMFHRVKAGDSQPAGTGLGLAICRGFVEAHGGTIRAE AGAGGQGTRIVIRLTVAEPPAPPPEDAE	20~~KdpD (2.1142E-117) ~~230,252~~Usp (3.41336E-22) ~~382,412~~DUF4118 (6.87556E-19) ~~511,537~~GAF (0.0000000000003262) ~~660,677~~HisKA (0.0000000000136009) ~~743,796~~HATPase_c (6.38362E-27) ~~901	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.1E-94	323.3	0.5	6.3E-94	322.7	0.3	1.3	1	A0A0C5LBU1_9SPHN	Histidine kinase (EC 2.7.13.3)	TS85_00375	Sphingomonas sp. WHSC-8	884	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. WHSC-8	1609977	>tr|A0A0C5LBU1|A0A0C5LBU1_9SPHN Histidine kinase OS=Sphingomonas sp. WHSC-8 GN=TS85_00375 PE=4 SV=1 MTDDRPDPEALLRATAQEGRGRLKLFLGAAPGVGKTYEMLREGVARLRAGVDVV IGIVETHGRAETEAQVQGLEIVPRRAVDYEGRSLDEMDVDAILARAPQLVLVDELA HTNVPGSRHDKRYQDVEELLAAGIDVYSTVNIQHLESLNDVVASFTKVRVRETLPD RVLENAEIEVVDIPPDELIERLREGKVYIPEEATRALGHFFSKSNLSALRELALRRAA QAVDAQMLDYLRAHALAGTWAGGDRVVVAVHELPGAAELVRAAKRVADALRAP WTAVHIETPRAAQFSDAENARLAATLHLASQLGAQVASVPAESVLAGLKRFTVEA RATQLIVGKSARSRWFELRHGSVVDRLVRETPGIAVHVLPMAEGAPAPRQRPRR GPGHGWGKPMGYAVSLGLTGLVTLVGASMGNVTNIGLLYLLPVMVAATRYGVRT GVVTGLASSLAYNFFFIPPTHTFTIQDPQNILTVLTLMAVAVVSSQLAARVRAQAVL AQRSAGQNSALAGFARLLTGTSKRDELGQILCAEVGRLLDASTVLLLPEHGELALV AAFPPEDRLEAIEQAAARWAFDHNQPTGRGSDTLTASEWLFHPLAAGGRVLGVM GLARPDATTVLRSDQLPLLLSLLDQAALALERMALEAEMATVTQLKERDRLRAALL SSVSHDLRTPLTTVLGMLAEMEPASPEQAGQLAAARSEAERLHRFVANLLDMVRI ESGALHQAIEPVDLAEAAASAVHDLRRALEGHAIRLDVSPELPFVSVDAQLFHHCLI NLLENAAKYGDSGSPITISARRQPSGMTLSVLDEGPGLAAGEEKRIFETFARIEGS DRKGGTGLGLAIVKGFAEAMGLRVDAANRADGAGACFTLRIPESHLRKGGGGE	18~~KdpD (4.3667E-119) ~~227,249~~Usp (7.03692E-35) ~~372,398~~DUF4118 (5.99172E-17) ~~494,522~~GAF (0.000000223896) ~~613,656~~HisKA (0.000000000851413) ~~717,770~~HATPase_c (6.52398E-24) ~~872	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4.6E-94	323.1	0.1	6.8E-94	322.6	0.1	1.3	1	Q0BVR9_GRABC	Histidine kinase (EC 2.7.13.3)	GbCGDNIH1_0185	Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	899	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Granulibacter, Granulibacter bethesdensis, Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	391165	>tr|Q0BVR9|Q0BVR9_GRABC Histidine kinase OS=Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1) GN=GbCGDNIH1_0185 PE=4 SV=1 MQDIRPERPDPDALLRQAEKEGQEGRRGRLKIFLGAAPGVGKTCEMLTTAHHLLR DGVDLVIGVVETHGRAGTAALVEGLEIIPLRSVPYRDRTMTEMDLDAILNRAPQMV LVDELAHGNVPGSRHPKRWMDVEELISAGIDVMTTVNIQHLESLNDIVASITRIRVR ETVPDRVLSEADEIELVDLTPNDLLQRMRDGKIYAPQAAGRAMLHYFSPGNLTALR ELALRQTAQQVDAQLLDHMKANAISGPWAAGERIMVWLTLQDRDVSLLRYGRRL ADHLHAPWIVLHVETGRDITEDARARMAGQMHLAQSLGAETVTIPGQDEALDALA YARAHNVTQIVAAHPDGHAGRMHWYQRVARWFSRSMTNRLIRAGGSFPIHIVAR SRDDDQDVVTPFAPEPRQAMPYVSSTLIIGVATGAAMLLRQILEVGNVSLTFLTAIL WVAVAYGLWPSLWASVLGMLCFNFFFLPPLYTFTIAAPENVVAMFFFLTTALIASH LGARVRNQAVVARHRADITQSLYQFSRRLSGIVTLDDLLWTACHQIATALERNAVI LMPEGDRLILRASYTPDEQIDADDLAAASWAWKNDRMAGRGSDTLPGVGWLFIP LRTGRGPVAVIGLDAHAEDHLLYPEQQQLLDALGDQAALAIERIGLAKDLDEARLT AETEKLRGALLTSLSHDLRTPLASILGAASSLHEYDALLTEQDRRELLLTIREEAERL NRFVANLLDMIRLEAGALQPRRERVDLAEVAASALSRAARILSDHPVRLEVAPDLP MPLLDDVLLEQVLFNLLDNAAKYTPPGTPISIVIGQQPGVLTIRVLDEGAGLATQDT ESVFEKFTRFRAADRSRPGTGLGLAIARGFIEAMGGGIAARNRSDRSGAEFTITLP VEAENR	25~~KdpD (1.75134E-118) ~~235,257~~Usp (2.04471E-27) ~~386,408~~DUF4118 (5.0037E-19) ~~508,534~~GAF (0.0000000000054789) ~~653,670~~HisKA (0.0000000000036496) ~~736,789~~HATPase_c (1.05321E-24) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.9E-94	323	0	7.6E-94	322.4	0	1.3	1	A4W858_ENT38	Histidine kinase (EC 2.7.13.3)	Ent638_1207	Enterobacter sp. (strain 638)	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Enterobacter, Enterobacter sp. (strain 638)	399742	>tr|A4W858|A4W858_ENT38 Histidine kinase OS=Enterobacter sp. (strain 638) GN=Ent638_1207 PE=4 SV=1 MTDEPVRPDPDRLLEQTAAPHRGKLKVFFGACAGVGKTYAMLAEAQRLRAQDLD ILIGVVETHGRKETAALLEGLATQPARRTSHRGRLVTEFDLDAALARRPALILMDEL AHSNAPGSRHPKRWQDVEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETV PDPFFDSADEVVLVDLPPDDLRQRLHEGKVYITGQAERAIEHFFRKGNLIALRELAL RRTADRVDDQMRAWRDRQGQDRVWHTRDAILLCIGHGSGNEKLVRTAARLAAK FGSVWHAVYVETPHLHALPEHQRRAILSALRLAQELGAETATLSDPAEDKAILRYA REHNLGKIVIGRRHHRRWFSRESFADKLAKRAPDLDLVIVALDDKPAPLPNRTTDV RPFGEKWRIQLRGCLVATVLCALITFVASQWLIAFDAANLVMIYLLGVVIVALLYGR WPSVLATVINVASFDLFFIAPRGTLAVSDVQYILTFAVMLTVGLIVGNLTAGVRYQA RIARYREQRTRHLYEMSKSLAVGRTPRDIVQTSEQFIRSTFHASSLILLPDEHGKLR PLTSASGMTPWDDAIARWSFDKGLPAGAGTDTLPGVPYLILPLRSADKNLGLVIVE PTHLRQLMIPEQQRLLETFTLLVASALERLALTASEEQARMASERESIRNSLLAALS HDLRTPLTVLFGQAEILTLDLAAENSPHAPQASEIRQHVLNTTRLVNNLLDMARIQS GGFNLKKEWLTLEEVVGSALKMLEPGLGGRHISLNMPEPLALIHVDGPLFERVLIN LLENAAKYAGSKAEIGLNADVANQALRLEIWDDGPGIPVGQEAAIFEKFARGNKES AIPGVGLGLAICQAIVEVHGGTIAAHNRPEGGACFCVTLPLDTPPELDELPEDL	20~~KdpD (1.39872E-124) ~~230,253~~Usp (1.77942E-39) ~~373,403~~DUF4118 (2.4022E-20) ~~501,527~~GAF (4.33268E-15) ~~644,661~~HisKA (0.00000000356241) ~~726,779~~HATPase_c (3.00534E-28) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	6E-94	322.7	0	9.1E-94	322.1	0	1.3	1	L0M5A0_ENTBF	Histidine kinase (EC 2.7.13.3)	D782_3155	Enterobacteriaceae bacterium (strain FGI 57)	896	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, unclassified Enterobacteriaceae (miscellaneous), Enterobacteriaceae bacterium (strain FGI 57)	693444	>tr|L0M5A0|L0M5A0_ENTBF Histidine kinase OS=Enterobacteriaceae bacterium (strain FGI 57) GN=D782_3155 PE=4 SV=1 MMTDEPQRPNPDRLLEQTASPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQG LDILAGVVETHGRKETSEMLKGLTVLPQKRLSWQGRYLHEFDLDAALARRPALVL MDELAHSNAPGSRHPKRWQDINELLEAGIDVFTTVNVQHLESLNDIVSGVTGIQVR ETVPDPFFDAADEVVLVDLPPDDLRQRLNEGKVYLAGQAERAIENFFRKGNLIALR ELALRRTADRVDEQMRAWRDTQGQEKVWHTRDAILLCVGHHTGSEKLVRTAARL AARLGSVWHAVYVETPTLHRLPEAQRRAILSSLRLAQELGAETATLSDPSEEKAVI RYAREHNLGKIVIGRQEKRHWWSGERFGDRLARHAPDLDLLVVAMDEKPDPLPS STRDPRSFFDKWQVQIRGYAVAFTLCTAITLIAAQWLMAFDAANLVMLYLLGVVIV ALFYGRWPSVLATVINVISFDLFFIAPRGTLAVSDVQYLLTFGVMLTVGLVIGNLTA GVRYQARVARYREQRTRHLYEMSKALAVGRSAEYIARTCEQYIQSTFHARSQVLL PDENDKLTPSTQQDGLTPWDDAIARWSFDKGLPAGAGTDTLPGVPYQILPLKSAS KTLGLVVVEPLNLRQLMIPEQQRLLETFTLLAASALERLALTASEEQARFASERESL RNSLLAALSHDLRTPLTVLFGQAEILTLDLASSGSPYAPQANEIRQHVLNTTRLVNN LLDMARIQSGGFNLNKEWLTLEEVVGSALRMLEPGLNGQQIALSLPDPLMLIHVDG PLFERVLINLLENAVKYAGPQARIGINAREQNHQLFLDIWDNGPGIAQGQEIRIFDK FSRGNKESAIPGVGLGLAICRAIVDIHGGTLSASNRPEGGACFHVTLPLESPPELEE FHEDM	21~~KdpD (5.93048E-127) ~~231,254~~Usp (2.88315E-40) ~~374,405~~DUF4118 (6.95123E-21) ~~502,532~~GAF (9.75649E-15) ~~645,662~~HisKA (0.0000000251172) ~~727,780~~HATPase_c (3.72252E-30) ~~881	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.9E-94	322.5	0	1E-93	322	0	1.3	1	G9Z513_9ENTR	Histidine kinase (EC 2.7.13.3)	HMPREF0880_02597	Yokenella regensburgei ATCC 43003	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yokenella, Yokenella regensburgei, Yokenella regensburgei ATCC 43003	1002368	>tr|G9Z513|G9Z513_9ENTR Histidine kinase OS=Yokenella regensburgei ATCC 43003 GN=HMPREF0880_02597 PE=4 SV=1 MTDEPLRPDPDRLLEQTASLHRGKLKVFFGACAGVGKTYAMLAEAQRLRAQGLDI LIGVVETHGRKETAAMLTGLATQPLKRISHRGRYVLEFDLDAALARRPALILMDELA HSNAQGSRHPKRWQDVEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETV PDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIGGQAERAIENFFRKGNLIALRELA LRRTADRVDDQMRAWRDRQGQEKVWHTRDAILLCIGHNTGSEKLVRTAARLAAK LGSVWHAVYVETPALHRLPEHQRRAILSALRLAQELGAETSTLSDPSEELAVLRYA REHNLGKIVIGRYNKRQWFHSRTFADRLSAHAPDLDVMIVALDEKPVPAPRTNDT RPWMEKWRVQLRGCAVAVALCAAITMVAMQWMYAFDAANLVMIYLLGVVVIALF YGRWPSVLATVINVISFDLFFIAPRGTLAVSDVQYVLTFGVMLTVGLVIGNLTAGVR YQARIARYREQRTRHLYEMSKALAVGRSAKDIATTSEQFIHSTFDARSQVLLPNDA GKLMPLTQQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLRSADRT HGLVVVEPSNLRQLMIPEQQRLLETFTLLVASALERLSLTESEEQSRLASERESIRN SLLAALSHDLRTPLTVLFGQAEILTLDLASEGSKHAPQANEIRQHVLNTTRLVNNLL DMARIQSGGFNLRKEWLTLEEVVGSALKTLEPTLGGRHIALSLPDPLMLVHVDGPL FERVLINLLENAAKYAGYRAQIGIKAETVGEHLQLDVWDNGPGIPPGQEQAIFDKF ARGTKESAIPGVGLGLAICEAIVDVHGGTISAWNRPEGGACFRVTLPLETPPQLED FHEDL	21~~KdpD (6.82162E-126) ~~230,253~~Usp (3.57569E-37) ~~373,426~~DUF4118 (7.63595E-19) ~~500,529~~GAF (1.76516E-15) ~~643,660~~HisKA (0.0000000045085) ~~725,778~~HATPase_c (3.29438E-30) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	7E-94	322.5	0.2	1.1E-93	321.9	0.1	1.3	1	Q3IYD7_RHOS4	Histidine kinase (EC 2.7.13.3)	kdpD RSP_1268	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	887	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides), Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	272943	>tr|Q3IYD7|Q3IYD7_RHOS4 Histidine kinase OS=Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158) GN=kdpD PE=4 SV=1 MADEDLRPEPEALLAEAAREGRGRLKIFLGAAPGVGKTFAMLEAARQRLREGTDV VAGVIETHGRAETEALVHDLPVVPRRPGYYRGRILSEMDLDALLARRPRLALIDELA HTNLEGSRHEKRWQDVEEVLAAGIDVWTTLNVQHVETLNDAVARITGIRVRETVP DRILDTADEIELIDLSPEDLIARLRAGKVYVPEQAARAVQNFFAKGNLTALRELAMR AAADRVDAQLREHMAANAIPGPWPAQERLLVCVSDSPAARNAIRAAKRSADRAR VEWIALSVTSPRIETLPEGARDDLALALRLAERLGATVASLQAGGDVAREILDFAR RNNVRRIIVGRPRPRSTLHALAHPFRERVAERLLRLGTEFEVTLVSAEPGRARPQA RRLPALSFPATGWALLATALASGAAWVVDRMLPVASLALLFMTAVIVVATRFGRW ASALTAVSGFFAYNFFFTEPRLTFTVHYRDQILTLGLFLAASLLTGGLAAELRARVD AQRAAADRMGKLYDFSRRVAAAAAFDDVVWAAVSHVSMTLACRTVLLVPEGERL AVAGGFPPEDRLELRDMSAARYAWQRGEEAGRGSATLPAADWLFLPIRAGERRL GVVGVAYEGGRSFSPVDRRLLDALIDQVALAMERVRLAEDLEGARLAAETDRLRT ALLSSVSHDLRTPLVTIIGAAGSLAEPGALPPEAQQALAETIREEGERLDRYVQNLL DMTRLGHGALKPAVQPSDLAELVGAARTRLAAVLRGHRLGTDLPPDLPAVLVDPV LTEQVLVNILDNAAKYAPPGSPITLAARLDAGRVVLSVADEGPGIPPADREKVFDM FYRVAGTDRRRAGTGLGLAICRGLLEAQGGTIRAEAARPDGQGTRILLTLPVAP	20~~KdpD (6.09076E-121) ~~230,252~~Usp (1.48771E-32) ~~380,403~~DUF4118 (0.00000000000236061) ~~500,528~~GAF (0.0000000000199854) ~~644,661~~HisKA (0.000000000000517158) ~~726,780~~HATPase_c (7.12646E-28) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.1E-94	322.5	2.5	9.9E-94	322	1.8	1.2	1	E0UCQ0_CYAP2	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Cyan7822_3294	Cyanothece sp. (strain PCC 7822)	378	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7822)	497965	>tr|E0UCQ0|E0UCQ0_CYAP2 Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Cyanothece sp. (strain PCC 7822) GN=Cyan7822_3294 PE=4 SV=1 MISKNELTEQPNLPLPYELPKKRRGKHKIYIGMSAGVGKTYRMLEEAHELKEQGID VVIGLLETHGREETAEVAEGLQIVPRKNINYGGVILTEMDTEAILARQPQLVLIDELA HTNVPGSPTDKRYKDVEIILEAGIDVFSTVNIQHFESLNDVVAKITGVVVREKIPDRL LDEADEVVVVDVTPETLQERLKEGKIYAPDKIDQALQNFFQRHHLVALRELALREV ADNLEEEAESFEPFNHHCCVKERILVCVSTYQHSVKLLRRGARIASQMKARLYGLY VSNPERFLTKDESLYIETCEKLCEQFGGKFLRVERVDVTKAIADVAHQYHITQVVL GQTQKSRWQLFLKGSPVQQLIGYLKDVDLHIIATKNHD	22-~-KdpD (3.34227E-122) ~~232,251~~Usp (1.84335E-43) ~~373	non-kinase	KdpD;Usp

	7.3E-94	322.5	1.3	1.3E-93	321.6	0.9	1.4	1	R6VWM4_9FIRM	Uncharacterized protein	BN746_00939	Erysipelotrichaceae bacterium CAG:64	635	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, environmental samples, Erysipelotrichaceae bacterium CAG:64	1262981	>tr|R6VWM4|R6VWM4_9FIRM Uncharacterized protein OS=Erysipelotrichaceae bacterium CAG:64 GN=BN746_00939 PE=4 SV=1 MKQGKLKIFFGYCAGVGKTYAMLEAAHERRREGMDVVIGYIEKHDRLDTIALMQG LECIALKAIMYHGITLEEFDLDQALQRHPQLILVDELAHTNVQGARHPKRYSDIQEL LHAGIDVYTTVNVQHLESLQDVVAGITRVQVQERIPDAVFDEADQVELVDIEPDELL ERLKRGKIYHKTAAQKAMHNFFVRDNLIALREIALRRCADRVNKRVSLKDRKSTRE HILLCLSPSRSNALVIRTAARMASAFFAEFTALYVENVNEEPLCREDLEQLEQNRRL AQHFHANIVSVAGENIAQQISEYAKISGVSKIVIGRSSPRPHSRARTLIDQLTLLAPD LEIYIIPDANVEPVKRKRHRLTHAHVFRHRDFMLTVLLFLGATGINLLMYHFQLPEA NIIMVYLLAIVLISYNTSSRVYGLGVSLLIVAVFNFFFTAPRFSMEAYDPAYAMTFAV LFIVSFIISTLTRTMRMQLKVNAMQAHRMELLLETSQQLQLAENMAQLGEEAVRQL YKLLNRTIIIYSVRNKTLQEPIIYHEHLNEEEEQKYLTENERAVAQWVLKNNRKAGV STSTLPYAKALYYSIRKKDRIYAVVGIALQQKEVLSPFERSMLATMLNEIALAMDSM RKQNHRRVNR	1~~KdpD (1.9228E-116) ~~211,226~~Usp (1.31271E-26) ~~347,372~~DUF4118 (1.24609E-14) ~~471,499~~GAF (0.0000250014) ~~623	non-kinase	KdpD;Usp;DUF4118;GAF

	7.3E-94	322.5	0	1.1E-93	321.9	0	1.3	1	I2BB58_SHIBC	Histidine kinase (EC 2.7.13.3)	kdpD EBL_c26830	Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Shimwellia, Shimwellia blattae (Escherichia blattae), Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	630626	>tr|I2BB58|I2BB58_SHIBC Histidine kinase OS=Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) GN=kdpD PE=4 SV=1 MTGEPDRPDPDQLLHQLSRPPRGKLKIFFGACAGVGKTYAMLQEARRLHQQGLN ILVGVVETHGRQETAALLASLPLLPPRRLLHRGRRIGEFDLDGALSRNPALVLVDEL AHSNAPGSRHPKRWQDVEELLAAGIDVFTTVNVQHLESLNDVVGGVTGVQVRET VPDPIFDAADEVVLVDLPPDDLRQRLHEGKVYISGQAERAIEHFFRKGNLIALRELA LRRTADRVDEQMRAWRAERGREKVWHTRDAILLCIGHTGDNDKLVRTAARLAGK LGSDWHAVFVETPRLHQLPPAQRRRILNALRLAQELGAQTATLSDPSEEKALVRY ARDHNLGKMITGRRTLHRWWPRPPFADRLARLAPDLDIMVVAVDEKAPADPRKT PDNRPFGEKWRVQIQGCLVAVALCALITLFARQFMMGFDAANLVMIYLLGVVVVA LFYGRWPSVLATVINVLSFDLFFIAPHGTLAVSDVQYLLTFSVMLVVGLTIGNLTAG VRYQARIARYREQRTRHLYEMSRALATTRSVRDIAATSEHFLGNSFRARCQVLTP DEHGKLTALTAPDSDPFWDDAIARWSFDKGLPAGAGTDTLPGMPWRVLPLSTPS QTLGLVVIEPENLRQLMVPEQQRLLETFTLLCATALERQLLATSEEQARIASEREQI RNALLSALSHDLRTPLTVLFGQAEILTLDLACAGSPHARQASEIREYILNTTRLVNNL LDMARIQSGGFNLHKEWLTLEEVVGSALKTLEPLAAGHPVTLDIPDPLALIQVDGP LFERVLINLLENAIKYAGPGAHISLHARCPQAMLEVDIRDNGPGIPSGQEQTIFDKF ARGSKESAIPGVGLGLAICRAIMDVHGGTITAENAPEGGAVFHLRVPQPPAPELDE NEVM	22~~KdpD (3.40878E-105) ~~230,253~~Usp (4.58602E-36) ~~373,403~~DUF4118 (9.33227E-21) ~~501,527~~GAF (0.00000000000794603) ~~644,661~~HisKA (0.0000000158814) ~~726,779~~HATPase_c (3.81209E-30) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	7.6E-94	322.4	2	1.5E-93	321.5	0.4	2.1	1	D6ZE67_SEGRD	Histidine kinase (EC 2.7.13.3)	Srot_0870	Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	856	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Segniliparaceae, Segniliparus, Segniliparus rotundus, Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	640132	>tr|D6ZE67|D6ZE67_SEGRD Histidine kinase OS=Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578) GN=Srot_0870 PE=4 SV=1 MESMSTEPAPDLQPTPPKRGQLRIYLGAAPGVGKTYAMLAEAHRCQEAGTDVVV AVVATHGREKTAALLDGLEIVPAARVSYRGTALEEMDLGAVLERAPQLALVDELAH TNAPGSAHEKRWQDVQVLLEAGIDVLSTVNVQHLESLNDVVAQITGATQQETVPD VFARSAAQVELVDITPEALRARMSHGEIYAPDKVDAALRNYFRAGNLTALRELALL WLADQVDAALAKYRREHRITDVWETRERVIVSVTGGPESQTLIRRARRIASRSGA ELMVLHVVRGDGLASAAETELGRLREFSANVGASLHTVVGDDVPTTLLEFARAVN ATQLVIGTSRRSRMAQLLDEGIGMRVVRESGKIDVHMVTHEEAGRRRALRPGLRS TRKTSWSAAVLAPPAAAWLMELAGPAVDFTSATAVFFAVVLLVSLLGGVAPAAFS AVVSGVLLNYFFAPPLRSFAVKSPGQVVTIFVMVGLGVAVAALVDFASSRARQAR QAAQEAELLTLFAGAVLRGADVSELLARAKETYGLRAVSLVRSGDVVSCAGEDAP TSEASARAAVQSPDGECVLLLDGPKTFAGRDRRVLEAVAAQAAALVRQADLAQE AALADGLAEADKLRRALLSAVSHDLRTPLAAVKAAVSSLRSDDVEFSPEDVGELLA TIEESADQLTALVGNLLDSSRLAAGVLAPQRRRVYVDEVAHRAILSLPAPRRARVQ VQPDVNAVLADPGLLERVLANLIDNALRYAPDSQVTVRSERQEGEVVISVVDHGP GIRADQRERAFEPFGRLSSAPDGRGDRDNSVGVGLGLSVVRGFAESMGGQVVV TQTPGGGATLQIWLPDANTAKRHAAETGAKA	17~~KdpD (1.03598E-108) ~~227,249~~Usp (3.6815E-22) ~~370,415~~DUF4118 (0.000000150364) ~~486,X,616~~HisKA (0.00000000000270746) ~~682,732~~HATPase_c (2.71338E-27) ~~839	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	7.6E-94	322.4	0.1	1.2E-93	321.7	0.1	1.3	1	D5WU13_KYRT2	Histidine kinase (EC 2.7.13.3)	Btus_0568	Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	905	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Kyrpidia, Kyrpidia tusciae, Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	562970	>tr|D5WU13|D5WU13_KYRT2 Histidine kinase OS=Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) GN=Btus_0568 PE=4 SV=1 MTKDERIPPRRDPDALLADLREEARRGKLTVFLGATAGVGKTYAMLESAHERLRQ GVDVVVGWVETHGRPETEALLQGLPVVPPKTLTYKNRTFQEMDLEGILARRPSLV LVDELAHTNIPGSRHAKRYLDVEELLAAGFDVFTTVNIQHLESLNDVVARITGVTVK ETVPDRVLETAYQVQLVDVPPDELLQRLREGKVYVPEVARQAARSFFRPGNVQA LRELALRYTAQKVDRQVEDYMRAHAIDGPWPAGERVMVCISPSPFSAQLIRVGRR MAAGLKAPWLVAYVESPSKPPGDAERIRVSKYLRLAEELGAETAVMTADRVAEEL VKLAKRRNVTQIIIGKPLHSRLEDWLRGSLVDQVIRGSEGVRIHVIPGKPGKTAMVA TRRWPRRRTAAKSRPWGQYGIALGMVIVWTVVLYLVEPVLGLVNVALLYLFPVLF SAVRWSLGPAAVAAVAGVLAFDYFFVPPTFSFTVADLRYALTFAVFLSVAVLTGRL ATGLRQQIRTIQRRETQTAALYALSRQMTAVSDLNAIAESIVVHVAESVDGEVALFL PDETGHLAVRRSTGSGAWLTGAQELATAQWVFHRGEPAGRGTQTLAEAEALYL PLRFERRVLGVLAVRPGNPGDIGEIPSEQRELLHAFAGLAAAAIARVRLAEQAKVA EVAAESERLRTALLNSITHDLRTPLASVIGSVTSLLEGDEIFDPKDRRELLMTIYQGA LRMNRLIANLLDMARIESGMMQLHKKWCDLEDVVGVALAQSEEWLHNREVHLNIP REMPMVLADDVLLERVMANLLGNAVKFSPPGSPIEVAAEVEDGAVEVSVTNRGAP IPEEELEKVFEKFYRAPGAHVQPGTGLGLAISKAIVEAHGGSIWAENIPGGVRVAF RLPADRPPELARREET	24~~KdpD (4.01008E-118) ~~234,256~~Usp (2.19892E-38) ~~378,415~~DUF4118 (0.0000000030535) ~~506,532~~GAF (0.000000115237) ~~633,672~~HisKA (0.00000000000126111) ~~738,791~~HATPase_c (6.63396E-28) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.7E-94	322.4	0	1.2E-93	321.8	0	1.3	1	A0A0A1B9F9_9ENTR	Histidine kinase (EC 2.7.13.3)	PSNIH2_18265	Pantoea sp. PSNIH2	887	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH2	1484157	sp|A0A0A1B9F9|A0A0A1B9F9_9ENTR Histidine kinase OS=Pantoea sp. PSNIH2 GN=PSNIH2_18265 PE=4 SV=1 MNDDIARPNPDALLQSGRHRGKLKIYFGACAGVGKTYAMLQEARRLRAQGLDVL VGIVETHEREETASLLEGLSVLPRRATGRSRYEEFDLDAALARRPAVILMDELAHS NVPGSRHPKRWQDIDELLEAGIDVMTTVNVQHLESLNDVVGGITGIQVRETVPDP FFDRADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALRELALR RTADRVDDQMRAWRDAQGREKVWHTRDAILLCIGDNTGSEKLVRTAARLASRLG SVWHAVYVETPRLYRLSEARRRNILRTLRLAQELGAETATLADSDEAQAVLRYAR EHNLGKIVIGRRPTRRWRRDSFADRLGQLGPDLDLLVVALEEATRELTGQLSDTR AFGEKWATQLRGMAAALLLCALITFCGQYWLPDFDPANGVMIYLLGVVIIALRYGR WPSVAATVMNILAFDLFFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRY QARVARYREQRARYLYELARSLSSALRHEDIAAAGQRSIFATLQARSALLLPDEKG ELVITGDSSLTLPPDGAIARWSFSKGQPAGAGTDTLPAMPWQMLALKTQEKRWG LLVVEPDNLRQLMIPEQQRLLETYCVLLANALARSEAASRLAAEREQLRNALLSAL SHDLRTPLTVLFGQAEMLMLDLSAENSTFTSQASQIREQTLSTIRLVSNMLDMARI QSGGLNLHQEWLLLEELVGSALTQLAAILPRDNVQLALPDGMVWLHGDSTLLERV FINLLENSVKYAGAQTPRGIRAVERAGRLEIEVWDSGPGIPAGQEEKIFDKFTRGD KESAVPGVGLGLAICKAIIETHGGQINARARAEGGASFLISLPQATPPALPEAEQEE LK	19~~KdpD (5.76948E-122) ~~226,249~~Usp (1.60439E-36) ~~368,407~~DUF4118 (6.37052E-20) ~~496,524~~GAF (0.0000000000042238) ~~639,651~~HisKA (0.0000000040967) ~~716,769~~HATPase_c (5.48273E-28) ~~870	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.8E-94	322.4	0.6	1.1E-93	321.9	0.4	1.2	1	A7I6Q3_METB6	Osmosensitive K+ channel His kinase sensor	Mboo_0896	Methanoregula boonei (strain 6A8)	658	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula boonei, Methanoregula boonei (strain 6A8)	456442	>tr|A7I6Q3|A7I6Q3_METB6 Osmosensitive K+ channel His kinase sensor OS=Methanoregula boonei (strain 6A8) GN=Mboo_0896 PE=4 SV=1 MPNPSDCRQDQRPDPDALLACVQKEELQKVRGKLKIFLGYIAGVGKTYEMLKAAH LRKDEGVDVRIGYIEPHGRKETEALMEGIPVIPNRTIEYHGVKLNEMDLDAILAAHP QLVLVDELAHTNVPGSRHLKRYQDVEELLAAGIDVYSTLNVQHIESLNDVVARITG VIIKEKIPDRVIDEAAEIEVVDLAPPELLQRLREGKVYVPEMAARAIEQFFNEGNLYA LRELALRRAAERVDNQMLAYMQTRSIPGPWAVGEYLLVCIGPGPLAERLIRTARR QADRINARWCAIYVETPTHHRLSLEAKEQVDRSLQLAEKLGATTASVFGLNVANT VLEYARQHNVTRIIIGKTLRPRWQEFVFGSVVDQLIHNSGPIDVYVISSGKDLPEKP AEAEPLLPASPPRDYVDSLTLVVAVTILGWLFHSLISPVNQLMFYLLAVVVIAFKRG LKPAIFTSVVGVLAFDFFFVPPYLTFRVSDTQYLVTFLGMIIVGSVISLLVARARRHA DAAQTRERETSTLYALSQDLAGALDADAIMNAVGQHIKEIFQWESAFFLPENGHLA AHAKSPGLVMDGDDLAVATWAFQHGTTAGYDTDTLHGSKLRYIPLRSTRGVLGIM AVQPAEANGVITYEQSRILTAFANQAALALERVNLAKPA	31~~KdpD (4.96405E-125) ~~239,262~~Usp (1.00358E-45) ~~384,408~~DUF4118 (1.45741E-18) ~~501,533~~GAF (0.0000000000176199) ~~651	non-kinase	KdpD;Usp;DUF4118;GAF

	8.2E-94	322.3	0.2	1.7E-93	321.3	0.1	1.5	1	F7UZ77_EEGSY	Histidine kinase (EC 2.7.13.3)	EGYY_06090	Eggerthella sp. (strain YY7918)	931	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, Eggerthella sp. (strain YY7918)	502558	>tr|F7UZ77|F7UZ77_EEGSY Histidine kinase OS=Eggerthella sp. (strain YY7918) GN=EGYY_06090 PE=4 SV=1 MADSTFDYALRRDPDAILRQIAEAEAAEGDTRGKLKIFFGYAAGVGKTYAMLEEAH AVLAKGFDVVVGYVEPHTRADTMALVEGLEQIPPHEVRHRTITLKEFDLDAVLARH PQIVLVDELAHTNAPGCRHRKRYQDVEELLRAGINVFTTVNVQHLEGLNDKIAGIT HVTVSERIPDRVFDEAASVELVDIEPDDLIERLEAGKVYSPDRAGTALANFFSQKNL TALREIALRRMAERLSRKAERAQEGQRVEAGEDVLVYVTEDPGNVKAIRAAANMA EAYRGTFTAVVMETSRSHKLDAARREALRTNVGVAEELGARIVTLHGDDIARQIAL YAQAAGVTHIVVGNTTGLRGGILAREGLVNRLTRLAHAAVVDVVPVQDLPAQFGR LREERGFRITAGDAWKAVASVAIATLLGLAIYGMGMAGSIVLMLYLLVALLFATRAD GFFFAVLASLGSMLAYNFFFTAPRFTLHAYGLNSSFVFVFLLLGTLLATSLAVRMK SQTESSARRAYRMEVLLESSRAIQSADDLNVCLRLAADQIVKLLNRPVVTYRLHSD GRLGEGDIRNVPGTKGADASEAELVSPSEAAVAAWAAANNERAGSTTDTLADAR CLYLPVSAKNVVYGVVGIVMDEMDDDDDFGAFEKNLVLMIVNECGQAAEQLVSTE DRRAMEVRVEKETLRSNLLRTISHDLRTPLTSISGDADMLLLDGDGMERAQRERL YRDIHDDAQWLIALVENLLSITRIENGTMEIDRQPEVVGEVVREALGHIDRRASEGR VRAEVTDELLMADMDARLIIQVIVNLVNNALTYSPVEGSVVVKASTVNEQDAPRVRI AVTDEGPGISAEDRAHLFDLFYNGSTGRPSGKSGDFKRGMGLGLPLCRSIVEVHG GTLEVRNVQPHGCEFSFSLPAVNADDVVSEQQREERRG	32~~KdpD (9.95615E-118) ~~240,259~~Usp (9.0321E-25) ~~381,408~~DUF4118 (0.00398225) ~~506,X,681~~HisKA (0.000000000112548) ~~747,800~~HATPase_c (1.69331E-24) ~~912	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.3E-94	322.3	0	1.3E-93	321.7	0	1.3	1	A6T6D6_KLEP7	Histidine kinase (EC 2.7.13.3)	kdpD KPN_00714	Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Klebsiella, Klebsiella pneumoniae, Klebsiella pneumoniae subsp. pneumoniae, Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	272620	>tr|A6T6D6|A6T6D6_KLEP7 Histidine kinase OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=kdpD PE=4 SV=1 MSDEPLRPDPDRLLQHTAAPHRGKLKVFFGACAGVGKTWAMLAEAQRLRAQGL DILIGVAETHGRKETAAMLQGLSTLPPRRLAHRGRYVYEFDLDAALARRPALILVDE LAHSNAPGSRHPKRWQDVDELLEAGIDVFTTVNVQHLESLNDVVSGITGVQVRET VPDPFFDAADDVVLVDLPPDDLRQRLNEGKVYIGGQAERAIENFFRKGNLIALREL ALRRTADRVDEQMRAWRDRQGQEKVWHTRDAILLCIGHNTGSEKLVRAAARLAA RLGSVWHAVYVETPSLHRLPEARRRAILAALRLAQELGAETATLSDPSEEKAVLHY AREHNLGKIVIGRQSKRRGWDRSGFADRLARHAPDLDLVVIALDEKPSPLPARGN DSRTALEKWRLQLQGCAVAVALCAIITLVAMQWLMAFEAANLVMLYLLGVVLIALV YGRWPSVLATVINVISFDLFFVAPRGTLAVSDVQYLLTFGVMLTVGLLIGNLTAGVR YQARVARYRERRTRHLYEMSKALAVGRSQQDIATTSERFIASTFQARSQLLLPDA QGKLLPLTHQPGLTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSAART WGLLVVEPENLRQLMIPEQQRLLETFTLLVASALERLTLTASEEQARLTSERESLR NSLLAALSHDLRTPLTVLFGQAEILTLDLASEGSKHAPQANEIRQHVLNTTRLVNNL LDMARIQSGGFNLHKEWLTLEEVVGSALRMLEPSLGGQHIQLDLPDPLQLVHVDG PLFERVLINLLENAHKYAGARASIGIRAEADARQLSLEVWDNGPGIPAGQEQTIFD KFARGNKESAIPGVGLGLAICQAIVDVHGGTISASNRPEGGASFRVTLPGETPPEL EELPEEL	20~~KdpD (6.27628E-126) ~~230,253~~Usp (1.50931E-28) ~~373,403~~DUF4118 (7.47591E-20) ~~501,527~~GAF (2.54147E-14) ~~644,661~~HisKA (0.00000000443041) ~~726,779~~HATPase_c (4.17225E-30) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.5E-94	322.2	0.3	1.4E-93	321.6	0.2	1.3	1	A0A0F2RQU5_9PROT	Histidine kinase	VR70_06055	Rhodospirillaceae bacterium BRH_c57	899	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), unclassified Rhodospirillaceae, Rhodospirillaceae bacterium BRH_c57	1629718	>tr|A0A0F2RQU5|A0A0F2RQU5_9PROT Histidine kinase OS=Rhodospirillaceae bacterium BRH_c57 GN=VR70_06055 PE=4 SV=1 MNDDRDDRPSPEALLAEAQREGRGRLKIFLGAAPGVGKTYAMLEAAHERMRESV DVVAGVVETHGRKETGALLKGVDTLAPRMVEYRDKTFREMDLDALLKRRPKIALV DELAHTNIPGSRHVKRWQDVEELLAAGIDVYSTLNIQHLDSINDIVEQISGVKVRETI PDSVLSTADEIELIDLPPEDLIKRLEEGKVYVPEQARRAVHSFFSLGNLTALREMAL RHAAERVDRQMVDYMRAHAIPGPWPARERVLVCIDAGVDADRLVRFAKRAAERR GAAWVAVTVETSQAHALTDAEKNRIDAAMRLAAQLGGDSATLQGDNVADAVVGF ARDRNCTQIVVGRARKAGWFGRVGKSVTESLIDKAGDFTVVLVGGDENEKPKPS APLPKPQTGWRVWLGYAFALVAAAAATGVCLLIDLYLPIANISVTYLLAVMIVAMKS GLRAGIMASVLSFLSFNFLFTEPRYTFAIADIHNITTVVFFLLAAVIVSNLAARLRTQV EATRESARRTTNLYDFGRKITAAATLDDVLWAVVHHVATTIHGKSLVLMPGEAGLY IAAGYPPEDQIDDKSAGAADWAWTHGNLAGRGSATLPTANWLFLPLTTGRGPVG VLGVQMMEDADMPSPTQLRLLETLADQAAVAIERTTLVADVETARVATERERLRA ALLSSLSHDLRTPLVSIMGAATTLGSYDEKLEAEGRQDLIQTIQDEAERLNRFVQNL LDMTKMGSGALKPRVDWVDLGDVVSAAVKRTERLARRHTIRIEIAPEMPLLCLDAI LMEQVFFNLLDNACKYAPPGTPIKVWAIKTAKHIAIEVADQGPGIPPEDREKVFDM FYRIDQADSQTAGTGLGLAICRGIVEAHGGSIHVEPGLHGIGTCIVIHLPLPPELSLD GAGTA	21~~KdpD (5.32019E-122) ~~231,253~~Usp (6.13892E-35) ~~376,413~~DUF4118 (2.12928E-15) ~~501,527~~GAF (9.09509E-15) ~~646,663~~HisKA (0.00000000000067659) ~~729,782~~HATPase_c (1.74452E-29) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	9E-94	322.2	0.2	1.3E-93	321.6	0.1	1.2	1	W0A6Z8_9SPHN	Histidine kinase (EC 2.7.13.3)	NX02_05670	Sphingomonas sanxanigenens DSM 19645 = NX02	889	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sanxanigenens, Sphingomonas sanxanigenens DSM 19645 = NX02	1123269	>tr|W0A6Z8|W0A6Z8_9SPHN Histidine kinase OS=Sphingomonas sanxanigenens DSM 19645 = NX02 GN=NX02_05670 PE=4 SV=1 MTSAPDRPDPEAFLRQAAQEGRGRLKLFLGAAPGVGKTYEMLSEGRQRREAGID IVIGVVETHGRRETEALVAGYEVIPRIDVDHRGHNLGEMDIDAILARRPQLVLVDEL AHTNAPSSRHPKRYQDVEELLDAGIDVYSTVNIQHVESLNDVVASFTRVRVRETV PDAMLEAAEIEVVDIPPDELIERLKEGKVYVPEEASRALGHFFSKSNLTALRELALR RAAQAVDAQMLDYVRQHALAGSFAVGERIIVAISEHPSGPGLVRAGKRLADALKA PWTVVHIETQRSQSLSDFERQRVADAMALASRLGAVTASIPAQRVVDGLRDFATE ARATQIVIGKSTRSWMFELRHGSVVDQLVRAIDGVAIHVLPGDGEVAREMPGAAA PRRPRGDLSDYLWTLAAVALCTAIARGLVELIDLGNVGMMFLVPVMFAAASFGLR AGLFAGVTASLAYNFFFLPPTGTLTVSNPENIISIFVLLGVALVTSQFAARVRTQADL AQSSARQNAALAGFSRLLTGAADQEALMQAICAEVARLFDVRTVLLLPSATGPQL RAAYPPEDRLDQIELAAAQWAIDNEQPAGRGSSTLTASDWLFHPLATTRGVLGVL GLAREDAGEPLRSDQMPLLMSLLDQAAIAFDRMALEGEMQDARQLRERDRLRSA LLSSVSHDLRTPLTSILSAVQQMRIEPRPDLVETVEDEAQRLNRFVANLLDMARVE AGALPLRIEATDLTDAVASAVHDTRRALAGHEIRLEIPPDMPLVRIDPQLFHHCLINL LDNTGRYADPDTPVTIAARRDAQGIALSIIDQGPGIPPGKESKLFETFTRLEGSDRA KGGTGLGLAIVKGFAEAMGLAVSARNVDPPGACFTITIPESAVISALDDQDLP	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sanxanigenens, Sphingomonas sanxanigenens DSM 19645 = NX02	20~~KdpD (2.90433E-120) ~~229,251~~Usp (1.02457E-35) ~~374,399~~DUF4118 (2.55963E-18) ~~498,524~~GAF (0.00000000103928) ~~643,660~~HisKA (0.000000000095136) ~~719,772~~HATPase_c (1.14471E-23) ~~874	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	9E-94	322.2	0.2	1.5E-93	321.4	0.1	1.4	1	D2ATK3_STRRD	Histidine kinase (EC 2.7.13.3)	Sros_3803	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	846	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	479432	>tr|D2ATK3|D2ATK3_STRRD Histidine kinase OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_3803 PE=4 SV=1 MSRARGRLRVYLGAAPGVGKTFAMLDEGHRRLARGTDVVVGLVEAHGRPRTAEL ADGMEVVPRRTVIYRETAFTELDVDAVIARGPKVALIDELAHTNVPGSRNAKRWQ DIEEILDAGIDVVSTVNIQHLESLNDVVRQITEVPQRETVPDEVVRRADAVQLVDMP PDGLRRRMAHGNIYAPEKVDAALSNYFRVGNLTALRELALLWVAGEVDEQLDQY RAEHGIEGTWEARERVVVALTGGPEGDTLIRRAARIAARTKGADLLAVHVTLSDGL GGADPARLARQRALVENLGGTYHQVVGENVPRALLDFAGGVNATQLVLGASRRG RLAHLFSRGVGLTATALSGSIDVHMIPHAEAGKGARRIRPGAALTRTRRLAGWAM ALLGIPVLTAALVPFRADLTLPNGILLFLLMVVGVALAGGMWPAVTAAVAGFLLLNY FFTPPFDRFTVSDPHNLLALSVYVLVAVMVSAVVDLAARRTREAARASADAEVLST LAGHVLRGESALPSLLARLRETFALTSVTLLERVGEPAPDDQSEPGAWRIVATSG GPPCGCPGAADTDVVIDGSLVLAACGRLLEASDRRVLEAFAAEAAVALRQERLRR EADLAGPLAEADRMRTALLAAVSHDLRTPLASARLAVESLSRGTEIEWSAEDRAELL ATADESLIKLDRLVANLLDMSRLQAGVLGLTLQPVALEEVIPRSIDDLGPLRDRVEG DVSVDLPEILADSALLERILVNVMSNAVRYSPAGKKVLITASRHGDHVEIRVVDRGP GIPAEAHDRVFMPFQRLGDRDNHTGVGLGLALSRGLAEAMGGTLTPEETPGGGL TMVLTLPTSSGARP	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	4~~KdpD (3.66E-118) ~~213,235~~Usp (1.70276E-18) ~~357,383~~DUF4118 (0.000000000370931) ~~477,X,620~~HisKA (0.00000000000577082) ~~686,737~~HATPase_c (3.35861E-28) ~~838	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1E-93	322	0.6	1.7E-93	321.3	0.4	1.4	1	Q0SHD3_RHOJR	Histidine kinase (EC 2.7.13.3)	kdpD RHA1_ro01229	Rhodococcus jostii (strain RHA1)	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus jostii, Rhodococcus jostii (strain RHA1)	101510	>tr|Q0SHD3|Q0SHD3_RHOJR Histidine kinase OS=Rhodococcus jostii (strain RHA1) GN=kdpD PE=4 SV=1 MSGTGTDGERRDAEHRRGELRIYLGAAPGVGKTFAMLGEAHRRRERGCDVVAA VVETHGRDRTAAQLGDLELVPPKLIAYRGTLGRELDVEAVLARRPALVLVDELAHT NTPGSVHEKRWQDVEILLAAGIDVLSTLNVQHLESLNDVVQRITGVVQQETVPDE VVRAATQVELVDITPEALRRRLSHGNIYAADKVDAALSNYFRKGNLTALRELALLW VADQVDAALAKYRAENKITDTWEARERVVVAVTGGLESETLVRRAGRIASRSSAE LIVVHVVRGDGLAGVSAPEMGKVRTLAASIGASLHSVVGDDVPTTLLDFARTANAT QLVLGTSRRSRWARIFDEGIGASVLHQSGSIDVHMVTHGESHRPRRLSPVGSRS RTAIAWIAAVLVPSVATLVMSAVDRWLGLVGEGALFFIVVLLVSLLGGVAPAAFSAL ISGLFLNYFFTPPVRSFTIAEPDNFITTVVLLVVAVAVAVLVDAAAKRSREARRASQ EAELLALFAGSVLRGADLGTLLEKVRETYGQDSVSVLHRDRGPVGSVGPHPPVSV DDADTVCEVGEGEYALALRGSELHARDRRVLLAVANQAVGMIRQTELAQEAGQA QALAEADRLRRSLLSAVSHDLRTPLAAVKAAASSLRSDDVDFSPEDTAELLATIEE SADVLTSLVGNLLDSSRLAAGVVTPTLRPVYLDEVVHRALVGLGIGGRTGTRARE RVEVDVGTVAAMADSGLLERVLANLIDNALRYGEDSVIRVGAAAVGDRAVVTVAD TGPGIPRGRADEMFAPFQRLGDRDTTTGVGLGLSVVRGFVDAMGGTISATDTPG GGLTMVVELAGAGGAHP	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus jostii, Rhodococcus jostii (strain RHA1)	15~~KdpD (7.87507E-117) ~~225,247~~Usp (2.05392E-31) ~~368,390~~DUF4118 (0.000000022426) ~~469,X,615~~HisKA (0.000000000000566735) ~~681,737~~HATPase_c (6.37608E-27) ~~837	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.1E-93	321.9	0	1.8E-93	321.2	0	1.3	1	A8AJC0_CITK8	Histidine kinase (EC 2.7.13.3)	CKO_02466	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter koseri (Citrobacter diversus), Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	290338	>tr|A8AJC0|A8AJC0_CITK8 Histidine kinase OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=CKO_02466 PE=4 SV=1 MVNEEPLRPDPDRLLEQTAAPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQGL DILTGVVETHGRKETAALLDGLSILPLKRQTHHGRHLSEFDLDAALARRPALILMDE LAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRET VPDPFFDAADEVVLVDLPPDDLRARLKEGKVYIAGQAERAIEHFFRKGNLIALRELA LRRTADRVDDQMRAWRSHPGEEKVWHTRDAILLCIGHNTGSEKLVRAAARLAAR LGSVWHAVYVETPALHRLPEKQRRAILSALRLAQELGAETATLSDPAEEKAVVRY AREHNLGKIVLGRPATQRWWRRDSFADRLAKQAPDLDQVVVALDDPPTRPLNQT PDTRAFKDKWRVQIQGCLVAIALCAVTTVIAVQWMVAFDAANLVMLYLLGVVIIALF YGRWPSVVATFINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGV RYQARVARYREQRTRHLYEMSKALAVGRSRQDIAATSEQFIASTFQARSQVLLPD ENGTLTPLTHQQGITPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSADKT HGLVVVEPGNLRQLMIPEQQRLLETFTLLVASALERLTLTASEELARLASERESIRN ALLAALSHDLRTPLTVLFGQAEILTLDLASEGSPHARQASEIRQHILNTTRLVNNLLD MARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLSHPINLSLPAPMTLVHVDGPLF ERVLINLLENAVKYAGSQAEIGIDAHVEDEHLQLDVWDNGPGIPDGQEKSIFDKFA RGNKESAVPGVGLGLAICQAIVEVHGGTISAHNRPQGGACFRVTLPQETAPELED FHEDM	21~~KdpD (1.91642E-127) ~~231,254~~Usp (3.02169E-31) ~~374,404~~DUF4118 (2.69858E-21) ~~502,530~~GAF (1.22344E-15) ~~645,662~~HisKA (0.00000000124227) ~~727,779~~HATPase_c (2.10556E-32) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.1E-93	321.8	2.7	1.7E-93	321.3	1.9	1.3	1	K9X9B6_9CHRO	Osmosensitive K channel His kinase sensor	Glo7428_0033	Gloeocapsa sp. PCC 7428	390	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	1173026	>tr|K9X9B6|K9X9B6_9CHRO Osmosensitive K channel His kinase sensor OS=Gloeocapsa sp. PCC 7428 GN=Glo7428_0033 PE=4 SV=1 MNKTEEPIVSENTTIRPARKGKHKIFIGMAPGVGKTYRMLEEAHALKQEGIDVVIGL LETHGRKETAQKADGLELIPRKEIVRGGLTLTEMDTEAILARSPQLALIDELAHTNV PGSEREKRYQDVEVILAAGIDVYSTVNIQHIESLNDLVARITGVVVRERVPDRLIEEA DEVVVIDVTPETLEERLLEGKIYAPEKIHQALANFFQRRNLIALRELALREVADNVEE DAIALTANSPNEQLAGQTCNIHERVLVCVSTYPNSLQLIRRGARLAGYMNAPLYAV FVANPDRFLTKAESLHLETCEHLCQEFGGTFIRVTNHNIAQAIADVAKQYRITQIVIG ESQRSRWKILLRGSLTQQLVRLLKNIDIHIISSEKNAEFNGVAPVG	18~~KdpD (4.8505E-131) ~~228,254~~Usp (4.6782E-49) ~~376	non-kinase	KdpD;Usp

	1.2E-93	321.8	0	2.2E-93	320.9	0	1.4	1	A8HY24_AZOC5	Histidine kinase (EC 2.7.13.3)	AZC_1568	Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	890	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Azorhizobium, Azorhizobium caulinodans, Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	438753	>tr|A8HY24|A8HY24_AZOC5 Histidine kinase OS=Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571) GN=AZC_1568 PE=4 SV=1 MGQEDKPRASPDALLAMVEREGKGKLRVFLGAAPGVGKTYAMLQAARAAKADG LDVVVGIVETHGRRETEAMLEGLPVLPRRPIHYRGRLVPEFDIEGALARRPKLLLVD EYAHSNVPGSRHPKRWQDVEDLLDAGIDVWTTLNIQHLESLNEVVQRITGVRVRE TVPDTAIQEADEVVMVDLPPDELLKRLAEGRVYVQDTAARAIERFFKPTNLTALRE LALRRVAARVDSDLIEHMQGGAIEGPWAAGERILVCVGPDASAQKVVREAKRLAD LADAPWLAVTVERPGHPLDATARARADAALRLAESLGAETRALVGSDLVEELLKV ARFENVTQIVVARARPSRLSRPFVRTLADALVREADGIAVHVLTFEEGERSAPRRR LPPVGGLDGYVAAAMAVSIATLLGEELTKHVALPNVSMIFLLAVLIPALFFGVWPAV FASLFSALAYNFFFIDPVYTFTIARPHEVLALVIFLVIAVIISAVAGRAREQAKASAQR VKAGRRLYDFTRKLSSLADAPEVAAGAASEIHAILSRAAVILSSTRGELHIAAAWPP EDRLDTASLSAARWAYEHGEPAGARTATLPSVPWLFIPLKARQGIIGVIGIEALSGE PLDAEGRVLLDALADQTASALERAALAGEMADVRSAAEAERVRNILLASISHDFRT PLSSILGASSSLIEYGARIDPEQRRDLLSQIREEADHLDSMVRNLLSMTRLEAGALD LRRDWVDVGEVVNQSVAAARRRGAIQHLTVRLGENLPLVRADQILLNQVLANIVG NAVRYAGASASIEVSAERVGDEVEIAVTDSGPGIPSGLLGHVFEKFVRAASDRAD GGEGAGLGLAIAKGIVEAHGGTITAESPPPGRASGLRLAFRLPVEPDTGP	21~~KdpD (8.04817E-120) ~~231,253~~Usp (2.14086E-26) ~~375,397~~DUF4118 (2.1164E-15) ~~496,525~~GAF (0.000000000000307449) ~~640,657~~HisKA (0.00000000000267404) ~~723,776~~HATPase_c (1.11634E-18) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.2E-93	321.8	0.3	2E-93	321	0.2	1.4	1	R6Q206_9CLOT	Uncharacterized protein	BN618_00210	Clostridium nexile CAG:348	664	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	1263069	>tr|R6Q206|R6Q206_9CLOT Uncharacterized protein OS=Clostridium nexile CAG:348 GN=BN618_00210 PE=4 SV=1 MEEMRPNSEQLLRRLKYEEEQKQTTRGKLKIFLGYAAGSGKTYTMLEAAHEAKKH GIDVVAGYIEPHDRPDTLKLTEGLEMIPPLWIEYKGVRFREFDLEQALKRKPKLILV DELAHTNVAGCRNHKRYQDVKELLRAGIDVYTTINIQHLESLNDLVGTITHIEVRER VPDRIFDHADQVEVIDIEPEDLIRRMQEGKIYQKQQAQRALDHFFRREKLAALREIT LRRTADRVNRIAEEERNIMGDMEYHTGEHVLVCISAAESSPKVIRSAARLAYAFHA KFTGIYVETPEMQEAGEKTKQSLQNHMELARSLGAKIVTVFGSDIGFQIAEYAVVG NVSKVVLGRTNHNRFIQKPRPELLEKLNNRAPNIDVYVIPDIKQKKIHTRMNIRSER WEKKWKRIFWGFAAITVVMILTTMVAFVLQKWNLPESNIIMVYILGVLLSSYISDNK LFAVYSSMFSVLAFNFFFTEPYLSLKAYDKGYPTTFLMLFIVGLFTAVQTRKLKLQN RESVKKAYRTEILLENSQKLRRCKSELEVWNQVAGQVGKLLNLSLIIYPVNEKGLL NDALVFPKKGVTKEQLEFLLDSQERAVAQWSAANHHRAGTCTHTLPTAKAMYIPI QNEKEVKGILGIYLEERRKLQEFEYGLLIAMLNETGVKLQDTFH	26~~KdpD (3.70712E-123) ~~234,255~~Usp (6.04674E-32) ~~378,407~~DUF4118 (6.86056E-16) ~~504,537~~GAF (0.000482837) ~~660	non-kinase	KdpD;Usp;DUF4118;GAF

	1.3E-93	321.7	0.7	2.1E-93	320.9	0.2	1.6	1	A0A075JHN9_9MICO	Histidine kinase (EC 2.7.13.3)	HX89_12865	Dermacoccus nishinomiyaensis	879	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Dermacoccaceae, Dermacoccus, Dermacoccus nishinomiyaensis	1274	>tr|A0A075JHN9|A0A075JHN9_9MICO Histidine kinase OS=Dermacoccus nishinomiyaensis GN=HX89_12865 PE=4 SV=1 MTRGTLRIYLGAAPGVGKTMAMLAEGRRRAERGTDVVVGFCETHGRTATAAALE GLEVMPRLRREYRGATLEEMDLDAVLRRAPQVALVDELAHTNVPGGRHEKRWQ DVEDLLAAGIDVVSTVNIQHLESLNDAAFAITGVLQRETVPDVVVRRAEQVELIDMA PEALRRRMAHGNVYKPEKVDAALANYFRQGNLTALRELALLWLADRVEESLTAYR SDHDIVGTWPTRHRVVVALSGGREGATLLRRAARIAARGSGGEMHAVFVVRDDG LRTAEADVVSGLRRLTEELGGTFHTVSGPDAAEAVLHYARGVNADQIVVGLSRRS RAQAMLRPGTGERIIAGSGEDIDVHVVTHELAHVGSSPTEREGLSTRRVRLGFLTS VTAPALLSALLVPLRSGVGLPLIVQLYLLLTVVVALIGGMAPAITAGVLSSLLINWFF TPPIGTLTISDPQNVVALVLFVVIGAAVSLVVHASARRAADVSASHQEATALAELSH TMLSSADQLALLLTRSLEMFDQDAAAVVRTRGPGRSVIASTDGYSDVAAQALPRE KTTVERIDDEHDLVLVGRPVPAERQRLLGAYAMHAAAVLHRRALLDLAESADTLAR DNKARTALLSAVSHDLRTPLAGIKAAVGSLRSDEVTFSPEDEAELLEAVETSADRL DALIGNLLDASRLQTGALVANPREIDLAEVVTPAVRALETPDRVTWHLDDAARHVV ADPGLLDRVLANVLENALRHGGSDGVVVTTSTLGPRVELRVADHGPGIPDEAREE IFRPFQRYGDAPAGDGIGLGLAVARGLTEAMGGMLEAETTPGGGVTMVIVLPAVA NAAGATSEAEPGAESEPESAPEARPQDAEADQPVDTRFADATTRGDS	3~~KdpD (1.65358E-113) ~~211,233~~Usp (4.75387E-20) ~~356,381~~DUF4118 (0.00000000000303431) ~~474,X,612~~HisKA (0.000000000000535419) ~~678,728~~HATPase_c (6.12064E-26) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.3E-93	321.7	0.2	1.8E-93	321.1	0.1	1.2	1	D7C419_STRBB	Sensory histidine kinase in two-component regulatory system wtih KdpE, regulation of potassium translocation	SBI_09267	Streptomyces bingchenggensis (strain BCW-1)	758	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7C419|D7C419_STRBB Sensory histidine kinase in two-component regulatory system wtih KdpE, regulation of potassium translocation OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_09267 PE=4 SV=1 MARGRLRIHLGAAPGVGKTYAMLQEGQRLRSLGTEVVIGLVEPHGRRPTAALAEG LETIPRHTLVHRGVSFTEMDLDAVLARRPQVALVDELAHTNVPGSRNAKRWQDVE ELLEAGIDVVTTLNVQHLESLNDVVRQITGVTQHETLPDEVARRADQIELVDLLPET LRRRLVHGDVYPPDRIEAALTHYFRVGNLTALRELALLWLADRVEEGLQRYRAEH GITAPWETRERILVGLTGGPEGETLIRRAARITACTPGSELLALHVVPGDGLARGD PAALSGQRSLVESMGGSYHQMTGEDIPEALLQFAEAENITQVVLGASRRGRFSLL LHAGVGQRTIHDSGPIDVHIVTHEAAAGASAPRLPRPGHGGTGPVRYWSALVGA ALLLPLMTLVLTGLRTGVGLSGALVLYLLAVVLAGLVGGRLPALLTAVAAGLLTDYY FTPPLHSFKVERGVDVVGLVVFLAAAWLVGSAAGTAARHTYQAVRATSEARALS RMAAAMMRGEPLPTLLEQVRENFSLTAVSLLERGTDHGPEPRWYVVASTGVRPP ERPYDADVEAPIDDRLTLAARGRGLSGDDRRILTACAAQIGVAHTQGGLARRGAG TDLDEQGRPRAAALYLRPVDLDEALTAALDDLGPGGHSISLRLPERLPDVIADAALL ARVLATLVADALRHSPPDAPPTLTAEALPDRLTVRIAGDTTGGAVDGERESPSLRL ARDLTEAMGGTVEHTSGGGAASVTITLPTVAQHPDPEG	1~~KdpD (1.63608E-118) ~~211,233~~Usp (1.06926E-26) ~~355,419~~DUF4118 (0.00365339) ~~474,X,664~~HATPase_c (0.000149664) ~~747	dysfunctional kinase	KdpD;Usp;DUF4118;X;HATPase_c

	1.5E-93	321.4	1.2	1.5E-93	321.4	0.8	1.4	1	B1XRS4_SYNP2	Potassium-dependent ATPase subunit D sensor protein, His kinase domain	kdpD SYNPCC7002_G0054	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR6) (Agmenellum quadruplicatum)	368	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	32049	>tr|B1XRS4|B1XRS4_SYNP2 Potassium-dependent ATPase subunit D sensor protein, His kinase domain OS=Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) GN=kdpD PE=4 SV=1 MYNPTAIAATNYQILPRRGKHKIFIGMAPGVGKTYRMLEEGHALKQDGVDVAIGLL EAHGREETTLKAEGLELIPRKQVYCRNVLLQEMDTEEILRRSPQLVLIDELAHTNIP GSKQEKRYQDVEKILNAGIDVYSTVNIQHLESLNDLVYRISGVVVRERIPDRIIDDAD EIVVVDVTPETLQERLQEGKIYAPEKIDQALQNFFRRSNLIALRELALREIADNIEEE SISETKNLHYNIRERVLVCISTYPNSIQLLRRGARIANHMNGQLFVLFVAPAGKFLS KSEALHIETCKRLCQEFTGEFLRIESPNIVTTIVKIATQERITQIVLGETRRSRFQLLF KGSIVQQLMRALPQVDIHIIANN	16~~KdpD (3.85165E-128) ~~226,244~~Usp (6.99861E-42) ~~366	non-kinase	KdpD;Usp
	1.6E-93	321.3	0.1	1.1E-92	318.7	0	2.3	1	E5ASX3_BURRH	Histidine kinase (EC 2.7.13.3)	RBRH_02494	Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454)	938	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia rhizoxinica, Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454)	882378	>tr|E5ASX3|E5ASX3_BURRH Histidine kinase OS=Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454) GN=RBRH_02494 PE=4 SV=1 MERPDPDELLDKLQREEEKKQRGKLKIFFGASAGVGKTFAMLQAARRCRDEGVD VVVGVAETHGRRETLALLDGLPSIPAARYPYRGKVLPEFDLNAALARRPQLILVDEL AHSNVPGARHLKRWQDVQELLDAGIDVYTTLNVQHLESLNDVIGQITGIRVWETIP DRIFDLADEVTLVDLPADELLARLRDGKVYLPQQAEHAVRHFFRKGNLIALRELALR RTADRVDAQMREYRADQSIERVWHARERIIACVGPGSESATLVRAAARLAASLKA DWLAVYVETPTLQRLPDTVRKRTLDALKLAAELGAETVTLDGPDAARTLLAYARM RNVSRLVAGVPRTRRWLAPSVGERLLQSASDIDVTLVGAGRAHQRRGARGDVRS FASLLGDERRSKLRYYAYAAAISAGITVVATELLHRIDLANLAMLYLLGVIFAAARLG RGPGVLISFLSVASFDFFFVPPRISLSVSDTQYLLTFAVMLLTSLTISHLTSSLRRQA RIATLRERRTSAMYAMTRELGAALATDQIIEIGMRHVAEVFQARVAILLPDSHDKVR QKVEEPDPAIMLQPPALDTDIAQWVYDQQKPAGQSTDTLPAADALYLPLKAPMRT RGVLALVVSRFEDLAVPEQRRMIDTFAAQIALALERVHYVEIAQDALVSMESERLR NSLLSAISHDLRTPLTAIVGFASMLAEQQSGGAPPRPQAERDLIEAIHEEALRMTRL VTNLLDMARLQAGAVRLNRQWLMLEEMVGAALAACRRSLAAHPVHTRVPAELPL LRLDPVLMEHLFANLFENAAKYTPTGAPLSIDAGVVEDGARRYVKVAIEDSGPGLP PGMQARVFDKFTRGEKESAKPGIGLGLAICRAIVDAHGGRIGAENRVDVQGRVLG ARFWFMLPADEVPPGSGEVLDEAQEQDADAARSGHVVSEITPKS	20~~KdpD (1.44534E-107) ~~230,252~~Usp (3.74418E-28) ~~372,413~~DUF4118 (1.04157E-18) ~~503,530~~GAF (8.59139E-18) ~~652,669~~HisKA (3.27942E-14) ~~738,791~~HATPase_c (9.43875E-23) ~~901	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.7E-93	321.2	0.1	2.6E-93	320.6	0	1.3	1	A0A089PQV0_PLUGE	Histidine kinase (EC 2.7.13.3)	LG71_21445	Pluralibacter gergoviae (Enterobacter gergoviae)	893	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pluralibacter, Pluralibacter gergoviae (Enterobacter gergoviae)	61647	>tr|A0A089PQV0|A0A089PQV0_PLUGE Histidine kinase OS=Pluralibacter gergoviae GN=LG71_21445 PE=4 SV=1 MTDDPLRPDPDRLLADAGRRHRGKLKVFFGACAGVGKTYAMLSEAQRLRAQGLD IVVGVVETHGRRETAALLDGLATLPPRRQHHRGRKVTEFALDAALARRPALILMDE LAHTNAAGSRHPKRWQDVEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIRVRET VPDPFFDAADDVVLVDLPADDLRQRLREGKVYIGGQAERAIEHFFRKGNLIALREL ALRRTADRVDSQMRDWRDRQGEEKVWHTRDAILLCVGHGGGSEKLVRTAARLA AKLGSAWHAVYVETPDLHRLPEHQRRSILAALRLAQELGAETATLADPQEDRAILR YAREHNLGKIIIGRRPQRGWRRASFADRLARLGPDLDLVIVALEERPPYPGRSSDM RPWHDRWRAQLRGCGVALALCALITLVASQFLTAFDAANLVMLYLLGVVIVALRY GRWPSVLATVVNVVSFDLFFIAPRGTLAVSDVQYVLTFGVMLTVGLTIGNLTAGVR YQARVARYREQRTRHLYEMSKALARGRSARDIAATSEAFIQSTFHARSLLLLPDGE DRLAPLTEGAAVAGWDEAIARWSFDKGQPAGAGTDTLPGVPWLSLPLKTAEKIH GVLIVEPGNRRQLMIPEQQRLLETCTLLVASALERLALTSSEEQARLASERESVRN ALLAALSHDLRTPLTVLFGQAEILTLDLAAAGSPHAAQASEIRQHVLNTARLVNNLL DMARIQSGGFNLRKEWLTLEEVVGSAIRTLEPGLGGRHIALSLGDPLTLIHVDGPL FERVLINLLENAVKYAGPDAQLGIRAAGQPEQLRIEVWDSGPGIPAGQEQAIFAKF ARGHKESAIPGVGLGLAICQAIVEVHGGTLSAHNRPAGGASFVVTLPPETPPALDD FTEDA	21~~KdpD (1.01702E-123) ~~230,253~~Usp (9.52751E-39) ~~372,402~~DUF4118 (9.50497E-19) ~~499,527~~GAF (0.000000000000154695) ~~642,659~~HisKA (0.00000000621311) ~~724,777~~HATPase_c (1.00729E-28) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2E-93	321	0.5	2E-93	321	0.4	1.5	1	B9JKR0_AGRRK	Histidine kinase (EC 2.7.13.3)	kdpDArad_9466	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	903	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Rhizobium radiobacter (Agrobacterium tumefaciens) (Agrobacterium radiobacter), Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	311403	>tr|B9JKR0|B9JKR0_AGRRK Histidine kinase OS=Agrobacterium radiobacter (strain K84 / ATCC BAA-868) GN=kdpD PE=4 SV=1 MPDDSRDTLNRPSPDALLEKARQETRGRLKIFLGAAPGVGKTYEMLLSGKAKIAD GVDVVVGVVETHGRRETQALLEGYEIIPRVNVDYKGRALDEMDLDAILNRRPGLVL VDELAHSNAHGSRHPKRYLDVKELLDRGIDVYTTLNIQHVESLNDVVSQITRVRVR ETVPDSIIDLADDVEIIDLTPDDLIKRLHDGKVYVSRTAERALTNYFTPGNLTALREL ALRRTAQRVDDQLLTHMQAHAIPGPWAAGERVLVSIDHHPRSASLVRYAARMAS RLRAPWAAVYVETNRAISLTEAQRDTIAATLRLAEQLGGEAITIPGREVAEELLRHS ASNNVTHIVIGSPKVGTWRDWSRASVSYELIRKAGDISVHVISGSDAEASPASRGV KSAPAPTPFQLRGYILATLYVAVALGVCVILDQVLDVRNLALVFLMAVLATAVTQGL RPALYSCLLGALAFNFFFLPPRYTLTISDPESVLAFFFFLGVAIIASNLTATVQRQAA SARQRARTTEDLYLFSKKLAGTGTLDDVLWATAFQLASMLKVRVVLLLPEDGTIAV KAGYPPDDTLDDADIAAARWAWEHNHAAGRGADTLPGAKRLYVPLRTGRTAVGV IGLDSDRRDGPLLTPEQQRLLDALADQAALAIERVQLVADVDRAKLAVEADRLRSA LLTSISHDLKTPLAAILGAAGTLRDYLETMSHEDRVDLLSTVVDESERLNRFIANLLD MTKIESGAMEPNYALHYGGDIVGSALRRGAKILARHRVETQMPADLPMVKVDPVL FEQVLFNLLDNAAKYAPEESTIRLEAWADVDNVVFRIMDEGPGIPPADLERVFDTF YRVRKGDQVRAGTGLGLSICRGFIEAMAGTITAGNRTDRQGAVFTIRLPKPTDLPK LDELK	~~734,787~~HATPase_c (2.03949E-29) ~~890	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.1E-93	320.9	0.7	4.9E-93	319.8	0.1	1.8	1	R6SSY4_9CLOT	Universal stress family protein	BN719_02215	Clostridium sp. CAG:58	666	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	1262824	>tr|R6SSY4|R6SSY4_9CLOT Universal stress family protein OS=Clostridium sp. CAG:58 GN=BN719_02215 PE=4 SV=1 MEEMRPDSEQLLKRIQYEEKREQEKNRGKMKVFLGYAAGTGKTYAMLEAAHEAE KSGIDVVAGYIEPHNRPDTEALREGLEEIPPLMVDYKGIQLREFDLDAALKRRPQLL LVDELAHTNVRGCRNEKRYQDVMELLQAGISVYSTVNIQHLESLNDLVGSITGIQV RERIPDYVFDQADQVEVIDIEPDDLIRRMKEGKIYGESQAERALSNFFRREKLVALR EIALRRTADRVSRMAEEERSLSDNQDYHTGEHILVCITAAPSSAKVIRTAARLADAF RGRLTGLVVETAKIREADEKTKAALRENMEIAKVLGARVVTVCGSDVASQIAQYAR ISNVSKIVLGRTNHLTIRPMYRSELLEKLTYLAPNIDVYIIPDMRQTKRYHPSQMEKR KKGDWRKTVLDLSLITAVMAAAAFLSLAFLKLGLSGTDQIILYLLGVLISSYIADRKIY SLYSALLSVVLYNFFCIEPLYSLKAYDRGDSVTFILLFFSGFFAAAMTRKLKQQNVE SAKIAYRTGLLLENSQRLRRCRREKEVWALTAAQAGKLLNLSVLIYPVDKKGRLGT AMVFPRPGMSEEEFSVCLSTREKGVAQWTAANGHRAGASTHTLPDSLALYLPIQ DEDQVKGVMGIYLEERRPIAEFEYNLLTAMLSEAAVKLKDTFPQE	25~~KdpD (8.78841E-124) ~~235,256~~Usp (5.83135E-32) ~~379,437~~DUF4118 (0.000000022686) ~~508,537~~GAF (0.0000032983) ~~659	non-kinase	KdpD;Usp;DUF4118;GAF

	2.4E-93	320.8	1.1	3.7E-93	320.2	0.8	1.3	1	A0A075K9I1_9FIRM	Histidine kinase (EC 2.7.13.3)	UFO1_0782	Pelosinus sp. UFO1	895	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Pelosinus, Pelosinus sp. UFO1	484770	>tr|A0A075K9I1|A0A075K9I1_9FIRM Histidine kinase OS=Pelosinus sp. UFO1 GN=UFO1_0782 PE=4 SV=1 MPEESKEKKRPDPDVLLTKLNKENRGKLTVFLGAAAGVGKTYTMLEIAHEMLASG VDVVIGWVETHKRVETEKMVEGLPRLPAREIEHRGRTLHEMDIDAILARKPKVVLV DELAHTNVAGSRHVRRFQDVEEILNAGIDVSTTLNIQHIESLNDIVAQITGVTVRETV PDSIVEQADQVQLIDIPPNELIKRLKEGKIYMPHQAELALNKFFRPGNINALRELSLR FTAYRVDKELNEYMQEHDIPGPWPAGERVMVCVSSSPFSAQLIRAARRLARGLQ AELLAVHIDTPRRLELSEKERDRIFRNMRLAEELGAKTISVVGKDLTEEILSMTREY NVTHLVVGKPLRGRIWEWLNGGAVVNKLIRYSGGVNIHVIQGNTEVKDEPKFKTL ATKATIPLWNYMAGVLMIFLITAGNWLWREYIESIHMMLYLVPVLLSAVWWGKGP SYVVALASVLLFDFFFIPPFFSFSVADLRYLWSLPLFLLVSFTIGGQTEKLRLEAMLA RQREKTTRALYSFSREIAAVVEVNAIVGILVEQAWQTLERPVAVFLPQDNGTLLLA AEAGTKKSGIDTSEQAVAIWAYEHSEIAGRCTETLPGARYMYLPLTTSDNTVGVL GIRIQEKMLTPVQRRLMEAWAGLAAIAVERVNLADQARRAALLVESDQLRTALFNS ISHELRTPLASIIGAVSGLLDVEGIYSGEDRKELLETVKEGANRMDRLVANLLDTAR LESGMMQLKIDWCDIEDITGIALRRVEESLNDRALLVRIPADLPLVKADCVLVELVL VNLLDNACKYSAPGSEIVITASQDEKVVRVSVADRGPGIPSEYLTRVFDKFYRVEQ PKSVSGTGLGLSICKGIIEAHGGTIHAENRPGGGTVMTFALPCDEQPPSNMV	23~~KdpD (9.1558E-119) ~~233,255~~Usp (9.99609E-42) ~~378,403~~DUF4118 (0.000134662) ~~493,528~~GAF (0.000000000000454555) ~~647,664~~HisKA (6.47151E-14) ~~730,792~~HATPase_c (1.61176E-27) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.4E-93	320.8	1.7	4E-93	320	1.2	1.4	1	K9UF76_9CHRO	Osmosensitive K+ channel His kinase sensor	Cha6605_2200	Chamaesiphon minutus PCC 6605	365	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Chamaesiphon, Chamaesiphon minutus, Chamaesiphon minutus PCC 6605	1173020	>tr|K9UF76|K9UF76_9CHRO Osmosensitive K+ channel His kinase sensor OS=Chamaesiphon minutus PCC 6605 GN=Cha6605_2200 PE=4 SV=1 MQTYRRGKHKIFIGMSPGVGKTYRMLEEGHRLRAEGIDVVIGLLETHNRAETIAKAI GLEQVPRQQITWQDVTLSEMDVPAILRRQPQLVLIDELAHTNIPGSDREKRYQDV EQILQAGIDVYSTVNIQHIESLNDTVAQLTGIVVRERIPDRVLEAADEVVVVDVTPET LQERLRDGKIYAPDKIDRSLNNFFQRRNLAALRELALREVADNIEEGTEQANGDAL VTASCNIHERVLVCISTYSNTIQLLRRGARVANYMHARFYVLFVNEPDRFLTKAESL HIATCERLCQEFGGEFLQVRAYKVLEAIVQTAQQYRITQIVMGESQKSRWQIFWK GSLTQQILRLLKNVDIHIISTSKSTTQ	5~~KdpD (4.61773E-120) ~~214,236~~Usp (1.65374E-43) ~~358	non-kinase	KdpD;Usp

	2.4E-93	320.8	4.1	3.2E-93	320.4	2.8	1.1	1	K8GCX6_9CYAN	Osmosensitive K+ channel His kinase sensor	OsccyDRAFT_4627	Oscillatoriales cyanobacterium JSC-12	377	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, unclassified Oscillatoriales, Oscillatoriales cyanobacterium JSC-12	864702	>tr|K8GCX6|K8GCX6_9CYAN Osmosensitive K+ channel His kinase sensor OS=Oscillatoriales cyanobacterium JSC-12 GN=OsccyDRAFT_4627 PE=4 SV=1 MAKPPLTSPVNTYHPVRRGKHKIFIGMAPGVGKTFKMLEEGHQLKQDGVDVVIGL LETHGRKETAEKAEGLEIVPRQQIEHNGIILTEMDTNAVLLRQPQLALVDELAHTNV PGSQREKRYQDVEVLLAAGIDVFSTVNIQHLESLNDLVARITGVVVRERIPDRLLEE ADEVVVVDVTPETLEERLREGKIYSMAKVEQALQNFFQRRNLIALRELALREVADN IEEEVLAEDINNTHSNAPYCNIHERVLVCVSTYPNAVQLIRRGARIAGYMHAPFYCL FVDDPDRFLTKPESLHIETCERLCKEFGGKFIRVTGNDKAKAIADVAKTYRVTQIVI GESQHSRWKLMLRGSLTHKLLRLLKNIDVHIISTDKTH	17~~KdpD (9.1245E-120) ~~226,250~~Usp (3.49737E-49) ~~372	non-kinase	KdpD;Usp
	2.5E-93	320.7	0.7	1.2E-92	318.5	0.2	2.1	1	B8GSR2_THISH	Histidine kinase (EC 2.7.13.3)	Tgr7_1885	Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	913	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Thioalkalivibrio, Thioalkalivibrio sulfidiphilus, Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	396588	>tr|B8GSR2|B8GSR2_THISH Histidine kinase OS=Thioalkalivibrio sulfidiphilus (strain HL-EbGR7) GN=Tgr7_1885 PE=4 SV=1 MGTEHTGQADALLGEIKRQTAGRLTVFLGAAPGVGKTYAMLARARELHRQGVDV VIGIVETHGRSETQTMVEGLPLLPRKKVEYQGRQLEEMDLDGLLGRKPAIALVDEL AHRNAPGSRHERRWQDVEELLNAGIDVYTTVNIQHLESLNDVVHQITGIRVSETVP DAVFERLRDIRLVDLPARELIERLNDGKVYLPEQAAQALQAFFSPSNLTALRELAM QTVADHVDADLRETRAARGLEGISIQRHVLIAIDGRGQSEYLVRAGARIAERRGAP WSVVTVETGRSADAALHTDDLYRTAPTRNMVARAEQQRLIEIDKAFALARNLGGE TEVLHNTDVTQALLDAAEARGARSIVIGRTRERPIVRIFNRTLTQQLLQRGARYELT IVSTPQARQRAMELQGLASGRLTGREVVLILLASVGAVGAAALAERTLGLQDLSLIF LVAVMLVASRTRMLSAVITAGLCFVAYNFFFIEPRYTFLISAHRGVATVLLFLAAALI AGRLASQLRMQVVALRAANTHATAMQNLGRHLAKAADLGQVIASGSSVLQSTLH AEAWIRINGEAGPTTAANHLTEKDLMAADWTQQHGQASGHYTDTLTHSSWLFLP VHSDKNTLGVAGLRFPSGMGRLSFEQRRLAESMVEDIGQAAQRTRLVSELEEAR VTGETERLRSALLSSVSHDLRSPLSSMIGAADSLARYAKDMGPEDQKSLLETIHVE GERLDRYIQNLLDMTRLGQQGLTLTRDWIGIDELVGSASRRLQRYEPDVRIEHDIP PDLPPIHVHPALIEQALFNVMENAAKFSPPGVPIRVQIRRTEDDQLRIDISDRGPGIP EDERRRIFDMFYSVERGDRGKQGTGLGLTIVQGIVGAHMGSVQALPGPEGKGTTI RLTLPWGGYANQEAKEHDGTS	22~~KdpD (2.60486E-120) ~~229,250~~Usp (2.21692E-28) ~~393,445~~DUF4118 (0.000141531) ~~488,X,673~~HisKA (0.00000000000171838) ~~739,792~~HATPase_c (7.54832E-23) ~~896	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2.5E-93	320.7	0	4.7E-93	319.8	0	1.4	1	A0A068QT51_9ENTR	Sensor protein kdpD (EC 2.7.13.3)	kdpD_XDD1_1326	Xenorhabdus doucetiae	738	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus doucetiae	351671	>tr|A0A068QT51|A0A068QT51_9ENTR Sensor protein kdpD OS=Xenorhabdus doucetiae GN=kdpD PE=4 SV=1 MAQNEPQRPDPDDLLTLANKKPRGKLKIFFGACAGVGKTYAMLQEAQRLLAQGL DVIVGVVETHERQETAALLQGLPQLPPKYFHYHERRIAAFDIDAALARHPAIILMDE LAFSNPKGCRHPKRWQDVEELLEAGIDVLTTINVQHLESLNDVVGGITGIRVRETIP DHIFDQADDVVLVDLPPDDLRQRLNDGKVYISGQAERAIEHFFRKGNLIALRELALR RTADRVDDQMRAFRDTQGREPVWHTRENLLLCIGYNAGNEKLIRKAARLAAKLDC VWHAVYVETPKLHRLPKNKRRTILQALKLAQDLGAETATLSDSHEEKAILRYAREH NLGKILIGRYYNSHTNFFGFKWHRDFSERLGKLGPDLDLIIVALEDKKRGDKEPKD NRTFNDKWRISIQGFLMAIVLCALITLFSRTFLLTLDQANLVAIYLLGVVIIALFYGRW PSVFAAFVNVISFDIFFVQPHWSLEVKNMQYLLTLTVMLIVGAVVGNLTAGIRYQA RVARYREQRTRHLYEITRELSKALNEEDVARISYHFLSNSFQAKTGLLLPDSNHHL HQVRSHNGGQMQIDNAIAKWCFEKKQPAGAGTDTLPGVPYQLLPIANPSQVFAV LAIESPNQHQLLVPEQQRLLQIFTGLIANALERLYLARSAESAKLEIEREQLRNSLLA ALSHDLLTPLTVLFGQTEMLMLDLSAENSPHTQQVNQIRQQILSTSRQVNNLLDMV PKEIPKQ	>~~KdpD (1.99942E-121) ~~231,254~~Usp (1.00105E-36) ~~379,410~~DUF4118 (1.03154E-20) ~~506,532~~GAF (2.33522E-15) ~~650,667~~HisKA (0.0000000189343) ~~730	dysfunctional kinase	KdpD;Usp;DUF4118;GAF;HisKA

	2.7E-93	320.6	0	4.3E-93	319.9	0	1.3	1	J7SKK9_MORMO	Histidine kinase (EC 2.7.13.3)	MU9_3392	Morganella morganii subsp. morganii KT	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Morganella, Morganella morganii (Proteus morganii), Morganella morganii subsp. morganii, Morganella morganii subsp. morganii KT	1124991	>tr|J7SKK9|J7SKK9_MORMO Histidine kinase OS=Morganella morganii subsp. morganii KT GN=MU9_3392 PE=4 SV=1 MYDEPLRPDPDQLLAQVTERPRGKLKIFFGACAGVGKTYAMLKEAQRLREQGIDV LAGVVETHGRSETAALLEGLRILPLKKHNYRGRQVAGFDLDRALAIHPAVILMDELA HTNIPGARHPKRWQDVEELLNAGIDVLTTINVQHLESLNDIVGGVTGVRVRETVPD PVFDAADEIVLVDLTPDDLLDRLREGKVYLPAQAERAIEHFFRKGNLLALRELALRR TTDRVDEQMRAWRERKGQEKVWHTRDAILVCLRPDGGNEKLVRAAARLAARLG SDWHAIFVETPARHKLPSPQRRTILTTLSLAQQLGATTATLAEPEESRAVIRYARE NNLGKIMIVRHERTSWWRRDKLQEQLSRSAADLDVVMIAPQDRQPENREKFSDN RPFLDKHKTDLQGCVVAALICAVTTLMAHHWLMAFDNANLVMLYILGVVVVARFY GRWPSVFATIINVISFDIFLINPKGTLAVSDMQYLLTFAVMMTVGLVIGSLTAGVRY QARVARYREQRTWHLYEMSKALAVARESDDIASVSCHFISHSLHARCEMLLPDEQ GNLIPAGGGVADNGRDDAIIRWSYDKGQPAGFGTGTLPGVPYQILPVCTTEKVYG VVIVEPYNRRQLLIPEQQRLLETLILLAAGALERRTLTEREAQSRLVSEREQVRNSL LAALSHDLRTPLTVLFGQAEILTLDLTSEGSPYAAQANEIRQHILSTTRLVNNLLDM ARIQSGGFNLNKEWLPLEEVIGSALQMLKPRFDTDSVQIDLNDPMQLICADGPLFE RVLINLLENAIKYAGPQAQIGIRSRLSDNMIDIEVWDNGPGIPAGQEAQIFEKFSRG QKESAIPGIGLGLAICRAIAEVHGGTILAGNRDGGGASFHIRLPCEDPPVIDEDDNP L	22~~KdpD (5.01135E-113) ~~214,253~~Usp (1.3453E-21) ~~373,403~~DUF4118 (2.32937E-18) ~~501,529~~GAF (0.00000000000456522) ~~644,661~~HisKA (0.000000000248982) ~~726,779~~HATPase_c (3.82244E-30) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.9E-93	320.5	0.1	4.7E-93	319.8	0.1	1.4	1	D5SYH6_PLAL2	Histidine kinase (EC 2.7.13.3)	Plim_1874	Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	895	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Planctopirus, Planctopirus limnophila (Planctomyces limnophilus), Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	521674	>tr|D5SYH6|D5SYH6_PLAL2 Histidine kinase OS=Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) GN=Plim_1874 PE=4 SV=1 MPDARPNPDDLLAKVQAEDTESTRGSLKVFFGYAAGVGKTYTMLENAQRAKAAG REVVVGYVEPHGRPETEALLAGLEVLPLREFEYRGVRLRDFDVDAALARNPDLLL VDELAHTNAVGCRHEKRWQDVEELLEAGINVWTTLNVQHIESLNDVIGQITGVTV RETVPDRAFDLADDLELVDITPEELLHRLKAGKVYVPDQAQRAIQSFFQKSNLTAL RELSLRQAARRIHTDVESARREKAAIQPWATAERLLVCVGPSPTTARVIRTARRMA AALDAPWLAVSVDLTGEPASSPRKQQVSQHFRLAERLGAETVTLAGQNVSETILD YARSRNVTKILIGKTNQPRWRRLLAGTVVDDLLEKSGDIDVYVIRGEEEKTAHAPA RTASTTQKLPYFWAVGLVSLTGLLAYGLRFLHLADAEANTVMLFLAAVAWTAFRY GRGPAVFASVLAVLVFDFFFVAPFHTFAVADTQYVVTFAVMLTIGLVISTLTSRLRA QIENTRLRERRTSSLYELGKQLSSLYGNVFLVGAAGGKVAEMVGGEVAIYLRQPS GPPELAFGHDTTIVKHSVSLPVAQWVIEHDQLAGAGTNTLPNAAALFFPLTGSQG THGAIAIRVPDTERLLDPEFRRLLDACANQLALALERDQLAIEAANARIQAEAEQVR SSLLSSVSHDLKTPLAAIAGASSSLLEATSLDEETRRQLLETVADEAARLNRLLENIL QMSKLDAGAAVPLCQWHVLEELVGSALHRTRRELAQHDVAVQLSSELPLLYVDG LLMEQVFVNLFENAARYTPEGTKVTIRAALDGDHVRIGISDNGPGLPAGAEERIFD KFYRASPTADGGRGSGLGLAICRAIIKAHGGTLVAANRPGGGAEFVIRLPVSKDAP QVMVE	24~~KdpD (5.9295E-119) ~~232,254~~Usp (8.54151E-42) ~~375,397~~DUF4118 (2.00072E-20) ~~500,530~~GAF (0.00000000029285) ~~646,675~~HisKA (0.000000000153179) ~~728,781~~HATPase_c (1.21722E-31) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.2E-93	320.3	2	4.1E-93	320	0.2	2	1	C6WWQ9_METML	Histidine kinase (EC 2.7.13.3)	Mmol_1452	Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540)	914	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylotenera, Methylotenera mobilis, Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540)	583345	>tr|C6WWQ9|C6WWQ9_METML Histidine kinase OS=Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540) GN=Mmol_1452 PE=4 SV=1 MNDDRPNPDLLLEKINKDAEKEKRGRLKIFFGACAGVGKTFAMLSTARTLRQEGL DVVVGIVETHGRIGTQSQLANLEVLPLKKLIYRERELTEFDLDAALARKPDLILVDEL AHSNVEGSRHPKRWQDVEELLIAGVDVYTTLNVQHIESLNDVVGQITGIRVSETIP DKVFDIADEVTLVDLPADELLQRLQDGKVYQPQQAKRAGKSFFRKGNLIALREMA LRRTADRVDSQMREYRTNSSISQVWQAKDRLLVCVGPDSESERLVRVAARLAQS LKSDWLAVYVETPKLQRISDKQRNLILKTLKLAETLGAETATLSGTKVAETVLSYAR SRNVTKLVVGKSTRTTLERLILPGVVDDLTNHATDIDLHVVSRERTLAERLATNHDN TDNLERASGDKSYAGYYIAAIVCAITAILSAQLLDYFELANVVMLYLLGVILISSKYGR GPGIFSSFISVATFDFFFVPPKLSFSVSDTQYLLIFAVMLVVALVISNLTANLRYQAM VAMNREKRSRALYDLGKSLASALTAAHIIEISIPHLSGIFKAKVAILLPDSQEKIVNTS LHKISNAKPDLNSNFDVDLAVAQWVYDHQQQAGFGTDTLPSAPALYIPLQAPMRT RGVLVILPDTNLSKGNRTIFLPEQRQLLDTFSSQIAIAIERVHYVEVAQEALISMESE RLRNSVLSAISHDLNTPLTTIIAAAGWLKQETEINDKRYEYVSMLNEQSIRMKNLVV NLLDMARLQSGKVKLNKQWQLLEEVVGTSLRTMSEVVSKHTIVIDMPHDLPLIEFD AVLIDRVLCNLLDNASKYSPAGNRIFISARTQQNDVWISVADEGSGLPENLENQLF EKFTRGEKESSKAGVGLGLSICKAIIEAHDGKIWANNKPPHGAIFTFSLPLGTPPSL PPDDDLV	22~~KdpD (7.00768E-121) ~~232,254~~Usp (2.76401E-44) ~~377,409~~DUF4118 (4.62241E-22) ~~507,537~~GAF (3.48397E-19) ~~664,681~~HisKA (0.0000000000116551) ~~745,798~~HATPase_c (6.86056E-29) ~~899	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.4E-93	320.3	0	6E-93	319.5	0	1.4	1	D8IRC8_HERSS	Histidine kinase (EC 2.7.13.3)	kdpD Hsero_3776	Herbaspirillum seropedicae (strain SmR1)	939	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herbaspirillum, Herbaspirillum seropedicae, Herbaspirillum seropedicae (strain SmR1)	757424	>tr|D8IRC8|D8IRC8_HERSS Histidine kinase OS=Herbaspirillum seropedicae (strain SmR1) GN=kdpD PE=4 SV=1 MLRLGSTGLLPLQCSNPDNPDMTTRPDPDDLLERVMRDEERQARGRLKIFFGFSA GVGKTFAMLEAAQALAAQGGDVVAGVVETHGRAETEAQLAGLARLPMRMVAYR DRQLPEFDLDAALERKPGVILVDELAHSNVPGSRHAKRWQDIDELLRAGIDVYTTL NVQHIESLNDVVGQITGIRVFETVPDHVFDEADDVMLVDIPPDELLARLQQGKVYL PQQAEKAGRNFFRKGNLIALREIALRRTADRVDADMRQYRADRSIAQLWQARECI VVAIGSGSGEERLIREAARLAAKLQAQWLAVHVDLPGQRQAMEARERVVSYLKLA HSLGAETASISGEELAAALLQFARSRNAGKLVIGQEEGGLRRLLRWPRGTLAQRIA RSGGEIDLYTIARSRTRHQHEPASPDSAASAAEALLTRRRRTRGTLWAVASCAITT TLAFLLDGKLHPANVIMLYLVGVMLVAMRYGRAASALVSVLSVLSFDFFFVDPRFSI TVSDAQYLLTLAVMLAVSLFISSLAARLRRQASVAMQREARAANLYMLGKELSALL TLDQILEIGRRHLAAVFGARIAFFLPDSADQLRLAEPEQDSGAAHVFRNVDAGVAQ WVYDNGQAAGKGTATLPSAAALYLPLTATMRTRGVLAFAIEAPSEEERQLAAAQL ALPENRQMLEIFCSQIAMAIERLHYAEVAQDALVTMESERLRNSLLSAISHDLRTPL TSLVGSADVLAANARLDDDARAMARTISEQSQKMVGLMNNLLDMARLQAGVVTL NRQWNALEELAGSALRLLAKALEGRQVDTRIAPELPLLRVDAVLLERVLANLVENAI KYSPPGTPIGISAHVEHGDGAPQVKVCVMDQGRGFPPTMTQHAFEKFTRGDNES ATPGVGLGLAICRAIIEAHQGRIWIAPQEAGQGATVCFTLPVETQPAPPEE	43~~KdpD (1.65755E-111) ~~252,275~~Usp (8.21562E-28) ~~398,433~~DUF4118 (1.48669E-19) ~~530,556~~GAF (3.19239E-16) ~~688,705~~HisKA (0.0000000000013677) ~~769,822~~HATPase_c (1.34905E-27) ~~928	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.4E-93	320.3	0.3	5.4E-93	319.6	0.2	1.3	1	R5WPC9_9FIRM	Uncharacterized protein	BN568_01735	Blautia sp. CAG:257	666	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	1262756	>tr|R5WPC9|R5WPC9_9FIRM Uncharacterized protein OS=Blautia sp. CAG:257 GN=BN568_01735 PE=4 SV=1 MEDTRPDSEYLLKKLQYEEEQKLKKNKGKLKIFLGYAAGSGKTYTMLEAAHEAKK HNTDVVAGYIEPHDRPDTRRQAEGLETIPPLVVEYKGVKLREFDLDRALERKPQLI LVDELAHTNAPGCRNEKRYQDVKELLRAGIDVYTTINIQHLESLNDLVGSITHIEVR ERIPDSVFDHADQVEVIDIEPEDLLARMKEGKIYKPVQAERAMNNFFKREKLAALR EITLRRTADRVNRIAEEERNITGDMDYHTGEHILACISAAESSAKVIRSAARLAYAFR GQFTGLYVETPAMQEADEKTKQGVRRNMELARALGAKIVTVYGSDIGSQVAEYA MVSNVSKVVLGRTNHRFFMRKPMAEVLEKLNSMAPNIDVYIIPDMKNRKAAGKYG HREGRRKAENAGMQALWEFGLINIILVLTTIAAWILQKFHLPESNIIMVYILGVLLSS YISDKKIYAVYSSLFSVLAFNFLFTEPYFSLKAYDKGYPTTFAMLFIVGLFTASQTRK LKLQNKESVKKAYRTEILLENSQKLRRCKSEKEVWQQAAAQVEKLLDLSLVIYPVN KDGLLGEAMLFPRQGTEKASLEPLLTSQEKAVAKWVAANHHRAGACTHTLPTAR GMYLPVQDEEQVKGVVGIFLEERRQIQEFKYGLLIAMLNETGVKLKDRF	32~~KdpD (1.56142E-119) ~~235,256~~Usp (3.21524E-31) ~~379,415~~DUF4118 (7.52405E-15) ~~507,537~~GAF (0.00000373654) ~~662	non-kinase	KdpD;Usp;DUF4118;GAF

	3.5E-93	320.2	0.2	6.3E-93	319.4	0.1	1.4	1	Q6ABI9_PROAC	Histidine kinase (EC 2.7.13.3)	PPA0118	Propionibacterium acnes (strain KPA171202 / DSM 16379)	830	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Propionibacterium, Propionibacterium acnes, Propionibacterium acnes (strain KPA171202 / DSM 16379)	267747	>tr|Q6ABI9|Q6ABI9_PROAC Histidine kinase OS=Propionibacterium acnes (strain KPA171202 / DSM 16379) GN=PPA0118 PE=4 SV=1 MAVRGRLRVLLGAAPGVGKTYAMLDEGKHLRAGGSDVVIAVVETHGRAATAAMT EGMEVIPRHYVECRGIELPEMDLDGVLAQHPDVALVDELAHTNAPGSRNEKRWQ DVEELLEAGIDVISTVNIQHIESLNDVVEQITGVPQRETVPDTVLRRASQVEVVDLA PQALRDRLSSGKVYPAERIDAALSNYFRLGNLTALRELALLWVADEVDHALADYRS EHGIDSRWEARERVVVALTGGREGETLLRRGARIAVRAGGGELLAVHVTTEDGLR SPHPGELARQRGLVDKLGGSFHQLVGDDIPETLIEFAKSVNATQLVIGASRRGKLS RLLTGHDVEADIIRASGAIDVHIVSHDAQAKALRLPRMGGSLSTRRRIAGFAVLAVL GPLLTLLLVSSRSPEALTTDVLAYELLAVVVALVGGAFSSLIAALASGFALDYFFTKP FYTVTVNEPLHLVALLLYLLTAALVSVVVDRAARKTRVARRAAAESGLLQSVAGLV LRGEDAVESLLSRATEAFGLSGARLMTDGKVVANWGTTSDQVTEHRIDDHTVVE FHGPEPDASERRLMSVIAAQLGTALEQHQLEETAKAVEPLAATDRVRTALLSAVG HDLRRPLAAATAAVSGLRSEWSKLSDQDRADLLETADEALSQLANLVTDLLDVSR LQSGVLGVSVMPVDPAEVIMPALDELSLGPADVEIDLGSDVPEMVADPALLQRVV VNLLSNALRYEPAGSRVRLAESSFANQVEIRVIDHGPGIPEDRRDDVMVPFQRLG DTDSSVGLGLGLALSKGFVEGMDGTLALEDTPGGGLTMVISLPRVGVEEASVQ	4~~KdpD (9.90711E-119) ~~212,234~~Usp (6.61465E-32) ~~357,X,601~~HisKA (0.00000000318754) ~~667,718~~HATPase_c (5.57946E-23) ~~819	kinase	KdpD;Usp;X;HisKA;HATPase_c
	3.5E-93	320.2	0.5	1E-92	318.7	0	1.9	1	B2U711_RALPJ	Histidine kinase (EC 2.7.13.3)	Rpic_3592	Ralstonia pickettii (strain 12J)	938	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia pickettii (Burkholderia pickettii), Ralstonia pickettii (strain 12J)	402626	>tr|B2U711|B2U711_RALPJ Histidine kinase OS=Ralstonia pickettii (strain 12J) GN=Rpic_3592 PE=4 SV=1 MPADQRPNPDQLLAELQSGQEQSARGKLRIYFGASAGVGKTYAMLAAAKAARAA GIDAVIGLVETHGRAETAALVADLEHLPTRQIEYKGRTLPEFDLDAALARKPALILVD ELAHSNVAGSRHPKRWQDIEDLLAAGIDVWTTVNVQHLDSLNEAVGSITGIRVWE TVPDAVFDAANEVILVDLPADELLRRLAEGKVYMPEQAQHAARNFFRKGNLIALRE LALRRTADRVDDDVQAYRRARRIENVWRTRETVVACLDPQGDGEQVIRSAARLA AQLECDWHAVAVVMPHLRAADARTERLHALLKLAQDAGAKVETLAGTNAVEAITG YIRRHNITKAVIGRPPEKRWRSARAIVVALRLAIGLERRLPSGDFAEALARHCPEVD VIRAAADPAHIQLTPRAAEVGRADVRSEAQRAADAQAGWLKPSYVAACVYVGVA TALSSLVRPVFDLANIVMLFLAAVVAVAMRHGRGPAALASVLSVALFDFFFVPPRF SFAVSDVQYLLTFGVMLAVGMLVGQLTAGLREQAEVAVQREAAAHALYEAAREL SAALTLDQIVSIGGRFVNATFGGRCAFFFVGLDGRLGAPQVAKPEGSTDAPSGMP NLDRVLADWTYQHGQPAGTGTHTLPSGSVLYLPLKAPMAIRGVLAVEPETFHVLA QPDNRRQIDACATLVAIAIERVHYVEVARDALVRIESERLRNSLLAAVSHDLRTPLT GLVGMAETLLRAQPPLPPLQAEAAAAIGQQAQRMRTMVTNLLDMARLQNQDVKL RLEWQSVEELVGAALQANPLPDHRVVVDHLAALPLIRCDGPLMERVLSNLLENAG KFAPAGTEVRISGEIVHDEARGNELRLRVRDHGPGVPAGSVQTIFEKFTRGEKES ATTGVGLGLAVCEAIVSAHHGRIWVEAPADGGACFVVALPAAEPPPVEDAEPIA	23~~KdpD (2.05216E-116) ~~233,256~~Usp (1.80811E-29) ~~390,433~~DUF4118 (2.70967E-23) ~~532,558~~GAF (0.00000000000009938) ~~684,701~~HisKA (0.000000000667415) ~~766,817~~HATPase_c (1.45984E-25) ~~923	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.6E-93	320.2	0	5.8E-93	319.5	0	1.3	1	R6ZQF8_9CLOT	Uncharacterized protein	BN593_00577	Clostridium sp. CAG:299	666	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:299	1262792	>tr|R6ZQF8|R6ZQF8_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:299 GN=BN593_00577 PE=4 SV=1 MQEERPDSEQLLKRLKYEEREQEKRTRGRLKIFLGYAAGSGKTYAMLEAAHEAKA HGIDVAAGYIEPHDRPDTQALTKGLEMLPPAFMEYKGMKLREFDLDGALKRKPQL LLVDELAHTNCRGCRNEKRYQDVKELLRAGISVYTTLNIQHLESLNDLVGSITHIDV RERIPDTVFDHADQVEVVDIEPEDLIERMKEGKIYRKEQADRALQNFFRRERLAAL REIALRRCADRVNRIAEEERSLLERQDYHTGEHILVCITAAPSSAKVIRTASRLADAF HGTLTGLCVETPDTQEAGEKTKEALRNNMELAKLLGAKIVTVFGSDVAAQIAQYAI VSNVSKIVLGRTNHFTMRPMYRSELLEKLTYMAPNIDIYIIPDMRQTKRWHPRQSA AKRQESWKKCAAGLAAATAVMLAATALALILRMFVFSEANTIMIYMMGVLLASCAA SRKLCALYSALLSVILFNFFFTEPLYSLKAYDQAYPITFLMLFLAGLFTATVTGKLKR QNMEISKTAYRTGILLENSQKLRRCKTREDVWRQAAVQAGKLLNLSILFYPVRKD GAVEEPLLFPRKGMDPEELKRCVNAQEKGVAQWTASNRRRAGACTHTLPDAMA MYLPVQDEEQIHAVMGIFLEERRPVAEFEYSLLTAMLNETGVKLKDFFIQS	27~~KdpD (4.41402E-124) ~~235,256~~Usp (1.60928E-33) ~~379,431~~DUF4118 (0.00000000000231714) ~~508,536~~GAF (0.0000253269) ~~657	non-kinase	KdpD;Usp;DUF4118;GAF

	3.7E-93	320.2	0.1	5.7E-93	319.5	0	1.3	1	Q7N6W8_PHOLL	Histidine kinase (EC 2.7.13.3)	kdpDplu1417	Photorhabdus luminescens subsp. laumondii (strain TT01)	897	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Photorhabdus, Photorhabdus luminescens (Xenorhabdus luminescens), Photorhabdus luminescens subsp. laumondii, Photorhabdus luminescens subsp. laumondii (strain TT01)	243265	>tr|Q7N6W8|Q7N6W8_PHOLL Histidine kinase OS=Photorhabdus luminescens subsp. laumondii (strain TT01) GN=kdpD PE=4 SV=1 MDQHEPQRPDPDELLTLVNEKQRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGL DVVIGVVETHERQGTAALLDGLPQLPLKQIYYRRRKISVFDLDAAIARHPAIILMDEL AFSNPHTNRHPKRWQDVEELLEAGIDVLTTINVQHLESLNDVVGDITGIRVRETIPD HIFDQANEIVLVDLPPDDLRQRLNEGKVYIPSQAERAIEHFFRKGNLIALRELALRRT ADRVDDQMRAFRDTQGHEPVWHTRDNLLLCIGNSSGNEKLIRTAARLAARLGCI WHAIYVETPKLYQLPEGKRRSILKALRLAHELGAETATLSDPNKEKAVLRYAREHN LGKILIGRRCTSKQKLFGWQWRSGFADRLGKLGPDLDLVIVALEERSHWDKEQD NRSVSEKWRVQIQGCLIAIALCTLITLFSRTFLLTLDKANLVTLYLLGVVVIALFYGRR PSIFAAFINVISFDIFFVQPHWSLAVTDMQYLLTFSVMLIVGVVVGNLTAGMRYQAR IARYREQRTRNLYEMTRELSRALNEEDIARTSYHFLTNGFQAKTGLFLPNDDGNLY QLTTNNGGHMLIDDAIAKWSFDKNLPAGAGTDTLPSVPYQLQPIATPSQTLAVLAI EPSYLRQLLIPEQQRLLQTFTGLIANALERLQLSRRAESAKLDTEREQLRNSLLAAL SHDLRTPLTVLFGQAEILMLDLSAEGSPHTKQVNQIRQQILSTSRLVNNLLDMARIQ SGGIQLNLEWQSLEEIVGSTLRSLEYALNRHPVAVSLPSDLLLHCDASLLERVFINL LENAIKYTDEQIPLGIKATTEKNQIHIEVWDAGKGIPPEQEQLIFDKFSRARKESAIP GVGLGLAICRAIIEIHQGKIWASNNEKGGASFHFVLPLEKPPEIITEEM	21~~KdpD (2.17693E-121) ~~231,254~~Usp (1.08358E-35) ~~379,407~~DUF4118 (7.96511E-22) ~~505,531~~GAF (3.2765E-15) ~~649,666~~HisKA (0.0000000000462128) ~~731,783~~HATPase_c (3.04986E-29) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.7E-93	320.1	0.1	6E-93	319.5	0.1	1.3	1	B0SY75_CAUSK	Histidine kinase (EC 2.7.13.3)	Caul_2695	Caulobacter sp. (strain K31)	897	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter sp. (strain K31)	366602	>tr|B0SY75|B0SY75_CAUSK Histidine kinase OS=Caulobacter sp. (strain K31) GN=Caul_2695 PE=4 SV=1 MAADDSRHAEKTRPDPEALLAAANRASRGRLKVFLGMAPGVGKTYEMLRAARRR KADGQDVLIGLVETHGRRETESLLRGMEVLPRKPIDHRGHVMMEFDLDTALARKP ALLLVDEYAHSNAPGSRHPKRWQDVEELLAAGIDVWTTLNVQHLESLVDVVQRIT GVRQRETVPDSALSRADAIELIDITPDELRERLTEGKVYVPETARLASENFFKVENL TALRELALRRAAQTVDDQLVAAMREKGVEGPWAAGERILVLVGGDAMASGLVRA GRRLSDMMMDAPWTVTHVDRLDQPVGGPAAAARLRDALKLAEQLGGTTVVLSG ADIVATVMAYARRNNVTQIVIGKSADSRWRELLGRSLAAALLREARGAAIHVVTEA THEPIVEPPRRRPAVGWTAYLISAACVAVATVAAWGLDVAFDRVDLGMIFLAAVLA AGVLRGLRPALAAATVAFLVYNYLFLDPRHSFAIGSPTDFLTLVVFWAVALAAGGL AGRVRDQGRDARRRASAVSALLAASRTFSAAAGREAAAKALAEQTAAAVGAKAV VLLPIHGELRPAAGAPTLDDLDAAPMAAARWAWEKGEAAGFGTGTLPQTRWTF WPLEGVRSRAGVAGVEAGAMVAGSEDERLLLALLEQGAVALERAELATEAVETE TLRRADRFRSALLNSISHDLRTPLSTVLGASTTLIDYGKGMTAAVRDDLLLSIREEA ERLNRYVGNLLDMTRLEGGALRLRTDWTDVRDVLGAAAERVSRRLGDRALVRDF PGELSLVRADSSLLEQAVVNILENAIAYSPAATRIEMAAYEDRSNVVISIEDEGRGIP TAELEQVFEKFRRMEEPTDRNQGAGLGLSISKGFIDAMGGRIAAASPIHDGRGTRI LISLPKAVATPHHLL	26~~KdpD (9.6172E-122) ~~236,258~~Usp (1.47451E-32) ~~382,431~~DUF4118 (0.00000405774) ~~487,X,663~~HisKA (0.000000000797189) ~~729,782~~HATPase_c (3.75907E-24) ~~886	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.3E-93	320	0.1	6.4E-93	319.4	0.1	1.3	1	E6WH82_PANSA	Histidine kinase (EC 2.7.13.3)	Pat9b_3780	Pantoea sp. (strain At-9b)	891	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. (strain At-9b)	592316	>tr|E6WH82|E6WH82_PANSA Histidine kinase OS=Pantoea sp. (strain At-9b) GN=Pat9b_3780 PE=4 SV=1 MNDELPRPDPDALLLNHSDSHRGKLKIYFGACAGVGKTYAMLQEAQRLRAQGLD VLAGVVETHGRDETAALLQGLAVLPRRATGRSRHAEFDLDAALARHPAVILMDEL AHTNVQGSRHPKRWQDIEELLDAGIDVITTVNVQHLESLNDVVGGVTGIQVRETV PDPFFDAADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALREL ALRRTADRVDDQMRAWRDQQGRDKVWHTRDAILLCIGDDTGSEKLVRTAARLAA RLGSEWHAVYVETPRLNRLPEARRRAILRTLQLAQELGAETATLSDPDEARAVLR YAREHNLGKIVTGRQPQRRWRRDSFAQRLGELGPDLDLLVVALDEPVRDAPSLM NGQRASAEKWRMQLRGCLMALVLCILVTAAGRWLLVEFDPANGVMIYLLAVVIVA LRFGRWPSVFATVINILAFDLFFVAPTGTVAVSDLQYLVTFAVMLAVGVIVGNLTAG VRYQARVARYREQRARHLYEMAKSLGSALTPQDIASTSQRVIEVTLQARSLLLLPD EQGELRAVGESSMGTPPDLAIAKWSYSKGQPAGAGTDTLPAVPYQILPLKSGNH CRGLLVVEPENLRQLMIPEQQRLVETFTVLIANALERMALSQSEAASRLAAEREQL RNALLSALSHDLRTPLTVLFGQAEMLMLDLASEQSKYVAQANQIREQTLSTIRLVS NMLDMARIQSGGLNLREEWVALDEVIGGALSSMGPSLKGHDFTLDLPAELVLIKG DSSMLERVFTNIIENSLKYAGNAAQHGIHAWRENARLEIAIWDSGPGIAPDALTRIF DKFTRGDKESAVPGVGLGLAICKTIVESHGGRIWAENRAEGGASFRLSLPLPPAP EISEDGLK	20~~KdpD (2.6381E-123) ~~228,251~~Usp (1.70469E-41) ~~370,402~~DUF4118 (2.49572E-22) ~~498,524~~GAF (6.63755E-15) ~~641,658~~HisKA (0.00000000065319) ~~723,776~~HATPase_c (2.28662E-29) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4.4E-93	319.9	0	6.8E-93	319.3	0	1.3	1	D5AKZ5_RHOCB	Histidine kinase (EC 2.7.13.3)	kdpD RCAP_rcc02255	Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)	897	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter capsulatus (Rhodopseudomonas capsulata), Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)	272942	>tr|D5AKZ5|D5AKZ5_RHOCB Histidine kinase OS=Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003) GN=kdpD PE=4 SV=1 MPAGDPEKRPDPDALLALSQRERPGRLKIFLGAAPGVGKTCAMLQEAHRLRAEG VDVVLGLIETHGRAETEALAAGLETLPRRHIDHRGQPLEEFDIDAALARRPALLVVD ELAHTNAPQSRHPKRWQDIRELLDAGIDVWTALNIQHLESLADVVARITGAPMRET VPDVLLQEAQDVVLVDIPPDELIARLKAGKVYLPQTARRAVEKFFTPGNLTALRELA LRRTAERVDDQMTEILRQKAIEGPWAAAERLLVCLVADGSSDALIRQTARLASALN ADWIALLLAPPGDPAQPDRRASEALRLVETLGGTAQRRTSADFAADILRVARREH VTQILLGHRPRGPLARLLRQSLAEALAARAEGIAVHLLPLPGPAPAAARRRLDALR RGLTRPGLPADLALAGLATTGVIAIGHALAAVMELPNLSMIFLAGVLICGTLRGTRA AVLAALLSCLGYNFFFIEPLHTFSIARPHEFLALLIFLVVASLTGSWTGRIRAQARAA LAQTRGVEAQAAFSRQLSAASSAEDVAWAMVTQVQGGLGGKAILLLVEGSELVP CAAWPPEEIADPVEMTAARWAFEKGEVAGWRTATLPNLRLRFHPLATPRHVVAV LGYEPPDRDQPLSVADEAKLAVAVEQAAVALDRALLVREAVKAAAMQENENIRDA LLASLGHDLRTPLAAITGAVTTLQRGETDLRPDQRTELLDTIGQEAARLNRFVGNLL EMSRIDQGVVKVRRDWVDVGDAIRLAAERARKTHPGRQTRVSLAPDLGFVRGDQ DLLSQVIFNLLDNAHKYGESEVSVHARNEGDQVAISVTDDGPGVKPADLERIFEKF FRAGGTDRRKPGTGLGLSICRGLVRAMGGTIKAESPAIRRRGTRLIVRLPLAELPQ DEEAR	22~~KdpD (2.10696E-117) ~~232,254~~Usp (7.04055E-21) ~~371,403~~DUF4118 (0.00000000000106515) ~~498,X,664~~HisKA (0.0000000000453392) ~~730,783~~HATPase_c (8.06031E-29) ~~885	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.9E-93	319.7	0.1	8.5E-93	319	0.1	1.4	1	A0A0B4Y426_9PROT	OmpR family two component system sensor histidine kinase	TH3_16300	Thalassospira xiamenensis M-5 = DSM 17429	883	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Thalassospira, Thalassospira xiamenensis, Thalassospira xiamenensis M-5 = DSM 17429	1123366	>tr|A0A0B4Y426|A0A0B4Y426_9PROT OmpR family two component system sensor histidine kinase OS=Thalassospira xiamenensis M-5 = DSM 17429 GN=TH3_16300 PE=4 SV=1 MTDEEDRPSPEALLEQTRKDDRGKLKIFLGAYPGVGKTYAMLQAAQERRKEGRD VIVGIVETHGRVETENLLRGLEALPRKRLLHRGRVFGEMDIDAIIWRKPEIALVDELA HTNVPGSRHEKRYQDIDELLDAGIDVYTTLNIQHLESLNDIVARISRVRVRETLPDS FLEKANEIELIDLPPDDLLQRLRDGKVYVIDQVGRALRHFFSKGNLTALRELAMRIA AERIDAQMLEYMRTHAVSGPWPTQDRLMVCLNESPVAKKLVRTAKRMAERQRV PWIALHVETPRDDRMANAEKDDIAEALRLAEQLGAEIVTLQAESHLAREISALASKR NVTRLLIGRPRRRRWTGLLRENVARKLLENAEGFDVTVIAADADEKKRSLISDNPF EPGSWRSRSLSWVFGSVTVATAAALFADRYVPLGNLSLIYLLAVLLTAIRCGMWP SIAVSLLSFISYNFFFTVPYYTLSVFHHEQLITIVFFLIVSVIVGNLAGRLRLQVDAMK TSGKRTANLYDFSRKIAAAASLDDVLWAAVHHVAATLDCQSMVLQPSTDGSLEIT AAYPPEDQLGLKDWGAAEWAWEHSKPAGWRSETLPTAEWLFMPVNTPQGPLG VLGVRFREDARTLGPSQRRLLEALVDQVAVAVERTRLATDIEEARLLSETEQLRAA LLSSVSHDLRTPLVSIIGSATTLSSYGDSMGEEDRGQLTQTILEESERLNRFVQNLL DMTRLGYGALQPKKEWSDLAEIIGRAVKHVRKYAGSRSFDVQVSPDLSPIQLDPV LIEQVLFNVLDNAVKHTADDGRITVKAKADKTRMVVEISDNGRGIPTEARQAVLMF STVCAQAIARWRARGLDCRSAVVLSRRMAEVSLHTTGRRGWAQRLS	22~~KdpD (1.35825E-119) ~~230,252~~Usp (1.7618E-36) ~~376,404~~DUF4118 (2.16752E-17) ~~499,527~~GAF (2.60977E-14) ~~647,664~~HisKA (0.0000000000141001) ~~730,783~~HATPase_c (0.00000000000107408) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5.1E-93	319.7	0.1	9.1E-93	318.9	0.1	1.4	1	R6R026_9CLOT	Histidine kinase (EC 2.7.13.3)	BN621_00577	Clostridium sp. CAG:352	900	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:352	1262798	>tr|R6R026|R6R026_9CLOT Histidine kinase OS=Clostridium sp. CAG:352 GN=BN621_00577 PE=4 SV=1 MDETRQSPEHFLKEIEKEKQNLNRGHLKIFFGYAAGVGKTYAMLKAAHSVKRHGI DVVAGYIEPHARPQTSALVNGLECLPNLVSEYNGITLSEFNLDAALARHPQLILVDE LAHTNAPVCRHTKRYQDIEELLNAGIDVYTTVNVQHIESLNDTVASITSIMVHERIPD SVFDNASQVELVDIEPQELIERLQAGKVYNPTQAERATENFFTVENLTALREIALRR CADRVNLLTETVRTKSHSDYHTDEHILVCLSSSPSNAKIIRTAARMANAFKGAFTAL FVETPDYQVMSEEDVKRLRSNMRLAEQLGAKIETVHGEDVSYQIAEFARLSGVSKI VIGRSSATRKSIFSKPTLTEKLIARVPNLDVHIIPDTGGKNTAYRAKKARKKNGIVFS VSDLLKSVAILILASCIGMLFRQLGFAEANIITVYVLGVLVTSVVTRHRVYSLISSIVSV LVFNFFFTDPQFTLQAYDQGYPVTFLIMFLAALLTSSLAVKLKEHAKQSAKAAYRT KVLFDTNQLLQQAKDKNEIVSATANQLIKLLGKDIVFYLTEGETLGEPHIFTVSGDK TDKEITGTKEEAVAEWVLKNNKHAGATTETLSNAKCLYLAVRVNSRVYGVVGIYIG NEPLDAFEKSILLSILGECALSLENEKNAREKEEAAILAKNEQLRANLLRAISHDLRT PLTSISGNASNLISNGNSFDEATKNQLYTDIYDDSMWLINLVENLLSVTRIEEGRLN LHITEDLVDDVITEALHHVNRKSVEHHITVRHKEDYLLAKMDAKLMVQVVINIVDNAI KYTPKGSNILIKTWKQGDKAVISIADDGDGIPDEMKERVFDMFYSGANKIADSRRS LGLGLSLCRSIVNAHAGKITVSDNTPHGTVFTITLPAGEVEIHE	23~~KdpD (1.2354E-118) ~~232,252~~Usp (2.76056E-40) ~~375,402~~DUF4118 (4.07752E-15) ~~503,529~~GAF (0.00000320239) ~~652,669~~HisKA (0.00000000227628) ~~735,790~~HATPase_c (8.99491E-27) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5.5E-93	319.6	0.2	9.6E-93	318.8	0.1	1.4	1	C5CPD0_VARPS	Histidine kinase (EC 2.7.13.3)	Vapar_4991	Variovorax paradoxus (strain S110)	920	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Variovorax, Variovorax paradoxus, Variovorax paradoxus (strain S110)	543728	>tr|C5CPD0|C5CPD0_VARPS Histidine kinase OS=Variovorax paradoxus (strain S110) GN=Vapar_4991 PE=4 SV=1 MSDIPRPDPDALLAQLRSDEARALRGKLRIYFGASAGVGKTWAMLSAAQRERAA GRDVLIGVAETHGRSETAALLAGLELLPLREVDHRGRRLAEFDLDAALARKPAVLL VDELAHTNAPGSRHAKRWQDVQELLAAGIEVWSALNVQHLESLNGTVGAITGVR VHETVPDTVLDEADEVVLVDVTPDELAARLAAGKVYLPQQAERAAQNFFRKGNLI ALREIALRRTAEHVEDDVRGWRVEQSGAAGRNGKDGQGGELQAWNTSGAILAC VGPHEGDAQTVRTAARLAGQLNVRWHAAYVETPRLQRLAAEERDRILAVLKLAEE LGAATAVLTGSDVAEQLAEQARRLNCATLVLGQPEPATGWRRWWPATPMPLPR ALARRAPALDIMEVGRADSSRRLSRAPIAATRADDDDHEKAPVHWPGYAWATAA SIALTLLCTPLAHVLELSNIVMLFMLGVVGVAMRFGRGPSALAALLNVAAFDYFFVP PRLSFAVSDVQYVLTFAIMLGVGLLVGQLMAGLRFAAGVSTSRERRARSLFELTR ELSAALESTQVVALGAAAVQGHFGGQALVLVTDAADQLVLPKSPPEGFDAQVAD WAFRHGQPAGLATATLAAQPWHYVPLQAPMRVRGVLALSPAQPRWLLIPEQAQ QLDTLARQIAIALERVHYVEVAQQAVVEMESERLRNALLGAISHDVRTPLTALIALA ESLQTLPPEAHAEAARAIVAQAHELHALVNNLLDMARLESGIAGGAVNLRRDWQS VEEVVGSAIRAARPALGPAVVQTALEPGLPLVEFDAVLIERVLVNLIENATKYGAPP IVVGARAEPGMLRLTVRDHGPGLPAALLGREQKLFDKFTRGETESATPGVGLGLA ICRAVVSAHGGEIAAANAQGGGAEFTVSLPRREPPETAEEAQP	25~~KdpD (1.12176E-109) ~~233,269~~Usp (2.32151E-28) ~~395,428~~DUF4118 (2.88072E-15) ~~525,556~~GAF (0.000000000172446) ~~668,685~~HisKA (0.0000000000299846) ~~747,804~~HATPase_c (7.01953E-23) ~~906	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5.7E-93	319.5	0	1.1E-92	318.7	0	1.5	1	B4ETV7_PROMH	Histidine kinase (EC 2.7.13.3)	kdpD PMI1227	Proteus mirabilis (strain HI4320)	900	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Proteus, Proteus mirabilis, Proteus mirabilis (strain HI4320)	529507	>tr|B4ETV7|B4ETV7_PROMH Histidine kinase OS=Proteus mirabilis (strain HI4320) GN=kdpD PE=4 SV=1 MEQAPQWQRPSPDDLLALTRAPHRGRLKIFFGACAGVGKTYAMLQEAQRLHQQ GIDVLAGVVETHQRQETAQQLEGLPLLPPLKLHYRGRKLSAFNLDAALARHPAVIL MDELAFSNPHKCRHPKRWQDVEELLDAGIDVLTTINVQHIESLNDIVGSITGIRVQE TIPDYIFDNADEVVMVDLPPDDLQQRLNEGKVYLAGQAERAIEHFFRKGNLIALREL ALRRMADRVDSQVKEFRDSQGGTPVWHTTDSLMVCLGAHGRNDKLVRTAARYA AAFGCQWHAIYVETPKLHQIGEHKRRAILHSLKLAQHLGARTAILSDNQAEKAVIRY AREHNLGKVIIGQRPYQKWQWLKRWVRMRFAERLARYAPDLHVISVALNEEEPR YKTKTFVPQNDKWRQNLKGYLTAIGLCLAITLFSRTFLLALDKANLVTLYLLGVVLIA LFFGRRPSIFAALINVISFDLFFVQPHFSLAVLDMQYLVTFSVMLIVGLVVGNLTAG MRYQTRVARYREQRTRHLFEMTRELSRALTLEEVVRTSYHFLSSAFDAKVCLLMP NHHGELTPYNAEGMGQLPIDSGIARWCWDKDQIAGAGTDTLPSVPYQLHPISAS QQVLAILAIEPNNLRQVLIPEQQQLLQTFNGLIANALERLQQAEMAEQSRINIEREQ LRNALLAALSHDLKTPLTVLFGQSEILLLDLSAEGSAHTEQVSQIRQQILTTSRLVNN LLDMARIQSGGIQVNLQWNLLQEIAGSAVRSLSYLLDKHPLQIDIPADLLLYCDSLLI ERVLTNLLENAVKYTASQTKLGIKATVEEDQIHVEVWDEGAGIPTEQLQLIFNKFSR AVKESAIPGVGLGLAICSAIIHLHEGKIWAENNKKGGASFHFVLPLKSLPNIDEIEIKQ	22~~KdpD (1.10468E-114) ~~232,255~~Usp (3.89623E-29) ~~378,408~~DUF4118 (4.00104E-20) ~~506,532~~GAF (1.67033E-17) ~~650,667~~HisKA (0.0000000000618114) ~~732,784~~HATPase_c (3.80488E-28) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.1E-93	319.4	1.1	9.6E-93	318.8	0.7	1.3	1	D4KH79_9FIRM	Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain	MHY_04990	Megamonas hypermegale ART12/1	516	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	657316	>tr|D4KH79|D4KH79_9FIRM Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain OS=Megamonas hypermegale ART12/1 GN=MHY_04990 PE=4 SV=1 MQLGGAYMPIIRKSPEKILEQIHIEEHESKRGKLKIFFGYAAGVGKTYAMLEAAHEA KKQGIDVVAGYIEPHARPATAALVNSLEVISPLVINHKDITLNEFNLDAAIKRNPQLIL VDELAHTNADGCRHIKRYQDIEELLKAGIDVYTTINVQHIESLNDIVASITKIIVRERIP DRIFDEAEQVELVDIEPSDLVTRLSEGKIYQKEQADRALGNFFTVENLTALREIALR RMADRVNKISLKVKNENNKDYYTNEHILVCLSSSPSNSKIIRTAARMANAFKAQFT ALFVQTSSFEKTSLENKKRLKENIHLAEQLGAKIEMVVGEDIPFQIAEFARLAGVSK LVIGRSIARNGFMRLMRKSFTDKLIEQLPNLDIHVIPDNKALFYKNFWKKSVNEREI CNTSDIITILVILIITSMIGMLFYSMNLGEANIMTVYILGVLIAALKTSKRLYSVVLSVLN VLAFDFLFIEPRYTFTAYDPVYIITFSVMFVSAFVTGGLTNKIKNKLYSLLN	29~~KdpD (2.23349E-127) ~~239,259~~Usp (2.30323E-37) ~~383,421~~DUF4118 (0.00000000000885699) ~~510	non-kinase	KdpD;Usp;DUF4118

	6.2E-93	319.4	2.3	9.8E-93	318.8	1.6	1.3	1	K9VXD8_9CYAN	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Cri9333_1267	Crinalium epipsammum PCC 9333	383	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Crinalium, Crinalium epipsammum, Crinalium epipsammum PCC 9333	1173022	>tr|K9VXD8|K9VXD8_9CYAN Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Crinalium epipsammum PCC 9333 GN=Cri9333_1267 PE=4 SV=1 MITQKDIANEISLDSTRVRSRRGKHKIFIGMAPGVGKTYRMLEEAHQLKQEGIDVVI GLLETHGRKETAQKSQGLEIITRQQIGRGDITLTEMDTDAILARQPQLILVDELAHT NVPGSPREKRYQDVEVILESGIDVYSTVNIQHIESLNDLVARITGVVVRERIPDRILD EANEVVVIDVTPETLEERLREGKIYAPEKIQQSLDNFFQRRNLIALRELALREIADNL EEDAINSTPKTKYCSVHERVMVCVSTYPNSVQLLRRGARIADYMRARLYVLFVAH PEKFLTKEESLHIETCEKLTREFGGEFLRATSHDVPQKIAEVAQEYRITQVVLGHS QKSRWQLLWRGSFVHQLLRYLKDIDLHIMASEKTVSKSLSEK	20~~KdpD (1.12415E-128) ~~230,249~~Usp (9.29474E-44) ~~371	non-kinase	KdpD;Usp
	6.3E-93	319.4	0.2	9.6E-93	318.8	0.1	1.3	1	A0A0A7PJB0_9SPHN	Histidine kinase (EC 2.7.13.3)	SKP52_16045	Sphingopyxis fribergensis	889	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingopyxis, Sphingopyxis fribergensis	1515612	>tr|A0A0A7PJB0|A0A0A7PJB0_9SPHN Histidine kinase OS=Sphingopyxis fribergensis GN=SKP52_16045 PE=4 SV=1 MTGNDRPSPEAFLRQAAQEGRGRLKVFLGAAPGVGKTWEMLTDGRQRREAGV DVVIGVVETHGRRETEALVHGHEIIPRRDVDHQGHSLGEMDIDAILARRPQLVLVD ELAHTNAPGSRHPKRYQDVEELLGAGIDVYSTINIQHVESLNDVVASFTRVRVRET VPDSILENAEIEVVDIPPDELIERLRDGKVYIPQEATRALTHFFSKSNLTALRELALR RAAQAVDAQMLEHVRSHALAGSFAVGERIVVAVSELPVAAELVRAGKRLADALKA PWSAVYIETRRSQGMTDDDRRQLADTLALASRLGASTATVPAASVVEGLRAFAAD ARATQVVIGKSSRPWWFEMRHGSVVDQLVRTIDDVAVHVLPGEPDAKAVSRSAV AIPGRWGKPSDYLLALAMVALMTALGRLLLAVIDLGNISLLYLVPVMFAAATFGLRA GLFAGLASSLAYNFFFLPPTGTLTVNNPENVVSILVLLGVAVVTSQFAARVRAQAD LAQSSARQNAALASFSRLLIAAPDQESLMQAICAEVGRLLDVRTALLLPSADGPML RAAVPPEDRLEQIERAAAQWAMDNEQPAGRGSSTLTASDWLFHPLRTTRGVLGV LGLTRDDAREPVRSDQVPLLMSLLDQASIALDRMELEEASLRTRQVDERDRLRSA LLSSVSHDLRTPLTTILSAAQEMRRHPSENLAETIETEALRLNRFVSNLLDMARVEA GALPMKVEATDLFDAAASAAHDTRASLLGHEVKVDISPNIPLVRVDPVLLHHCLINL LDNAGRYADPGTPIVIRARRAADAIFMSIIDQGPGIAPGNEKRVFDTFTRLEGSDRA KHGTGLGLAIVKGFAEAMGLSVEAGNNDDPLGACFTIRIPETLIITHLDDKEVP	19~~KdpD (7.27575E-118) ~~228,250~~Usp (3.5662E-36) ~~373,398~~DUF4118 (4.29687E-18) ~~497,523~~GAF (0.000000000624399) ~~642,659~~HisKA (0.0000000000681373) ~~718,771~~HATPase_c (3.39612E-22) ~~874	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.3E-93	319.4	0.1	1.4E-92	318.3	0	1.6	1	Q0K8I9_CUPNH	Histidine kinase (EC 2.7.13.3)	kdpD 1 H16_A2600	Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	949	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus necator (Alcaligenes eutrophus) (Ralstonia eutropha), Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	381666	>tr|Q0K8I9|Q0K8I9_CUPNH Histidine kinase OS=Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) GN=kdpD1 PE=4 SV=1 MPEPRQPDDPRPDPDHLLQRMQAAGERAARGCLRIYFGASAGVGKTFAMLAAA RAQREQGGDVVVGVVETHGRAETEALAEGIERVPLRRVDYRGRTLQEFDLDAAL ARRPALILVDELAHSNAPGSRHPKRWQDIAELLSAGIDVWTTVNVQHLDSLNQAV AGITGIRVRETVPDTVFDDAGEVVLVDLPADELLRRLREGRVYVPEQARHAVQHF FRKGNLIALRELALRRTADRVDDDVRAYRQEASIEPVWRTREAVLACVGHGSDAA QVVRSARRLAGQLDCDCHVVTVSVPRLAPVPDAQREQLDQAMRLAEALGARTET LAGSDMVAAVAGYVRRHNLTKVLIGRTPARWADGGASLSGRMHALLARALAPWL GARAWLFGRTSFADALAAACPEIDVIRVADDSVRQETPADAPVLPGTEPPQADAR PAQWPGLLWAVAWCAGATALSALARPWFDLVNIAMLFLLAVAGVALRHGRTAGA FAALVAVGAFDFFFVPPQLSFAVTDVQYLVTFLVMLAVGLVIGQLTAGLREQAQVS VQRETDARTLYELARELSAALTDAQIVGIGSRFLRAAFDARAAFFLVGADGRLLPA ATAPEAGGAAQSDAVDHVLAQWVFNHGQPAGTGTDTLPSGTVLYLPLKAPMQV RGVLAVEPRTWRAFAQPALRRQVDVFATLIAIAIERLHYVEVAQQALLAMESERLR SSLLAAVSHDLRTPLTSLIGMAETLQRGTTPLAPEVAETVGAMRDQARRMHAMVA NLLDMARLQSRSVALRKEWQSFEELAGAALASLRDALARHRVVVADLSALPLVEC DGVLMERVLCNLLENAAKYTAPGTEIRVRGELSDDAVHLVVEDDGPGVPAAMAR QVFEKFTRGERESATTGVGLGLAVCEAIVQAHGGSIRVEPVHARAQGEGTGARF VVTLPRGNPPVLELEAAGLPA	(5.44568E-22) ~~541,595~~GAF (0.000000000000298902) ~~690,707~~HisKA (7.39726E-14) ~~772,825~~HATPase_c (3.58596E-28) ~~932	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.7E-93	319.3	0.1	1.2E-92	318.4	0	1.5	1	A0A0C1Q9F8_9ACTN	Histidine kinase (Fragment)	LK07_36815	Streptomyces pluripotens	606	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pluripotens	1355015	>tr|A0A0C1Q9F8|A0A0C1Q9F8_9ACTN Histidine kinase (Fragment) OS=Streptomyces pluripotens GN=LK07_36815 PE=4 SV=1 MPADQRPNPDQLLAELQSGKEQSARGKLRIYFGASAGVGKTYAMLAAAKAARAA GIDAIIGLVETHGRAETAALVADLEHLPTRQIEYKGRTLPEFDLDAALARKPALILVD ELAHSNVAGSRHPKRWQDIEDLLAAGIDVWTTVNVQHLDSLNEAVGSITGIRVWE TVPDAVFDAANEVILVDLPADELLRRLAEGKVYMPEQAQHAARNFFRKGNLIALRE LALRRTADRVDDDVQAYRRARRIENVWRTRETVVACLDPQGDGEQVIRSAARLA AQLECDWHAVAVVMPHLRAADARTERLHALLKLAEDAGAKVETLAGTNAVEAITG YIRRHNITKAVIGRPPEKRWRSARAVVVALRLAIGLERRLPSGDFAEALARHCPEV DVIRAAADPAHIQLQPRAAEVGRADVRSEAQRAADAQAGWLKPAYVAACVYVGV ATALSSLVRPVFDLANIVMLFLAAVVAVAMRHGRGPAALASVLSVALFDFFFVPPR FSFAVSDVQYLLTFGVMLAVGMLVGQLTAGLREQAEVAVQREAAAHALYEAAREL SAALTLDQIVSIGGRFVNATFGGRCAFFFVGLDGRLGAPQVAKPEGSTDAPSG	>~~KdpD (1.06624E-118) ~~233,256~~Usp (8.67786E-30) ~~390,432~~DUF4118 (2.39327E-23) ~~532,X	non-kinase	KdpD;Usp;DUF4118;X;

	6.9E-93	319.3	0	1.2E-92	318.4	0	1.4	1	A2SIR9_METPP	Histidine kinase (EC 2.7.13.3)	Mpe_A2503	Methylibium petroleiphilum (strain PM1)	906	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Methylibium, Methylibium petroleiphilum, Methylibium petroleiphilum (strain PM1)	420662	>tr|A2SIR9|A2SIR9_METPP Histidine kinase OS=Methylibium petroleiphilum (strain PM1) GN=Mpe_A2503 PE=4 SV=1 MTESRPDPDQLLVQLRDDEARAARGRLRIYFGASAGVGKTCAMLTAARKLRDDG VDVLAGVVETHGRAETQALLHGLELLPPAVVRHRDRTLPEFDLDAALARRPALLLV DELAHSNVSGSRHPKRWQDVEELLDAGIDVYTTLNVQHLESLNDVVSGITGIRVH ETLPDTFFDRADEVVLVDTPADELIERLKAGKVYLPAQAERAVGHFFRKGNLMALR ELALRRTADRVEDDVQAYRVEQAIAPVWKTEAALLCCIGPRDDSDHVVRSAARLA QQLAVAWHAVYVETPALQRLPAAQRERILQTVKLAGELGAVTAVLSAQDVATALA AHAREHNLSKLLMGHNRERPWWRRDTFSQRLARLAPDVDLIEVGEGQRHAMPV TRERQGEGRLAPGRPEGYLWAAAACALTTLVALPLQPVFELANIVMLFLLAVVGV ALRFGRGPAVLAAFLNVAAFDFFFVAPQLSFAVSDVQYLLTFAVMLVVGLLTGQLT AGLRYQASVATHREARSRALFELARDLSGELLTDQVVHTAEQAIEREFRGRARTF LQDEAGRLQWPRSGADAPGLDLGTAQWVLDHGDAAGLGTDTLPGTAWLYLPLK APMRSRGVLALQPTQPRLLLVPEQRRQLETFAVLTAIALERVHYVEVAQQATVQIE SERLRNSLLSALSHDLRTPLAALYGLADTLVDGTQGEAQEMARALGAEARRLNAM VGKLLDMARLQSGAVQLDRQWQPIEEVVGSALRSLGPALARHPVRTELPDGLPL VCFDAALIERVLCNLLENAAKYTPSGSAVTIGARVQGEELVVSVSDLGPGLPAGRE EALFEKFVRGERESATAGVGLGLAICRAIVEAHGGHIRAGRGDGPPERPGASFGF SLPLGTPPALPQPEAVTVDAALDGAVP	22~~KdpD (1.73831E-118) ~~232,255~~Usp (6.89754E-37) ~~375,402~~DUF4118 (2.23184E-21) ~~501,575~~GAF (0.0000000000454645) ~~644,661~~HisKA (0.000000000207282) ~~723,776~~HATPase_c (7.4781E-25) ~~881	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	7E-93	319.2	0.1	1.1E-92	318.6	0.1	1.3	1	F7QKF0_9BRAD	Histidine kinase (EC 2.7.13.3)	kdpDCSIRO_2045	Bradyrhizobiaceae bacterium SG-6C	896	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, unclassified Bradyrhizobiaceae, Bradyrhizobiaceae bacterium SG-6C	709797	>tr|F7QKF0|F7QKF0_9BRAD Histidine kinase OS=Bradyrhizobiaceae bacterium SG-6C GN=kdpD PE=4 SV=1 MPHEETKRASPDALLARAGREGRGRLKIFLGAAPGVGKTYAMLTAARSEKAGGK DVAAGLIETHGRRETEQLVEDFEVLPRKPIVYRNQVMREFDLDAALARRPEILLVD EYAHTNVPGSRHPKRWQDIDELLRAGINVWTTLNIQHLESLNDVVQKISKVRVRET VPDKVFDNADEVILVDFPPDELLRRLAEGKVYVQDTAARAVDNFFKPQNLTALREL ALRRAAERVDAALVESMQAQAIEGPWAAGERILACVGPDQISPSVVRAAKRLADL MDAPWMAVTVERPGAYADSATRRRLDDIMKLAESLGAETQTLTGTDLPAELLRFA KFENVTQIVVGRAPGGFFSELLRRSLPHELVRRTRDIAIHLVTREADGTVKPVPSS RRWISETFNWQHFIYAALTVGGAVGAGEILTRLTPIPNLSIVFLLAVLFIAMNFGIWP AVFASLLSFLAYNFFFISPVHTLTVAEPYELLALLIFLVVAIASAAMAARVREQARVS ADRVRATRRLYEFTRRLSGLASPEDVAEGAASEIHISLRRPVVVLLARNDDIVLTAA WPPEDDLDAAAMTAARWAYNHGEAAGTNTGTLPIIPWLFTPLKIGDKVLGTIGVA TAKDTPSLDSEERALLDTLCEQAAAALERASLAGEMVDAKTATEAERVRNTLLASI SHDFRTPLSSILGAATSLLDYDDKLDAASKNDLLGQIKEEAEGLDEMVRNLLAMTRI DAGALELRSDWIDLREVAARVVNAARRRGALQTFAIELPAELPLVRADAILIEQAIG NIVTNAVLHTPHQARIVIDAETGASEVRLRFTDDGPGIAPDILPRIFGRFVKGEALKS ASADGGQGTGLGLAIAKGIMEAHHGTIVAESPVAHGHGTRFTMVFPQKELAA	21~~KdpD (6.06062E-119) ~~231,253~~Usp (1.59614E-35) ~~375,400~~DUF4118 (0.00000000000145239) ~~486,526~~GAF (0.0000000025086) ~~645,662~~HisKA (0.0000000000461413) ~~728,781~~HATPase_c (4.43182E-27) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	7E-93	319.2	0.1	1E-92	318.7	0	1.3	1	E1SHK7_PANVC	Histidine kinase (EC 2.7.13.3)	kdpDPvag_3065	Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	892	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea vagans, Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	712898	>tr|E1SHK7|E1SHK7_PANVC Histidine kinase OS=Pantoea vagans (strain C9-1) GN=kdpD PE=4 SV=1 MNHDEPQRPDPDALLQANRESHRGQLKIYFGACAGVGKTYAMLQEAQRLRAQG LDVLIGVVETHERPETAQLLTGLTLLPRRATGRSRHAEFDLDAALARHPAVILMDEL AHTNVQGSRHPKRWQDIEELLEAGIDVLTTVNVQHLESLNDVVGGVTGIQVRETV PDPFFDSADEVVLVDLPPDDLRQRLKEGKVYIGDRAERAIENFFRKGNLFALRELA LRRTADRVDDQMRAWRDQQGRDRVWHTRDAILLCIGDDSGSEKLVRTAARLAA RLGSEWHAVYVETPRLNRLPEARRRAILRTLQLAQELGAETATLSEPDEAEAVLG YAREHNLGKIVTGRRPLRRWRRDSFAERLGQLGPDLDLLVVALDEPLKDAPHPLP DGRVTSEKWRIQLRGVMMALVLCIVVTAAGQSVLINFDPANCVMIYLLAVVIVALRY GRWPSVIATVMNIVAFDLFFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVR YQARVARYREQRARQLYEMAKSLGSALTPQDIAATSQRVLDATLQARCLLLLPDE QGELQPVGEALPASEPDRAIAKWSYSKGQPAGAGTDTLPAVPYQILPLKSGAHCR GLLVVEPQNLRQLMIPEQQRLVETFTVLIANALERMALSHSEAASRLSAEREQLRN ALLSALSHDLRTPLTVLFGQAEMLMLDLASDNSKYVPQASQIREQTLSTIRLVSNM LDMARIQSGGLNLREEWLALEEVIGGALSSMAPSLKGHEVQLDLPDDIVLIKGDST LLERVFTNLIENSLKYAGNSAPRGIRAWRAATRLEIAVWDSGPGVAEDDLTRIFDK FWRGDKESAVPGVGLGLAICKTIIESHGGQIWAENRPEGGAAFRLSLPLPPVPEIS DEGLK	21~~KdpD (6.3179E-120) ~~229,252~~Usp (8.85194E-36) ~~371,403~~DUF4118 (2.02809E-21) ~~499,525~~GAF (0.000000000000110258) ~~642,659~~HisKA (0.000000000546041) ~~724,777~~HATPase_c (1.16064E-29) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.4E-93	319.2	1.6	1.4E-92	318.2	1.1	1.5	1	A0A0D6T9R0_9RHOB	Histidine kinase (EC 2.7.13.3)	SY26_17625	Paracoccus sp. 361	888	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 361	1603292	>tr|A0A0D6T9R0|A0A0D6T9R0_9RHOB Histidine kinase OS=Paracoccus sp. 361 GN=SY26_17625 PE=4 SV=1 MTELRPEPDALLAQAEREGRGRLKIFLGAAPGVGKTYAMLEAARRRAAEGVDVVA AVVETHGRAETEALLQGLDLLPKRAQFYRERILHEMDLDALLERRPQLALIDELAH SNIPGSRHDKRWQDVEEVLAAGIDVLTTLNVQHLETLNDRVARISGVRVRETVPD AVLARADEVELIDLPTEELIERLRAGKVYVQDQIARAVQNFFSKGNLTALRELAMRA AADRVDAQLREHMRANAIGGPWPAQERILVALTESPVARTLVRTAKRMADRARV EWVAVTVTSARSEALSDPDRDALAQALRLAERLGGEVATLSAAGPVADEILDYAR RRNVSRILLGRPRPRPWWRRIGRQNVARAVTEAGRDFEVTVVSDPQRTPTPPAV RHWSVDRDPRAYAKATLTVIAASLLALSADRIFPVTSLSLIFMTGVIVVAVRQGLWP SLYASCLSFLTYNFFFTDPRNTFLVIRQDQIMTLLLFLIASGLTGNLAARLRDRALAQ RDIAMRTNLLYDFARQVAGAGSAVEVLRAAAIHVGAALGCDTVVMRPGPLGRPVI EVAEPPRDTLALRDASAADYAWTRGEEAGRGSGTLPASDWLFLPVGTEGRRLAI LGIAYPDGRSLAPMDRRLLDAMTDQTGIALERIALQADLEQALVTSEAERLRAALLS SVSHDLRTPLVSIIGAASSLADPALDLAAPARASMAATIRDEGERLDRYIQNLLDMT RLGHGALVPKRVPADLREIAGSARHRLRGALRDHRVEVAVPDDLPQVLVDPLLIEQ VVMNLLDNAAKYAPEGSRIDVTARVDGARAELSVGDDGPGIPPDARGRVFDMFY RVAEGDGQRAGTGLGLAIARGIVEAHGGTIAAHPARADGRGTRITLTLPLDTPA	(7.40427E-118) ~~228,250~~Usp (2.08524E-25) ~~375,397~~DUF4118 (4.10866E-14) ~~497,526~~GAF (0.00000798145) ~~642,659~~HisKA (0.000000000532491) ~~725,778~~HATPase_c (3.48219E-28) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.9E-93	319.1	0.1	1.5E-92	318.2	0	1.5	1	R5T4S6_9CLOT	Sensor histidine kinase KdpD	BN544_02002	Clostridium hathewayi CAG:224	680	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	1263067	>tr|R5T4S6|R5T4S6_9CLOT Sensor histidine kinase KdpD OS=Clostridium hathewayi CAG:224 GN=BN544_02002 PE=4 SV=1 MKKNDIDEMDKKRDPEKILQEIKEQEEELEETDIKRRGKLKIFFGYAAGVGKTYAM LDTAGEAKAAGADVVAGYIEPHARPDTIALLEGLEVLPPKLIDHKGIKLREFNLDAAL WRKPEILLVDELAHTNAEGCRHRKRFQDIQELLDAGIDVYTTVNVQHLESLHDIVA SITHIRVNERVPDRIFDEADKIELVDIEPEELLTRLAAGKIYGKNQAGRAMSNFFTKE NLTALREIALRRTADQVNKAVMKERQAAGRDYYTGEHVLVCLSPSPTNEKVIRTAA RMAGAFRAELSAVVVETLEAAEREDKVRKTMENNITLAKQFGAKVVTLYGDDIAE QIAGYAKNNGVSKIVIGRTVRPTGLSAIVRRRRNLIDRLIALVPGMDIYVIPDVRAAV QKHRHLTGKNSAAVEPARVAVDATAAVFLLASATILGQGIEACGLGEMNQIMIYIM AVILISGFSRYRVTGVMASAASVLLFNFFFTVPRFTFQAVASVYPFTFLTMLLCALT VSSLAARLKRQVRLSKEESEKMQILIAISNKLKLAADSDEILDICAKQVMKLLEKNVII YHAVGGEVKQPRVYLSNDAEEMAGGILLNEDETAVAGWVCKNCHKAGCTTNTLP GAAGLYIPIQKDGRVFGVIGIDLKEGAPIKPNDKNVLHVILDETAVVLKAQMIHGYL	35~~KdpD (2.39703E-123) ~~245,265~~Usp (6.15466E-36) ~~391,422~~DUF4118 (0.000000000388533) ~~521,547~~GAF (0.0000372185) ~~671	non-kinase	KdpD;Usp;DUF4118;GAF

	8.3E-93	319	0.1	1.4E-92	318.3	0	1.4	1	C3MF86_RHISN	Histidine kinase (EC 2.7.13.3)	NGR_c01200	Rhizobium sp. (strain NGR234)	894	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Sinorhizobium fredii group, Rhizobium fredii (Sinorhizobium fredii), Rhizobium sp. (strain NGR234)	394	>tr|C3MF86|C3MF86_RHISN Histidine kinase OS=Rhizobium sp. (strain NGR234) GN=NGR_c01200 PE=4 SV=1 MPEIDRDPASRPDPDALLALAEKGGRGKLTVFLGAAPGVGKTYAMLMRAQRLKE EGADIVIGLVETHGRSETAALLEGLEVLPRREVAHGGRTLHEFDLDAALARHPRIIV VDELAHTNFGESRHPKRYQDIEELVDAGIDVWTALNIQHLESLSDIVAQIAGVPVRE RIPDTVLNRADEVLLVDLPPAELIDRLKEGKVYLPDSAKRAVDNFFRLGNLTALREL ALRRTADRVDDQMVDYLKQNAIEGPWPASERLLVCIGPDPLSEKVVRTASRLASG LNADWIVVSVERADREAADGEAMRQLDETFRLAEQLGAETRRIIGSDFVEEILKLA RRENATQIVIGARRHRFPLNLFRASLPDALAKRVSGIGIHLVTGKIEPVARTRRRSK QLLPEGLERALAIAGGTVGLATVLGLLIEQFIILQNISLLYLLAVLASAVYAGYFAALA AALFSVVAYNFFFIEPVNTFTVAEPHEVFALFVFLAAAALAGGLASRIREQAKTARN RATATQALYDFSRKLSGTANADDVLWAAVTQMQSTLRRNAVMLLPEDGDIALRAA WPPDTELTVSDMIAARWAFEKKEAAGNDTGTLPNSPFQFRPLMSPQGVVGVCG FLQEDSPLEINEERALAAILDQTAIAVDRARLSRESLDQAAQLEGEKFRAALLSSLS HDLTTPLATIGSAVISLRQLGEGTPKDAREDLLKSIEEESGRLTRFVTNLLDMNRIE AGTINARRDRVDVAEVVHDAVERARKYFPGRVFETSIALGLPAMRGDGVLLGQVL FNLLDNANRFGGDEPVSIYARREGDEVVLSVTDLGKGIAPADLEHVFDKFFRKGK PDGRSLGTGLGLTISRSFVEAMGGRIKAESPALRRRGTRISMRFPAAEAELSN	24~~KdpD (2.31693E-125) ~~234,256~~Usp (1.17225E-37) ~~379,X,529~~GAF (0.0000507582) ~~646,663~~HisKA (0.000000673496) ~~729,782~~HATPase_c (1.20416E-24) ~~885	kinase	KdpD;Usp;X;GAF;HisKA;HATPase_c
	8.9E-93	318.9	0.9	1.6E-92	318.1	0.6	1.4	1	K9STD0_9SYNE	Osmosensitive K+ channel His kinase sensor	Syn7502_01086	Synechococcus sp. PCC 7502	361	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. PCC 7502	1173263	>tr|K9STD0|K9STD0_9SYNE Osmosensitive K+ channel His kinase sensor OS=Synechococcus sp. PCC 7502 GN=Syn7502_01086 PE=4 SV=1 MTPNRRGKHKIFIGMSPGVGKTYKMLEEGHRLLSEGVDVVIGLLETHNREETANK AIGLELIPRQQVPWQGITLPEMDTKAILARQPQLVLVDELAHTNVPGSEREKRYQD VEVILAAGIDVYSTVNIQHIESLNDTVAKITGVIVRERIPDRILEAADEIIVVDVTPETL QERLKDGKIYAPDKIDQSLNNFFQRHHLIALRELALREIADNIDAEGIEEESPQNNFY NVQERVLVCVSTYPNSLQLLRRGARICTYMHGQLYVLFVEDPDRFLTKSETLHIEN CQRLCQDFKGEFIRVREYNIAKAITQTAQKHRITQIVMGESQKSRWQMLLKGSLT QTILRQLKNVDIHIISTSDRP	5~~KdpD (1.14486E-127) ~~214,234~~Usp (6.54485E-42) ~~356	non-kinase	KdpD;Usp

	9.1E-93	318.9	0.4	1.7E-92	318	0.2	1.5	1	R6QGF3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN583_01050	Anaerostipes sp. CAG:276	902	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, environmental samples, Anaerostipes sp. CAG:276	1262699	>tr|R6QGF3|R6QGF3_9FIRM Histidine kinase OS=Anaerostipes sp. CAG:276 GN=BN583_01050 PE=4 SV=1 MEEEMRRNPDRILKQIHREETEQARASGKLKIFFGYAAGVGKTYSMLKAAHDALE QGRDTVIGYIEPHTRPETMALVKGLETVPVKEIEYNGMNLRELDLDGVIKRHPQLV LVDELAHTNGMGCRHKKRYQDVEEILKAGIDVYTTVNVQHIESLNDIVASITGVIVR ERIPDSVFDNADSVELADIEPEDLLKRLKAGKIYREAQAGKAMQNFFIESNLVALRE IALRRTADRVNHISEQQKEQEGKEGYYTDEHILICLSPSPSNQKVIRTASRMSRAF HGKFTAVFVKTEAADKISLDDEQRLVENVRLAEQLGAKITTIFGEDIPEQIAGYAKA AGVSKIVIGRSVNRSVFAARHNFADRLSALAPNLDIYIIPDQQAAPDSGRRTFWNK EKIRVRSEDVIRTASIFVFVTALGLWFQSIGFSESNIITIYILGTLITALVTEYRFYSLLF SVCSVLCFNFLFIQPLFTLNVYGSGYPVTFAIMLLSALISGNLMTRVKQQARAASIQ AYRTGILLETNRRLQNAADREEIIELSSKQMTRLLDRAIIFYDAEDDRLLEPRTYGNK TQTDFSRYLTHEERAVAEWVRKNNKHAGATTDTLPGAKGLYLAVRSADHVHGVI GICLEKTKLDTFEKELMISMLDEIGLALEKDKIAASQKEAELKAQREEFRANLLRSIS HDLRTPLTSISGNAGVLRQSSDQISEEKKQELYTDIYDDAMWLINLVENLLSVTRIE NGTMKIEKEPEIVEEVILEAVKHIDRRKNEHHIHIRIDDDMMMADMDAKLMIQVIINL VDNAIKYTGKGSHIDISAEKKNGKVLIEVADDGEGISDEAKTRLFDMFYTGSKTVAD SRRSMGMGLALCKSIVQAHGGTITVRDRKPRGTVFSFELQAEEVIVHG	28~~KdpD (4.19832E-119) ~~235,256~~Usp (5.00128E-32) ~~378,410~~DUF4118 (1.43606E-16) ~~505,531~~GAF (0.0000242252) ~~654,671~~HisKA (0.000000000301534) ~~737,792~~HATPase_c (2.44051E-27) ~~893	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	9.9E-93	318.8	0.2	1.5E-92	318.2	0.1	1.3	1	M4S5E9_9SPHN	Histidine kinase (EC 2.7.13.3)	G432_12260	Sphingomonas sp. MM-1	888	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. MM-1	745310	>tr|M4S5E9|M4S5E9_9SPHN Histidine kinase OS=Sphingomonas sp. MM-1 GN=G432_12260 PE=4 SV=1 MALSGDGRPDPDALLRAAAQEGRGRLKIFLGAAPGVGKTYEMLSDGAAQRQEG RDVVVGVVETHGRVETEALVRGHELIPRREVPYQGRILHEMDLDALLERAPELVLV DELAHTNAPGSRHPKRYQDVEELLAAGIDVYTTVNIQHIESLNDVVASFTRVRVRE TVPDGILEMADIEVVDIPPDELIERLKAGKVYLPREATRALTHFFSKSNLSALRELAL RRAAQAVDAQMLEHVRALGVGGTWAASERIVVAVSELPGADGLVRAAKRIADAL HAPWTAVYIETPRAQTFGAGEHRSLAAVMNLATQLGGVVATVPATSIVAGLKAYL TDARATQLIVGKSQRSRWFELRHGSVVDRLVRETPGVAVHVLPLESPPPRTGGF RIHNAWGSRSGYAWTAAMVAGVTAIASGLFHVLDLGNVALLYLLPVMAAATLFGL RTGLFAGLTSSLAYNFFFLPPTGTLTVNNPENVISILVLLGVAIATSQLTARVRAQAD MASSSARTNAALAGFLRRLTGIGDPMELARAICEDIARLFDLRVVLLVPNGGGLSL QAASHPGCDLETMELAAARWAFDTSAPAGRGSGTLASSDWYFQPLRAGDRTQG VLGLAKEDGGDPLRADQLPLLTSLVDQAALVMERFRLEEEMRDVESVRTRDRLR QALLSSVSHDLRTPLTAVIAAADQLDHGATPDLIGTIKAESARLNRFVSNLLDMARV EAGALKLNIEAIDLSDAVTGAAHDARRALEGHPVRLDVPPDLPLVRADPQLLHHCL LNLLDNAGRYGDPGTEIVIEGRHLFGHIRLAVLDNGPGLPPGREAEVFETFRRFEG SDRAIGGTGLGLAIVKAFAEAMGMSVEASNREDGSGASFALMFPSPLIVRDVAQG SV	21~~KdpD (4.77072E-119) ~~230,252~~Usp (9.13073E-37) ~~375,398~~DUF4118 (4.52933E-17) ~~497,523~~GAF (0.000000000429041) ~~642,659~~HisKA (0.00000000116109) ~~718,780~~HATPase_c (1.90369E-18) ~~874	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1E-92	318.7	0.2	1.8E-92	317.9	0.2	1.4	1	B2FJW7_STRMK	Histidine kinase (EC 2.7.13.3)	kdpD Smlt0405	Stenotrophomonas maltophilia (strain K279a)	886	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Stenotrophomonas, Stenotrophomonas maltophilia group, Stenotrophomonas maltophilia (Pseudomonas maltophilia) (Xanthomonas maltophilia), Stenotrophomonas maltophilia (strain K279a)	522373	>tr|B2FJW7|B2FJW7_STRMK Histidine kinase OS=Stenotrophomonas maltophilia (strain K279a) GN=kdpD PE=4 SV=1 MTDARTRQADALVEGLQREAGGKLTVFLGAAPGVGKTYAMLTRAQEQLRRGVDL VVGLVETHGRADTQALLEGLPQLPLKDVAYHGHALQEMDLDAVLARHPALVLVDE LAHRNAPGSRHERRWQDVMELLDAGIDVWTTVNIQHLESLNDVVMRITGVRVSE TVPDGVLDRLHDIVLVDLPPRELIARLQQGKVYVPEQAAQALQAFFSPANLTALRE LAMQEAADRVDSSLREARAARGESNLPLRRGVLVAIDGGGQSEYLVRVARRIAER RDAPWTVVTVQGRRQDEATRREIDAAFALARRLGGDAELLHGSSIADALLDHAAH NGVSTLVLGRTRERPLARMFNRTLTQQLIQRGAHYEITIISTPQARARSRREGLLP PMRGISYEPVQALIATALACAVAWLAERWVGMADLSMVFIVAVVLVAARTRASVA VMAAILCFLAYNFLFIAPRFTFAIGARQGVITVFLFLAAALVAGRLASRLRMQVIALR AANRHARARQQLGRQLASAAGNGEVAQAGRHALEQAMDVPAWLRIGADTATGG RSQPGDTDLAAADWALRHGQPSGRFTDTLAGAQWWFLPLLDGEDRAIGVAGLY LPGAQARLLPEQRQLAEAMVDDIAQAALRTRLVAELEQAHVSNETERLRSALLSSV SHDLRSPLAAMIGSADSLASYGAAMDTADRRALLDTILVEGERLDRYIQNLLDMTR LGHEGLKINRDWIGVDELIGSAARRLQRYQPKVRLELDIPATLAPIWVHPALVEQA VFNVMENAAKFSPPDAAVQVQARELDGQLRIDVIDAGPGIPDDERARIFDMFYSV ERGDRGRHGTGLGLTICQGMVGAHGGSVQALPGRDGRGTLIRITLPLLKPASHDE PDSD	19~~KdpD (4.95346E-123) ~~229,251~~Usp (1.90056E-31) ~~370,395~~DUF4118 (0.0000000206816) ~~491,X,650~~HisKA (0.0000000000160418) ~~716,770~~HATPase_c (2.29384E-22) ~~872	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1E-92	318.7	0.3	1.7E-92	318	0.2	1.3	1	J7J0P9_DESMD	Osmosensitive K+ channel histidine kinase	Desmer_2979	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	671	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	768704	>tr|J7J0P9|J7J0P9_DESMD Osmosensitive K+ channel histidine kinase OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=Desmer_2979 PE=4 SV=1 MKKEKRIDPDELLASLEKEGLGKLTIFLGAAAGVGKTYAMLEAAKEKLSEGMDVVV GLAETHGRAETKALLEGLPVIPTKPQDYKGKTFYEMDLDAILARRPQIALVDELAHT NVAGSRHKKRFMDVQELLAAGINVYTTLNIQHLETLNDIVAQITGVTVRETVPDQIL ETAFQILDIDPPEELIQRLKDGKVYVAGQATEALKNFFRPGNINALRELALRYTAKK VDRQLESYMRVHGIAGPWPTGEKVLVCISASPFSAKLIRVAKRMAASQNAEWFAV HVEPHLHRLSGNEADRDSMAKNLRLAEQLGAEIIGLTGDDIAEEILHLAAKRNVSQII IGKPEHTRFWTFVHGSVVDKVIRHSQGISIHVIPGSQQETGQRNYPAERVKKKGIS PQLVHSSSVPYILAPLLMTLMISIITPISSFLGIVNISMLFLLPVLISAARWGRLPAVIT AAMGAITLDFFFVPPIFTFTVADIRYVLSFAIFMLVGIITGTLSDRLKKQINYSRQREN RVSALYALSRDIAAVSQLDDVLESIVNNVSSTLEGQVVLLLPNEKGKLVLQRDSGL NNFLNDSELAVASWVFDKGRKAGKGTETLGAATALYLPLSTEQGVQGVLGICFNT TEVQFDSERIRLLEAFAGLTAMAINRIKLSEQARRTLCQSHSCY	22~~KdpD (3.47822E-122) ~~229,251~~Usp (2.35415E-39) ~~375,407~~DUF4118 (1.25163E-16) ~~507,534~~GAF (6.04295E-14) ~~653	non-kinase	KdpD;Usp;DUF4118;GAF

	1.1E-92	318.6	0	5.2E-92	316.4	0	2	1	J9SQL2_9ACTN	Histidine kinase (EC 2.7.13.3)	KTR9_4019	Gordonia sp. KTR9	849	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia sp. KTR9	337191	>tr|J9SQL2|J9SQL2_9ACTN Histidine kinase OS=Gordonia sp. KTR9 GN=KTR9_4019 PE=4 SV=1 MSSAAGHPEGRGKLRVFLGCAPGVGKTYEMLAQARTLVDEGTDVVIGVVESHGR VATAALVEGLETIPRISRSYRGTPLEDMDLDAVLARRPEVALVDELAHTNIPGSRNR KRWEDIEELLGAGIDVYSTINIQHLASLNDVVAQITGVVQRETVPDDIVRGADEIELV DIDPQALRQRLSAGKVYPGGRVDGALANYFRQGNLTALRELALLWLADQVDDKLA DYRAAHSITETWEARERVVVAVTGGAESPTLLRRASRIASRSSAELLAVHVVRGD GLTGVGVDLAALKELAAGFGARIHTVVGDDIPDTLLEFARGVNATQLVLGTSRRPR WQRIFDEGVGAAVVSDSGRIDVHMVTHDETSRRSRLDIRDTRFRRPLSWLFAVLV PAGVTGVLQLLDPWLGFASQSALYFVAVLAVSMLGGILPAALSAVISGLLLNFFFT DPRFTFTISQPDNLITILVMLMIAIAVAALVDSATVRRAQAQDAAREAELLALFSSVV LGGADVPVLLERFRETYDQSAVSVVRRTSRAGRVVEAAVGESPPVSPEDADTVC VVPGEKFELLLRGPKLGARDRRVLAAVAGQAAGAVQRHALEAEAATAEALARTDE LRRALLSAVGHDLRTPLAAAKAAVSSLRSDDVTFSPEDTAELLATVDESVDHLTSL VGNLLDSSRLAAGAVRPHRQRTFLPEVVHRAAAAVARTDREPALTFDLGHAWAY TDPGLLERALANLIDNARRHGGGHVEVTARLTPADPPRCEIRIIDHGPGLPVVDRD QIFAAFHQGGDTSGASSGVGLGLSVAQGFVTAIGGVLGVEDTPGGGATMVVDLP ATDDLDVPVETAGPVR	9~~KdpD (8.23618E-113) ~~219,241~~Usp (1.96259E-31) ~~361,384~~DUF4118 (9.65536E-15) ~~478,X,612~~HisKA (0.0000000000205007) ~~678,729~~HATPase_c (4.17386E-21) ~~832	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.1E-92	318.6	1.2	1.6E-92	318	0.1	1.8	1	C8WN67_EGGLE	Histidine kinase (EC 2.7.13.3)	Elen_2843	Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (Eubacterium lentum)	926	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, Eggerthella lenta, Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (Eubacterium lentum)	479437	>tr|C8WN67|C8WN67_EGGLE Histidine kinase OS=Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) GN=Elen_2843 PE=4 SV=1 MDYEARRDPDAILRQIVEEEAAEGDTRGKLKIFFGYAAGVGKTYAMLEEAHAVLEK GFDVVVGYVEPHTRADTMALVDGLEQISPSTVQHRGISLREFDLDAVLARHPQIVL VDELAHTNAPGCRHRKRYQDVEELLRAGINVFTTVNVQHLEGLNDKIAAITHVSVA ERIPDRIFDQAASVELVDIEPDDLIERLEAGKIYLPDRARTALGNFFSRKNLAALREI ALRRMADRLTRKAECTEAGARVEAGEDVLVYVTHNTGNVKAIRAAANMAESYHG ALTAVVVESSQSKKFDSDQRGRLRANIDLAEELGAHVVTLFGDDIAQQLAQYAVT AGATHIVVGNATGGLSVRSLLRESLVSRLMKLAHGAVVDVVPTKDLPAQYGRLSE ATGFRLTGADVWRALASVAIATAIGLAIYSLGLAGSVVLMLYLIVALLIATRADGFFY ALFVSMGSVFAYNFFFTIPRFTLHAVGLNYPIIFAFLLVGTFAASSLAIRMKRQAEST ARRAYRMEVLLESSRKLQGARNADECFRLAAEQVIKLLNRPVVMYRLGIDGRLAK PVVHDVPGTLGGDAGACALASPEESAVAAWSAANNERAGATTDTLADSQCLYLPI HSKDAVFGVAGIAMDDIDGEEDFGAFEKNLLLAILDECGQTTEQIVFAEDRRRMEM RMEKETLRANLLRTISHDLRTPLTSISGDADMLLHDRGALSAQQKEHLYRDIHDDA CWLVTLVENLLSITRIDNGTLQLAEQPELVADVVREALQHVDRRAGRRRVDVELE DELLMADMDARLIVQVIINLVNNAVSYTPADGRIVVSARRVVEHDRPRVRIAVADE GPGISEEDRKHIFDMFYNGSTGRRGGKSGDFKRGMGLGLSLCRSIVEVHGGTLD VRNVNPHGSEFSFTLAAVEAGDVVARSTEEARG	27~~KdpD (4.60949E-118) ~~235,254~~Usp (2.06724E-24) ~~377,404~~DUF4118 (0.000000000934154) ~~502,X,677~~HisKA (0.00000000191871) ~~743,796~~HATPase_c (4.68589E-28) ~~908	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.1E-92	318.6	0.3	1.7E-92	318	0.2	1.3	1	A0A0C9M332_SPHPI	Histidine kinase (EC 2.7.13.3)	kdpDSP6_31_00020	Sphingomonas paucimobilis NBRC 13935	888	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas paucimobilis (Pseudomonas paucimobilis), Sphingomonas paucimobilis NBRC 13935	1219050	>tr|A0A0C9M332|A0A0C9M332_SPHPI Histidine kinase OS=Sphingomonas paucimobilis NBRC 13935 GN=kdpD PE=4 SV=1 MTAGEPRPDPDALLRAAEREGRGRLKIFLGAAPGVGKTFEMLSEGAARRRDGVD VVVAVVETHGRVETEALVRGQEVMPRRAVPYEGRTLHEMDLDAVLARAPRLALV DELAHTNAPGSRHPKRYQDVEELLDAGIDVYTTVNIQHIESLNDVVASFTRVRVRE TVPDRILEAAEIEVVDIPPDELIERLKAGKVYLPQEATRALSHFFSKSNLSALRELAL RRAAQAVDAQMLDHVRSLGVGGQWAAGERLVVAVSELPGADELVRAAKRTADA LRAPWTALFIDTPRTATLGEAQHRRLAATMTLATQLGAAVATVPAPSVVEGIRAFL TDARATQLVVGKAKRSRWFELRHGSVVDRLVRETPGVTVHVLPVGEAPVERERT KRRGQWGSPIGYGLTLLGVAAVTALASALFHILNLGNVALLYLLPVMAAASLYGLR TGLFAGIASSLAYNFFFLPPVGTLSVSNPENVISIFVLLGVAVATSQLTSRVRAQAD LAAASARDNATLAGFLHRLSGLADPAEAARVICEDIALLFEVQAVLLTPSPAGLAVQ AATKPDYRLETMEMAAAHWAFDTGTPAGKGSATLAASEWLFQPLKAGNRTLAVL GLAREAGGEPVRADRLPLLTGLIDQAALILERLRLESEVRDVDAVRTRDRLRAALLS SVSHDLRTPLTAVMAAAAQLRQGATPELVSTIEGEAARLNRFVANLLDMARVEAG ALKLKIEAIDLSDAVTGAAHDARRALEGHAVRLDVPPDLPLVRADPQLLHHCLLNLL DNAGRYGDPGTEIVIEGRHRHGSLRLSVLDHGPGLPPGREAEVFETFRRLEGSDR VAGGTGLGLAIVKAFAEAMGLTVEAGNREDGAGAAFALCFPRELIMRDGAPEGM A	20~~KdpD (8.32001E-111) ~~229,251~~Usp (1.10636E-34) ~~374,397~~DUF4118 (6.47769E-18) ~~494,522~~GAF (0.00000987319) ~~641,658~~HisKA (0.0000000013013) ~~717,779~~HATPase_c (5.19554E-17) ~~873	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.1E-92	318.6	2.1	2E-92	317.7	0.2	2.1	1	KDPD_CLOAB	Sensor protein KdpD (EC 2.7.13.3)	kdpDCA_C3678	Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	900	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium acetobutylicum, Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	272562	>sp|P94608|KDPD_CLOAB Sensor protein KdpD OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) GN=kdpD PE=3 SV=2 MDINYERPDPYYLLNKIDKEEKNKNRGKLKIFFGYAAGVGKTYAMLRAAHYMKEL GKDIVIGYIEPHARMDTMSLTKGLPQIPVKNIDYKGVILREFDVDKALLRKPEIILVDE LAHTNAKSQRNKKRWKDIEELLDAGIDVYTTLNVQHIESLNDIVANITHVSVRETIPD KVFDDADKVELIDIEPDELLKRFTDGKIYRKEQVKRAFNNFFTKNNLYALREIALRR TADRVNFEIEIARLSKGQITVMATSDQILACIGTSPSSARIIRTAARMAESYHSKWIA LYVDTGRSLGKADKETLNANFNLVELLGGELVTVHGENVADQIIRYAELRNTTKIVI GKNHKRTGTLLHFYAKDVVDKLMDSNSYIDVYMIPNSSYYRDHKNSILSKISIQHKG SVKDVLKAIIIMAITTDIAELFSYMGFKDVNVIMIFILGVIIVYMATKGQIMGIISSIAAVL VFNYRFTEPKNSFIVYDKSYLVTFPIMMIVAFIIGSLTNKVQKEAQDSNMREKRTQT LYIVSGKLLSAVGTSEVVSIGIKYISRLVNRNVICYLADTSNKLSTPFVYKKDKGAKE EIIMSKDENAAAYWTFLNGKESGCGTSTFYRAKGYYIPIKIKNKVLGVIGVSCPSGP LRPQKKAVVDTVTGQIAIALDREILSKEQEKSKVEIERERLRSNLLRSISHDLRSPLA GIKGAASTILENGELIDEKRKQELINGIYEDTEWLIRLIENLLSMTKFDEGNTKIKKDV ELVEEVVSEAVQRSSKYFKNHKIKVSVPEDVIMVSMDGSLIEQVIINLLDNASKFSP KGSTIEIKVYEKKKDVVFEIIDEGQGISEDILPNIFDRFFTNGSKISDSRRGVGLGLAI CKSIVEAHGGKIEAVNKGSGGAIFKFNIPKEL	24~~KdpD (8.17085E-132) ~~234,257~~Usp (3.22953E-40) ~~379,407~~DUF4118 (7.48065E-14) ~~507,534~~GAF (0.0000330086) ~~657,674~~HisKA (0.000000000000820826) ~~740,793~~HATPase_c (7.3625E-28) ~~896	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.1E-92	318.6	0.7	1.8E-92	317.9	0.5	1.3	1	U5RTD5_9CLOT	Histidine kinase (EC 2.7.13.3)	CAETHG_1797	Clostridium autoethanogenum DSM 10061	911	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium autoethanogenum, Clostridium autoethanogenum DSM 10061	1341692	>tr|U5RTD5|U5RTD5_9CLOT Histidine kinase OS=Clostridium autoethanogenum DSM 10061 GN=CAETHG_1797 PE=4 SV=1 MEVIIIDYNERPDPYRILNKVEKEDSESERGKLKIFFGYAAGVGKTYSMLREAHDIK NLGKDIVIGYIESHERLETMDLTKGIESINTKVIDYRGVILKEFDLDAALLRKPEIILVD ELAHTNAKGKRHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDVVESITHISVRETIP DKVFDNADKVEIIDIEPDELLKRFSDGKVYARDQVKSAFHNFFTKSNLYALREIALR KTADRVNYEIETARLSKGQITVVPASDQILACISSSPSSLRVIRTAARMAEVYHSKW IVVYVETTKSQKLSKEDRKRLNSYFNLGEQLGGEVVTIYGDDIADQVIQYAKFRNIT KIIIGKNNKKTSKVFHFYAKDVVDKLMDSNSYIDVYVIPNSLYDRKSNKITKKFSKEF NLSLKEAIKAALILSIVTCAAIIFDYVGFSEANVIMIFILGVIIVYMQTTGYLMGIISSLV GVSIFNYLFVPPKRSFHFYDKNYLITFIMILIEAFVIGNLTNKIQQDADESYTREKRTQ TLYRVTSKLLSAVGNSDVVSIAIKYLSRLVDRTVVCYLSIDNKLSTPFVYYLDELKKD DLILNKDEAAVAYWSFLKGREAGSGTDTFYGARGYYIPVKVQNKILGVIGVSCEKD FLSHDQKFIVETVTGQMAIALDREILVGQQEKSKVEIERERLRSNLLRSISHDLRSP LAGIKGAVSTIIENGKFIPEKTKEDLLNGIYDDTEWLISLVENLLSMTKFDEGNMKIN KNLELVEEVVSEAVQRSSKYFKDHKIKVEVPKKLIMVPMDGNLIEQVLINLIQNAAK FSKKQSFIQIKVYESVDDVFFEVIDDGIGISDKILPHIFDRFFTNGSSIADSRRGVGL GLTICKSIVEAHCGTIEAENKKEGGAIFRFNIPKGESTSNELM	28~~KdpD (9.15649E-123) ~~238,261~~Usp (6.68043E-43) ~~385,412~~DUF4118 (0.000000000000279045) ~~512,541~~GAF (0.00130861) ~~661,678~~HisKA (0.000000000163033) ~~744,797~~HATPase_c (3.12919E-26) ~~900	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.1E-92	318.5	2.2	1.5E-92	318.2	1.6	1.1	1	K9V5I3_9CYAN	Osmosensitive K channel His kinase sensor	Cal6303_4152	Calothrix sp. PCC 6303	369	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix parietina, Calothrix sp. PCC 6303	1170562	>tr|K9V5I3|K9V5I3_9CYAN Osmosensitive K channel His kinase sensor OS=Calothrix sp. PCC 6303 GN=Cal6303_4152 PE=4 SV=1 MLSSPDTTYNRSSRRGKHKIFIGMAPGVGKTYKMLEEAHQIRTEGMDVVIGILETH GRRETAEKAVGLEAIPRQDLVVNNVTLNEMDTDAIITRSPQLVLVDELAHTNVPGS PREKRYQDVEVILSSGIDVYSTVNIQHLESLNDIVARITGIVVRERIPDRLLDEADEV VVIDVTPETLEERLREGKIYAPEKIEQSLGNFFQRRNLIALRELALREVADTVEDDA KSSAFTVASCNIHERVLVCLSTYPNSIQLLRRGARIANYMNARLYAVFISNPERFLS KEESLHVETSSKLCEEFGGEFLRGTSQNVAEEIAKFATKLHITQIVIGESQQPGWK RWIRRSFTQRLMELIRYQNIDLHIIATHK	13~~KdpD (5.56341E-127) ~~223,242~~Usp (3.90014E-40) ~~366	non-kinase	KdpD;Usp
	1.2E-92	318.5	0.2	2.9E-92	317.2	0	1.7	1	A9C186_DELAS	Histidine kinase (EC 2.7.13.3)	Daci_5921	Delftia acidovorans (strain DSM 14801 / SPH-1)	904	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Delftia, Delftia acidovorans (Pseudomonas acidovorans) (Comamonas acidovorans), Delftia acidovorans (strain DSM 14801 / SPH-1)	398578	>tr|A9C186|A9C186_DELAS Histidine kinase OS=Delftia acidovorans (strain DSM 14801 / SPH-1) GN=Daci_5921 PE=4 SV=1 MPISSSAEPAPPGMPRPDPDALVARLRHERAQEGRGKLRIYFGSNAGVGKTYAM LAAAQRERQGGREVLVGLVETHGRKETAQQLHGLEQLPLRELPHQGRTLREFDL DAALARHPRVLLLDELAHSNAPGSRHPKRWQDVQELLDAGIDVWTTINVQHLESL NDVVGGIVGITVRETVPDQIFDDADEVIVVDISPDELLRRLKDGKVYMLEQAERASR NFFRRGNLLALRELALRRTADRVDEDMRDYRRERSIGTVWPARERLLVAVAGRA GDDALVRQVARMARRLDADWMVVYVDAPQRQHRPRSVQAAVLKTLALAARLGA ETATLPGADVAEALVAFARERNASRLVLAQPPRPAWSPWRWWTRSLPDRITHLH PDIDVLVLSGGSSAARTEAAPAATSALPRRAPLPWKGYAGVTLACLAATALAEQLL RVFDPANVVMLFLLIVVLSSLRWGRGPGAWAALLSVLCFDYFFVPPRGSFHVNDT QYLFTFVLMLGVALVCGQLMARLRHEARVAAERERRAGALARLARDLSGALTQE QVVEIALRTVSGVFDAQAGLLLPDADERLRPAGGGPCAMDDSIARWAMDHGQQA GQGTDTLPAAPARYVPLAAPVRMRGVLVLQLRAPQRLEVPEEQRLLEACASQVAL ALERQHFVAVAQQTQIAMEGERMRNTLLSAVSHDLRTPLTTILGAAEAAQRHVPP GGAADMLEQVRIQAQAMQRLVENLLDMARLQQGGVHLQREWLPLDEVVGSALR QMRARLGQHLVSTDVPASLPLLQLDALLMERVLVNLLDNAAKYTPAGTPLAISARV QDGELLLSVRDGGPGLPSHLPVETLFEPFTRGTAESTVSGIGLGLALVRSIVEAHG GRIEAAAARPGPGTIFTLRFPVPEQPALD	33~~KdpD (2.55703E-107) ~~243,265~~Usp (7.56805E-32) ~~390,436~~DUF4118 (4.84071E-20) ~~516,544~~GAF (7.8336E-17) ~~659,676~~HisKA (0.00000000000198015) ~~739,792~~HATPase_c (1.21452E-26) ~~895	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.2E-92	318.4	0	2E-92	317.8	0	1.3	1	Q2W609_MAGSA	Histidine kinase (EC 2.7.13.3)	amb1912	Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	898	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum magneticum, Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	342108	>tr|Q2W609|Q2W609_MAGSA Histidine kinase OS=Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) GN=amb1912 PE=4 SV=1 MIGMSEPQRPSPDALLAQARREGRGRLKIFLGAAPGVGKTYAMLCAAHERLKDG VDVVAGVVETHGRKETEALVKGLDVLPARLVEYRGREFREMDLDALISRRPAIALV DELAHANVPGSRHLKRWQDVEEVLAAGINVYATLNIQHLESLNDVVERISGVKVRE TLPDGVLAGADEIELIDLPPADLIKRLNEGKVYVPEQARRAVGHFFSPGNLTALRE MALRHAAERVDAQMVDYMRSNAIAGPWPARERIMVCIDERADSDRLVRVAKRAA DRRGAAWVAVTVETSHTLTLPEADKDRVAAAMRLAAQLGGETAHLQGDDVVAVV LACAAERNATQIVVGRPRRLRLLDHFAATVTDRLVERGGAFNVLVVGDDSEDARK VPKPTAVQPEPQDWPGLALALAAAGAATGLGFAIDLWLSVASISVAYLLAVMVVA MWIGLRPGILASVASFLAFNFFFTEPRFTFAVSDVQNLLTLAFFLIAAFIVSGMASRL RAQVQASRESARRTVNLYEFGRKVTGAATQDDVLWAVVHHVADTIRGRSLVLMP VEGRLSVMAGYPPEDHLDDKSAAAAEWAWSHGKPAGRGSATLPAALWLFLPLR TGRSAVGVLGVQMSEDADLPSPAQMRLLETLADQAAVAIERTTLVSDIEAARVAT ERERLRSALLSSLSHDLRTPLVSIMGAASSLISYDDILGPADRRDLAQTVQDEAERL NRFVQNLLDMTRLGSGTLKPRIDWADLSDIVGGAVERAARLTRSHAVKVDIDPDM PLLCVDAVLLGQVFFNLLDNACKYSPPGTGIKVWARRAADHISIEVADQGPGIPEA DREKVFDMFYRVGLTDSQPAGTGLGLAICRGIVEAHGGTIRAEAGLHGSGTAIIIRL PLPPSPDVAGEEA	22~~KdpD (7.78604E-112) ~~232,254~~Usp (4.2646E-35) ~~377,432~~DUF4118 (1.06973E-15) ~~501,527~~GAF (0.0000000000064628) ~~646,675~~HisKA (0.00000000105173) ~~729,782~~HATPase_c (1.44647E-29) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.3E-92	318.3	0.1	1.9E-92	317.8	0.1	1.2	1	D4GDC9_PANAM	Histidine kinase (EC 2.7.13.3)	kdpD PANA_3787	Pantoea ananatis (strain LMG 20103)	891	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea ananas (Erwinia uredovora), Pantoea ananatis (strain LMG 20103)	706191	>tr|D4GDC9|D4GDC9_PANAM Histidine kinase OS=Pantoea ananatis (strain LMG 20103) GN=kdpD PE=4 SV=1 MNHEPLRPDPDALLQTSSDSHRGKLKIYFGACAGVGKTYAMLQEAQRLRAQGLD VLVGVVETHERPETAQLLNGLVLLPRRATGRSRHAEFDLDAALARHPAVILMDELA HTNVKGSRHPKRWQDIEELLEAGIDVLTTVNVQHLESLNDVVGGVTGIQVRETVP DPFFDAADEVVLVDLPPDDLRQRLKEGKVYIGDRAERAIENFFRKGNLYALRELAL RRTADRVDDQMRAWRDSQGRDRVWHTRDAILLCIGDDTGSEKLVRTAARLAARL GSEWHAVYVETPRLNRLPEARRRAILRTLKLAQDMGAETATLSDPDEAQAVLRYA REHNLGKIVTGRRPARRWRRDSFAERLGQLGPDLDLLVVALNEPIQDAPHPLAED RVNSDKWRLQLRGVLMALVLCIVVTAAGQSVLISFDPANCVMIYLLAVVIVALRYG RWPSVIATVMNIIAFDLFFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRY QARVARYREQRTRQLYEMAKSLGSGLTPEDIAATSQRVLEATLQARCLLLLPDEQ GELHTLGNALPGNEPDWAIAKWSFSKGQPAGAGTDTLPAVPYQILPLKVGDLCR GLLVVEPQNVRQLMVPEQQRLLETFTVLIANALERMALSQSEAASRLSAEREQLR NALLSALSHDLRTPLTVLFGQAEMLMLDLASDNSKYVPQASQIREQTLSTIRLVSN MLDMARIQSGGLNLREEWLALEEVIGGALSSMAPSLKGREVELDLPEDIVLIKGDS TLLERVFTNLIENSLKYAGNCAPRGIRAWCENTRLEIAIWDGGPGIAQNDLTRIFDK FSRGDKESAVPGVGLGLAICKTIIESHGGQIWAENRAEGGACFRLSLPLPPVPEIS PEGLK	20~~KdpD (4.49495E-122) ~~228,251~~Usp (1.6975E-35) ~~370,402~~DUF4118 (2.14445E-21) ~~498,524~~GAF (2.47732E-14) ~~641,658~~HisKA (0.000000000438066) ~~723,776~~HATPase_c (1.79512E-28) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.4E-92	318.3	0.2	1.4E-92	318.3	0.2	1.7	1	R6H926_9FIRM	Histidine kinase (EC 2.7.13.3)	BN490_00090	Firmicutes bacterium CAG:137	900	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:137	1263004	>tr|R6H926|R6H926_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:137 GN=BN490_00090 PE=4 SV=1 MEIPRQNPDQLLRAIRNDTESKKRGKLKIFFGYAAGVGKTYAMLQAAHQAKANGT EVVAGYIEPHSRPQTSALLDGLEQLPVKQVLYGEMILREFDIDSALKRKPQLILVDE LAHTNGSGSRHAKRYQDVQELLSAGIDVYTTVNVQHIESLNDTVASITGVLVRERI PDSVFDQADQVELVDIEPTELLERMASGNIYQGDQAERAAVNFFTVENLTALREIA LRRCADRVNLLTESARIQSRGDYHTDEHILVCLSSSPSNAKIIRTAARMARAFRGN FTALFVETPATTEMNEDDKKRLRENIRLAGQLGAHIETVYGEDVPYQIAEFARLSG VSKIVIGRSTATRKSIFSKPTLTERLIANAPNLDIHVIPDASSGAVCQKRRNHRFHVT AVPVRDLAKSILVLLASTLVGYVFYTMGFSEANIVSVYIFGVLVISVITTSRFCGAVA SVVSVLVFNFFFTVPRFTFRFNNPNYLVTFPIMFMVALLTGSLATRLKNNAKQSAN AAYRTKILFETNQLLQRETEEQAVVKATAGQLLKLLQKDIVVYLANGQELDAPSIFR TPDSNQCELVSENEKAVAAWVLRNNKHAGATTDTLSSAKCLYLAIRVNQQVYGVV GVAMNDVPLDSFENSVLLSILGECALALENIKNAREKEEAAIMAKNEQLRANLLRAI SHDLRTPLTSISGNADNLLANYQKMDDDTRKRTFTDIYEDSMWLINLVENLLAITRI EGGQVHLTQSVELMDEVVAEALRHINRKSREHTIRVSSSEDLILASIDAKLIVQVIIN LLDNAIKYTPAGSVIEVHTEKNNASQQVLVSVSDDGPGIPDDQKTHIFDMFYSGAN KIADSRRSLGLGLSLCKSIVSAHGGTIWVTDRDPKGTVFTFTLPAGEVELHE	22~~KdpD (1.35346E-123) ~~232,252~~Usp (1.60558E-37) ~~375,401~~DUF4118 (0.000000000325936) ~~502,528~~GAF (0.00394801) ~~650,667~~HisKA (0.000000000265631) ~~733,786~~HATPase_c (3.95737E-29) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.4E-92	318.2	0.8	2.4E-92	317.5	0.5	1.4	1	F5XJC8_MICPN	Histidine kinase (EC 2.7.13.3)	kdpD MLP_28140	Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	868	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Microlunatus, Microlunatus phosphovorus, Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	1032480	>tr|F5XJC8|F5XJC8_MICPN Histidine kinase OS=Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1) GN=kdpD PE=4 SV=1 MQVAAVGHTGGVERGILRVYLGAAPGVGKTFAMLQEGQRRAERGTDVVVAFVE THSRAKTAAALDGLEVLPRRQVDHGGLLVDELDLEAVLARRPKVALVDELAHTNA VDASSEQRRNPKRWQDVETILAAGIDVITTVNIQHLESLNDVVTSITGVRQRETVP DRVVRSADSIELVDMSPEALRRRLAHGNVYPADKIDAALSNYFREGNLTALRELAL LWLADRVDAGLERYRGRHHITGTWPARERVVVGISGGPESIALMRRAARIASRSA GGEWLAVYVSRQDGLAAVSPAALERLRVAAEELGGEFQAVVAHDSATGLLDVAR GVNATQVLIGASRRSRISALLQPGVGEEVIAGSGEIDVHVVTHDYARRAGRQRRS RRTLSRRRQVAGYLLAVVGTVVVSLALLATSDLHGLPTESMLLLTLVVGTALLGGM WPSVIAAVLSSLALNFLFVPPTRTFTIADPENAFAIVLFVLVGVAVASVVDRSARRT QEAQEARMEANTLAVLAHSLLQSGDDPEELLRQTGEALGMTGARLIRTAGDPLVG ENAVEENAVEETVAVWGEPGSTVESSRVAAGPNLQLMLHGRPLNATDQRLLTAY AAHFAVLEERRRAEQESVRVRLLDEGNRTKTALLAAVSHDLRSPLAAIKAATSSLR NTAIAWSPHDREELLATVEESADRLDALVANLLDMSRLQTQLVTALTTEVDLLSAA EWTLANIAGADGIAVSGPDDLPPALADPGLLDRVIANVVENALKYGPASPITITGSS WTTPSGELRATLRIVDRGPGVPAEALDAIFEPFQRLGDVPAGGGVGLGLAVARGL AEAMGGTVTAEETPGGGLTVIIDLPSAGPNPPPAEDNL	13~~KdpD (2.52997E-114) ~~227,249~~Usp (2.20585E-27) ~~371,397~~DUF4118 (0.00000000000189404) ~~496,X,633~~HisKA (0.00000000000316147) ~~699,749~~HATPase_c (0.00000000000002289) ~~854	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.5E-92	318.1	0.1	2.3E-92	317.6	0.1	1.3	1	E3JB50_FRASU	Histidine kinase (EC 2.7.13.3)	FraEuI1c_6701	Frankia sp. (strain EuI1c)	913	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain EuI1c)	298654	>tr|E3JB50|E3JB50_FRASU Histidine kinase OS=Frankia sp. (strain EuI1c) GN=FraEuI1c_6701 PE=4 SV=1 MTSDAVDGPRRGRLRIYLGAAPGVGKTYAMLSEGHRRAGRGTDTVIGLVETHGR HLTAEMIGEFEIVPRRTVYHRGARFTEMDVDAVLARKPALALVDEYAHSNVPGSR NAKRWQDVEDLLGAGIDVVTTLNIQHLESLNDVVSTITGVPQRETIPDAVVRAADQ VELVDMAPEALRRRMAHGNVYAADKVDAALANYFRVGNLTALRELALLWVAGKV EEQLDDYRVDHGITDTWEARERVVVAITGGPEGDTLIRRAARIAARSTGGSDLLAV HVSRPDGLVTGADPAALARQRALVESLGGSYHLVLGDNVPKALLDFARAENATQL VLGASRRGRFAHLVSRGVGVTTTARSGSIDVHLVTHEESSAGGRGTRIPGEDGSK SGGAWVLGAGRARRRASSLTLSASRQLAGFTLAGGALALLTVLATSSRQEVNLTS DTLLYLLVVVASAFIGGIWPALAAAVAASLLLNFYFTPPLHTWTIDDRNNAFALAAF VAVAIAVSRVVDLARRRSVQAARASAEAETLATLAGTVLRSEHPLPAILERVREGF GMTSVTLLAARSGDDASNPPPPGSGRDLWEIVANVGPRPAEHPSDGDVEVPAG RFTLVLRGRPLPAADRRLLAGFAAQAATAAERLRLAQEAASVKPLAEADRVRSALL TAVSHDLRTPLAAAKAAVTGLRAEDVVWSPEERAELVATADESLDRLTTLVENLLD MSRLQAGVLSVFPRAVHVEDVVALALDCLGPDAVGVRIQVSADPEVPAMRADPVL LERVIANVVANAIRFSPAGSPPLVSASTLGDRVQIRVVDRGPGVPKTDRDAIFQPF QRLGDRDNTVGTGLGLALSRGLTEAMNGTLTPEDTPGGGLTMVVELPAASGTTE EAVDPATSGGPATSGGPEPSGGPATSGGPR	9~~KdpD (7.59854E-117) ~~219,241~~Usp (4.37116E-21) ~~365,X,655~~HisKA (0.00000000000195196) ~~721,774~~HATPase_c (9.30371E-25) ~~875	kinase	KdpD;Usp;X;HisKA;HATPase_c

	1.6E-92	318.1	1.4	2.5E-92	317.4	1	1.3	1	R6R2Y2_9FIRM	Uncharacterized protein	BN652_02355	Firmicutes bacterium CAG:424	675	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	1263022	>tr|R6R2Y2|R6R2Y2_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:424 GN=BN652_02355 PE=4 SV=1 MEKEEYERPDSSQLLRRLQFEEEEKLKKSRGKLKIFLGYAAGSGKTYAMLKAAHE AKKHHIDVVAGYVEPHARPDTQALVKGLETIAPMEIAYKGVKLREFDLDAALKRNP RLILVDELAHTNVKGCRNEKRYQDVKELLRAGIDVYTTMNIQHLESLNDIVGNVTHI EVRERVPDKVFDHADQVEVIDIEPEELIERMKEGKIYGTLQAERALENFFRREKLVA LREITLRRTADRVNRIAEEERNALGEMDYHTGEHVLVCISPSPSNAKVIRTASRLAY AFHASFTGIYVETPKMQEADEKNKAAVKNHMDLARALGADIVTVYGTDIAYQIVEY AIVGNISKIVMGRSRKQWMFGKSRSEVLEQLTYRAPNIDVYIIPDMKHTKEYREKG KSSEKKEESGKMVLLELGEITAIMALSTMAAYIFQWFRLSEANLIMVYMVGVLLSS YVADKKIYALYSALISVLSFNFFFTEPYFSLKAYDKGSPVTFAMLFAVGFFMASMTR QLKAQTRESAKKAYRTEILLENSRKLRRCRTREEVWKQVAAQVGKLLNLSIIIYPVD KKGNLEEPMLFPRKGMGLPELKENVNGKERAVAQWAASNRHRAGTCTHTLPDA NAMYLPVQSTEEVKGVMGILLEERRPVKDFEYGLLIAMLNETGVKLQDTFLEKEIKI N	28~~KdpD (9.08415E-122) ~~238,259~~Usp (3.40886E-37) ~~382,411~~DUF4118 (0.00000000000078062) ~~512,540~~GAF (0.000000440509) ~~664	non-kinase	KdpD;Usp;DUF4118;GAF

	1.6E-92	318.1	0.1	1.2E-90	312	0	2.4	2	Q0K2T7_CUPNH	Histidine kinase (EC 2.7.13.3)	kdpD2 H16_B0895	Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	948	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus necator (Alcaligenes eutrophus) (Ralstonia eutropha), Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	381666	>tr|Q0K2T7|Q0K2T7_CUPNH Histidine kinase OS=Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) GN=kdpD2 PE=4 SV=1 MPDAELREAGSRPDPDALLQMVQEEGARASRGKLRVYFGASAGVGKTFAMLTA ARTASARGTDAVIGIVETHGRAETEALIAGIERLPMKDVPYRERVLQEFDLDAALVR RPALVLVDELAHSNAPGSRHPKRWQDIQELQAAGIDVWTTVNVQHLDSLNEAVG GITGIRVWETVPDVVFDSADEVVLVDLPADELLRRLKEGKVYLPEQARHAARNFF RKGNLIALRELALRRTADRVDSDVRAWRQSEAVQGVWRTREAVLACIGSGDDAE QVVRSARRLAGQLDCDWHVVTIATPRLAPPSDFAKTRLQTAMRLAEELGARTETL AGNDMVQAIVGYVRRHNLTKVVIGRAPADWRRGGASVAERARSLLGLALTPFVN APAWLFGRRSFADALALGCPEIDIIRVAADTTRVDLRPRHGTEAPDAPAPGDGAT RKDYLWAAAWCAGATALSALAFPWFDVVNIAMLFLAAVVGVALRHGRGPAALAS VLAVAAFDFFFVPPRLSFAVSDVQYLLTFLVLLSVGLVIGQLTAGLREQAQVAVQR ENDARTLYELARELSAALVPNQIVSIASRFLRAAFDANSAFFLVSAEGRLLPPVSDV EQHDTGARTDSIDRVLAEWVFDHGQPAGTGTHTLPGSTVLYLPLKAPMQTRGVL AVEPAVSRAFAQPALRRQVDVFCTLIAIAIERLHYVEVAQLALLSMESERLRSSLLA AVSHDLRTPLTSLIGMAETMQRSDPGLAPSLAETVAAMLEQARRMRTMVVNLLD MAKLQGREVRMSKEWQSVEELVGASLAAMREALEHHRVVVVDLSRVPLVECDA VLIERVLCNLLENAAKYTPAGTEIRLSAAPVDDEIRIAVEDDGPGVPKGKERQIFEK FTRGERESATAGVGLGLAVCEAIVQAHGGRIWVEPAQRPDRPGGQAGARFLVAL PRGNPPAVEPEQTDA	29~~KdpD (6.33579E-118) ~~239,262~~Usp (6.94588E-32) ~~360,454~~DUF4118 (0.00000000000042746) ~~540,567~~GAF (2.50938E-16) ~~690,707~~HisKA (0.000000000000373313) ~~772,825~~HATPase_c (2.09923E-28) ~~933	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.6E-92	318.1	3	2.4E-92	317.5	2.1	1.2	1	K9XY83_STAC7	Osmosensitive K channel His kinase sensor	Sta7437_4020	Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	374	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Stanieria, Stanieria cyanosphaera, Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	111780	>tr|K9XY83|K9XY83_STAC7 Osmosensitive K channel His kinase sensor OS=Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437) GN=Sta7437_4020 PE=4 SV=1 MIEGNKITDSSAYQFFQRRGKHRIYIGMSPGVGKTYRMLQEAKGLLEEGIDVVIGL LETHGREETAEAASGLELIPRQQIKRGNHTLTEMDTEAILKRQPQLVLIDELAHTNV PGSQREKRYQDVEVVLAAGIDVFSTVNIQHLESLNDLVAKITGVVVRERIPDRILDE ADEVVVVDVTPETLQERLREGKIYTLDKIERSLQNFFQRHNLVALRELALRREIADNL EEIAESTTPKDKYCSIQERVLVCISTHPNSSHLLRRGARLASQMRSRLYVLYVNNP DRFLTKDESLYLEMCEKLSEQIGGEFIRVDSNNITTAIAQTAKKYFITQIVLGQTRRS RWQLLLRSSPVQELLKVLHDVDLHIIATNNNSR	18~~KdpD (7.34473E-117) ~~227,246~~Usp (2.95741E-44) ~~368	non-kinase	KdpD;Usp

	1.6E-92	318.1	0.1	2.5E-92	317.5	0	1.3	1	A0A099GBC0_9RHOB	Histidine kinase (EC 2.7.13.3)	IX56_15165	Paracoccus sp. 5503	921	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 5503	1525717	>tr|A0A099GBC0|A0A099GBC0_9RHOB Histidine kinase OS=Paracoccus sp. 5503 GN=IX56_15165 PE=4 SV=1 MTDAPRPDPERFLAEANAEAGVTTAAGRGRLKIFLGASPGVGKTYAMLEEAGAR ARAGTDVTVALAETHGRAETAALLARLDQMPRRVVTYRDRQLTEMDLDALLARRP GLALIDELAHSNVPGSRHPKRWQDVEEVLAAGIDVYTTLNIQHIESLNDLVARITGV RVQETVPDAVLQMADEIKLIDLPPEDLIQRMREGKVYMPAEAGRALGNFFSKPNLT ALRELALRTAASRVDAEMLALTRGTGRAAAQDRLMVCLDDPATAKGLVRAGRRM TDRARIPWVVATVVTPAVEAQGPQAAGAMTDALQLAERLGAQARTLRSEGDVAA AFLDAARQLNVTRLIVGRATRAGWRDRIAALIRPPLAQTLLAQAEGFEVTVLDPAP DRPSPPQPPTSPAPATEPAARWRETDWRAGPGRDWGRIAVAALGAAVAGTLAA WPFWSILPVASLAVIYLVGVLAVGMRLGTAGAVAAAVLSFLAYNYFFTEPYYSLQV SAEESVVALLVFTISAVFTGTLAGRLKRQVEFMRVTQARTETLYDFARKIASATTTD DVLWAAAAHIARTLECHSLILMPDATGALQQVQGFPSIEEGLDAHALAAARWAYE KDQPAGRDTDTLPTAGWMFIPLATQGAPLGVIGLRFTDPARRMDPETRRLLVAVE DQVAVAVERMAVEDDLERARLTSETEKLRAALLNSVSHDLRTPLVTVIGALSAVEA GGLSPAQERGLVVEALDEARRLDRFVGNLLGMTRLGHGALVPRRAAVAVAEVIG RARADLSRVLARFRVAVEIDPATPPLAVDPVLIGQALVNLLENASKYAPEGSTIRLT AAPVPEGVALTVIDEGPGIPVAERSRVFDLFHRAVQGDGQPAGTGLGLAIVKGMV EANGGTVAAIAPPDGRGAAIRLLLPAAAAAAAEDADA	26~~KdpD (8.59928E-115) ~~236,255~~Usp (3.17786E-17) ~~382,436~~DUF4118 (0.00000661526) ~~524,550~~GAF (0.000000000868009) ~~671,688~~HisKA (0.0000000288298) ~~752,805~~HATPase_c (8.79346E-21) ~~899	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.6E-92	318.1	0.1	2.5E-92	317.4	0	1.3	1	A0A0A8F065_9ACTN	Sensory histidine kinase in two-component regulatory system wtih KdpE	GZL_08794	Streptomyces sp. 769	837	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	1262452	>tr|A0A0A8F065|A0A0A8F065_9ACTN Sensory histidine kinase in two-component regulatory system wtih KdpE OS=Streptomyces sp. 769 GN=GZL_08794 PE=4 SV=1 MARGRLRIFLGAAPGVGKTYAMLAEGQRLRALGTEVVVGFVEPHGRRPTAAMAE GLETIPRRALRHRGARFTEMDPDAVLARRPQVALVDELAHSNVPGTRNAKRWQD VEELLDAGIDVVTTLNVQHLESLNDVVRQITGVRQRETLPDEVARRADQIELVDLP PEVLRRRMVHGDIYPADRIESALTHYFRVGNLTALREIALLWLADRVEEGLQRYRA EHGIVAPWETRERILVALNGGPEGETLIRRAARISARTPGTELLALHVVPEDGLTHV DPSVLDAQRTLLESLGGSFHQTTGEDVVEALLQFAEAENVTQIVLGASRHGRVAS LLRAGVGERTIKGSGPIDVHIVTHEEAAASAALRLPRPGNGMGPRRLGAAAAGAV VLLPLLTLLLTVVRGPMGLAGALVLYLLVVVVVVALVGGVVPALLAAVAAALLADYSFI APVHSFDIERPDEIVALVVFVVTAVLVGTAAGAAARHTRQAARAIAEARTLSRLAA GVLRGQDLPALVEMIRENFGLSAVSLLERDPRASPVPRWYVVASAGDHPPERPY EAEVESPVDDLLTLAARGPGLSSQDRRLLDACAAELGLAHARGRIAGPAGLGDPL AEAERTRASLLLAAGRDLRAPLRTAEDALGRLRRRGGERAPDERRLLETARAAVH RAAQLVTDLDDLSRLHAGALDLYLRPVDLNEAWGAALDDLGPGGHSIVLRLPEYL PDVIADAALLTRALTALAADALRHSPPGRPPVVTAETHDGRVAIRVADGSGGEGA AAAGRSGSRADSLALRLSRDLAEAMDGSLRTSGRGSAFTVTLSLPSSAPGRPRR GKRPKHST	1~~KdpD (3.10106E-115) ~~211,233~~Usp (6.44063E-28) ~~355,X,743~~HATPase_c (0.16)~~820	dysfunctional kinase	KdpD;Usp;X;HATPase_c

	1.6E-92	318.1	0.7	2.6E-92	317.4	0.5	1.3	1	R5TPN1_9FIRM	Universal stress family protein	BN481_00424	Ruminococcus gnavus CAG:126	550	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	1263106	>tr|R5TPN1|R5TPN1_9FIRM Universal stress family protein OS=Ruminococcus gnavus CAG:126 GN=BN481_00424 PE=4 SV=1 MTEENRPDPGLLLKKLQYEEKEKEKQTKGKLKIFLGYAAGSGKTYAMLEAAHEAK KHQVDVVAGYIEPHARPDTQAMAEGLEEIPPLMVDYKGIQLREFNLDAALERKPKL ILVDELAHTNVRGSRNEKRYQDVRELLRAGINVYTTMNIQHLESLNDLVGNITNIEV KERVPDSVFDQADQVEVIDIEPEDLIERMKEGKIYGPVQAERALENFFRREKLVAL REIALRRSADRVNRIAEEERNILGNTGYHTGEHILACISAAPSSAKVIRTAARLSYAF HAQFTALYVETPAMQEAGEKTKQTLKSHLELAKALGAKIVTVYGEDAAYQIAEYAI VSNVSKVVMGRTNHRGIWRRPRIEVMEKLTHMAPNIDVYIIPDIRKATHKREVQIQ RRRKTSWKNVLLDLAEITGVMAAATLAAYVLWLFRLPESNIIMIYILGILLSSYIANKK IYALYSSLISVFAFNFFFTEPYFSLKAYDKGYPTTFVMLFLVGLFTATLTRSLKQQS RESAKKAYRMEILLENSQKLRRCKSKQEVWTQVAGRQESF	31~~KdpD (8.17056E-121) ~~236,257~~Usp (1.82744E-35) ~~380,408~~DUF4118 (4.16815E-15) ~~509	non-kinase	KdpD;Usp;DUF4118
	1.6E-92	318	1	3E-92	317.2	0.2	1.8	1	A5N880_CLOK5	Histidine kinase (EC 2.7.13.3)	kdpD CKL_1469	Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	898	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium kluyveri, Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	431943	>tr|A5N880|A5N880_CLOK5 Histidine kinase OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=kdpD PE=4 SV=1 MGIHQTNSNLLTEQLLNMSTEKRQGRLRIYFGYAAGVGKTCAMLNDAHEMKKDGI DVVAGYIEPHARPETMVLLNGLELLPPLEVLYNGIMLKEFDLDSALKRKPQLVLVDE LAHSNAVACRHKKRYQDVEELLHAGIDVYTTINVQHIESLNDVVASITGISVRERIPD SVFDSADQVELVDIEPDDLIDRLNKGKVYGREQAQRALVNFFTKEKLVALREIALR RTADQVNRVAVLNNKQSKNGGHYTNEHILVCLSSAPSNAKVIRTAARMADAFHGT FTALLVETPQIKELSEKNMIKLRENLRLAEQLSAQIATVYGEDIPMQIAEYATASRVS KIVIGRSNHVKKWFAKTNFVDRLITLAPNLDIYIIPDTQSSFYVKIYKFTKPLELSLPDI FKSAGILFICTLIGLWFDSLGFSESNIIMVYILGVLFNAMVTKGKIYSAVASILSVLVF NYFFTYPYFSLLAYDPGYPVTFLVMLMASFIVSTLTKRVKEQARYSAQKAYRTEVL LETNRKLQQARDKSEIFSETAHQLVKLLDRTVIFYPEQHNTLSEPLVFPKDGWEDY FKIYLKTDERAVAEWVYKNNKRAGATTNTLSAAKCLYLAVRSSDMVFAVVGIVMD KKVPLEAFEKSLMIAMLGDCALSLEKEKLNERQKQISMQIQQEKLRGNLLRTISHDL RTPLTSISGNAGILMGNSKVLSEAQKKGLYTDIYDDSMWLINLVENILSITRIEDGKI NLNLQPELLEEIIAEALCHINRNSVNYHIETIVEDELIMAKVDSRLIIQVIINIVDNAIKYT PPGSHIVISAKRRKQFILVEIADDGPGIEDEAKDRLFDMFYTVDNIHGDSRRGLGLG LSLCKSIVHAHGGTIYVKDNIPQGTVICFTLQAQEVKLS	22~~KdpD (2.17125E-119) ~~232,253~~Usp (5.96982E-37) ~~375,399~~DUF4118 (3.46786E-16) ~~500,X,668~~HisKA (0.0000000124787) ~~734,787~~HATPase_c (3.33696E-28) ~~890	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.7E-92	318	0.5	2.7E-92	317.3	0.3	1.3	1	Q9A7X5_CAUCR	Histidine kinase (EC 2.7.13.3)	CC_1594	Caulobacter crescentus (strain ATCC 19089 / CB15)	892	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter vibrioides (Caulobacter crescentus), Caulobacter crescentus (strain ATCC 19089 / CB15)	190650	>tr|Q9A7X5|Q9A7X5_CAUCR Histidine kinase OS=Caulobacter crescentus (strain ATCC 19089 / CB15) GN=CC_1594 PE=4 SV=1 MPVDDPKRPDPEALLAAANKARRGRLKVFLGMAPGVGKTYEMLRAARRRKAEGA DVLIGVVETHGRRETESLLRGMDVLPRRPIEHRGRVQMEFDIDAALERKPKILLVD EYAHSNAIGSRHPKRWQDVEELLAAGIDVWTTLNVQHLESLVDVVQRITGVRQRE TVPDSALSRADDIELVDITPDELRERMAAGKVYVPETARLAADNFFKVENLTALREL ALRRAAQTVDDQLIATMREKGVEGPWAAGERILVLVSGDAMAATLVRAGRRLSD MMMDAPWIVTHVERTDRPLARDGDAARLREAYRLAEQLGGATVALSGGDIVDTV MAYARRHNVTQIVIGKSVESRWRELLERSLAGALLREARGVAVHVVTEAAPEREP RPPAPLRPDRWRGYAVGALFIAAATLAAWGLDVAFNRVDLGMIFLTAVLAAGVLH GLRPALAAATVAFLVYNCLFLEPRYSFVVGSPTDFITLVVFWAVALASGGLAGRVR EQALGSQRRAAAVTTLLAASRTFSAASGRDAVAKALAEQVSAAAGGLAVVLLPQG DEIALAHGSPELAPLDAAQMAAARWAWDKGEVAGFGTGTLPQSRWTFWPLDGV RARTGVAGLAAGAAPLGADQERLVLALLEQGAVALERSQLAAEAVETETLRRADR FRSALMNSVSHDLRTPLSTVLGASTTLIDYGDKLAKPVREDLVVSIREEAERLNRY VANLLDMTRIEGGALRLRTDWIDVRDVLNAAADRVSRRLGGRELARDFPRELSLIQ ADASLLEQVVVNVLENAIAYSPPEARIEMAAYEDRANVVISIEDEGRGIPTSELERV FDKFRRMEEPSDRTQGAGLGLSIAKGFIDALGGRIAAASPIHDGRGTRILISLPKTV TTPHHLL	21~~KdpD (3.51939E-123) ~~231,253~~Usp (1.22407E-39) ~~377,399~~DUF4118 (0.000000000114198) ~~498,X,658~~HisKA (0.0000000011793) ~~724,777~~HATPase_c (7.0379E-24) ~~881	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.7E-92	317.9	1.6	2.6E-92	317.4	1.1	1.3	1	K9VHA8_9CYAN	Osmosensitive K channel His kinase sensor	Osc7112_2130	Oscillatoria nigro-viridis PCC 7112	383	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria nigro-viridis, Oscillatoria nigro-viridis PCC 7112	179408	>tr|K9VHA8|K9VHA8_9CYAN Osmosensitive K channel His kinase sensor OS=Oscillatoria nigro-viridis PCC 7112 GN=Osc7112_2130 PE=4 SV=1 MIHSSELTNNPDAVYAQPNRTYDRTPRRGKHKIFIGMAPGVGKTFRMLEEGHRLK SEGIDVVIGLLETHGRKETAAKAEGLEIVPKKQMRRGEKMLAEMDTDAVIERRPQL ALIDELAHTNIPGSLREKRYQDVEEILNAGIDVFSTLNIQHIESLNDLVARITGVVVRE RVPDPVLEDADEIVVVDVTPETLEERLLEGKIYAPEKIEQSLENFFQRRHLIALRELA LREVADNVEDDAATLKGQSCNIHERVLVCISTYPNSLQLLRRGARIASYMNAPFYA VFVNDPDRFLTKAESLHVETCEKLCQEFKGQFLRVNGTNIAKVISEVAKQYRITQIV IGESQQSRWHLLLRGSLTQQLVRSLKHVDLHIIATEKSGLSN	26~~KdpD (3.62407E-129) ~~236,253~~Usp (3.16567E-44) ~~375	non-kinase	KdpD;Usp

	1.9E-92	317.8	0	3.1E-92	317.2	0	1.3	1	A0A068R7B7_9ENTR	Histidine kinase (EC 2.7.13.3)	kdpD XPG1_2374	Xenorhabdus poinarii	895	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus poinarii	40577	>tr|A0A068R7B7|A0A068R7B7_9ENTR Histidine kinase OS=Xenorhabdus poinarii GN=kdpD PE=4 SV=1 MAQHEPQRPDPDELLTLANAKPRGKLKIFFGACAGVGKTYAMLQEAQRLLAQGL DVIVGVVETHERQETAALLKGLPQLPAKYVHHHKRRIATFDIDAALARHPAIILMDEL AFSNPKGCRHPKRWQDVEELLETGIDVLTTINVQHLESLNDIVGGITGVRVRETIP DHIFDQADDVVLVDLPPDDLRQRLNDGKVYISGQAERAIEHFFRKGNLIALRELALR RTADRVDEQMRAFRDTHGREPVWHTRENLLLCIGDNAGNEKLIRKAARLAAKLNC VWHAVYVETPKLHRLPESKRHAILQSLKLAQDLGAETATLSDPHQEKAILRYAREH NLGKILIGRYYGSQPNILGFKWHRDFSERLGKLGPDLDLIIVALEDKKRGDKELKDN RTSHDKWFVPVQGFLVAVVLCVLITFFSWAFLVTLDQANLVTLYLLGVVMIALFYG RWPSVFAAFINVISFDLFFVQPHWSLAVKDMQYLLTLTVMLIVGAVVGNLTAGIRY QARIARYREQRTRHLYEITRELSKALSEEDIARISYHFLSNSFQAKTGLLLPDCHHH LYQISAHNGGQMRIDEAIAKWCFDKKQPAGAGTDTLPGVPYQLLPIATPAQVFAVL AIESPNLRQLLVPEQQRLLHIFTGLIANALERLHLARKAESAKLDAEREQLHHSLLV ALSHDLRTPLTVLFDQSKVLMRDLAGGNSPYTQQVNQIHQQILSTSRLVNNLLDM ARLQSGEIQLNLEWHSLEDIVDNAFRSLAYALNHYTVALSLPNDLLLYCDATLLERV FINLLENAIKYTHEKTPLGILATIEKVTSQQLHVEVWDAGTGIPPGQEKHIFEPFSYA NQASPIRGIGSGLAICRSIIEIHGGKIWTANNKKGGASFHFLLPLAAPKN	23~~KdpD (1.14697E-119) ~~231,254~~Usp (7.5118E-35) ~~379,407~~DUF4118 (5.09004E-22) ~~506,532~~GAF (5.90852E-16) ~~650,667~~HisKA (0.000000340102) ~~732,784~~HATPase_c (1.72378E-23) ~~888	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2E-92	317.8	1.4	2.6E-92	317.4	1	1.1	1	K9PA50_CYAGP	Osmosensitive K+ channel His kinase sensor	Cyagr_3178	Cyanobium gracile (strain ATCC 27147 / PCC 6307)	364	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobium, Cyanobium gracile, Cyanobium gracile (strain ATCC 27147 / PCC 6307)	292564	>tr|K9PA50|K9PA50_CYAGP Osmosensitive K+ channel His kinase sensor OS=Cyanobium gracile (strain ATCC 27147 / PCC 6307) GN=Cyagr_3178 PE=4 SV=1 MIRSSRGRGRHKVFIGMAPGVGKTCRMLQEGRELLKEGTDVVIGLLETHGRQETI RQAEGLEQVPRKQLLYQGVTLEELDVAAVLERRPQLVLVDELAHTNIPGSERKKR WQDVEALLLSGLDVYSTLNIQHLESLNDLVAELTGVVVRERIPNRVLEQADEVVLV DVTPETLQERLKEGKVYAPEKVPQALANFFQRRHLVALRELSLREVADRVEEEEP TAAGLRERVMVCVSAYPSATRLLRRAARLASTMDAPLLALTIQDPGRFLSRQETLR LEACATLCQDVGGTFLRIESSDVLGTIARVARERRITQIVLGQTLRSRWQVLLRRPI SERLQQLLRGLSIDLHLISDTTAPGADAEP	7~~KdpD (4.07094E-121) ~~216,229~~Usp (1.58029E-25) ~~353	non-kinase	KdpD;Usp

	2E-92	317.7	0.8	3.1E-92	317.1	0.6	1.3	1	C7JIB3_ACEP3	Two component sensor histidine kinase KdpD	kdpDAPA01_40530APA01_43130	Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)	895	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acetobacter, Acetobacter pasteurianus (Acetobacter turbidans), Acetobacter pasteurianus subsp. pasteurianus, Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)	634452	>tr|C7JIB3|C7JIB3_ACEP3 Two component sensor histidine kinase KdpD OS=Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153) GN=kdpD PE=4 SV=1 MEAHLIRPDPDALLRQTVLDGESRKRGRLKVFLGAAPGVGKTFEMLTVAHQLQRD GVDVVIGVVETHGRAETAALVNGLELVPLRTMTYRDRMAQEMDLDAVLRRAPCV AAVDELAHTNVPGSRHPKRWMDVEELLAAGIDVLTTVNIQHLESLNDIVASITRIRV RETVPDHVIGDADEVELIDLTPNDLLQRMRDGKIYAEHTAGRAMLHYFSPGNLTAL RELALRQTAQQVDAQLVDHMKANAIVGPWAAGERIMVCLTLQDGDASLLRYGKR LADHLHAPWIVLHVETNRDLSDAARATMASQMHLAQSLGAELVTIPGQDVALDAV AYARTQNVTQIVAAHPVGRGWSARVRQWLGRSTTERLIQFAQGFPVHVVPRSP GENAPTEQLLNIAPFTARPYVVGTLIVLGALVVALLLRQSFEVSNVSLAFLTAILGVA VAYGLWPSLWASLMAMLCFNFFFLPPFYTLTIAAPDNVVALFFFLVTALIASNLGA RVRNQAVVARHRADITQSLYHFSRTITGILQLEDLLWSASHQIATMLDCDVAMLLP DGEILKVKASYNGGKAVGAADLAAATWAWKNNKVAGRGSDNLPGGRWLFIPLRT GRGPVAVIGLHAERTGPILDLEQQGLLDALADQTASAIESILLAGELDQARLDVETD KLRGALLTSISHDLRTPLASILGATSSLESYGEELDENARKELLSTIHDEADRLNRFV ANLLDMTRLEAGALQPRKERVDIGEVIASALCRAARLLSDHETEMVIEPDLPMLLLD DVLLEQALFNILDNAGKYTPVGTKIVVTASVAADTLLIRVTDEGEGFAAHDPETAFS KFKRFKSADRSRPGTGLGLAISRGFIEALGGKIVSRNRKDCSGAELVMTFPLDEKN TK	25~~KdpD (1.05915E-107) ~~234,256~~Usp (3.28833E-32) ~~381,428~~DUF4118 (0.000000000000011521) ~~503,530~~GAF (0.0000000000332955) ~~647,665~~HisKA (0.00000000000040447) ~~731,784~~HATPase_c (4.77293E-20) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2E-92	317.7	1.1	3.9E-92	316.8	0.2	1.9	1	F4GEN7_ALIDK	Histidine kinase (EC 2.7.13.3)	Alide2_1439	Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	909	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Alicycliphilus, Alicycliphilus denitrificans, Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	596154	>tr|F4GEN7|F4GEN7_ALIDK Histidine kinase OS=Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601) GN=Alide2_1439 PE=4 SV=1 MGAENTQQADALVGELRRQAAGRLTVFLGAAPGVGKTYAMLARARELHRQGIDV VIGIVETHGRAETMALVEGLPQVPRRQVGYQGRMLDEMDLDGLLARRPAIALVDE LAHRNAPGSRHERRWQDVQELLDAGIDVYTTVNVQHLESLNDVVHQITGIRVSET VPDAVFERLRDIRLVDLPARELIERLNQGKVYLPEQAAQALQAFFSPSNLTALRELA MQTVAEHVDADLRETRTARGLADIAIQRHVLVAIDGRGQSEYLVRAGARIAERRGA PWSVVSVDTGRSAGAALHAEDLERAAPGQARHSAAHAEQQRQRELDQAFALAR SLGGETEALHNTDVTQALLDAAAARGARSIVIGRTRERPVARIFNRTLTQQLLQRG ARYELTIVSTPQARQRALRLQGLAGERLARGEPALIALATLGATAAAALAERFVGL EDLSTVFLIAVLLVASRTRMVAAAITAVLCFLAYDFLFIEPRFTFLISAQRGVATVLLF LAAALIAGRLASRLRMQVIALRAANTHATAMQNLARQLSKAADLGQVITASASVLQ STLNAQAWIRINGESGPAAAAQHLDEKDKAAAEWSQQHGQPSGRYTDTLAHCA WWFLPVHSDRETLGVVGLRFPAGMGRLPFEQRRLAESMTEDIGQAALRARLVSE LEAARVTGETERLRSALLSSVSHDLRSPLSSMIGAADSLARYGQDMGAQDRGSLL ETIRVEGERLDRYIQNLLDMTRLGQQGLALSRDWIGVDELVGSAVRRLQRYEPAV KVESSIDAGIGPVHVHPALIEQAIFNVLENAAKFSPPGEPIRVQALREEGGLLRIDIS DRGPGIPEDERRRIFDMFYSVERGDRGKQGTGLGLTIVQGIVGAHMGRVEALPG PDGRGTTIRLTLPLGEPLPAQEG	22~~KdpD (1.31422E-119) ~~229,250~~Usp (7.95852E-28) ~~395,448~~DUF4118 (0.000186845) ~~490,X,675~~HisKA (0.0000000000286571) ~~741,794~~HATPase_c (1.00441E-23) ~~898	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.2E-92	317.6	0.1	3.4E-92	317	0	1.3	1	A5V6B3_SPHWW	Histidine kinase (EC 2.7.13.3)	Swit_1465	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	895	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas wittichii, Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	392499	>tr|A5V6B3|A5V6B3_SPHWW Histidine kinase OS=Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273) GN=Swit_1465 PE=4 SV=1 MIHPPEPARADPDALLRAAAREARGRLKLFLGAAPGVGKTYEMLSEGAARLREGE DVVVGVVETHGRRETEALTRPFEIIPRRVSEHHGRPLSEMDIDAILARAPQLVLVDE LAHSNAPGSRHPKRWQDVEELLAAGIDVYSTINIQHVESLNDVVASFTRVRVRETV PDHVLEQAEIEIVDIPPDELIERLKDGKVYVPEEASRALSHFFSKSNLSALRELALRR AAQAVDAQMLDHLRAHALGGTFAGGDRVLVAVSERPEAEALVRAAKRLADALRA PWTAIHVETGRSSGFGAAERERLARTLALAAQLGGGTASVPATDVVSGLAGYAR DYRATQLVLGKSSRSWWFELRHGSVVDRIVRSAEGVAVHVLPIAGQAGAGLAAR RTWREGLEARPFLWSLAMVAATVASAVGLRQLLDLNNVAMLFLLPVLAAAGRFGL RPGLFAGLVSALAYNFFLLPPLYTLSISNPENVIAFFVLLIVAVVTSQLAARMRAQAE LANRSARQNAALAGFAQRIADAANPDELAQAICGEIARLFNVNAMLFMPSPAGAAL VAAVPTGHEPDQLDLAAANWTLEKGKPAGRGSDTLTASDWLFQPIAKGDRTLAA LAVAHVDPDGAAIRSDELPLLLSLAHQSALAMDRMQLAEAMRELDVVRSRDRLRA ALLSSVGHDLRTPLTTIRSAIGELGQSALAPTDAAIVDALDGEVERLDRFVGNLLDM ARAQAGAITLAIEPIDLTDAVASAVHAVRKTLDGHDILLDIPPELPMVRADPQLLHHV LINLLDNAGRYAHPGTPLRIGARRGPDGLSLAIRDEGPGLPEGKETAVFETFTRFD GSDRARGGTGLGLAIARDFAAAMEVDIRAERCADPQGARFTLSWPDRLVVRIDPE ALA	28~~KdpD (1.87655E-103) ~~231,253~~Usp (1.54031E-41) ~~376,399~~DUF4118 (2.3564E-20) ~~499,525~~GAF (0.00000255026) ~~645,662~~HisKA (0.0000000296748) ~~725,778~~HATPase_c (1.59365E-21) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.2E-92	317.6	0.1	3.4E-92	317	0.1	1.3	1	A0A0A0Z0J6_9ENTR	Histidine kinase (EC 2.7.13.3)	PSNIH1_04915	Pantoea sp. PSNIH1	891	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH1	1484158	>tr|A0A0A0Z0J6|A0A0A0Z0J6_9ENTR Histidine kinase OS=Pantoea sp. PSNIH1 GN=PSNIH1_04915 PE=4 SV=1 MNDELPRPDPDALLLSHSDSHRGKLKIYFGACAGVGKTFAMLQEAQRLRAQGLD VLAGIVETHNRAETAALLHGLTLLPRRTTGRSHHTEFDLDAALARHPAVILMDELAH TNVQGARHPKRWQDIDELLDAGIDVITTVNVQHLESLNDVVAGITGIQVRETVPDP FFDSADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALRELALRR TADRVDDQMRAWRDQQGRDRVWHTRDAILLCIGDDTGSEKLVRTAARLAARLGS VWHAVYVETPRLHRLPEAQRRAILRTLQLAQELGAETATLADPDEVRAVLRYARE HNLGKIVAGRQPHRRFRRDSFAQRLGELGPDLDLLVVALDEPLRPALHAASSKPV SSDKWRLRLRGCIMALLLCLAVTFIGRGLLAEFDSANAVMIYLLSVVLVALRYGRW PSVFATVINIVAFDLMFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRYQA RVARYREQRARYLYEMAKSLGSALTPQDIAATAQRVIEVTLQARSQLLLPDEQGEL QATGPDLRGTPPDAGIAKWSYSKGQPAGAGTDTLPAVPYQIVPLKSGQQCRGLL VVEPENLRQLMIPEQQRLVETFTVLIANALERMALTQSEAASRLAAEREQLRNALL SALSHDLRTPLTVLFGQAEMLMLDLAHAQSPFVAQAGQIREQTLSTIRLVSNMLDM ARIQSGGLQLREEWVALDEVIDGALRSMGPMLKGHAFELALPSELVLIKGDSAML ERVFSNLIENSLKYAGNAAQHGIRAWRDGSRLEIGVWDSGPGIAGDSLTQIFEKFA RGDKESAVPGVGLGLAISKTITEAHRGRIWAENRASGGAEFRLSLPLAPPEISEA ALK	20~~KdpD (2.20877E-120) ~~228,251~~Usp (2.72445E-39) ~~370,402~~DUF4118 (1.87347E-20) ~~498,524~~GAF (8.08039E-14) ~~641,658~~HisKA (0.00000000552893) ~~723,776~~HATPase_c (8.97483E-27) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.3E-92	317.5	0.8	3.5E-92	317	0.6	1.3	1	K9RWZ7_SYNP3	Osmosensitive K+ channel His kinase sensor	Syn6312_2733	Synechococcus sp. (strain ATCC 27167 / PCC 6312)	373	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27167 / PCC 6312)	195253	>tr|K9RWZ7|K9RWZ7_SYNP3 Osmosensitive K+ channel His kinase sensor OS=Synechococcus sp. (strain ATCC 27167 / PCC 6312) GN=Syn6312_2733 PE=4 SV=1 MKNPSETELHTLSTKNHLGPSRRGKHKIFIGMCPGVGKTYRMLEEGRRLKQEGLD VVIGLLETHGRKETQERATGLELIPRKALSWQGKTFTEMDIEATIERKPQLALIDEL AHTNVPGSEREKRYQDVEVILQAGIDVYSTVNIQHLESLNDLVFKISSVVVRERIPD RLLDEADEVVVVDVTPETLQQRLKEGKIYAPEKIDQALQNFFQRQTLTLLRELSLR EIADSVEEDVREMQQDYCNIQERVLVCISTYPNSVQLLRRGGRIAHYMNARLYVLF VADPNRFLSKSESLYIETCERLCQELPGEFIRIESVDIVGTIAQVVQEKHITQIVIGES RRSRWQTLLRGSVSQKLMRKLATVDLHIIANTP	21~~KdpD (1.58582E-116) ~~231,248~~Usp (1.64414E-44) ~~370	non-kinase	KdpD;Usp

	2.3E-92	317.5	1.1	6.5E-92	316.1	0.1	2	1	A0A060QKY1_9PROT	Histidine kinase (EC 2.7.13.3)	ASAP_2241	Asaia platycodi SF2.1	923	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Asaia, Asaia platycodi, Asaia platycodi SF2.1	1382230	>tr|A0A060QKY1|A0A060QKY1_9PROT Histidine kinase OS=Asaia platycodi SF2.1 GN=ASAP_2241 PE=4 SV=1 MNRRSRQTEPGNAMTRQDYDRPDPDALLRQGCGERRRGRLKIFLGAAPGVGKT FEMLSSARHLMQEGVDLAIGVVETHGRAETQALVEGLPVIAAGSVAYRGQILREM DLDAILARRPTLALVDELAHSNAPGSRHPKRWMDVEELLNAGIDVFTTVNIQHLES LNDIVASITRVRVRETVPDHVIESADELELVDLTPGDLLQRMRDGKIYAAHTAGRAL LHYFSPGNLTALRELALRQTAQQVDAQLVDHMKANAIAGPWAAGERVMVCLTLQ DGDAGLVRYGKRLADRLHAPWIVLHVETSRDLTEEARARMASQMHLAQSLGAET VTVPGHDIALDALAYARAQNVTQIVAAHPAGTGWLGRLRQLIGRSTTERLIQRSEN FPVHVVPRSGEAMDHRIYENPPPRFSPYLASTAIVLCALGLALLLRQGFEVSNVSL AFLTAILGVAVAYGLGPSLWASIFGMLCFNFFFLPPLYTLTIAAPDNVVALFFFFATA LIAGNLGARVRSQAVVARHRAEITQSLYRFSRTITGMSTLDDLLCSVTRQIATLLDC HVVLLMPDGGRLAVQAQSDKAHPPGEDDLAAASWAWKHSRLAGRGSDSLPGV QWLFIPLRTARGPVAVIGLYREKPGQLLDAEQQSLLDALADQTASALESLLLTRDL DRVRLEAETDRLRGALLTSISHDLRTPLASILGAASSLRDYGEVLGEEGRSELLSTL TDEAERLNRFVGNLLDMTRIEAGALPLRHDSVDCAEVAATALARAAKLLEHHHVTL DTASTLPMLDLDAVLLEQSLFNILDNAAKYTPAETAITLRLAMRHSRLVIAIEDEGPG FGDRDPAEIFGKFTRFAAADTARAGTGLGLAIARGFVEAMGGDIEAANRTDRQGA VFTLRFPLPASQAMRQIVPDRTGPETRDGRKSL	36~~KdpD (4.70974E-118) ~~245,267~~Usp (1.05595E-34) ~~392,437~~DUF4118 (0.00000000000008298) ~~512,538~~GAF (0.00000000000117341) ~~656,674~~HisKA (0.000000000000982559) ~~740,793~~HATPase_c (4.76741E-22) ~~896	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.4E-92	317.5	0	4.4E-92	316.6	0	1.5	1	D7A9S8_STAND	Histidine kinase (EC 2.7.13.3)	Snov_1545	Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	903	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Starkeya, Starkeya novella (Thiobacillus novellus), Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	639283	>tr|D7A9S8|D7A9S8_STAND Histidine kinase OS=Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113) GN=Snov_1545 PE=4 SV=1 MSVQDPPRADPEALLAAAEREARGKLRIYLGAAPGVGKTYAMLSAARAAKAAGG DVVIGIVETHGRAETEALIEGIESLPRKGVPYRGRLVPEFDLDAALARQPGLLLVDE YAHSNVDGSRHPKRWQDVQDLLAAGIDVWTTLNIQHVESLNDVVQRITGVRVRE TVPDTALQKADEIILVDLPSDELIKRLADGKVYVEDTATRAVQSFFKPSNLTALREL ALRRVAARVDSDLLERMQGAAIEGPWAAGERILVCVGPDIAAERVVREAKRLADL MDASWFAVTVERPGHVMAGGDRRRLEAGMRLAETLGAETRSLVAADVASELLRF ARFENVTQIIIGKARRWWLARLLRGPLADALVKQADGVAIHVVTAEASEVPARRRF QPPPAGQLAGYSAAVLSVGAATVTGLFLTRFVALPNVSMLYLLAVLLPALLYGVW PAILASTLSFLAYNFFFIDPVETFTVARPHELLALLIFLIVAVLISTIAGRAREQARIAA QRMRATRRLYEFTRKLSALPDRSSVAEAAAVELHTVLGRPSVILLSEHGDLSIAAA WPPEDRLDTGSMTAASWAFEHGEAAGAGTGTLPSVPWLFRPLGGMAGGTAGG APIGVVGIERDPTMPVLDAESESILGTLSEQTAAALVRTMLSAEVTRARTAAETER VRNILLASISHDFRTPLASILGAATSLIDYGPDIPPEVRRDLLAQMRDEAENLDHMV RNLLSMTRLEAGALEIHKDWVDAVELMNRAVSAVRRRGATQRFVVTSAPDLPLIQ ADQSLMDQALGNVVANAVRYAGKEARIGLAATVIDNELVIAVTDDGPGIPTQTLPH VFEKFVRASRGAADGGDGSGLGLAITKGIVEAHGGRVAGRSPAPGQRNGTRITM KLPLPAHAPEGEGKS	24~~KdpD (1.73542E-112) ~~231,253~~Usp (1.07585E-37) ~~375,440~~DUF4118 (0.000000827379) ~~497,X,665~~HisKA (0.00000000000928626) ~~731,786~~HATPase_c (8.31622E-15) ~~890	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.7E-92	317.3	0.1	4.9E-92	316.5	0.1	1.4	1	A9F786_SORC5	Histidine kinase (EC 2.7.13.3)	kdpDsce1355	Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	910	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Sorangiineae, Polyangiaceae, Sorangium, Sorangium cellulosum (Polyangium cellulosum), Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	448385	>tr|A9F786|A9F786_SORC5 Histidine kinase OS=Sorangium cellulosum (strain So ce56) GN=kdpD PE=4 SV=1 MADASDERPDPEALLAAAREEEERGKVGKLKIFFGAAPGVGKTYAMLEAARSLRG EAVDVVVGWVETHGRAETEALLDEPPPLPRLPAVEVEHRGRTLREFDLEAALKRR PKLLVVDELAHTNAPGLRHPKRWQDVMDLLDAGIDVHTTVNVQHIESLNDVVAQV TGVVVRETVPDSMIERADEIELIDLPPDDLLERLREGKVYLSEQIERAASNFFRKGN LIALRELALRRTAERVDDQMRGYMRAHGIQKTWAVAERIAVCVGPSPMSARLIRA TRRMAGGLKAEWHAVYVQTPAQARLSEADRERVDRNLALAERLGATTVQLHGAE VAGEVLRYARQHNVNKIVVGKPTHPRWKDLIYGSLLDDLVRQSGDIDVHVIQGAA EAAKPEPGAPERRGLRPLAYAWGACVAVICTLVSWLMHPFSDLANLIMVYLLGVV FVASRFGAGPSVLASVLGVAAFDFFFVRPYLTFAVGDLRYLVTFAIMLGVGLVIASL TARIRGQAESASEREQRTAALYAMSRELAALRGIDELSLSAARHVREVFGADAVVL LPGADGRLAARAGTAEDLVAGERERAVAEWAYARGKAAGAGTDTLPSASAMHLP LQGSAGPIGVLSVRPSRPWPFLDLSRRELLGAFATQTALALERALLARQAQRARL EAQAEELRNALLSSVSHDLRTPLATITGAAGALLDDGNDGAALDLAARRDLTQTVL EEAQRLERLVRNLLDMTRLESGALAVRKEWLPLEEVVGAALNRVEEHLRGREISIE LDRATELVPMDGVLIEQVLINLLENALKYSPAGSPIGIRGFTEGNVATLEINDRGPGI PPGEEEAIFEKFYRGRGHTQRGIGLGLTICRGIVTAHGGRVAAENRPHGGAAFRV TLPIEGRPPNLARPELPAAAGA	25~~KdpD (3.63389E-111) ~~238,260~~Usp (7.25764E-46) ~~382,405~~DUF4118 (4.9917E-20) ~~505,532~~GAF (0.0000000000602704) ~~645,668~~HisKA (0.000000000000531594) ~~737,790~~HATPase_c (2.8771E-27) ~~890	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.8E-92	317.3	3.2	3.9E-92	316.8	2.2	1.2	1	K9QY28_NOSS7	Osmosensitive K+ channel His kinase sensor	Nos7524_4781	Nostoc sp. (strain ATCC 29411 / PCC 7524)	362	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain ATCC 29411 / PCC 7524)	28072	>tr|K9QY28|K9QY28_NOSS7 Osmosensitive K+ channel His kinase sensor OS=Nostoc sp. (strain ATCC 29411 / PCC 7524) GN=Nos7524_4781 PE=4 SV=1 MYATRRGKHKIFIGMAPGVGKTYQMLEEAKALKQEGIDVVIGLLETHGRKETADKS NGLEILPRRQIVRGDLTLTEMDTDAILQRSPQLVLIDELAHTNVPGSLRTKRYEDVE VILAAGIDVYSTMNVQHLESLNDVVARITSVVVRERVPDRILEAADEIVVVDVTPETL QERLLEGKIYAPAKIQQALEHFFQRRNLIALRELALREVADNIEEEAIANTPNGQFC NIQERVLVCVSTYPNSVQLLRRGARLAGYMNAPFYVVFVSDPDHFLTKEESLHIDT CEKLCQEFGGTFIRINSNNIAKAIAEVAEQNRITQIVIGESQRSRWQILLKGSLTQKL MRLLKNIDLHIIGSEKTTHK	5~~KdpD (1.07578E-127) ~~214,233~~Usp (8.79033E-49) ~~355	non-kinase	KdpD;Usp
	3E-92	317.2	0.2	4.7E-92	316.5	0.1	1.3	1	B9K2I0_AGRVS	Histidine kinase (EC 2.7.13.3)	kdpDAvi_6071	Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	902	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium vitis (Rhizobium vitis), Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	311402	>tr|B9K2I0|B9K2I0_AGRVS Histidine kinase OS=Agrobacterium vitis (strain S4 / ATCC BAA-846) GN=kdpD PE=4 SV=1 MSDAQRDTNRRPDPDALLGLANRDGRGKLTIFLGAAPGVGKTYAMLSRARGQKT AGIDIVIGLVETHGRSETELLTDGLETLPRKQIAYKDRVLEEFDIDAALARRPAVIIVD ELAHSNVPESRHPKRHQDIEELLAAGIDVWTALNIQHLESLSEIVTQITGVQVRETV PDRVLKQADVVVLIDLPPEELIVRLREGKIYLPDNARRATDSFFRLGNLTALRELAL RRTADRVDDQMVDYLKQNAIEGPWRTGERLLVCIGPDALSEKVVRTASNLASGM NARWLVVSLEQADQADENPGDQTRIEELFRLAERFGAETRRVQGRDFVHEILRLA KKEHVTQIVIGAPKRSRWQRLFRRSLPDALLDVRSGMGIHLVTGEAAPEKTKRVG LTKTFSLKSLPVRPRDIITALITTTVAVIGARGIIHFVALPNVSMLFLLAVLVSALREGY VAAVLTSVLSALAYNFFFISPVFTLTIAAPHEVFAFVMFIAAALIAGGIAARIRAQGQI AARRATQTQILYDVSSKLAGTVDADGVVWTAVSQLNGIIKRPVALLSPQNGTLALR SCWPPDTELGVAEMAAARFALEKGETAGAGTGTLPNSKLQFRPLRSPAGTLAVC GHEMTGEPLDPMEERALSAILDQVTIALDRANLTIRSVEDQARLERERFQSTLLSSI SHDLRTPLATITGAVTSLKEFGERMPVESRRDLLQSIEEEGERLSRFVGNLLDMTR IEAGALEAKHDWVDLNDVISDSIARARRVAPATEISASIAKDLPLLRADSLLLGQVLF NLIDNACKHGGGEPVTVYARADDTVLSLSVTDMGKGISEKDIDRIFEKFYRRGKGA DGRKPGTGLGLAIAKGFVEAMGGTITVESPAVKRIGTRFTLRFPLENMEKDRAEA	25~~KdpD (4.08072E-120) ~~234,256~~Usp (1.07901E-33) ~~379,408~~DUF4118 (0.00000000079178) ~~490,533~~GAF (0.000159446) ~~650,667~~HisKA (0.00000000000507637) ~~733,786~~HATPase_c (2.21488E-27) ~~890	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.3E-92	317.1	0.4	5.2E-92	316.4	0.3	1.3	1	B5EH77_GEOBB	Histidine kinase (EC 2.7.13.3)	kdpD Gbem_2605	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	892	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	404380	>tr|B5EH77|B5EH77_GEOBB Histidine kinase OS=Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622) GN=kdpD PE=4 SV=1 MRDDAARPSPETLLKVAKAEEEAQSGRGKLKIFLGYAPGVGKTYAMLEAAQMRK REGRDVVAAYVESHGRAETDLLLEGLEVIPKLRIEYQGVQLSEMDIDTVLARKPQIA LVDELAHTNAVGSRHEKRWQDVEELIYAGIDVYTTVNVQHFDSLNDIVAQITGVVV RETVPDKLLDLALEIRVVDIPPEDLLERLREGKVYIPEKAMLATEKFFKPGNLMALR ELSLRRAASRVDDQMRAYMEARSIAGPWPAAEKLLVCVSGSPYSEKLIRTTRRLA DEVKARWHTVYIETPGLSKHARENRERVWRDLRLAESLGAEVATLSSASVAQALV EFAVHNNVTKIVVGKPKKPRWREFLRQPLVDEIIRLSGPVDVYVVSIAATGETPKA AQVHPKKPVQWTGYLKGSALVVAVTLLCKVLQGFLAPTNLMMIYLLGLVLAATKL GRRPAVLTALLSVLAFDFFFVPPRLTFAVADTEYLITFIALFTVGFVISTLVSQTRER AESIREREEQTATLYYLSRDLTVASDLRGILAATLKNIEDSVGGMVAVLLPEGERLE LQAASGGLTLDTKEHAVADWSFRNSSPAGRGTETLGSSELLYLPLLTSGDVLGVL GVRLKSETEYTSPLTRRLLHAFATQTAFAIERVLLVKQAEQAQILRARENLERALLN SISHDLRTPLVSISGALGALRDRTTYLEEESRRDLLEAAWEEAGRLNRFVGNLLDM TRLEAGAMKPKRVPSDLQDLIGCALASLEPQLSKRKLTVRVDPGLPLVSMDMVLM TQVLVNLLDNALKYAPSNELIELESRALDGKVTLKVADRGPGVPPQDLERIFDKFY RVPVPEGAGGTGLGLSICKGIVEAHGGTIHAENREGGGLKITVQLPVEGEGHG	25~~KdpD (2.11039E-118) ~~235,257~~Usp (2.17304E-44) ~~380,404~~DUF4118 (2.03976E-19) ~~503,529~~GAF (0.0000000003194) ~~647,664~~HisKA (0.000000000410465) ~~730,785~~HATPase_c (3.9722E-32) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.3E-92	317	0	3.9E-91	313.5	0	2.1	1	A0A052IKP7_9BORD	Histidine kinase (EC 2.7.13.3)	L539_3539	Bordetella hinzii 5132	907	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella hinzii, Bordetella hinzii 5132	1331257	>tr|A0A052IKP7|A0A052IKP7_9BORD Histidine kinase OS=Bordetella hinzii 5132 GN=L539_3539 PE=4 SV=1 MAEPGARRPDPDRLLQSLRQEEQAARRGRLRIYFGASAGVGKTYAMLAGAHAQ MAQGTDVLAGVVETHGRQETRRLLEGLPQLPPRQLPYRGRELPEFDLEGALRRR PGLVLLDELAHSNAPGAQHAKRWQDVQDLLHAGIDVWTTLNVQHLESLNEAVGG ITGVRVWETVPDDIFDQADEIILVDLSADELLRRLKDGKVYVPEQARHATRNFFRK GNLIALRELALRRTAEHVDEDVQAYRRDAAIQPVWRTREALAACIGPDGDAEHLV RSAHRLAQQLDCEWHAITIEGLRVQPPPEGQARRLERALALAESLGAHCETLAGT DRVEATARYARRHNVTKIVVGRAQGGWARVPWLDRLLTPGRLWHGRGFAEQLA RACPDIDILRVAAPAHAPAPPAGREPPSPARAAPRRWSGYGWALAYCALATGVS QAAFPLLHQTNIVMFYLLAVVGVALRHGRGPAALASVVSVPLFDYFFVQPISSFAV SDVQYVLTFAVLLGVGLLIGQLTAGLRAQAETSVKREADARALYEFARELSSALQS EQIVQAAETFLKAAFDADSALYILGLDDRLRLAASCRMAPEPALAQWVQDHGQPA GAGTRTLANSPLLYLPLAAPMRVRGVLVLRTARPVAASPAAWRQAQAYATLIAIAV ERLHYVEVAQQALLNVEYEKLRNSLLAAVSHDLRTPLTGLIGMTETLARGSPDAAT QEQALAIRDQARRMHLMVVNLLDMARLQSHGAPLKREWQSIEELVGAALATMRE TLRAHRLRVLPLSDLPLVECDGILIERVLCNLLENAAKYSPPGGAITLEGQVRGEVL QVSVTDQGPGIAPGREELVFQKFTRGERESPLPGVGLGLSVCRAIIQTHHGRIWV EPAPGGQGARFAFELPLGQPPAIETETP	25~~KdpD (2.55611E-117) ~~235,258~~Usp (1.48904E-32) ~~389,420~~DUF4118 (1.33613E-19) ~~519,547~~GAF (1.24569E-14) ~~659,676~~HisKA (0.000000000000267863) ~~739,792~~HATPase_c (4.02449E-28) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.4E-92	317	0.5	8.8E-90	309.1	0	2.4	2	A0A0C4Y5W5_9BURK	Histidine kinase (EC 2.7.13.3)	RR42_m0094	Cupriavidus basilensis	977	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus basilensis	68895	>tr|A0A0C4Y5W5|A0A0C4Y5W5_9BURK Histidine kinase OS=Cupriavidus basilensis GN=RR42_m0094 PE=4 SV=1 MPDTAQRDAPGRPDPDALLQRMQQEGERAARGKLRVYFGASAGVGKTFAMLTA ARALREQGSDVVIGVVETHGRAETEALIAGLERLPMKAMPHHKLDDRVLQEFDLD GALARRPALILVDELAHSNASGSRHPKRWQDIEELLSAGIDVWTTVNVQHLDSLN EAVGGITGIRVWETVPDTVFDDADEVILVDLPADELLRRLRDGKVYLPEQARTAAT NFFRKGNLIALRELALRRTADRVDDDVRAYRHAESIRPVWRTREAVLACIGTGDDA AQVVKSARRLAGQLDCDWHVVTVATPRLAPLGGHERANIEEAMRLAEELGARTE TLAGSDIVQAVAGYVRRHNLTKVVVGRAPGNWRRSGGSLLARGRALLALGLSPFL GARAWLFGRHSFADSLALGCPEIDVIRVAADAMGADTRGRAQPAGGRADVREDP APNDDSSVVAHRIDYLWAVAWCGGASLLSALTRPWFDLVNIAMLFLAAVVGVALR HGRGPAALASVLSVAAFDFFFVPPRMSFAVSDVQYLVTFAVLLTVGLVIGQLTAGL REQAQVSVERETDARTLYELARELSAALMPEQIIDISSRFLQAALGARSAFFLVSPK GRLLPPVIDPTQRGNDAIDPVLAQWVFDHGQPAGTGTHTLPGSTVLYLPLKAPMQ TRGVLAVEPQKWRAFARPERRRQIDVFATLIAIAIERLHYVEVAQQALVSMESERL RSSLLAAVSHDLRTPLTSLIGMAETMQRTEPPLPASLSETVDAMREQALRMRTMV VNLLDMARLQSRDVRMQKEWQSLEELVGAALAGMRDALSRHRVSVADLSALPLV ECDAVLMERVLCNLLENAAKYTPPGTGIRISGEVAETEVRLAVADDGPGVPRGQE LSIFQKFTRGERESATAGVGLGLAVCEAIVQAHGGRIWVESVNADHTGARFVVAL PRGNPPAIEPEPPEALESALLAAHGNGGVPVAHDAANKESS	29~~KdpD (9.00623E-120) ~~242,265~~Usp (2.25299E-31) ~~371,453~~DUF4118 (8.75719E-23) ~~552,579~~GAF (7.72505E-18) ~~698,715~~HisKA (0.000000000000182756) ~~780,833~~HATPase_c (1.36855E-26) ~~936	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.5E-92	317	0.8	6E-91	312.9	0.1	2	2	A0A0D1XG31_ANEMI	Strain NCTC 7096 contig_275, whole genome shotgun sequence	TS65_28105	Aneurinibacillus migulanus (Bacillus migulanus)	383	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Aneurinibacillus group, Aneurinibacillus, Aneurinibacillus migulanus (Bacillus migulanus)	47500	>tr|A0A0D1XG31|A0A0D1XG31_ANEMI Strain NCTC 7096 contig_275, whole genome shotgun sequence OS=Aneurinibacillus migulanus GN=TS65_28105 PE=4 SV=1 MGDEKRKTPEELLKIIEREQRGYLKIFIGAAPGVGKTYMMLREGNEMLEKGIDIVIG LVETHGRAETAAQIGNLPVFPLKSVQYKGREFQEMDVDGLLTRRPQYVIVDELAH TNVPGSKNKKRYEDVMELVKAGIHVITAMNIQHLESLNDTVKQLTGVKVRERVPD WILNEAAEVQLIDTPPEKLRDRLKAGLIYKPEKIEQSLQNFFRTGNLNALREIALREV ADDVDERLESYKQENGIDGMRGANEKILVCVNYRPNAERLIRRGWRIASRLKCQL YILNIPLYSVQEMDDATRKQMRLLEKLAKDLNAEFHIRASAGRKPEQVIIDFVNEKGI TQIVLGQSARSRWEEIAKGSIVNRIMKGTKYVDILIVADGVDYRE	19~~KdpD (6.33087E-119) ~~229,251~~Usp (2.2003E-39) ~~376	non-kinase	KdpD;Usp
	3.8E-92	316.8	0.5	6.2E-92	316.2	0.4	1.3	1	D5VJC0_CAUST	Histidine kinase (EC 2.7.13.3)	Cseg_1856	Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (Mycoplana segnis)	892	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter segnis, Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (Mycoplana segnis)	509190	>tr|D5VJC0|D5VJC0_CAUST Histidine kinase OS=Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) GN=Cseg_1856 PE=4 SV=1 MPADEPKRPDPEALLAAANKARRGRLKVFLGMAPGVGKTYEMLRAARRRKAEGA DVLIGVVETHGRRETESLLRGMEVLPRKPIEHRGRVQMEFDIDAALARKPKILLVD EYAHSNAIGSRHPKRWQDVEELLAAGVDVWTTLNVQHLESLVDVVQRITGVRQR ETVPDSALSRADDIELVDITPSELRERMAAGKVYVPETARLAADNFFKVENLTALR ELALRRAAQTVDDQLVATMREKGVEGPWAAGERILVLVSGDTMAASLVRAGRRL SDMMMDAPWTVAHVERTDRPLAKDGDAARLREAYRLAEQLGGATVGLTGGDIV DTVMAYARRHNVTQIVIGKSVESRWRERLGRSLATALLREARGAAVHVVTEAAHE PQPKPTRPLGQGLWQGYAVGALFIGVATLAAWGLDVTFDRVDLGMIFLAAVLAA GVLHGLRPALAAATVAFVVYNYLFLEPRYSLAVGAPTDFITLVVFWAVALASGGLA GRVRDQALGSQRRAAAVTTLLAASRTLSAATGRDAVARALAEQVSAAAGGRSLV LLPEGEEIAPAFGSPSLEMLDAAQMAAARWAWEKGEPAGFGTGTLPQARWTFW PLDGVRARTGVAGVEAGAAPPGSDHERLVLALLEQGAVALERSQLASEAVEAETL RRADRFRSALMNSVSHDLRTPLSTVLGASTTLIDYGDKLAKPVRDDLVVSIREEAE RLNRYVANLLDMTRIEGGALRLRTDWIDVRDVLNAAAERVSRRLGGRELARDYPR ELSLVQADASLLEQVVVNVLENAIAYSPPEARIEMAAYEDRSNVVISIEDEGRGIPT SELERVFDKFRRMEEPSDRSQGAGLGLSIAKGFIDALGGRIAAASPIHDGKGTRILI SLPKGVATPHHLL	21~~KdpD (3.67214E-123) ~~231,253~~Usp (6.8613E-38) ~~377,399~~DUF4118 (0.0000000000435312) ~~498,X,658~~HisKA (0.000000000647993) ~~724,777~~HATPase_c (5.06607E-24) ~~881	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.2E-92	316.7	0	7.5E-92	315.9	0	1.4	1	G0AB27_COLFT	Histidine kinase (EC 2.7.13.3)	kdpD CFU_1320	Collimonas fungivorans (strain Ter331)	926	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Collimonas, Collimonas fungivorans, Collimonas fungivorans (strain Ter331)	1005048	>tr|G0AB27|G0AB27_COLFT Histidine kinase OS=Collimonas fungivorans (strain Ter331) GN=kdpD PE=4 SV=1 MSSPYSNDDLRPDPDALLARLQVQESLVGRGKLRIYFGASAGVGKTYAMLSAAHK LHGEGRDVLAGVIESHGRAETAALLNGLELLPMKQVAYRDKHLPEFDLDAALQRK PSLVLVDELAHSNAAGSRHPKRWQDVEELLNAGIDVFTTLNVQHLESLNDVVGGI TGIRVAETLPDTVFDAADEVVLVDLPADELLNRLKLGKVYKLPQAERASRNFFRKG NLIALRELALRRTADRLQGDVQAYRIEKSIGAVWQTDAALLACVGPSPNAEHVIRG TARLATQLNAEWHAVYVETPKLQRLPSAKRERILKTLKLAQDLGATTAVLAGSEVA EVVAGYARSHNFSKIIIGRSQRRFPWQASHSARIAAQARDIDLIAIGASSASTAEKA EEGVGGILPRHLPMQGRIEWWGYAWALAVCVLVTLLATPILPFFDLANIVMLYLLA EVLIAIRYGRGPAIFVALLSIASFDFFFVPPRFSFAVSDFQYLLTFGVMLAVGLTITHL TSGLRYQARIASDREARSRALFEFARALSGVLQTEQIFETSGQFLQRSFQAKTLLLI PDEAGRLSLPAVIPDDVAHVAAALDMGIAQWAFDNASSAGIGTDTLPASSYLYLPL VAPMRTRGVLVILPHNRRWILIPEQQQQLYTFATLTAIALERVHYVEVAQDALVRM ESERLRNSLLSALSHDLRTPLTALIGLSESLVLSKPPLQQHQQVLATALHSEMLRM SALVTNLLDMARIQSGEVKLNLQWQPFEEVVGSALRASGSALHGHQVEIRVAHEL PLVHFDAVLIERVLCNLLENAAKYTPAGSHIVLAAAVNARFLTVTIADDGPGLPSGM EDTIFEKFTRGERESAKPGVGLGLAICRAIVEAHGGTIRAHSGRHGTSGAEFIFTIP LGAPPSMPDLEEHEPSAGSMEKDSEKT	29~~KdpD (1.96499E-122) ~~238,261~~Usp (8.89021E-39) ~~380,413~~DUF4118 (6.75712E-21) ~~512,539~~GAF (6.05406E-15) ~~660,677~~HisKA (0.0000000000138288) ~~742,795~~HATPase_c (1.21208E-27) ~~898	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.4E-92	316.6	1	7.1E-92	316	0.7	1.3	1	A0A0C2TN58_BACBA	Histidine kinase (EC 2.7.13.3)	SD77_1461	Bacillus badius	898	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus badius	1455	>tr|A0A0C2TN58|A0A0C2TN58_BACBA Histidine kinase OS=Bacillus badius GN=SD77_1461 PE=4 SV=1 MEDQRPSPEVFLAKMEAEQEAAAGKLKIFLGYAAGVGKTYAMLDAAHQAKQLGK DVVVGYIERHPRPETLALLEGLEQIPAKSIEYKGKIFQELDIDKVIERQPEIVLIDELA HTNVPVMRHLKRFGDVEELLAKGMDVYTTVNIQHIESLHDVVEDITGIKVRERIPDY VIDQASQIKLVDIEPDELIQRLKEGKVYPPKQAEKAIDSFFRKQNLVALREIALRRTA DTVYYKTAKESFKQNVQIEEHLLVGLSSSPTNAKVIRTAARIAQALHGKFTALYVQR AEKGEASPADVERLQQHMKLSEQLGGHVVIVQEEDVAAALASYAHISGVTKLVIG RTAIKRKWWQPSSKISQRLNEYAPSLAIHIVPDQENEPIYLPEMKAHLYFEWMDGL KMLAVFSLASLMGLFFFQMGYSEANIITIYILGVLILAIWSSGWMMSIISSAAAVLLF NFLFTEPRLSFEAYHRDYPITFFIMFLSGIITSSLTKRIKEQAAAAIRKSYRTEVLLET NRKLHHAKSIDEIITQGVSQIVKLVEKPVNFFEIDHRLIAKSLFFRTDTLSNSENRAIE GLFGNANELGVVNWVANNKRIAGVSTDIFPEAGAYYLPVISGGEVKGVIGIALSKH DPLPAFERHVLHAVINDFSLAFDKWYLQKLHAQVVREAELQQMRANLLRAISHDL RTPLTSISGNADILLTNTEQIPEGDKIRLYQDIYSNSKWLVQMVENLLAVSKLDDGQ LAIELQPELVEDIVQEALLHVVRLNNTHNISYQAEPELLLALMDARLIIQVLINIIDNAL TYTPAGSDISIVAKEAGDAVLFSISDNGPGIEDSLKAKLFEPFTTGKAQRSDSRRGL GLGLALCQTILHLHGSELTVSDNKPQGTTFSFSLKKGMVAI	24~~KdpD (7.54799E-118) ~~231,249~~Usp (2.46064E-31) ~~372,396~~DUF4118 (1.34834E-14) ~~496,X,669~~HisKA (0.000000000414223) ~~735,788~~HATPase_c (4.28385E-27) ~~891	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.4E-92	316.6	0	6.4E-92	316.1	0	1.2	1	A0A0A8F4C3_9ACTN	Histidine kinase (EC 2.7.13.3)	GZL_08788	Streptomyces sp. 769	865	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	1262452	>tr|A0A0A8F4C3|A0A0A8F4C3_9ACTN Histidine kinase OS=Streptomyces sp. 769 GN=GZL_08788 PE=4 SV=1 MVREGLSVAPNRVAAEASDARPGKLKVFLGAAPGVGKTYRMLDEGRRRLRRGT DVVVAYAECHGRQYTEEMLDGLEMVPRLHRSYRGSTFTELDLDAVLARRPAVAL VDELPHTNVPGGRNAKRWQDIDELLAAGIDVVTTVNVQHLESLNDVVEKITGVPQ RETVPDDVVRRADQIELVDMPAEALRRRMAHGNIYQPEKVDAALAHYFRIGNLTAL RELALLWVAGRVDETLQKYRSEHGIGTVWETRERVVVALTGGPEGETLIRRAERI ADRPRALNSVRAGGTPISGGDLLAVHVARSDGLAYASPAALAKQRALVESLGGSY HSVVGDHVPTALLDFARAENATQLVLGTSRRSWFSRLVAPRGIGEDTVELSGDID VHLVTHEGAGRGRRLPVPGRQLPHARRVVGPVAGLVLPLLLTTVLTHTRGALNLT SEALLFMVTVVGVACLGGVVSALLASLAASLLLNYYFIPPSGEFTITEPNNALALAV FALVAVTVAALVDRSLRLSRRAASATAEAETLSSMAGTILRGEQGVSVLLERTRET FGMESAELVPRAGQETDADEERDDLVKVPAGPDRLLVLRGRRLPASEHRVLTAFA AHLAAALDHARLMEAAAQVEPVKAADRLRTALLAAVSHDLRTPLASGRAAISSLRS PDVVFSPAERNELLATAEESLIELNRLVDNLLDMSRLRAGALSLSLQPTAFADVLPL ALATLPATPVRIAFQGLAEVRDVLADPPLLERVIANLVTNAVRHCAASQRVLITASS LGSRVELRVVDQGPGLPPEDRDRIFVPFQRLGDRDNTSGLGLGLALSRGLAEAM GGTLDPEDTPGGGLTMVLSLPAAPVAEPVEAVELG	20~~KdpD (4.13389E-113) ~~230,252~~Usp (3.17719E-28) ~~388,X,632~~HisKA (0.0000000000187723) ~~698,749~~HATPase_c (5.4852E-28) ~~850	kinase	KdpD;Usp;X;HisKA;HATPase_c

	4.7E-92	316.6	1	6.3E-92	316.1	0.7	1.2	1	B2J4W2_NOSP7	Osmosensitive K+ channel signal transduction histidine kinase, sensor domain protein	Npun_R0299	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	384	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	63737	>tr|B2J4W2|B2J4W2_NOSP7 Osmosensitive K+ channel signal transduction histidine kinase, sensor domain protein OS=Nostoc punctiforme (strain ATCC 29133 / PCC 73102) GN=Npun_R0299 PE=4 SV=1 MSDNNTGSNGTAPLNSGSYSLYPVRRRGKHKIFIGMAPGVGKTYRMLEEGHALK QEGIDVIVGLLETHGRKDTEEKAEGLEILPRKQYPRGELMLTDMDTDAILKRSPQL ALIDELAHTNVPGSPREKRYEDVEVVLAAGIDVYSTMNVQHLESLNDLVARITGVV VRERVPDRILDEADEIVVVDVTPETLQERLLEGKIYAPQKIQQSLDNFFQRRNLIAL RELALREVADNVEENAIATTPNGQSCNIHERVLVCISTYPNSVQLLRRGARLASYM NAPLYTLFVADPERFLTKEESLHIHTCEKLCNEFEGTFLRVTNSNVANAIAEVAEKY RITQIVIGESQRSRWQMLLKGSLTQKLVRLLKNIDLHIIASEKMVLSK	26~~KdpD (9.11975E-130) ~~235,254~~Usp (9.49215E-45) ~~376	non-kinase	KdpD;Usp
	4.8E-92	316.5	0.1	1E-91	315.4	0.1	1.6	1	B0SYJ4_CAUSK	Histidine kinase (EC 2.7.13.3)	Caul_4239	Caulobacter sp. (strain K31)	894	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter sp. (strain K31)	366602	>tr|B0SYJ4|B0SYJ4_CAUSK Histidine kinase OS=Caulobacter sp. (strain K31) GN=Caul_4239 PE=4 SV=1 MPAEEPKRPDPEALLAAANKAGRGRLKVFLGMAPGVGKTYEMLRAARRRKAEG QDVLIGLVETHGRRETESLLRGMEVMPRRPLEHKGRTHLEFDIDAALARKPKLLLV DEYAHSNAPGSRHPKRWQDVEELLAAGIDIWTTLNVQHLESLVDVVQRITGVRQR ETVPDSALSRADDIEVVDITPDELRERMGAGKVYVPETARLASENFFKVENLTALR ELALRRAAQTVDDQLVAAMREKGVEGPWAAGERILVLVGGDAMSSSLVRAGRRL SDMMMDAPWTVTHVERSDRSGPSPLAATRLRDALKLAEQLGGTTVVMTGVDIVA TVMAYARRNNVTQIVIGKSAGNRWNELTGRSLAAALLREARGEAIHVVTEAAHTH GDVPVERSRKRGPGWPAYVTGAAFVGLATLVAWGLDTAFDRVDLGMIYLAAVLA AGVMYGLRPALAAATAAFLVYNYLFLAPRYSLQIGSPTDFLTLIVFWAVALATGGL AGRVRDQARGSQRRAAAVSTLLAAARTLSGATGRQLVAQAIADQVAATAGAKAV VFIPLNGDLTPAAGAPSLEPLGAAPMAAARWAWERGETAGFGTATLPHAEWTF WPLEGVRGRAGVAGVEAGAMAQGSDDERLVLGLLDQGAIALERADLAADAVEAE TLRRADRFRSALLNSISHDLRTPLSTVLGASSTLTEYGDKMEPAVRADLMVSIREE AERLNRYVANLLDMTRLEGGALRLRNDWIDVRDVLGAAADRVTRRLGGRPLTRD FPSELSLVRADASLLEQVVVNILENAIAYSPPGAQIEMAAYEDRGNIVISIEDEGRGI PPAELERVFEKFRRRMEEPTDRTGGVGLGLSIAKGFIDAMNGRIAAASPIHDGKGTR ILISLPKAVHTPKDLL	21~~KdpD (2.33614E-122) ~~231,253~~Usp (5.90763E-33) ~~377,405~~DUF4118 (0.00000000523292) ~~500,X,660~~HisKA (0.000000000194074) ~~726,779~~HATPase_c (7.09388E-27) ~~883	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.9E-92	316.5	0.2	9.1E-92	315.6	0.1	1.5	1	D9QFM8_BRESC	Histidine kinase (EC 2.7.13.3)	Bresu_3237	Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (Caulobacter subvibrioides)	902	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas, Brevundimonas subvibrioides, Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (Caulobacter subvibrioides)	633149	>tr|D9QFM8|D9QFM8_BRESC Histidine kinase OS=Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) GN=Bresu_3237 PE=4 SV=1 MSPDPPVEAGRLSRRPRRGRLKVFLGMSPGVGKTYEMLRAARRRKAEGGDVVV GVVETHGRKETESLLRGLEVMARRPIEHRDRTLLEFDIDGAIARRPELLLVDEYAH SNAPGSRHPKRWQDVEEILDAGIDVWTTLNVQHLESLSDVVLRITGVRQREAVPD SALSRADDIEVVDITPEELRKRLEEGKVYVPETARLASQNFFRIENLTALRELALRR AAQTVDDQLVATLRERGVQGPWAAGERVLVLIGGDGMAGMLVRTGRRMSDMM MDAPWTVATVDRPSSASGDVGRAQRLAEAFKLAEQLGGRTVLLTGDDVVRTVSD YAHRNNITQIVLGRSVVTGWRARFSEVFGRSLAAELLRAARGVAIHVVTDAATPDT PASRPAVPAGERLWDGRGYAIGAAFVAFATGLALLLDRSFERVDLGVLYLSAVLA AGVLYGLRPALAAATAAFLVYNFLFLEPRYSFAIGSPTDFLTLFVFWAVATVTGVLA GRVREQARRAQRRASAVSALLVASQSLSAAEDRGTAARVLAEQTAAAAGARAVV LLPEGEDIAVAALAPLKAGATEPPHTLSPADMAAARWAWERGEAAGHGTGTLPQ TRWTFRPLNGVRKRSGVAGVEAAAALAPGSDEERLALAVMDQGAVALERAELAGQ ALETETLRRTDRFRGALMNSVSHDLRTPLSTVLGSATTLIDYGETLKPEVRADLLT SIREEAERLNRYVGDLLDMTRLEGGGLNVKADWTDVRDVLNAAAERVSWRLGTR DLTRDFPADLSLVMLDQGLLEQAVVNILENAIAYSPDGSRIELAAYEDRGSVVISIE DEGRGIPTAELERVFDKFRRMDEPSDRSQGAGLGLAIAKGFVEAMNGRIAAASPI HGDLGTRVLISLPKAIATHHQLL	22~~KdpD (1.55093E-110) ~~226,248~~Usp (5.4013E-34) ~~376,406~~DUF4118 (0.0000000148723) ~~500,X,668~~HisKA (0.00000000000522414) ~~734,787~~HATPase_c (1.77035E-24) ~~891	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	5.2E-92	316.4	0.7	8.4E-91	312.5	0.1	2.2	1	A0A0H3M1M8_BORBR	Two component sensor protein	kdpDBB3920	Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	931	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella bronchiseptica (Alcaligenes bronchisepticus), Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	257310	>tr|A0A0H3M1M8|A0A0H3M1M8_BORBR Two component sensor protein OS=Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) GN=kdpD PE=4 SV=1 MRAACARPFPTRHTHPMADPGNDRLDPDRLLQTLEQAQSDARRGRLRIYFGACA GVGKTYAMLAAARAQAAQGVDVVAGLVETHGRADTAALLDTLPALPLQTLDFQG RRLREFDLQAAVARRPRLLLLDELAHTNAPGARHAKRWQDVEELLAAGIDVWTTL NVQHLESLNEAVGGITGVRVRETVPDSVFDAADEIILVDLSADELLRRLREGRVYV PEQARHASRHFFRKGNLIALRELALRRTAEHVDDDVRAYRHERAIEPVWRTREAV VACIDADPHAEHVLRSAHRLAQQLDCEWHAITIEAPRVAPLPRAGRARLDQALALA ETLGAHVETVAGTDMVDAATRYMRRHNITKAVVGRDAWRRRGLSGLLDAALTPG RLLRRRSFADALASACPEADIVRVGAPSAATAAPRRDPRSWRNASAPAGHAAAG AYLWALAYCAAATLASRLAFPVLHQTNIVMIFLLAVVAAALRHGRGPAALASVVSV ALFDFFFVQPLASFAVSDVQYLLTFAVLLTVGLLIGQLTAGLRQQARAAARREADA RGLYEFARELSAALQPEQIAGAASAFLNAAFGARGALYILGLDDRLRLAPGAGDAA LEPALAQWAFDHGQACGAGTDTLSNSPVLYLPLRAPMRVRGVLALHHAGPPLYS AAPARRQLDAYATLIAIAIERLHYVEVAQQALLSIESERLRNALLAAVSHDLRTPLTS LLGMAETLQRSPAAMTPAALETVAAMQDQARRMHALVVNLLDMARLQSHDAPLR RQWQSVEELVGSALAAMNAALQDRPVTVAPLSALPLVECDGILIERVLCNLLENAA KYTPPGSAIHIDALADAHTLQVRVADDGAGVAQADRQRIFEKFARGQRESATPGA GLGLAVCRAILDAHQGRIWVEPARRLRGACFVFALPLTPPPAVPPEPA	41~~KdpD (6.11683E-110) ~~251,274~~Usp (1.1443E-32) ~~394,440~~DUF4118 (1.49392E-19) ~~534,566~~GAF (0.000000000000796096) ~~681,698~~HisKA (0.000000000001871) ~~763,816~~HATPase_c (1.38296E-28) ~~918	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5.2E-92	316.4	0	1E-91	315.4	0	1.5	1	A0A0F2S4I1_9RHOB	Histidine kinase	VR71_00125	Roseovarius sp. BRH_c41	884	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseovarius, Roseovarius sp. BRH_c41	1629709	>tr|A0A0F2S4I1|A0A0F2S4I1_9RHOB Histidine kinase OS=Roseovarius sp. BRH_c41 GN=VR71_00125 PE=4 SV=1 MTDDARPSPDALLREAQREGRGTLKIFLGAAPGVGKTYEMLLEGAEKIEAGADVVI GLVETHGRDETEALVAPLPVIPRRKIDYKGQTLTEMDLDAVLERRPKIVLVDELAHT NAPGSRHPKRWQDIEELRAAGIDVMTTVNIQHVESLNDVVGSFTHVRVRETVPDK VFEEAEIELIDLPPEDLISRLGDGKVYVPDQARHALDHFFSKGNLLALRELALRHAA QYVEARIQEHKSVTGKDIGYAGGQRILVAISQEAGGEQVIRAAKRLADALKAPLIAL YVETPSAERFGDAEKTQLAGNLSLAASLGATLQSVPATSVQDAILAHCRDVSATQ LVLGKSRRQGGWWRRRDPIVQDILDRTTGVAIHVIPFDEQVRGRDWRNFVPRGS WTGDAVAIGSVAALTLAAFLAQGWISRGPIDLLYLLPVIVSASLYGFRAGLIAAIAAG IAYNFFFLPPFYTVIIYGPANIITAVLLVVVAIITGQLAARARAAAALAMRSARENAGL ARFATRLGAASNTQETAQLIRDELRSLLAVQTIVLHPSADGVTISAFGQTKPQLSPV DRAAAEWVMDHGEEAGIGTNTLTASAWQFRPLKTSLGTLAVLGFRGPHGRDPIP TERAALAESLIDQAALAHERLKLEADMRDMEVVRQRDNLRAALLASLSHDLRTPLT AVTAAAEALSATGDEAELVETVRSEARRLNRFLSDLLDLTRIEEGAVTPDLVPTDLT DVIASALGDLSKSLTGRKVLTSIDPNLPLVRADAVLLNHALLNLVDNAAKYSPQDAP IEIIARMGRRGPVIDVLDSGPGIPQGSEQRIFDRFARGETSDRTGGSGLGLAIVKGF AAAMGFTVEAARRQGGGSRFTIRIPSTAIIQVSLEDIA	19~~KdpD (1.00552E-109) ~~212,250~~Usp (8.95754E-31) ~~373,421~~DUF4118 (0.000000113901) ~~487,X,656~~HisKA (0.0000000000257815) ~~716,769~~HATPase_c (5.25386E-26) ~~870	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	5.5E-92	316.3	0.2	7E-92	316	0.2	1.1	1	F8I8U6_SULAT	Osmosensitive K channel His kinase sensor	kdpDTPY_3241	Sulfobacillus acidophilus (strain TPY)	360	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiales incertae sedis, Clostridiales Family XVII. Incertae Sedis, Sulfobacillus, Sulfobacillus acidophilus, Sulfobacillus acidophilus (strain TPY)	1051632	>tr|F8I8U6|F8I8U6_SULAT Osmosensitive K channel His kinase sensor OS=Sulfobacillus acidophilus (strain TPY) GN=kdpD PE=4 SV=1 MPNEGWGRLTIYVGAAPGVGKTYKMLQDANDWLARGVDVVAGFIETHGRRETA DQIGRLEVLPRKRINYQGHTYEELDTDAVIRRRPAVVLIDELAHSNVPGSRHAKRY EDIEDILRAGIDVVTTVNIQHLESLQDKVEHITGVKVRERVPDRIMDLADEIKLIDVTP QTLQERLMNGQIYAPDKIEAALSHFFQPGKLSALRELALLEVADDVDQRLGSAEVV HPERILVCVNYRPHSEKLIRRGWRIADRLKAELYVLVVVTEPLSPDEQRDLERIRDL SRQFRATFILRSADQRNVGPVIVEVAESLRVSQIVIGQPQNARNGPLGWTSPNPID YVLRHAEFMDLHVVSSTRESSAN	7~~KdpD (2.10485E-117) ~~214,228~~Usp (4.71039E-32) ~~352	non-kinase	KdpD;Usp
	5.7E-92	316.3	0.3	9.8E-92	315.5	0.2	1.4	1	A0A023Y7L0_9GAMM	Histidine kinase (EC 2.7.13.3)	DX03_18410	Stenotrophomonas rhizophila	886	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Stenotrophomonas, Stenotrophomonas rhizophila	216778	>tr|A0A023Y7L0|A0A023Y7L0_9GAMM Histidine kinase OS=Stenotrophomonas rhizophila GN=DX03_18410 PE=4 SV=1 MSDPRTRQADALVERLQREAGGKLTVFLGAAPGVGKTFSMLSRAHEQLRRGVDV VVGLVETHGRAETSALLEGLPQVPLLQRDYQQHVLGEMDLDAVLARHPALVLVDE LAHRNVPGSRHERRWQDVMELLEAGIDVWTTVNIQHLESLNDVVMRITGVRVSE TVPDAVLDRLHDIVLVDIPPRELIERLQQGKVYVPEQAAQALQAFFSPANLTALREL AMQEAADRVDSSLRETRAARGEGNLPLRRRVLVAIDGGGQSEYLVRVGRRIAER RDAPWTVVTVQGRRNDEATRREIDAAFALARRLGGEAELLHGSSIADALLDHAAH NSVSTLILGRTRERPVARMLNRTLTQQLIQRGAHYEITIIGTPQARARARRTGLSVP SRSTGQDTLLALGATAIACLVALVAERWVGLYDLSMVFIVAVVMVAARSRTSAAVI AAALCFLAYNFFFIAPRFTFAISARQGVITVFLFLAAALVAGRLASRLRMQVLALRAA NRHANARQALGRQLTRAASNEEVAQAGREALEQAMDAPAWLRIGQDTSTSGSA APGDTDLAAADWARRHGQPSGRFTDTLAGAEWWFLPLLDGDDRAIGVAGMRFA RNAPRLTPEQRQLAEAMVDDIAQAALRTQLVADLEKAHVSNETERLRSALLSSVS HDLRSPLAAMIGSADSLGSYADAMDAQDRRALLDTILVEGERLDRYIQNLLDMTRL GHEGLQINRDWIGVDELVGSAARRLQRYQPEVQLKLDIPATLAPIWVHPALVEQA VFNVMENAAKFSPPGAAVEVQARLVEGELRIDVLDAGPGIPDDERARIFDMFYSV ERGDRGRHGTGLGLTICQGMIGAHGGSVQALPGRDGRGTLIRITLPLLQPHPADD HDDP	19~~KdpD (2.08221E-121) ~~229,250~~Usp (2.62423E-30) ~~370,397~~DUF4118 (0.00000000000202648) ~~491,X,650~~HisKA (0.0000000000753208) ~~716,770~~HATPase_c (1.70618E-21) ~~872	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	6.4E-92	316.1	0.4	1.2E-91	315.2	0.3	1.5	1	C5C3W2_BEUC1	Histidine kinase (EC 2.7.13.3)	Bcav_3779	Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	857	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Beutenbergiaceae, Beutenbergia, Beutenbergia cavernae, Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	471853	>tr|C5C3W2|C5C3W2_BEUC1 Histidine kinase OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432) GN=Bcav_3779 PE=4 SV=1 MSDPAVDPGSAPSAGAEPGRRPGRLTVYLGAAPGVGKTYAMLDEAQRRRSRGT DVVVGLVETHGRAATLEKIGDLEIVPRRVVRHRGVELTELDTEAVIARGPEVALVD ELAHTNAPGSPHPKRWEDVADLLAAGIDVVTTVNVQHLESLNEDVEAITGVRQKE TVPDHVVRAADQIQLVDMSPQALRRRLAHGNVYRADQIDASLASYFREGNLTALR ELALLWLADRVDDALTQYRTEHAIAGVWPARERIVVAVTGGPESATLLRRGARIAE RAAGSELLAVHVLATDGLPTAPPAVIAADRALVESLGGTFHTVVGEDVPSAVVDFA QGANATMVVVGVSRHSRWREALLGSTSTEIARLAGAIDVHLVTHERARSGARPLA SSALSPSRRLAGWVLAFVAPLALTGLLVLVQEDVSASTELMLFLAAAVGVALVGG RWPAVACAAASFLCLNWFFTEPTGRFTIADPENLLALVVFVLVAAAVASVVDLAAR RASQAYRARAEASTLAALSRSVLSGEDTADAVVSRLAETFQLAHVALEERVAERA PWTTIAEAARSTASPGGGGSGSGSDSDDDRTIVRIDDTRRLVLTGRPLPAGDRQV LEAFGTQAGIVLEHRRLSARAEKARILEEADATRTALLAAVSHDLRTPLASIRAAVD GLRSDAVALDPDDEAALVDTAATSTARLEQLIDNLLDASRLESGALSPVLRDVSLD EIVPLAVDPFADHVSLEVPDDLPLVHTDPGLLERVVANIVANAVRHAPGGVPVRVL AARAGDSVELRVEDRGPGLDDARKARMFEPFQRLGDVSGTGLGLGLAVAAGLSR AVGATIAPEDTPGGGLTMVLTVPMAGG	19~~KdpD (9.68986E-111) ~~230,252~~Usp (3.56346E-29) ~~374,399~~DUF4118 (0.0000000649977) ~~474,X,638~~HisKA (0.000000000000971262) ~~704,752~~HATPase_c (5.40613E-21) ~~852	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	6.4E-92	316.1	0.1	1E-91	315.5	0.1	1.3	1	A0A0F0CBD6_9CLOT	Sensor protein KdpD (EC 2.7.13.3)	kdpD_4CLFS41_46290	Clostridium sp. FS41	663	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. FS41	1609975	>tr|A0A0F0CBD6|A0A0F0CBD6_9CLOT Sensor protein KdpD OS=Clostridium sp. FS41 GN=kdpD_4 PE=4 SV=1 MEKEWDGRPDPELLLRQNFPDSNNKGRGKLKIFFGYAAGVGKTFAMLEAARQEK AGGRDVVVGYIEPHDRPDTLALLDGLELLTPKYVEYKGITLREFDLDGVLIRHPDLV LVDELAHTNAQGCRHKKRYQDVTELLDAGINVYTTVNVQHLESLHDIVASITHVRV NERIPDRVFDNAAQVELVDIGPEELRQRLEEGKIYHREQADRASISFFTAQNLSAL REIALRRTADRVNREVIRERDAAGKDYFTGEHVLVCLSPSPTNAKVIRTAARMASA FHADFTAVLVETEHLKKEHVRISRSMEANINLAKQFRANVITLYGDDIVEQVASYAR QNGISKIVIGRTVRTRHSIFAKPTLIDRLIKAVPNMDIYVIPDASARERKRNGGTEQK RRVGSDLLKTALVMAFCTAMSLILDHYQLGIINAAMIYMMGTMLSAYLTRAGWCGL LASVASVLLFNFFFTEPRYTLQADASIYPFTFAAMLVCALVTSSMASRLKREAAKG EAESRYMQILFDINRNLRKGSTGEEILDICGTLVRNLLKRNIVIYDTREGRTDRMKIY PASENEDSARLTSLFKQQSEAAVAFWVYKNRHKAGATTDTLPGAQARYTPVYKD DRVYAVIGVEMKGGDTIQPNDKNVLNIIAEETSYRLGDMKEGCPR	25~~KdpD (2.54532E-113) ~~235,255~~Usp (3.67268E-34) ~~378,401~~DUF4118 (0.0000000000460281) ~~502,530~~GAF (0.0000679823) ~~651	non-kinase	KdpD;Usp;DUF4118;GAF

	7.6E-92	315.9	1.8	1E-91	315.4	1.2	1.2	1	B7KBV1_CYAP7	Osmosensitive K channel His kinase sensor	PCC7424_4719	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	377	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	65393	>tr|B7KBV1|B7KBV1_CYAP7 Osmosensitive K channel His kinase sensor OS=Cyanothece sp. (strain PCC 7424) GN=PCC7424_4719 PE=4 SV=1 MNSTPYESLNKSESGKHRIYIGMAPGVGKTYRMLQEANSLREEGIDVVIGLLETHG REETAEQVERLEQVPLKEITYQGKPLKEMDVEAIITRQPQIVLVDELAHTNIPGSLR EKRYQDVEFLLNLGINVFSTVNIQHFESLNDVVAKITGVLVRERIPDRLLDEADEVIV VDATPEILQERLIEGKIYKPEKIEQSLRNFFQRRNLVALRELALREVANNIEEIEELE GEGNYCCVQERVLVCLSTYSQSSRLLRRGARLANQMKARLYALFVEDPERFLSK DEIFYLEWCQQLCQDFGGEFLRVTHPDVAKAIAEVAEQHHITQVVIGQSLKSRWN LLLKGSIVQRLMRYLKEVDLHIIATTFVTIFYVHKFLLF	15~~KdpD (2.0957E-121) ~~219,240~~Usp (1.87622E-42) ~~362	non-kinase	KdpD;Usp
	8.2E-92	315.8	2.9	8.5E-92	315.7	0.7	1.9	1	A6V7N5_PSEA7	Histidine kinase (EC 2.7.13.3)	PSPA7_3716	Pseudomonas aeruginosa (strain PA7)	914	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	381754	>tr|A6V7N5|A6V7N5_PSEA7 Histidine kinase OS=Pseudomonas aeruginosa (strain PA7) GN=PSPA7_3716 PE=4 SV=1 MRAEQTEQADALLGELERQTAGRLTVFLGAAPGVGKTYAMLVRARELHHQGVDV VVGIVETHGRGETQTMVEGLSLLPRKKVEYQGRQLEEMDLDGLLARKPAIALVDE LAHRNVPGSRHERRWQDVEELLDAGIDVYTTVNVQHLESVNDVVHQITGVRVSE TVPDAVFERLRDIRLVDLPARELIERLNQGKVYLPEQAAQALQAFFSPSNLTALREL AMQTVAEHVDADLREKRAARGLEGISIQRHVLIAVDGRGHSEYLVRAGAKIAERR GAPWSVVTVETGRSADAALHTDEMDRAAPTLNRMARDEQQRLMEIDKAFALARN LGGETEVMHNTDVTQALLDAAAARGAKSIVIGRTRERPFARIFNRTLTQQLLLRGA RYELTIISTPQARQRSLRLPDITGERLTWREALLILMASLGAVGTAALAERTLGLQD LSMVFLVAVILVASRTRMASAVITATLCFLAYNFFFIEPRYTFLISAHRGVATVMLFL AAALIAGRLASRLRMQVVALRAANTHAMAMQNLGRRLAKAADLGQVITAGASILQ STLHAEVWIRINGESGPATSAGRLADKDLTAADWTQQHDQASGRYTDTLTNSAW WFLPVSSDKDTLGVVGLRFPPNMGRLSFEQRRLAESMVEDIGQTALRTRLVSELE VARVTGETERLRSALLSSVSHDLRSPLSSMIGAADSLARYGKDMGLEDQQSLLETI HVEGERLDRYIQNLLDMTRLGQQGLTLTRDWIGIDELVGSASRRLQRYEPDARIE HEIPAELTPIHVHPALIEQALFNVMENAAKFSPPGEPVRVQVRRTNDDQLQIDVSD RGPGIPEEERRRIFDMFYSVERGDRGKQGTGLGLTIVQGIVGAHMGSVEALPGPE GRGTTIRLTLPWGGYSNQEAKENDGTSQ	22~~KdpD (9.77E-118) ~~229,250~~Usp (1.81398E-26) ~~393,414~~DUF4118 (0.000000000440189) ~~514,X,673~~HisKA (0.0000000000041507) ~~739,792~~HATPase_c (1.8297E-23) ~~896	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	8.4E-92	315.7	0.2	1.5E-91	314.9	0.2	1.4	1	A1TJ27_ACIAC	Histidine kinase (EC 2.7.13.3)	Aave_0358	Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	932	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax citrulli (Acidovorax avenae subsp. citrulli), Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	397945	>tr|A1TJ27|A1TJ27_ACIAC Histidine kinase OS=Acidovorax citrulli (strain AAC00-1) GN=Aave_0358 PE=4 SV=1 MPTDLRPDPDALIAQMRAEEQRVQRGKLRIYFGANAGVGKTWSMLGAAQRERQ AGRDVLVGVVETHGRAETAALLEGLPVLPRRTLEHSGRKRTEFDLDAALQRRPAV LLVDELAHSNVPGSRHAKRWQDVQELVAAGIEVWTALNVQHLESLNGTVGAITGV RVHETVPDTVLDEADEVVLVDATPDELAARLAAGKVYLPQQAERAAQNFFRKGNL IALREIALRRTAEHVEDDVRGWRVEQSGGGHGVPPAWNTSGALLACVGPHEDAA HTVRTAARLAGQLNVRWHAAYVETPRLQRLPARERDRILAVLQLAEGLGAETAVL TGDAVAPPLAEHARQLNCATVVVGRARRRTGLGRWWPVPGTAQAIGAAAPTLEI VEAGEPGSSRRLPAAPWRPAGDPAGAGAQEDGGRPSVRWPGYGAAVAASVAV TLLALPLSGVLELTNIVMLYLLGVVGVAMRFGRVPAALAALLNVAAFDFVFVSPQLS FAVSDVQYLVTFGVMLGVGLLVGQLTAGLRFSAGVSAGREQRMRSLFELTRELS AALEASQVVDIGVRAVQQHFGGQAVVLPLDDTDRLAVPAVPPAGFDPSVADWTL RHGRSAGLGTATLAAQGWRYVPLTAPMRVRGVLALAPARPRWLLIPEQAQHLET LARQVAIALERVHYVEVAQRAVLDMESERLRNALLGAISHDVRTPLTALIALAESLP AQPDEALPAASQAIVQQAHQLHALVSNLLDMARLESGLAGGSVRLRRDWQSVEE VVGSAIRAARPALGALEVRTALPADLPLVEFDAVLIERVLVNLLENAAKYGALPIDIA AEALPGTLRIRVRDHGPGLPAALRGREHTLFDKFTRGQSESPTPGVGLGLAICRA VVLAHGGDIAASGAGAGPGAEFTVTLPRRNPPAVGEAAELPDEDASDSPGADRN LS	24~~KdpD (1.99069E-115) ~~233,261~~Usp (5.4299E-25) ~~356,434~~DUF4118 (0.00000000000458702) ~~520,551~~GAF (0.00000000000128167) ~~663,680~~HisKA (0.000000000547159) ~~742,799~~HATPase_c (3.52845E-18) ~~881	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.5E-92	315.7	0.2	1.3E-91	315	0.1	1.3	1	S0EVC4_CHTCT	Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain (EC 2.7.13.3)	CCALI_01549	Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	382	cellular organisms, Bacteria, Armatimonadetes, Chthonomonadetes, Chthonomonadales, Chthonomonadaceae, Chthonomonas, Chthonomonas calidirosea, Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	1303518	>tr|S0EVC4|S0EVC4_CHTCT Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain OS=Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49) GN=CCALI_01549 PE=4 SV=1 MVSDAQEERPDPDALLARIKAEEPQQRGRLKIFLGFAAGVGKTYEMLSEANRRKQ RGQDVVIGYVETHGRKGTEAQIGDLEIIPRKKIEYRGRVFEEMDTEAILRRKPQWV VVDELAHTNVPGSERPKRWQDVEYLRDHGISVLTTLNVQHLESLNDTVYDITGIRV RETVPDSLLHEAEIVMVDITPRALIHRLERGEIYPSDKIQSALNNWFREGNLNALREI ALREVAQEVDRDLSDYRKEQRIKKTWATKDRIMVCIAPELASMRLLRRGWRIAQR LDADIVAVYVENRPLTPEQQEQFRSVLALADQLKIPVVTLHGEVADQLISYAKEHQI TQIVIGHSSRSRFQEFLKGSIIHRLTQELRNIDILIVAPPEDEAL	26~~KdpD (8.07489E-121) ~~234,256~~Usp (8.03126E-35) ~~375	non-kinase	KdpD;Usp

	8.8E-92	315.7	0	1.4E-91	315	0	1.3	1	D7BWR2_STRBB	Histidine kinase (EC 2.7.13.3)	SBI_00297	Streptomyces bingchenggensis (strain BCW-1)	823	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7BWR2|D7BWR2_STRBB Histidine kinase OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_00297 PE=4 SV=1 MNDVRPGRLKVYLGAAPGVGKTYRMLDEGRRRASRGADVVVGFVECHGRPRTE AMLDGLEVVPRAHCDYRGGKFQEMDLAAVLARRPQVAIVDEFAHSNVPGGHNSK RWQDVEELLAAGVDVITAVNIQHLASLNDVVEKITRVPQGETVPDEVVRRAQQIEL VDMEPEGLRRRMAHGNIYAPEKVDAALANYFRPGNLTALRQLALLWVADQVDEA LQMYRTEHGIGRVWETRERVVVALTGGLEGDTLIRRAARIADRSAGGDLLAVHVT RSDGLAVGSSHASLARQRRLVEDLGGSYHSVVGDDVGTALVEFARAEHATQLVL GTSRRGRIERFLGGCGTGETVVGMSGDIDVHMVTHERAGRGMLLPSRRRTLSLV RRVAGPVAGLVLPVLLTVLLDRARGTFNLTSEALLFLLTVVGVACIGGVASAVIASV TASLLLNYWFIPPIGAFTLDNADALVALGVFAIVAATVAGVVDRSLRLSRRSARATA EAETMSSLAGTIVRGGATIPALLERTRETFGMESADLVHHEQTPDEEGVTVVPAG PGAFLVLRGRTLPSSGRRVLAAFAAHVGSAVERTRLAEAAAEIEPVKAADRMRTA LLRAVGHDLRTPLAAGWAAVTSLRSRDVEFSDEDRDELLATADESLAKLNRLVEN LLDLSRLQAGVLTLDLRATTLEEVLPAALADIPDVEVRDLEEIPAVMADPPLLERVIA NLVGNAARHSPPGGQVALTASAHAGRVEVRVVDRGPGLPQTGRERIFEPFQRLG DTDNTTGLGLGLALSKGLTEAMDGTLVPEDTPGGGLTMVLSLPFAERTVYSR	5~~KdpD (9.93707E-109) ~~214,236~~Usp (2.35964E-28) ~~360,414~~DUF4118 (0.000000242342) ~~481,X,599~~HisKA (0.0000000028115) ~~665,712~~HATPase_c (1.61192E-24) ~~813	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.8E-92	315.7	0.2	1.5E-91	314.9	0.2	1.4	1	D1BKY0_SANKS	Histidine kinase (EC 2.7.13.3)	Sked_27030	Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	853	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Sanguibacteraceae, Sanguibacter, Sanguibacter keddieii, Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	446469	>tr|D1BKY0|D1BKY0_SANKS Histidine kinase OS=Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74) GN=Sked_27030 PE=4 SV=1 MGDTRTGRLTVYLGAAPGVGKTFAMLDEARRRARGTDVVVGLVETHGRQATA EQVGDLEVLPRAVVPYRGTELGELDVAGVLARAPEVVLVDELAHTNAPGSTHPKR WQDVADLLEAGIDVVTTVNVQHLESLGDDVHAITGVRQRETVPDHVVRSADQVQ LVDLSPDALRRRLAHGNVYRAEQIDASLSSYFRVGNLTALRELALLWLADSVDDAL TRYRSDHAIDGTWPARERIVVAVTGGPEGETLLRRGARIAQRTAGSELLAVHVLA TDGLPSAPPAAIASDRDLTRALGGTFHTVVGEDVPSAVVDFARGVNATMIVVGVS RHSRVREALLGSSSAQTAQLAGSIDVHLVTHDHARSGSPLRRRWSALSRTRQVS GWALAVVLPAVLTGLVWWFRGDVSLTTELMLFLAGTVGVALVGGLWPAVVTALV SFVCVNWFFTPPTGMLTVSNPENALALVVFVVVAVSVASVVDLAARRTAQAYRAR AEASTLAALSRSVLSGDDSADAVVSRLAETFAVSEVRLEERTGAKAPWVTVAQTH RAGQRGGVDAEASTVRIDDDRRLVVVGRTLPASDQQVLEAFAAQAGIVLEYRRLR EAASQAAVLEQADATRTALLAAVSHDLRTPLASIRAAIDGLSAADVQLDAEDQAAL LDTIGGSTARLEALIANLLDLSRIQTGSVRAVLVARSVDEIVPVAVDGFAPGQVDLD VPDNLPLVLTDAGLLERAVANVVANAVRFSPAGVPVLVTASARPGEVEIRVVDRG PGLDDDRKQRMFEPFQRLGDTSPDGLGLGLAVAQGLVRAVGATVVVDDTPGGG LTMVLTVPTAEGSTAAPAVPTAESLSDRGGA	5~~KdpD (1.2123E-109) ~~214,236~~Usp (1.48323E-28) ~~358,384~~DUF4118 (0.00000000012698) ~~459,X,614~~HisKA (0.000000000000152865) ~~680,742~~HATPase_c (7.71771E-16) ~~829	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	9.4E-92	315.6	2.2	1.3E-91	315.1	1.6	1.2	1	R5Y2K9_9BACE	Histidine kinase KdpD domain protein	BN496_01537	Bacteroides sp. CAG:144	377	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:144	1262736	>tr|R5Y2K9|R5Y2K9_9BACE Histidine kinase KdpD domain protein OS=Bacteroides sp. CAG:144 GN=BN496_01537 PE=4 SV=1 MQNEENNNVQYFLDLIRRSRRGKFKVYIGMIAGVGKTYRMLQEAHELLENGVDVQ IGYVETHGRAGTEAQLVGLPVIPRKKIFYKGKELEEMDLEAILQRHPEIVVVDELAH TNVEGCRNRKRWEDVLELLDAGINVISAINIQHIESLNDEVKDIAGIEVKERVPDRIL QEADEVVNIDLTAEELIARLKAGKIYRPEKVQTALNNFFKTENILQLRELALKEVAFR IERKVESEVIPTSNAPARREKVLACISSNEQTPRHIIRKAYRLASRYNTSFIALYVQT HREDPDRISLASQRYLINHFELVTELGGTIKQVAADSVTDVIIDVCRENQITVVCMG QPSFSMPNVLFSIGRYRKFMKALAEMRIDLIIIS	19~~KdpD (2.4606E-127) ~~229,249~~Usp (2.55758E-25) ~~345	non-kinase	KdpD;Usp
	9.8E-92	315.5	0.1	1.6E-91	314.8	0	1.4	1	E2Q1F8_STRC2	Sensory histidine kinase in two-component regulatory system wtih KdpE (EC 2.7.13.3)	kdpD SCLAV_5517	Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces clavuligerus, Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	443255	>tr|E2Q1F8|E2Q1F8_STRC2 Sensory histidine kinase in two-component regulatory system wtih KdpE OS=Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602) GN=kdpD PE=4 SV=1 MAQGRLRIYLGAAPGVGKTYAMLAEGRRLAAEGADVVVALVEPHGRRLTAAMAE GLPSVPRRRVVHRGVRLTEMDVAAVLARRPGIALVDELAHTTVPGSRNPRRWQD VEELLDAGIDVITTLNIQHLESLNDVVEEITGVRQHETLPDPVARRADQIELVDLEPE ALRRRMTHGDIYPPDRIETALTHYFRVGNLTALRELALLWLADRVEEGLQRYRAEH GISAPWETRERILVGLTGGREGGTVIRRAARISARTPGSELLALHVVPGDGLADPV PLAEQRALVESLGGTYHQVTGDDIAAALLGFARTENVTQIVLGASRRGRVMSVVR TGVGRRTIRGSGPIDVHIVTHEEAGGPVPRPGSGSGRAPGPGRHRWSPYRDRR WWAALALAAVLPPALALVLTAPGTGVGPAGALLLCLLLVVVIALVGGLWPALLAAV VSAVLADRWFAAPGRSLSGARADELLAPAVFLAVAVLVGLAAGTAARRARRAGR AAAEAAALSRLATEMMRGRELPALVEQIRENFGLTSLSLLLRETAAGVRTRWYVV AAAGERPPERPEDADVEALADSGLTLAGRGRALGTDDYRVFAACGAQLAVAYSR GVLARRAAETDTRATAERTRASLLLRAGRELRAVLRTADEALVRLGHGAGTRADE ARLLGTAQLSVRRAERLVADLETLNRLHGGALATVLRPVDVGEVLTASLDELGPG GRTVEVSVPDGLPEVIADAAQLARALTALIADALRNSAPGAPPSVVARALPGKLAV RVTDGGSPAPPAGDRPPGARAEGIAQRLSRELTEAMGGALTAAGTRGGRFTVTL TLPAVAPPARPGPDGTPGPG	1~~KdpD (6.58844E-107) ~~211,233~~Usp (5.12258E-26) ~~353,431~~DUF4118 (0.0033583) ~~481,X,737~~HATPase_c (0.00490232) ~~827	dysfunctional kinase	KdpD;Usp;DUF4118;X;HATPase_c

	9.9E-92	315.5	0.2	1.8E-91	314.6	0.1	1.5	1	R5JHY9_9FIRM	Histidine kinase (EC 2.7.13.3)	BN781_00700	Coprococcus sp. CAG:782	899	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus sp. CAG:782	1262863	>tr|R5JHY9|R5JHY9_9FIRM Histidine kinase OS=Coprococcus sp. CAG:782 GN=BN781_00700 PE=4 SV=1 MSESRHNPDQLLKEIQADEEKRNKGHLKIFFGYAAGVGKTYAMLEAAHMEKQQGI DVVVGYVEPHACPKTAALLNGLEVLPTREVFYNGMILDEFDIGMALKRKPQLILVD ELAHTNAEGCRHAKRYQDIEELLNAGIDVYTTVNVQHIESLCDTVASITEIVVRERIP DSIFDNADQVELIDIEPQDLINRLNTGNVYRQTQEKQAVENFFTIENLTALREISLRR CADRVNILTENTRIKNHGDYHTGEHILVCLSSSPSNAKIIRTAAKMASAFKGEFTAL FVETPDFSVMSEENVKRLRSNICLAEQLGAKIETVYGEDVPFQIAEFTRLSGVSKIV IGRSSATKRHLLSKPTLTEKLIDYAPNLDVHIIPDAVSNAAVYQLRGGRKKTHIVFSV TDTLKSTAILILSSLVGMIFQKFGFDEANIITVFVLAVLVTAVITKHQIYSLISSIVSVLV FSFLFTEPQFTLQAYDQGYPVTFIIMLLAAFLTSSLAIRIKNQAKQAAQSAYRTKVLF DTNQLLQQAKDKNEIVSATSNQLIKLLRRDIVFYLADGEVLDTPHIFSVTEENLESCI SENEKAVAGWVLKNNKRAGATTGTLSNAKCLYLAVHSSSMVYGVIGIVMGEIPLD PFENSILLSILGECALALENEKNAREKQEAAILAKNEQLRANLLRAISHDLRTPLTSIS GNASNLLSNGDYFDNDTKKQLYMDIYDDSMWLINLVENLLAVTRIEEGRLNLRITE DLMDDVITEALHHINRKSEEHHISVESKEEFLLAKMDAKLIVQVIINIVDNAIKYTPKN SHIVIRTEKRGKQAIVSISDDGNGIADEIKPRIFDMFYSGANQIADSRRSLGLGLSLC KSIINAHGGELTVSDNLPHGTVFTFTLPAGEVKIYE	23~~KdpD (1.54788E-119) ~~232,252~~Usp (5.64904E-37) ~~375,403~~DUF4118 (0.0000000000288563) ~~503,X,668~~HisKA (0.000000000346235) ~~734,787~~HATPase_c (6.60057E-28) ~~890	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1E-91	315.5	1.2	1.4E-91	315	0.8	1.2	1	K9TR56_9CYAN	Osmosensitive K+ channel His kinase sensor	Oscil6304_4995	Oscillatoria acuminata PCC 6304	375	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria acuminata, Oscillatoria acuminata PCC 6304	56110	>tr|K9TR56|K9TR56_9CYAN Osmosensitive K+ channel His kinase sensor OS=Oscillatoria acuminata PCC 6304 GN=Oscil6304_4995 PE=4 SV=1 MDFSEQLPESDSLYQPSRRRGKHKIYIGMAPGVGKTFRMLEEALALKQEGIDVVV GLLETHGRRETAEKAEGLEIIPRQKVQRGGIFLTEMDVDGILARAPQLVLVDELAHT NIPGSLREKRYQDVEFILEAGIDVYSTVNIQHLESLNDLVARITGVVVRERIPDRLLE EASEVLVVDITPETLEERLREGKIYAPAKIQQSLANFFQRRNLVALRELALREVADNI EETELSGTSHGLTCSIQERVLVCVSTYPKSLLLIRRGARLANYMNAPFYVMFVSSP ERFLTKAESLHIETCEKLCEEFGGEFVRIESRDIKEAISKIAAQYRITQIVLGETRRSR WDLLWRGSIVQQLMRSLPEIDLHIIANTSKET	19~~KdpD (4.05718E-126) ~~228,247~~Usp (1.67844E-44) ~~369	non-kinase	KdpD;Usp

	1.1E-91	315.3	0.7	1.9E-90	311.3	0.1	2.2	1	Q7VVZ6_BORPE	Two component sensor protein	kdpDBP2483	Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	904	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella pertussis, Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	257313	>tr|Q7VVZ6|Q7VVZ6_BORPE Two component sensor protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) GN=kdpD PE=4 SV=1 MADPGNDRLDPDRLLQTLEQAQSDARRGRLRIYFGACAGVGKTYAMLAAARAQA AQGVDVVAGLVETHGRADTAALLDTLPALPLQTLDFQGRRLREFDLQATVARRPR LLLLDELAHTNAPGARHAKRWQDVEELLAAGIDVWTTLNVQHLESLNEAVGGITG VRVRETVPDSVFDAADEIILVDLSADELLRRLREGRVYVPEQARHASRHFFRKGNL IALRELALRRTAEHVDDDVRAYRHERAIEPVWRTREAVVACIDADPHAEHVLRSAH RLAQQLDCEWHAITIEAPRVAPLPRAGRARLDQALALAETLGAHVETVAGTDMVD AATRYMRRHNITKAVVGRDAWRRRGLSGLLDAALTPGRLLRRRSFADVLASACP EADIVRVGAPSAATAAPRRDPRSWRNASAPAGHAAAGAYLWALAYCAAATLASR LAFPVLHQTNIVMIFLLAVVAAALRHGRGPAALASVVSVALFDFFFVQPLASFAVSD VQYLLTFAVLLTVGLLIGQLTAGLRQQARAAARREADARGLYEFARELSAALQPEQ IAGAASAFLNAAFGARGALYILGLDDRLRLAPGAGDAALEPTLAQWAFDHGQACG AGTDTLSNSPVLYLPLRAPMRVRGVLALHHAGPPLYSAAPARRQLDAYATLIAIAIE RLHYVEVAQQALLSIESERLRNALLAAVSHDLRTPLTSLLGMAETLQRSPAAMTPA ALETVAAMQDQARRMHALVVNLLDMARLQSHDAPLRRQWQSVEELVGSALAAM NAALQDRPVTVAPLSALPLVKCDGILIERVLCNLLENAAKYTPPGSAIHIDALADAHT LQVRVADDGAGVAQADRQRIFEKFARGQRESAPPPAQASGWRYAAPSWTPTRA ASGSSRPGACAAPASSSRCR	25~~KdpD (2.31029E-110) ~~235,258~~Usp (6.66891E-34) ~~380,424~~DUF4118 (6.39791E-20) ~~518,550~~GAF (0.00000000000053548) ~~665,682~~HisKA (0.00000000000117747) ~~747,800~~HATPase_c (0.000000000000251722) ~~862	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.2E-91	315.2	1.8	1.2E-91	315.2	1.3	1.7	1	Q31MG0_SYNE7	Potassium-transporting ATPase D chain	Synpcc7942_1729	Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	370	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus elongatus, Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	1140	>tr|Q31MG0|Q31MG0_SYNE7 Potassium-transporting ATPase D chain OS=Synechococcus elongatus (strain PCC 7942) GN=Synpcc7942_1729 PE=4 SV=1 MTTLLKARRGRHKVFIGMAPGVGKTYRMLQEGQQLHSEGLDVVIGLLETHGRQE TRQQAQGLELVAPRQLDYNGVVLSEVDIEAILQRQPQLVLIDELAHTNAPGSEHEK RYQDVELLLAAGLDVYSTVNIQHLESLNDLVARITGVIVRERIPDRLLEEADEVVVV DVTPETLEERLREGRIYALDKVPQALTNFFRRHHLVALRELALRSVADSIEEQAAG TRTGAISVRERVLVCLSTHPQSIRLLRRAARLSGAMDARLYVLFVADPQRFLTKAE VLQLETCDRLCGMFEGAFLRVESTDVVGAIVKVATEQRVTQVVIGESPTSRRLW WWQRPLTDRLLQRLRGQGIDLHIISFPGDHPDSELDD	7~~KdpD (8.26272E-110) ~~217,234~~Usp (9.25394E-37) ~~358	non-kinase	KdpD;Usp

	1.3E-91	315.1	3.6	1.8E-91	314.7	2.5	1.2	1	K9Z6H6_CYAAP	Osmosensitive K channel His kinase sensor	Cyan10605_2262	Cyanobacterium aponinum (strain PCC 10605)	359	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobacterium, Cyanobacterium aponinum, Cyanobacterium aponinum (strain PCC 10605)	755178	>tr|K9Z6H6|K9Z6H6_CYAAP Osmosensitive K channel His kinase sensor OS=Cyanobacterium aponinum (strain PCC 10605) GN=Cyan10605_2262 PE=4 SV=1 MLRKQGKHKIFIGMAPGVGKTYKMLQDANILKKQGIDVVIGLLETHNRQETLLQADGLEIIPRKFISQDNLTLTEMDTEAIINRHPQLVLIDELAHTNIPNSRYQKRYQDVEEILKAGIDVYSTVNIQHLESLNDLIAKITGVVVRERIPDRILDEADQVVVIDVTPETLEERLLAGKIYASNKIEQSLQNFFQRKNLIALRELALREVADTVEEEGEESIPFAQSYLIQERVLVCVSTYPNSLRLLRRGARLANYMNAPLFVLFVKNPDHFLSKTEALHIETCQQLCRDFEGTFLRVEDYNVASVIALIAEQEKITQIVIGESRQSRWKQLLRGSFTQKLMRLIWKKQIDLHIIATNH	4~~KdpD (1.77855E-123) ~~213,232~~Usp (8.88706E-30) ~~356	non-kinase	KdpD;Usp
	1.3E-91	315.1	0	2.4E-91	314.2	0	1.4	1	V4IXB4_9ACTN	Histidine kinase (EC 2.7.13.3)	B590_05719	Streptomyces sp. PVA 94-07	852	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. PVA 94-07	1223307	>tr|V4IXB4|V4IXB4_9ACTN Histidine kinase OS=Streptomyces sp. PVA 94-07 GN=B590_05719 PE=4 SV=1 MGRGTLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVIGFVAHHDRPRTRALLEGLELIEPLGGPDGDGGTPQTREMDVEAVLARRPAVALVDELAHTNASGARNAKRWQDVEELLAAGISVISTVNIQHLESLGDVVEAITGVRQQETVPDEVVRRADQIELVDMSPQALRRRLAHGNVYQSDKVDAALSNYFRPGNLTALRELALLWTADRADEYLQKYRGEHNIRSTWQARERIVVGLTGGPEGRTLLRRAARMAAKGSGSEILAVYIARRDGGLTTASPKELALQRTLVEDLGGSFHHVIGDDIPSALLEFARGVNATQIVLGSSRRKSWQYVFGPGVGATVARESTPDLDVHIVTHEEVGQGRGLPVARGARLGRSRILWGWFIAVCGPALLAIVLSSLDHGPGLANDVLLFLSLTVGAALVGGLLPALASAALCSALLNFYFTPPTRTLTISDPENIVAIVISFAVAVAVASAVDLAARRTHQAARLRAESEILSFLAGSVLRGATTLDALLERVRETFAMESVALLEREGDRTPWTCAGSVGPRPLERPEDADVDMPVGDHMALALCGRVLPAEDRRVLAAFAAQAAVVLDRQRLQDEADQARRLAEGNRIRTALLAAVSHDLRTPLAAIKASVTSLRSDDVAWSEQDEAELLESIEHGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSAQLDIPETLPMAVDPGLLERSVANVVENAVKYAPEGAPVLVAASALGDRVELRVMDHGPGVPDDAKDRIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLTLRAVTGPRAGARTVLPAQVTS	1~~KdpD (2.03489E-109) ~~213,236~~Usp (1.50732E-29) ~~360,X,616~~HisKA (0.000000000000137299) ~~682,731~~HATPase_c (2.72648E-25) ~~832	kinase	KdpD;Usp;X;HisKA;HATPase_c

	1.4E-91	315	1.3	2.6E-91	314.1	0.9	1.5	1	B1HTG2_LYSSC	Histidine kinase (EC 2.7.13.3)	kdpD Bsph_3682	Lysinibacillus sphaericus (strain C3-41)	895	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus sphaericus (Bacillus sphaericus), Lysinibacillus sphaericus (strain C3-41)	444177	>tr|B1HTG2|B1HTG2_LYSSC Histidine kinase OS=Lysinibacillus sphaericus (strain C3-41) GN=kdpD PE=4 SV=1 MENTRPTPEMFLARLQQEEHSIGKLKIFLGYAAGVGKTYAMLDAAHQAKKLGKDV VVGYVEPHPRPETLALLEGLEQIPTKKITYKGKIFQELDIDAVLQRKPEIVLIDELAHS NVPSMRHKKRFGDVEELLAKGIHVFTTVNIQHIESLHDLVEEITEIKVRERIPDYLID QAAQIKVVDIEPDELIQRLQDGKVYVKQQAEKALDSFFRKQNLVSLREIALRRTAD TINYQQLNSNESVRNYVQIEEHLLVGISSSPTNAKVIRTTARLAQALHGKFTALYVQ NMQAHERNHADSERLQQYIKLVEQLGGHVVIVQEDDIAAALANYAQISGVTKLVIG RSSMRKKWWQPNAKISDRLNEYVPNLSIHIVPDQENEQFYFPRIKNKLAFEWLDL FKMFIVFSVISIVGLYLYSIGISEPNIITIYILGVLILAIWSSGWLMSIISSIVAVLLFNYFF TEPRFSFDAYHRDYPMTFFIMFLSGVITSSLTKKIKEQTIIAIRKSYRMEVLLETNRR LQHAKSIEEIITEGMSQIVKLVEKPVQFFEIDNRVIGKSTFFRNDKISTIENQKIATLF NNPNEHGVVNWVTNNKHVAGVSTDIFPEVHAYYIPVISNGNVRGVIGIALSKLLPLP AFERNILHAIINDFSFAMDKWYLQKLHEEVAREAEMEQMRANLLRAISHDLRTPLT AISGNADILLNNAPLIPDIEKNKLYEDIFNNSKWLVQMVENLLAVSRLEDGQFALEIQ LELVEDIIQEALSHVVHQNSSHKISYQIEPEFLLSLMDARLMIQVFINIIDNALTYTPP GSDITILVKECDGLVNFSISDNGPGIDDSLKSSLFEPFTTGKVQRSDSRRGLGLGLA LCQTILKLHGSQITVSDNKPQGTIFNFSLKKE	23~~KdpD (1.58174E-117) ~~230,250~~Usp (1.65349E-33) ~~373,396~~DUF4118 (1.96245E-14) ~~497,579~~GAF (0.00120247) ~~653,670~~HisKA (0.0000000000613368) ~~736,791~~HATPase_c (4.90627E-24) ~~892	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.4E-91	315	0.2	2.3E-91	314.3	0.1	1.4	1	H6MWK3_GORPV	Histidine kinase (EC 2.7.13.3)	kdpD GPOL_c44110	Gordonia polyisoprenivorans (strain DSM 44266 / VH2)	848	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia polyisoprenivorans, Gordonia polyisoprenivorans (strain DSM 44266 / VH2)	1112204	>tr|H6MWK3|H6MWK3_GORPV Histidine kinase OS=Gordonia polyisoprenivorans (strain DSM 44266 / VH2) GN=kdpD PE=4 SV=1 MVSTADARGTLEVFLGCAPGVGKTYEMLAHAHDLIGEGADVVIAVVESHGRSATA GLIEGIEVIPRRRIVYRGTELEEMDLDAVLARHPQVALVDELAHSNVPGSANAKRW QDIDVLRDAGIDVLTTVNIQHLESLNDVVAQITGVTQRETVPDAVVRAADQIELVDI APQALRQRLSAGKVYPSGRIDGALANYFRQGNLTALRELALLWLADRVDDNLADY RAAHAITDTWEARERVVVAITGGAESSTLIRRASRIASRSSAELIVVHVVRGDGLA GRSGVELSELTELAAGFGARVHSIVGDDIPTTLLEFARGVNATQLVLGTSRRPRW KRIFDEGVGATVVASSGRIDVHMVTHEETAKRNRLDIRETRFHRPLSWVLAVVVPL VMTGILAILDRWLGFASETALFFVTVLAISMLGGVAPAALSAVVSGVLLNYFFTAPR FTLTINEPDNLITILVMLVIAIAVAALVDSATVRRVQAQRAAREAELLAVFSDAVLGG ADVAGLLERVRETYDQRAVSVVRRRADGTVEVSAAVGEDPPHRDSEADTVLPAR GDEYELLLCGASPEAQDRRVLTAVATQATAALERADLEAGAAAARALAQTDELRR ALLSAVSHDLRTPLAGAKAAVSSLRSEEVTFSPEDTAELLATIEESVDQLSALVANL LDSSRLEAGAIRPNMARTYLVEVVHRAANRSGPAAAGIAFRFGHVWAWTDGGLL ERVLANLIDNAVRHGGGQVEVATSLDESDPQSPRTIIEVVDHGPGIPVERREQIFD DFRQGFDRNGSDGGVGLGLSVAQGFTSTMGGNLAVVDTPGGGTTMVVDLPAIE QSEQSAPAEGVAHG	7~~KdpD (6.00293E-114) ~~216,238~~Usp (2.57E-31) ~~359,382~~DUF4118 (0.0000000000517284) ~~476,X,610~~HisKA (0.0000000000116952) ~~676,725~~HATPase_c (2.41333E-22) ~~830	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.5E-91	314.9	0.7	1.8E-90	311.4	0.1	2.2	1	X4Z2T7_9BORD	Sensor protein KdpD (EC 2.7.13.3)	kdpD D560_0215	Bordetella holmesii ATCC 51541	884	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella holmesii, Bordetella holmesii ATCC 51541	1247649	>tr|X4Z2T7|X4Z2T7_9BORD Sensor protein KdpD OS=Bordetella holmesii ATCC 51541 GN=kdpD PE=4 SV=1 MADPGNDRLDPDRLLQTLEQAQSDARRGRLRIYFGACAGVGKTYAMLAAARAQA AQGVDVVAGLVETHGRADTAALLDTLPALPLQTLDFQGRRLREFDLQATVARRPR LLLLDELAHTNAPGARHAKRWQDVEELLAAGIDVWTTLNVQHLESLNEAVGGITG VRVRETVPDSVFDAADEIILVDLSADELLRRLREGRVYVPEQARHASRHFFRKGNL IALRELALRRTAEHVDDDVRAYRHERAIEPVWRTREAVVACIDADPHAEHVLRSAH RLAQQLDCEWHAITIEAPRVAPLPRAGRARLDQALALAETLGAHVETVAGTDMVD AATRYMRRHNITKAVVGRDAWRRRGLSGLLDAALTPGRLLRRRSFADALASACP EADIVRVGAPSAATAAPRRDPRSWRNASAPAGHAAAGAYLWALAYCAAATLASR LAFPVLHQTNIVMIFLLAVVAAALRHGRGPAALASVVSVALFDFFFVQPLASFAVSD VQYLLTFAVLLTVGLLVGQLTAGLRQQARAAARREADARGLYEFARELSAALQPE QIAGAASAFLNAAFGARGALYILGLDDRLRLAPGAGDAALEPTLAQWAFDHGQAC GAGTDTLSNSPVLYLSLRAPMRVRGVLALHHAGPPLYSAAPARRQLDAYATLIAIAI ERLHYVEVAQQALLSIESERLRNALLTAVSHDLRTPLTSLLGMAETLQRSPAAMTP AALETVAAMQDQARRMHALVVNLLDMARLQSHDAPLRRQWQSVEELVGSALAA MNAALQDRPVTVAPLSALPLVKCDGILIERVLCNLLENAAKYTPPGSAIHIDALADR QRIFEKFARGQRESAPPAQASGWRYAAPSWTPTRAASGSSRPGACAAPASSSR CR	25~~KdpD (1.04039E-110) ~~235,258~~Usp (3.80447E-33) ~~378,424~~DUF4118 (8.2903E-20) ~~518,550~~GAF (0.0000000000138752) ~~665,682~~HisKA (0.0000000000052747) ~~747,800~~HATPase_c (0.00222281) ~~843	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.5E-91	314.9	2.8	2.3E-91	314.3	1.9	1.3	1	B7JXL2_CYAP8	Osmosensitive K channel His kinase sensor	PCC8801_0684	Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	368	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	41431	>tr|B7JXL2|B7JXL2_CYAP8 Osmosensitive K channel His kinase sensor OS=Cyanothece sp. (strain PCC 8801) GN=PCC8801_0684 PE=4 SV=1 MIAQNQLAQPFFSASHSGKHRIYIGMAPGVGKTYRMLQDAQALKEEGMDVVIGLL ETHNREETAEQAEGLEQIPLLEVNYQNKSLKEMNVEEILARSPQLVLIDELAHTNVP GSLREKRYQDVEYILESGINVFSTVNIQHLESLNDLVAKITGVVVRERIPDRLLDEA DEVVVVDVTPEILQERLEDGKIYDVHKIEQSLSNFFQYRNLTALRELALREVADNLE ELAEEQSGHKGSNGVQERILVSVSTNPQSSRLVRRGARLVSQLKGRLYVLFVCDP DRFLSKDEGLYIEMCERLCQELGGEFLRVSHPDIVKGIIEVAQQYHITQIVIGHTRQ PRWKWFFKRTIVQRLIGSLNGIDLHIIAGS	15~~KdpD (1.29821E-112) ~~225,244~~Usp (1.24281E-41) ~~366	non-kinase	KdpD;Usp
	1.5E-91	314.9	0	2.4E-91	314.2	0	1.3	1	D3UX99_XENBS	Histidine kinase (EC 2.7.13.3)	kdpDXBJ1_1070	Xenorhabdus bovienii (strain SS-2004)	905	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus bovienii, Xenorhabdus bovienii (strain SS-2004)	406818	>tr|D3UX99|D3UX99_XENBS Histidine kinase OS=Xenorhabdus bovienii (strain SS-2004) GN=kdpD PE=4 SV=1 MDQIEPLRPDPDDLLALANEKPRGKLKIFFGACAGVGKTYAMLQEAQRLLSQGLD VIAGVVETHERQETAALLTGLPQLPLKHIRYHERRIAAFDIDAAIARYPAIILMDELAF SNPHSSRHPKRWQDVEELLEAGIDVLTTINVQHLESLNDVVGAITGIRVRETIPDHI FDHADDVVLVDIPPDDLRQRLNDGKVYISGQAERAIEHFFRKGNLIALRELALRRTA DRVDDQMRAFRDTRGKEPVWHTRDNLLLCIGCNAGNEKLIRTAARLAAKLGCEW HAVYVETPKLHRLPEIKRRTILKALKLAQELGAETATLSDPHEERAILRYAREHNLG KILVGRYHGSHSTSFSDKWLGFKWRPDFVERLGKLGPDLDLIIVALEDKKRWDKE QRDNRAFHEKWRIQIHGFLIAIILCTLITLFSHTFLLTLDKANLVTLYLLGVVIIALFYG RWPSVFAAFINVISFDIFFVQPRWSLAVTDMQYLLTFTVMLIVGVVVGNLTAGIRY QARVARYREQRTRHLYEITRELSRALNEEDVARISYHFLSNSFQAKTGLLLPDNNA RLYQVKSNNGGQMQIDEAIAKWSFDKKQPAGAGTDTLPGVPYQLFPIATASQVFA VLAIESPNLRQLLVPEQQRLLQTFTGLIANALERLHLSRRAESAKLETEREQLRNSL LAALSHDLRTPLTVLFGQTEILMLDLSTENSPHTQQVNQIRQQILSTSRLVNNLLDM ARIQSGGIQLNLEWHSLEEIVGSALRSLEYTLSRYTVELSLSANLLLHCDACLLERV FINLLENAIKYTHEQTPLGIRATTEYKQVHIEIWDAGSGIPQGQEQVIFDKFSRVRK ESAIPGVGLGLAICRAIIEIHGGHIWAANNKKGGASFHFVLPLEEVPKIEEVIEEM	23~~KdpD (2.55199E-108) ~~231,254~~Usp (2.86673E-35) ~~384,412~~DUF4118 (3.18142E-21) ~~511,537~~GAF (6.74244E-17) ~~655,672~~HisKA (0.0000000000192553) ~~737,789~~HATPase_c (1.82897E-26) ~~890	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.6E-91	314.8	0.1	3.4E-91	313.8	0.1	1.6	1	D0IYP3_COMT2	Histidine kinase (EC 2.7.13.3)	CtCNB1_0533	Comamonas testosteroni (strain CNB-2)	897	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Comamonas, Comamonas testosteroni (Pseudomonas testosteroni), Comamonas testosteroni CNB-1, Comamonas testosteroni (strain CNB-2)	688245	>tr|D0IYP3|D0IYP3_COMT2 Histidine kinase OS=Comamonas testosteroni (strain CNB-2) GN=CtCNB1_0533 PE=4 SV=1 MPSSTPSSAAQRPDPDALVAQLQADRQRAHLGKLRIYFGSNAGVGKTYSMLAAA QRERQAGRKVLVGLVETHGRAETEQQLHDLELLPRRTLVYQGRQLDEFDLDAAL ARRPEVLLLDELAHSNVSGSRHPKRWQDVQELLEAGIEVWTTLNVQHLESLNDVV GGIVGIQVHETVPDHIFDDADEVIVVDIPPEELLKRLKSGKVYPLEQAERASRNFFR QGNLLALRELALRRTADRVDEDMRDYRRERSIGDVWPTRERLLVGVGGRAGDDA LVRQVARLARRLEADWVVVYVDAPERQHRPRAAQEAVLKTLALAARLGAETATIP GAHVAQALVDFARERNASHLVLARVHEPLSRWLRWRASSLSEQIAALDPGLDVLL LSVKQSKNESTLRLPAAREKTIPWKGYAGVTLACLAATAVAELLLRVFDPANVVML FLLVVVLSAVRWGRGPGAWAALLSVLLFDFYFVPPRNSFSVNDTQYLFTFSLMLG VALVCGQLTARLRHEARVAAERERRAGALARLARDLSGALTQEQVTQIALTTISGV FDAQTGLLVPDADERLQLAPGSEAQIDTSVGRWSMEHGQMAGHGTDTLAAAPAL YVPLMAPVRSRGVLVLQLRAPQRLRVPEERRLLEACASQIALALERVHFVEVAQQ TQIAMEGERMRNTLLSAVSHDLRTPLTGILGAAQAALPHAPQGPAHHMLVQIRNQ AQALQQLVDNLLAMARLQQGGVQLKREWLPVDELVGSALAQMRERLAAHALQTS LPADLPLLQLDAVLMERVLVNLLDNAIKYTPEGTTITVAASVADGDCVLSVQDAGP GLPVHLSAEQLFEPFTRGQAESAVFGMGLGLALAQRIVQAHGGRLRVAQADPGP GTIFSVHLPVPEQPAMDE	29~~KdpD (3.23472E-102) ~~239,261~~Usp (2.20231E-29) ~~386,416~~DUF4118 (0.00000000000122731) ~~508,536~~GAF (2.38775E-14) ~~651,668~~HisKA (0.0000000000300767) ~~731,784~~HATPase_c (3.13309E-27) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.7E-91	314.7	0.5	3.4E-91	313.7	0.4	1.5	1	R4K6B5_CLOPA	Histidine kinase (EC 2.7.13.3)	Clopa_3992	Clostridium pasteurianum BC1	880	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium pasteurianum, Clostridium pasteurianum BC1	86416	>tr|R4K6B5|R4K6B5_CLOPA Histidine kinase OS=Clostridium pasteurianum BC1 GN=Clopa_3992 PE=4 SV=1 MRGKLKIFFGYAAGVGKTYEMLREAQEIKESGEDIVIGYIEPHARPETIALTKGLEKI ELKTIRYKGSTFREFDIDKALIRKPKIILVDELAHTNGIGQRNRKRWQDIEELLAAGI DVYTTVNVQHIESLNDVVENITHISVRETIPDKIFDEAEKVEIVDIEPDELLNRFKSGK IYRIEQVKRALLNFFTRNNLYALREIALRRIADRVNYEVESGRLAKREITVIPASEQIL ACISPSPSSAKVIRTAARMAENYHSKFVVLYISTTKAENLSKEDKKRLNLNFSLAEK LGGEIAQLYGDNVADQIIQYAKFRNITKLVIGKNYKRSSKILHFYAKDVVDKLMDSN AYIDVYVIPNSLYKKKREKLIRKLNRWNNFSLKEISESILIIGIATGIAQIFDYMGLNDT NEIMILILGVIIVYIRTTGYFIGVIASIVGVLMFNFLFTEPKYSLEIYDKNYLITFTIMLIVA FIVGNLTNRIQKESNNSYTREKRTQTLYMVSSKLLSAVGASDVISIGIKYTSRLINRT VVAYLSEDNKLSASFVYNNKSENENEILNRDENAVAYWCLLNGKEAGKGTDTFYG AKGYYVPIKIQEKILGVIGVSCLQGFLEPEQKFIVQTITGQIAIALDREILSSEQETSK VQIERERLRSNLLRSISHDLRSPLAGIKGSISTILEKGKVISEKTKEELLNGIYDDTEW LIRLVENLLSMTKFDEGNMDIIRNMELVEEVVSEAVQRSSKYSKDHKIKVNVPEKII MVPMDGNLIEQVIINLLDNAAKFSPKYSIIEIKVYESEEDVIFQVIDNGCGIEEKILSNI FERFFTNGSKISDSRRGVGLGLAICKSIVEAHGGKITAANKKGGGAIFTFNIPKKHE NLKK	2~~KdpD (4.13926E-123) ~~210,233~~Usp (8.00178E-41) ~~357,385~~DUF4118 (2.69554E-16) ~~484,513~~GAF (0.0000943404) ~~632,649~~HisKA (0.000000000099328) ~~715,768~~HATPase_c (1.02193E-28) ~~871	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.7E-91	314.7	0	3.6E-91	313.6	0	1.6	1	C4XK61_DESMR	Histidine kinase (EC 2.7.13.3)	kdpDDMR_09250	Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	889	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio magneticus, Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	573370	>tr|C4XK61|C4XK61_DESMR Histidine kinase OS=Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1) GN=kdpD PE=4 SV=1 MHDEDNRPDPDALLAMVQREEENKRRGQLRIFLGMAPGVGKTYAMLEAARLKMT EGVEPLVGIVETHGRQDTEALLYGMSILPRQRIDYRGHALEEFDLNTALAKRPSLIL VDELAHTNAPGCRHPKRWQDVEELLEHGLDVWTTLNVQHLESLNDIVAQITGVRV RETVPDAVLAKAQSVILVDLPPEDLRQRLTEGKVYLPKQAEWAGENFFRVGNLNA LRELALRQTANRVGTEVLVYRRGHAIETTWPTAERILVCVGPSPYSATLVRTAKRL ADGLHADWHALFIQKSPEGTSTDQAMANLRLAQELGAQTHVLTGADVAKLVVGF ARQHNVTRIVIGKPLTRNLLDVLRGSPVDQLVRESGEIDVHVIKGQDPRLPAARRP PPALAKGRWKDLPAALGIVAASTAACFAMYPYFELANLIMVYLVGVLAASIWLSRR ASAAASVLSVLAFDFCFVPPRFSFSVTDVAYLVTFAVMFLVALVLSSMASRVKAQA DSAVQLERQASELSDFSRNLATTRGAANLLLVAHEHITRIFGCTTFALLPNTEGKLE DAFVSEANETLTDKDVGVAQWVFDNGKPAGLTTQTLAESDALYLPLPGTEAILGV MGLRPDSPDAADSLELPDRRRLLEAVVHQTALALDVDRLEERAKKTLVEAEREKL RAALLSTVTHDFKTPLSAIAGSAESLLALGEATTPEVRRSLEENIAQEASRLERLVD NLLRIAALESGSVVPDIKLIPIEDVVGSALARLDATLAGHAVHLDIPDDLPPIPMDEVL MEQVLINLLENAAKHTPLGTEILVSAAIRGHKAVIEVRDAGPGLPPGDPEKLFERFQ RGDRSSTSGYGLGLAICRAVVKAHGGSITADRNRPAGAAFTVILPLYANE	24~~KdpD (3.11374E-114) ~~234,256~~Usp (1.72234E-39) ~~374,401~~DUF4118 (1.40316E-16) ~~498,528~~GAF (0.000000187099) ~~646,664~~HisKA (0.00000000011512) ~~729,783~~HATPase_c (1.96573E-29) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.8E-91	314.7	0.2	3.4E-91	313.7	0	1.6	1	A0JW43_ARTS2	Histidine kinase (EC 2.7.13.3)	Arth_1878	Arthrobacter sp. (strain FB24)	883	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. (strain FB24)	290399	>tr|A0JW43|A0JW43_ARTS2 Histidine kinase OS=Arthrobacter sp. (strain FB24) GN=Arth_1878 PE=4 SV=1 MARGTLRIFLGAAPGVGKTYEMLEEAHRLSKRGEDVVVAFAMDHGRSDTRALLD GLEVIPPRRLPYRGTEFEEMDLDAVLARAPETAIVDEYAHTNIPGSRHTKRWEDID ELLNAGINVLSTVNIQHLASLGDVVNAITDVRQAETVPDEIVRRADQIHLVDISPELL RQRLGDGKIYSADKIDAALSNYFRLGNLTALRELALLWLADRVDEGLARYREENDI QATWPARERIVVGLTGSPEGEVLIRRGARILNRVNGGDLLAVHVRAADGVAEESP RALEAQRRLIQDLGGSYHVVAGEDPASALLDFARSVNATQIVVGISRHKKLAGLLG ALLGGGIGTRVVRDSGDIDVHMVSHPLGGRGTGPVRQRDLGRVRVTAGFVLAAV LPALLQLMLSANSEPNIATAVLIQLSGSVLVALIGGLWPAIVAALWSSLLVNYYSTP PVGTLTISDPQNLLALLVFVGVSAAVAVVVDISARRSKEASRARAEATTLGDLTRSA ARAEDTVKGLLEQALDVFQVSGAALYTSAGDTGTEAPGGTGWRSVAEAGAVPPA GPDTADNIEQIDPTTRLVLTGRTLPASDRRLLGAFGVHLAAQLERQQLAASRREVL RLAESNTMRTSILRAVSHDLRTPLAGIKLAVGGLLQHGVTYTPEEERDLLQTIDACA DRLDLLVGNLLDMSRISADSVNPLLRPVRWSEVVPAALHGTPQGRVRVELPANMP EIDADPGMLERVIANIVENAVKYAPDSEIVLVGAVGGFRSATIAGRPASELRIIDHG QGVPAERVVEMFRPFQRLDDIPQTTGVGLGLAVAKGFTEAMGGTLRAEETPGGG LTMVIRLPLSTGLAIDDGDRQAPVQPQSLLARRTDSRPFQPSATENP	1~~KdpD (4.96228E-110) ~~211,233~~Usp (3.03936E-26) ~~359,385~~DUF4118 (0.000000399156) ~~463,X,619~~HisKA (0.00000000000135246) ~~685,734~~HATPase_c (2.19973E-21) ~~843	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.8E-91	314.7	0.1	2.5E-91	314.2	0.1	1.2	1	A0A059VV35_STRA9	Histidine kinase (EC 2.7.13.3)	DC74_380	Streptomyces albulus	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	68570	>tr|A0A059VV35|A0A059VV35_STRA9 Histidine kinase OS=Streptomyces albulus GN=DC74_380 PE=4 SV=1 MAPRVTAEAAGERQGKLKVFLGAAPGVGKTYRMLDEGRRRLRRGTDVVVAYAE CHGRQHTEEMLDGLEVVPRLHRAYRGSTFSELDLDAVLARGPAVALVDELPHTNV PGGRNAKRWQDIDELLAAGIDVVTTVNVQHLESLNDVVEKITGVPQRETVPDEVV RRAHQIELVDMPAEALRRRMAHGNIYQPEKVDAALAHYFRIGNLTALRELALLWVA GRVDETLQKYRSEHGIGTVWETRERVVVALTGGPEGETLIRRAERIADRSSGGDL LAVHVARSDGLAYASPAALAKQRALVESLGGSYHSVVGDHVPTALLDFARAENAT QLVLGTSRRSWFSRLVAPRGIGEDTVELSGDIDVHMVTHERAGRGQRLSIPGRQL PHARRIAGPVAGLVLPFVLTAVLTHIRGPLNLTSEALLFLATVVGVACLGGVVSALL ASLTASLLLNYYFIPPSREFTITEANNALALAVFALVAVTVAALVDRSLRLSRRAASA TAEAETLSSMAGTILRGDQGVSVLLERTRETFGMASAELVPRAEQEPGTEAEEEA EGLVKVPAGPDRLLVLRGRRLPASEHRVLTAFAAHLAAALDHARLMEAAAEVEPV KAADRLRTALLAAVSHDLRTPLASGRAAISSLRSTDVAFTAAERSELLATAEDSLIE LNRLVDNLLDMSRLRAGALSLHLQPTAFADVLPLSLATLAAAPVRIASRGLAEVCD VLADPPLLERVIANLVTNAVRHSGAAESVLITASAMGPRVELRVIDRGPGLRPEDR DRIFVPFQRLGDRDNTSGLGLGLALSRGLAEAMGGTLSPEDTPGGGLTMVLSLRA ATAGDAVEADTP	12~~KdpD (2.15338E-112) ~~222,244~~Usp (2.88691E-29) ~~367,X,613~~HisKA (0.0000000000514381) ~~679,730~~HATPase_c (1.71755E-26) ~~831	kinase	KdpD;Usp;X;HisKA;HATPase_c
	1.8E-91	314.7	0.7	1.1E-90	312.1	0	2.2	1	Q1LSE9_CUPMC	Histidine kinase (EC 2.7.13.3)	kdpDRmet_0041	Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	967	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus metallidurans, Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	266264	>tr|Q1LSE9|Q1LSE9_CUPMC Histidine kinase OS=Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) GN=kdpD PE=4 SV=1 MYAWQSPAWHNHRHQPPLPMTDPDARPDPDALLQRMQAERARAARGKLRVYF GASAGVGKTFAMLGAARALREQGVDVVVGVVETHGRAETEALLDGLERLPLREV PYRDRVLAEFDLDGALARRPALILVDELAHSNAAGSRHPKRWQDIQELQATGIDV WTTVNVQHLDSLNQAVGGITGVRVWETVPDAVFDGADEVVLVDLPADELLRRLR EGKVYLPDQARHAARNFFRKGNLIALRELALRRTADRVDDDVRAYRHAESIDLVW RTREALVACIGAGDDAEQVVRSAQRLAGQLDCDWHVVTIATPQLMPPSNEVRAR MRAAMQLAEELGARTETLAGNDMVKAVAGYVRRHNLTKVLLGRAPADWYARGN WIDKGRALLARALSPLLGVGNRLFGRQMFADALAAGCPEIDVIRVAADSTRADLRP RVQEGLSTEAHDAEAEAELARVRRHNYGWAVVWCMAATFLSTLTRPWFDLVNIA MLFLVAVVGVALRHGRGPAALASVISVAAFDFFFVPPRMSFAVSDVQYLLTFFVLL TVGLVIGQLTAGLREQAQVSVRRETDARTLYELARELSAALTAQQIVEIGGRFLRA AFDADGTFFLVAENGRLMPMAGGEKTPEPRTGKGDAIDKVLAQWVFDHGQPAG TGTHTLPGSTVLYLPLKAPMQTRGVLAVEPRAWRALADPALRRQADVFATLIAIAI ERIHYVDVAQRALVSIESERLRSSLLAAVSHDLRTPLTGLIGMAETLQRAEMPLPAS VAETVEAMRVQAQRMRTMVVNLLDMARLQHHDLALKRGWQSLEELIGAALASMR DVLGRHHVEVMNLVELPLVECDDVLMERVLCNLLENAAKYTPAGTAIRIRGAVVG DEVQLSVEDEGPGVQSGQERYIFEKFTRGERESATSGVGLGLAVCEAIMQAHGG RIWVEAAHPHGSRFTLALPRGNPPAIEPESLDEPIPDHH	43~~KdpD (2.45004E-112) ~~253,276~~Usp (2.39786E-26) ~~375,459~~DUF4118 (3.09444E-23) ~~559,587~~GAF (6.74302E-17) ~~710,727~~HisKA (8.77552E-14) ~~792,845~~HATPase_c (6.61734E-27) ~~946	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.8E-91	314.7	0.1	2.9E-91	314	0	1.3	1	Q5GW24_XANOR	Histidine kinase (EC 2.7.13.3)	kdpD XOO3843	Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85)	886	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas oryzae, Xanthomonas oryzae pv. oryzae, Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85)	291331	>tr|Q5GW24|Q5GW24_XANOR Histidine kinase OS=Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85) GN=kdpD PE=4 SV=1 MNDARTQQADALIGELQREHGGRLTVFLGAAPGVGKTYAMLSRARERLRQGMD VVAGVVETHGRSETAALLEGLPLLPRARVSYQGRMLEELDLDALLARKPRLALIDE LAHRNVPGSRHERRWQDIVELLDAGIDVYTTVNIQHLESLNDIVLRITGVRVSETVP DAVFDRLRDIVLVDLPPRELIERLQQGKVYLPEQATQALQAFFSPSNLTALRELAM QTAADRVDSDLRDTQAARGLPGTAALRRRVVVAIDGRGSSDYLVRVARRLSERR DAPWTVVTVQTRTVTDAAWRLEIDRAFALTRRLGGDTSLLHGTNVADALLDFAAQ NGISTLVLGRTRERPLARMFNRTLTQQLLQRGAHYELVIVSSADARARARQRWRH PRQWLQRYDLVFAAIAAAGAVGVAWLLQRWTDINDLSMVFIVAVVLVASRTRMAA AVVAALLSFVAYNFFFIEPRFTLQISARQGVVTVCMFLIAALVAGRLASRLRSQVLA LRAANAHANVLQALARQLSTAADLGQVLEAGRRALATALDADVWLRLEQRESDA PTSFGALDRSAADWTQRHGQPAGRFTDTLAGAQWWCLPVRHERGTLGVAALRF RQGVQRPGLEQRRLAEAMVEDIGQAALRTRLVADLEGARVSGETERLRSALLSSV SHDLRSPLASMIGSASSLASYGDAMDAHDRHSLLDTIQLEGERLDRYIQNLLDMTR LGHTGLTVNRDWIGVDELIGSATRRLQRYQPDVRLQLDLAADLPAIWVHPALVEQ AIFNVLENAAKFSPPGIAVTVQATLRSGALQIDIGDQGPGIPEDERARIFDMFYSVE RGDRGRNGTGLGLAICQGMIGAHGGSVEALAGAHGHGTTIRITLPLLVPAAPPRP DAD	19~~KdpD (1.39335E-114) ~~229,251~~Usp (1.74718E-26) ~~372,411~~DUF4118 (0.00000977775) ~~495,521~~GAF (0.00160309) ~~630,650~~HisKA (0.000000000206875) ~~716,770~~HATPase_c (3.8803E-23) ~~872	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.1E-91	314.4	0.1	3.1E-91	313.8	0.1	1.3	1	C6WFG8_ACTMD	Histidine kinase (EC 2.7.13.3)	Amir_1955	Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	902	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Actinosynnema, Actinosynnema mirum, Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	446462	>tr|C6WFG8|C6WFG8_ACTMD Histidine kinase OS=Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971) GN=Amir_1955 PE=4 SV=1 MSVLPSPPVVGTGTRSPPADPTAPTAHTDPVVDTKRKRGELRIYLGAAPGVGKTF ALLNEAHRRRERGADVVVGLVEAHDRARTAELLDGLEQIPRRTTHHDGEPRSELD LEAVLRRAPAVVVVDELAHTNPPGAGNPKRWQDVEDLLDAGIDVLTTLNVHHLES LSDVVRRITGVDQRETVPDEVVRRAEQVELVDLTPEALRRRLAHGNVYPAHKVDA ALADYFRPGNLAALRELALLWVADQVDVALQRYRADQRITDTWETRERVVVAITG GPESEPLIRRARRIALSAAAELLVVTVLPVAPRATGPDAPDAPSRFRRLTEDLGAT YHTVVGDDVPTALLEFARGVNATQLVLGASRRSRLARAFDGGVGAAVIARSDSID VHMVPHDESPEPPRRHPDRNPLTPSRQALGWLLSVLLPLVVTGIGTALAEDITFST DLVGFFLATVVVALVGGLGPAVFAALIGAGMLNFFFTQPYYSLTVSAQENLLTLLV MVTVAVLVALVVDRAARLASQAARARTEAALLASYARTVLAGPDPLARLLEQVRE NFAQESATLLERVDHDWTPVASAGPNPCADPDEADVDVPVNPDVHLALRGRPLA AGDRRALEGAAGQALLALRHQRMSAQAEDARRLAETTQLRTALLSAVGHDLRTPL TSIKASVGSLRDVELSLSAEDTAELLEAVELSADRLTGLVDNLLDSSRLATGAVTPV FKAIGYDEAVAAALAGVDERDRVLVEVREDLPPVRADLGLLERVVANVVDNALRH GSRRPAPRASGGPDAAGPGAAGPRVAGPEATTPEVGFPEVAVRASAHGDRVEL RVVDHGPGVPRHTTEAVFAPFQRLGDRDAAPGIGLGLSVAKGFTEAMGGAITAE DTPGGGLTIVVSLPAAGPQTP	37~~KdpD (2.53535E-100) ~~246,268~~Usp (2.20991E-29) ~~391,447~~DUF4118 (0.0000000163056) ~~499,X,645~~HisKA (0.0000000000243346) ~~710,760~~HATPase_c (1.92264E-21) ~~894	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.1E-91	314.4	0	3.2E-91	313.8	0	1.3	1	A0A0F7CQ87_9ACTN	Osmosensitive K channel His kinase sensor	SXIM_45970	Streptomyces xiamenensis	869	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces xiamenensis	408015	>tr|A0A0F7CQ87|A0A0F7CQ87_9ACTN Osmosensitive K channel His kinase sensor OS=Streptomyces xiamenensis GN=SXIM_45970 PE=4 SV=1 MARRGTLRIYLGAAPGVGKTYAMLSEAHRRAERGTDIVVGFVETHDRPRTEALLR GLETVPRRPPPGAGRGEMDTEAVLRRAPAVACVDELAHSNAPGSRHDKRWRDI DTLLDAGIDVISTVNIQHLESLADVVAAITGVRQRETVPDAVVRRADQIELVDMTPE ALRRRMAHGNIYAPDKVDAALSHYFRPGNLTALRELALLWTADRVDAYLQRYRTE QGIRSTWYARERIVVALTGGPEGSTLIRRAARMAAKSSGGEILAVHVSRADRLTAV SPRELASQRTLVEQLGGTFHHVIGDDISSALLDFARGVNANQIVLGSSRRKTWQY AFGPGVGASVARDSGPDLDVHIVTHAEVARGRGLPNARGARLGRSRTVAGWLIG LAGPPLLTVLLAAPPRPLAEFASDVLLFLSVTVLAALVGGFYPGLVSAALATLLLDY FFTEPLREWGVGSGHDVITVVIFFAIALAVASVVDMSAQRTQQAARLRAESETLTV LAGSVLRGEDTLRALLGRARETFGMDCAALLERDHDGGRWRCVGSVSAIADNPR PLLRPQDADVDVPVGEHTMLVLSGRVLPAEDRRVLSAFAAQAATILDRQRLLTEAA RAHKLAEGNRIRTALLAAVSHDLRTPLAAIKASVSSLRSDDVEWSPQDRAGLLESI EDGADRLDQLVGNLLDMSRLHTGTVRPLIRRTGLDEVVLRALAGVPVDVVDLDVP ESLPWVAADPGLLERSVANIVENAVKYRPPDTRVLVRGSALGNQVELRVVDRGP GVPDADKGRIFEPFQRHGDIPRGNGVGLGLAVARGFTEAMGGTLDAEDTPGGG MTMVLTLPTDIPAPAAAGAGAPAERESEQGEQGGAHAPGTRGR	2~~KdpD (4.45641E-115) ~~210,232~~Usp (3.7972E-29) ~~355,382~~DUF4118 (0.000000836932) ~~478,507~~GAF (0.00425801) ~~600,617~~HisKA (0.000000000000103023) ~~683,732~~HATPase_c (5.61304E-24) ~~833	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.2E-91	314.3	2.3	3E-91	313.9	1.6	1.2	1	K7W0T7_9NOST	Osmosensitive potassium channel histidine kinase sensor protein	kdpDANA_C11902	Anabaena sp. 90	373	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena sp. 90	46234	>tr|K7W0T7|K7W0T7_9NOST Osmosensitive potassium channel histidine kinase sensor protein OS=Anabaena sp. 90 GN=kdpD PE=4 SV=1 MFNPSTPSPDSSYIRPARRGKHKIFIGMAPGVGKTYRMLEEAHQLKKDGIDVVIGL LETHGRKDTAVKAIGLEVIPRKVIIHKNINLEEMDTEGIFKRSPQLVLVDELAHTNIP GSAREKRYQDVELILAEGIDVYSTVNIQHLESLNDLVARITGVVVRERIPDLLLDEAD AVVVIDVTPETLEERLREGKIYTPDKIEQSLENFFQRRNLIALRELALREVADTVEEE ANTSISAGQICNVHERVLVCVSTYPNSIQLLRRGARLANYMNAKLYTLFIADPERFL SKEESLHIDTCEKLCLEFAGEFLHIKNHNVSQTIAQIAATYHITQIVIGESQQPRWKR FFKRSFTQRLLELIRNQNIDLHIIATEK	17~~KdpD (1.6718E-128) ~~227,246~~Usp (8.12645E-41) ~~370	non-kinase	KdpD;Usp
	2.3E-91	314.3	0	3.8E-91	313.6	0	1.4	1	W0UXS5_9BURK	Histidine kinase (EC 2.7.13.3)	kdpDGJA_695	Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	910	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Janthinobacterium, Janthinobacterium agaricidamnosum, Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	1349767	>tr|W0UXS5|W0UXS5_9BURK Histidine kinase OS=Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628 GN=kdpD PE=4 SV=1 MLPNDSQRPDPDALLAQVQAQEKKASRGKLRIYFGASAGVGKTCAMLAAAHKMQ DDGQQLLVGIVETHGRRDTAALLEGLPLLPLKQIVYRGKNLAEFDLDEALLRRPPLI LMDELAHSNAPGSRHPKRWQDVEELLDAGIDVLSTVNVQHLESLNDVVGGITGVR VAETLPDTVFDRADEVVLVDLPADELLTRLKLGKVYQPQQAERASQNFFRKGNLIA LRELALRRTADRIQDDVQAYRVEKSINPIWKTGAALLACIGPRPGAEHVIRSTARLA SQLNAEWHALYVETPQLQHLPPAERERILKTLKLAQDLGARTAVVSNSDIAGAIVD YARAGNISKVIVGRGRRNWPWRIAHARRIAQLAPDVDLIEIGQPAAQAGAASQPA ARDGEEGADAGRRPSRHWRYLVAAGASVLTALLVLPMLAYLDLANIAMLFLLTVVL VAVRFGRGPAALASLVGVACFDFVFVPPRYSFAVGDFQYVITFGVMLAVGLIIGHL TAGLRFQARVASHREARARALYEFARELSGVLQTEQIFEITRDFIQRAFQARATLLI PDDDGRLQMTQQAGDIHAQQLALLDLGIAQWSFDHAEAAGIGTDTLPAASVFYLP LIAPMRTRGILALLPDNRRWLLVPEQRQHLDTFAALAAIALERVHYIDVAQGALVQ MESERLRNSLLAALSHDLRTPLTSLVGLSESLVMSKPGLAPEQLTMARSLQEETLR MSALVSNLLDMARIESGQVRLNLQWQALEEVVGSALRASRSQLTCHQVQTRLER DLPLVSYDAVLIERVLCNLLENAAKYTPPGSSITIAADVRGAWLQVSVYDDGPGLP AGREEAIFEKFTRGERESNKPGVGLGLAICRAIVEAHGGKIRAGQSPIHGAAIEFTL PLGTPPAMPELDLELPH	25~~KdpD (2.20101E-110) ~~235,258~~Usp (1.20344E-37) ~~376,409~~DUF4118 (3.97917E-19) ~~509,536~~GAF (3.2791E-16) ~~657,674~~HisKA (0.0000000000389524) ~~739,792~~HATPase_c (1.86482E-28) ~~893	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.3E-91	314.3	0.2	3.7E-91	313.6	0.1	1.3	1	A0A0F5L0B4_9RHIZ	Histidine kinase	VW35_18790	Devosia soli	892	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia soli	361041	>tr|A0A0F5L0B4|A0A0F5L0B4_9RHIZ Histidine kinase OS=Devosia soli GN=VW35_18790 PE=4 SV=1 MEEPRRPDPEALLAETQKAHRGRLKVFLGMAPGVGKTYEMLRQARRRKVEGLDV VVGLVETHGRKETESLLRGLEVLPRAPIDYKGRTLLEFDIDGSLKRRPELLIVDEYA HTNAAGSRHPKRWQDVEEILAAGIDVWTTLNVQHLESLVDVVLKITGVRQRETVP DSALSRADDIEVVDITPAELRERMAAGKVYVPETARLAIDNFFKPENLTALRELALR RAAQTVDDQLNAAMRVKGLEGPWAAGDRILVLVSDDPMASNLVRQGRRLSDTM GDAPWIAAHVARGRRDDGEAGTTSRLTDALKLAEQLGATTVVLTGDDLVKAVLAY AGKNNVTQIVIGKGPDRRIREILGLSLAAELLRAARGVAIHVVTEPGESQPRQRWR MARSLRQGWTQHLIGLVYVVAAAGLAYLLDVRFERADLGMIFLAAILAAAVIHGLG PGLVAGGFAFLLYNFLFLSPRYSFAIGSPTDLLTLFVFLAVALATGLLAGRSRDRAN EAQRRAGDVSSLLVATRAFSRAPTKADAAQALAEQVTAATGARSVVLLPKGDDIA PATGAPELTALNEGAMAAARWAWERGDAAGHGTGTLPQTSWTFRPLDGVRNR TGVIGVEAHSSLPGSDEEKLLTALADGGAIAIERAELALQAVEGETLRRSDRFRSAL LNSVSHDLRTPLSTVLGASSTLIELGDKLDPAVKDDLVVSIREEAERLNHYIGNLLD MTRLEGGGVTLRLQSCDVEEVLRAAAARLSRRLGEHSVAYDFPAALPRVIVDPGL LEQAIVNILENAIAYSPDNTEISIAAYEDRAKVIISIEDEGKGIPTDELERVFDKFRRLE EPTDRGKGVGLGLSITKGFIEAMGGTIVAASPIHGDKGTRMLIGLNKSPEDVWKEK	19~~KdpD (3.10383E-122) ~~229,251~~Usp (3.92144E-32) ~~375,438~~DUF4118 (0.00000000202972) ~~498,527~~GAF (0.000164765) ~~641,658~~HisKA (0.0000000000454198) ~~724,777~~HATPase_c (5.26586E-24) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.4E-91	314.2	0.1	3.8E-91	313.6	0	1.3	1	Q92XJ2_RHIME	Histidine kinase (EC 2.7.13.3)	SMa2327	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	896	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Rhizobium meliloti (Ensifer meliloti) (Sinorhizobium meliloti), Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	266834	>tr|Q92XJ2|Q92XJ2_RHIME Histidine kinase OS=Rhizobium meliloti (strain 1021) GN=SMa2327 PE=4 SV=1 MPHNDRDLKSRPDPDALLALAEQGRRGKLTVFLGAAPGVGKTFAMLTRARRLKE EGGDIVIGLVETHGRGETAALLEGLEVLPRRQVLHNGRTLHEFDLDAALARRPRVI LVDELAHTNFGESRHPKRYQDIEELVDAGIDVWTALNIQHLESLSDVVAHIAGVPV RERVPDTVLNRADDVLLVDLPPAELIERLKEGKVYLPDNAKRAADRFFRLGNLTAL RELALRRTADRVDDQMVDYLRQNAIEGPWGAAERLLVCIGPDPLSEKVVRTASRL ASSLNADWMVVSVERAEAESSGAMRQLDETFRLAEQLGAETRRIIGNDFVEEILKL ARREHATQIVIGTRRHYFPLRLFRRSLPDALAARAAGIAIHLVTDGSAPAVKPAARR RSTLPDGWGRGVAIATGTAAAATALGLLIEQFVVLQNISLLFLLAVLVSATYAGYVA AIAAALISILAYNFCFIEPVGTFTVAEPHEVFALFVFLAAAMLAGGLASRVREQAKTA RRRAAATQALYDFSRKLSGTANAEDVLWAAVTQIHATLRRNAALLPEDGDVRLM AAWPPDTELGLTDTMAGRWAFEKKEAAGNGTGTLPNSPFQFRPLMSPHGVVGV FGFLQEDKPLEINEERALAAILDQTAIAVDRARLSRESLDQAAQLEGEKFLAALLSSI SHDLRTPLATITGAVTSLRQLGERMSEESRDDLLKSIEEESGRLTRFVANLLDMTRI EAGTVNAKRDWVDVADVVHSAVERARKYFPGRVFETSIAPDLPLIRGDSVLLGQVI FNLLDNANRFGGDEPVSIYGRREEDEIVLSVTDLGKGIAPADLDRVFDKFFRKGKP DGRSLGTGLGLSISKGFVEAMDGRIKAESPAMKRRGTRISMRFPVAETGITEKER G	24~~KdpD (8.07348E-127) ~~234,256~~Usp (5.78793E-34) ~~377,X,527~~GAF (0.000000387749) ~~644,661~~HisKA (0.000000000269098) ~~727,780~~HATPase_c (1.03139E-22) ~~883	kinase	KdpD;Usp;X;GAF;HisKA;HATPase_c
	2.5E-91	314.2	0.8	2.5E-91	314.2	0.5	1.6	1	G7M3P4_9CLOT	Histidine kinase (EC 2.7.13.3)	CDLVIII_3973	Clostridium sp. DL-VIII	905	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. DL-VIII	641107	>tr|G7M3P4|G7M3P4_9CLOT Histidine kinase OS=Clostridium sp. DL-VIII GN=CDLVIII_3973 PE=4 SV=1 MDINERPDPQYLLNQIRKEENESSRGKLKIFFGYAAGVGKSYAMLVEAHDVKRLG KDVVIGYIEPHARAETMALVNGIENIGVKVINYRGITLKEFDLDKALVRKPEIILVDEL AHTNAATERHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDIVESITHIAVRETIPDK VFDDADKVELIDIEPDELLNRFSEGKVYSREQTRKAFNNFFTKNNLFALREIALRRT ADRVNYEVESVRLSKSQITVMPTSDVVLACISPSPSSARVIRTATRMAEAHHSKWI ALYVEGTKSKNLGKEDRERLNSHFNLAEQLGGEVVTAYGDNAVEQIIQYAKFRNV TKIIIGKNHKKPNNLFHFYAKDIVDKLMESNSYIDVYVIPNSTFDKKREKTIKKNKYS SKISKKETLIAVVIMLITTIVALCIDYLGFSAANVIMIFILGVIIVNIKTRGYILGFISSIVSI LLFNYLFTEPRYSLEVYDKSYIATFPIMLIVTFTIGTLTSKIQREALNSSKRENITQILY RVSRKLLSATGTADVVGIGIKYLSRLLERTVICYLGQENKLSTPFIYTATKGEKDRTL LSKDEEAVAYWTFLNDKECGAGTNTFHGAKGYYMPLKSHGKVLGVLGVSCINGP LKPEQKFIFETVASQIYIALDREILAEIQKKSNLEIESERLRSNLLRSISHDLRSPLAGI KGSVSTIIETGNLISEKTRGELLQSVYDDTEWLIRLVENLLSMTRFDGGDMKVKKDD TELVEEVVYEAVQRISKRSTAHEIKVTVPEDVIMAPMDGSLIEQVLINLIDNAIKFTPK NSLIEVKVYENEKDIIFEVIDNGTGIAEDILPHIFDRFFTNGDKISDSRRGVGLGLAIC KSIVEGHGGTITADNRESQEGAIFKFNIPKEGNSDGQ	23~~KdpD (3.2864E-123) ~~233,256~~Usp (1.0762E-40) ~~380,407~~DUF4118 (8.47856E-15) ~~507,534~~GAF (0.00000374643) ~~656,673~~HisKA (0.000000000100332) ~~739,792~~HATPase_c (4.15009E-27) ~~896	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.7E-91	314	1.3	4.4E-91	313.4	0.9	1.3	1	A0A0F0KN13_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpD RL72_02373	Microbacterium azadirachtae	923	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium azadirachtae	582680	>tr|A0A0F0KN13|A0A0F0KN13_9MICO Sensor protein KdpD OS=Microbacterium azadirachtae GN=kdpD PE=4 SV=1 MSVSEGVSAMAERRREGGSARGRLRVLLGAAPGVGKTYEMLGEGRRLDELGRD VVIGVVETHGRAATLAQTQGIEQVPRRIVSHRGVQLDELDLDAVLARRPELALIDE MAHTNAPGSRNAKRWQDVQELLDAGIDVITTVNVQHIESLNAVVEKITGVVQQET VPDEVIRDADEVEVVDLAPQTLRDRLSAGQVYPAERIDAALSNYFRLGNLTALREL ALLWLADEVDSALRSYRSQHGIDSAWQTRERVVVALTGGPEGETLLRRGARIAAR SAGGELLAVHVTTQDGLRGDRPGALTQQRGLVESLGGSYHQLVGDDVAGTLVEF AQSVDASQLVIGVSRRSRLSAALTGPGIGAEIIRRSGDIDVHIVTHSAAGRRGPLPTI RGGALGWRRQLIGFAVALIGGPLLSWLLFSLKAPGSITSDVLSYQLLVVVVALIGGL RPALFAAVLSGFTLDFLFVEPLFTVTIADPLHALALVLYVVIAVLVSIVVDQAARRAR AAQRASGEAELLAAVAGNVLRGDSAPTALVARAREAFGLSGIRLLSPDGDVLAVD GEPLGGNVPGGDPEHAAHDAHGPEARTTTATAGASATADGAQPPRPPRVETVP VGTAADGRPRAILELHGGDLDAAGRRLLDAIVAQLAAAIEHTDLRETAKEAAVLAET DQVRSALLSALSHDLRRPLAAAVAAVGGLRGAHRLSAEDRAELVETADESLATLS RLVTDLLDVSRVQAGVLAVSLGRVDAGGGVVSALDELSLGPDEVELALDPALPPL RADPVLLQRVLVNLLTNAVRHSPAGDRVIVSTSRLGERAEIRVADRGEGIPEDQRE SAFLPFQRHGDTDNTTGLGLGLALSRGFAEGMGGTLTAEDTPGGGLTMVVSLPL DDAGLDVSTRPDPGAEYDTLRTSHREPRSDDEGGTR	19~~KdpD (4.96191E-115) ~~229,251~~Usp (5.3398E-30) ~~374,397~~DUF4118 (0.00000000000611587) ~~495,X,668~~HisKA (0.000266113) ~~733,784~~HATPase_c (5.54073E-28) ~~885	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.9E-91	314	0.4	5.3E-91	313.1	0	1.6	1	E3HLX8_ACHXA	Histidine kinase (EC 2.7.13.3)	kdpD AXYL_01191	Achromobacter xylosoxidans (strain A8)	928	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Achromobacter, Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans), Achromobacter xylosoxidans (strain A8)	762376	>tr|E3HLX8|E3HLX8_ACHXA Histidine kinase OS=Achromobacter xylosoxidans (strain A8) GN=kdpD PE=4 SV=1 MADIAGERPDPDALLKTLDDAARQAVRGKLRVYFGSSAGVGKTYAMLVAARAQA AQGVEVLAGIVETHGRRETATLLEGLPVLPLQDVPYRSHVLKEFDLDGALARHPDL VLVDELAHSNAPGSRHAKRWQDIQELLAAGIDVWTTLNVQHLDSLNEAVGSITGV RVWETVPDEVFDAADEVILVDLSADELLRRLKEGKVYLPEQARHATRNFFRKGNLI ALRELALRRTADHVDDDVQAYRRDRAIEPVWRTREAVVACIGPDVDAEYVIRSAH RLSQQLECDLHVVTIDTPRAAPPPQAEQERIQRSLALADALGARSETLAGGDMVD AVVRYVRRHNITKAIIGRTRASGLQRLRLSLSAVLTAAISPGWLWRRHSFADMLAA GCPEIDIIRLGAPPLPAAAAPGRDPLTLGQRARLGADERNPRPLAGYAWALCYCA AATALSALAFPALHQTNIVMLFLLAVVAVALRHGRGPAALASVISVGLFDFFFVQPL ASFAVSDVQYLLTFGVLLSVGLLIGQLTAGLRLQAQASVKREADARSLYEFARELS SALLPEQIVTLAGAFVHATFGSRCALYILGMDDRLKLASPAADDMPPLESALAQWV YDHGQPAGAGTATLSNSELLYLPLKAPMRTRGVLALAAPRRSLFSNPDSRRQIEA YATLIAIALERLHYVEVAQQALVSMESEKLRNSLLAAVSHDLRTPLTSLVGMTDTLM RQQAALPPGIHDTIRAMRDQAQRMHALVVNLLDMARLQNRDTPLRLEWQSIEELV GASLAAMREPLAAHRVAVDSLSQLPLVECDGVLIERVLCNLLENAAKYTPAGSTLR VHADVHEGELRVAVSDNGPGVPPGAERRIFEKFTRGDRESATPGVGLGLAVCEAI IAAHHGKIWVEHAPGQESGAQFVFTLPLGTPPPIQSETP	27~~KdpD (2.14842E-119) ~~235,258~~Usp (3.29748E-30) ~~394,457~~DUF4118 (7.126E-17) ~~531,560~~GAF (4.93711E-14) ~~677,694~~HisKA (0.0000000000151152) ~~759,812~~HATPase_c (6.63165E-29) ~~915	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.9E-91	313.9	0.2	4.7E-91	313.3	0.1	1.3	1	D3RSE1_ALLVD	Histidine kinase (EC 2.7.13.3)	Alvin_1161	Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	891	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Allochromatium, Allochromatium vinosum (Chromatium vinosum), Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	572477	>tr|D3RSE1|D3RSE1_ALLVD Histidine kinase OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) GN=Alvin_1161 PE=4 SV=1 MNATADDRPDPQALLSAIERERHGALKIFLGASPGVGKTYKMLEAAREARREGAD IIIGIIESHGRQETEALCEGLESIPLMQMAYRGAQFRELNLDAILKRAPAVVLIDELAH RNIPGTRHLRRYQDIEELLEHGIDVWTTVNIQHLESLNDVVARITGVRMRETVPDT VLSEARDVVLVDLTPRELIERLKQGKVYIPEQARAALDGFFSPTNLAALRELALQTV AERIDRDVREVMRSQGVTGPWPVRARIVVAIDGIGNGEELVRLGRRLAERRRAP WSAVFVDRGDTGPEQQAGVERTFDLAARLGGETLTLRGHDPVEELLAFAREQNA TTLVVGRSRHRPLAGFFSQSLSQRLLRCGEDFEITFVSSRVARVRRRRHWFRRLE PMRDYVLTLAVVAAATGIAAVIEPLVPLPNLSLVFLTAVLLVAVRTAIRPALIAAVLSA AAYNFFFTEPRFTLAMHRTHELATVGFFLIMGLIGGQLAGRLRHQVLALRGTNEQT QRLLSLSRRLATAVDLPTIHRESTTAIAEHLHVPVVLLAPGDSGRLAQAAASQDEV VLNDKAWSAAQWAYDHRQPSGFQTQTLSAIDWRFLPLAIEQECFGVLGVYRPNP GFQSEQLAAIDALITQVTMAMARTRLTTTLEQAKVAEETERLRSALLSSVSHDLRT PLASMIGAASSLRSLDEALSTDDRRELLDSVISEGERLNRYIQNLLDMTRLGHGTLK LERDWIGIDDILNSALRRTRELLHHCRLIRHIEPGLPLLYVHPALIEQALVNVIENAAK FSPEGSEVRVAAMRDDGELLITVADEGPGIPADHREKVFNMFFTGGEGDRGKHG SGLGLAICSGMIGAHGGRIEALPGPGGRGTTIATHLPLIEPPDDDNEERA	21~~KdpD (1.93826E-113) ~~231,253~~Usp (8.8133E-33) ~~370,395~~DUF4118 (4.13849E-17) ~~494,531~~GAF (0.0000638361) ~~638,655~~HisKA (7.64142E-14) ~~721,774~~HATPase_c (4.15674E-23) ~~873	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.1E-91	313.9	0.7	5.8E-91	313	0.5	1.5	1	E8N7S7_MICTS	Histidine kinase (EC 2.7.13.3)	MTES_1369	Microbacterium testaceum (strain StLB037)	852	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium testaceum (Aureobacterium testaceum) (Brevibacterium testaceum), Microbacterium testaceum (strain StLB037)	979556	>tr|E8N7S7|E8N7S7_MICTS Histidine kinase OS=Microbacterium testaceum (strain StLB037) GN=MTES_1369 PE=4 SV=1 MLAGIHRRRVVRRGTLRVLLGMAPGVGKTYEMLEEGRRLAAEGRDVVIAVVETH GRAATAAQAEGLEVVPRRPVAHRGVALDEMDLAAVIARHPDLALVDELAHTNAPG SANDKRWTDVEELLDAGIDVITTVNVQHIASLNDVVEKITGVTQRETVPDAVVRAA DQIEVVDLAPQSLRDRLSAGFVYPAERIDAALSNYFRLGNLTALRELALLWLADEV DSALQRYRTEHGIEGSWQARERVVVALTGGSEGETLLRRGARIAARSAGGELLA VHVSTQDGLRTSNPAALETQRALVEQLGGTYHQVVGDDVATALVDFARSVNASQ LVIGVSRRGRLGAALTGPGIGNTVIRESGDIDVHIVNHARAGGRFALPRLTGPALS MKRRILGFVTALVGGPIISLLLLATGSDDSITTDVLSYQLLVVIVALIGGIWPAVFAAV LSGLTLDFLFIAPLHTVTISDPVHAIALVLYVVIAMLVSVVVDQAARRARAARRASAE AELLATVAGSVLRGEVAVPALVSRAREAFGLAGVRLIAADGRVLATDGEPVRDDR RTTVPVGDGRATLELHGGDLDAGARRLLDVVVAQLAAALERADLAETAAEAGALA ETDQVRSALLSAVSHDLRRPLASAVAALGGLRAAGDHLSEDDRRELIETADESLAT LSVLVTDLLDVSRVQAGVLAVSLAPVDAADVVIAALDELDLGPDEVELALDPDLPSL RADAVLLQRVLVNVLANAQRYTPEGVRVRIATSRLGGIAEIRVIDHGPGIAVERRDD MFSPFQRLGDTDNTAGLGLGLALSRGFAEGMGGTLVPEDTPGGGLTMVVTLPVA EGGAEAVASGIREDAP	12~~KdpD (4.43074E-114) ~~221,243~~Usp (1.57747E-30) ~~366,402~~DUF4118 (0.00000000504511) ~~487,X,615~~HisKA (0.00000000303265) ~~681,732~~HATPase_c (1.05131E-23) ~~833	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.2E-91	313.8	0.3	5.9E-91	312.9	0.2	1.5	1	D4M4P0_9FIRM	Histidine kinase (EC 2.7.13.3)	RTO_16100	Ruminococcus torques L2-14	899	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, [Ruminococcus] torques, Ruminococcus torques L2-14	657313	>tr|D4M4P0|D4M4P0_9FIRM Histidine kinase OS=Ruminococcus torques L2-14 GN=RTO_16100 PE=4 SV=1 MSESRHNPDQLLKEIQADEEKRNKGHLKIFFGYAAGVGKTYAMLEAAHMEKQQGI DVVAGYVEPHAHPKTAALLNGLEVLPTREVFYNGMILDEFDIGMALKRKPQLILVD ELAHTNAEGCRHAKRYQDIKELLNAGIDVYTTVNVQHIESLCDTVASITEIVVRERIP DSIFDNADQVELIDIEPQDLINRLNTGNVYRQTQEKQAVENFFTIENLTALREISLRR CADRVNILTENTRIKNHGDYHTGEHILVCLSSSPSNAKIIRTAAKMASAFKGEFTAL FVETPDFSVMSEENVKRLRSNICLAEQLGAKIETVYGEDVPFQIAEFTRLSGVSKIV IGRSSATKRHLLSKPTLTEKLIDYAPNLDVHIIPDTVSNAAVYQLREGRKKNHIVFSV TDTLKSTAILILSSLVGMIFQKFGFDEANIITVFVLGVLVTAVITKHQIYSLISSIVSVLV FNFLFTEPQFTLQAYDQGYPVTFIIMLLAAFLTGSLAIRIKNQAKQAAQSAYRTKVL FDTNQLLQQAKDKNEIVSATSNQLIKLLRKDIVFYLADGEVLDTPHIFSVTEENLESC ISENEKAVAGWVLKNNKRAGATTGTLSNAKCLYLAVRSSSMVYGVIGIVMGEIPLD PFENSILLSILGECALALENEKNAREKQEAAILAKNEQLRANLLRAISHDLRTPLTSIS GNASNLLSNGDFFDNDTKKQLYMDIYDDSMWLINLVENLLAVTRIEEGRLNLRITE DLMDDVITEALHHINRKSEEHHISVESKEEFLLAKMDAKLIVQVIINIVDNAIKYTPKN SHIVIRTEKRGKQAIVSISDDGNGIADEIKPRIFDMFYSGANQIADSRRSLGLGLSLC KSIINAHGGELTVSDNLPHGTVFTFTLPAGEVKVYE	23~~KdpD (1.40208E-118) ~~232,252~~Usp (4.78401E-37) ~~375,403~~DUF4118 (0.00000000000678613) ~~503,X,668~~HisKA (0.000000000327017) ~~734,787~~HATPase_c (6.92882E-28) ~~890	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.5E-91	313.7	3.3	4.7E-91	313.3	2.3	1.2	1	K9WPQ8_9CYAN	Osmosensitive K+ channel His kinase sensor	Mic7113_5929	Microcoleus sp. PCC 7113	384	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	1173027	>tr|K9WPQ8|K9WPQ8_9CYAN Osmosensitive K+ channel His kinase sensor OS=Microcoleus sp. PCC 7113 GN=Mic7113_5929 PE=4 SV=1 MIHQNEIANQLNSTEPNDTLSRRRRGKHKMFIGMAPGVGKTYRMLEEAHRLKEEG IDVVIGLLETHGREETADKAVGLEMMPKKLIVHGGVTLGEMDTDAILERQPQLVLV DELAHTNIPGSLREKRYQDVEVILETGIDVYSTVNIQHLESLNDLVAKITGVVVRERI PDRILDEATEVVVVDVTPETLQERLIEGKIYAPEKIEQSLQNFFQKRHLVALRELALR EVADNIEESAEKNSTPAAQFCNVHERVLVCISTYPNSAQLLRRGARLATVMRSRLY ALFVDHPERFLTRDESLYIETCKNFCLEFGGEFICVKSANVADAIAATARQYHITQVI LGQSHKSRWEILWRGSLVQKLVRYLKDVDLHIIATEKKEFKRF	24~~KdpD (2.98303E-127) ~~233,253~~Usp (2.93248E-42) ~~375	non-kinase	KdpD;Usp
	3.5E-91	313.7	0.3	6E-91	312.9	0.2	1.4	1	C4IDW5_CLOBU	Histidine kinase (EC 2.7.13.3)	CLP_3545	Clostridium butyricum E4 str. BoNT E BL5262	896	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	632245	>tr|C4IDW5|C4IDW5_CLOBU Histidine kinase OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_3545 PE=4 SV=1 MVYERPNPDDVLKAISKEHKKNGKLKIFFGYAAGVGKTFAMLEAAHKSKESGIDVV AGYIEPHTRVETLNLLNGLEMLPNLKVDYKGISLNEFNIDGALERKPDLILVDELAHS NAVGCRHVKRYQDIKELLDNGIDVYTTVNVQHIESLNDIVASITGIIVKERIPDSVFD NADQIELVDIEPEDLIQRLNEGKIYRTDQAKRALLNFFTKEKLVALREIALRRTADAV NKKIDIERERTKNSYYTEEHLLICLSSSPSNAKVIRTAARMADAFHGLFTALFVETTD TKEFQDENRVRLERNLKLAEQLGARIATVYGDDIAWQISEYAKLSGVSKIVLGRST TKKGLFKTKKTLVDKLTEIAPNIDIYIIPDNSKQKQTKIKLKANLYKFDMVDIAKTFGIL FLSTILALIFFEFGYSEANIITIYIFGVLLTSITTSGKRCGILMSILAVLTFNFLFTDPRFT FQAYDKSYPVTFAVMFISSIVTSKLATKVKLEAQQSTRKAYRTEVLLETSQKLQIAK SKEDIFNKTAYQTKKLLDKTIILYKSEKGVLAEPLVFKHENDKDVLEYISEEEKAVAQ WTLKNKKHAGATTNTLPGAKCLYLSIRNHEKAFGVIGIPLEKDEFLEAFEKNLLIAVL GESALALEKEEINQSKNKIYIKAEQEKLRSNLLRSISHDLRTPLTSISGNAGILINNSEI LSEEKKKSLYLDIYDDSMWLINLVENLLSITRIENGTMKINTEPELVEEVIEEAICHIN RKVSEHKINTVIEDDLLMAKMDSGLIIQVIINIINNAIKYTPKDSIITITSKRKNNMAVIEI SDNGKGINEESKEKLFDMFFTDNNKFGDGRRGLGLGLALCKSIIDAHEGCIYVRDN KPNGAIFGFTLHIEEVKINE	20~~KdpD (1.49902E-120) ~~230,250~~Usp (3.93196E-37) ~~373,397~~DUF4118 (4.78142E-16) ~~496,524~~GAF (0.000292447) ~~648,665~~HisKA (0.0000000138116) ~~731,797~~HATPase_c (0.00000000789602) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.6E-91	313.7	0.1	6.5E-91	312.8	0	1.4	1	A0A0A8DVX1_9XANT	Histidine kinase (EC 2.7.13.3)	SB85_09135	Xanthomonas sacchari	892	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas sacchari	56458	>tr|A0A0A8DVX1|A0A0A8DVX1_9XANT Histidine kinase OS=Xanthomonas sacchari GN=SB85_09135 PE=4 SV=1 MPDPRTQQADALIGELQRERGGRLTVFLGAAPGVGKTYAMLSRARQLQQQGSNL VVGVVETHGRAETAALLEGLTVQPRRRLEYRGRTLDEMDLDALLALRPPLVLVDE LAHRNAPGSRHERRWQDVQELLDAGIDVYSTVNIQHLESLNDVVHRITGVRVSET VPDAIFDRLRDIVLVDLPPRELIERLQQGKVYLPEQAGQALQAFFSPSNLAALRELA MQTAADRVDNDLRDVQAAQGRTSVALRRTVMVAIDGRGQSDYLVRVARRLAERR GAPWTVVTVQTQAQPDADWQLEIDRAFALARRLGGEAALLHGANVADALLDHAA RSGVSTLVLGRTRERPLARMINRTLTQQLLQRGAHYELVIISSPEARARARRRWR SPAHWLSRDDLLFATVASALAVVVAWIAESWVGIDDLSMVFIVAVVMVASKTRMT AAVLAALLSFFSYNFFFIEPRFTFQIGARQGVVTVLLFLVAALVAGRLASRLRMQVL ALRAVNAQTTALQRLGRELTSAADLGQVLEAGRRALAGTLDAEAWLRLQPLERAH DGADDYAPTMAAVDRSAADWAQRHGQATGRFTDTLAGASWWFLPVRHERGTI GVVGLRFGAGVQRPGLEQQRLAEAMVEDIGQAALRTRLVADLESARVSGETERL RSALLSSVSHDLRSPLAAMIGAASSLSSYGKAMDAEDRRSLLDTIQMEGERLDRYI QNLLDMTRLGHTGLTLNRDWIGVDELIGSAARRLQRYQPQVRLDIALAAELPTLW VHPALVEQAIFNVLENAAKFSPADAAIRVAAGMVEGRLRIDISDRGPGIPEDERARI FDMFYSVERGDRGRHGTGLGLTICQGMIGAHGGSVEALPGPDGRGTTIRITLPLIE PAAPPSRPDAD	19~~KdpD (8.97406E-121) ~~229,251~~Usp (1.44693E-30) ~~371,423~~DUF4118 (0.00000000360435) ~~492,520~~GAF (0.000113705) ~~635,655~~HisKA (0.0000000000393616) ~~721,775~~HATPase_c (2.05774E-23) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.9E-91	313.6	0.1	8.7E-91	312.4	0	1.6	1	D5X2Y5_THIK1	Histidine kinase (EC 2.7.13.3)	Tint_0068	Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	914	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Thiomonas, Thiomonas intermedia (Thiobacillus intermedius), Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	75379	>tr|D5X2Y5|D5X2Y5_THIK1 Histidine kinase OS=Thiomonas intermedia (strain K12) GN=Tint_0068 PE=4 SV=1 MTDPDIRPSPDALLAQVQQDAEQAQRGRLKLFFGASPGVGKTYAMLMAARRLRD EGVDVCVGLVETHGRAETARLLEGLEQIPLREVRHGAHLLREFDPAAALARRPAV LLVDELAHSNAPGSRHPKRWQDVEELLDAGIDLYTTLNVQHLESVSDIVGGITGVQ VRETLPDRIFERADEVVLVDLPPDDLLQRLKDGKVYLPEQAAHAVRNFFRKGNLLA LRQLALRLTAEQVEGEMRDYRSRRVGGAVWDAAEALLVCAGPRDDIGLVRAAAR LADALHARWHVITVETPALQGASEAQRDHALALLQRARDLGAQTAMLAGPHAAE AALAYARTHNLNRVVLGRASRWPWWRRVLGRSTTAVLARQAPDLDLILITRDARS PLTALAGLHPALPSADALMRRYLAALLISGAITLLASPLRSYFDLSNTVMLFMLGVV AVALRFGRGPAALAAVVNVLAFDFFYVPPRFSFAVSDVQYVFTFSVMLGVGLLIGH LTSHLHFQARVAGQRERRTHDLYELSRELSGALTVDQVAEIGTRVVQASFRCRAT LLVLGLDERLQPSADVAADALLPFDAELARWCLQRGAPAGQGTDTLPGAPLFYLP LKAPMRVRGVLVVDPGNTRLSTIPELRRLLETCATQIAIALERIHFVSVAQDTLLAM QAERMRNSLLSALSHDLRTPLTALVGTAEVLSTRLAAHPPGDAATLHGQALSLLQ QSRRLARMVDDLLDMARLQSGQVTLRQDWQSVEELVGSALRAVDAAALAQHPL QIDLPADFPLVRADAVLLERVLVNLLDNALKFTPPGTPLGVRARVRGAEAEITVWD RGPGLPAGRERAVFETFTRGDPESPIPGVGLGLAICRAIVEAHGGRVTAANAPEG GAAFNVRLPLHEMPPLDAAAELGTEPAGPTP	24~~KdpD (1.65042E-103) ~~234,284~~Usp (1.49644E-14) ~~379,405~~DUF4118 (2.9765E-19) ~~502,531~~GAF (2.25699E-14) ~~650,667~~HisKA (0.000000000163765) ~~736,790~~HATPase_c (5.11699E-28) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.6E-91	313.3	0.1	7.6E-91	312.6	0.1	1.4	1	S6AQD9_PSERE	Histidine kinase (EC 2.7.13.3)	kdpDPCA10_22360	Pseudomonas resinovorans NBRC 106553	882	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas resinovorans, Pseudomonas resinovorans NBRC 106553	1245471	>tr|S6AQD9|S6AQD9_PSERE Histidine kinase OS=Pseudomonas resinovorans NBRC 106553 GN=kdpD PE=4 SV=1 MSDTRRADALLADMPQGGRGRLKVFLGAAPGVGKTYAMLQAAQAQLRQGVDLR AGVVETHGRAETEAMLAGLPQQPLRRFDYRGMALTEMDLDGILAQPPKLVLVDEL AHTNAPGSRHAKRWQDVEELLDAGVDVYTTVNVQHLEALNDQVHDITGVQVRET LPDWVLQEADEILLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELA MQTAAARVDADLNRRYRQRGLEAPAVRGRLLVGIDGDHQAERLVRHASRVAERR HLPWSVVYVDTGGARSEEVRSRLQGAQQLAERLGGEVVTLRGESVAKGLVQHA AERRASLLLVGRSRQRLRRRLLGRGLAERLLRLGEGLEVSVLDTEVDRRPPSPRA THHTRLLDYGLAVVAAITASLVAWAVAHTLELPNISLVFLAAVLLVAVRSSLGPALL CAGLSFIAYDFLFIPPTFSLTIARQEDVLTLLFFLLMAGLTGNLASRQRRQLDALRDT QSETTALLDLSRKLTAATDRQAVLNVAVQQFETWRDVEVCLLSRGRDGVWKVEA GAQRLLADQERAAAEWSWQHDQPAGLGTDTLPGGRWWWLPLSGEEGPLVLLG VSPRDEAPLPVGRRRLIAALGQPLAQALARAQLAEELEAARLHGETEQLRSALLAS VSHDLRTPLTAMRGSIDSLLSLGEAIPMDDRRELLEGTRDEAERLDRYIQNLLDMT RLGHGGLKLARDWVAPVDIVASALQRLRPVLAPLQVETGVPEQLPLLYVHAALIEQ ALVNVLENAARFSPSGGRLRVAVEADEAELRFSVADQGPGIPPDERERIFDMFYT AARGDRGGQGTGLGLAICQGMVGAHGGRVTVGEGLDHRGATLTLHLPLHPQPQ LEEE	17~~KdpD (6.15347E-123) ~~227,248~~Usp (4.92714E-21) ~~365,390~~DUF4118 (3.88034E-17) ~~489,X,649~~HisKA (0.000000000000277641) ~~715,768~~HATPase_c (1.38497E-26) ~~871	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.6E-91	313.3	0.2	7.2E-91	312.7	0.1	1.3	1	A0A097EJN6_9SPHN	Histidine kinase (EC 2.7.13.3)	MC45_17045	Sphingomonas taxi	886	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas taxi	1549858	>tr|A0A097EJN6|A0A097EJN6_9SPHN Histidine kinase OS=Sphingomonas taxi GN=MC45_17045 PE=4 SV=1 MSDAAARPDPDALLRHAAQEGRGRLKIFLGAAPGVGKTYEMLSEGAARAREGVD VVIGVVETHGRSETEALTRGYTIVPRRIVPHEGHGLAEMDIDAILARAPRLVLVDEL AHSNAPGSRHAKRYQDVEELLAAGIDVYSTVNIQHVESLNDVVAGFTRVRVRETV PDRILELAEIEVVDIPPDELIERLKAGKVYLPQEATRALAHFFSKTNLSALRELALRR AAQAVDAQMLDHVRALGVGGTWAGGERVVVAVSEAAGVESLVRAAKRLADALH APWTAVFVETPRTQAFAAVEHRQVAKVMTLATQLGGAAAAVPAQTVLAGLKAYV GEARATQLIVGKSTRSRWFELRHGSIVDRLVRETPDIAIHVLPMPAAVRGRRAAPV DRWGSRSGYVWTGAMVAAVTGVASALFHILDLGNVALLYLLPVMMAASLFGLWT GLFAGLASSIAYNFFFLPPTGTLTISNPENVVSVLVLLGIAIATSHLTARVRAQADIAA ASARTNAALAGFLRQLTRLNDPVAVAQAICDEVGQLFGLHTVMLVAEGAGLAVQA ANGSDYRLETMEMAAAQWAYDGGAPAGRGSATLAASQWFFQPLVTGERTLGVL GLANEAGGDPLRPDQIPLFLNLIEQATLAFERLRLEIETRDLGAMRERERLRTALLS SVSHDLRTPLTAVIAAAAQLHHGATPDLIATIEGEAARLHRFVANLLDMARVEAGAL TLRMEAVDLADAVAGAAHDARRALDGHAVQLDVPPDLPLVRADQQLLHHCLLNLL DNAGRYADPGTPIRVEARHRYGVILLSVEDEGPGLPPGREAEVFDTFRRFAGSDR AIGGTGLGLAIVKAFAAAMGIGVEAANRQDRPGARFGLSFPAALIVRDMVEEGD	20~~KdpD (9.34891E-114) ~~229,251~~Usp (4.51817E-33) ~~374,396~~DUF4118 (5.25962E-17) ~~493,521~~GAF (0.00000184882) ~~640,657~~HisKA (0.00000001075) ~~716,778~~HATPase_c (9.87198E-18) ~~872	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5E-91	313.2	1.6	7.4E-91	312.6	1.1	1.3	1	KDPD_SYNY3	Putative sensor protein KdpD (EC 2.7.3.-)	kdpD slr1731	Synechocystis sp. (strain PCC 6803 / Kazusa)	370	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechocystis, Synechocystis sp. PCC 6803, Synechocystis sp. (strain PCC 6803 / Kazusa)	1111708	>sp|P73870|KDPD_SYNY3 Putative sensor protein KdpD OS=Synechocystis sp. (strain PCC 6803 / Kazusa) GN=kdpD PE=3 SV=1 MIHAGQSSSLTPAASPPHRRGKHKIFIGMAPGVGKTYRMLEEGQQLKQEGFDVVI GLLETHGREETAQKAIGLEQVPLRTMIWQGRSLLEMDTGAILARSPQLALVDELAH TNIPGAEREKRYQDVELILAAGIDVYSTINIQHLESLNDLVYKISGVVVRERVPDRLL DEADEVVVVDVTPETLQERLQEGKIYAQDKINQALQNFFKRQNLVALRELALREVA NNIEENSRHDQQTNHCAVHERILVCISTYPNSIQLLRRGGRIASQMNGRLFVLFVA PTNQFLSKVEALHVETCQHLTQEFEGEFIRQESDNVVGAIAQVATTYRITQIVLGES RRSRWHLLIKGSIIQRLMRCLPTVDLHIIANG	18~~KdpD (3.52355E-120) ~~228,246~~Usp (1.82614E-44) ~~368	non-kinase	KdpD;Usp

	5.4E-91	313.1	1.8	9.4E-91	312.3	1.2	1.4	1	B1WP54_CYAA5	Potassium-transporting ATPase D chain	kdpDcce_3885	Cyanothece sp. (strain ATCC 51142)	370	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain ATCC 51142)	43989	>tr|B1WP54|B1WP54_CYAA5 Potassium-transporting ATPase D chain OS=Cyanothece sp. (strain ATCC 51142) GN=kdpD PE=4 SV=1 MLSQNNITPSLLSVSHRGKHRIYIGMAPGVGKTYRMLQDAQALKEQGTDVVIGLLE THNREETAEQAEGLERIPLLAVNYQNISLKEMNVDGILARSPQLVLVDELAHTNVP GSLHEKRYQDVEYLLESGLNVFSTVNIQHLESLKDLVIKITGISVRERIPDRLLDEAD EVVVVDITPEILQERLQDGKIYDLHKIEQSLNNFFQYRNLVALRELALREVADNLEEL STEKSGKESSNGVQERILVTISTNPNSSRLIRRGARLVSQLKGRLYVLFVSHPEQF LSKNDTLYLEMCEQLCQSLGGEFLQITHVDVVKAIAETAKQYHITQIVIGQTQQSR WKLFLQGSIVQRLIRHLKEIDLHIIALPVL	15~~KdpD (1.80841E-121) ~~225,244~~Usp (2.99637E-42) ~~366	non-kinase	KdpD;Usp

	5.4E-91	313.1	0.2	8.8E-91	312.4	0.1	1.3	1	E6U9J4_ETHHY	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Ethha_1754	Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	377	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ethanoligenens, Ethanoligenens harbinense, Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	663278	>tr|E6U9J4|E6U9J4_ETHHY Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3) GN=Ethha_1754 PE=4 SV=1 MSDKRLTPEEALNICNSQSRGTLKIFLGYAPGVGKTFAMLNEANRRLKYGQDIVIG YVENHGREETDSQIGDLGVLPRKTILYNGVELSELDVDAILQRKPDTVLIDELAHTNI PGSKNKKRYEDVLEILSHGINVISTLNIQHLESLNDVIFQITGIRVNETLPDNILQQAD EVVVVDLTPDALQNRLRRGAVYRPEKVPQALKNFFRKGNLNALRELVLRQAAEDV DEDLDAYMKRKGIKDNWHTVERLMVCISSSPNSKKLIRRGARIANRYKCEWHVVS VNSTRLFFDNHTETDQKMLESHEQLARQLGAEVIELTGRSVSETLAVYANQKHITQ IIMGQSARTKVETFFRGSTVNKLIKMVKNVEIHLIPIG	20~~KdpD (2.3756E-119) ~~228,250~~Usp (4.08413E-43) ~~375	non-kinase	KdpD;Usp
	5.4E-91	313.1	0	1.3E-90	311.8	0	1.7	1	B2IIP8_BEII9	Histidine kinase (EC 2.7.13.3)	Bind_1099	Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	896	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Beijerinckia, Beijerinckia indica, Beijerinckia indica subsp. indica, Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	395963	>tr|B2IIP8|B2IIP8_BEII9 Histidine kinase OS=Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712) GN=Bind_1099 PE=4 SV=1 MKEQPTHSEPNALMVKTGNVRRGRLKVFLGMSPGVGKTYEMLRAARRRKAEGG DVVIGVVETHGRRETEALLRGLEILSRRPIDYRDRSFLEFDIDAALARKPALLLIDEY AHSNVPGSRHPKRWQDVQEVLAVGIDVWTTLNVQHLESLVDVVWKITGVRQRET VPDSALSNADEIEVVDITPSELRQRLAAGKVYVPETAQLASEKFFKPENLTALRELA LRRAAQTIDDQLMGEMKRAGVEGPWAAGERILVLIGADTMAHSLIRAARRLSDMM MNAPWTVAHVEIANRAPPDTVSVARLNEAFKLAEQLGGSTVVLTGNDLIDSAFAY ARQSNITQIMVGKSRRVWWWKWRNRSLAHALLDKATGVALHVITEAAPDHLMPP VPPARPVQNRWSDYVLGIGLVAAATFLSYFLDRAFEHTDLGMIFLSAVLAVGVLFG LRPALVAATLAFLTYNFLFLDPRYSFAIGSPTDVLTLLVFLAVALATGGLAGRVRDQ ASATARRASAISALLAASRRLSAVSTKDEAAKALAEQVSAAARGKAVVLLPIAETIA PAATASTTTPLSTADMGTADMAAARWAWEKGESAGAGTGTLPNAAWTFRPLQG LRTRSGVVGIEAKATSQEDERFVAALLDQGAVALERAELAAKAAEAEAWKRSDQL RSALLNSISHDLRTPLSTVLGSATTLIDYGKTLDSAVSVDLLESIREEAERLNRYVG NLLNMTRLEGGALNPRSEWTDVRDVLNAAAQRVSRRLGKRKLVTDYPPTLSPITT DAALLEQAVVNILENAIAYSPDDTDVEIAVYEDPRNIVISIEDEGRGIPTAELSRVFEK FRRMEEISDRGKGVGLGLSISKGFVDAMGGRIAAASPIHGDKGTRVLISLPKMAVI PQGST	21~~KdpD (8.82085E-121) ~~230,252~~Usp (4.2476E-32) ~~376,400~~DUF4118 (1.01013E-14) ~~499,X,662~~HisKA (0.0000000000286302) ~~728,781~~HATPase_c (1.26786E-25) ~~885	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	5.8E-91	313	0.2	9.5E-90	309	0	2.2	1	Q2KWC3_BORA1	Two component sensor kinase (EC 2.7.3.-) (Fragment)	kdpDBAV2704	Bordetella avium (strain 197N)	922	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella avium, Bordetella avium (strain 197N)	360910	>tr|Q2KWC3|Q2KWC3_BORA1 Two component sensor kinase (Fragment) OS=Bordetella avium (strain 197N) GN=kdpD PE=4 SV=1 VPHSFPASMTVPGANRPDPDLLLHTLDQAAAAARRGRLRIYFGASAGVGKTYAML AGARAQIAQGVQVLAGVIETHGRKETQQLLDGLPLLPPKTLAYRGHVLREFDLEG ALQRRPALLLLDELAHSNAPGSRHAKRWQDVQDLLHAGIDVWTTLNVQHLDSLNE AVGGITGVRVWETVPDDIFDQADEIILVDLSADELLRRLKDGKVYVPDQARHATHH FFRKGNLIALRELALRRTADHVDDDVQAYRRDAAIQPVWRTRETVAACIGPDADA AHVVRNAHRLAQQLDCEWHVITIEGLNIRPGQPHGGLEQALALAETLGAHAEILAG ADRVEAAARYARRHNVTKMVVGRGQARRRLAPQLDRLLAPGWLWQRHSFADEL ARACPDIDILRVAAPAHAPVAPVQHDPLTASGSRQAATPAPRRWPDYGWALAYC LFATAVSKLAFPLLHQTNIVMFYLLAVVGVALRHGRGPAALASVISVGLFDYFFVQP ISSFAVSDVQYLLTFAVLLGVGLLIGQLTAGLHAQAETSVKREADARALYEFARELS SALLPEQIVQAADTFLKAAFDADSALYILGMDDRLQLAATPPPSMAAPEPSLAQWV QDHGQAAGAGTATLSNSPLLYVPLAAPMRVRGVLVLQTSHPIASAPASWRQVQA YATLIAIGLERLHYVEVAQHALLNVESEKLRNSLLAAVSHDLRTPLTGLIGMTETLAR SATDAAVQEQANAIRDQARRMHRMVVNLLDMARLQSQGTPLKREWQSVEELAG AALANMRETLRGHQVRVLPLSELPLVECDGMLIERVFCNLLENAAKYSPEGGTITL EGRVSDDALQVSVSDQGPGVAPGSEDRIFQKFTRGERESALPGVGLGLSVCRAI VQAHQGRIWVEPAPGGQGARFIFELPLGQPPTIDHELS	40~~KdpD (3.92454E-105) ~~243,266~~Usp (3.71294E-27) ~~395,432~~DUF4118 (2.17903E-19) ~~526,558~~GAF (0.000000000000208694) ~~674,691~~HisKA (9.28004E-14) ~~754,807~~HATPase_c (3.31234E-30) ~~909	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	6.9E-91	312.7	2.1	9.6E-91	312.3	1.5	1.2	1	K9WYH7_9NOST	Osmosensitive K+ channel His kinase sensor	Cylst_2653	Cylindrospermum stagnale PCC 7417	396	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Cylindrospermum, Cylindrospermum stagnale, Cylindrospermum stagnale PCC 7417	56107	>tr|K9WYH7|K9WYH7_9NOST Osmosensitive K+ channel His kinase sensor OS=Cylindrospermum stagnale PCC 7417 GN=Cylst_2653 PE=4 SV=1 MMITQREMLNDTNTGSADTKPLTSASSAMSLARRGKHKIFIGMAPGVGKTYRMLE EGHALKQEGIDVVIGLLETHGRKETAAKAEGLEIVKNRQVPHGELMLTEMDTEAIIR RSPQLVLIDELAHTNVPGSPRKKRYEDVEVILAAGIDVYSTMNIQHLESLNDLVARI TGVVVRERVSDRILEAADEVVVVDVTPETLEERLIEGKIYAPPKIEQALDNFFQRRN LIALRELALREVANNVEEEAIASTPNGQFYNIQERVLVCVSTYPNSVQLLRRGARLA SYMNAPLYTLFVADPHHFLTKEESLHVDTCQKLCKEFAGTFIRVTNNNVAQAIAQE AHKHHITQIVIGASQRSRWQLLLKGSLIQTLVHLLKNVDLHIIASEKKSSSQAENSG	32~~KdpD (4.10847E-119) ~~242,261~~Usp (3.81575E-45) ~~383	non-kinase	KdpD;Usp

	8.2E-91	312.5	0	1.5E-90	311.6	0	1.5	1	D8ML40_ERWBE	Histidine kinase (EC 2.7.13.3)	kdpDEbC_43370	Erwinia billingiae (strain Eb661)	889	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Erwinia, Erwinia billingiae, Erwinia billingiae (strain Eb661)	634500	>tr|D8ML40|D8ML40_ERWBE Histidine kinase OS=Erwinia billingiae (strain Eb661) GN=kdpD PE=4 SV=1 MNDELHRPDPDSLLLQATESGRGKLKIYFGACAGVGKTWAMLQEARRLRAQGLE VLVGVVETHGREETAALLDGLTVLPRKATGQNRHPEFDLDAALARHPAVILMDELA HTNAPGSRHPKRWQDIEELLDAGMDVMTTVNVQHLESLNDVVGGVTGIRVRETV PDPFFDAADEVVLVDLPADDLRQRLKEGKVYIGDRAERAIENFFRKGNLFALRELA LRRTADRVDDQMRAWRDSQGREKVVWHTRDAILLCIGDNTGSEKLVRTAARLAAR LDSVWHAVYVETPRLHRLSEARRRGILRTLQLAQDLGAETATLSDPDDANAVLRY AREHNLGKIILGRRSARRWRRDSFAERLGKLGPDLDMVIVALDEPVSAPASALAD NRPGGDKWRNPLRGCLASLILCSLVTLAGRWLLPGVDSVNLVMVYLLAVVVVALR YGRWPSVVATVLNIVAFDLVFVMPTGTIAVSDVQYLVTFGVMLAVGVIVGNLTAGV RYQARVARYREQRARHLYEMAKTLSRALSQQDIAQALPRSLDTTLQARSELLLPD EQGELVAVGESRLNNVPDNAIARWSFDKGQPAGAGTDTLPGVPWQILPLKSGNE TLGLLVLEPLNLRQLMIPEQQRLVETFTVLIANALERIALSQREAVSRLAAEREQLR NALLSALSHDLRTPLTVLFGQAEILTLDLATEGSKHAIQASEMREQTLNTIRLVNNLL DMARLQSGGFSLRAEWMALEELIGSTLKMMAPSLGNRKVALALPQEMLLIHVDGP LMERVLTNLLENALKYAGDDAQIGIRAGVQAQRLEIEVWDSGPGIPGGQETQIFEK FSRGNKESAVPGVGLGLAICQAIVSIHEGKIRAENRAEGGARFIITLPVKEPPVIEEY Q	20~~KdpD (4.4394E-120) ~~228,251~~Usp (4.52389E-34) ~~370,400~~DUF4118 (0.00000000000700095) ~~498,524~~GAF (5.43205E-14) ~~641,658~~HisKA (0.00000000775261) ~~723,776~~HATPase_c (8.04794E-28) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.6E-91	312.4	0.2	2.2E-90	311.1	0.2	1.7	1	D7B3Y2_NOCDD	Histidine kinase (EC 2.7.13.3)	Ndas_1513	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	832	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	446468	>tr|D7B3Y2|D7B3Y2_NOCDD Histidine kinase OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_1513 PE=4 SV=1 MRRGRLRVFLGAAPGVGKTHTMLEEGRRLRDEGRDVVVAIVETHGREAVAALLD GMETVPRTAVSHRGVGLTEMDLDAVLARRPQVALVDEFAHTNAPGARHGKRWE DVARLCAAGVDVITTVNIQHIESLNDVVQRITGAPQRETVPDRVLRAADQIELVDLA PQALRDRLAAGRVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALMDYR AEHRIDSTWEARERVVVALTGGPEGETLLRRGARIAARSGSGELLALHVSGQEGL RDARPEALAAQRVLTERLGGTFHQVVGDDIPRSLVEFARAVNATQLVIGISRRGRL LTALTGPGVGATVIRESGPIDVHMVNHAAAARGPALPRLGGALSLRRRLAGFALSL VAGPLLTWMLAAERSPEALVADVLTYQLLVVVVALVGGIWPALYTAVMSAVTLDLL FIEPVLQIRIDHPVHLGALVLYALNAVLVSYVVDQAARRTRAAQRAGAEFELLATVA GSVLRGQDALRALVGRTREAFALDAVRLRSDGAVLSSAGEAPPGAEPTVVAVGE RASLELHGAELGASERRLLEVIATQIDAALEHQDLRATASEVGPLAENDQVRSALL SAVSHDLRRPLAAVTTAVSSLRLSGVDWSPGDRDELLATAEESLATLTALVTDLLD VSRLQAGVLAVSAHDTDVDEVILPALDELGLGPADVDLELDPDLPAVRADAGLLQR AIVNLLANAVRFSPPGRGARVATSAFGAAAQIRVIDHGPGVSPDRLDQLFVPFQRL GDTDNTTGLGLGLALSRGFVEGMGGRLTAEDTPGGGLTMVISLPLAERPGPGED A	1~~KdpD (1.81407E-112) ~~211,233~~Usp (9.35595E-29) ~~356,X,602~~HisKA (0.0000000425132) ~~668,719~~HATPase_c (4.64181E-26) ~~820	kinase	KdpD;Usp;X;HisKA;HATPase_c
	8.8E-91	312.4	0	1.3E-90	311.8	0	1.3	1	D3VAM2_XENNA	Histidine kinase (EC 2.7.13.3)	kdpDXNC1_1395	Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	904	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus nematophila (Achromobacter nematophilus), Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	406817	>tr|D3VAM2|D3VAM2_XENNA Histidine kinase OS=Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6) GN=kdpD PE=4 SV=1 MLQNELQRPDPDDLLTLANENPRGKLKIFFGACAGVGKTYAMLQEAQRLLAQGLD IIVGTVETHERQETAALLQGLPQLSPKYLRHNNRRVAAFDIDAALARHPAIILMDELA FSNPQGCRHPKRWQDVDELLEAGIDVLTTINVQHLESLNDIVGTITGIRVRETIPDH IFDQANDVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRELALRRT ADRVDEQMRAFRDTKGKEPVWHTRDNLLLCIGYNAGNEKLIRTAARLAAKLDCA WHAVYVETPKLHRLPEGKRRTILKALRLAQDLGAETATLSDSSEEKAILRYAREHN LGKILIGRYHDSHSNLFSRKWRPDFAERLGKLGPELDLIIVALENRKHWDKEPKDN RSFNEKWRVQIQGCIMAIILCTLTTLFSRTFLLTLDKANLVTLYLLGVVIIALFYDRW SSVFAAFINVISFDLFFVQPHWSLAVKDMQYLLTFTVMLIVGVVVGNLTAGIRYQA RVARHREQRTRYLYEITRELSRALNEEDVARISYHFLSNSFQAKTGLLLPDIHHHLY QVKSNNGGQMQVDEGIAKWCFEKKQPAGAGTDTLPGVPYQLLPIATPSQVFAVL AIESANLRHLLVPEQQRLLQTFTGVIANALERLHLTRSAESAKLETEREQLRNSLLA ALSHDLRTPLTILFGQTEILMLDLSAENSPHTQQVNQIRQQILSTSRLVNNLLDMARI QSGGIQLNLEWYPLEEIVGSALRSLDYSLHRYNVELTLSTHLFLHCDAALLERVFIN LLENAIKYTHEQTPLGIQATIEQETEKKQVHIEIWDAGSGIPSGQEQLIFEKFSRASK ESVIPGVGLGLAICQAIIEIHGGNIWATGNQKGGASFHFVLPLEDPPKIEDVQEDM	23~~KdpD (3.36359E-117) ~~231,254~~Usp (3.22768E-37) ~~379,410~~DUF4118 (3.97282E-19) ~~506,532~~GAF (5.72811E-15) ~~650,667~~HisKA (0.0000000000462696) ~~732,784~~HATPase_c (2.99107E-26) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.2E-90	312	0.1	2E-90	311.2	0.1	1.4	1	D2UFZ5_XANAP	Histidine kinase (EC 2.7.13.3)	KdpD XALc_2829	Xanthomonas albilineans (strain GPE PC73 / CFBP 7063)	892	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas albilineans, Xanthomonas albilineans (strain GPE PC73 / CFBP 7063)	380358	>tr|D2UFZ5|D2UFZ5_XANAP Histidine kinase OS=Xanthomonas albilineans (strain GPE PC73 / CFBP 7063) GN=KdpD PE=4 SV=1 MSDLRTQQADALIGELKRERGGRLTVFLGAAPGVGKTYAMLSRARQLQQQGSVL VIGVVETHGRVETAALLEGLTVQPRRRVEYRGRTLDEMDLDALLALRPPLVLVDEL AHRNAPGSRHERRWQDVEELLDAGIDVYSTVNIQHLESLNDVVHRITGVRVSETV PDAMFDRLRDIVLVDLPPRELIERLQQGKVYLPEQAGQALQAFFSPSNLAALRELA MQTAADRVDNDLRDVQAAQGRPGLALRRRVMVAIDGRGQSDYLVRVARRVAER RGSPWTVVTVQTQAQPEEAWQLEIDRAFALARRLGGDAALLRGSSVADALLDHA ARNGVSTLLLGRTRERPLARMINRTLTQQLLQRGAHYELVIISSPEARARSRRRWR SPGHWLSRDDLAFAMVASALAVVVAWIAERWVGIDDLSMVFIVAVVMVAAKTRM AAAVLAALLSFFGYNFFFIEPRFTFQIGTRQGVVTVLLFLVAALVAGRLASRLRSQV LALRAANAQTTALQRLGRELTSAADLGQVLDAGRHALSTTLDAEAWVRLQPLEAA HAGADDYAPSMAAVDRSAADWAQRHGQATGRFTDTLAGASWWFLPVRHERGA IGVVGLRFAAGVQRPGLEQQRLAEAMVEDIGQAALRTRLVADLESARVSGETEHL RSALLSSVSHDLRSPLAAMIGAASSLSSYGQAMSAEDRRSLLDTIQMEGERLDRYI QNLLDMTRLGHNGLTLNRDWIGVDELIGSAARRLQRYQPEVLLDIVLAADLPTLWV HPALVEQAVFNVLENAAKFSPPDTAIRVAAMMVEGRLRIDIADRGPGIPEDERARIF DMFYSVERGDRGRHGTGLGLTICQGMIGAHGGSVEALPGPDGRGTTIRITLPLIEP AAPPRRPDAD	19~~KdpD (2.7046E-120) ~~229,250~~Usp (1.57413E-21) ~~371,423~~DUF4118 (0.000532811) ~~494,520~~GAF (0.000354159) ~~635,655~~HisKA (0.00000000000844371) ~~721,775~~HATPase_c (2.42511E-23) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.2E-90	312	0.3	1.9E-90	311.3	0.1	1.4	1	A0A0F2QZQ0_9PSED	Histidine kinase (Fragment)	VR76_04385	Pseudomonas sp. BRH_c35	364	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. BRH_c35	1629711	>tr|A0A0F2QZQ0|A0A0F2QZQ0_9PSED Histidine kinase (Fragment) OS=Pseudomonas sp. BRH_c35 GN=VR76_04385 PE=4 SV=1 MSDALRADALLDDVPREGRGRLKVFLGAAPGVGKTYAMLQAAQRQKRLGCDLRV GVVETHGRAETEAMLVGLPEQPLIRSEYRGITLAEMDLDGLLAARPRVVLVDELAH SNAPGSRHSKRWQDVLELLEAGIDVYTTVNVQHLESLNDQVRAITGIQVRETVPD WILQEADDILLIDLPPRELLERLREGKVYVPDQARAAIDAFFTQTNLTALRELAMQT AAARVDAELNRRYRLQGQSAPAVRGRLLVGIHGNDAAEGLVRHAARVAERRHLP WSVVYVNTGASRGETELAHLQAAQQLAERLGGEVVELRGERVARTLIDHAYERR ATLLLVGRSGARRGLKRVFMRSVAEQLIAAGQGL	17~~KdpD (2.98086E-120) ~~227,248~~Usp (4.85552E-24) ~~358	non-kinase	KdpD;Usp

	1.2E-90	312	1.3	2.1E-90	311.2	0.9	1.4	1	R7G954_9FIRM	Universal stress family protein	BN631_00316	Eubacterium dolichum CAG:375	629	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium dolichum CAG:375	1263076	>tr|R7G954|R7G954_9FIRM Universal stress family protein OS=Eubacterium dolichum CAG:375 GN=BN631_00316 PE=4 SV=1 MQRKGRLKIFFGYCAGVGKTYSMLKEAHEKAQEGVDVVIGYIEPHDRKETISLIDG LEQLDKKEILYKKHRFYELDLDLALQRHPKLILVDELAHTNAIGSRHKKRYSDIEELL RAGIDVYTTINVQHLESLHDTVAMITRIQVNERIPDHIFDDADDVKLVDIEVDDLIQRL KDGKIYHKNQTKRALENFFVRDNLIALREIAMRRCADRINLITSTANKAFSKEHIMV CLGASPTNQKVIRTAARMVQAFHADFTALYVETSQADWITQKAKNQLQANLELAR HLKADIVSTYGDDIAYQISQYAKNAHVSKLVLGRSYQKPSIFRKTTLVDQLSKLAPEI EIYIIPDQQSGAMKKKYRTLLKSKFNMQEAIITITVLLVTTLFAIFLDSFHVHITSIVLLY VLASCFIGMMTFYPLYNLIATLLSLLLIDIFFVEPRFSLLMDSKEYPIMFLVMMIVSLSI SMMGHRLKKEKMLASLHAHSMEVILQTSQRLQVLNTYHEIMEETCYQLFQLLHRPI IFYPVKHQELQDGVLYKACDFPAIKEQLTSIEEIAVAKWVFTNNKNAGATTNTLSHS KALYLAIRKGSCVYGVVGIRINTSNDLLPFEKNLLKAILNETALAMSSIAQQ	3~~KdpD (2.50056E-117) ~~212,227~~Usp (9.82308E-32) ~~349,372~~DUF4118 (0.0000344375) ~~474,503~~GAF (0.00135929) ~~623	non-kinase	KdpD;Usp;DUF4118;GAF

	1.2E-90	312	3	1.9E-90	311.3	2.1	1.3	1	C1F834_ACIC5	Osmosensitive K+ channel His kinase sensor domain/universal stress family protein	ACP_0080	Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	387	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Acidobacterium, Acidobacterium capsulatum, Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	240015	>tr|C1F834|C1F834_ACIC5 Osmosensitive K+ channel His kinase sensor domain/universal stress family protein OS=Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161) GN=ACP_0080 PE=4 SV=1 MNQPDNASINIPLRAPRELHLQREDVARLRIYLGAAPGVGKTYRMLQDAHRLHDQ GVDVVVGFVEAHGRAETVSLTEGLEMIPRHQVPYRSVTLEEMDVDAILARKPHTV VVDELAHTNVPGSRHRKRYEDVLELLDAGIHVMTAVNIQHIETLNDAVSRSASTQI RETIPDSILKRADEVVNVDVTVDELRTRLREGKIYAPEKVELALANFFRKGNLNMLR ELALRTTAEKVGSAASEYRRTQGLEQAPMPEKVMVCFSARTGSERLLRVGARIAG RLATQWYAVYVERPGTSRHHDDADAQRRIEDFERMAADLGAKVVMLKKKNVADA LVEFAKQENISHVVFGQSARSRFDIFLRGSVINRFLAEMRETTVQVVPMNKKEKK	28~~KdpD (1.05465E-116) ~~234,255~~Usp (1.73952E-32) ~~380	non-kinase	KdpD;Usp
	1.2E-90	311.9	0.4	2.8E-90	310.7	0.3	1.6	1	Q2IPD8_ANADE	Histidine kinase (EC 2.7.13.3)	Adeh_0892	Anaeromyxobacter dehalogenans (strain 2CP-C)	902	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Anaeromyxobacteraceae, Anaeromyxobacter, Anaeromyxobacter dehalogenans, Anaeromyxobacter dehalogenans (strain 2CP-C)	290397	>tr|Q2IPD8|Q2IPD8_ANADE Histidine kinase OS=Anaeromyxobacter dehalogenans (strain 2CP-C) GN=Adeh_0892 PE=4 SV=1 MTSPDQRPDPDALLAHARAEEDRARRARFKVFFGFAPGVGKTYRMLQVARDLVA EGVEVVIGAVETHGRYDTAGLMLGLEVLPRRALPHHGRVVEEFDLDAALARRPRIL LLDELAHANAPGSRHAKRWQDVVELLAAGIEVYTTLNVQHVESLNDVVAQITHVQ VRETIPDSILDRADEVELVDVAPEELLERLREGKVYVPEQAALAREHFFKRGNLLAL RELALRRMADRADVDVLAFREAHGVRRAWATAERVLVCVGHAPDSARIVRAGRR IAAGLRAPWFAAAVEATGQPPLPQEDRDRLEAHLRLAESLGAEVVRLSGVRVSDG ILDFARRRNVSRIVLGKPRHPRWRDRLRGSLVDEVIRGSGDIEVHVLAGTDGDGP GRAAPARREGPTPLREHLRAVAIMGVTTALAAAARALLHVPDVEMLFLLGVMVVA LTSGRRASVVAAVLAVTCYDFFFVPPSFTLGVTDARYLLTFAMMLGVGVVIGTLTL RLREQQQAAVARERRTSAVYALGKELAAAADAAGVGAACVGAVAEAFDCAAVFL VAKDRETLEPLAAVPAGEALTAGARAVAQWAHEHGRPAGRGTDTLPGEPVLCLP LRTSGDVLAILALRAPRERTLDGEQRELVESLGRHAAVALDRVRLADEARRSALRA RTEELRSGLLSAVSHDLRTPLAAITGASTLLLDAAVADPAVRRELVATVVEEAERLE RLVSDLLDMTRLDSGVVEPRREWVPLVEVVGAAMNRVERALGNRPVAIALRDDLP LLSIDPILIEQLLVNLLENATKYTPPGTEISVAAVREGGTLVIEVADRGPGIPAGEEE RIFERFHRAARPGVRGVGLGLPIARAIAQAHGGRLTAASRPGGGSVFRLTLPVQS PPPAPPEPAPPRGGPA	24~~KdpD (6.30911E-101) ~~218,256~~Usp (9.47298E-40) ~~379,429~~DUF4118 (0.0000000005307) ~~502,536~~GAF (9.87157E-16) ~~647,664~~HisKA (2.41127E-14) ~~729,782~~HATPase_c (1.26335E-29) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.3E-90	311.8	0.4	2.3E-90	311	0.3	1.4	1	B2TMJ4_CLOBB	Osmosensitive K+ channel histidine kinase KdpD (EC 2.7.3.-) (Sensor protein KdpD) (EC 2.7.13.3)	CLL_A0981 CB17B0916	Clostridium botulinum (strain Eklund 17B / Type B)	900	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum B, Clostridium botulinum (strain Eklund 17B / Type B)	935198	>tr|B2TMJ4|B2TMJ4_CLOBB Osmosensitive K+ channel histidine kinase KdpD OS=Clostridium botulinum (strain Eklund 17B / Type B) GN=CLL_A0981 PE=4 SV=1 MIDERPDPDEILKKISSDENNKQGKLKIFFGYAAGVGKTYAMLEAAHIAKNSGIDVV AGYIEPHTRVETLALLDGLKMLPNLKVKYKGITLNEFDLDSAINRKPKLILVDELAHS NAYGCRHMKRYQDIQELLNNGIDVYTTINVQHIESLNDIVASITGIVVRERIPDSVFD NANQVELVDIEPDDLITRLDNGKVYKTDQARRALINFFTKEKLVALREIALRRTADA VNKKIENKRDEIKSTYYTEEHILICLSSSPSNTKVIRTAARMAFAFHGLFTALFVETS NSKDLSLENKKILETNLKLAEQLGAKIATVYGDDVANQISQYAKISGVSKIVIGRSNN KKSWFNNKKTLVDKLTEFAPNIDIYIIPDNLKAYKRNSSEKLKKITLPHFTVMDLIKTT AILGAVTATGVIFYNLGYSEANIINIYILGVLLTSITTTGKSCGLLVSILGVLVFNFLFTN PRFTFQAYDKSYPITFFVMLVSSIISSKLATRVKIEAKQSAEKAYRTEVLLETSQKLQ MAKNKEEIFNKILIQIEKLLDKSVILYPADNEVLLEPIVFKKNRTINIKEFITEDERAVA QWVFKNKKHAGSTTNTLPGAKCLYMAIRNHEKSFAVVAIPIDKDETLDSFKKNLLIA ILAESALSLEKEYINETKNEIYMKAEQEKLRSNLLRAISHDLRTPLTSISGNAGILMG NSRVLDESRKQRLYTDIYDDSMWLINLVENLLSVTRIENGTMDIELQPELIDEVIQE SLQHINRESSNYNIEVEVEDELLMAKMDSGLIIQVIINIVNNAVKYTPKGSNIKIFGKK QGKSVVIEISDDGCGIEDSMKGKLFDMFFTLNSTSADGRRGLGLGLSLCKSIINAH GGEVYVRDNEPKGTIFGFTLQCEEVIYSE	22~~KdpD (1.88212E-121) ~~231,251~~Usp (1.92787E-35) ~~374,401~~DUF4118 (2.63203E-14) ~~500,528~~GAF (0.00000177102) ~~652,669~~HisKA (0.000000000239218) ~~735,799~~HATPase_c (1.99991E-19) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.4E-90	311.7	0.3	2E-90	311.2	0.2	1.2	1	Q02CX3_SOLUE	Osmosensitive K+ channel His kinase sensor	Acid_0077	Solibacter usitatus (strain Ellin6076)	345	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Solibacteres, Solibacterales, Solibacteraceae, Candidatus Solibacter, Solibacter usitatus, Solibacter usitatus (strain Ellin6076)	234267	>tr|Q02CX3|Q02CX3_SOLUE Osmosensitive K+ channel His kinase sensor OS=Solibacter usitatus (strain Ellin6076) GN=Acid_0077 PE=4 SV=1 MSRPGQLKIYLGYAAGVGKTYRMLEEAQALRAKDIDVVIGYFEPHGRQETIDKTE GLETVPRRAIQYGGTRFEEMDLDAVLRRKPAVAVVDEFAHSNIPGSGNEKRWQD VHALLDAGINVLTTMNVQHLESLNDQVWQVTGVRVRETVPDWVVDEADEVVLVD LTPRALRNRIDRGVVYASEKARRALDNFFTEANLTALRELAIRHTAHEVEDKLLDPR REERILICLTGRPSSANLIRRGKRVADYLQGDCLAVHVAPGAVCDENVRRHMSFA RNLRIETHVLEGEDVPSVIAEFARSHKITQIFMGRSSARPWWKRFGETVVQRMVR LARDMQITIVAERRR	2~~KdpD (6.26984E-117) ~~212,224~~Usp (1.54758E-27) ~~341	non-kinase	KdpD;Usp

	1.5E-90	311.6	0.1	2.6E-90	310.8	0.1	1.4	1	S6C135_9ACTN	Histidine kinase (EC 2.7.13.3)	AEQU_1604	Adlercreutzia equolificiens DSM 19450	943	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Adlercreutzia, Adlercreutzia equolificiens, Adlercreutzia equolificiens DSM 19450	1384484	>tr|S6C135|S6C135_9ACTN Histidine kinase OS=Adlercreutzia equolificiens DSM 19450 GN=AEQU_1604 PE=4 SV=1 MAEVRERWEIGGGRGDPDAILQRIREEEEAGEAERFEGRGRLKVFFGYAAGVGK TFAMLTEAHRVQDEGVDVVVGYVEPHTRADTLALLDGLEVLPVKSVKHRNVALRE FDLDVALKRRPQVVLVDELAHTNAPGCRHRKRYQDVEELLRAGIDVYTTVNVQHL EGLNDKIASVTAVAPSERIPDRVFDAADSVEVVDLEPADLIKRLRSGKIYAPERIGS ALSHFFSRSNLAALREIALRRAADRLTRASAATVPHAAGGEDVLVLVTADAAAPRVI RAAAGMAEAFGGSCTALVVESGGGEGAEGRSKGDAALARSIALAEEMGAHIVTLT GDDPVQPVALYAAAAGIRRIVVPSMPGRIGLLGCGDVASRLMRAAPEAMVTAVPA VDAPSVLERLRTYASFRLTASDVFRALLAIAVATALGEVAWLASPTPSIILMTYLLVA LLLATRADGFLYAVLVALGSVVAYSFFFTAPRYTFHAYSLSAPIIFTVLLIGTLGASSL AIRLKRQATTAARRAYRTEVLLESSREFQAVVSLGACLETAAAQVVKILDRPVVMY QVDGAAHGGLLPPRVFDVPGSGGGDAEKLDLAAPGEMAVASWVAANGEAAGAT TDTLREARCLYLPIRSKDRVFGVAGLVMEQGDDDFGSFERNLLVALLDECGQAAE ALALASERKNLAVKAEKEALRSNLLRAISHDLRTPLTSISGDADMLLASGDVLDEAQ RKRLTSDIHEDANWLINLVENLLSVTRLDDGDVEVSRAPELVSDVLADALRHVSRS VSEHRLTVEIEDEFLLAQMDGRLIVQVVVNLLNNAIAYTPAGSSIRLTAHRERSASGG DRVVVAVADDGPGIPPAEQARVFDLFYHGGRVGTGCEDGEGGDARRGMGLGLS LCRSILRAHGSDIVLRDAYPHGCVFSFALPAAELREEAPVGVVEEGSADVER	38~~KdpD (2.04428E-116) ~~247,264~~Usp (0.000000000000291302) ~~386,413~~DUF4118 (0.0000000310886) ~~511,537~~GAF (0.00356985) ~~659,686~~HisKA (0.000000000116721) ~~752,805~~HATPase_c (4.00038E-23) ~~920	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.6E-90	311.6	0.7	2.6E-90	310.8	0.5	1.4	1	D0L4M9_GORB4	Histidine kinase (EC 2.7.13.3)	Gbro_4089	Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia bronchialis, Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	526226	>tr|D0L4M9|D0L4M9_GORB4 Histidine kinase OS=Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) GN=Gbro_4089 PE=4 SV=1 MADSGDGRAGDGRGRLEVFLGCAPGVGKTYEMLATARGLIDEGSDVVVAVVES HGRSATAALVEGLEVVERTSVAYRDATLEEMDLEAVLERHPQVALVDEMAHTNAP GLRNTKRWQDIEVLRDAGIDVLTTINIQHLESLNDVVAQITGVTQRETVPDEAVRA ADQIELVDIDPQALRQRLTAGKVYPGRRIDGALTNYFRQGNLTALRELALLWLADR VDDTLADYRAANAITATWEARERVVVAITGGPESAALIRRASRIASRSSAELVVVH VVRGDGLAQRTPIDMTALRDLAAGFGAKIHTVVGDDVPATLLEFARGVNATQLVL GTSRRPRWQRILDEGVGATVVRESGRIDVHMVTHEETRRRHRLDIRETRFHRPLS WAAAVLVPLAVTGILMLLDPWLGFSSESALFFVAVLAVSMLGGIAPAVLSAVVSGL LLNYFLTNPRYTFTIDEPDNLITIMVMLMIAIAVAVLVDSATVRRAQAQRAGRDAELL SLFSTTVLGGADVPALLEKVRETYDQRGVTLIRRPKRGAPVIESKVGTEPPADEQA ATTVCPVPGGEFEMWLTGPELGGRDRRVLTSVATQAAGAVQRRQLESEAAEAA ALAQTDELRRALLSAVSHDLRTPLAAAKAAVSSLRSTDVTFSPEDTEELLATIEEST DQLSALVGNLLDSSRLAAGVVRPELRRTYLAEVIHRALYAVDRRSVDTPDVTVDLQ QEWAYTDAGLLERALANLVDNAVRHGGDEVRVQARPDGTRCVIRVIDHGRGIPP EQRERVFTAFQQYGDRNGSSTGVGLGLSVAQGFVRAVGGSISVSGTPGGGTTM EVSLPMFASPAEAGEL	16~~KdpD (6.80052E-107) ~~221,243~~Usp (1.02814E-32) ~~364,387~~DUF4118 (3.52315E-15) ~~481,X,615~~HisKA (0.000000000000389831) ~~681,733~~HATPase_c (2.29785E-27) ~~833	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.6E-90	311.6	0	2.8E-90	310.8	0	1.4	1	B2VJK1_ERWT9	Histidine kinase (EC 2.7.13.3)	kdpDETA_33620	Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	890	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Erwinia, Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	338565	>tr|B2VJK1|B2VJK1_ERWT9 Histidine kinase OS=Erwinia tasmaniensis (strain DSM 17950 / Et1/99) GN=kdpD PE=4 SV=1 MNDELQRPDPDALLRQAVESHRGKLKIYFGACAGVGKTWSMLQEARRLRAQGLE VLVGVVETHDRPETAALLSGLTVLPRRATGPQRRPEFDLDAALARHPAVILMDELA HSNTPGSRHPKRWQDIDELLEAGIDVMTTVNVQHLESLNDVVGGVTGIRVRETVP DPFFDAADEVVLVDLPPDDLRQRLKEGKVYIGESAERAIENFFRKGNLIALRELALR RTADRVDDQMRAWRDTQGREKVWHTRDAILLCIGDNSGSEKLVRSAARLAARLD SVWHAVYVETPRLYRLSETRRRGILRTLQLAQDLGAETATLSDPSEASAVLRYAR EHNLGKIIIGRRPTRRWWRESFAERVGELGPDLDILIVALDDPPPDSVSSLAERVD SQEGKRGSQLRGCAAALLLCMLVTLAGRWLLPAVDSVNLVMVYLLSVVIVALRYG RWPSVVATLLNILAFDLVFVAPTGTMVVSDVQYLVTFGVMLAVGVIVGNLTAGVRY QARVARYREQRAHHLYETAKALSRALTQRDIASTLQRSVESTLQARSELYLPDEH GELVPVGAAHLSAVPDRAIARWSFDKGQPAGAGTDTLPGVQWQMLPLKSGSDM LGLLILEPLNLRQLMIPEQQRLVETFTVLIANALERMALSQREAASRLAAEREQLRN ALLSALSHDLRTPLTVLFGQAEILTLDLASANSPYAGQASAMREQTLNTIRLVNNLL DMARLQSGGFSLRREWMALDELIGSALRQLAPLLADRPVTLDLPAELLLIDVDGPL MERVLVNLLENALKYAGDKAQIGIRARAVAQRLELEVWDTGPGIAPDQQQLIFEKF SRGDKESTVPGVGLGLAICQAIVTLHEGKIHAENRPQGGVSFVISLPLTAPPMLEE YT	20~~KdpD (1.2538E-118) ~~228,251~~Usp (2.16181E-37) ~~370,401~~DUF4118 (6.80192E-21) ~~499,525~~GAF (0.000000000161844) ~~642,659~~HisKA (0.00000000284288) ~~724,777~~HATPase_c (9.74458E-31) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.6E-90	311.5	0.8	2.3E-90	311	0.6	1.2	1	D7BJE2_MEISD	Translation initiation factor IF-2	Mesil_3494	Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	370	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Meiothermus, Meiothermus silvanus, Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	526227	>tr|D7BJE2|D7BJE2_MEISD Translation initiation factor IF-2 OS=Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) GN=Mesil_3494 PE=4 SV=1 MEPAAPDPQQLLEAILKSGRGRHKIYVGAAAGVGKTYRALQELRERLEAGVDAVV GYLETHGRADTARMAEGLPIFPRKQLEYKGVVLPEMDLEGLLARRPALVLVDELA HTNVPGSKNAKRYQDVEELLQAGISVISTMNIQHLESLNDLVARLTGVRVKERVPD RVLLEADEVILVDVTPEVLQERLRAGKIYPKAKIEQALANFFTAENLAVLRELALRSV ADKVEEDASVGEDSPAIKERIAVAVTPSPKDALLIRRGARMAQRMRGELHVVHVR NRRLSREEERVLDSHRIITESLEGRFHSLEGRDVAKALADFAKEYGITQLVLGENS NPTWRDFFRLSIIQRLIYLTHDIDIHIMDRRAEER	18~~KdpD (4.77796E-120) ~~228,244~~Usp (1.20881E-36) ~~362	non-kinase	KdpD;Usp
	1.6E-90	311.5	0.1	2.7E-90	310.8	0.1	1.4	1	D2R314_PIRSD	Histidine kinase (EC 2.7.13.3)	Psta_4097	Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	909	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Pirellula, Pirellula staleyi, Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	530564	>tr|D2R314|D2R314_PIRSD Histidine kinase OS=Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) GN=Psta_4097 PE=4 SV=1 MTDSRPNPDALLALAEDEQKLDDTTTGKRGSLRIFFGYAAGVGKTYGMLEAAQAA RREGRDVVVGYIEPHARKETQALAADFETLPTKQLSYRGVTLREFDVDAALARKA EITLVDELAHTNAEGSRHEKRWQDIEELCASGLHVWTTLNVQHLESLNDVIGQITG VQVRETIPDHVFDAADQLELIDITPEELLGRLEAGKIYLPEQAKRAIQSFFQRSNLSA LRELSLRQAARRVHTDVESARRARSVRQPWATTDRLLVCVGPSPTTARVIRTAKR MASALDAPWIAVSVDLTGASSTSPASQQIAEHFRLAERLGAETVTLPGQRMTETIL EYARTRNVTKILIGKTDQPRWKRLLMGTVVDEILEQSGEIDVYVIHGEKDQAARVA TPPARPPIDYWLYGKAAVPVGLAGLAALAMKRWHFADAEANTVMIFLAAVAWAA FRFGRGPAIVASLLAVTIFDFFFVPPFHTFAVADTQYIVTFAVMLAIALLISTLTSRLR AQLEAMRDRQRRTAALYELGKQLSSLYGSSFLAKAAGEKIAEMVGGEVAIYLDRH APSPELVFGARSSIALQHGSSAVAHWVIQHGQMAGAGTSTLPSAVGLFLPLIGSQ RVHGAMAVAVASAARLQQPELRQLLESCASQLAISIERDALVVEAADARVKAEAE QVRSSLLSSVSHDLKTPLAAIAGASSTLLEASSLPPSTREQLLQTVAEEAVRLGRLL ENILQMSKLDAGASPPHLEWHMLEEIVGSSIRRIEKSLTQHQLIIQIPEQLPLLRLDG LLMEQVFVNLLENAARYTTAGSTISVRAVVEGQEVRVTVADNGPGLPAGAEEKVF DKFYRAFPSADGGRGSGLGLAICRAIVKVHGGRIEAANLPAGGAEFVIHLPLAQDI PQVPLSPSDSSRAS	27~~KdpD (1.21932E-117) ~~237,259~~Usp (2.5635E-39) ~~380,407~~DUF4118 (1.09889E-18) ~~506,536~~GAF (0.000183883) ~~652,681~~HisKA (0.00000000506713) ~~734,787~~HATPase_c (5.1623E-29) ~~889	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.6E-90	311.5	0.1	2.6E-90	310.8	0.1	1.3	1	Q1QJ49_NITHX	Histidine kinase (EC 2.7.13.3)	Nham_2991	Nitrobacter hamburgensis (strain X14 / DSM 10229)	894	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Nitrobacter, Nitrobacter hamburgensis, Nitrobacter hamburgensis (strain X14 / DSM 10229)	323097	>tr|Q1QJ49|Q1QJ49_NITHX Histidine kinase OS=Nitrobacter hamburgensis (strain X14 / DSM 10229) GN=Nham_2991 PE=4 SV=1 MSGEPATRASPDALLALAKKEGRGHLKIFLGAAPGVGKTYAMLAAARSEIAGGRN VVVGLVETHGRRETDQMLDGFEVLARKPIVYRNQVMHEFDLDAARARKPGLLLVD EYAHTNVPGSRHPKRWQDIDELLRAGIDVWTTLNIQHLESLNDVVQKISKVRVRET VPDKVFDQADEVVLVDFPPDELLKRLAEGKVYVQDTAARAVENFFKPQNLTALRE LAMRRAAERVDASLIERMQAQAIDGPWAAGERILACIGPDPVSPTVVRTAKRLADL MDAPWIAVTVERPGASLNSAARQRLDEVMKLAESLGAETQTLTGADLPAELLRFA KFENVTQIVVGRSRGGFFSELLRRSLPYELVRRTQDIAIHLVTRESDVSEPASGWL LHNRSPLRPLPFVYATLTVAAALAVSKVLTELMPIPNLSMVFMLSVLVSAINFGVWP AIYASVLSFFIYNFFFIPPLYNFTIAEPYELLALVIFLVVAIVTSAMAGRVRDQARVSA GRVRAMRRLYEFTRRLSGLATRDGIAEGAAGEIHASLARPVVVLLAEGDGLALTAA WPPEDALDTATMTAARWAYNHAEPAGADTGTLPIIPWYFVPLRIGDKALGVIGVA KDKDTPPLDSEARTLLDTLSEQTAAALERAALASEMVSARTATETERVRNTLLASV SHDFRTPLSSILGAATSLLSYGDKIGAAAKTDLLGQIKQETEGLDEMVRNLLAITRID SGALELRRDWIDLREIVERVASAARRRSAPQRIDITMPPDLPLVRADAALAEQAIGN VVANAIVHTSKETHIVIDAQSGLSDITVRVTDNGPGIGSDILPHVFNRFVRGNGADD VHDGGEGTGLGLAIARGIMEAHGGSITVDSPVEGQPGARFVMVFPREDGAT	323097	>tr|Q1QJ49|Q1QJ49_NITHX Histidine kinase OS=Nitrobacter hamburgensis (strain X14 / DSM 10229) GN=Nham_2991 PE=4 SV=1 MSGEPATRASPDALLALAKKEGRGHLKIFLGAAPGVGKTYAMLAAARSEIAGGRN VVVGLVETHGRRETDQMLDGFEVLARKPIVYRNQVMHEFDLDAARARKPGLLLVD EYAHTNVPGSRHPKRWQDIDELLRAGIDVWTTLNIQHLESLNDVVQKISKVRVRET VPDKVFDQADEVVLVDFPPDELLKRLAEGKVYVQDTAARAVENFFKPQNLTALRE LAMRRAAERVDASLIERMQAQAIDGPWAAGERILACIGPDPVSPTVVRTAKRLADL MDAPWIAVTVERPGASLNSAARQRLDEVMKLAESLGAETQTLTGADLPAELLRFA KFENVTQIVVGRSRGGFFSELLRRSLPYELVRRTQDIAIHLVTRESDVSEPASGWL LHNRSPLRPLPFVYATLTVAAALAVSKVLTELMPIPNLSMVFMLSVLVSAINFGVWP AIYASVLSFFIYNFFFIPPLYNFTIAEPYELLALVIFLVVAIVTSAMAGRVRDQARVSA GRVRAMRRLYEFTRRLSGLATRDGIAEGAAGEIHASLARPVVVLLAEGDGLALTAA WPPEDALDTATMTAARWAYNHAEPAGADTGTLPIIPWYFVPLRIGDKALGVIGVA KDKDTPPLDSEARTLLDTLSEQTAAALERAALASEMVSARTATETERVRNTLLASV SHDFRTPLSSILGAATSLLSYGDKIGAAAKTDLLGQIKQETEGLDEMVRNLLAITRID SGALELRRDWIDLREIVERVASAARRRSAPQRIDITMPPDLPLVRADAALAEQAIGN VVANAIVHTSKETHIVIDAQSGLSDITVRVTDNGPGIGSDILPHVFNRFVRGNGADD VHDGGEGTGLGLAIARGIMEAHGGSITVDSPVEGQPGARFVMVFPREDGAT	21~~KdpD (1.67569E-116) ~~231,253~~Usp (1.18621E-38) ~~375,414~~DUF4118 (4.27321E-15) ~~499,527~~GAF (0.0000000688941) ~~638,661~~HisKA (0.000000000178129) ~~727,781~~HATPase_c (9.00759E-25) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.8E-90	311.4	0.4	3.1E-90	310.6	0.3	1.4	1	R5FAQ5_9CLOT	Uncharacterized protein	BN723_02738	Clostridium bolteae CAG:59	664	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	1263064	>tr|R5FAQ5|R5FAQ5_9CLOT Uncharacterized protein OS=Clostridium bolteae CAG:59 GN=BN723_02738 PE=4 SV=1 MDGQRDERPDPELLLKQNFPRESDKARGRLKIFFGYAAGVGKTYAMLEAARQEK AAGRDVVAGYIEPHDRPDTMELLAGMELLTPMAVTYKGIILKEFDLDAALMRRPDLI LVDELAHTNAQGCRHKKRYQDVIELLDAGINVYTTVNVQHLESLHDIVASITHVRVY ERIPDDIFDDAGQVELVDIAPEELRQRLEDGKIYHKDQADKASVRFFTVENLSALRE IALRRTADRVNREVVRERDAAGKDYYTGEHVLVCLSPSPTNARVIRTAARMAGAF HADFTAVLVETADMKREHAKISRSMEANINLAKQFRANVITLYGDDIVQQIAGYAR RNGISKIVIGRTVRKRSFLHLKSTIIDRLIKAVPNMDVYVIPDAAARENGKIKKPENG RKYSMDILKTGLIMAGCTFLSMVLDHYKLGIINVAMIYMMGTMLAAYVTRAGTYGF LASVASVLLFNFFFTPPRYTFQADGSIYPFTFAAMLVCALITSSMAARLKREAEKSE AESGYMQILFGINRNLRKGTTREEILDICGRLVQSLLKRNIVIYDMLDGKMNRMKIY PASEREDASSLTSLFKNPDEMAVAAWVYKNHHKAGATTDTLPGARARYTPVYKD DTVYAVIGVEMKGGDIIKPNDKNVLNIIAEETSYRLKDMSGPRICR	25~~KdpD (1.4993E-117) ~~235,255~~Usp (4.43648E-38) ~~378,401~~DUF4118 (0.00000000000901618) ~~502,530~~GAF (0.000170915) ~~651	non-kinase	KdpD;Usp;DUF4118;GAF

	1.8E-90	311.4	0.3	1.8E-90	311.4	0.2	1.8	1	N8S5C4_ACIGI	Histidine kinase (EC 2.7.13.3)	F981_02738	Acinetobacter guillouiae CIP 63.46	880	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter guillouiae (Acinetobacter genomosp. 11), Acinetobacter guillouiae CIP 63.46	1217655	>tr|N8S5C4|N8S5C4_ACIGI Histidine kinase OS=Acinetobacter guillouiae CIP 63.46 GN=F981_02738 PE=4 SV=1 MSDYRNNKADVLLQHTQRYQSGRLTIFLGAAPGVGKTFAMLVRAHELALQGIDIVI GYVETHGRIETENLISGLVIIPRKTIEYQGHSLEEMDLDAVLASKPSIVLVDEFAHSN MPNSRHEKRWQDINELLDAGIDVFTTMNIQHLESLNDVVYQITGIRVTETVPDRVF ERIRDIRLIDLPVNELLERLNQGKVYVPEQAEQALQRFFNSSNLTALRELAMQTVA SHVDTDVRENFAIQGLVPIPLKNHILIMIEGNGQAEALVRAGCRIAENRQANWTVV VFSKDSKISEKQDNLSSREIERALNLTRQLGGMTEILYGQQHAKTLFDYVMDRGIS TLVLAQSHRKAFTFGVVNFVDQLLKYQPSFELSIVPILAEHRQQSFFQDTHSFLSL REMFYVLSTTMISIVIASLGEKYLGIEELSVIFITAVVFVASKTRMLAAVLSALLFFFA YNFFFISPKFTLQISAHQGVITVVAFLGAALISSRLASRLREQVTALKTANSYNSIMQ DLGQKLSTAIDLKQVQEIAENSLSKNLNAEIWFYFPESSISSLEVINNKEKISADWTF KNHQPSGRFTQTLTENDWWFLPLLASKQCFGVVGVKFLKNVSVLNTEQKQLTET MVEYIAQAISRTQLTKALEIANVSSETERLRSALLSSVSHDLRSPLASMIGAADTLS NYRHSMDEQDQDSLLEAIHLEGERLDRYIQNLLDMTRLGHEGLSLKRDWIGVDELI GSAVRRLKRYMPHSLVEVDLPEQTLSLFVHAALIEQAIFNVLENAAKFSPENKAVTI KVLQLNENEIEISISDQGLGIPEDERERIFDMFYTMERGDRGQYGTGLGLTIVKAIIG AHMGKISASSAKNNQGTCIRMQLPIQQIG	22~~KdpD (3.63144E-119) ~~229,250~~Usp (1.07956E-15) ~~374,X,651~~HisKA (0.00000000000698261) ~~717,770~~HATPase_c (2.96728E-22) ~~874	kinase	KdpD;Usp;X;HisKA;HATPase_c
	2.1E-90	311.2	0.1	3.7E-90	310.3	0.1	1.4	1	R7C3W0_9BURK	Histidine kinase (EC 2.7.13.3)	BN641_00699	Sutterella sp. CAG:397	907	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Sutterellaceae, Sutterella, environmental samples, Sutterella sp. CAG:397	1262976	>tr|R7C3W0|R7C3W0_9BURK Histidine kinase OS=Sutterella sp. CAG:397 GN=BN641_00699 PE=4 SV=1 MPDNASNTKTADQILKEVQKERRGKLKLFFGAAPGVGKTYAMLQEVQEKRAQGL DVLVGWVDTHARKDTEAMLAGLEVLPRKTIVHRGFKYQEFDIDEVLKRRPGLVVV DELAHSNAPGSRHPKRWQDVEELLDAGINVYTALNVQHLESLNNVVERMIGVTVN ETVPDRLFDEANEVRLVDLPPADLIARLKAGKVYLRQTIEAALGSFFKQGNLLALRE LSLKRMAERADAETNARRVLSQTPDLTTEGIVLWLGNASGAEELVRSCSRLSATQ QRNWHVVWYDDGTAGEKRRLEMMHCLALAEELGAATQVLSGFEEERAVCDYAR THGASTIAVSKAYMNFWRRRRLMNEAEDLRILEMTALPTETEKDTVQTTGLFAITE RDGWWQSCVVTAVVALILMWLEPYIKPANAVMVLLIPTLIISMRYGRAPGVLTALL SSAAFIVLFVEPPFSFAVDDPSYLIVPFVMLLVAAGTGTLFARLRRISDQANDRTAH MRMLFTLSRELGKSLMVEEVAEILEKHAFSDLGAKIELWSSGGTVSDVKRLTANIK NVDRAIVLWCVEHGDEAGRGTHTLPYSPYLYLPLRGQMRVHGVIVFSVDEPDRW LDPEMRRVATAVADLAALALERLHYIDVSQKTLVEMESDRFRHALIQELGDELQVP LSDLTEGAEALSAKLSVQNSPEAAEGRKLLSDVRRMSRLTGNLLEMSRLQSSGFE LEAKKTPIAELFEESLDEIAPSQRQQFHIVTNIAKDCPAEVSVDPALIRRLLVNLLDN AVKYCSAGCTIELSAEASAGNVLISVSDNGPGLPGGDVNRLFDPFKRGVKTGNGA VAGVGLGLAISRTIARVHGAQLIGKNNADGPGCTFTLILPLPEEEEAEEEAKEKETE KDGKPLVTAPAEVAADKA	21~~KdpD (5.20914E-114) ~~230,261~~Usp (0.00000000182837) ~~361,392~~DUF4118 (1.1472E-17) ~~487,556~~GAF (0.0000330077) ~~615,X,767~~HATPase_c (1.95256E-24) ~~871	dysfunctional kinase	KdpD;Usp;DUF4118;GAF;X;HATPase_c
	2.1E-90	311.2	0.1	3.5E-90	310.4	0.1	1.3	1	A0A023NTT4_9GAMM	Histidine kinase (EC 2.7.13.3)	CH75_16325	Dyella jiangningensis	888	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Dyella, Dyella jiangningensis	1379159	>tr|A0A023NTT4|A0A023NTT4_9GAMM Histidine kinase OS=Dyella jiangningensis GN=CH75_16325 PE=4 SV=1 MSEPSREARADALLDSVQEENGRRLKIFLGAAPGVGKTYAMLSAARELKRQGIDV VVGLVETHGRAETQALLEGLEMLPRRKVNYRGRDFTEFDLDAALQRRPAVILVDE LAHSNLPGGRHERRWQDIAELLDAGIEVYSALNVQHLESLNDQVRRITNVTVRETV PDAFLDRARDIVLVDLPPRELIQRLKQGKVYVPETAVAALDAFFSPTNLVALRELAV DTVAGHVDSDLREQMLARGGAMPVRRRVMAAIDGHSQSEYLVRIARRIAERRGA PWSVAFVDTGATLDKGRRERLDAAMRLARRLGGDTVVLRGHAIADELIAHADREG IGQIILGRTRERPLARMLGRSLTQLLLRRGAHLELTIIATPAERAKSRLRLRMPGGK GRRDEYVFATGATLAAFGLSFIADRYLSVANLALIFLMAVMVVAARTRMTVAVYTAI LCFLGYNFFFAPPRYTLAIANFDDVLAVCLFLVAALVCSRLATRLASQVESLRAAHA NARALLSLGQRLSTSTDAAGIRKVGVDALSHVLHCDAAILARDASQVLRVVATAPR DFSLTTQDLGAASWSEQHMEQAGRYTDTLNAAPCWVLPLGSADNPLGVAALRFP PEQGEPPVDERSLALAMVQDIGQALQRARLADELEGARVQGETERLRNALLSSVS HDLRSPLASMIGSAGTLASYGDQLPAGERRELLEAILGEGQRLDRYIQNLLDMTRL GHGTLKLNRDWTDVAEIVAASSNRLRKLFPDLRLDIALPSKTILLYVHPALIEQALFN ILENAARFSPPGEAVRIVVRPNGEKVQIDVIDRGPGIPEDERARIFDMFYSVSRGD RAPQGTGLGLAICRGMIGAHGGSVEALPGDGVGTTIRITLPLPAPPENNA	24~~KdpD (2.79196E-117) ~~230,250~~Usp (1.82502E-26) ~~371,395~~DUF4118 (0.00000000000192115) ~~494,529~~GAF (0.00427211) ~~640,657~~HisKA (0.00000000000562234) ~~723,776~~HATPase_c (2.09886E-27) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.1E-90	311.1	1	3.3E-90	310.5	0.7	1.3	1	B0JYA9_MICAN	Potassium-transporting P-type ATPase D chain	MAE_53250	Microcystis aeruginosa (strain NIES-843)	372	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Microcystis, Microcystis aeruginosa, Microcystis aeruginosa (strain NIES-843)	449447	>tr|B0JYA9|B0JYA9_MICAN Potassium-transporting P-type ATPase D chain OS=Microcystis aeruginosa (strain NIES-843) GN=MAE_53250 PE=4 SV=1 MRRGRHKIFIGMAPGVGKTYKMLEEGHSLRKQGTDVVIGLLETHGRKETAEKAG GLEIVPRKILEKEGFTLSEMDTEAIIARSPQLCLIDELAHTNAPSSEREKRFQDVEIIL SRGIDVYSTVNIQHIESLNDLVARITGVVVRERIPDRILEEADEVIVVDVTAETLEERL LAGKIYAPEKIEQSLNNFFQRRNLIALRELALREVADTVEEEASNSTKFIGQSCPVH ERVLVCISTYPNSLRLLRRGARIAGYMNAEFFVIFVDNPERFLTREEALHIETCERL CREFEGKFLRVKSYQVAAAIAEVAERERITQIVIGESLQSRWKHFIKGSFTQKLMR LIWQKNIDLHIIATDPKVPIKDARAKGVKR	1~~KdpD (5.71467E-123) ~~211,231~~Usp (6.14856E-35) ~~355	non-kinase	KdpD;Usp

	2.2E-90	311.1	2.8	3.5E-90	310.4	1.9	1.3	1	Q8A523_BACTN	FrrC, osmosensitive K+ channel histidine kinase	BT_2421	Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	377	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides thetaiotaomicron, Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	226186	>tr|Q8A523|Q8A523_BACTN FrrC, osmosensitive K+ channel histidine kinase OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) GN=BT_2421 PE=4 SV=1 MDMDREQSVQHFLDLIKKSHRGKFKIYIGMIAGVGKSYRMLQEAHELLENGVDVQI GYIETHGRAGTEALMQGLPVIPRRKIFYKGKELEEMDVDAIIRLHPEIVIVDELAHTN VEGSLNEKRWQDVMTLLDEGINVISAINIQHIESVNEEVQEITGIEVKERVPDSVLQ EADEVVNIDLTAEELISRLKAGKIYRPEKIQTALDNFFRTENILQLRELALKEVALRVE KKVENEVVMGVSVGIRHEKFMACISSHEKTPRRIIRKAARLATRYNTTFVALYVQT PRESMDRIDLASQRYLLNHFKLVAELGGEVIQVQSKDILGSIVKVCRDKQISSVCM GTPNLRFPHAICSILGYRKFLNNLSQANVDLIILA	19~~KdpD (4.88474E-127) ~~229,249~~Usp (7.6806E-29) ~~377	non-kinase	KdpD;Usp
	2.2E-90	311.1	0.2	1.1E-89	308.8	0	2	1	E1VQU2_9GAMM	Histidine kinase (EC 2.7.13.3)	kdpDHDN1F_36010	gamma proteobacterium HdN1	903	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, unclassified Gammaproteobacteria (miscellaneous), gamma proteobacterium HdN1	83406	>tr|E1VQU2|E1VQU2_9GAMM Histidine kinase OS=gamma proteobacterium HdN1 GN=kdpD PE=4 SV=1 MSSEQSIQANALLGEIRRQSGGRLTVFLGAAPGVGKTFAMLTRARELLRQGVDVV AGIIETHGRSETLALLDGLPVLPRKKLEYKGRWLEEMDLDGLLARRPAIALVDELAH SNVPGSRHEKRWQDVEELLDAGVDVYTTINVQHLESLNDVVHQITGVRVSETVPD VVFSRLRDIRLVDLPARELIERLNQGKVYLPEQASQALQAFFSPSNLTALRELAMQ TVAGHVDADLRETRMARGLENISIQHHVMIAIDGQGHSEYLVRAGARIAERRAAS WSVVTVETGRAAIATLQVNDLERAPRAHDPAARAEQQRLSEIDRAFALARNLGGE TEALHNTDVTQALLDAAAVRNAKTIVIGRTRERPIARLFNRTMTQQLLQRGARYEL TIISTPQMPARTRDWPLASHLRLPGRETLLILVASLGAVGIAAIAERYLDLQDLSLIFL VAVMLVASRTRMLAAAIAAVLCFLAYNFFFIEPRFTLLISAHRGVATVLLFLAAALIA GRLASQLRMQVVALSAANTHTTLLQKLGHGLASAADLGQVMTAGTAVLQNTLSA QAWIRIDATRIPADLTFTEKDLMAADWTLQHGRECGRYTDTLGNCPWWFLPLQT DGNSFGVIGLKFPESAGRPTFEQRRLAESMVTDIGQAALRTRLVSELEAARVGGE TERLKVALLSSVSHDLRSPLSSIIGSADSLVCYGKDMSEEDRQSLLEAIRLEGERLD RYIQNLLDMTRLGHEGMTLVRDWIGVDELVGSASRRLQRYQPEVRIECSIPEDLP PIHVHPALIEQALFNVMENAARFSPRDEPVIVNVSGEPGAHLQIRISDAGPGIPEAE RSRIFDMFYSVERGDRGTQGTGLGLTIVQGIIGAHMGSVEALPGPDGRGTTIRLTL PWGHFPHRS	22~~KdpD (1.23489E-121) ~~229,250~~Usp (2.00488E-26) ~~393,418~~DUF4118 (0.00000232402) ~~483,X,671~~HisKA (0.000000000417354) ~~737,790~~HATPase_c (2.54308E-22) ~~894	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2.2E-90	311.1	0.3	4.6E-90	310.1	0.1	1.6	1	A0A068NN19_9BACT	Histidine kinase (EC 2.7.13.3)	OP10G_0757	Fimbriimonas ginsengisoli Gsoil 348	879	cellular organisms, Bacteria, Armatimonadetes, Fimbriimonadia, Fimbriimonadales, Fimbriimonadaceae, Fimbriimonas, Fimbriimonas ginsengisoli, Fimbriimonas ginsengisoli Gsoil 348	661478	>tr|A0A068NN19|A0A068NN19_9BACT Histidine kinase OS=Fimbriimonas ginsengisoli Gsoil 348 GN=OP10G_0757 PE=4 SV=1 MLRIAQREMTERTRGRLKIFLGMSAGVGKTYAMLSEAHEQIARGIDLVVGYAETH GRKETEALLVGLPSLPLREVEHRGILLKEFDIDEALRRRPRLLVVDELPHTNAPGSR HLKRYQDVEELLAAGIDVHTAINIQHVESLRDVVASMTGVFVQETVPDTFIDAADEI ELVDIPPDELRQRVQEGKVYVPAQTERALEGFFCRGNLLALRELALRRAADRVDA EIQSFRRADASPGSMGSRQRILVCVAPNRLGERVIRAAARYGTAMHAQVLAISVIS DRQTNRSDEDRDRAERAMRLAEALGMETLSRSGHDIVAEILTVARQRGAGLIIVGK PIRSRWHELVRGSVVDDLVRRSGDIDVHVITGESETPSERPTPIQVADARPEEYAA SVLAVAATTALCFLLSPWVHLSNLIMLYLLAVGLVSTRVGRGPSLLSAILSVAAFDF FFVSPRYTFAVSDVEFLPTFVVMFAVSVILSGLNSRFRRQAADAASRERRTSALYE VSRDMAASRTKQEIAEAAARRIGDEFDTDVAVLLPDARSMLTVVVPSVTSFEADD SEMAVAQWAFEHGKPAGAGTDTLPGSAAMYLPLRASRGSVGALALSPRSKSEAL TLAQRTLLETFATGLAVALERTLLAKESHEARLQAESEKMRNALLSSISHDLRTPLT AIAGAASAMRERGGAEQELAETIYEESMRLNLQVQNLLDMTRLNSGEIRPNVEWQ SLEELIAAALDRTRVVLSDRPVEIHIPSDLPLLELDGALMEKVFANLFENAAVHAQG NSPIEVSAWAGDETVYVEVSDRGPGIPVGSEATIFERFQRPKRDGDGGRFGLGL AICRAIVRLHGGRIWAKNRTGGGSTFVIELPKPDRAPEVPVG	14~~KdpD (2.41379E-105) ~~206,244~~Usp (9.65402E-34) ~~367,390~~DUF4118 (1.21375E-22) ~~489,517~~GAF (2.38162E-14) ~~635,652~~HisKA (0.00000000000346717) ~~713,766~~HATPase_c (3.36347E-29) ~~867	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.3E-90	311	2.2	3.1E-90	310.6	1.5	1.2	1	R7JDL5_9PORP	Osmosensitive K+ channel His kinase sensor domain protein	BN646_01831	Parabacteroides sp. CAG:409	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides sp. CAG:409	1262913	>tr|R7JDL5|R7JDL5_9PORP Osmosensitive K+ channel His kinase sensor domain protein OS=Parabacteroides sp. CAG:409 GN=BN646_01831 PE=4 SV=1 MANREESVRHFLNLIKRSQRGAFKIYIGMIAGVGKTYKMLQEAHEMLDNGIDVQIG YVETHGRASTEAQLKGLPVIPRKKIFYKGKELEEMDLDAILQLHPELVIVDELAHTN VDGCRNEKRWQDVMDLLEAGINVISAVNIQHIESLNEDIKGIAGIEVKERIPDKVLEE ADEVVNIDLTAEELINRLKAGKIYKTEKIQTALSNFFKTENILQLRELALKEVAFRVEK KVETEVIPEEKAVHRELYLACISSNAKTPRHIIRRTARLASRYNTDFMALYVQTPSE SPDRINLSVQRHLLNHFKLVTELGGELIQVASPDIIQAIIDVCHERHITTVCIGQPTLN WSKIFKIHRYGYFLKNLSAMDIKLIIFPQ	18~~KdpD (4.56377E-124) ~~228,249~~Usp (2.90379E-29) ~~371	non-kinase	KdpD;Usp

	2.4E-90	311	1.6	3.2E-90	310.6	1.1	1.2	1	Q8YPF2_NOSS1	Potassium-dependent ATPase subunit D	all4242	Nostoc sp. (strain PCC 7120 / UTEX 2576)	377	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	103690	>tr|Q8YPF2|Q8YPF2_NOSS1 Potassium-dependent ATPase subunit D OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=all4242 PE=4 SV=1 MYPVKRGKHKIFIGMAPGVGKTYRMLEEAQALKQEGIDVVIGLLETHGRKETADK AAGLEVVPRQQIARGGLTLTEMDTDAILKRCLSTSRYGSTPQLVLVDELAHTNVPG SPREKRYEDVEIILAAGIDVYSTMNVQHLESLNDVVAKITGVVVRERVPDRILKEAD EVVVVDVTPETLQERLIEGKIYAPQKIQQSLDNFFQRRNLIALRELALREVADNVEE EAIPGVNASTANGQFCNIHERVLVCISTYPQSVQLLRRGARLANYMNAPLYVVFVA NPEQFLTKEESLHIDTCEKLCKEFAGTFIRVTSGDIGKAIAQVAEQYRITQIVIGESQ RSRWQILLKGSLTHKLVRLLKNIDLHIIATEKTPSAKR	5~~KdpD (7.48427E-124) ~~223,246~~Usp (3.34889E-48) ~~368	non-kinase	KdpD;Usp

	2.5E-90	310.9	0	4E-89	307	0	2.5	1	D1CGX0_THET1	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Tter_2088	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	384	cellular organisms, Bacteria, unclassified Bacteria, Thermobaculum, Thermobaculum terrenum, Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	525904	>tr|D1CGX0|D1CGX0_THET1 Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Thermobaculum terrenum (strain ATCC BAA-798 / YNP1) GN=Tter_2088 PE=4 SV=1 MEERRPSAEEMLERVRRQAGSGSRGRLKIYLGMAAGVGKTYAALMELHRRKSR GTDCVVGWVETHGRPKTLEALRGLEVVPPRRCEYKGRMVEEMDTEAIIRRRPAV ALVDELAHTNVPGCARHEKRWQEVQDILDHGITVISTLNVQHIESFADLVEDITGSP VRERVPDWVVDQADELELVDMSPHSLRQRIRHGNVYPPEQVEAALRGFFREGNL SALRELALRKMAERAEQDLEAYMRQHDIEQIWPVGDKVLVAIDAHPRSRILIQRG WRRAQRYGTDLLVAFVETPAWARASPEARRQLAQLLQYAEDLGAKCLRSQGQDI AAQLLELAKEHNVGTVVLGRPRGSRWRHLLRGSVPERLLWKAKDIDLIIVADQAE QD	22~~KdpD (2.2724E-113) ~~232,255~~Usp (6.62116E-34) ~~378	non-kinase	KdpD;Usp
	2.5E-90	310.9	0.4	2.5E-90	310.9	0.3	1.8	1	N8ZKG9_9GAMM	Histidine kinase (EC 2.7.13.3)	F960_01562	Acinetobacter gerneri DSM 14967 = CIP 107464	888	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter gerneri, Acinetobacter gerneri DSM 14967 = CIP 107464	1120926	>tr|N8ZKG9|N8ZKG9_9GAMM Histidine kinase OS=Acinetobacter gerneri DSM 14967 = CIP 107464 GN=F960_01562 PE=4 SV=1 MSENRDNKADVLLQHTKRYQSGRLTIFLGAAPGVGKTYAMLVRAHDLFQQGVDIV IAYVETHGRAETDHLVDGLPIIARKMVSYQGHQLQEMDLDAVLEKKPHIVLVDEFA HTNMPGSRHEKRWQDINELLDAGIDVFTTMNIQHLESLNDVVLQITGVRVLETVPD RVFERIRDIRLIDLPVNELIERLNQGKVYVPEQASHALKGFFTPSNLTALRELAMQT VASHVDSDVRENFAIQGIAPIPLKNHILVLIEAKGKAEALVRAGCRLAENRLATWTV VAFFKDNATSDALKLDEHSREIETALNLARQLGGMTEILYGEKHAKVLSEYAIERGI STIVLAQQNESILQKYFQPSLIDHLLKNHPKFELSIVPIQENHQVKSKHLNKRYLLSL SETLFVLLITICSIAIASLSEKYLGISEISIIFITAVVFIASKTRMMAATTAAILLFLSYDFF FILPKFTFDISAPKGFITIVAFLAAALIASRLASRLKEQVNALKAANRYNSIMQDLSQK LSVAANLEQVLDIALNQLSQNLKAKIWFNLAENAPYLEQINHHTLSQKEKISADWTF KNSQPSGKFTQTLTENEWWFLPLLASKQCLGVVGIKFEYSISQMTLEQKRLAEAM IENIAQAISRTQLTQDLELAKVSSETEKLRSALLSSVSHDLRSPLASMIGAADTLSNY RHNMNQQDQDDLLQAIHLEGERLDRYIQNLLDMTRLGHEGLTLRRDWIGVDELVG SAVRRLKRYLPKIKVNVKFSEANLSLFVHAALIEQAIFNVLENAAKFSPEDEAVELD VEKLNDQQIQISITDQGQGIPEDERNRIFDMFYTMQRGDRGQYGTGLGLTIVKAIIG AHMGQISASSGRQQKGTCIRIVLPIQQMISA	22~~KdpD (3.58707E-120) ~~229,250~~Usp (2.37184E-19) ~~376,399~~DUF4118 (0.00000000348473) ~~498,524~~GAF (0.000318654) ~~640,657~~HisKA (0.0000000000254543) ~~723,776~~HATPase_c (2.22521E-23) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.6E-90	310.9	2.3	3.4E-90	310.5	1.6	1.1	1	F2IFU5_FLUTR	Osmosensitive K channel His kinase sensor	Fluta_0548	Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Cryomorphaceae, Fluviicola, Fluviicola taffensis, Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	755732	>tr|F2IFU5|F2IFU5_FLUTR Osmosensitive K channel His kinase sensor OS=Fluviicola taffensis (strain DSM 16823 / RW262 / RW262) GN=Fluta_0548 PE=4 SV=1 MTEKENNVQHFLDLIKRSRRGKFKIYIGMSAGVGKTYRMLQESHALLKSGIDVKIG YIETHDREETQSLLDGLPIIPRKHVFYKGKDVEEMDLQAIINLRPEVVIVDELAHTNIE GSKNKKRWQDILDILEAGINVISAVNIQHIESLNTQIRQITGIEVEERIPDSVLQMADE VVNIDLTSDELITRLKEGKVYKADKIQRALSNFFRSENILQLRELALKEVASQVERKV EIEVPSNVSFRHEKLLACISSNEKTAKKVIRKTARLSRYYNSKWFVLYVQIPAENND KIPLDKQRHLINNFKLATELGAEVIRLEAKNVTDGIMQVAEEKKITTLCIGKPHFNLL KIILATSIFNKLLTKLVASDIDLVILS	18~~KdpD (1.55641E-120) ~~228,246~~Usp (1.3562E-30) ~~374	non-kinase	KdpD;Usp
	2.6E-90	310.8	0.9	4.8E-90	310	0.6	1.5	1	Q187D8_PEPD6	Histidine kinase (EC 2.7.13.3)	kdpD CD630_18290	Peptoclostridium difficile (strain 630) (Clostridium difficile)	900	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptoclostridium, Peptoclostridium difficile (Clostridium difficile), Peptoclostridium difficile (strain 630) (Clostridium difficile)	272563	>tr|Q187D8|Q187D8_PEPD6 Histidine kinase OS=Peptoclostridium difficile (strain 630) GN=kdpD PE=4 SV=1 MDRPNPDILLEKIKNEEEKLSRGQLKIFFGYAAGVGKTYSMLESAQNLKKVGVDVV VGYIEPHTRPETLALLDGLEILPVKEIEYKSIKLKEFDLDAALERKPEVILVDEFAHSN VAGLRHTKRWQDIEELLLAGINVYTTVNVQHLESLNDIVEIITNVSVKETIPDKFLDT NTQLELIDVEPDVLLERFNEGKIYKKEQATRAKNNFFIKDNLVALREIALRKTAERV NKEVQMTRLSKGDVTVIPTSDTLLACISPSPSSAKVIRTASRISDSTFAKWIALYVET PNTARLPFDEQKQLQNNLKLAKKLGGEIIVLHGENIIEQILRIAKLRNVTKIVIGRNHS SNKRFSKRFKKDIVDKLIDEVDYIDIHIIPYKFASDVKYKTKKDKSSIKSKFKISKVDFI KLIFITLMISILAYAVQSMGFIRENILLIYMLGVVLVSMWTKGYSTGIISSVFNIVLLNY FFTAPLYTLSIADSNYIVTLVVFSIVGIITSTLTSKIQHEAETAAKREENTKMIYQIIKG FLRLSNKDDIVNKGIELLSLSLSRDVICYLNVDKHNKSKLYKKNTNNKDKNDLDSED EKAVASWVLSNSTVAGNDTDTLPGSKGYYIPIVGMNLTLGVVGISCIDSKLDTEDIS LIETIIAQMAIALDREILSEAKENTNLEIERERLRSNLLRAVSHDLRTPLAGISGAVSTI IKNKGTIGQDIIDELLSGVYEDTQWLIRLVENLLSMTKIDEGKLEVKKHSELVEEIISE ALQKIKKRIENALIDINIPEQILFVPMDAKLIEQVLINLIDNSLKYSKEDCKIEINVYEKD DYVWFEVSDNGPGISKELKKHIFDRFFTGEEGAKDSRKGVGLGLSICKSIIQAHKG EIMVENNKDKGSTFKFSLPKENE	22~~KdpD (1.14233E-108) ~~230,253~~Usp (6.18197E-42) ~~377,406~~DUF4118 (1.31302E-16) ~~505,533~~GAF (0.0000126306) ~~656,673~~HisKA (0.0000000227628) ~~739,792~~HATPase_c (1.10753E-29) ~~895	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.7E-90	310.8	0	4.5E-90	310.1	0	1.3	1	E3GLH5_EUBLK	Histidine kinase (EC 2.7.13.3)	ELI_1562	Eubacterium limosum (strain KIST612)	907	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium limosum, Eubacterium limosum (strain KIST612)	903814	>tr|E3GLH5|E3GLH5_EUBLK Histidine kinase OS=Eubacterium limosum (strain KIST612) GN=ELI_1562 PE=4 SV=1 MDFQDERPNPERLLKEINEEERRSREDEEGIGHLKIFFGYCAGVGKTYAMLEEAQ QLYKKGVDVLVGYVEPHTRPETMAMLEGLPAIPPQVVDYKGITLRDFDLDKALEKK PKVIIVDEFAHTNPEGFRNKKRYQDIEELLNAGIDVYTTVNVQHIESLNDVVGSITGII VHERVPDYVFDKADKIKLVDIDPEELLKRFEEGKVYAPEKADLAKRRFFTVENLNAL REIAMRKAADRIVSGAGNKKKKVPFSKMLVCVGPSPSSAHCIRTTARIADAFHIPW VALYVKTSDRTYADISERKNLQDNMNLAEQLGAEIVTMQGDDMAMVISEYIKQSGI TNVVIGKGRNKPNPFKEDLEDQLLSMNPGIEIHIVPDSQAEKTSGGIPKKRLSWLS KRILSLHFSLKDFGKTVLTLVLATAISFGLRELNLGDQNIIMVYLLSILVISRLTVGYLY GICASVFGVLLFNFFFTEPYFTFNATNPTYPVTFIVMLLVALMTSALTNGIKVQAKM AVMNERRTEILYELSKKLLITRGLENIVTLTNESLTSIFERSVIFYTQNPDEKNRGTF MQGPEETSGAFMQSKEEEAVAHWVFQNKKAAGNGTDTLVGAKGFYMPVVSQG RVLGVIGISCVEEMLPPKRRAFLKMIVSQVAMALERQRLSDEQGKARLETEKEKM RSNFLRAISHDLRTPLTGILGSSSALLENIGELDISTQKKLLRDIKDDSEWIIRMVENL LSVTRIGEGKVDLKKHPEAVEEIVGEAVAIIRKRFDHTDIKVEVPDTLLMVSMDGTLI EQVMINLMENAIKYAGSHPVLDVKVQNLGKKARFIVGDNGEGISETMLPHIFEGYM GDEEKSSDSRRGMGIGLTICKSIVDAHGGTLKARNKQEGGAEFSFELPVEEDDNN ES	32~~KdpD (9.79353E-117) ~~239,254~~Usp (1.22663E-37) ~~375,411~~DUF4118 (1.98482E-18) ~~509,536~~GAF (0.000000144342) ~~658,675~~HisKA (5.04448E-14) ~~741,794~~HATPase_c (1.14503E-23) ~~897	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.7E-90	310.8	0	4.9E-90	309.9	0	1.4	1	C1D7X3_LARHH	Histidine kinase (EC 2.7.13.3)	kdpD LHK_01575	Laribacter hongkongensis (strain HLHK9)	877	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Laribacter, Laribacter hongkongensis, Laribacter hongkongensis (strain HLHK9)	557598	>tr|C1D7X3|C1D7X3_LARHH Histidine kinase OS=Laribacter hongkongensis (strain HLHK9) GN=kdpD PE=4 SV=1 MDDLRPDPDRLLAALQADEQRAARGKLTIFFGACAGVGKTFAMLQALRQQREAG CEGLVGIVETHGRQETARLLEGLPMLPSRRVAYRGHDLAEFDLDAALALHPPLIVV DELAHSNVEGSRHRKRWQDVAELLAAGIDVYTALNVQHLESLNDIVAGITGIPVRE TVPDRVFDEADEVRLVDLPPDELLSRLAAGKVYLPDAAERARQHFFRKGNLIALRE LALRRTADRVDAQMRAYRADRDIQPVWEARDRLLVCVGGEGGDRLVREAARLAA RLQTDWIAVHVDAPRGGRRVREEALQALKLAASLGAEITTLSGGQVEEVLAAYAR SRNATKLLCGVRPQSGRRWRWQRALPERIVARHPDLDVILVSSGEAARTAPRIW HPGRPVWRDYGWATLACAATTVLSALLLQVFAPANVIMLLLLTVVLVAIRWGRGP GAWAALLAVGCFDFFFVPPYWSFTVNDTQYLFTFVLMLGVALLIGQLAASLRQAA DIAQLREFRAKALARLARELSGALQTEQIVSIATEQLEPLLTVRIAVLLPDAHETLKA VGALPVDREVAQWVYDNQQEAGAGTQTLSATDIRYVPLKAPMRTRGVLALQLTD SRMPDEPEWRHLLDGCCAQIALALERVHYVEVAQDALVSMEGERMRNTLLSAVS HDLRTPITAIAGLAGTLEKKLADPAQQELAHAIHGEATQMNRLVSNLLDMARLQSG GVKLRLDWQSLEEVVGSALGQLRPVLARHPVQVALPAELPLLEFDALLIERVLVNL LDNAAKYTPVGSGIRISARLDNGWLRLRVDDEGPGLPEPAESLFQPFVRGVRESA TSGAGLGLALCRLIVEAHGGTIATENRHEGGARFVVALPVKTAVPEEIE	22~~KdpD (1.91906E-115) ~~232,254~~Usp (1.18538E-28) ~~373,395~~DUF4118 (7.83815E-14) ~~494,521~~GAF (0.0000000302988) ~~633,650~~HisKA (0.000000000000146149) ~~713,766~~HATPase_c (9.19811E-29) ~~866	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3E-90	310.6	0.9	5.8E-90	309.7	0.6	1.5	1	X2GN40_9BACI	Histidine kinase (EC 2.7.13.3)	T479_15025	Lysinibacillus varians	901	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus varians	1145276	>tr|X2GN40|X2GN40_9BACI Histidine kinase OS=Lysinibacillus varians GN=T479_15025 PE=4 SV=1 MEKMRPTPEELLTRFHQEQTTVGRLKIFIGYAAGVGKTYAMLDAAHLAKKLGKDV VIGYIEPHPRPETLALLDGLEQIPTRTIHYKGRTFQELDIDAVLERKPEIVLIDELAHS NVPVMRHTKRFGDVEELLAKGIHVYTTVNIQHIESLHDVVEEITGVKVRERIPDYLID QAALIKIVDIEPDELIQRLIEGKIYSKQQAEKALASFFRKQNLVALREIALRRTADTIN YKQINDSESIRQTTQIEEHILVGISSSPTNAKVIRTAARLAQALHGKFTALYVQKVKE GDDNDANSERLQQHIKLTEQLGGHVVIVQENDVAAALANYAQMSGVTKLVLGRTV MKKKWWQPNAKIIDRLNDYVPNLAIHIVPDQENEQFYFPDLRNRLTFEWLDLLKM SVVFSLASCLALFFFTMGVSESNIITIYILSVLILAIWSSGWLMTIISSAVAVLLFNFLF TEPRFSLEAYHRDYPMTFMIMFFSGIITSSLTKKIKEQAIVAVRKSYRMEVLLETNR KLQHAKSIEDIITEGMSQIVKLVEKPVQFFEIENNMIAKSVFFPTPTLSNTENTKVAT LFKNTNELGVVHWVINNNHFAGVSTDIFPEVNGYYLPVLSSGSVKGVVGIALSKQT PLPAFERHILNAIMNDFSFALDKWYLQNLNEKVAREAELEQMRANLLRAISHDLRT PLTTISGNADILLTNTVQIPDIEKTRLYEDIYKNSRWLVQMVENLLAVSMLEDGQFA LEMQLELVEDIIQEALLHVIPRNNTHHISYHVEPELVMALMDARLIIQVLINIINNALTY TPAGSDISFIAKEEGEYVHFSIADNGPGIDDSLKEKLFEPFITGKVQRSDSRRGLGL GLALCQTILTLHDSKLVVEDNYPNGTIFRFTLKKGVVSIDE	23~~KdpD (4.31217E-115) ~~230,250~~Usp (1.73757E-34) ~~373,396~~DUF4118 (0.000000000000930365) ~~497,X,670~~HisKA (0.000000000597273) ~~735,789~~HATPase_c (9.41947E-25) ~~892	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.9E-90	310.3	0.3	6.7E-90	309.5	0.2	1.4	1	A0A0D5LS15_9RHIZ	Histidine kinase (EC 2.7.13.3)	TM49_16175	Martelella endophytica	888	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	1486262	>tr|A0A0D5LS15|A0A0D5LS15_9RHIZ Histidine kinase OS=Martelella endophytica GN=TM49_16175 PE=4 SV=1 MPEQTRPDPEALLPAAKREGRGRLKIFLGAAPGVGKTYAMLDAAARLARSGTHVL VGLVETHGRAETEAMLHDLTVLPRRPFFHNGRILHELDVDALIAARPDLALIDELAH SNLSDSRHQKRWQDVEDVLAAGIDVFTTLNVQHVETLNDMVARITGVRVRETVPN RILAEADEIELIDLPPDELIERLRAGKVYVEDQAARAVANFFAKGNLTALRELALRTA ADRIDRQLQEHMAAHAIAGPWPTQERIMVVMPQEASGQDVIRAGKRAADRARVE WLALGISRLREGRPSAGGANTLRLAEQLGARISLLEVEDDGATEVIARAGRENVR RILMPRPRRRTLFARLMRPSLHERLYDGLLRKAGDFELTLVSEEAVASPAKAEPVR VSEPFSLRQIAIVTGALGVTTGIAALLRPVFPITSLSLLFMTVVVAVAARMGRKPALV AAGLSFLCFNFFFTEPLYTLRIWDQTQFLTLVLLVISSMLTGNLAARLRERVIAQKA AAERTAKLYEFSRRAAAAASFGDVVWAAVSHVSAVLGGHAVLLAPVGNGRLDIVG SSPAEDHLPAREMTAARYSFEHGEPTGRGSSTLPAVDWLFLPLVASDRCIGVLGV RSEDGNAALAGERGLAEALADQVALALERIRLSEDLAQTRVSSEAERLRTALLSSV SHDLRTPLVSILGAAESLENPGLTDHARGILTETIRDEGERLDRYIQNLLDMTRLGH GALKLRTSATDLRELAGAARRRLGGPLRDHPLEIGIAEDLPAADIDPLLIEQVLINILD NAAKYSGIGSAIYLGADLTGNAITVWIEDDGPGFPPEAMHHVFDMFWRAEQGDG MPMGAGLGLAICRGIVEAHGGTISAGAAHARGRGARIEFTVPLAGRS	19~~KdpD (2.58061E-112) ~~229,251~~Usp (1.09983E-14) ~~376,399~~DUF4118 (5.01557E-14) ~~499,528~~GAF (0.00000000000190374) ~~644,661~~HisKA (0.000000000000352998) ~~725,778~~HATPase_c (2.13244E-22) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.3E-90	310.1	0	7.1E-90	309.4	0	1.4	1	W0HXN9_9ENTR	Histidine kinase (EC 2.7.13.3)	kdpD Sant_3534	Sodalis praecaptivus	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Sodalis (tsetse S-endosymbionts), Sodalis praecaptivus	1239307	>tr|W0HXN9|W0HXN9_9ENTR Histidine kinase OS=Sodalis praecaptivus GN=kdpD PE=4 SV=1 MTDEPLRPDPDVLLAQADNDGRGKLKIYFGACAGVGKTWAMLQEARRLRAQGLD VVAGVVETHGRQETAALLEGLEMLKPRATGRRRHQAFDLDAALARRPAVILMDEL AHSNAPGARHPKRWQDIEELLEAGIDVLTTVNVQHLESLNDVVSGVTGVRVRETV PDPFFDAAAEVVLVDLPPDDLLVRLKQGKVYVGDRAERAIENFFRKGNLFALRELA LRRTADRVDGQMRAWRDARGREEKVWHTRDAVLLCIGASTGSEKLVRTAARLAA KLGSEWHAVTVETPTLYRRGEARRRATLRTLQLAQKMGAVTATLSDPDEAKAVL RYAREHNLGKIILGRPPQRRWRFANRFHRRLSRLGPDVDLLIVALDDVPDTSLARA EDGRGMGNGWRQNMRGALAAAALCALITLVCQWLPGVSPINLVMIYLLGVVLIAIV FGRLPSVAAALLNIVAFDLFFVAPAGSFAVSDAEYLVTFTVMLAVGLLTGNLTAGV RYQARVARHREQRARYLYEMADGLSRVRRPEAIAHICQRVVSAALLARCEIWLPD RQGELQGPAQSMMHTVPDAAIVKWSFDKGQVAGAGTDTLPGVPYKILPLTSSGR TLGLLIIEPSNVRHLMIPEQQRLLETFLVLIAGALERLELTRREQLSRLAAEREELRN SLLAALSHDLRTPLTVLFGQAEILMLNLSAEGSRYVHQADELRRQTLSTIRLVNNML DMARIEADGFRPQTDWIALEEIIGSALKSLEGVVSARHVRLDLPREMILLRADGPLL ERVFVNLLENAQKYAGQGAEIGIRAEKRTDTLTITVWDNGPGLPVGKENQLFDKF TRGHQESAIPGVGMGLAICRAIVEMHQGEIYAANRPSGGACFTIILPLPPAPALEEP LQEDA	21~~KdpD (1.1147E-117) ~~228,252~~Usp (1.01327E-34) ~~372,411~~DUF4118 (1.67777E-18) ~~499,527~~GAF (0.000000000042235) ~~642,659~~HisKA (0.00000000314452) ~~724,777~~HATPase_c (1.24907E-29) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4.4E-90	310.1	1.8	5.9E-90	309.7	1.3	1.2	1	R5I937_9PORP	Osmosensitive K+ channel His kinase sensor domain protein	BN472_02765	Tannerella sp. CAG:118	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:118	1262978	>tr|R5I937|R5I937_9PORP Osmosensitive K+ channel His kinase sensor domain protein OS=Tannerella sp. CAG:118 GN=BN472_02765 PE=4 SV=1 MNNEESVQHFLELIKKSRRGKFKIYIGMIAGVGKSYRMLQEAHDLLDNGVDVQIGY IETHKRAGTEALLEGLPIIPRKKIFYKGKELEEMDLEAILRIHPEIVIVDELAHTNVEGS ANKKRWQDVMALLDAGINVISAVNIQHIESLNEEVQGISGIEVKERIPDSVLQEADE VVNIDLTAEELINRLKAGKIYKPEKIATALNNFFKTENILQLRELALKEVALRVEKKVE NEVVISNVGVRHEKFLACISSNEKTPRKIIRKTARLATRYNASFVALYVQTPQESPD RISLASQRHLINHFKLVTELGGEVVQVQSPHVTESIIKVCKEKQITTICMGQPAFKLP QAYIKIHYYKKFIHFLAQANIDLLILA	17~~KdpD (5.67491E-128) ~~227,246~~Usp (1.11426E-28) ~~374	non-kinase	KdpD;Usp

	4.4E-90	310.1	0.5	8.6E-90	309.2	0.3	1.5	1	R6N6Z4_9FIRM	Sensor histidine kinase KdpD	BN627_01443	Lachnospiraceae bacterium CAG:364	675	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	1262983	>tr|R6N6Z4|R6N6Z4_9FIRM Sensor histidine kinase KdpD OS=Lachnospiraceae bacterium CAG:364 GN=BN627_01443 PE=4 SV=1 MSSDRSTPEEILKRIQAEEKQKENEKRGKLYIFLGYAAGVGKTCAMLDTAQELKKK GIDVVAGYIEPHARWETSMREKGLEKIPPLMVPYKGIELREFNLDAALKRKPQILLV DELAHTNANGLRHKKRYEDIEELLDAGIDVYTTVNIQHLESLNDIVENITKIHVKERIP DGVFDEAEQVKLIDIEPDLLITRLKEGKIYKTVQAERALQNFFAKEKLIALREIALRR MADKVNQIAQQERLLSEKQEEGEGYQGEHILTCISTAPSCERVIRSASRMAYAFH ARFTALYVETTRLQNADASVKKIRDDNLHLAEMLGAKIVTVFGDDVAFQIAEYARV SGVTKLVLGRTNHKILFGQKKGNITDEISEYSPNLDIFIIPDMGHTGKKKYFLFSPTN SEKRKKTEKLGADILKEAFMLGIATAVGLLFQKLGFLNADIIMVYLLGILLLSLYTARR YIAVSSAVFSVLLFDWFFVEPFYSFNFYSGKYSATFGIMLLFSIIISAIISTEKHQAKE SAKMMYRTELLLDNSRRMRRVESVKELLTELSDKVLKLMNLSVVFYVQKEGKLTG PWLFPKPGISKAELGKTVDTKEKAVVDWVMTNRKRAGCCTHTLPEANAIYLPIKTS DEIYGVMGIVLEEKREIPPFEYGLLTAMLNEAALVFARLIYGRKEKP	>~~KdpD (1.98856E-116) ~~235,259~~Usp (7.59823E-33) ~~382,417~~DUF4118 (0.00000235999) ~~499,540~~GAF (0.000000646184) ~~666	non-kinase	KdpD;Usp;DUF4118;GAF

	4.8E-90	310	0.2	1E-89	308.9	0.1	1.6	1	D7B4M1_NOCDD	Histidine kinase (EC 2.7.13.3)	Ndas_1632	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	844	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	446468	>tr|D7B4M1|D7B4M1_NOCDD Histidine kinase OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_1632 PE=4 SV=1 MTRGHLRVYLGAAPGVGKTYRMLDEAHRRRDRGADVVIGFVESHGRAMTEAMV DDLETIPRAVLTHRGARLEEMDLDAVLARRPQVVLVDDLAHANAPGARNARRWQ DIEALLEAGITVLSTLDVQHLESLNDVVERVTGTRQSETVPDAWVRGADQIELVDM TPEALRRRLAHGNVYGPDRIDAALGHRFRADTLTALRELALLWLAGRVDDELRRH RGEHRAASAWQTRERVVVGLSGGPGGEALIRRAARIAGRGRGVELLAVHVALGD GPVGADPALLARQRVLVEDLGGTYHQVLGEDVPAALTAFAQGVDATQLVLGASG RGRLARLLRPGVGAATAALSESIDVHLVTLEEAERGSGRARSGAVSRRRRLAGYA LALTALALLVFGTGVPHSEEYLSGGILLVFATVTATALVGGLWPALAAAFSGFVVLN LFFTEPYETLVVNQPGNLLTLVVFVFVAVAVSVVVDKAARRTREAARASAEAQTLA TVAGSVLRGSRPLEALLERLRETFSLESVALLERRPQASSRPDHRNDPGAWEAVA SVGELPHSAPGGADVDVPVDEGLTLVLHGHRPRAGERRIIEAFAAQAAVALRQER LAQEAAAAGTLAEADRMRTALLAAVSHDLRAPLASAKASVTSLRSREVRFSEEVQ AELLATADESLDRLTRLVTDLLDMSRLQAGVLGVTVTGLSLRESVFAVLDDLGEQG RAVRVRVPEELPEVAADPGLLERVLANVVGNALRFSPHDRPPSVTASWTGDQVE LLVADHGPGVPEHERERMFVPFQRLGDTDAATGLGLGLALARGLMEAMGGSLLP ETTPGGGLTLRLVLPVAGAAG	3~~KdpD (5.09907E-105) ~~211,233~~Usp (6.44538E-23) ~~355,391~~DUF4118 (0.00184372) ~~461,X,619~~HisKA (0.0000000000166307) ~~685,736~~HATPase_c (1.12498E-23) ~~837	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	5.2E-90	309.9	0.1	8.1E-90	309.2	0.1	1.3	1	S5YHT4_PARAH	Histidine kinase (EC 2.7.13.3)	JCM7686_pAMI4p337	Paracoccus aminophilus JCM 7686	905	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus aminophilus, Paracoccus aminophilus JCM 7686	1367847	>tr|S5YHT4|S5YHT4_PARAH Histidine kinase OS=Paracoccus aminophilus JCM 7686 GN=JCM7686_pAMI4p337 PE=4 SV=1 MNHDAPRPDPETFLAAADIEAGEPAGTERGRGRLKIFLGASPGVGKTYAMLEEAS AVHRAGGDVIVALAETHGRAETAALLSQLDQIPRRLVTYRGRQISEMDLDGLLARQ PRLALIDELAHSNVPGDRHPKRWQDVEEVLDAGIDVYTTLNIQHIESLNDVVARITG VRVQETVPDAILQRASEIRLIDLSAEDLIKRMREGKVYMPAEAGRALLNFFSKPNLT ALRELALRTAASRVDAEMLALTRGSGRPSAQDRLMVCLEDPATAKALVRAGRRM TDRARIPWIAATVITPDIERQGPGAAGAMTDALALAERLGAEIQILRADHADVVDEL LASARRRKVSRLILGRVPRTGWRARVHARFFTPLSERILEQAADLEVTILSPSGEP SPPKVKPRRSAAGWPRLSAEALAVTAVSTLIATPFDRILPVASLAVIYLVGVLSIGM RRGTAGAVLASVMSFLAYNYFFTSPYYSLRVASHESIVALLVFTVSALFTGSLAGR LKRQVEFMRVTQARTETLYDFARKIASASTTDDVLWAAAAHIAHSLECESLILMPD EGGDLRQVQGFPAIQEDLAPPIFAAALWAYQKNTPAGSGTDTLPALDWMFLPLAT QGAPIGAIGVRFFDATRGRDPETRRMLSAVEDQVAVAVERIKIESDLERARLASQT EILRAALLNSVSHDLRTPLVTVIGSLSALDQGDLPPETTAALVRGALSEAERLDRYV ANLLSMTRLGHGALVARRAPTDVAELIGRAQSDLAAPLAPFRVAITLPKDLPPIMVD PVLIGQSLINLMENATKYAPEGSTIRLTAQPEDKGVALMIEDEGPGIPQEQRTRVFE LFHRAIQGDGQPAGTGIGLAIVKGMIEANDGKVEAIEPPSGKGAAIRLWLPVADSL EESHGA	30~~KdpD (8.03895E-115) ~~239,258~~Usp (2.56366E-23) ~~387,11~~DUF4118 (5.62012E-14) ~~509,535~~GAF (0.000000209232) ~~656,675~~HisKA (0.00000000401279) ~~737,790~~HATPase_c (2.14814E-20) ~~893	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5.3E-90	309.8	1.8	8.6E-90	309.1	1.3	1.3	1	A0A099W3W6_9LIST	Histidine kinase	EP56_12795	Listeriaceae bacterium FSL A5-0209	383	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, unclassified Listeriaceae, Listeriaceae bacterium FSL A5-0209	1497679	>tr|A0A099W3W6|A0A099W3W6_9LIST Histidine kinase OS=Listeriaceae bacterium FSL A5-0209 GN=EP56_12795 PE=4 SV=1 MSEEADFSFRRKSPEEILAEIERLKKGKLKIYIGSAPGVGKTYRMLSEAQDLRKEGI DVVIGLVETHNRPETAAMIGNLETIPLKEIPYKGTVFQDLDVEAILARNPDVVVIDEL AHTNIPGSKHSKRYQDVLEILDHRINVLSAVNIQHLESLHDAVQTVTGVKVRERIPD HLLDTASEVILIDVSAETLQKRLREGKIYASHKINQSLENFFTQRNLSALREMALRE VADDVDDKTDKTEAKLRAAAVNEKILVCVKNDDNAEKLIRRGWRIANRLRAELFILT AIPGSLSDLDPYTRKKYESWKKLANEFDAHFLIETNHNRKIFSVITEVAKKHHITQIIL GQSVKTRLEELTKGSVVNAIMRETDGIDIHIVADSRKN	25~~KdpD (2.21842E-111) ~~229,253~~Usp (4.42511E-35) ~~378	non-kinase	KdpD;Usp
	5.6E-90	309.8	0	9.4E-90	309	0	1.4	1	B8J1F2_DESDA	Histidine kinase (EC 2.7.13.3)	Ddes_1680	Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	961	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio desulfuricans, Desulfovibrio desulfuricans subsp. desulfuricans, Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	525146	>tr|B8J1F2|B8J1F2_DESDA Histidine kinase OS=Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949) GN=Ddes_1680 PE=4 SV=1 MTDKHTRPDPDALLAQLRQTGTPQGIQADELSGGHLPVRGTLKIFFGYAAGVGKT YAMLRAAHTAAEQGQDIVVGYVEPHPRPETAALLQGLESLAPLRLEYRGIPLHELD VDAVLDRKPEIALVDELAHSNAIGCRNRKRYQDVEELLQGGISVWTTVNVQHLESL NDVVAAMTGVAVRERVPDSVFDGADHVELVDLEPDELMARLREGKIYAQAQAQH ALGHFFLPANLIALRETALRRMADRINRRAIPAEPGSREAARQVKEHILICLSGAPS NARVIRTAARMAEAFHADFTALFVRNNTSGHNDTQSLGTLRKNTRLAEDLGAAIVT AQGEDIPVQIAEYARMSGVSKIVIGRSPASGWLRRGKTLVERLAELAPEMETYIIPD AEPISRNASRPGTLYRMVRAFRGTAPRSWRQWGATAALLAICTMTGLIMSSMGM PNAVITGLYMLGVLGVSILTTGPWYGVTASILGVALFDFLFVAPRFSLTVYDDGYLS LFAAMLIVSAAASAITGRARSQARQSAARALHTELLLGNSRRLQKAENENAILAEAA RQFGTLLGCDAVLYPVYNGHLETRRIFPYYTAAQASREPGRPHTLPRQLAKGQTE CTHRTEKDELAVAQWVAKNGRPAGAGTDSLPGARLCYIPISSRTTVLAVAGLDVS PGSASPLNAADSKNIVLALAGECAMAVEKERLARANADIAVRAQQEKLRADVLRS VSHDLRTPLTAICGNAAMLAAGGDIEMQRRKSLARAIEEDARYLVEMVENLLALTR LEQYGFTLRLAPELMEDIIREALAVTRRRAAAHNIRVDMADALLMARMDARLMVQV LVNLLDNAVKYTPAGTTIRISAQADGARARLEVADNGPGISAEEKTRIFDMFHSAVI KKGDSRRGMGVGLALCRSIVQAHGGDLRVHDNTPRGAVFSLDLQREIEEGPVPE SLRETPPTGTGARE	39~~KdpD (2.38321E-113) ~~247,268~~Usp (5.42718E-29) ~~390,422~~DUF4118 (0.000000000000214371) ~~524,X,715~~HisKA (0.00000000039714) ~~780,835~~HATPase_c (4.53607E-29) ~~936	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	5.9E-90	309.7	2.6	1.1E-89	308.8	1.8	1.4	1	S0GLV5_9PORP	Two-component system, OmpR family, sensor histidine kinase KdpD	C803_05528	Parabacteroides goldsteinii dnLKV18	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides goldsteinii, Parabacteroides goldsteinii dnLKV18	1235789	>tr|S0GLV5|S0GLV5_9PORP Two-component system, OmpR family, sensor histidine kinase KdpD OS=Parabacteroides goldsteinii dnLKV18 GN=C803_05528 PE=4 SV=1 MDREQSVQHFLDLLKKSRRGNFKIYIGMIAGVGKTYRMLQEAHELLRSGIDVQVG YVETHGRVETEALVEGLPLIPRRRSFYKGKEVEEMDLQAILNIHPEVVIVDELAHTNI EGSKNEKRWQDVTDILEAGISVITAVNIQHLEGLNEDVQDITGIEIKERIPDSVLEQA DEVVNIDLTADELVKRLRAGKIYKPEKIQTALNNFFKSENILQLRELALKEVALRVEK KVENAVPVNTGVRHEKFLACISSQEKTPRKVIRKAARLATRYNTKFFVLYVQMPCE SIDRIPLANQRYLSNHFKLAAELGGEIIQVQSKSIPDSIIEVCREKQISTVCIGKPAFT LVSVFRACFQYRKLLNSLSQMNIDLIILA	17~~KdpD (5.10234E-122) ~~227,245~~Usp (2.60035E-27) ~~342	non-kinase	KdpD;Usp

	6.1E-90	309.6	2.1	8.3E-90	309.2	1.4	1.2	1	R5NG41_9BACT	Histidine kinase KdpD domain protein	BN471_01401	Paraprevotella clara CAG:116	377	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Paraprevotella, environmental samples, Paraprevotella clara CAG:116	1263095	>tr|R5NG41|R5NG41_9BACT Histidine kinase KdpD domain protein OS=Paraprevotella clara CAG:116 GN=BN471_01401 PE=4 SV=1 MEENENGNAQRFLELIRRSRRGKFKIYIGMIAGVGKTYRMLSEAHDLLKNGIDVQI GYVETHGRPGTVAMLEGLPVIPRKKVFYKGKEIEEMDLETILQVHPELVIVDELAHT NVEGSRNTKRWEDVMELLDAGINVVSALNIQHIESLSEDVKSITGINVAERVPDKVL QEADEVVNIDLTAEDLITRLKAGNIYKKEKIQTALNNFFKTENILQLRELALKEVAFR VERKVESEVTPLAPAQTRREKILACVSSNEHTPRHIIRKAYRLSTRYSTSFIALHVQ TPKESPDRIKLSSQRYLLNYFQLVTELGGKVEQMSSPNVTDAIVQFCKENQVTTV CMGRPAFEMPEMFFKIGRYKRFLQQLSEMRIDLIIVA	19~~KdpD (7.67789E-123) ~~229,249~~Usp (1.72681E-23) ~~377	non-kinase	KdpD;Usp
	6.9E-90	309.5	3	9.3E-90	309	2.1	1.2	1	R5VP67_9PORP	Uncharacterized protein	BN709_01654	Odoribacter laneus CAG:561	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter laneus CAG:561	1263089	>tr|R5VP67|R5VP67_9PORP Uncharacterized protein OS=Odoribacter laneus CAG:561 GN=BN709_01654 PE=4 SV=1 MDKEQSVQHFLDLIKRSRRGKFKIYIGMIAGVGKTYRMLQEAHQLLESGIDVQVGY IETHGRVNTEKQLEGLPVIPRRKVFYKGKELEEMDLQAILHLHPEIVLVDELAHTNIE GSKNEKRWQDVLDLLDAGINVISAVNIQHIESLNEEVQDIAGIEVKERIPDSVLEQA DEVVNIDLTAEELVTRLKAGNIYKPEKIQIALDNFFKSENILQLRELALKEVALRVEKK VENEVIDNVGVRHEKFLACISSAEKTPRRIIRKTARLATHYNCKFAVLYVQTPRESA DRIPLANQRYLLNHFKLASELRGEVIQIQSENVIDSIIQVCKERQISTVCMGKPDFSF WNIFRKALRYRKLVNHLALLNIDLIILAAR	17~~KdpD (1.04744E-122) ~~227,245~~Usp (1.03003E-26) ~~373	non-kinase	KdpD;Usp

	7.3E-90	309.4	0.7	9.3E-90	309	0.5	1.1	1	R5W558_9BACT	Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain	BN505_00832	Alistipes sp. CAG:157	370	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes sp. CAG:157	1262692	>tr|R5W558|R5W558_9BACT Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain OS=Alistipes sp. CAG:157 GN=BN505_00832 PE=4 SV=1 MDKQDSVQRFLELIRRSHRGKFKIYIGMSAGVGKTYRMLQEAHQLLEAGVDVRIG YIETHGRPDTEALLEGLPVVPLRKLFYKGKELEEMDTQAIINLHPEIVIVDELAHTNIE GSGNPKRWQDVMQILEAGISVISAVNIQHIEGLNESVQEITGVEIRERIPDSVLAMA DEVVNIDLTAEELINRLKAGKIYKPDKINAALNNFFTQDNILQLRELALKEVAMRVEK KVENEITAGDKPHRDRLLAVIDSSEKRSRRVIRKTARMATHINAPFSVLYIQSDRET ADRIPLANQRYLINNLNLASELGGEIRRIHSNRPVETILEVCREQKVSFVCIARPEFS PVKGILGFWKLTGRLSRMNIDLLILS	17~~KdpD (1.67581E-121) ~~227,245~~Usp (1.00336E-21) ~~370	non-kinase	KdpD;Usp
	7.8E-90	309.3	1.1	1.3E-89	308.6	0.8	1.3	1	Q8Y3Z9_LISMO	Histidine kinase (EC 2.7.13.3)	lmo2679	Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	896	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, Listeria, Listeria monocytogenes, Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	169963	>tr|Q8Y3Z9|Q8Y3Z9_LISMO Histidine kinase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) GN=lmo2679 PE=4 SV=1 METNRPSPDALLVNLQEETDSSVGKLKIYFGFAAGVGKTYAMLSDAKDQLAAGVD VVAGYIEPHARVETLRMLEGIPIISPKAINHKNIALKEFDLDEALKRKPELILVDELAH TNAAGVRNKKRFQDVEELLQAGIDVYTTVNVQHIESLNDIVEGITKVAVRETIPDYV FDEADRVKLIDIEPDELLKRLEQGKIYQPERAQTAMQNFFTRENLKLLREIAMRKAA DRISHEYDQTGVYPEKRASSKWLVCIGTSPSSAKLIRWTARTAEAFRAPWTALYIE NEENDYMTKAEKKCLRETMELAERLGAEIVTLAGHDIAETVAEYARLTGVTNIVVG KSRRRMGLRSLFEEDFEDRLITHLDNVDMHIIPSSHPKAKKRRMKMRFKSFLTWH DMAKMVLLLALATAICVGLSEFGIGDQNVIMVYILSVLIISRVTSGYVYGVLGSIIGV MLFNFFFTSPLYTFNTIQAGYPVTFGIMLLVALITSALTVRIKTQASLAVERERRTEV LYEINKQLLVTRNLKGIINLTNEYILHLFSRSVIFYSADPAKSNEGIFVQAEGKEDAS ALLSADEEAVAHWVFKNKKRAGAGTDTLMGAFGYYMPVMSQGKVLGVIGVSCSP EEGPLTQDNRIFLRMISSQVALALERQYLSEEQRQIVIESAKEKMRSNLLRAISHDL RTPLTGIIGASSALLEKEDELDKETERNLIRGIKDDSGWLIRMVENLLSVTRISEGLV SLERAPEAVEEIVGEAVGRIKKRFRDRTIHVKVPRDLLMVPMDGTLIEQVLINLMEN ALRHGGTGAEVWVDVTKTKQSAIFSVRDNGKGIPENRLADLFDTFAVEARERSD MSRGLGLGLSICMSIIRAHDGTLEAKNNKHGGATFWFTLPLDGGDGK	24~~KdpD (5.92334E-125) ~~231,249~~Usp (2.01335E-46) ~~373,397~~DUF4118 (2.18454E-16) ~~498,534~~GAF (0.000000219942) ~~649,666~~HisKA (0.0000000000152426) ~~732,785~~HATPase_c (3.66867E-26) ~~888	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	8.1E-90	309.2	1.1	4.2E-89	306.9	0.1	2	1	U5LHJ2_9BACI	Histidine kinase	N288_25405	Bacillus infantis NRRL B-14911	382	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus infantis, Bacillus infantis NRRL B-14911	1367477	>tr|U5LHJ2|U5LHJ2_9BACI Histidine kinase OS=Bacillus infantis NRRL B-14911 GN=N288_25405 PE=4 SV=1 MKQNHPYFRRRTPEEILHEITESSRGKLKLYVGAAPGVGKSYKMLQDASDLKKEG KDVVIGFIETHGRIETEEQIKDLEQVPIKIIPYKGKKFYELNVEAIIERKPDLVIVDELA HANIPGSENPKRYMDVSLILDAGIDVFSAVNIQHLESVNDIVQQITGVKVRERVPDT FVQKAYEIQLIDIPPETLRKRLSDGKIYAPEKIEQSLSHFFTINNLSALRELSLREIAN DVDERIEQISGSLENGPIGVNEKILVCVQYGPTAEKLIRRGWRMAHRMKAELYILN VTAEKRSDSSPVNEQKIKEWQMLAEQFNATIILEEKRSRKPAAVIIEVAKKLNVTQIL LGQSARTRWEEIKKGSIVNMIMRETSNIDIHIVADGR	23~~KdpD (1.72478E-115) ~~233,254~~Usp (4.30831E-40) ~~379	non-kinase	KdpD;Usp

	8.2E-90	309.2	3.1	1.3E-89	308.5	2.2	1.3	1	D6D7W0_9BACE	Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain (EC 2.7.13.3)	BXY_09400	Bacteroides xylanisolvens XB1A	376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides xylanisolvens, Bacteroides xylanisolvens XB1A	657309	>tr|D6D7W0|D6D7W0_9BACE Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain OS=Bacteroides xylanisolvens XB1A GN=BXY_09400 PE=4 SV=1 MDDREQSVQHFLDLIKRSQRGKFKVYIGMIAGVGKSYRMLQEAHELLENGVDVKI GYIETHGRAGTEALLQGLPVIPRRKIFYKGKELEEMDVDAIIRIHPEIVIVDELAHTNV EGSLNEKRWQDVITLLDEGINVISAINIQHIESVNEEVQEITGIEVKERVPDSVLQEA DEVVNIDLTAEELIARLKAGKIYRPEKIQTALDNFFRTENILQLRELALKEVALRVEKK VENEVMMGVAVGLRHEKFMACISSHEKTPRRIIRKAAKLATRYNTTFIALYVQTPR ESMDRIDLASQRYLLNHFKLVAELGGEVVQVQSKDILGSIVKVCKEKQISTVCMGT PNLRLPYAICSILGYRKFLNNLSQANVDLIILA	18~~KdpD (1.70316E-126) ~~228,248~~Usp (7.25998E-28) ~~376	non-kinase	KdpD;Usp

	8.8E-90	309.1	2.8	1.4E-89	308.4	2	1.3	1	F6D4T4_METPW	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	MSWAN_1124	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	651	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	868131	>tr|F6D4T4|F6D4T4_METPW Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1) GN=MSWAN_1124 PE=4 SV=1 MTEIKRPDPDELLSQIKEEESKQDQNKGYLKIFLGYVAGVGKTYRMLSEARVLNEN KKDVVVGIAETHGRKETQDLLKGLEVIPQRKIKYKEILLEEFDIDAVLKRKPDYVMV DELAHTNVPGSRHLKRYNDVEELLSQGITVYTTLNIQHIESVNDIIKQITGVQVKETV PDRIIQMTDKIELVDLPTGELIERLKEGKVYIPEKAKQAMERFFRERNLVALRELALR YTTTHIDYDMDYFLKQEKIIGPWDASNRIMVCISSNSSSEKLIRVAHRFSDLFNVEY FAVYVDPSYKFNMKSEEVIQLDKNLKLAEELDANLFRLAGNKISDEIVSFAKSKNITL IIMGHSRRSRFQKIFEGSVINKVIQKSQAQVLILENENKEFIKTKNVKKPYFSLKKEL KPYTVSILSIGLTSLICFVIRPYIEAINIPMIFIIPVVISGLVSGRKAGILSSVLAVGVFDF LFVQPYYSFSVSDVRFVPTFLVLLIVGIITSFLADVVKKQVENTRQREQFIASLYDFS KDLLISQSLRDILGRSTQYISELFNYDVIILMQDDQKRLNIVSRFGDHVSFDDNECG VSNWVFEHQKSAGRTTETLSSSKWYHIPLKVPSGILGVLAIATDESIDNEKKHLIES FASIVSLTMSNSIKE	26~~KdpD (2.65272E-113) ~~235,257~~Usp (8.82855E-35) ~~373,404~~DUF4118 (1.10651E-18) ~~504,530~~GAF (0.000000000525271) ~~647	non-kinase	KdpD;Usp;DUF4118;GAF

	9.2E-90	309.1	0.1	1.8E-89	308.1	0.1	1.5	1	U1ZQF9_9BURK	Histidine kinase (EC 2.7.13.3)	N879_04860	Alcaligenes sp. EGD-AK7	889	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Alcaligenes, Alcaligenes sp. EGD-AK7	1386079	>tr|U1ZQF9|U1ZQF9_9BURK Histidine kinase OS=Alcaligenes sp. EGD-AK7 GN=N879_04860 PE=4 SV=1 MSLEDRPDPDELLQVIGEDPHQPRRGQLKIFFGACAGVGKTYAMLKEAHQRQSE GVSVAIGIVETHGRQETQALIDGLPVLPRKEYQRQGRAVTEFDLDAALASGYQLLL VDELAHSNIEGSRHAKRWQDVEELLDAGIDVYTALNVQHLDSLNEVVGGIVGVRV RETVPDRIFDRAADVLLVDLPPDDLLSRLSAGKVYLADSVAHARQNFFRRGNLIAL RELALRRVADRVNADVHVYRISHAIRTVWPTRELLMVCVSADSAQEALIREGARLA QQLQTPWIVLHVDTPQESGQIKAQEALVRLAASAQHAGAEFANIAGQDVAHTILAY ARQRNATKLILGNSSARSIWPWRTRLSERLARSNPEIGLLLLRMDTVQRPIRPLEL EQPMAQGKALSIASIICVVTTLLAEKLLPFFELSNVIMLFLITVVFIALRLGRLAGVWA SLLSVAFFDFFFVEPRYSFSVTDTQYVFTFGVMLGVALIIGQLAAKLQAEARAARD GERRAAALTRVSRDLAGALALEQVLAVCRDTLEPLFEMQVVLVVPDQQNQLVATR HTGFVELSVAQWVFDHMEAAGNGTETLSGASALYLPLKGPMAPRGVLVVQSGG AASLRTPDGRRLLDACCFTLAQALERIHYVEIAQDTVLRMEGEKMRNTLLSAVSHD LRTPLTVIRGLAETLEQPKGLSETERTDIARSIRIESDELRRQVSNLLDLARMQSEG VKLHKEWHALGEIVGIAVARCSAALQPRKVVTEFAADLPLIEVDGVLLERVVTNLLD NAAKYTPVTSTISLRGLCSGQFMYLMISDDGPGLPPGDPERLFDTFTRGQKESSV AGVGLGLGLCRTIIAAHGGTISAKPRMPHGVIFEIRLPWKAAPRMDDDELLT	23~~KdpD (1.96843E-106) ~~233,256~~Usp (6.62438E-27) ~~375,404~~DUF4118 (3.22239E-18) ~~498,525~~GAF (0.0000000715266) ~~638,655~~HisKA (0.00000000000220453) ~~720,773~~HATPase_c (7.85144E-24) ~~874	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	9.3E-90	309	1.1	1.5E-89	308.4	0.2	1.7	1	Q883V3_PSESM	Histidine kinase (EC 2.7.13.3)	kdpD PSPTO_2245	Pseudomonas syringae pv. tomato (strain DC3000)	887	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas syringae group, Pseudomonas syringae group genomosp. 3, Pseudomonas syringae pv. tomato, Pseudomonas syringae pv. tomato (strain DC3000)	223283	>tr|Q883V3|Q883V3_PSESM Histidine kinase OS=Pseudomonas syringae pv. tomato (strain DC3000) GN=kdpD PE=1 SV=1 MSDSGRADALLAQLPREGRGRLKVFLGAAPGVGKTYAMLQAAHAQLRQGVRVM AGVVETHGRAETEALLNGLPQQPLLRTEYRGMTLEEMDLDALLKAAPSLVLVDEL AHTNAPGSRHTKRWQDIQELLAAGIDVYTTVNVQHLESLNDQVRGITGVQVRETL PDWVLQEAFDLVLIDLPPRELLERLRDGKVYVPEQARAAIDAFFTQTNLTALREMA MQTAAAQVDNDLAQGYRQLGQSAPAVRGRMLVGIDGDMHAERLVRHASRVAQR RHLPWSAVHVDDGQTLDEQSRARLQNAQQLAERLGGEAVSLRAGEVARTLVQH AIERRASVVLVGQSRRHWRRRVFGGGVAARLLREGHGLEISVLDDSEELPDQPP RARPAREVVWFDYGLAFVATLIASLVAWGVAGVLALPNISLIFLAAVLLVAVRSSM GPALACAGLSFLAYDFLFIPPPSFSLNIQREEDVLTLLFFLLMSALTGKLAARQRRQL QALRDTQEQTSELLDLSRKMTAATDRKAVLNAAEQHFSGWKELYLCLVDRDTQG GLVVETGGPLTFSEAERAAADWAWQHDQPAGSGTGTLPSGRWWWWPITAEE GPLALLGVCAREGQSFTDQHRRLLAALTQPLAQALARAQLAQELEAARLHGETEQ LRSALLASVSHDLRTPLTSMRGSIDSLLALGEAIALEDRRELLEGTRDEAERLDRYI QNLLDMTRLGHGALKLARDWVSPADIVGSALNRLRAVLTPLQVSTQVTGDLPLLY VHAALIEQALVNVLENAARFSPLGGRLQVTAGVVDSELFFSVSDEGPGIPEDERAK IFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGRLTVEEGIDGLGTRITLFLPLQ AQPDAEMEEPA	17~~KdpD (2.31834E-121) ~~227,248~~Usp (7.97106E-36) ~~365,392~~DUF4118 (4.11961E-18) ~~491,546~~GAF (0.00893144) ~~624,651~~HisKA (0.000000000000282655) ~~717,770~~HATPase_c (1.35716E-24) ~~873	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	9.5E-90	309	0	2E-89	308	0	1.6	1	Q4K7X9_PSEF5	Histidine kinase (EC 2.7.13.3)	kdpD_2 PFL_4570	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	890	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	220664	>tr|Q4K7X9|Q4K7X9_PSEF5 Histidine kinase OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=kdpD_2 PE=4 SV=1 MPPRDGRPDPDALLEKLQQEEQAAQRGKLRIYFGSNAGVGKTCAMLTAARNEVA QGRDVVAGVVETHGRRETAELLQGLQVLERHRLMHRDYALPEFDLDAALARHPA VLLVDELAHSNVPGSRHPKRWQDVEELLRAGIDVWTTLNVQHLESLNDIVSGIIGI RVRETVPDHLFDEAHEVLVIDLPPDDLLRRLKDGKVYLGPQAERASRHFFRKGNLL ALRELTLRRTADRVDAQMRDYRRERSINALWPARERLLVGIAGDPADERLVREAA RLAQKLEADWMVVHVASAQRRGAGAARYAAAMKTLALAAEFGAETATLPGMDV AEALVACAREHNANRLVLGHYPRKVWQFWHQSVSDRISRQHPEIDQIVIANGPLS RRPAPVDKPEAGLPPSRAPAYLWASLACFAATAVAALLLKVFDPANVVMLFLLTVV LVALRYGRGPGVWAAMLAVLCFDFFFVQPVWSFTVNDTQYFFTFALMLGIALITG QLTARLRHEARTAAAGERRATSLAGLARELSAALTEEQICAVALRTFSGVFEARVG LALPDAENRVRALSANTLAIDESIAQWAYDHDQPAGRGTDTLAAAKGCYLPLKAP MRVRGVLVLEAEDAERLKEPEEQRLLEACMSQLAIALERVHYVEVAQSTVLQMEG ERMRNTLLAAISHDLRTPLTTIIGAADAALPHAAQGPLKHLLAGIHDQASSMQRLIE NLLDMARMQERGVRLNRQWNSLEEIVGSALRQLREPLAGHQLRVAMAPQLPLVE VDALLLERVLVNLLDNAAKYTPAGTLVQISARQVDQQIILQVSDSGPGCPKGSSPA SLFEAFSRGQQESAVAGIGLGLALAKRIVEAHGGRIEAQPHADAGLSFVITLPAGQ PPSMETL	24~~KdpD (1.03935E-111) ~~234,256~~Usp (5.62132E-28) ~~378,429~~DUF4118 (3.92327E-20) ~~501,529~~GAF (1.58996E-14) ~~644,661~~HisKA (0.00000000012683) ~~724,777~~HATPase_c (8.75509E-25) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	9.7E-90	309	0.3	1.4E-89	308.4	0.2	1.3	1	G8Q1U4_PSEFL	Histidine kinase (EC 2.7.13.3)	kdpDPSF113_1668	Pseudomonas fluorescens F113	883	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens F113	1114970	>tr|G8Q1U4|G8Q1U4_PSEFL Histidine kinase OS=Pseudomonas fluorescens F113 GN=kdpD PE=4 SV=1 MSDSGRADALLANLPRNDRGRLKVFLGAAPGVGKTYAMLQAAHTQLRQGVKVIA GVVETHGRSETEALLGGLAQQPLVRSEYRGVMLEEMDLDGLLAAHPTLVLVDELA HSNAPGSRHAKRWQDIQELLTAGIDVYTTVNVQHLESLNDQVRGITGVQVRETLP DWVLQEADELLLIDLPPRELLERLRDGKVYVPEQARAAIDAFFTQTNLTALRELAM QTAAAQVDNDLTQGYRQLGQAAPAVRGRLLVGVDGDVQAERLVRHASRVAQRR HLPWSLVHVDNGSARDEPSRQRLQNAQQLAERLGGEVVLLRAGEVARTLIQHAS ERRATLLLVGQSRPRLRRRLFGGGLASRLLRDARGLEINVLDSDEQPRPARVRSN AVQTGFDYVLALTATVAASALAWGISGWLALPNISLVFLMAVLLVAVRSSLGPALA CAALSFLAYDFLFIPPNFSFTIQREEDVLTLVFFLLMAALTGNLAARQRRQLQALRD TQQETGELLDLSRKLTAATDRQAVISAAAQHLNGWHDLQLCLLNRDNQGGWKIE SGEPLTFTEAERAAADWSWQHDQPAGAGTGTLPSGRWWWWPLSAEGGPLALL GVCPKEGKPLSGQRRRLLAALSQPLAQALARAQLAQDLEAARLHGETEQLRSALL ASVSHDLRTPLTAMRGSIDSLLALGEAIPLADRRELLEGTRDEAERLDRYIQNLLDM TRLGHGALKLARDWVSPADIVGSALNRLRAVLAPLALSVEVPAELPLLYVHAALIEQ ALVNVLENAARFSPAQGQLLLSAGATDSEVFFAVADEGPGIPEEERAKIFDMFYTA ARGDRGGQGTGLGLAICQGMVGAHGGRISVADGLDGRGTCITLHLPLQAQPGM DDEA	19~~KdpD (2.12087E-120) ~~227,248~~Usp (1.69667E-30) ~~365,390~~DUF4118 (7.16204E-20) ~~489,X,649~~HisKA (0.000000000000436485) ~~715,768~~HATPase_c (9.74591E-26) ~~871	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	9.9E-90	309	3.4	2.3E-89	307.8	2.4	1.6	1	F8L2N8_PARAV	Histidine kinase (EC 2.7.13.3)	kdpDPUV_26190	Parachlamydia acanthamoebae (strain UV7)	876	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Parachlamydiaceae, Parachlamydia, Parachlamydia acanthamoebae, Parachlamydia acanthamoebae (strain UV7)	765952	>tr|F8L2N8|F8L2N8_PARAV Histidine kinase OS=Parachlamydia acanthamoebae (strain UV7) GN=kdpD PE=4 SV=1 MSEQERPAPEDFLRMTEIQESEEKGQLKIFLGMAAGVGKTYAMLEEAQALQKEG VNVVIGIVDTHGRSETSALVSGLKKIPEKVITYRDREFQELDLDAIILLKPDVVLVDEL AHTNIPGKRHNKRWQDVLEILDHGIDVYTTLNVQHIESLKDVVHGITGVVVQETVP DLIIEKAASIQLVDLTTDELLQRLKEGKVYLPEQSKIATQNFFKKDKLTALREIVLRYA ADKVDRDLRQMEPTGERSTLWRAREKFLVAVSQSPYSQKLIRRACRMAVNFDAP WIALYVNNERILNEQDSQQLTKNLQLARNLGAEVVTIKNPTIAEGIQSIVRQKGVTQ ILLGRSLEKTVFGTSTYFSLPDLLAAECPEVDIHILRQDKDASYTKKMLFLPFSHIPFI NYIYVFLFAGLFTLANFFLAPFVGYETIGVIYLLGILLLSLFFTKGPIIFAAFLFALCWD FFFIPPIWGFEVSKKEDIALLVLYIMTAASTGILVDRARGHKEMFQKSEETTRLLYD VVKKIASGPSTQEIFKSVKEELDRFFKGKFEIIVKQLGNGLKFDDSNSLLTNDMEKN TAIWAFENGKEAGWSTDTLPSANNLYIPLKGFHEIVGILVFKPDTAKNLSPEEKNFI YTIGGQLTGHIERKFSEEETKQNEQLKLMERVHKTILDRISHEFSDPIVSIQTSVQIL KDQNKDSLEVQKIDNAAETLSKILTNVLAMAQLSEGLVPLNLSLQDVKELIHECCFN VKRAQNGHRLNIHIDEKIPLIPIDFYLIEILLYNLLFNAFEYSPSDSTIEVEAKKLDKYV VISVADEGKGIPEDQLETIFEKFFRLPEETGPGMGLGLAIAKTIAEVHKGKLKVENL PVKGAKFSLYLPIKI	22~~KdpD (1.92465E-111) ~~232,254~~Usp (1.31238E-26) ~~375,399~~DUF4118 (0.00000000120007) ~~497,525~~GAF (0.00000963079) ~~642,669~~HisKA (0.00229859) ~~719,772~~HATPase_c (5.78851E-26) ~~872	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1E-89	308.9	1.2	1.5E-89	308.4	0.8	1.2	1	R5PNT1_9PORP	Osmosensitive K+ channel histidine kinase	BN783_01721	Odoribacter sp. CAG:788	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter sp. CAG:788	1262909	>tr|R5PNT1|R5PNT1_9PORP Osmosensitive K+ channel histidine kinase OS=Odoribacter sp. CAG:788 GN=BN783_01721 PE=4 SV=1 MSREENVQHFLDLIRRSRRGKFKIYIGMIAGVGKTYRMLQEAHELLENGIDVQIGYI ETHGRAGTEALRDGLPMIPRKGIFYKGKELEEMDLDRILLLHPELVIVDELAHTNVE GSRNEKRWQDVLELLDAGINVISAVNIQHIESLNEEVRSIAGIEVKERIPDKVLQDA DEVVNIDLTAEELINRLKAGKIYRPEKIQVALNNFFKTENILQLRELALKEVAFRVEK KVENEVVSGDVGVRHEKFLACISTNEKTPRHIIRKAARLATHYNTTFITLYVQTPGE RSDRIDLASQRHLLNHFKLATELGGEVVQIVSPHVIDTIIEICRSRQITTVCMGQPAF QMPSSLLKISKYRKFLRALKEMSIDLIILA	17~~KdpD (2.99731E-125) ~~227,246~~Usp (1.70723E-25) ~~343	non-kinase	KdpD;Usp
	1E-89	308.9	0.2	1.7E-89	308.2	0.1	1.4	1	G5KAR6_9STRE	Histidine kinase (EC 2.7.13.3)	STRPS_2029	Streptococcus pseudoporcinus LQ 940-04	881	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pseudoporcinus, Streptococcus pseudoporcinus LQ 940-04	875093	>tr|G5KAR6|G5KAR6_9STRE Histidine kinase OS=Streptococcus pseudoporcinus LQ 940-04 GN=STRPS_2029 PE=4 SV=1 MQTGKLRIYFGYAAGVGKTYAMLNEAQKAKKAGVDVLAGYIEPHNRPETMALLAG LEQLSPKSITYKGITLKEFDIDAALKRQPRIILVDELAHTNCFGSRNKKRYQDIRELL CAGIDVYTTVNVQHIESLNDVIETITGIQVNERIPDAVFNQADQIELVDIEPLDLLERL DKGKIYAKSQANLAKHHFFTEEKLIALREIALRKAADQINQSAIRSEKVKASLVTKEH VLVCVSPSPYASHVIRAASRLASAFNADFTALYIGSLDRESPNQKADNKLRQHLEL AEQLGAKVSIVDADNVSKQIVDYAKLSHVSKLVVGKSSDKTIWPKENIVEVLSQSV PDLDIFVIPNARGKKEPYHDKFSFVSWIPKWQFSFSDLLKTLAMLLLVTLTGLLFRY WNFSVDNIITIYILGVQVNAVWTKGKLSSVVSSILSVLCFNYFFTEPYYTFVAFSPN YPITFIIMLIAGLITSSLIKRIQEQARLSTEKSYRTELLLQTNKGLSQADTIPAILEELAV QVKKLLDRDVVIYPVIAGTLEDPKYFSASQSLQTLTDYDQLNERGVVEWVLHNNK RAGATTNTLSAAKFLYLSVREKDHVFAIIGILMDDKATVDLFEKSVILAVLGEAALAL EKERLREEQQKIELKMQKEQLRANLLRAISHDLRTPLTSISGQARLMMETGETLEK QQLTELATYIYDDSMWLINLIENLLSITKLDNDMTLSLSTNIFDEMVEEALKHVDRHL KHHNFILDLSDDLLMAKMDGPLIVQVLINIINNAVKYTPEGSRITLTSKRKDQNLVVE VSDDGPGISDQAKEKIFDLFYTSENASADGKRGLGIGLSLCKSIITAHGGTIYVHDNI PKGVIIGFTLPLVGVPVLHEK	4~~KdpD (2.08745E-117) ~~211,230~~Usp (3.53111E-30) ~~351,439~~DUF4118 (0.00000209771) ~~481,X,649~~HisKA (0.0000000000450689) ~~715,767~~HATPase_c (2.91535E-26) ~~870	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.1E-89	308.9	0.5	1.5E-89	308.4	0.3	1.2	1	K9ZA22_ANACC	Osmosensitive K channel His kinase sensor	Anacy_0431	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	372	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	272123	>tr|K9ZA22|K9ZA22_ANACC Osmosensitive K channel His kinase sensor OS=Anabaena cylindrica (strain ATCC 27899 / PCC 7122) GN=Anacy_0431 PE=4 SV=1 MLTDANSSLYLKRRGKHKIFIGMAPGVGKTYKMLEEGQLLKQEGIDVVIGLLETHG RKETIQKSEGLEIIPPQLMLLSDLMFPEMDTDAIINRFPQLVLIDELAHTNIPGSLREK RYEDVEIILAAGIDVYSTMNVQHLESLNDLVARITGIVVRERLPDRILEAADEVVLVDI TPETLQERLLEGKIYAPQKIQQSLDNFFQRRNLIALRELALREVADNVEGEALASIP TGQFCNIHERVLVCVSTYPNSVQLLRRGARLAGYMNAPMYVLFVADPQRFLSKAE SLHVDTCEKLCKEFTGTFIRVNSNNIADAIAEVAEKYHITQIVIGESQRSRWEILFKG SLTQKLVRLLKNVDLHIIATEKTSSSKN	12~~KdpD (4.13238E-125) ~~222,241~~Usp (8.83841E-47) ~~363	non-kinase	KdpD;Usp

	1.1E-89	308.8	2.2	1.6E-89	308.3	1.5	1.2	1	R7EMA6_9BACE	Uncharacterized protein	BN594_00615	Bacteroides uniformis CAG:3	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides uniformis CAG:3	1263055	>tr|R7EMA6|R7EMA6_9BACE Uncharacterized protein OS=Bacteroides uniformis CAG:3 GN=BN594_00615 PE=4 SV=1 MSREESVQHFLDLIKKSRRGKFKVYIGMIAGVGKSYRMLQEAHELLDNGVDVKIG YIETHGRAGTDAMLEGLPVVPRRKIFYKGKELEEMDLDAIIQIHPEIVVVDELAHTN VEGSRNEKRWQDVMDLLDEGINVISAVNIQHIESVNEEVQGISGIEVKERIPDSVLQ EADEVVNIDLTAEELIARLKAGKIYKPEKVSTALNNFFKTENILQLRELALKEVALRV EKKVENEVVTSVGVRHERFLACISSNEKTPRRIIRKAARLATRYNTSFVALYVQTPR ESTDRIGLANQRYLLNHFKLVTELGGEVVQVQSPDVLGSIVDTCREKQITTVCMGS PSLSFPKSLFMILKYRKFVRDLAQVNIDLIILA	17~~KdpD (1.33729E-127) ~~227,245~~Usp (5.59695E-29) ~~373	non-kinase	KdpD;Usp
	1.4E-89	308.5	2	2.3E-89	307.8	1.4	1.3	1	R6LFS2_9BACE	Histidine kinase KdpD domain protein	BN507_02372	Bacteroides clarus CAG:160	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides clarus CAG:160	1263039	>tr|R6LFS2|R6LFS2_9BACE Histidine kinase KdpD domain protein OS=Bacteroides clarus CAG:160 GN=BN507_02372 PE=4 SV=1 MSREESVQHFLDLIKKSRRGKFKVYIGMIAGVGKTYRMLQEAHDLLDNGVDVNIG YVETHGRAGTEAVLAGLPVIPRRKIFYKGKELEEMDLDAIIRIHPEIVIVDELAHTNV EGSRNEKRWQDVMDLLDEGINVISAVNIQHIESINEEVQGISGIEVKERIPDSVLEE ADEVVNIDLTAEELITRLKAGKIYKPDKVALALNNFFKTENILQLRELALKEVALRVE KKVENEVVVSSVGVRHEKFMACISSHEKTPRRIIRKAARLATRYNTSFVALYVQTP RESADRIALANQRHLLNHFKLVTELGGEVMQVQSKDVPGSIVTACREKQITTVCM GSPSFALPQSLFMVLRYRKFVSELAQANIDLIILA	17~~KdpD (1.29041E-126) ~~227,246~~Usp (1.86086E-26) ~~374	non-kinase	KdpD;Usp

	1.4E-89	308.5	0.4	2.1E-89	307.9	0.3	1.3	1	L0DJW0_SINAD	Osmosensitive K+ channel His kinase sensor	Sinac_5539	Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	377	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Singulisphaera, Singulisphaera acidiphila, Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	886293	>tr|L0DJW0|L0DJW0_SINAD Osmosensitive K+ channel His kinase sensor OS=Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10) GN=Sinac_5539 PE=4 SV=1 MSTLEPGRPSPEHFLNLIRRQERGRLKVYLGSAAGVGKTYSMLREGQRLKKQGV DVAIGIVETHGRVETAEQLGDLEIIPPVVIEYRGVTLREMDLDGILARRPTVCLVDEL AHTNAPGSRHGKRYQDVEELLRVGIHVITTVNIQHLESLYDEVERVTGVKVKERLP DSVLGEADQIVNVDISAEDLLERLNAGKVYPPERAERALENFFTSANLTRLREFTLA EMAHLIDRRTRRTEADRSQASATERVMVGMSSRSPNAPALMRKAARLADRLNAP WYAVYIQTPAEDLTRIDAATQRVLGKNLELAQQLGGIPMTFRGKDVASTISAFAHE YGIKVIIVGKTNQPWHRRLLRGSILEQILNQSEGVDVMVVDV	22~~KdpD (2.29166E-115) ~~228,250~~Usp (3.14704E-34) ~~375	non-kinase	KdpD;Usp

	1.4E-89	308.4	4	2E-89	308	2.7	1.2	1	Q11TL2_CYTH3	Sensor kinase for the kdp operon (EC 2.7.3.-)	kdpDCHU_1986	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Cytophaga, Cytophaga hutchinsonii, Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	269798	>tr|Q11TL2|Q11TL2_CYTH3 Sensor kinase for the kdp operon OS=Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469) GN=kdpD PE=4 SV=1 MSEKDKTVQHFLDLIKKSRKGKFKIYIGMSAGVGKSYRMLQEAHALLKNGIDVKIG FIETHNRKETHALLEGLPVVPRRKLFYKGKELEEMDVQAIINLRPEVVIVDELAHTNI EGSKNEKRWQDVIEILEAGINVISAVNIQHIESLNEEVKTITGVEVKERIPDSILTQAD EVVNIDLTADELIIRLKEGKIYQEEKIQAALQNFFKSDHILQLRELALKEVASQVERK VETEVTKTHAIKHERFLACISSNDHAAKEVIRKTARLANYYHSKWYVLYIQTPNEHA DKIALDKQRHLINNFKLATELGAEIIKVESASVTKMIVSQAIERNITTICIGKPRLNVFK IIWRTNVLNTLFKKLSSNNIDLVILS	18~~KdpD (8.77212E-120) ~~228,246~~Usp (8.10779E-37) ~~374	non-kinase	KdpD;Usp

	1.4E-89	308.4	2.9	1.4E-89	308.4	2	1.4	1	R6DK25_9BACE	Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain	BN772_03518	Bacteroides sp. CAG:754	376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:754	1262750	>tr|R6DK25|R6DK25_9BACE Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain OS=Bacteroides sp. CAG:754 GN=BN772_03518 PE=4 SV=1 MDDREQSVQHFLDLIKRSHRGKFKIYIGMIAGVGKSYRMLQEAHELLENGVDVQIG YIETHGRTGTEMLLEGLPVIPRRKIFYKGKELEEMDTDAIIRIHPEIVIVDELAHTNVE GSLNEKRWQDVMTLLDEGINVISAINIQHIESVNEEVQEITGIEVKERVPDSVLQEA DEVVNIDLTAEELITRLKAGKIYRPEKIQTALDNFFRTENILQLRELALKEVALRVEKK VENEVVMGVAVGLRHEKFMACISSHEKTPRRIIRKAARLATRYNTTFIALYVQTPKE SMERIDLASQRYLLNHFKLVTELGGEVVQVQSKDILGSIVEVCKEKQISTVCMGSP DMRLPYAICSILGYRKFLNNLSQANIDLIILA	18~~KdpD (1.09008E-126) ~~228,248~~Usp (6.84439E-28) ~~376	non-kinase	KdpD;Usp
	1.4E-89	308.4	0	2.7E-89	307.5	0	1.5	1	A5FWF2_ACICJ	Histidine kinase (EC 2.7.13.3)	Acry_0713	Acidiphilium cryptum (strain JF-5)	867	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acidiphilium, Acidiphilium cryptum, Acidiphilium cryptum (strain JF-5)	349163	>tr|A5FWF2|A5FWF2_ACICJ Histidine kinase OS=Acidiphilium cryptum (strain JF-5) GN=Acry_0713 PE=4 SV=1 MGSASPENRPDPDALLARANSDGRGQLKIFLGAAPGVGKTWEMLAAARRRFETG TDVVVGLVETHGRAETAEQLADLPVLPRRIVPYRGRLLEEFDLDAALKRRPALLLV DELAHANAPGLRHAKRWQDVAALLEAGINVWTTLNVQHLESLNDQVARITGIRVA ETLPDTVLGLADDIELIDLPPEELRTRLKQGLVYRPDVARRALGGFFRPGNLAALRE MALRRVAQHVDRDIAAYMRAQAIAGPWPAAERVMAVVEAGEAAEQVVRHASRLA EALRAPFFAFHAERAATGMAVQPALDLAIQLGGTVETTTNADVFAALLDAAARQN VAHIVIARGRGRWRWRRGLASRLARGARAYALHVVPDPAASRPAPPHRAPPPKL MPFGISLGIMILTTIGGFALRGVLPAEAMGYVFTAIVVGMASLYGRSVGIFAALTGF VLWNFFFLPPIYTLSVTNPRDVTALFAFLVVGVLTGSLAGRVRAEAETARTRIEALR RITLFGRALAQVSDEAGLAAVVEAEARALAGEAVLLLARDDGLPRAGGFDEAAVA AAEFAWRNRVATGMGTTTLPASAWRFQPLATEAGAIGVLGVRPETPPAEPVIQTL GALADQAALAAERLRLATSAAEARAHESTQRLRTALLSSLSHDLRTPLTAIRGAAE TLAEADGELPEATRRDLLASIVEDVGRMTRFLANITGMARIETGEIVARHEKVDLAP VVEHAVARVKEAFHTAVNIPEDAATVRADPALLEQVLVNLLENAVKYGPEGGAISV FARRAGDSVVLSVADEGVGIPPEDLPHVFNSFFRVVRGDRVAPGTGLGLAIARAF VEAMGGTIAAESPRRDLPADGLPGTIIRVELPVP	23~~KdpD (4.11556E-114) ~~232,254~~Usp (4.44242E-14) ~~367,387~~DUF4118 (0.0000000000115499) ~~487,X,639~~HisKA (0.0000000000690139) ~~705,755~~HATPase_c (2.34419E-28) ~~864	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.5E-89	308.4	1.5	2.2E-89	307.8	1	1.3	1	R7NT34_9BACE	Osmosensitive K+ channel histidine kinase	BN821_00360	Bacteroides sp. CAG:98	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:98	1262754	>tr|R7NT34|R7NT34_9BACE Osmosensitive K+ channel histidine kinase OS=Bacteroides sp. CAG:98 GN=BN821_00360 PE=4 SV=1 MEREENVKHFLDLIRRSRRGKFKIYIGMIAGVGKSYRMLQEAHEMQENGLDVQIG YIETHGRTGTEALLEGLTIIPRKKIFYKGKEIEEMDLDSILRLHPELVIIDELAHTNIEG SRNEKRWQDVMELLDAGINIISAVNIQHIESLNEEVKGIAGIEVKERIPDKVLQDADE VVNIDLTAEELINRLKAGKIYRPEKIELALNNFFKTENILQLRELALKEVAFRVEKKVE NEIVSIDKGVRHEKFLACISSNEKTPRHIIRKAARLASRYNTVFSALYVQTPVESTER INLASQRHLLNHFKLVTELGGEVLQVASANVLDEIIKTCQEKQITTICMGQPAFKMP STLFSISKYKKFLASLAQMNIDLIILA	17~~KdpD (4.21823E-124) ~~227,246~~Usp (3.76923E-26) ~~374	non-kinase	KdpD;Usp
	1.5E-89	308.4	0	2.4E-89	307.7	0	1.4	1	A0A0A8UWB8_LEGHA	Sensor protein kdpD (EC 2.7.13.3)	kdpDLHA_2382	Legionella hackeliae	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella hackeliae	449	>tr|A0A0A8UWB8|A0A0A8UWB8_LEGHA Sensor protein kdpD OS=Legionella hackeliae GN=kdpD PE=4 SV=1 MMGADNQRPDPDVLLAQVQSQEKQASKGKLRIYFGASAGVGKTYAMLVEARKLK EDGCDVIVGLVETHGRKETEALLSGLPLLPRKSILYRNKELYDFDIDAALEKHPQLIL VDELAHSNIPGMRHPKRWQDVEELLEAGIDVFTTLNVQHLESLNDAIGGITNIHIAE TVPDTIFDKADEVVMVDITADDLLLRLKAGKVYQGPQGELAAQNFFRKGNLIALRE LALRRTAERLEDDVQAYRIEQSIDKIWKTDTALLACVGERPGAEYVIRNTARLACQ LNAEWHVIYVETPALMRLPFSKKQYALNALKLAEELGATTSIVTGDDVALAIADYAR NQNFSKIVLGRRRPSLRFWHSSILSRLAAYAPDFDLLVIGDLDKAGNSLDVQDISKP VKEKKEYAHYLVAVGAIFFTVLISKILEPYFSLINISLLLLLTSLLIAIRFGRGPALVASLI AAGSLDFFFIEPRYSFLIADWQQGIMMCLIVAIALITGHLTANLRYQVFIKGQRESRT HVLYKFAYELSSALLTEPILETTRTYIQHAFSARAWLLLPDDDGQLQLPTDEETFQA SEMQNLDMGIAQWAFDHKESAGLGTDTLPGNSFFYLPLVAPMRTRGLLVIQPKIS QWLQRPEERQQLDTFAALAAIALERVHFIQVAQEALVHMESERMRNKVLANLSYD LQTPLASLINLSESLVKSDSLLTPLQQELANSLKNEILHMDSLIKNLFEIARIKTGELK LNLQWHHFDTILINVSHAMNAKMTTHHIETLLEGNLPLVYLDNLLIERVLIALLDSTC KYTPKGTSIILSATSHDNNLKIAIYDKGSILSSGRAKALWKKLKRGFRIDLEIAICGAII EAHGGNIQLGHSPEGGTSIICSLPIKPVPELIIEE	25~~KdpD (5.96731E-118) ~~235,258~~Usp (1.00427E-38) ~~378,443~~DUF4118 (0.00000000590066) ~~504,534~~GAF (0.000000000000032389) ~~652,669~~HisKA (0.00000016472) ~~734,787~~HATPase_c (0.000000116834) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.6E-89	308.3	0.4	2.9E-89	307.4	0	1.6	1	A4SZG6_POLSQ	Histidine kinase (EC 2.7.13.3)	Pnuc_1667	Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1)	897	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Polynucleobacter, Polynucleobacter necessarius, Polynucleobacter necessarius subsp. asymbioticus, Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1)	312153	>tr|A4SZG6|A4SZG6_POLSQ Histidine kinase OS=Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1) GN=Pnuc_1667 PE=4 SV=1 MPESRPDPDQLLAQIQSQEIQSGRGKLKIFFGANAGVGKTYAMLSAAHEQSKNKR VIAGVVETHGRKDTIAMLDGIEVLPLKEIDYRGKKLKEFNLDQALIEKPDLILMDELA HSNAAGSRHPKRWQDVEELLAAGIDVYSTINVQHIETLNDIVGGITGVRVWETVPD HIFDSADEVVLVDLPPDELLQRLKDGKVYLPQQAERATQNFFRKGNLIALRELALR RSADRLDGEIIKYRKDNSVSNVWKTRESILACIGPGDEAENVIRSAARVAAQLQIP WHAIYVETPKLQNLSQKSRERILKTISMAEEMGAKVVTVGGNDAVESIISYAREHN LSRVIVGTGALSRWQIWRRAFSESISRRAPDLDILKIAQGTNSTSIARDSFDIESWM WQLKAPWQSYALSLLICGIAGVVATPLNSIVELPNIAMLFLLAVVLVSVKYGLGPSF MASAVNVLVFDFFFVPPRFSFSVSDAQYVFTFAVMLVVGLITAKLTTGLTYQAKVA NRREQRVKSLYEMSRDLSGALMPEQVAEISQHFVEIEFKAKSILLLADDDNQLSEIII NKKSNLQADLSIAQWAFDKSKEAGNGTDSLPGAPLLYIPLRAPMRTRGILVIDAPS STRLKSPEQRRLLDTFARLLAISLERIHYVSVAQSSTVQIESERLRNSLLSAISHDLR TPLTALVGLTDALEMLDAPLTSEQKEIAVLLREKALKMSSQVSNLLDMARLQSGAV QLNKQWFLIEEAIGAAIKSVESASEGRHITVTLPPDLPLLNFDAVLIERVFINLLENAY KYTPKNSSVSIGASVSSPQSVEIWVQDDGPGLPKGKEEDIFRKFERGNKEGAISG VGLGLTICRAIIEAHGGKITGKTMAGGGARFTFSLPRGNPPKIDIEDQ	22~~KdpD (7.94073E-121) ~~231,254~~Usp (1.12818E-37) ~~375,404~~DUF4118 (1.45708E-19) ~~503,530~~GAF (2.03459E-16) ~~647,664~~HisKA (0.0000000000780934) ~~729,782~~HATPase_c (2.31643E-25) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.7E-89	308.2	1	2.7E-89	307.6	0.7	1.3	1	B2UR94_AKKM8	Osmosensitive K channel His kinase sensor	Amuc_1154	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	375	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales, Akkermansiaceae, Akkermansia, Akkermansia muciniphila, Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	349741	>tr|B2UR94|B2UR94_AKKM8 Osmosensitive K channel His kinase sensor OS=Akkermansia muciniphila (strain ATCC BAA-835 / Muc) GN=Amuc_1154 PE=4 SV=1 MIDGSNGAEHFLDLIRRSRRGKFKIYIGMMAGVGKTYRMLQEAHELLNNGIDVRIG YVETHGRPGTEAMLRGVPVIPRKVVFYKGREIEEMDLDAILQARPELVIVDELAHT NVEGSRHRKRWEDVMELLDANINVISAINIQHIESLSGEVKEITGIEMKERVPDRILQ EADEVVNIDLTSEELIGRLKAGKIYRPEKIQIALDNFFRTENILQLRELALKEVAFRVE KKVETEVFPAVSSARREKILACISSNEQTPRHIIRKAYRISSRYSTSFIALYVQTPRE SPDRINLASQRHLLNHFKLVAELGGTVKQVSAEDIPQAIIATCREYHITAICMGHPA FKMPGAMFKILGYKQFLRVLSEMKIDLIIIA	18~~KdpD (1.10599E-122) ~~228,247~~Usp (5.67198E-26) ~~375	non-kinase	KdpD;Usp

	1.8E-89	308.1	0	3.2E-89	307.3	0	1.4	1	I0HQX2_RUBGI	Histidine kinase (EC 2.7.13.3)	kdpD RGE_20680	Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	901	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Rubrivivax, Rubrivivax gelatinosus (Rhodocyclus gelatinosus) (Rhodopseudomonas gelatinosa), Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	983917	>tr|I0HQX2|I0HQX2_RUBGI Histidine kinase OS=Rubrivivax gelatinosus (strain NBRC 100245 / IL144) GN=kdpD PE=4 SV=1 MNEPSRPDPDSLLRDVQQDEARARRGRLKIFFGASAGVGKTWAMLAAARDALAH GVPLTVGLVETHSRRDTAAMAEGLPQLPRKRCTYRGRELEEFDLDAALAFGATHE DALVLVDELAHSNVAGSRHPKRWQDVEELLAAGVDVWTTMNVQHLESLNDVVG GITGIRVRETVPDRVFDEADEVVVVDLPPDELLARLKAGKVYLPPQAERAATNFFR KGNLLALRELALRRTADRVDGEMLAWRRRNRVETVWPNREALLAAVAPGGHGE TVVRRCARLAAQLDLPWHAVMVETPALQRLGPEARREALQQLKLAESLGATTATP SAPDAADGLVRYAREHNLSRLVLGRGRRRLPWQRPTVERVAALAGELDVVQVGT AGAPAPRAAGPAPAAEGAGWAGYAAAAGACVLTALAATPLRDVLELSNIVMIFLL AVVGVGLRFGRGPAVAAAFFGVALFDFFFVQPRFSFAVSDVQYLLTFGVMLAVAL AIGQLTAGLKVQAAAAMQRERRVRRLYEMTRDLSAALLPAQVAEIGARFVAAEFG ARCALYATDEHDELQRLPGGEAEADEGVVSWAFRHGRAAGAGTDTLPASRCLVL PLKAPMRQRGVLAIEAGDTAALGPETMRLMETCASLLAISLERLHYVDVAQQSAL QIESERLRNSLLSAISHDLRTPLAALVGLADTLALAPPGPAPRGLVDAIRESARRMA ALVGNLLDMARLQAGAVRLRRAWQPLEEVVGSALAACRPVLQGRPVTVVLADGL PLLSLDAVLFERVLVNLLENAARYTPAGSALAIRAEALDQTVRLVVDDQGPGLPPG REEALFEKFERGERESATPGVGLGLAISRAIVQAHGGTIHGANRLEGGRVAGARF TIELPRGTPPEDDGSAAAAADEDIR	23~~KdpD (3.23512E-106) ~~237,260~~Usp (1.64411E-22) ~~379,410~~DUF4118 (0.00000000000117824) ~~502,529~~GAF (3.30803E-14) ~~642,659~~HisKA (0.000000000000783684) ~~722,775~~HATPase_c (4.17839E-25) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.9E-89	308.1	4.5	2.9E-89	307.4	3.1	1.3	1	R7LGH1_9BACT	Sensor histidine kinase KdpD	BN805_00525	Prevotella sp. CAG:891	379	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:891	1262937	>tr|R7LGH1|R7LGH1_9BACT Sensor histidine kinase KdpD OS=Prevotella sp. CAG:891 GN=BN805_00525 PE=4 SV=1 MKDRKDREENAKHFLQLIRRSQRGVFKVYIGMIAGVGKTYRMLQEAHEMLDNGIN VQIGYVETHGRVATEELLAGLPVIPRKKIYYKGKELEEMDLDAILLLRPELVVVDELA HTNVEGSRHEKRWQDVMELLEAGINVITAVNIQHIESLNEEVKGIAGIEVKERIPDK VLEEADEVVNIDLTAEELINRLKAGKIYRKEKVQTALNHFFKTENILQLRELALKEVA FRVERKVENELVTVEKGVHRERFLVCISSNEKTPRRLIRRTARLATRYDTDFLVLYV QTPAEHPDRIPLATQRHLLNHFKLAAELGGELIQRASPDVIDTIQAVCKERQVTTLC IGQPAFTYVSTLVHLKRYRSFLRFLSDENIKLIIFPQ	21~~KdpD (3.19994E-119) ~~231,250~~Usp (9.19462E-28) ~~347	non-kinase	KdpD;Usp

	2.1E-89	307.9	1.5	3.5E-89	307.2	1.1	1.3	1	R5MM88_9BACE	Osmosensitive K+ channel His kinase sensor domain protein	BN711_02301	Bacteroides intestinalis CAG:564	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides intestinalis CAG:564	1263049	>tr|R5MM88|R5MM88_9BACE Osmosensitive K+ channel His kinase sensor domain protein OS=Bacteroides intestinalis CAG:564 GN=BN711_02301 PE=4 SV=1 MDREQNVQHFLDLIKKSRRGKFKIYIGMIAGVGKSYRMLQEAHDLLDNGVDVQIG YIETHGRAGTEALLAGLPVIPRRRIFYKGKELEEMDLEGIIRIHPEIVIVDELAHTNVE GSRNEKRWQDVMDLLDEGINVISAVNIQHIESVNEEVQGISGIEVKERIPDSVLQEA DEVVNIDLTAEELITRLKAGKIYRPEKVQTALTNFFRTENILQLRELALKEVALRVEK KVENEVVISSVGVRHEKFLACISSHEKTPRRIIRKAARLATRYNTSFIALYVQTPRES ADRIDLASQRYLLNQFKLVTELDGEVLQVQSKDVLDAIIRTCKERQITSVCMGSPAF RFPQSLFMVLKYRKFVSELAQANIDLIILA	17~~KdpD (6.25348E-126) ~~227,246~~Usp (2.19921E-28) ~~374	non-kinase	KdpD;Usp

	2.3E-89	307.8	2.6	3.3E-89	307.2	1.8	1.3	1	E6STB8_BACT6	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Bache_0219	Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides helcogenes, Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	693979	>tr|E6STB8|E6STB8_BACT6 Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108) GN=Bache_0219 PE=4 SV=1 MSREENVRHFLDLIRESRRGKFKVYIGMIAGVGKSYRMLQEAHDLLDNGVDVRIG YIETHGRAGTDAQLEGLPVIPRRKIFYKGKELEEMDLDTIILMHPEIVVVDELAHTNV EGSRNEKRWQDVMELLEEGINVISAVNIQHIESVNEEVQSISGIEVKERIPDSVLQK ADEVVNIDLTAEELIARLKTGKIYKPEKVSVALNNFFRTENILQLRELALKEVAMQVE KKVKNEVVAGVGVRHEKFLACISSHEKTPRRIIRKAARLATRYNTSFAALYVQTPR ESADRINLASQRYLLNHFRLVTELNGEVVQVQSGNILDAIVTTCKERQITTVCMGG PSFPLLRSLFMILKYRKFMDDLAQENIDLIILA	17~~KdpD (1.33326E-123) ~~227,245~~Usp (3.67174E-26) ~~373	non-kinase	KdpD;Usp

	2.5E-89	307.6	2.4	3.4E-89	307.2	1.7	1.2	1	W0F294_9SPHI	FrrC, osmosensitive K+ channel histidine kinase	NIASO_10395	Niabella soli DSM 19437	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Niabella, Niabella soli, Niabella soli DSM 19437	929713	>tr|W0F294|W0F294_9SPHI FrrC, osmosensitive K+ channel histidine kinase OS=Niabella soli DSM 19437 GN=NIASO_10395 PE=4 SV=1 MPDKDHTAQHFLDLIKKSRRGKFKVYLGMSAGVGKTYRMLQEAHSLLRGGIDVKI GYIETHNRAETHALLEGLPLVPRRRLFYKGKELEELDVQAVINLRPEVVIVDELAHT NIEGSKNEKRWQDVVEILDAGINVISAVNIQHIESLNQEVKEITGVEVKERIPDSVLA QADEVVNIDLTADELITRLKEGKIYEPAKIETALNNFFKNDHILQLRELALKEAASQV ERKVETELTLPGAIKREKFLACISSNEKTAKTVIRKTARLANYYNSKWYLLYVQTSR ENADKIALDKQRHLINNFKLAMELGAEIIKIENENVAKAIIEQCEERRITTICIGKPHLN LTRIILATNVFNELLKKLSANEVDLVILS	18~~KdpD (6.22645E-118) ~~228,246~~Usp (8.24069E-31) ~~374	non-kinase	KdpD;Usp

	2.8E-89	307.5	2.2	4.3E-89	306.9	1.6	1.3	1	A6L5B7_BACV8	Osmosensitive K+ channel histidine kinase	BVU_3252	Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides vulgatus, Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	435590	>tr|A6L5B7|A6L5B7_BACV8 Osmosensitive K+ channel histidine kinase OS=Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154) GN=BVU_3252 PE=4 SV=1 MEDREESVQHFLDLIKRSRRGKFKIYIGMIAGVGKSYRMLQEAHEMLENGVDVQI GYIETHGRAGTVAMLEGLPVISRKKIFYKGKEVEEMDLDAILQLHPELVIVDELAHT NIEGSRNEKRWQDVMELLDAGINVISAVNIQHIESLNEDVKGIAGIEVKERIPDKVL QDADEVVNIDLTAEELINRLKAGKIYRPEKIQLALNNFFKTENILQLRELALKEVAFR VEKKVENEIVTGEKGIRHEKFLACISSNERTPRHIIRKAARLASRYNTVFFALYVQTP AESTERIPLATQRHLLNHFKLVTELGGEVIQVSSSDIMGEIIKTCRQRGITTVCMGH PAFKMPGALFSLSKYRKFLHSLAEMDIDLIILA	18~~KdpD (3.96982E-126) ~~228,247~~Usp (1.04734E-27) ~~375	non-kinase	KdpD;Usp

	3.1E-89	307.4	1.6	4.2E-89	306.9	1.1	1.2	1	M0QSC5_MYXSD	Osmosensitive K+ channel histidine kinase sensor subunit	MYSTI_00155	Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	388	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus stipitatus, Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	1278073	>tr|M0QSC5|M0QSC5_MYXSD Osmosensitive K+ channel histidine kinase sensor subunit OS=Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8) GN=MYSTI_00155 PE=4 SV=1 MTTRRSRAEDFLELVERGRRGRLKLYIGFAAGVGKTYRMLEEAHALERRGVDVVL GFVETHGRQETEALVAGLEVVPREKHTYRDVTVEEMDLDAVLARKPQVVVVDEL AHTNLPVCRHRKRYQDVQELLDAGINVIGAFNVQHLESLNDLVERTTGVVVRETLP DSFLKGADQVVNLDLAVEDLHERLRAGKIYAEDKVPRALESFFKGENLSTLRELAL REVAESLDRATAGQSSRPGEEAQQKGAEWGRVLVALSSHPPRAATLLRRGSRLA GRLNTDWFVVYVETPREAPHLIDSEAQRHLLTNIEKAKELGAEVVRLRSKDPVEAI LDFARSHGVGHIIVGRSHQPWWKRAVGRAADVRLLREGEGFDIHVVAFHAPDEE KRP	18~~KdpD (2.62928E-117) ~~228,252~~Usp (1.49994E-40) ~~378	non-kinase	KdpD;Usp
	3.1E-89	307.3	0.9	3.1E-89	307.3	0.6	1.7	1	B0VM40_ACIBS	Histidine kinase (EC 2.7.13.3)	kdpDABSDF1600	Acinetobacter baumannii (strain SDF)	884	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter calcoaceticus/baumannii complex, Acinetobacter baumannii, Acinetobacter baumannii (strain SDF)	509170	>tr|B0VM40|B0VM40_ACIBS Histidine kinase OS=Acinetobacter baumannii (strain SDF) GN=kdpD PE=4 SV=1 MQSNRENQAEALLNHVNRYQAGRLTVFLGAAPGVGKTYAMLARAKELFQQGTD VVVGIVETHGRIETLKILEGLPQIARKEMQYQRHTLEEMDLDAILLRHPQIVLVDELA HRNVPNSRHERRWQDVNELLDAGIDVFTTINIQHLESLNDVVYQITGIRVNETVPD RVFDRIRDIRLIDLPVSELIERLHQGKVYVPEQANLALQGFFSISNLTALRELAMQCV AEHVDSDLKESYASKGLKSISLQNELMIAIDGQGSSEYLVRAGCRLAERNGAIWTV VNVARSLDFGQSSGNSYKKEYIEIDRAFELARQLGGRTEVLYGHRVASVLMDAAV DRGISNLVIGKSISPWWLKLFKKNLAQQLLNQENSIALTILHPEQGTKKINQLEKPS FLSLKESVFVLAVTCASIFIAHFAEVLFGIEDFSVIFIISVLIVATKTRMLAAVVAALICF LAYNFFFIAPRYTFQISAHQGVVTVVAFFAAALIAGRLASQLRQQVLSLKAANAYTT VMQDLARKLSSAVNLEEVMQTGRMTLETQLQTKVWISIRDKVISSDIELNDKEKVT AEWCLKHRQPCGRFTDTLSQSNWCFLPLLEQKNSLGIVGIYFKDELVSLNFEQKK LTESVIEYIAQAVLRTQLVDELEQAKVISETERLRSALLSSVSHDLRSPLASIIGAADT LAHFKAEMTEQDQQDLLETIHLEGERLDRYIQNLLDMTRLGHEGLTLKRDWVGVD ELIGSATRRLKRYKPDTQVVVQLPEQQISLYVHPALVEQAIFNVLENAANFSPPDE PVMIRAQLSSEDEVKIEIEDRGAGIPEDERHRIFDIFYTMERGDRGKFGTGLGLTIV KAIIGAHMGTIEAFSGRQNKGTLIQIKLPLHPVKE	22~~KdpD (3.59125E-117) ~~229,251~~Usp (2.05575E-24) ~~377,401~~DUF4118 (0.0000000012037) ~~499,X,654~~HisKA (0.000000000000941286) ~~720,774~~HATPase_c (4.76603E-21) ~~877	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.6E-89	307.1	1	7.2E-89	306.1	0.3	1.7	1	D3F9J1_CONWI	Osmosensitive K channel His kinase sensor	Cwoe_0725	Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	391	cellular organisms, Bacteria, Actinobacteria, Thermoleophilia, Solirubrobacterales, Conexibacteraceae, Conexibacter, Conexibacter woesei, Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	469383	>tr|D3F9J1|D3F9J1_CONWI Osmosensitive K channel His kinase sensor OS=Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577) GN=Cwoe_0725 PE=4 SV=1 MEAATRSRTGRLKVFLGMAAGVGKTYRMLQEGQAEAESGRDVVIGYLEPHGRAETTAQARGLEVVPRQRVEHRGAFLEEMDLRGILSRAPELCLIDELAHTNAPGLLHAKRYEDVAAVLAAGIDVFSTVNVQHLESLNDTVAELTTTRVRETVPDEVLGEADELVLIDLTPEALIERLRAGKVYPRERIESALNNFFRIEHLSALREVALRQVAEEVEARRVVGPLPARRSGDGERIALSAAPAAIGERLLALVTPAPVSQRVVRRAWRSAQRLGADLDLLWVQPAGRELKPEQAEQLDALRRLAVVLGAHLLVEPGDDLVAVVRRVAHDRRTTYVLIGEPRPRNALRRLLRPSLPSRLLDALPGIDVRIVADRTRRAAAVDEQQEWSGEA	7~~KdpD (1.22714E-108) ~~217,249~~Usp (5.87203E-22) ~~372	non-kinase	KdpD;Usp

	3.8E-89	307	0.5	5.7E-89	306.5	0.3	1.3	1	H8MWB8_CORCM	Osmosensitive K+ channel histidine kinase sensor subunit	kdpD COCOR_07863	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	387	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, Corallococcus coralloides (Myxococcus coralloides), Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	1144275	>tr|H8MWB8|H8MWB8_CORCM Osmosensitive K+ channel histidine kinase sensor subunit OS=Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) GN=kdpD PE=4 SV=1 MTTRRPRAEDFLELVERGRRGRLKLYIGFAAGVGKTFRMLEEAHALKARGVDVVL GFVETHGRPETEALVEGLEAVPRQRLTYRDVTVEELDLDAILARKPQVAIVDELAH TNAPVCRHRKRYQDVQELLAAGINVIGAFNVQHLESLNDLVERNTGVTVRETLPD SFLKTADQVVNLDLAVEDLHERLKAGKIYAPDKVPHALERFFTGDNLSTLRELALR EVAESLDRATTGRQARAGEDASQKGGAWGRVMVALSSHPPRAATLLRRGSRMA GRLNTDWFVVYVETPREAPNLIDAEAQRHLLTNIEKAKELGAEVVRLRSSDPVAAL LDFARSHGVGHIIIGRSHQAKWRQRLGMTADARLLREGEGFDIHVVSFESHEEKR P	18~~KdpD (2.70358E-119) ~~228,252~~Usp (7.46163E-39) ~~378	non-kinase	KdpD;Usp
	4E-89	307	0.1	6E-89	306.4	0.1	1.3	1	Q4K8P7_PSEF5	Histidine kinase (EC 2.7.13.3)	kdpD_1 PFL_4294	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	883	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	220664	>tr|Q4K8P7|Q4K8P7_PSEF5 Histidine kinase OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=kdpD_1 PE=4 SV=1 MSDSGRADALLAELPRDGRGRLKVFLGAAPGVGKTYAMLQAAHSQLRQGVKVLA GVVETHGRAETEALLSGLPQQPLVRSEYRGVLLEEMDLDGLLKAKPKLVLVDELA HSNAPGSRHAKRWQDIQELLAAGIDVFTTVNVQHLESLNDQVRGITGVQVRETLP DWVLQEAYELLLVDLPPRELLERLRDGKVYVPEQARAAIDAFFTQTNLTALRELAM QTAAAQVDNDLAQGYRQLGQAAPAVRGRLLVGIDGDAQAERLVRHASRVAQRR HLPWSLVHVDNGRLRDEQARLRLQAAQQLAERLGGEVVLLRAGEVAKTLIQHAAE RRASLLLVGQSRRRWRRRWFGGGLAARLLRNADGLEINVLDSEPQPHQPGLRVK HSLIWFDYVLAVLATLLASALAWGVASVLPLPNISLVFLAAVLLVAVRSSLGPALAC AALSFLSYDFLFIPPNFSLAIQREEDVLTLLFFLLMAALTGNLAARQRRQLQALRDT QEETGELLDLSRKLTAATDRQAVISAAAQHLNGRDELRVCLINRDGQGGWKVETG GSPQFSEAERAAADWAWQHDQPAGLGTGTLPFGRWWWWPLSVDDGPLGLLG VCPREGEEFSGQRRRLLTALSQPLAQALARARLAEDLEAARLHGETEQLRSALLA SVSHDLRTPLTSMRGSIDSLLALGEAIPLEDRRELLEGTRDEAERLDRYIQNLLDMT RLGHGALKLARDWVAPGDIVGSALNRLRAVLAPLQVATELPADLPLLYVHAALIEQ ALVNVLENAARFSPLQGHLQLKVSASEQELSFAVSDEGPGIPEDERAKIFDMFYTA ARGDRGGQGTGLGLAICQGMVGAHGGHISVAEGIGGKGTCITLHLPLQTQPELES DL	18~~KdpD (5.22387E-121) ~~227,248~~Usp (7.03407E-28) ~~365,405~~DUF4118 (0.00000000274391) ~~489,X,649~~HisKA (0.000000000000184095) ~~715,768~~HATPase_c (1.31607E-25) ~~871	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4E-89	307	0.1	7.7E-89	306	0	1.5	1	A0A0F5LAG7_9RHIZ	Histidine kinase	VW29_17360	Devosia limi DSM 17137	891	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia limi, Devosia limi DSM 17137	1121477	>tr|A0A0F5LAG7|A0A0F5LAG7_9RHIZ Histidine kinase OS=Devosia limi DSM 17137 GN=VW29_17360 PE=4 SV=1 MTDNNDTLRPDPAALLELAARETRGKLTIFLGAAPGVGKTYAMLTRARQRRAEGV EIVIGLVETHGRAETAALLEGLEILPRRAGRQAGRTYDEFDLDAALRRKPAIIIVDEL AHSNDADARHPKRYQDIAELLAAGIDVWTALNVQHLESLSDLVARIAGVPVRETVP DIVLQKADEVVLVDLPPSELIARLREGKVYLPENAGRAAEGFFKPANLTALRELALR RTADRVDDQMADIWRQQAVEGPWTTGERLLVCVGPDQLSEKVVRTASRLAVGL NARWIVLSLSGASNPIPPPARAARLEATLHLAERLGAEIRRATVDDFVAEILRIARRE NITQIVVGRPRPGLLPRRSLPEALLRAAGDIGVYMVPGQGDAPRNPLRLRRRTLP QWALTLALPFVATGLITVLGLGLSQLVALQNLSMLFLVAVLVSALLGGRFAALLAAG LSFLAYNFFFIDPVRTFTIARPHEVLALAIFVGVAVVTGSLAARLREQMGRARQAVR NTQALYDFSRKLSAAYGLDNVLTATAGHLQTTLGLDTVLLASLDGGELELQVAWP PDQNLDATAMTAARWAHDKREPAGFLTATLPAVPYLFLPIRSEQRLVGVVGLKLN AERGPLTPDEGRQVAAILEQAAIAIDRARLVRDNARIALEKEGEKLQTALLSSLSHD LRTPLASITGAVTTLRQLGDRMNGETRADLLMSIEEETGRLNRFVTNLFDMTRIES GAVKPRRDPVDLLALITNVVERARALDPALVVETSIADAMPPVLADPALLDPVLFNL LDNARKYAGTALPVTIFVRVDNGMATIAVTDQGKGIPPGELEAIFDKFYRRAKGDH RAAGTGLGLSIARGFVEAMGGTLKAESPAMRRRGTRFTIRLPLAEGARS	24~~KdpD (1.48827E-113) ~~232,254~~Usp (1.16681E-26) ~~374,398~~DUF4118 (1.0467E-15) ~~497,524~~GAF (0.0000000000253282) ~~643,660~~HisKA (0.0000000034094) ~~726,782~~HATPase_c (5.82922E-26) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.1E-89	306.9	0.1	7.5E-89	306.1	0.1	1.4	1	U7DEJ3_PSEFL	Histidine kinase (EC 2.7.13.3)	B723_08545	Pseudomonas fluorescens NCIMB 11764	883	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens NCIMB 11764	1221522	>tr|U7DEJ3|U7DEJ3_PSEFL Histidine kinase OS=Pseudomonas fluorescens NCIMB 11764 GN=B723_08545 PE=4 SV=1 MSDSGRADALLADLPRDGRGRLKVFLGAAPGVGKTYAMLQAAHTQLRQGVKLIA GVVETHGRAETEALLGGLPQQPLVRSEYRGVTLEEMDLDGLLAAKPKLVLVDELA HTNAPGSRHAKRWQDIQELLAAGIDVYTTVNVQHLESLNDQVRGITGVQVRETLP DWVLQEAYELLLIDLPPRELLERLRDGKVYVPEQARAAIDAYFSQTNLTALRELAM QTAAAQVDNDLAQGYRQLGQAAPTVRGRLLVGVDGDAQAERLVRHASRVAQRR HLPWSLVHVDNGSVRDEQSRLRLQSAQQLAERLGGEVVLLRAGEVAKTLIQHAT ERRASLVLVGQSRQRLRRRLFGGGLAARLLRHARGLEINVIDSDHEQDPPRQRPV QSLVWFDYALALVATVLATALAWAVASVLPLPNISLVFLAAVLLVAVRSSLGPALAC AALSFLTYDFLFIPPNFSFSIQREEDVLTLLFFLLMAALTGNLAARQRRQLQALRDT QEETTELLDLSRKLTAATDRQAVVNAAAQHLEGWSDLQLCLLNRDGQSGWKVET GGPLEFSEAERAAADWAWQHDQPAGAGTGTLPFGRWWWWPLSVEDGPLALL GVCAKEGQTLSGQRRRLLTALSQPLAQALARAQLAEDLEAARLHGETEQLRSALL ASVSHDLRTPLTSMRGSIDSLLALGEAIPLEDRRELLEGTRDEAERLDRYIQNLLDM TRLGHGALKLARDWVSPADIVGSALNRLRAVLAPLQVSTQVPAELPLLYVHAALIE QALVNVLENAARFSPPHGRLQLLAGADDSELFFSVSDEGPGIPEEERAKIFDMFYT AARGDRGGQGTGLGLAICQGMVGAHGGRISVGDGIEGRGTCITLHLPLQEQPDV DSEG	18~~KdpD (2.48437E-121) ~~227,248~~Usp (4.34583E-27) ~~368,390~~DUF4118 (3.66957E-14) ~~489,X,649~~HisKA (0.000000000000150495) ~~715,768~~HATPase_c (6.1205E-26) ~~871	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.2E-89	306.9	1.9	5.6E-89	306.5	1.3	1.1	1	Q1DFX3_MYXXD	Osmosensitive K+ channel His kinase sensor domain/universal stress domain protein	MXAN_0167	Myxococcus xanthus (strain DK 1622)	389	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus xanthus, Myxococcus xanthus (strain DK 1622)	246197	>tr|Q1DFX3|Q1DFX3_MYXXD Osmosensitive K+ channel His kinase sensor domain/universal stress domain protein OS=Myxococcus xanthus (strain DK 1622) GN=MXAN_0167 PE=4 SV=1 MTMTRRSRAEDFLELVERGRRGRLKLYIGFAAGVGKTYRMLEEAHALKRRGVDV VLGFVESHDRADTQALVEGLEVVPRKQYSYRDVTVEEMDLDAVLARKPQVAVVD ELAHTNLPVCRHRKRYQDVQALLDAGINVIGAFNVQHLESLNDLVERATGVAVRET LPDSFLKAADQVVNLDLAVEDLHERLRTGKIYAKDKVPRALERFFTEENLATLRELA LREVAESLDRATARPPPGEGDEGSQRSAAWGRVLVALSSYPRHAATLMRRGSR MAGRLNTDWFVVYVETPREAPHLIDAEAQRHLLTNIEKAKELGAEVVRLRARDPV EGILDFARSHGVGHIIVGRSHQPWWKQRLGRAVDMRLVREGRGFDIHVVAFEPR EEGRRP	19~~KdpD (8.28285E-121) ~~229,253~~Usp (5.58921E-41) ~~379	non-kinase	KdpD;Usp
	4.3E-89	306.9	0.1	7.3E-89	306.1	0.1	1.4	1	A5GAF9_GEOUR	Histidine kinase (EC 2.7.13.3)	Gura_1224	Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	889	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter uraniireducens, Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	351605	>tr|A5GAF9|A5GAF9_GEOUR Histidine kinase OS=Geobacter uraniireducens (strain Rf4) GN=Gura_1224 PE=4 SV=1 MTDNDDKRPSPEALLKLAQAEEKEDGRGKLKIFLGYAAGVGKTYAMLEAGWQRK MEGRDVVAAYVESHGRFETDSLLSMSGVEIIPKAQIEHMGVLLPELDTDAVLARKP QIALVDELAHTNARGSRHEKRWQDVEEILASGIDVYTTVNIQHFESLNDIVAQITGV VVRETVPDRLLDEAAEIRLVDIPPDELLQRLHEGKVYIPKQATLAMEKFFKPGNLIAL RELSLRRAAVRVDEEMRAYMETRSIAGPWPAAERLLVCVSGSPFGEKLIRSTRRL ADEMKAHWYTVYIETPGSGKHVQENRERVWKDLRLAESLGGEVATVSATSVADS VIDFAVKHNVTKIVVGKPTKPRWMEFLNPPLVDQIIRRSGTIDVYVVSIEPSEKSEG TALARRKSPSPWSGYMKSLALVAAATLACELVRPFLAPTNMVMAYLLAVVLAALR LGLKPAIVTAFLGILAFDFFFVPPRLTFAVADTEYLITFVALFTVGVVISTLVARSRER AEAIRKREVQTASLYYLSRDLAVSADIGAVLDAVAKNFGESFNGRLAVLIPEGERLE IKAASREMQLDTKELAVADWAFRNRQSAGHGTETLSSARLLYLPLQTSASVLGVL GVELEDEADYANTQSRRLLDAFTTQTTLAIERVQLGKQAAQALILQGRETLERALL NSVSHDLRTPLVSITGALGTLRDKEHRLSDTRRRELLDAAWEEAGRLNRFVGNLL DMTRLEAGAVTLKEEPCDIQDLVGCALAALEQRIGAREVKVQLPDGLPLVKLDMAL MTQVLVNLLDNALKYSPHASIIDIAARVDDGRLTLEVSDRGPGVPESDLKRIFDKFY RIPVPEGAGGTGLGLSICKGIVEAHHGKIRAENRDGGGLRVIATLPVK	26~~KdpD (1.15235E-114) ~~237,259~~Usp (5.29755E-42) ~~382,430~~DUF4118 (8.81965E-19) ~~505,531~~GAF (0.0000000159054) ~~649,666~~HisKA (0.00000000115186) ~~732,787~~HATPase_c (3.49449E-31) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4.7E-89	306.7	0.1	7.4E-89	306.1	0.1	1.3	1	Q8PCL9_XANCP	Histidine kinase (EC 2.7.13.3)	kdpD XCC0705	Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	886	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas campestris, Xanthomonas campestris pv. campestris, Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	190485	>tr|Q8PCL9|Q8PCL9_XANCP Histidine kinase OS=Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25) GN=kdpD PE=4 SV=1 MSDARTQQADALIGELQREHGGRLTVFLGAAPGVGKTYAMLSRARERLRQGVDV VAGVVETHGRSETAALLDGVPLLPRVQVSYQGHALEELALDALLARKPQLALIDEL AHRNVPGSRHERRWQDTVELLDAGIDVYTTVNIQHLESLNDIVLRITGVRVSETVP DAVFDRLRDIVLVDLPPRELIERLQQGKVYLPEQASQALQAFFSPSNLTALRELAM QTAADRVDSDLRDTQAARGLPGTAALRRHVVVAIDGRGSSDYLVRVARRLSERR DAPWTVVTVQTRTVADAAWQLEIDRAFALTRRLGGDTALLHGANVADALLDFASQ NGVSTLVLGRTRERPLARMFNRTLTQQLLQRGAHYELVIVSSGDARARARQRWR NPGQWLQRYDLAYAAIAAAAAVAVAWVIQRWTDIDDLSMVFIVAVVLVASRTRMA AAVIAALLSFVAYNFFFIEPRFTLHISARQGVVTVCLFLIAALVAGRLASRLRSQVLA LRAANAHANALQALARQLSTAADLGQVLEAGRRALASALDAEVWLRLEQCESEAP TSFSALDRNAADWTQRHGQPAGRFTDTLAGAQWWCLPVRHERGTLGVAALRFR QQLQRPGLEQRRLAEAMVEDIGQAALRTRLVADLEGARVSGETERLRSALLSSVS HDLRSPLASMIGSASSLAEYGEAMDATDRRSLLETIQLEGERLDRYIQNLLDMTRL GHTGLTLKRDWIGVDELIGSATRRLQRYQPQVRLQLDLAPELPAIWVHPALVEQAI FNVLENAAKFSPPGVAVTVQARLQSGALQIEIGDQGPGIPEDERARIFDMFYSVER GDRGRHGTGLGLTICQGMIGAHGGSVEALAGPHGHGTTIRITLPLLVPAASPRPD AD	19~~KdpD (1.67896E-115) ~~229,251~~Usp (7.9026E-27) ~~372,424~~DUF4118 (0.0000000000238775) ~~495,521~~GAF (0.00166421) ~~630,650~~HisKA (0.0000000000604826) ~~716,770~~HATPase_c (1.0525E-23) ~~872	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.9E-89	306.7	0.8	9.2E-89	305.8	0.6	1.5	1	B7J5L6_ACIF2	Histidine kinase (EC 2.7.13.3)	kdpD AFE_2229	Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	913	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus ferrooxidans (Thiobacillus ferrooxidans), Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	243159	>tr|B7J5L6|B7J5L6_ACIF2 Histidine kinase OS=Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) GN=kdpD PE=4 SV=1 MATEDRKDGRPDPDALLAQVQQEEQARQRGRLKIFFGAAPGVGKTYAMLRYGQ QEMAKGVDVLVGIVETHQRSETQTLADALPTLPRVHLAYKNVVLEEFDLDAALAR RPGLLLLDELAHSNAPGSRHKKRWQDLEELLDAGLSVATTVNVQHLESVHEVVQ QITGIQVQETLPDQIIQQADEVILVDISDEDLLQRLKEGKVYLGDRGQRAMTHFFRK GNLIALRQLALRLAADRVDLELRQFHQQNPEEGRRSGSRDRLLVAVSGRPEDEHL VRAAYHLATAQRADWLVIHVDTPRGLLQRPQTQAWIWNHLHLAESLGAETARLT GVNIGAEVLAYARLRDVTQIVLGQTQGLRKFLWWWPGSLTAHLLNSERGIDVVIH PLPVKKAIPEDRRRLRNQQYLGIVDTPLRRRTRNRAFVISGTIGLALSGLAWSLGAYL GFAGVFMLYMLGAVGTALMYGRWPSLITFIAAVVSYYSFGLDRGLPTTVGSLAYF ALILSLILLISQLVARSREQELMARIRERRARNLYQLVQALSSARGVEGILNASIEKLH QTLGIAVAFWLPLVDNAGGPLQMFPASTDLEAPQRNLRAAARWSFLNKKNAGMS TDTLADIPALFMPMLSGERALGVMMLSDLDLRRAPVDWLRFLETVARLIAVALDSA QASLQRTEADVRLRVEQLQNALLGAVSHDLRTPLAGVLGTATTLQRNAQGLTAEE HDLLENIREQTQKMEHTVDRILHMAALQSGRLHIKKEWVPLEDLLVTARDQVKAVC ADRPFQVRISKDLPLLLVDPQLMVQVLTNLLENACRYSPSGRAIELEAYANDAEITV CVIDHGFGVPPGREEEIFLRFSQVKPPHGLGGSGLGLAICAAIIELHGGRIWVRNR VAVRGAVFCFTVPREPEPPMPSDGD	28~~KdpD (2.93998E-106) ~~237,260~~Usp (3.30249E-31) ~~382,427~~DUF4118 (0.00212445) ~~495,542~~GAF (0.00000000049239) ~~662,680~~HisKA (0.00000000024862) ~~744,800~~HATPase_c (1.17874E-16) ~~900	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5.5E-89	306.5	2.6	7E-89	306.2	1.8	1.1	1	C6VYH1_DYAFD	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Dfer_0381	Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	371	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Dyadobacter, Dyadobacter fermentans, Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	471854	>tr|C6VYH1|C6VYH1_DYAFD Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114) GN=Dfer_0381 PE=4 SV=1 METSAEHFLQLIKQSRRGKFKIYIGMSAGVGKTYRMLQEAHALLRTGIDVKIGYIET HNRKETHELLEGLPVIPRRKLFYKGKELDEFDVQAVITLRPEVVIVDELAHSNIEGS KHAKRWQDVLDILEAGINVISAVNIQHIESLNQEVREITGVEVAERIPDKVLGMADE VVNIDLTADELITRLKEGKIYREEKIQAALQNFFKPQHILQLRELALKEVASQVERKV ESEIQPGMVLKHERFLACISSNEKTARNVIRKTARLANYYHSSWFLLYVQTPGESA SRIGLAKQRHLINNFKLATELGGNVIKMESGSIARTIVEVAEKNKITTICIGKPHLNLF KVILATNVFNGLLNKMSSSDIDLVILS	15~~KdpD (1.0034E-119) ~~225,243~~Usp (5.90423E-29) ~~371	non-kinase	KdpD;Usp

	6.1E-89	306.4	1	9.9E-89	305.7	0.7	1.3	1	Q0PAK0_CAMJE	Truncated KdpD protein (EC 2.7.3.-)	kdpDCj0679	Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	606	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Campylobacter, Campylobacter jejuni, Campylobacter jejuni subsp. jejuni, Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	192222	>tr|Q0PAK0|Q0PAK0_CAMJE Truncated KdpD protein OS=Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168) GN=kdpD PE=4 SV=1 MQRQSPEQILKKLEVKAKEEEKNKLVKLKIFLGYAAGSGKTYAMLSEARTLRDNG VDVVLGYIEPHDRPETMALAQGFESIANLEIPYKNIVLKEFDLDATLKRKPALVLVDE LAHTNAKGLRNEKRFQDIEELLKAGIDVYTTLNIQHLESLNDLVANISKIEVKERIPD RIFDEADQVELVDIEPNKLLKRMQDGKIYKEKQAKLALENFFRQERLIALREIALRRL ASRVNLRASEQRLINDDLAYHTGEHILVCINASNAKVIRAAARLALAFHAKLSALYIK NPNIKEAKALEENIELAKSFDAKIISVYDDIARQIAEYSSLSNVSKIVLGKNKDKKSLK KRFLKLSLKKHPILIYILSMKIKFLLLKYEVKKSFDFLGFLKITGVLLLATFIAFVFHKFN TQPSNIVMIFILAVFASSFISDNKIFAFYSSLVSVLIYNFFFLEPIFSLKVHDSGNIITFT TMFIVGFLTAVFTRRLKLQSKELTKRAYRTAILLENSENLARVKSKQELWEQLGNQ ALKLLNLPIIIYPINKNNILSKPLLFFNDDKQMLKNCFSADEIAIAQWVATNKERAGVC TNTLPNANAMYLPIEDGKKLKGL	27~~KdpD (4.48022E-117) ~~233,254~~Usp (7.10705E-18) ~~337,386~~DUF4118 (0.000000000000051276) ~~485,X	non-kinase	KdpD;Usp;DUF4118;X;

	6.2E-89	306.4	0.6	6.2E-89	306.4	0.4	1.4	1	D4ZNR6_ARTPN	K+-transporting ATPase D chain	NIES39_O07180	Arthrospira platensis (strain NIES-39 / IAM M-135) (Spirulina platensis)	370	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Arthrospira, Arthrospira platensis (Spirulina platensis), Arthrospira platensis (strain NIES-39 / IAM M-135) (Spirulina platensis)	696747	>tr|D4ZNR6|D4ZNR6_ARTPN K+-transporting ATPase D chain OS=Arthrospira platensis (strain NIES-39 / IAM M-135) GN=NIES39_O07180 PE=4 SV=1 MFQTSLCITPPNPPQSIALGKHKVFIGMAPGVGKTYRMLEEAQQLKQEGFDVVIGI LETHGRADTAEKAVGLEQVPLKQINWLFRTLTELDTSAVLARCPQLVLVDELAHTN IPGSERQKRYQDVFWILEAGIDVYSTINIQHLESLNDLVHKISGVVVRERVPDRLLD EADEVIVVDVTPETLQERLQEGKIYASAKIDRALHNFFQRRNLVALRELALRFVADN IEDNGRQSHSQSYCNIQERVLVCVSTYPSSIRLLRRGARIANQMNGRLSVLFVAHP HQFLSKSEALHIETCKRMCQEFEGEFLRVESDDVVTAILDTAVEQHITQIVLGETRR SRWQLLIKGSIVQRLMRGLPQVDLHIIGTDH	20~~KdpD (2.21518E-122) ~~227,245~~Usp (1.176E-45) ~~367	non-kinase	KdpD;Usp
	6.5E-89	306.3	0	9.9E-89	305.7	0	1.3	1	E8RRF1_ASTEC	Histidine kinase (EC 2.7.13.3)	Astex_0655	Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	886	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Asticcacaulis, Asticcacaulis excentricus, Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	573065	>tr|E8RRF1|E8RRF1_ASTEC Histidine kinase OS=Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48) GN=Astex_0655 PE=4 SV=1 MKAETRPDPDKLLALFSHDTGGLSRGRLKIFFGASAGVGKTFAMLSEARRLLAEG RNVIIGVAEHHNRPETLALFDGLPVLPQKTIDHRGVSVREFDLDAALQLKPDLILVD EYAHTNAPGSRHPKRWQDIEELLENGIDVFTTLNVQHLESLNDVVARLTGVVWVKE TVPDVAFDEADEIALIDIPPEDLLQRLSEGKVYVAEGAPQRAADNFFKKGNLGRLR ELALRRAAERVDADNDAFSAAMGQSEAATGDKILVLVGPDALSERLIRHTKRMAD RSRAPWSALYLQTDRHETLSDKARLRVEHHLRLAEKLGGRVVRLIAGGAAATILGY ARHNGFTRLVLGHSRPVWWRFGLPSLSQKLMAQGAGLEITTLTADQIEVGSRDPI GHTLLATPPRTYLMAGVAVGVSTLLGLPFREMIDPDSLVMLYLTGVVIVAARYGIG PSVLASVLSVAAFNWFFIKPYYSFTFDNISYVLTFAVMLATSLIVGSLTARLSLHVRL ARRGEAESRLLYDLSRALSAARGLEDIGDAVQRGLTAAFDVEVALWNNGAQITGV PEIDPRELGAMQWVAQNRQIAGRHTDTLPSARALYVPLPSEPGVLGLTPRDRDR QFTGAEWLVFETVASLIASALQRARQSLEAESARVETENEKLRNVLLASVSHDLKT PLTVMNGAVASLLKMRKKLPREAVDELTSLWGHLTGLQKFVANLLRMAAITSGQL KLNFGPYLIQEIAGAALQRIDPQKGDRQLRTLTAGQIPMVNIDGALIEQVLINLLENAI AHTSDDGIITLSFEGDADRVRVRVSDNGPGLPAGEEAQIFEKFHRAGGLSSDRLS TDRSGQSNGLGLAICKGIIEAHGGLIYAKTNPTGGASFIFTLPAYTHPV	25~~KdpD (2.9732E-115) ~~234,255~~Usp (1.27535E-31) ~~374,401~~DUF4118 (4.46976E-17) ~~497,527~~GAF (0.00000325614) ~~635,652~~HisKA (0.000137175) ~~716,770~~HATPase_c (1.29841E-28) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.1E-89	306.1	1.1	1.4E-88	305.2	0.4	1.7	1	A0A0F2C8J6_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpDRS85_01850	Microbacterium sp. SA39	854	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium sp. SA39	1263625	>tr|A0A0F2C8J6|A0A0F2C8J6_9MICO Sensor protein KdpD OS=Microbacterium sp. SA39 GN=kdpD PE=4 SV=1 MSREHSRRGRLRVLLGAAPGVGKTFEMLAEGRRLRDEGHDVVIAIVETHERAATQ AQTVGLEEVPRRIDDHRGVPLTELDLDAVLSRAPEIALVDELAHTNSPGSRHPKR WQDVDELLAAGIDVITTVNVQHVESLNAVVEKITGVAQQETIPDAVVRAADEIEVV DLAPQSLRDRLSAGLVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALRT YRAEQGIEGTWQARERVVVALTGGPEGETLLRRGARIAARSAGGELLAVHVSAQ DGLRDETPGALAAQRTLVESLGGSYHQVVGDDIPATLVEFAQGADATQLVIGVSR RGRLAAALTGPGIGSEVIRRSGDIDVHIVTHAAAGGRLALPRMTGGALGWRRQVL GFAVALVFGPLLSWVMFAFRSPESITAEVLAYQLLVVVVALIGGIRPAVFAAVLSGI TLDFLFVAPLFTITVAHPLHVLALALYVVIAILVSIIVDQAARRARTAQRAAAEAELLA AVAGNVLRGDNAVLAMVSRTREAFGLSGVRLLSPDGDVLASDGEPVADGRSTTV PVGVGANGSPRATLELHGQPLAGPERRLLDAIVAQLSAAIEHTDLRATALEAEALA ETDQVRSALLSAVSHDIRRPLASAVAAIGGLRGAHELSASDRAELLATADESLATLS ALVTDLLDVSRVQAGVLAVSATRLDATAPVLAAVDELGLGPSDVELALDSALPALH ADPVLLQRVLVNVLANAHRHAPSGSRVLVSTSALGERAEIRIIDRGAGVAPERRDSI FQPFQRFGDTDNTTGLGLGLALSRGFTEGMGGTLTPEDTPGGGLTMVISLPLAAT SPTLRQAQESHMTEDTE	6~~KdpD (1.73471E-112) ~~216,238~~Usp (9.15303E-29) ~~361,389~~DUF4118 (0.00000000603261) ~~482,X,615~~HisKA (0.0000000143933) ~~680,731~~HATPase_c (1.42434E-22) ~~832	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	7.3E-89	306.1	1	1.3E-88	305.3	0.7	1.4	1	W0JK97_DESAE	Histidine kinase	DESACE_07650	Desulfurella acetivorans A63	652	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfurellales, Desulfurellaceae, Desulfurella, Desulfurella acetivorans, Desulfurella acetivorans A63	694431	>tr|W0JK97|W0JK97_DESAE Histidine kinase OS=Desulfurella acetivorans A63 GN=DESACE_07650 PE=4 SV=1 MQENDIKRPSPEELLEVAKQQEASEQKKGKLTIYLGYAPGVGKTYTMLSDAHLRK KEGIDVVVGYAETHGRVETEKLLEGLEVIEPLIVDYKGLKLKEVNFEKIIQRKPQLVII DELAHTNPPNFKNVKRYQDVEEILNAGIDVYTALNVQHIESLNDLVYQITNIAIKETV PDKFIEQASEIKLVDLTPEELLKRLDATAPVLAAVDELGLGPSDVELALDSALPALH RIVADSVDGKMRSYMKQHAIAGPWAVKEKVLVGIFASPYAEQLVRATYRFATEIDA QWIAVHVETQKNQYFTDQEKAWLNKAFDLVRSLGGQIVWIKGDDITTEIVNYAKS QNVTKIVIGKPRKFSMFSPTIPEKLIMQTEFIDVYLIAPKDKKPQEFLKKKKYGIKNIK DYLYSTINIGAVTLLSLILKNHLNHSSLMSIFLAALVLNALIFEIPAVIVSIVISVLVFDFF FIPPQYTFYISNFNYLISFLVYVVVIVFISVLATKLKTKVNLLKESQLRELSLYELSNNL VMASTKEQVLSILINHIKKLFNVEAAIFIADENNKLKVGAKTKDFEINSETLGIANWSF INKKNAGFGTDTISNATALYIPMITTNGVFGVIAINLKQLNKPVTIDQTVAIDAIAHLG AIALERLKLMRCS	27~~KdpD (1.52678E-113) ~~236,258~~Usp (5.02857E-32) ~~378,401~~DUF4118 (0.0000000321014) ~~500,528~~GAF (0.0000000371551) ~~645	non-kinase	KdpD;Usp;DUF4118;GAF

	7.7E-89	306	0	1.2E-88	305.4	0	1.3	1	V6KD61_STRRC	Histidine kinase (EC 2.7.13.3)	M878_19690	Streptomyces roseochromogenus subsp. oscitans DS 12.976	1000	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	1352936	>tr|V6KD61|V6KD61_STRRC Histidine kinase OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_19690 PE=4 SV=1 MSDVRPGRLKVYLGAAPGVGKTYRMLDEGRRRAARGADVVVGFAECHGRPHTE AMLDGLDTVPRASCSYRGGQFQEMDLAAVLTRRPQVAIVDEIAHSNVPGEGRNP KRWQDIEALLDAGIEVITALNIQHLESLNDVVEKITGVPQHETVPDEVVRRAWQIEL VDMPPEGLRRRMAHGNIYAPEKIDAALANYFRPGNLQALRQLALLWTADRVDEAL QEYRSQHGIGRVWETRERVVVALTGGPEGDTLVRRAARIADRSAGGDLLAVHVA RSDGLAAGVSHASLARQRRLVEDLGGSYHSVVGDDVATALVEFARAENATQLVL GTSRRGRLTRFLTGPGTGETVTELSGDIDVHRVTHERAGRGTLLPSRRRTLSTAR LIAGPVAGLVLPVLLTALLAQLRGTLNLTSEALLFLLAVVGVACIGGVASAVIASVTA SLLLNYWFIPPIGAFTLNDPNALVGLTVFAVVAAIVAAVVDRSLRLSRRSARATAEA ETMSSLAGSIVRGEATIPALLERTRETFGMESADLVDEPPDAAGPDAGRLDPGRL DAGGLDAGGAQVFGSHVVRSHASGSHVGGADMGGSCVGGGDGAGSHVGGVD GAGPHVAGADTGGSYVVGVDGAGSHVGGADMGGSYVAGADAAGSHTVGSHEA GPHAAGSEAGGPRAAGFHSASSGAVFVSAGLHVAGADACGSPTVVPHVAGSHA AGATAVPAGPGAWLVLRGRTLSSSERRVLAAFAAHVGSAVERARLAEAAAEVEP VKAADRLRTALLRAVGHDLRTPLAAGWAAVTSLRSRDVAFSDEDRDELLATADES MAKLNRLVENLLDLSRLEAGALTLNLRATTLEEVLPLALADVPGVRVTDMEGIPAVL ADPPLLERVIANLVGNAARHTPPGKQVLVTASVLAGRVELRVVDRGPGLPADGRD RLFEPFQRLGDTDNTTGLGLGLALARGLTEAMNGTLSPEDTPGGGLTMVVSLPFA GRRVGAEASEQSVGGP	5~~KdpD (9.0558E-101) ~~215,237~~Usp (1.05563E-29) ~~361,391~~DUF4118 (0.0000000143939) ~~469,X,767~~HisKA (0.00000000177203) ~~833,880~~HATPase_c (6.82399E-25) ~~981	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.4E-89	305.9	0.1	1.5E-88	305.1	0	1.4	1	A0A0F5FWK2_9RHIZ	Histidine kinase	VE25_03050	Devosia geojensis	894	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia geojensis	443610	>tr|A0A0F5FWK2|A0A0F5FWK2_9RHIZ Histidine kinase OS=Devosia geojensis GN=VE25_03050 PE=4 SV=1 MSDTNADIRPDPRAFLKLAAGEGRGKLTVFLGAAPGVGKTYAMLARAQQRKVEG TDIVIGLVETHGRPETARLMEGLEVLPRRKGERSGTTYDEFDLDAALQRKPAIIIVD ELAHSNDAAARHPKRYQDIAELIAAGIDVWTALNVQHLESQSDLVSRIAGVPVRET VPDVVLKNADEVVLVDLPPAELIQRLKEGKVYLPDNAGRAVEGFFRPENLTALREL ALRRTADRVDDQMADIWRQQAVEGPWITSERLLVCVGPDPLSEKVVRTASRMAL GLNARWMVLSLSRSADPIPDADKAARLEATLVLAERLGAEVRRVVADDFVAEILKI ARRENITQIVVGRMRAGLLTRLTRRSLPDALIASAEGIGIHLVPEAERPSASSLTPR RRSLPEWLATFGLPAATVGAITLLGLGISQLLALQNLSILYLLSVLVCAILVGRAAALL AAVFSFLTYNFFFIEPTGTFTIAKPHEVLTLVIFACVALVTGTLASRLRDQVERARQA VRNTQALYDFSRRLSAAYGLENVLTATAAQLHAMLGKGAVLLTPGETGTLELQVA WPPDQALDDTAMTAARWAHDKREPAGFMTGTLPAVPYLFLPIRSDQRIAGVVGL SRDMAQGPLSPDEDRQVSAVLEQAALAIDRARLVRENAKVAVAKEGEKLQTALLS SLSHDLRTPLASITGAVTSLRQLGEKMSVETRADLLTSIEEETGRLTRFVGNLFDM TRIESGMIKPRREPVELEPLIGEVIARAGKLDPALKVETSIAEAMPPALADAQLLEQ VLFNLLDNARKYAGTAEPVAVYVRREEDMAVISVTDQGRGIPEDEIEAVFEKFHRR ARGDGRPAGTGLGLSIARGFVTAMGGTIKAESPAVRKRGTRFVVRLPLALEGTA	22~~KdpD (3.89033E-113) ~~232,254~~Usp (2.29708E-30) ~~377,397~~DUF4118 (4.52085E-14) ~~500,527~~GAF (0.00000000175669) ~~646,663~~HisKA (0.00000000250424) ~~729,782~~HATPase_c (2.85564E-28) ~~886	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	9.4E-89	305.8	0	1.2E-88	305.4	0	1.1	1	X1X445_ACYPI	Uncharacterized protein		Acyrthosiphon pisum (Pea aphid)	517	cellular organisms, Eukaryota, Opisthokonta, Metazoa, Eumetazoa, Bilateria, Protostomia, Ecdysozoa, Panarthropoda, Arthropoda, Mandibulata, Pancrustacea, Hexapoda, Insecta, Dicondylia, Pterygota (winged insects), Neoptera, Paraneoptera, Hemiptera, Sternorrhyncha, Aphidiformes, Aphidomorpha (aphids), Aphidoidea, Aphididae (aphids), Aphidinae, Macrosiphini, Acyrthosiphon, Acyrthosiphon pisum (Pea aphid)	7029	>tr|X1X445|X1X445_ACYPI Uncharacterized protein OS=Acyrthosiphon pisum PE=4 SV=1 RPDPDALVLNHSDSHRGKLKIYFGACAGVGKTSPCCREAQRLRAQGLDVLAGVV ETHGREETAALLNGLAVLPRRATGRSRHAEFDLDAALARHPAVILMDELAHTNVQ GSRHPKRWQDIEELLEAGIDVITTVNVQHLESLNDVVGGVTGIQVRETVPDPFFDS ADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALRELALRRTAD RVDDQMRAWRDQQGRDKVWHTRDAILLCIGDDTGSEKLVRTAARLAARLGSEW HAVYVETPRLNRLPEARRRAILRTLQLAQELGAETATLSDPDEARAVLRYAREHNL GKIVTGRQPQRRWRRDSFAQRLGQLGPDLDLLVVALDEPVRDAPHPMGGKQAN SDKWRLHLRGCLMAIALCILVTIVVAGYWWSSIRANGVMIYLLAVVSATPAAAGLA TRAPAESTLLSPNPLVLPTTTQSPHPCLPARLCGWRISCRWRGEAQSADSSAAH HSSAVVQAHCGKSWSAPAMAGRSVG	14~~KdpD (3.83911E-122) ~~222,245~~Usp (6.83984E-42) ~~364,X	non-kinase	KdpD;Usp;X;
	9.6E-89	305.7	0.3	1.9E-88	304.8	0.2	1.5	1	Q88FD9_PSEPK	Histidine kinase (EC 2.7.13.3)	kdpD PP_4158	Pseudomonas putida (strain KT2440)	884	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas putida (Arthrobacter siderocapsulatus), Pseudomonas putida (strain KT2440)	160488	>tr|Q88FD9|Q88FD9_PSEPK Histidine kinase OS=Pseudomonas putida (strain KT2440) GN=kdpD PE=4 SV=1 MSDSARADALLANLPRTGRGRLKVFLGAAPGVGKTFAMLQAAHAQQRQGVQVL AGVVETHGRAETEALLGGLHQQPLLRSQYRGVTLEEMDLDGLLRAAPALALVDEL AHTNAPGSRHAKRWQDVQELLAAGIDVYTTVNVQHLESLNDKVRDITGVQVRETL PDWVLQEAFELVLIDLPPRELLERLREGKVYVPEQARAAIDAYFSQTNLTALRELA MQTAAAQVDADLAHGYRQRGQEAPALRGRLLVGIDGDDQAERLVRHASRVAQR RHLPWSLVHVDNGRLRDETARHRLQAAQQLAERLGGEVVLLRAGEVARTLIQHA VERRASLVLVGQSRNRLRRRLFGAGVAARLLRESRGLEINVLDRDVQPPAPRSAV RRVWVWRHYLLALLATVMAAGLAWAVSSVLALPNISLVFLAAVLLVAVRSSLGPAL ACAALSFLVYDFLFIPPNFSFTIQREEDVLTLVFFLLMAALTGNLAARQRRQLQALR ETQAQTSQLLDLSRRLTVATDRQAIFKAAGQHLDGWQDAQVCLLERNAEGQLQV ASGEACTFSDTERAAADWAWQHGQAAGHGSDTLPNGRWWWWPLAVDDQPLA LLGVRPRNGQPLSDPRRRLLTALGQPLAQALARARLAEQLEAARLHGETEQLRSA LLASVSHDLRTPLTAMRGSIDSLLALGDAIPAEDRRELLEGTRNEAERLDRYIQNLL DMTRLGHGGLKLARDWVAPADIVGSALNRLRVVLAPLRVHTDVPTELPLLFVHAA LIEQALVNVLENAARFSPANGRLELQVAVHDDQLRLTVSDQGPGIPEADREKIFDM FYTAARGDRGGQGTGLGLAICQGMIGAHGGQILVGEGIDGQGTSITLCLPLPPQP EAESETP	18~~KdpD (8.60373E-111) ~~227,248~~Usp (1.87446E-29) ~~365,389~~DUF4118 (1.36702E-19) ~~48,X,649~~HisKA (0.0000000000000519565) ~~715,768~~HATPase_c (2.32701E-26) ~~871	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	9.7E-89	305.7	0.9	1.5E-88	305.1	0.6	1.3	1	A0A089YR56_9PSED	Histidine kinase (EC 2.7.13.3)	LT40_01790	Pseudomonas rhizosphaerae	878	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas rhizosphaerae	216142	>tr|A0A089YR56|A0A089YR56_9PSED Histidine kinase OS=Pseudomonas rhizosphaerae GN=LT40_01790 PE=4 SV=1 MSDSGRADALLAALPRNGRGRLKVFLGAAPGVGKTYAMLQAAHARQRQGIEVLA AVVQTHGRAETEALLVGLPQQALRRSQYRDVILEEMDLDAVLAARPALALVDELA HSNAPGSRHAKRWQDVQDLLAAGIDVYTTVNVQHLESLNDQVQSITGVQVRETL PDWVVQEADDLLLIDLPPRELLERLREGKVYVPEQARAAIDAFFTQTNLSALRELA MQTAAAQVDDDLHEGYRSLGQQAPSVRGRLLVGIVADEQAERLVRHASRVARRR HLPWSVVHVDNGRLLDETARQRLQLAQQIAERLGGEVVELRDAEVARTLLQHAG DRRANLILVGQSRRRRFGAGLAERLLRSHSGVEINVLARAQVQPSKPRRPRPVGR WREYVLALLATLLASGLAWAVAQVLDLPNISLVFLAAVLLVAVRSSPGPALSCAAL SFLAYDFLFIPPNFSLSIQRQEDVLTLLFFLLMAALTGNLAARQRQQLSALRETQAH TAQLLELSRLLAAATDRQAVFSAAAQHLHGWPGLDICLLERGEQGWKVAHGSAA PFTTTELAAAQWAGNHAQPAGLGTATLPAGRWWWLPVTLEGRVLALLAVAERQ PGRLDGHGRRLLGALVQPVAQALARADLAHDLEAARLHGETEQLRSALLASVSHD LRTPLTAMRGSIDSLLALGSALAPDDRQALLEVTRDEAERLDRYIQNLLDMTRLGH GALKLARDWVAVGDIVASAVGRLRAPLAPLQVQVQVPAQLPLLYVHAALIEQALVN VLENAARFSPVGGRLQVSARVRDDSLLLAVSDEGPGIPEAERTKIFDMFYTAARG DRGGQGTGLGLAICQGMVGAHGGRVEVSSGIDGQGTCIALCLPLRAQPGADADT	18~~KdpD (3.30946E-116) ~~227,248~~Usp (7.03663E-24) ~~365,401~~DUF4118 (0.000000141823) ~~485,511~~GAF (0.000090766) ~~627,644~~HisKA (0.000000000000353906) ~~710,763~~HATPase_c (1.79044E-25) ~~866	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.2E-88	305.4	2.7	1.2E-88	305.4	1.9	1.4	1	A7GLG6_BACCN	Osmosensitive K channel His kinase sensor	Bcer98_0627	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	381	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cytotoxicus, Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	315749	>tr|A7GLG6|A7GLG6_BACCN Osmosensitive K channel His kinase sensor OS=Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98) GN=Bcer98_0627 PE=4 SV=1 MYAEEYEPKFQRRSPEDYLEEIQRMNRGKLKLYVGAAPGVGKTYKMLLDAHEMK KEGLDVVIGLVETHGRKETEAAILDLEIIPLQEIEYKRKRFYELNVEKIIKRAPQVVVV DELAHSNIPGAKHKKRYMDVEELLEAGISVLSAFNIQHLESVHDIVEQITNIKVRERI PDCILQKANEIQLVDVTPEVLRKRLRDGKIYKEEKIKQSLEHFFTINNLGALRELSLR EVADDMDEKMSQSLIEPIGVKEKILVCVQYSLAAEKLIRRGWRMANRLNAELFVLN VERGNVESISAGRRQIIAEWKALTKQFEATFLLEEAKGRKPAAVMIEVAKRLQVTQI LLGQSARTRWEEICKGSIVNEIMRETKYIDIHIVADQRK	25~~KdpD (4.19754E-111) ~~235,252~~Usp (3.95331E-39) ~~377	non-kinase	KdpD;Usp

	1.3E-88	305.3	2.3	1.9E-88	304.8	1.6	1.2	1	R7DKZ6_9PORP	Uncharacterized protein	BN686_00682	Tannerella sp. CAG:51	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:51	1262979	>tr|R7DKZ6|R7DKZ6_9PORP Uncharacterized protein OS=Tannerella sp. CAG:51 GN=BN686_00682 PE=4 SV=1 MDKEKSVQHFLDLIKQSRRGKFKIYIGMIAGVGKTYRMLQEAHQLLESGVDVQIGY VETHGRTDTDAQLKGLPVIPRRKIFYKGKELEEMDVEAIIRIRPEIVIVDELAHTNVE GSLNEKRWQDVLQLLDEGINVISAVNIQHIEALNDEIQRISGIEVKERIPDSVLEEAD EVVNIDLTAEELLARLKAGKIYRSDKVEWALSHFFNADNILQLRELALKEVALRVAK KVEDEVVVGNVGVRHEKILVCISTNEKTPRKLIRKAARLAIHHNTQFSVLYVQTPKE SADRIPLAVQRHLLNHFKLATELGGEVIQLQKSNVIDGIIEACANNHITKCCIGKPEL SFFSAVFSIMNYKKLVDFLSTSNIDLIILA	17~~KdpD (2.2949E-121) ~~227,246~~Usp (2.24863E-24) ~~374	non-kinase	KdpD;Usp
	1.3E-88	305.3	0.9	2.9E-88	304.2	0.3	1.8	1	A0A077F967_9PSED	Histidine kinase (EC 2.7.13.3)	PSAKL28_17460	Pseudomonas alkylphenolia	886	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas alkylphenolia	237609	>tr|A0A077F967|A0A077F967_9PSED Histidine kinase OS=Pseudomonas alkylphenolia GN=PSAKL28_17460 PE=4 SV=1 MSDSNSERADALLAGLPREGRGRLKVFLGAAPGVGKTYAMLQAAHAQVRQGVQ VLAAVVETHGRAETESLLAGLAQQPLVRSKYRGVQLEEMDLDGLLKAAPQLALVD ELAHSNAPGSRHAKRWQDVQELLAAGIDVYTTVNVQHLESLNDQVRGITGVQVR ETLPDWVLQEAFELVLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRE LAMQTAAAQVDADLAHGYRQLGQDAPSLRGRLLVGVDGDAQAERLVRHASRVA QRRHLPWSLVHVDNGKLRDETARQRLQAAQQLAERLGGEVVLLRAGEVAKTLIQ HALERRANLVLVGQSRDRLRRRLFGAGVATRLLREAHGLEINVLDRDERPEPQSA AVKKVWVWRHYLLALVATVLAAGISWGVSGVLALPNISLVFLAAVLLVAVRSSLGP ALACAAMSFLTYDFLFIPPNFSFSIQREEDVLTSLFFLLMAALTGNLAARQRRQLQA LRETQEQTNQLLDLSRKLTAATDRQAVFNAAGQHLDGWNDLQVCLLERDVEGRL QVASAASVQFNDNERAAADWAWQHDQAAGLGSDTLPNGRWWWWPLSVEEQP LALLGVRPRQGQSLTAQRRRLLKALSQPLAQALARARLAEQLEAARLHGETEQLR SALLASVSHDLRTPLTAMRGSIDSLLALGEAIPQADRQELLEGTRNEAERLDRYIQN LLDMTRLGHGGLKLARDWVAPTDIVGSALNRLRVVLAPLQVSTEVPDGLPLLFVH AALIEQALVNVLENAARFSPVNGRLQLQVSADDEQLRFAVSDEGPGIPAADREKIF DMFYTAARGDRGGQGTGLGLAICQGMIGAHGGHILVGEGIDGHGTCITLCLPLPT PPEPESEAP	19~~KdpD (5.11795E-118) ~~229,250~~Usp (2.79571E-28) ~~367,391~~DUF4118 (1.27522E-18) ~~491,X,651~~HisKA (0.00000000000127096) ~~717,770~~HATPase_c (1.69162E-24) ~~870	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.6E-88	305	0.4	2.6E-88	304.3	0.3	1.4	1	A0KED2_AERHH	Histidine kinase (EC 2.7.13.3)	AHA_0014	Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	862	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Aeromonas, Aeromonas hydrophila, Aeromonas hydrophila subsp. hydrophila, Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	380703	>tr|A0KED2|A0KED2_AERHH Histidine kinase OS=Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240) GN=AHA_0014 PE=4 SV=1 MRDEVRADALLASLEQEHRGKLKVFLGAAPGVGKTYAMLQAVREQAKEGVDILIG VVETHGRQETLALLDKLAIQPRKLHLHRQQRLEEMDLDGLLARKPAIAVVDELAHS NAPGSRHEKRWQDVEELLGAGIDVYTTLNVQHLESLNDLVWQLTGVRVKETLPD QVLLEADSLVLIDLPPKELLGRLKEGKVYVPHQAKAALQSFFSLNNLTALRELAMQ TAASHVEGDLQLQWQAAGKTTLPLRGKLMVCLGDQHGAALVRYGHRFAQRRQL PWLVVHIDSKGQRSVELEQALALASQLGAKVLTLSSPAVADTLLETAEQQQVSQL LLGKPHKAPWRRSLVQHLLKQAQGLEITLVDTEKRKPSLGLKPLHPKDIRQSLLAV AIMGTTSAAVWGLSHWLPPASLPMLFVLGVLATALTTSLMPAILAAVLGFVGHNLL FTAPYFSLSVASHSDLLTLFVLLIVGITAGRLASRQRQQLIGLRETQQLGNALLSLS QGLATASSPEEVLRQGSQAISLALGQPVFALDQHYQHRAGSTQHKPGQTDKAAI DWCLAQKQSAGAHTATLNAAEAQYHHLSDELVLGIVLANPLASSAEHQLQALLTDI RAALARIDLNERLADSQLQAETDRMRAALLSSVSHDLKTPLATIMGAGSTLLEYGD RISSEDRSELLHSVQDEARRLHSYVQNLLDMTRIGSPDFQLKRDWVDLADLVENA RRRLDSSWRQHKLLVHFDQQIPRLYVHGALIEQVLVNILDNASRYSPAGTPIEFKV MLADPDLILDIIDIGVGIAESDRDKIFNLFYTQPVGDCGSRGTGLGLAISRAMIEAHG GRIWAFSGPNGNGTCMRISLPLALNAAAA	17~~KdpD (1.60465E-116) ~~227,248~~Usp (9.36775E-25) ~~359,382~~DUF4118 (0.00000000000863693) ~~480,X,631~~HisKA (0.0000000000454122) ~~697,750~~HATPase_c (5.84817E-23) ~~852	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.6E-88	305	0.1	2.4E-88	304.4	0.1	1.3	1	A6V7F6_PSEA7	Histidine kinase (EC 2.7.13.3)	kdpD PSPA7_3637	Pseudomonas aeruginosa (strain PA7)	885	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	381754	>tr|A6V7F6|A6V7F6_PSEA7 Histidine kinase OS=Pseudomonas aeruginosa (strain PA7) GN=kdpD PE=4 SV=1 MTDTARADALLADLPGDGRGRLKVFLGAAPGVGKTFAMLQAAQAQLRQGVKLRA GVVETHSRAETEALLAGVPQQPLRSLEYRGMKLQEMDLDGLLADPPALALVDELA HSNVPGSRHAKRWQDIQELLAAGIDVYTTVNVQHLESLNDQVRDITGVQVRETVP DWVLQEAYEIVLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELAM QTAAARVDADLAHRYRQRGEEAPALRGRLLVGIDGDEQAERLVRHACRVAERRH LPWSVVHVDTGGLRGEQARMRLQGAQQLAERLGGEIVVLRAGEVARTLLQHARE RRASLVLVGQSRRRWYRRAFGGGLAGRLLRDGQGLEISALDSEADLRPAEPRPR YPLAWNDYLLALLATALASGLAWGVAHLLELPNISLVFLMAVLLVAVRSSLMPALLC AVASFLAYDFLFIPPHFSFAIHRHEDLLSLAFFLFMAGLTGNLAARQRRQLEALRDT QEETSLLLELSRKLTAATDRQAVLAAAAQQFEGWQDVEVCLLGQVNGEWKTEAG AQRPLTDQERVAADWAWSHDQPAGLGTGTLPGGRWWWWPLSAEEGPLALLGI APLDGQPLSPQRRRLLAALGQPLAQALARARLAEDLEAARLHGETEQLRSALLAS VSHDLRTPLTAMRGSIDSLLALGEAIPPADRRELLESTRDEAERLDRYIQNLLDMTR LGHGGLKLARDWVAPGDIVGSALNRLRAVLAPYRVQAIVGNDLPLLYVHAALIEQA LINVLENAARFSPSQGRLRVEVSQGDAELRFAVSDEGPGIPLAEREKIFDMFYTAA RGDRGGQGTGLGLAICQGMIGAHGGRISVGEGLDGRGTTLVLHLPLHPQPDLGQ LEADE	18~~KdpD (1.99307E-121) ~~227,248~~Usp (1.30925E-31) ~~365,405~~DUF4118 (7.94576E-14) ~~489,X,648~~HisKA (7.14152E-14) ~~714,767~~HATPase_c (4.4664E-26) ~~870	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.7E-88	305	0	3.2E-88	304	0	1.5	1	A5FU13_ACICJ	Histidine kinase (EC 2.7.13.3)	Acry_3493	Acidiphilium cryptum (strain JF-5)	867	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acidiphilium, Acidiphilium cryptum, Acidiphilium cryptum (strain JF-5)	349163	>tr|A5FU13|A5FU13_ACICJ Histidine kinase OS=Acidiphilium cryptum (strain JF-5) GN=Acry_3493 PE=4 SV=1 MGSASPENRPDPDALLARANSDGRGQLKIFLGAAPGVGKTWEMLAAARRRFETG TDVVAGLVETHGRAETAEQLADLPVLPRRIVPYRGRLLEEFDLDSALKRRPALLLV DELAHANAPGLRHAKRWQDVAALLEAGINVWTTLNVQHLESLNDQVARITGIRVA ETLPDTVLGLADDIELIDLPPEELRTRLKQGLVYRPDVARRALGGFFRPGNLAALRE MALRRVAQHVDRDIAAYMRAQAIAGPWPAAERVMAVVEAGEAAEQVVRHASRLA EALRAPFFAFHAERAATGMAVQPALDLAIQLGGTVETTTNADVFAALLDAAARQN VAHIVIARGRGRWRWRRGLASRLARGARAYALHVVPDPAASRPAPPHRAPPPKL MPFGISLGIMIVTTIGGFALRGVLPAEAMGYVFTAIVVGMASLYGRSVGIFAALTGF VLWNFFFLPPIYTLSVTNPRDVTALFAFLVVGVLTGSLAGRVRAEAETARTRIEALR RITLFGRALAQVSDEAGLAAVVEAEARALAGEAVLLLARGDGLPRAGGFDEAAVA AAEFAWRNRVATGMGTTTLPASAWRFQPLATEAGAIGVLGVRPETPPAEPVIQTL SALADQAALAAERLRLATSAAEARAHESTQRLRTALLSSLSHDLRTPLTAIRGAAET LAEADGELPEATRRDLLASIVEDVGRMTRFLANITGMARIETGEIVARHEKVDLAPV VEHAVARVKEAFHTAVNIPEDAATVRADPALLEQVLVNLLENAVKYGPEGGAISVF ARRAGDSVVLSVADEGVGIPPEDLPHVFDSFFRVVRGDRVAPGTGLGLAIARAFV EAMGGTIAAESPRRDLPADGLPGTIIRVELPVP	23~~KdpD (2.94869E-113) ~~232,254~~Usp (4.31871E-14) ~~367,387~~DUF4118 (0.0000000000171432) ~~487,X,639~~HisKA (0.0000000000633345) ~~705,755~~HATPase_c (1.06629E-28) ~~864	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.7E-88	305	0.7	3.9E-88	303.7	0.3	1.7	1	A0A0F0LD98_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpDRS83_00569	Microbacterium oxydans	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium oxydans	82380	>tr|A0A0F0LD98|A0A0F0LD98_9MICO Sensor protein KdpD OS=Microbacterium oxydans GN=kdpD PE=4 SV=1 MTRERRGRLRVLLGAAPGVGKTFEMLVEGRRLLDEGRDVMIAVVETHDRAATRA QTVGLPEIPRRTDVHRGVPLTELDLDAVLARRPEIALVDELAHTNIPGSRHPKRWQ DVDALLDAGIDVITTVNVQHIESLNAVVEKITGIAQQETIPDAVVRAADEIEVVDLAP QSLRDRLAAGVVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALRSYRAD HGIEGAWQARERVVVALTGGPEGETLLRRGARIAARSAGGELLAVHISTQDGLRD ETPGALAAQRALVESLGGSYHQIIGDDIPGTLVEFAQGADATQLVIGVSRRGRLMA ALTGPGIGSEVIRRSGDIDVHIVTHAAAGGRVALPRITGGALGWRRQVLGFAVAVV FGPLLSWVMFTFRSPESITSEVLAYQLLVVVVALIGGIRPAVFAAVLSGITLDLLFVA PLFTITIAHPLHVLALVLYVVIAILVSLIVDQAARRARTAKRATAEAELLAAVAGNVLR GDNSVLALVSRTREAFGLSGVRLLSPTGEVLACDGEPLADGRATSVPVGSDGTP RAMLELHGDSLDAPARRLLDAIVAQLAAAIEHTDLRETAKEVAALAETDQVRSALLS ALSHDLRRPLASAVAAIGGLRGAHELSADDRAELLATADESLATLSTLVTDLLDVSR VQAGVLAVSSAPMDATGPILAAVDELGLGPADVDLSLDPNLPLLQADAVLLQRVLV NVLANAHRYAPDGTRVLISTSALGERAEIRIADRGEGVPAERRDSIFQPFQRFGDT DNTTGLGLGLALSRGFAEGMGGSLTPEDTPGGGLTMVISLPLAEADPLRHAQESL EETE	4~~KdpD (1.13447E-114) ~~214,236~~Usp (4.86183E-29) ~~359,387~~DUF4118 (0.00000000642391) ~~480,X,611~~HisKA (0.00000000783989) ~~676,727~~HATPase_c (4.22505E-23) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.7E-88	304.9	0.2	2.9E-88	304.1	0.1	1.4	1	A0A077LKJ0_9PSED	Histidine kinase (EC 2.7.13.3)	PSCI_3959	Pseudomonas sp. StFLB209	880	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. StFLB209	1028989	>tr|A0A077LKJ0|A0A077LKJ0_9PSED Histidine kinase OS=Pseudomonas sp. StFLB209 GN=PSCI_3959 PE=4 SV=1 MSDSSRADAILAQLPRDGRGRLKIFLGAAPGVGKTYAMLQAAHSRMRQGVNLLA AVVQTHGRAETEALLVGLPQLPMLRREYRGMTLEEMDLDGVLRAAPALVLVDELA HSNVPGSRHDKRWQDVHELLAAGIDVYTTVNVQHLESLNDQIRAITGVQVRETLP DWVLQEAFELVLIDLPPRELLERLRDGKVYVPEQARAAIDAFFSQTNLTALRELAM QTAAAQVDNDLAQGYRQRGEQAPAVRGRLLVGIDGDIQADLLVRHASRVAERRH LPWSLVHVDADRPLDEQGRAYLQGAQQLAERLGGEVVTLRAGEVARTLLQHAVE RRASVVMVGQSRHLWRRRLFGGGVAGRLLREAHGLEISVLDSQALPDRPRQRAP IKGLDYALAVLATALASGVAWGIAGILALPNISLIFLMAVLLVAVRSSVGPALFCALLS FLAYDFLFMPPNFSLSIQREEDVLTLVFFLLMAALTGQLASRQRRQFKALRATQEQ TSTVLDLSRKLTAATDRQAVLSAAEQHLSGWPELQLCLLGRDQNASWVVELGGP LTFSEAERVAADWAWQHDQAAGLDTGTLPSGRWWWWPVSAEEGPLALLGVCP RPGHRFTAQHRRLLSALSQPLAQALARAQLVQDLESARLHGETEQLRSALLASVS HDLRTPLTAMRGSIDSLLALGEAIPLDDRRELLEGTRDEAERLDRYIQNLLDMTRLG HGSLKLARDWVAPADIVGSALGRLRAVLAPLQVEVQMAAELPLLYVHAALIEQALV NVLENAARFSPVGGVLRVHSRVSEGELQLLVSDQGAGIPEAERAKIFDMFYTAAR GDRGGPGTGLGLAICQGMVGAHGGRVTVAEGIDGLGTCMTLHLPLPAQPQADSE	18~~KdpD (8.53863E-117) ~~227,248~~Usp (1.05552E-29) ~~365,400~~DUF4118 (1.17323E-16) ~~487,533~~GAF (0.00102664) ~~630,647~~HisKA (0.000000000000282075) ~~713,766~~HATPase_c (1.29711E-23) ~~869	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.9E-88	304.8	0.5	3.3E-88	304	0.4	1.4	1	A0A0F0LTG6_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpDRR49_02066	Microbacterium ginsengisoli	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium ginsengisoli	400772	>tr|A0A0F0LTG6|A0A0F0LTG6_9MICO Sensor protein KdpD OS=Microbacterium ginsengisoli GN=kdpD PE=4 SV=1 MRRGRLRVLLGAAPGVGKTYAMLEEGHRLSAEGADVVVGVVETHGRAATAALTR GLEVVPLRRDRHRGVSLDELDVEAVITRHPSVALIDELAHTNAPGSAHAKRWEDV EQLRDAGIDVITTVNVQHIASLSDVIEQITGTVQRETVPDAVVRGADQIEVVDLAPQ SLRDRLSAGLVYPAERVDAALSNYFRLGNLTALRELALLWLADEVDSALKQYRAE HDIDGTWTTRERVVVALTGGPEGETLIRRGARIAARSAGGELLAVHVLSQDGLRG ATPGALATQRALVEQLGGTYHQLVGDDVAHTLVEFARSVNASQLVIGVSRRSRM SAALTGSGIGATVIRDSGDIDVHIVTHSAAGGKLRLPRVRGGALSRGRRLLGFAVA LVGGPLLSWLLFSFRSDDSITSDVLAYQLLVVIVALVGGIWPALFAAVLSGFTLDYL FVQPLFTITIAHPLHALALGLYVVIAILVSYIVDQAARRARVAERATAEARLLATIAGS VLRGDSAVEALVSRAREAFGLHAVRLVGEGGTVLAEDVADGPAPANAACTRLPV GARVGGAPRATLELTGDEPDGASRRLLDVIVAQLAAAIDHLELTAAAREADALAET DQVRSALLSAVSHDLRRPLAAAVAAVGGLRAADVRLSPTDRAELLETADESLRTLS MLVTDLLDVSRVQAGVLAVSLAPVDAAGALLAALDELGYGPDEVEVALDPDLPPLV ADPVLLQRVLVNLLANARRFAAPGTHVVVTTSRLGELAQIRVIDRGPGVPADRRDD IFAPFQRQGDTDNTTGLGLGLAISRGFTEGMGGTLTPEDTPGGGLTMVVELPVQP AAETTTQGAR	1~~KdpD (3.85656E-112) ~~211,233~~Usp (8.27437E-31) ~~356,379~~DUF4118 (0.0000000000770134) ~~477,X,613~~HisKA (0.000445695) ~~679,730~~HATPase_c (3.73936E-24) ~~831	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2E-88	304.7	1.7	2.7E-88	304.3	1.2	1.2	1	C6X583_FLAB3	Osmosensitive K+ channel histidine kinase kdpD (EC 2.7.3.-)	FIC_01121	Flavobacteriaceae bacterium (strain 3519-10)	416	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, unclassified Flavobacteriaceae, Flavobacteriaceae bacterium (strain 3519-10)	531844	>tr|C6X583|C6X583_FLAB3 Osmosensitive K+ channel histidine kinase kdpD OS=Flavobacteriaceae bacterium (strain 3519-10) GN=FIC_01121 PE=4 SV=1 MFTMTEVSALAAYLPQPLWPSVFRITGKTRLLLHKKPTSPKKMDEERKTAEHFLQ LIKKSRRGKFKLYIGMSAGVGKTFRMLQEAHTLLRSGIDVKIGYIETHRREETAALL EGLPLIPRRTLFYKGKELEEFDVQAVINLRPEVVIIDELAHTNIEGSKNQKRWQDVF EILDAGINVISAVNIQHIESLNDEIRNITGISVQERIPDSVVAQADEVVNIDLTADELIA RLKEGKIYNAEKIEAALTNFFQSDHILQLRELALKEVATQVNRKVETEVLKPNTLKH ERFLACISSNEKSAKTIIKKTARLANYYHSKWFVLYVQTPAENADKIALSKQRHLIN NYKLATELGAEIISISHSSIPKAIISQVEEKKITTVCIGKPRLTLWNLIMATGTFPLLLK KLAAEKVDTVILS	60~~KdpD (2.40343E-118) ~~270,288~~Usp (1.4488E-22) ~~392	non-kinase	KdpD;Usp
	2E-88	304.7	0.1	2.8E-88	304.2	0	1.2	1	A0A0A1CX93_9MICC	Histidine kinase (EC 2.7.13.3)	ART_2196	Arthrobacter sp. PAMC25486	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. PAMC25486	1494608	>tr|A0A0A1CX93|A0A0A1CX93_9MICC Histidine kinase OS=Arthrobacter sp. PAMC25486 GN=ART_2196 PE=4 SV=1 MTRGILRIFLGSAPGVGKTYSMLEEGHAQAAAGVDVVAGVILDHGRAQTRAQLAG LESVPTQHLSYRGSDFQELDVAALLARRPALALVDEYAHSNIPGAGNAKRWQDVE ELLAAGIDVYSTVNVQHLASLRDVVESITGVRQQETIPDDVVRRAEQIELVDIPPELL RQRLSTGHVYAADKVDAALANYFRLGNLTALRELALLWLADRVEEGVAAYRHSH GIAENWPTRERVVVGLSGGAEGEVLLRRAARILSRVSGGELLAVHVPRSDGVSG DAPSALEGQRQLVTDLGGSYHSVGGEDPARALLDFARNAGATQIVIGSSRRKPRL GFLLGAGVGARVVRDAGDMDVHMVPHPHSAAGGVVRNRGELNRKRVVAGFALA VVLPVLVQLGTGPLSLQTTMVIQLAAAIGVALVGGLWPAILAAVWGSLLLNYFSAP PVGNLTINDPENLLALLVFLVVAVAVALAVDQSARRSREAVQAGAEAATLSELARG ILASQDTVQVFLEQVRDHFGMRSVALFATAAPPGTWHLAASVGEEPPQNPAAAD TVEEVSDHWVLGLSGRILPARDRRLLSAFGAHLLALEQREALSETQRENVQLSQD NNIRTSVLRAVSHDLRTPLAGIKLAVSSLRQTEVTFSPEDEAELLATIEHYSDRMDA LVGNLLDMSRLSAQMVRPVAGPVTWQEVLPGALHGVPSERVRRELPPNMPPIEA DPGLLERVIANIVENAVKYAPDSDILVVGSVGGSGSATINGRPASELRVIDHGRGV PAAEVMAMFRPFQRLDDVSYGPHGGSGVGLGLAVAKGFTEIMGGVLEAEQTPG GGLTMTIRMPLSTGIVRTLP	3~~KdpD (8.21449E-106) ~~211,233~~Usp (2.12514E-25) ~~356,377~~DUF4118 (0.000260071) ~~452,X,606~~HisKA (0.0000000000076768) ~~672,721~~HATPase_c (2.7726E-17) ~~833	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2.2E-88	304.6	1	2.8E-88	304.2	0.7	1.1	1	H1ZCI4_MYROD	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Myrod_0222	Myroides odoratus DSM 2801	376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Myroides, Myroides odoratus (Flavobacterium odoratum), Myroides odoratus DSM 2801	929704	>tr|H1ZCI4|H1ZCI4_MYROD Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Myroides odoratus DSM 2801 GN=Myrod_0222 PE=4 SV=1 MERETRQSAEDFLALIRRAKRGKFKVYIGMSAGVGKTYRMLMEARDLQRNGIDVK LGFIETHNRQETHALLAGLPLIPRKEVFYKGKMVEELDLEAILKEHPEIVIIDELAHSN IAGSKNAKRWQDVMEILEAGINVISALNIQHIESLNNAVKDITSIDVMERVPDKVLQE ADEVVNIDLTADDLIERLKEGKIYPPAKVPAALQNFFTSSNILQLRELALKEVASHVE NKVASEVSMSVSAKPSRFMACISSNDKHAKNVIRKTARLASYLNSKWYVLYVQTP KEHPDKIALDKQRHLINNFKLATELGAEIIKSEHPNIAKAIMMQVEQRQVTTICIGKP RLRLYQIILATNVFNQLLKKLTSLPIDIIIFSK	19~~KdpD (4.18219E-118) ~~229,247~~Usp (1.89891E-30) ~~375	non-kinase	KdpD;Usp

	2.2E-88	304.5	3.7	2.2E-88	304.5	2.5	1.4	1	R5V113_9BACE	Uncharacterized protein	BN535_00850	Bacteroides caccae CAG:21	376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides caccae CAG:21	1263037	>tr|R5V113|R5V113_9BACE Uncharacterized protein OS=Bacteroides caccae CAG:21 GN=BN535_00850 PE=4 SV=1 MDDREQSVQHFLDLIKRSHRGKFKIYIGMIAGVGKSYRMLQEAHELLENGVDVQIG YVETHGRVGTEAMLQGLPVISRRKIFYKGKELEEMDLDTIIRIHPEIVIVDELAHTNV EGSLNEKRWQDVMALLDEGINVISAINIQHIESVNEEVQEITGIEVKERVPDSVLQE ADEVVNIDLTAEELIARLKAGKIYRPEKIQTALDNFFRTENILQLRELALKEVALRVEK KVENEVVMGVAVGLRHEKFMACISSHEKTPRRIIRKAAKLATRYNTTFIALYVQTPK ESMDRIGLARQRYLLNHFKLVTELGGEVVQVQSRDILGSIVEICKEKQISTVCMGS PDLKLPYAICSILGYRKFLNNLSRANVDLIILA	18~~KdpD (6.88942E-125) ~~228,248~~Usp (3.39384E-24) ~~376	non-kinase	KdpD;Usp
	2.2E-88	304.5	0.2	4.2E-88	303.6	0.1	1.5	1	A0A0F2JLF4_9FIRM	Osmosensitive K+ channel histidine kinase KdpD	UF75_0351	Desulfosporosinus sp. I2	881	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	1617025	>tr|A0A0F2JLF4|A0A0F2JLF4_9FIRM Osmosensitive K+ channel histidine kinase KdpD OS=Desulfosporosinus sp. I2 GN=UF75_0351 PE=4 SV=1 MAKGKLTIFLGAASGVGKTYAMLEAALGRLSEGIDVVVGLVETHGRADTEAMLKE LTVIPWGTRDYLGRTFHELDLDAVLTRRPQLVVIDELAHTNIEGSRHKKRYMDVKE LLSAGINVYTTLNIQNLETLNDIVTQITGITVQETVPDQVLEAASQIQLIDIPPEELIQR LKDGKVYVPGQETEGFRNFFRPGNINALRELALRYTAQRVDRQLESYRRIHGIDG PWATGEKILVCISASPFSAQLIRIAKRMTEKVQGELLAVHVETLRRFPSSESEKDS MAKNLRLAEELGAEVIGLTGNSVAEVILGLARKRNVSQILIGKPQHTRLWEIIHGSV VDKVIRQSQGVSIHVIPGNQQEAGSAQIQTLEIRNSPKLIPYLASSLMVIVMTLVLTL VSPFLGLVNISLAYLLPILLSAARWGTLPAIATAFMGTIAFDLFFVPPIFKFTVADLRY LISFVIFMLVGLITGTLSERLKKQVNYSRQRENSISALYSLSRDIAAVDNLEAVLDCIV SNVSETLEGQVMLLLPNEKAQLVLRKHSGLNDFLDQPEFSVATWVYERGLKAGY GTETLGTAKALYLPLRTEQGTQGVLGIYIKERKAQFDPEGMRLLEAFTGLSAVAIN RVKLAEQARETLTLVESERLRTALFNSLSHDLRTPLASIIGAVTGLLEDQNVVYSPE VRKELLKTILHGAERMNRFISNLLDMARLESGMLSLKKDWCDLQDILGVAINRLGD TLTRRPLDIDIQEGLPLVQADGILIEQVLINLLDNALKYSEAASKILISIRQQERQLEIVI ANRGPNIPETDLSKVFDKFYRLSSPLQVSGTGLGLAICKGLIEAHGGDIWAENNKL GGVTITFTLPLTDQCFGIVPEMDEGE	1~~KdpD (7.92257E-108) ~~211,233~~Usp (6.85486E-38) ~~356,380~~DUF4118 (1.79028E-16) ~~480,506~~GAF (0.00000000148999) ~~626,643~~HisKA (0.00000000000192135) ~~710,763~~HATPase_c (7.01755E-28) ~~864	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.4E-88	304.4	0.1	3.5E-88	303.9	0	1.3	1	A0A0F2TAZ5_9ACTN	Uncharacterized protein	VM95_26865	Streptomyces rubellomurinus	794	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rubellomurinus	359131	>tr|A0A0F2TAZ5|A0A0F2TAZ5_9ACTN Uncharacterized protein OS=Streptomyces rubellomurinus GN=VM95_26865 PE=4 SV=1 MAGKLRVFLGAAPGVGKTYAMLREGRRLRGEGLDVVVGLVETYGRRGTQEQLG DLPVLPRRLVRYRGTDLTELDVDALLARRASLALVDELAHTDVPGGRNAKRWQDV RELLDAGIDVATTLNIQHLESLNDVVEQITGVAQRETIPDEVVRAADRIELVDLSPDA LRTRMAQGEVYPPDRVDVALDHYFRAGNLGALRELALLWLADRVEEELADYRAR HGIRAPWETKERIVVALNGAAQGEHLIRRGARTATRVHGDLIGVHVRLDDGTAER EPPALAAQRDLLRELHGSFVEVSGGDVARALVDFARTESATQILLGPTSRSRLREL ATGSVINRVIRLAGPIDVRVLPPPEPGLLTVPPAPRRRRPALVPVRRRRLAWLLGP AGVVTLAWALSPLRGSLGLSGALLCLLLAVAGTARLGGLLPAAGATAAGALAADY FFTTPWHSLTVGRGADLAALVLFLAVAGVIAHLIDGLTRRSQQAGRARAEAAVLTR LAGETVESGPRVLPDLVAELRQVFGLDGAAVLVRTGALWLPAASAGAAVPLRPEE ASFSVDLGDGAVLVLRGTPLTEEDTRLLGPYVTQLKLARERERLAAQASAAEVLA HTDALHTALLEALGRDLRAPLAAVRQEAERMPGPDGRRVGAQVERMERLVANLL DLSRLRAGVMPVVLRPTVVAEVVRAAAEGVPGVRIDLGAGLPRVIADPGLLERAFT DVLAAAGAGPVVVDAGVVAGRVDVRVTVPGGEAAVQEGAGQPVVRGFVEAMN GELAVEEAPGGGTAYVISLARAVA	3~~KdpD (1.53661E-108) ~~210,232~~Usp (2.39353E-25) ~~353,X,617~~HisKA (0.00101652) ~~670,754~~HATPase_c (0.00951405) ~~789	kinase	KdpD;Usp;X;HisKA;HATPase_c

	2.4E-88	304.4	0.4	2.4E-88	304.4	0.3	1.7	1	V5XHB1_MYCNE	Histidine kinase	D174_21905	Mycobacterium neoaurum VKM Ac-1815D	593	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	700508	>tr|V5XHB1|V5XHB1_MYCNE Histidine kinase OS=Mycobacterium neoaurum VKM Ac-1815D GN=D174_21905 PE=4 SV=1 MGILGRKRADLRIYLGAAPGVGKTYSMLGEAQRRMSRGTDVVAAVIETHGRRHTA QQLAGIEMVPPIVIEYQGARHAEIDVEAVLARRPQVVLVDELAHTNTPGSRNAHR WQDVEEFLDAGITVISTVNVQHLESLHDVVGHITGITEQQRIPDEIVRAADQIELVDI TPEALRRRITHGNVFGRDRIDAALDDYFRPGNLSALRQLALLWLADQVDAALAKY RTDKNITDTWEARERVVVAVSGGPESETLVRRASRIASRSGAELKVLHIVQGDGL VAITPQQKKMLRELAASLGATMHTVVGEDVAATLLDFARSANATQLVIGTSRRSR WARMFDEGIGAQVIAQSGNVDVHMVTHPEAHTGISWSRSSLHRRRFWSWLTAV AIPAIICAATTGLPEGALGIGGQSALFFTGVVAVALIGGIAPAALCAVLSGVLLTYFLV SPVHSFAVYDSDSVVTIAVLLVVAVAVAVVVDRAAHRAAEARRAAREAELLALFAD AALRDADLDVLLDRLREAYGQRAVSIVSADGTVLAGVGHDPCTDVEAADTAIDVA DHDHWLLLSGKTLTTRDRRVLSAVAEQAVSMIRRQSA	7~~KdpD (1.88289E-107) ~~216,238~~Usp (4.19507E-35) ~~359,382~~DUF4118 (0.000008087) ~~462,X	non-kinase	KdpD;Usp;DUF4118;X;

	2.6E-88	304.3	3.5	3.5E-88	303.9	2.4	1.2	1	A0A0C1FPQ1_9FLAO	Histidine kinase	OA93_21600	Flavobacterium sp. KMS	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium sp. KMS	1566023	>tr|A0A0C1FPQ1|A0A0C1FPQ1_9FLAO Histidine kinase OS=Flavobacterium sp. KMS GN=OA93_21600 PE=4 SV=1 MDNEKENNVKHFLDLIQKSRKGKFKVYIGMSAGVGKTFRMLQEAHTLLKNGIDVKI GYIETHNRKETHELLDGLPVIPRRSIFYKGKQLEEMDVQAIINLRPEVVIVDELAHTN IEGSKNEKRWQDVLEILESGINVISAVNIQHIESLNEDVKRITNVDVKERIPDNVLRL ADEVVNIDLTSEDLIDRLKEGKIYTEDKIQTALNNFFKSDQILQLRELALKEVASQVL RKVENEVPKTQALRHEKLLACISSNERTAKNIIRKTARLASYYNSDWYVLYVQLPR ESSDKIALDKQRHLINNFKLATQLGAEVIKIESTNITDTMLKVVEQKEITTVCIGKPHF NFFKVILATSIFRRLLTRLSLSNVDLVILS	19~~KdpD (8.29478E-117) ~~229,247~~Usp (1.14568E-29) ~~375	non-kinase	KdpD;Usp
	2.7E-88	304.3	0.8	5.1E-88	303.4	0.6	1.5	1	Q8F1M3_LEPIN	Histidine kinase (EC 2.7.13.3)	kdpD LA_3109	Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	870	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira interrogans, Leptospira interrogans serovar Lai, Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	189518	>tr|Q8F1M3|Q8F1M3_LEPIN Histidine kinase OS=Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) GN=kdpD PE=4 SV=1 MIKDTRLDPDELLRKIQKEEQKEISGRLKVFFGMVAGVGKTYAMLNAARGLKKEG VDVVVGYIETHGRKETEELLEGLEILPRKKIEHREIEFEEMDIDSILRRKPEVVLVDE FAHTNIPGSRHVKRYQDVIEILNHSINVFTTLNVQHLESQVESVEKNTSVKIRETIPD SILDMADEIVLIDLSPDDLRKRLQEGKVYVPEKANLAGDYFFKKENLTFLRETALNY TARHVNVALDSEKFREKILVSIGSNPNSYSLLRYAKRLAYERNGELFAIYNQTRENL TKENLSQLEKNLSFARELGCEILYAADEDTAEAILRISGQKSITRVVIEKSDTNWW WRWNSTASKLARIPSNFELCLVPYSFISGEESVLNRFLRTSSGGKQYLTSLTLILLA TCISLFLEPIAGYWSISLLYLFFVSGIGSFFSKGPTVLAGLLSGIFWDFLFIPPRYTFF IEKLEDVLMFGAFLFISIIIGNVTSRLRQKEKVLVNRELRLTTLYELSKELGHARDVR RISEIGAEYLGKVFQTEIVILLENQGNIDFNSSRAGNFFPDPKETAVSNWVYKNKIP AGKFTDTLSLSLGTYFPMIAPGKVIGVIGVVLNERLNLDQENLLLTMGNQIALALER ELLSEETRTRYLANQSERLYTIIFNSLSHELKTPLSSIRGAVTALLEPEIENSREARV ELLNEINESSMILNLLLGNLLDMSRYESGFLKLRMDWHDPSDLIHVVVRRLRQTVK NSHCVIHLPENPVPTWMDFTLMEQALFNVVFNAVQISPEGTPVFIELICRKDKIQYI VEDEGPGIPKEDLEKIFEKFYRSKNRNHVGSGLGLSISKSIVETHGGTLTAENRTIV GARFCIEIPIKSS	26~~KdpD (1.28846E-103) ~~233,245~~Usp (5.06249E-19) ~~364,387~~DUF4118 (0.000000000000135552) ~~487,513~~GAF (0.0000000000053259) ~~629,655~~HisKA (0.000176703) ~~697,765~~HATPase_c (2.40073E-24) ~~865	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.7E-88	304.2	0.9	3.7E-88	303.8	0.6	1.2	1	D4IJZ0_9BACT	Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain (EC 2.7.13.3)	AL1_06430	Alistipes shahii WAL 8301	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, Alistipes shahii, Alistipes shahii WAL 8301	717959	>tr|D4IJZ0|D4IJZ0_9BACT Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain OS=Alistipes shahii WAL 8301 GN=AL1_06430 PE=4 SV=1 MERQDSVQRFLELIRRSHRGKFKVYIGMSAGVGKTCRMLQEARQLLDAGVDVRI GYIETHGRAGTEALVEGLPLVPRRRLFYKGKELEEMDTQAIVNLRPEIVVVDELAH TNIEGSENPKRWQDVMQILDAGISVISAVNIQHIEGLNEVVEEITGIEIRERVPDSVL AMADEVVNIDLTADELIERLKAGKIYRPDKIAAALGNFFTQDNLLQLRELALKEVALR VEKKVDSEVTGSETFRRDKLLAVIDSSEKRARRVIRKTARMATHLNAAFTVLYVQG DREADDRIPLARQRYLINNLNLATELGGEVRRIRSNSPVESIAGVCREQKINIVCIGR PEFSLFSLLKSAIRLRRLTVRLSRMNIDLFIFS	17~~KdpD (6.7923E-117) ~~227,245~~Usp (1.09477E-19) ~~373	non-kinase	KdpD;Usp
	2.9E-88	304.2	0.4	4.9E-88	303.4	0.3	1.4	1	A0A0F5VG60_9GAMM	Histidine kinase	KY46_04840	Photobacterium halotolerans	889	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	265726	>tr|A0A0F5VG60|A0A0F5VG60_9GAMM Histidine kinase OS=Photobacterium halotolerans GN=KY46_04840 PE=4 SV=1 MTDNTARSQQADALLSKLKQEEKGKLTVFLGAAPGVGKTYAMLSAAKERLQQGA DVVVGLVETHGREETEAMLVELEVMPRKEIGYHNTYLTEFDLDSALERRPELILVD ELAHTNVPGSRHKRRYQDVDELLSAGIDVYTTVNIQHLVSLNDLVMQITGVRVRET VPDSFIDDAYDIRFIDLPPVNLVERLQQGKVYLPEYARLAMDTFFSISNLTALRELA MKRVIEQVDAHLINELEAKSEKADFILKDKLLVLISTNSDHSYLIRIGRQIADRRQIPW TVVWVDTGKTQDLQRRKRLNDAMVMAKELGASAEVLRGSSTYRSILPFLNEHRIN TVLVGAGTRRQFLWQRKRLYQQLIESGLPVEVSVYRAPEQLKMPKEPELRLSPLG DKKGHIFGIVSTAVATVFALLLQQVLSSGNLVLLYVIAILAVGLKFGARPALATAIWS FLSFNFFLTAPTFTFKVHSQDDVATLIFLVCIGLISGPAASRIRNQFILLKESNQYAET LRELAQELSVADDENALWKSVNRHIERAVHVKCYSVMAGKDDHKQFVPLLLTPLK HIDHSAIDWVFQHGRTAGRFTDTLSASQMTVIPVLQEKKVIAVVALCWDKSQTQF NPFEQELVHAMLQQASSTWQRIHLVSDLESARVKTEVEQIRSALLSSVSHDLKSPL SAMMGAAESLRVFDKQLNEQDRFDLLDTILQESRRLDSYIQNLLDMTKLGHGTLKI ERDWVSVDDIIGSALSRLKRYFPSVKVDYIRHNEPPLLYVHAALIEQALFNILENAV RYSPEEEPITIVMDTTQNQCRVSIEDQGPGIPKAAQKEIFNMFYVVSDGDQKKQNT GMGLAICKGMISAHGGKVRAVDGAGGRGTRIEVELPLDYPNMKQE	21~~KdpD (2.00234E-116) ~~231,253~~Usp (7.69666E-15) ~~369,401~~DUF4118 (0.0000000000365974) ~~496,522~~GAF (0.00103817) ~~636,657~~HisKA (0.00000000000140556) ~~723,776~~HATPase_c (7.70108E-24) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.1E-88	304.1	0.1	4.8E-88	303.5	0.1	1.3	1	Q9I389_PSEAE	Histidine kinase (EC 2.7.13.3)	kdpD PA1636	Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	885	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	208964	sp|Q9I389|Q9I389_PSEAE Histidine kinase OS=Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228) GN=kdpD PE=4 SV=1 MTDTARADALLADLPADGRGRLKVFLGAAPGVGKTFAMLQAAQAQLRQGVKLRA GVVETHSRAETESLLAGVPQQPLRSLEYRGMKLQEMDLDGLLADPPALALVDELA HSNVPGSRHAKRWQDIQELLAAGIDVYTTVNVQHLESLNDQVRDITGVQVRETVP DWVLQEAYEIVLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELAM QTAAARVDADLNHRYRQRGEEAPALRGRLLVGIDGDEQAERLVRHACRVAERRH LPWSVVHVDTGGLRGEQARMRLQGAQQLAERLGGEIVVLRAGEVARTLLQHARE RRASLVLVGQSRRRWYRRAFGGGLAGRLLRDGQGLEISALDSEADLRPAEPRPR YPVVWNDYLLALLATALASGLAWIVAHLLELPNISLVFLMAVLLVAVRSSLMPALLC AVASFLAYDFLFIPPHFSFAIHRHEDLLSLAFFLFMAGLTGNLAARQRRQLEALRDT QEETSLLLELSRKLTAATDRQAVLAAAAQQFDDWKDVEVCLLGQVNGEWKTEAG VQRQLADQERVAADWAWAHDQPAGLGTGTLPGGRWWWWPLSAEEGPLALLG VAPLDGQPLSPQRRRLLAALGQPLAQALARARLAEDLEAARLHGETEQLRSALLA SVSHDLRTPLTAMRGSIDSLLALGEAIPPADRRELLESTRDEAERLDRYIQNLLDMT RLGHGGLKLARDWVAPGDIVGSALNRLRAVLAPYRVQAIVANDLPLLYVHAALIEQ ALINVLENAARFSPNHGRLRIEVSQDAAELRFAVSDEGPGIPEAEREKIFDMFYTAA RGDRGGQGTGLGLAICQGMIGAHGGRISVGEGLDGRGTTLVLHLPLHPQPDLGQ LEGDE	18~~KdpD (1.02212E-120) ~~227,248~~Usp (1.7193E-31) ~~365,405~~DUF4118 (4.53798E-14) ~~489,X,648~~HisKA (7.63804E-14) ~~714,767~~HATPase_c (9.46546E-27) ~~870	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.6E-88	303.8	0.8	5.9E-88	303.2	0.5	1.3	1	F0TA31_METLA	Osmosensitive K channel His kinase sensor	Metbo_1758	Methanobacterium lacus (strain AL-21)	651	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium lacus (strain AL-21)	877455	>tr|F0TA31|F0TA31_METLA Osmosensitive K channel His kinase sensor OS=Methanobacterium lacus (strain AL-21) GN=Metbo_1758 PE=4 SV=1 MKPQYSRPDPDELLRKIKEEERSNKSKKGHLKIFLGYVAGVGKTYRMLSEAGFLC QKGYDVVAGVVETHGRADTEKLLQGLNIIHKKEIEYNGITIGELDIDKILDVRPEFVL VDELAHTNVPGSRNLKRYQDVEELLKAGINVYSTLNIQHIESINDIVYQITGVKVKET VPDKIIDLADKIELVDLPIDELIDRLKDGKVYIPEKAKDAMNKFFTKRNLVALREMAL RYATVHVDYDMDHYLKKENILGPWETSNKIMACISPNNSSRRLIRIAHRFSDRFNA EWFAVYVEPSYKIRQSPDELRKLEINLQLAEKLDGKVFRLTGSISDEITKFADSENIT LIMMGHSRRSRLKELIEGSIINQVIQKSDAQVLVVENEKQETEVTDTVNSMDFKPY GRNIKPYLFSFLSISFTVFLCYLIRPFIEAINIPMIFIIPVVFTSLIYGRKAGILASILAVIS FDFFFVLPYYSLSVADVRFIPTFLVLLIVGIITSLLADSVRNQVRVTRQREKFISALYD FSKDLLSSQDLNDIVDRSTKYISETFNSDVLIMLPDEEGRLVTYMNSEDSDFNDND MGVSNWVFKQDKSAGYGTDTLSSSRWYQVPLGVQNTTIGVIAIAPKGPMGNEQK HLVEAFARVVALALSNSIQT	26~~KdpD (2.09484E-113) ~~236,258~~Usp (1.13074E-33) ~~378,405~~DUF4118 (7.10739E-20) ~~505,531~~GAF (0.0000000000270243) ~~647	non-kinase	KdpD;Usp;DUF4118;GAF

	3.7E-88	303.8	0.2	8.6E-88	302.6	0	1.7	1	A0A060B975_9GAMM	Histidine kinase (EC 2.7.13.3)	FF32_12940	Halomonas campaniensis	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas campaniensis	213554	>tr|A0A060B975|A0A060B975_9GAMM Histidine kinase OS=Halomonas campaniensis GN=FF32_12940 PE=4 SV=1 MYSADQRPDPNTLLKAARREARGCLRVFLGAAPGVGKTYTMLRTARERAEEGED IVIGVVESHGRADTEALCDGVARLPLAPLKHHGRTFYEFDIDAALARRPTILLVDEL AHRNIPGSRHPRRYQDIEELLDAGIDVWTTVNVQHLESLNDDVARITGIRMRETVP DALLERARDVSLVDLTPDELLERLRRGKVYIPEQARAAMEGYFNESNLNALRELAI QTMAERVDADVKVAMDAGGRAGPWPVRPHLLVVINGSEDDVSLVRAAHRMAER RLAVWRAVYVDKGIASPEQQLAIEQVFSLVTRLGGDSIRLQGHSQLSEVLNYARSI NATTIVVGREAKRRWWKWSRPLAQRLMAHAEAFDIVVVAKGAVKQHANRWRHG WKLRPPQLLATSLAVTASLGVAVMLEPWLELANLSLVFLVAVLFSAVWAGTAMAM FSAIASFLVFNFFFTEPRLTFAMVERGQLLTAVFFLLVAVVVGQLAGRGRRRLIALR ASRDQTQLLLRYAEQLSTATDSASAAKIGVDTLVQCFAVPTVFIESAESANEVRVV HALPDSVRLDMTAKQAAVWSWQHQKPSGQGTDTLSQQAWRLIPLTVQGEKVG MLALKLSESLKALTYERESLIDTLVRQLSMALERTRLVAELNTTRVSEENERLRSAL LSSVSHDLRTPLSSIIGSASSLIELKPQLSDSDQRELLDGILSESERLNRYIQNLLDM TRLGHGTLKIERDWVAFDDVINSALKRLGQSLKHVVVRKSWPPSLPLLYVHPALVE QALVNVLDNAQRFSPPGGELSIKAHFTEGDPATLVITVEDQGPGISPELREQVFDM FYSGGDGDRSAHGSGLGLAICRGMIGAHGGTIMAGTGESGRGTAIIITLPLLGADI RRSDEE	20~~KdpD (1.91697E-113) ~~230,252~~Usp (2.33846E-24) ~~371,392~~DUF4118 (0.0000000635309) ~~492,548~~GAF (0.00000776492) ~~639,656~~HisKA (5.18047E-14) ~~722,776~~HATPase_c (1.44543E-23) ~~881	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.8E-88	303.8	1.1	5E-88	303.4	0.7	1.1	1	Q09AI1_STIAD	Sensor protein (EC 2.7.3.-) (Sensor protein KdpD) (EC 2.7.3.-)	kdpD STAUR_0220 STIAU_2786	Stigmatella aurantiaca (strain DW4/3-1)	390	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Cystobacteraceae, Stigmatella, Stigmatella aurantiaca, Stigmatella aurantiaca (strain DW4/3-1)	378806	>tr|Q09AI1|Q09AI1_STIAD Sensor protein OS=Stigmatella aurantiaca (strain DW4/3-1) GN=kdpD PE=4 SV=1 MAGRTRRTRAEDFLELVERGRRGRLKLYIGFAAGVGKTYRMLEEAHALKKRGVD VVLGFVETHGRAETEALVAGLESVPRRAFTYRDVTVEEMDLEAVLARKPQVAVVD ELAHTNVPLCRHTKRYQDVQELLAAGINIIGAFNVQHLESLNGLVERATGVTVRETI PDSFLKSADQVVNLDLAVEDLHERLKAGKIYALDKVPHALERFFTQENLSTLRELAL REVAESLDRATTGQQARAGEEPQGKGGGWGRVLVALSSHPPRAATLLRRGSRM AGRLNTDWFVVYVETPREAPNLIDAEAQRHLLANIEKAKELGAEVVRLRGKDPVE AILDFARSHGVGHIILGRSHQPWWKQLLGRSADIRLLREGAGFDLHVVSFDSPQE ERRP	20~~KdpD (6.93272E-118) ~~230,254~~Usp (4.00516E-43) ~~380	non-kinase	KdpD;Usp

	4.1E-88	303.7	0.8	5.6E-88	303.2	0.6	1.2	1	K9QGM4_9NOSO	Osmosensitive K channel His kinase sensor	Nos7107_3963	Nostoc sp. PCC 7107	386	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	317936	>tr|K9QGM4|K9QGM4_9NOSO Osmosensitive K channel His kinase sensor OS=Nostoc sp. PCC 7107 GN=Nos7107_3963 PE=4 SV=1 MLDNTNSGAAINSSYPVRRGKHKIFIGMAPGVGKTYRMLEEGNALKQEGIDVVIGL LETHGRKDTAEKAVGLEIIPRKEISRGGLTLTEMDTETILQRCLPTSSYGSKSQLVL VDELAHTNVPGSPREKRYQDVEVILAAGIDVYSTMNVQHLESLNDLVARITGVVVR ERVPDRILEAADEVVVVDVTPETLQERLLEGKIYAQPKIQQALDNFFQRRNLIALRE LALREVADNIEEDAIASTPNGQFCNIHERVLVCISTYPNSLQLLRRGARLANYMNAP LYVVFVADPERFLSKDESLHIHNCEKLCQEFAGTFLRVTNGNIAQAIAEVAEKYRIT QIVIGESQRSRWQILLKGSLTQKLVRLLKNIDIHIIASDKNSSVKI	18~~KdpD (3.53377E-120) ~~236,255~~Usp (1.46011E-47) ~~377	non-kinase	KdpD;Usp
	4.3E-88	303.6	0.4	8.7E-88	302.6	0.3	1.5	1	V2UDL0_9GAMM	Histidine kinase (EC 2.7.13.3)	P255_00724	Acinetobacter brisouii CIP 110357	881	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter brisouii, Acinetobacter brisouii CIP 110357	1341683	>tr|V2UDL0|V2UDL0_9GAMM Histidine kinase OS=Acinetobacter brisouii CIP 110357 GN=P255_00724 PE=4 SV=1 MQIDRNNKADAWLAHSQREQSGRLTIFLGAAPGVGKTYAMLTRAHELMQQGQH VVVGVVETHGRSDTERLIQGLHVIPRKSLEYQGRMLEEMDLDQILKLKPQIVLVDE LAHRNVPNSRHEYRWQDVNELLDAGIDVYSTLNIQHLESLNDVVYQITGIRVTETV PDALLKRLKDIRLVDLPVPELLERMNHGKIYFADVAPHALQGFFKAANLTALRDLAI QTVAGQVDIDYREKFVAQGQIIPIQNHVLLAIDGSEFSEDLVRRAHRIAERRNATW SVISIQKSKAETTQIFTVTKAFNLARKLGADTYLLYSNHIASTILQAAYDYGASNILLG KSPQKSLWQRLFSDHIADQLLEKQHPFEITFVQPLKAQNNQTSPNDAAHSSWRE QGLAFTQREVFESIIIVLLGLIVAAISDHFIGYSDLALIFIVTVLLVAIRARMLITIISVFIC FLLYNYFFIEPRFTFMISAERGVITIITFIVSALLVGRLANQLRAQVLSLRAANSVSLQ LQELERKLSACVDIEQVLNVAKQHLETSLNATVWLKVENQSLGDPSVLNEKDQIAA DWTQKNAKPCGRFTNTLTNSDWWFIPLNLVKEYGVIAIRFNQNAQTISFELQRLTE LMIEDIAQTVARVQLSLQLENSRVVAETEKLRSALLSSVSHDLRSPLAAMIGSADTL KYYGEQMSESDRHELLDTIHIEGERLDRYIQNLLDMTRLGHQGLTLARDWIGVDEL IGSATQRLKRYQPNVKIDVTLADDLPQLYVHPALIEQAIFNVLENAAKFSPDDMPIKI SIQQEDDFLQINIEDQGVGIPEDEREQIFDMFYTMQRGDRGKTGTGLGLAIVKAIIG AHMGSIEALAGTHGQGTLIKIRLPLHQD	22~~KdpD (2.20983E-103) ~~229,249~~Usp (4.90384E-27) ~~369,402~~DUF4118 (0.000000000865481) ~~500,X,654~~HisKA (0.000000000018543) ~~720,773~~HATPase_c (8.33256E-24) ~~876	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.5E-88	303.6	3	5.9E-88	303.2	2.1	1.1	1	A0A0E9MTD1_9SPHI	Two-component histidine kinase KdpD	FPE01S_01_00290	Flavihumibacter petaseus NBRC 106054	371	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Flavihumibacter, Flavihumibacter petaseus, Flavihumibacter petaseus NBRC 106054	1220578	>tr|A0A0E9MTD1|A0A0E9MTD1_9SPHI Two-component histidine kinase KdpD OS=Flavihumibacter petaseus NBRC 106054 GN=FPE01S_01_00290 PE=4 SV=1 METIATDWPDRRKEQKGKLKIYIGMSAGVGKTYRMLQEAHTLLRNGINLKIGYVET HRRQETEALVPGLPLLPRRKVFYKGKELDEMDVQAIILLHPQVVVVDELAHSNIPG SRNEKRWQDVLDILEAGIDVITAVNIQHIESINDDVKAITGIEVKERVPDKVLQLADE VVNIDLTAQELITRLKEGKIYDHAKVQQALTNFFQPEKILQLRELALKEVAGQVERK VDYEVAAGNRQWRHERFLACISSNHETAQHIIRKTARMASYYNSRWYVLYVQTP REAADKIPLAAQRHLINNFKNATELGGDIVQRQSRNVAEAIMALIEEKGITTVCIGKP HFHLWQIILKTNVFNHLLKTLSKNDVDLVILS	14~~KdpD (2.0536E-115) ~~224,243~~Usp (2.37336E-30) ~~371	non-kinase	KdpD;Usp
	4.7E-88	303.5	0.2	6.9E-88	302.9	0.1	1.2	1	C3K5J9_PSEFS	Histidine kinase (EC 2.7.13.3)	kdpD PFLU_1679	Pseudomonas fluorescens (strain SBW25)	883	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens (strain SBW25)	216595	>tr|C3K5J9|C3K5J9_PSEFS Histidine kinase OS=Pseudomonas fluorescens (strain SBW25) GN=kdpD PE=4 SV=1 MSDSGRADALLADLPRDGRGRLKVFLGAAPGVGKTYAMLQAAHTQLRQGVRLVA GVVETHGRAETEALLSGLPQQPLLRSEYRGVMLEEMDLDGLLAAKPRLVLVDELA HSNAPGSRHEKRWQDIQELLAAGINVFTTVNVQHLESLNDQVRGITGVQVRETLP DWVLQEADELLLIDLPSRELLERLRDGKVYVPEQARAAIDAFFTQTNLMALRELAM QTAAAHVDDDLAQGYRQLGQSAPAVRGRLLVGVDGDAQAERLVRHASRVAQRR HLPWSLVHIDNGRARDEQSRLRLQNAQQLAERLGGEVVLLRAGEVAKTLIQHAAE RRASLLLVGQSRMRWRRRLFGGGLAARLLRHARGLEINILDSDDMPASPRLPEVR GLVWFDYALAVVATVVAAAVAWAVSSVLPLPNISLVFLAAVLLVAVRSSLGPSLVC AGLSFMTYDFLFIPPNFSFSIQREEDVLTLLFFLLMAALTGNLAARQRRQLQALRDT QEETSELLDLSRKLTAATDRQAVISAAAHHLEGWSDLDLCLVNRDGQGGWAIETG GPLTLTEAERAAADWAWQHDQPAGMGTGTLPFGRWWWWPLSGEEGPLGLLG VSPKPGLELSGQRRRLLTALSQPLAQALARAQLAQELESARLHGETEQLRSALLA SVSHDLRTPLTSMRGSIDSLLALGEAIPLEDRRELLEGTRDEAERLDRYIQNLLDMT RLGHGALKLARDWVSPGDIVGSALGRLRAVLAPLQVSADVPPELPLLYVHAALIEQ ALVNVLENAARFSPPQGRLQLSAGVLDNQLFFAVADEGPGIPEDERAKIFDMFYT AARGDRGGQGTGLGLAICQGMVGAHGGHISVADGIDGRGTCITLFLPLPTQPGLE REA	18~~KdpD (9.98527E-120) ~~227,248~~Usp (2.58562E-32) ~~368,411~~DUF4118 (0.000000144168) ~~489,X,649~~HisKA (0.000000000000255101) ~~715,768~~HATPase_c (1.34478E-24) ~~871	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.7E-88	303.5	2.9	6.3E-88	303.1	2	1.2	1	R5J7D2_9BACE	Uncharacterized protein	BN523_02396	Bacteroides sp. CAG:189	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:189	1262737	>tr|R5J7D2|R5J7D2_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:189 GN=BN523_02396 PE=4 SV=1 MEREESVQHFLDLIKKSRRGKFKIYIGMIAGVGKTYRMLQEARELLDNGVDVRIGY VETHGRAGTEAMLEGLPVISRRKIFYKGKELEEMDLETIIRIHPEIVVVDELAHTNVE GSLNEKRWQDVMTLLDEGINVISAINIQHIESVNEEVQDICGIEVKERVPDSVLQEA DEVVNIDLTAEELITRLKAGKIYRPEKIEMALNNFFKTENILQLRELALKEVALRVEKK VENEVVASVGIRHERFMACISSHEKSPRRIIRKVARLATRYNTSFIALYVQTPRESM DRIDLASQRYLLNHFKLVAELGGEVVQVQSKDILKSIVDVCREKQITTICMGSPNLRI PKVFSTVFGYKKFLADLAQANVDLIILAVE	17~~KdpD (8.67199E-124) ~~227,245~~Usp (7.64832E-28) ~~344	non-kinase	KdpD;Usp

	4.8E-88	303.4	2.5	6.4E-88	303	1.7	1.1	1	F8EK06_RUNSL	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Runsl_3028	Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Runella, Runella slithyformis, Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	761193	>tr|F8EK06|F8EK06_RUNSL Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4) GN=Runsl_3028 PE=4 SV=1 MPGPIEQNAQYFLDLIKKSKRGKFKVYIGMSAGVGKTYRMLQEAHTLLRNGVDIKI GSVETHRRADTHALLEGLPLIPHRTVFYRGKELEEMDLQAILNLHPEVVIVDELAHS NIQGSKNEKRWQDVIDILDAGINVISAVNIQHLESLNEDVFRITGIEVKETVPDSLLQ QADEVVNIDLTAAELITRLKEGKIYDHTKIETALSNFFKADKILQLRELALKEVASQV ERKVELEVPGNTTFRAERFVACISSNHEIAKKILRKTARLASYYQGKWYVLYVQTS GEDTDKIGLATQRHLINNFKLATELGAEVIRVKSNEVAQTIFDTAQKHSITTVCIGKP HGNFWKNLTGNSLFFRLLRKVSDTDIDLVVIS	19~~KdpD (1.05356E-116) ~~229,247~~Usp (4.48656E-32) ~~375	non-kinase	KdpD;Usp
	5.5E-88	303.3	0.7	8.5E-88	302.6	0.5	1.3	1	F9ZTB7_ACICS	Histidine kinase (EC 2.7.13.3)	Atc_0284	Acidithiobacillus caldus (strain SM-1)	927	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus caldus, Acidithiobacillus caldus (strain SM-1)	990288	>tr|F9ZTB7|F9ZTB7_ACICS Histidine kinase OS=Acidithiobacillus caldus (strain SM-1) GN=Atc_0284 PE=4 SV=1 MMLESEGATAGHKEPMSDDITEDRPDPDALLAAVQKEEAAKQRGRLKIFFGAAPG VGKTYAMLRYGLDEMNKGRDVLIGVVETHQRSDTQALADALPQLPLREAQHRNV TLKEFDLDAALQRRPGLLLLDELAHSNAPGSRHQKRWQDLEELLDAGIHVATTVN VQHLESVNEVVRAITGVQVRETVPDRVIAEAEELTLVDISDTDLLQRLKEGKVYLGE RGERAMANFFRKGNLIALRQLAMRIAADRVDLELRQFNAENPEDSKSGGVRERLL VAIGMYPEDEHLVRAGYHLATALRCPWIVVHVDTPRGLLQKPEEQAWLWSHLHL AERLGAETVRLTGVDVAAEILAYAELRDVTQILVGQAQGLRRYIWWWPGSLLGKL LNRRRRMDVVVHPLPLKKAVSEESLERSRQYLGMTISPEQRRQRNRALAIGAGLG IGLSLLALALNPLLGLPSVFLLYLVGTVGTALHYGRWPSIIALSSALVTFYAFGLSRG LPATLGSLVTFGIILALAVLISQLVARSREQENMARMRERRARNLYTLVQALSRLRS APEILTTAAEQIHSTLGLSTAFWLPAGADDGLPLRLLPEDTDLGEQRDGLQSAAV WVFQHGRPAGMGTDTLSGLPALMLPISAGERVLGVMMVSDVEIRRTPADWLRY METITRLVAVALESARTFQRRSEADLHLQLERMQSALLSAVSHDLRTPLTTILGSLG TLERLHGTLPEAEQQQLIRDIRTETERMSQTMERILRVAALLSGGAELHKEWVPLT DILGSARRERQSPCADRPFNVQIPADLPLLHGDPTLLTQVLGNLIENACRYTPPGT AVDIQAWANPQEIFVCVIDHGYGIPPGRERELFERFSRVKPPVGTGGSGLGLAIAQ SVLQMHGGRIWASNQVMNRGAKFCFSLPREAPPSLPQEE	41~~KdpD (1.71547E-107) ~~251,274~~Usp (5.41364E-32) ~~396,461~~DUF4118 (0.000005284) ~~529,558~~GAF (0.0000000000509684) ~~676,694~~HisKA (0.00000000000744245) ~~759,813~~HATPase_c (5.96857E-25) ~~915	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5.5E-88	303.3	0.7	9.8E-88	302.4	0.5	1.4	1	J7IUW2_DESMD	Histidine kinase (EC 2.7.13.3)	Desmer_0442	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	891	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	768704	>tr|J7IUW2|J7IUW2_DESMD Histidine kinase OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=Desmer_0442 PE=4 SV=1 MPKGKLTIFLGAAYGVGKTYAMLEAAIGRLSEGIDVVVGFVETHSRTDTEAMVQKL TVIPTRYLNYKGKISREMDLEAVLTRHPQLVLIDELAHTNAEGSRHKKRYMDVKELL SEGINVYTTMNIQDLETLNDIVAQITGVTVGETVPDQMLEIASQIQLIDIPPEELIQRL KDGKVHVPDQETEGFKNFFRMGNINALRELALRYTAQRVDRQLESYRRVHGIAVP WPTGEKILVCISASPFSAQLIRIAKRMTEKVQGELLAVHVETLRRFPSSEAEKDSM AKNLRLAEELGAEIIGLTGNGVAEAILEAAKKRNVSQIIIGKPEHTRFWEILHGSVVD KVIRQSQGISIHVIPGNKQEVGLSQIHRLKKNEDTGAKTQQRIFPQIIPYLVSGLMIT LMTLFFRGLSPFFGLVNISLAYVLPILISAARWGTLPAIATALMGTIAFDLFFVPPIFK FTVADLRYLISFAIFLWVGVITGTLSDRLKKQVNYSRQRQNSISALYSLSRDIAAVD DLEAVLDSIVSNVSKTLEGQVMLLLPNEQAQLALRKNSGSDDFLDRQELSVATWV YERGLKAGSGTETLGTAKALYLPLRTEQGMQGVLGIYSSDRKANLDPERFRLLEA FTGLAAMAINRVKLAEQARESLSLIESERLRTALFNSLSHDLRTPLASIIGGVTGLLE DQNLVYSPEVRKELLKTILHGAERMNRFISNLLDMARLESGMLRLKKDWCDLQDIV GVAIKRLGDTLTRRPLDINIQENLPLVQADGILIEQVLVNLLDNALKYSEAASKIKVSI RQQENHLEIVVSNRGQSIPETDLSKVFDKFYRLSSPLQVSGTGLGLAICKGFIEAH GGNIWAENNTLGGVTITFTLPLTNQFLGIVPEMDEGE	3~~KdpD (5.61857E-106) ~~211,233~~Usp (7.32271E-40) ~~356,390~~DUF4118 (9.51436E-16) ~~490,516~~GAF (0.0000000000173509) ~~636,653~~HisKA (0.00000000000789523) ~~720,773~~HATPase_c (2.26649E-28) ~~874	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	5.7E-88	303.2	1.6	9E-88	302.5	1.1	1.3	1	R6KEZ9_9BACE	Uncharacterized protein	BN506_01194	Bacteroides cellulosilyticus CAG:158	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides cellulosilyticus CAG:158	1263038	>tr|R6KEZ9|R6KEZ9_9BACE Uncharacterized protein OS=Bacteroides cellulosilyticus CAG:158 GN=BN506_01194 PE=4 SV=1 MNREESVQHFLDLIKKSRRGKFKIYIGMIAGVGKSYRMLQEAHDLLDNGVDVQIGY VETHGRAGTEVLLEGLPVIPRRKIFYKAKELEEMDLEGIIRIHPDIVIVDELAHTNVE GSRNEKRWQDVMDLLDEGINVISAVNIQHIESVNEEVQGISGIEVKERIPDSVLQEA DEVVNIDLTAEELITRLKAGKIYKPEKVPMALNNFFKTENILQLRELALKEVALRVEK KVENEVVVSSVGVRHEKFLACISSKEKTPRRIIRKAARLATRYNTSFIALYVQTPRE SADRIDLASQRYLLNHFKLVTELDGEVVQVQSKDVLDAIIRTCKERQITSVCMGSP SFRLPQSLFMVLKYRKFVNDLAQANVDLIILA	17~~KdpD (1.86511E-124) ~~227,246~~Usp (1.31757E-28) ~~374	non-kinase	KdpD;Usp

	7E-88	302.9	0.2	1.1E-87	302.3	0.1	1.3	1	A0A089WM28_9PSED	Histidine kinase (EC 2.7.13.3)	LK03_14250	Pseudomonas cremoricolorata	894	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas cremoricolorata	157783	[illegible] cremoricolorata GN=LK03_14250 PE=4 SV=1 MTDSSGAAASGAAALRADALLTALPAQGRGRLKVFLGAAPGVGKTYAMLQAAHE RQRQGVRLLAAVVQTHGRSETEALSLGLPQVPLLRHEYRGVLLEEMDLDAVLAAA PQLALVDELAHSNVPGSRHAKRWQDVQELLAAGIDVYTTVNVQHLESLNDKVCGI TGVQVRETVPDWVVQEAFELVLIDLPPRELLERLRQGKVYVPEQARAAIDAFFSQ TNLGALRELAMQTAAAQVDADVAQGYRQRGEQAPALQGRLLVGVDGDDQAEAL VRHASRVAQRRHLPWSVVHVERGAARDEGSRQCLQAAQQLAERLGGEVVVLRA GEVARTLLGHAAERRASVLLVGQSRRRWWRRWLSGGVAQRLLREPSGLEISVLD GQAARPARVRGEPGRWVAGHYLLAILATALAAGLAWAVSSVLELPNISLVFLAAVL LVAVRSSLGPALVCALLSFLAYDYLFIAPSYSLSIRREEDVLTLLFFLLMAALTGKLA ARQRRQLQVLRDTQDETRQLLELSQHLALATDRKAVLAAAVTHLEQAAGQPVTVV QRLADGGFSPLSGPAQALPVSAQAAAHWAWQHGQAAGAGTDTLPDSPFWWW PLRVEDRPLALLGVKVAPSAALSRRRLRLLRGLAQPLAQALARVELAEQLEAARLQ GETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALDQALSGADRRELLEGTRDEAE RLDRYIQNLLDMTRLGHGSLALARDWVAPADIVGSALHRLRTLLAPLRVERQMAG DLPLLYVHAALIEQALVNVLENAARFSPRDGRILLQVAVEGEQLRLAISDQGPGIPL AERSKIFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGRIEVDDGADGQGTCI TLCLPLPAQPDADAEAP	28~~KdpD (2.68676E-112) ~~232,258~~Usp (1.21939E-25) ~~375,425~~DUF4118 (0.000000197815) ~~499,X,659~~HisKA (0.000000000000099518) ~~725,778~~HATPase_c (9.90575E-26) ~~881	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	7.1E-88	302.9	0.6	1.3E-87	302	0.1	1.7	1	M1E8G4_9FIRM	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Thena_0832	Thermodesulfobium narugense DSM 14796	644	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermodesulfobiaceae, Thermodesulfobium, Thermodesulfobium narugense, Thermodesulfobium narugense DSM 14796	747365	>tr|M1E8G4|M1E8G4_9FIRM Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Thermodesulfobium narugense DSM 14796 GN=Thena_0832 PE=4 SV=1 MKDDDLKRPTPEEMLQVAKSEEKAKKGQLTIYLGYAPGVGKTYSMLSDAHLRKNEGIDIVVGYAETHNRPETEKLLEGLEVIPPLIVEYKGIKLKEVDFEKILKRRPQIAIIDELAHTNPPSFTNSKRYQDIEELLNAGIDVYTAVNVQHIESFKDIVLQVSKISIKETVPDSFFQQAFEIKLVDITPEELLKRLKEGKIYVENMAKSAIDQYFKVGNLLALRQIALRVVADSVDEKMRLYMIQHAIAGPWSIKKKVLVGVFASPYAKQLVRATYRFANEIDAQWIALHVETQKNKTFTKEEIDWLNGALDLVRTLGGQIVWLKGDDAAKEIIDYAKSHNVTKIVIGKPKKFSLFSRSIPEKLITGTKNIDIYMLDLKEEKINLKKKKIEFIYSNQYVIALFNIFVVSIFGYILREYLNNINMISLFFLALIFNALFLQFLPVLLSTFASLLIFDFLFIQPYYSFAISDLNYFLTFIVYSVAVLTINILASKLKTIIKTLKESQKREIGLYEFSTDLVMARNINQVLSLTINHIKKLFLFETAIFIREKEKIKLGAKTEKFEISPEIKGIASWCLINKKAAGLGTETFSNTNSLYLPMLTAKDSYGVIAIKITNKKNFKIDDRIALDAITRLSAMALERIYNLA	24~~KdpD (5.14668E-112) ~~234,256~~Usp (1.7135E-30) ~~375,396~~DUF4118 (0.000000492008) ~~494,522~~GAF (0.0000227208) ~~639	non-kinase	KdpD;Usp;DUF4118;GAF

	7.1E-88	302.9	2	1.3E-87	302	1.4	1.4	1	C2W4C0_BACCE	Sensor histidine kinase KdpD	bcere0022_6220	Bacillus cereus Rock3-44	381	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock3-44	526986	>tr|C2W4C0|C2W4C0_BACCE Sensor histidine kinase KdpD OS=Bacillus cereus Rock3-44 GN=bcere0022_6220 PE=4 SV=1 MYAENDEPTFQRRSPEEYLEEIRRMNQGKLKLYVGAAPGVGKSYKMLFDAREMK KEGTDIVIGLIETHGRKETEEAIADLEKVPLKEIKYKGKVFYELDVEAIIKRAPQVVVV DELAHSNIPGSKRKKRYMDVEELLDAGISVLSAFNIQHLESVHDIVEQITNVKVRERI PDFILQKANEIQLVDVTPEVLRKRLIDGKIYKEEKIQQSLRNFFTVNNLGALRELSLR EVADDMDDKISQSVTEPIGVKEKILVCVQYSSTAEKLIRRGWRMADRLNAELYVLN VEREKIESLSVSKRQTIDEWKSLTNQFYATFLLEETKGRKPADVIIEVAKRLQVTQIL LGQSARTRWEEIRKGSIVNEIMRETQYIDIHIVADQRV	25~~KdpD (3.97819E-113) ~~235,252~~Usp (2.04434E-41) ~~377	non-kinase	KdpD;Usp

	7.6E-88	302.8	0	1.1E-87	302.2	0	1.3	1	A0A024HDR4_PSEKB	Two-component sensor KdpD	kdpd1PKB_1850	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	473	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas knackmussii, Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	1301098	>tr|A0A024HDR4|A0A024HDR4_PSEKB Two-component sensor KdpD OS=Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13) GN=kdpd1 PE=4 SV=1 MTDPKRADALLAEVERNGRGRLKVFLGAAPGVGKTYAMLLAAQGQLRQGVKLRA GVVETHGRAETEALLVGLPQQPPLRSEYRGIRLTEMDLDGLLRDPPQLALVDELA HTNAPGSRHAKRWQDIQELLSAGIDVYTTVNVQHLESLNDQVRDITGVQVRETVP DWVLQEADELLLVDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELTM QTAAARVDADLAQRYRQLGSEAPAVRGRLLVAVDGEHNAERLVRHASRVAERRH LPWTLVHVDTGGARDEQSRLHLQNAQQLAERLGGEILQLRGGEVARTLVEHARE RRASVILVGRSRQRWYRRLFGGGLAARLLRLGEGLEISVLDSEADLAPAGPRARE RGHWRDYLLAAGAAGGARGPALAPAPWPGGCRNCWRYPISPWCSSPPCCWW RCAAACGLRWLAQCCRSWPTTSCSSPRASRSPSSAKRTY	18~~KdpD (2.00005E-126) ~~227,248~~Usp (4.87669E-35) ~~365,X	non-kinase	KdpD;Usp;X;

	7.7E-88	302.8	0.1	1.2E-87	302.2	0	1.3	1	B4U8E6_HYDS0	Osmosensitive K channel His kinase sensor	HY04AAS1_0720	Hydrogenobaculum sp. (strain Y04AAS1)	643	cellular organisms, Bacteria, Aquificae, Aquificales, Aquificaceae, Hydrogenobaculum, Hydrogenobaculum sp. (strain Y04AAS1)	380749	>tr|B4U8E6|B4U8E6_HYDS0 Osmosensitive K channel His kinase sensor OS=Hydrogenobaculum sp. (strain Y04AAS1) GN=HY04AAS1_0720 PE=4 SV=1 MEEERPIPESLLEIAEEKQKRGKLTIYLGAMPGVGKTYAMLNDAHIKKQEGIDIKVG FVETHGRKETEKLLEGLDTIPSLEVDYSGIKLKEINLDEILRIKPQICIIDELPHTNPPM FRNKKRYQDIEEVLNAGIDVWTAMNVQHMESISDIVYQITGVRVRETIPDEFVKNA DEIKLIDLPPEELIQRLKEGKVYVPDLAQEAIKRYFRPGNIMALRELSMRIAADKLNK KLNTYMKEHAIAGPWAIKERIVVGIYASPFAEHLVRATYRVANEIDAEWIAIYVETEK HAYLTDKELDWLQKALELAKSLGAEIVWIKDDDVPNAIIRYIKSHNINKIIMGKPKKF PIFRGSIFRKIAQNTKYVDIFMLDPPIAEAELFNISKKRINFPKLYLPKIYNIFIGLFLVF LATFIGLQFRNYLNQLNLVFLFLLALSLAALMLDTYSTIFATLISIVIFDYFFVPPYYSF AISDINYFLSYTVFALMIVFINLLSIRLKRNLKKLQKSEEKSNVLFELSRKLLRINSKEE CISITIRYVKMFVEDMAIFLKAKDSIHMEALTKNININDRVKTIVQWCIKNKKPAGVST QTFSEDPYFYIPLIYKDDVYGVMIFDMSKSKETNYETISILETIADLFTASIVKYT	20~~KdpD (2.96922E-115) ~~227,251~~Usp (4.60725E-34) ~~367,447~~DUF4118 (0.00105819) ~~499,525~~GAF (0.000000464438) ~~639	non-kinase	KdpD;Usp;DUF4118;GAF

	7.9E-88	302.7	0.5	1.4E-87	301.9	0.4	1.4	1	A0A0F2SJA7_9FIRM	Histidine kinase	VR66_04095	Peptococcaceae bacterium BRH_c23	891	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c23	1629714	>tr|A0A0F2SJA7|A0A0F2SJA7_9FIRM Histidine kinase OS=Peptococcaceae bacterium BRH_c23 GN=VR66_04095 PE=4 SV=1 MVKGKLTIFLGAASGVGKTYAMLESALGRLSEGVDVVVGLVETHGRADTEAMLN GFTVIPRRSQEYMDRIFFEMDLDAVLTRRPQLVLIDELAHTNVDGSRHKKRYMDV KELLSAGINVYTTLNIQDLETLNDIVTQITGVAVRETVPDQVLEIASQIQLIDIPPEELI QRLKDGKVYVSDQETEGLKDFFRPGNINALRELALLYTAQRVDRQLESYRQDHGI NGPWPTGEKILVCISASPFSAQLIRIAKRMTEKVQGQLFAVHVETLRRLPSSEAEK DSMAKNLRLAEELGAEVIGLTGNGVAEAILELARKRNVSQIIIGKPAHTRFWELIHG SVVDKVIRQSQGISIHVIPGRPPEAGKAQIKAVKNGEEAGTKPQGWNSPKIIPYLAS SLMIIGMTLVFTLVHPFLGLVNISLLYLLPILISAALWGTLPAIVTAIMGTIAFDLFFVP PFFKFTVADLRYLISFAIFMLVGLITGTLSDRLKKQVNYSRQRENNISALYSLSRDIA AVDNLDAVLDCIVSNVSKTLEGQVMLLLPNEKAQLVLRKDSGLINSLDKCELSVAT WVYERGLKAGHGTETLGTAKAQYLPLSTEQGTQGVLGININESNTQFDPERIRLL EAFTGLAAMAINRVKLAEQARESLSLVESERLRTALFNSLSHDLRTPLASIIGAVTG LLEDKNVIYSPEVRKELLKTILYGAERMNRFISNLLDMARLESGMLRLNKEWCDLQ DIIGVAINRLGDTLTRRPLDIDIQEGLPLVQADGILIEQVLINLLDNALKYSEAASKIMI SIRQQGNQLEIVVANRGHGIPEADLSKVFDKFYRLSSPLQVSGTGLGLAICKGLIEA HGGDIWAENNKLGGVTITFTLPLTDQFLGIVPEMNEGE	3~~KdpD (7.85169E-110) ~~211,233~~Usp (5.78677E-40) ~~356,390~~DUF4118 (2.07696E-17) ~~490,516~~GAF (0.000000000154838) ~~636,653~~HisKA (0.00000000000449046) ~~720,773~~HATPase_c (3.05232E-30) ~~874	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.1E-88	302.7	3.6	1.1E-87	302.3	2.5	1.2	1	A5FIH2_FLAJ1	Osmosensitive K+ channel His kinase sensor	Fjoh_1971	Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) (Cytophaga johnsonae)	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobigroup, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium johnsoniae (Cytophaga johnsonae), Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) (Cytophaga johnsonae)	376686	>tr|A5FIH2|A5FIH2_FLAJ1 Osmosensitive K+ channel His kinase sensor OS=Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) GN=Fjoh_1971 PE=4 SV=1 MENENNNAQHFLDLIQKSRKGKFKIYIGMSAGVGKTFRMLQEAHSLLKNGIDVKIG YIETHMRKETHELLAGLPIIPRRTIFYKGKELEELDVQAIINLRPEVVIVDELAHTNVE GSKNEKRWQDVLEILEAGINVISAVNIQHIESLNEDVKRITNIDVQERIPDNVLRLAD EVVNIDLTSEDLIARLKEGKIYTADKIQTALTNFFKSEQILQLRELALKEVASQVVRK VESEVPNLHALRHEKLLACISSNEKTAKIIIRKAARLASYYNGSWYVLYVETPQESS NRIALDKQRHLINNFKLAVQLGAEVIKLENSNITDAILTTVEEKQITTVCIGKPHFNLF KVILSTTIFRRLLNKLSLSNVDLVILS	18~~KdpD (2.76634E-116) ~~228,246~~Usp (6.88482E-28) ~~374	non-kinase	KdpD;Usp

	8.2E-88	302.7	2.5	1.1E-87	302.2	1.7	1.2	1	E8U858_DEIML	Osmosensitive K channel His kinase sensor	Deima_1598	Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	371	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus maricopensis, Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	709986	>tr|E8U858|E8U858_DEIML Osmosensitive K channel His kinase sensor OS=Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34) GN=Deima_1598 PE=4 SV=1 MSDPTPERQPERLTRPDAERARGHHKIFVGAAAGVGKTYRALTELREHREAGQD AIIGVLETHGRQDTARAADGLPIQPRREVKYKGVQLSEMDLAGLLERRPDMVLVD ELAHSNAPGSKNEKRYEDVEELLQAGINVISTVNIQHLESLNDLVARLTGVRVRER VPDHVVQDADEVILVDVTPQVLQDRLRAGKIYAADKVEQALKNFFTDENLGALREL ALRQVAEAVQAETEETTEHSSGVKERILVALGAEPESGRLLRRGGRMAKRLGGDL IALYVSTGRLSRDQSKTLDGLRAITESLGGTFVTAPARGGVGHTLVQYVREHGVT QVILGESSRTRFQEFLRGSIIHQVLRDTRNVDVYVISRDK	21~~KdpD (3.78352E-113) ~~230,247~~Usp (1.11066E-33) ~~368	non-kinase	KdpD;Usp

	9.2E-88	302.5	2.6	1.2E-87	302.1	1.8	1.1	1	F0S644_PSESL	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Pedsa_1588	Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Pseudopedobacter, Pseudopedobacter saltans, Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	762903	>tr|F0S644|F0S644_PSESL Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) GN=Pedsa_1588 PE=4 SV=1 MTEKDQTVQQFLDLIKKSRRGKFKVYIGMSAGVGKTFRMLQEAHSLLRNGIDLKIG YIETHNRKETHDLLEGLPVIPRRKLFYKGKELEELDVQAVINLRPEVVIIDELAHTNIE GSKNEKRWQDVLDILDAGINVISAVNIQHIESLNEEVRAITGIEVKERIPDSVIAEAD EVVNIDLTADELITRLKEGKIYEAAKIETALNNFFKSEHILQLRELALKEVASQVERKV ESEVTLTGAAKREKFLACISSNEKTAKNVIRKTARLANYYNSKWSVLYVQTPRESP DKIALDKQRHLINNFKLATELGANIIKVENGNISKAIMEQCEQRKITTICIGKPHLSLIH ILATNVFNGLLRKLSANDIDLVILS	18~~KdpD (1.94538E-118) ~~228,246~~Usp (9.8028E-32) ~~374	non-kinase	KdpD;Usp
	9.9E-88	302.4	0.3	1.8E-87	301.6	0.2	1.4	1	C6RQT2_ACIRA	Histidine kinase (EC 2.7.13.3)	ACIRA0001_0651	Acinetobacter radioresistens SK82	886	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter radioresistens, Acinetobacter radioresistens SK82	596318	>tr|C6RQT2|C6RQT2_ACIRA Histidine kinase OS=Acinetobacter radioresistens SK82 GN=ACIRA0001_0651 PE=4 SV=1 MTNIQTNKADILLQQVKRHQTGHMTIFLGAAPGVGKTFAMLSRAHELYGQGQNVA IGYIETHGRLETEELVAGLPVIPRKIVEYKNHNLEEMDLDSILQIHPDIVLVDELAHQN IPGSRHKKRWQNINELLDAGIDVFTTMNIQHLESLNDVIFQITGIRVKETVPDQILERI RDIRLIDLPVNELLERLNQGKVYVPDQAAHALKSFFNIANLTALRELAIQTVAHHIDID AREQFDVKGLSLTPLNNHVLIMIQGNQNSEALVRIGSRIAERRNAKWTVAAFLTTA SGHNPISFETHSTGREIERALHLARQLGGMTDILYGKNYAGTLYNFACERGISILVL EQESRPLFYSWLRPPLAHQLLKYQLAFELSIVPVQQGKPQAYRFNRQNYVLNLKE LIFVLITTITSILIAKLSVQYLKVEELSLIFITAVIFVAANTRMTAAMLAAILFFFAYNFFFI PPTLTFQISAHKSVITVVAFLAAALIAGRLASRLREQVVALRSANSYNSIMQDLGQK LSVAVDLQQVIEIGQNSLEKSLNVQVWFKLSDETALSSDENLLTEKEKISANWTLK NHQPSGRFTQTLSESAWWFLPLLASKECIGVIGLNISENQREMNIEQRRLAEAMV EYITQAITRTQLSKELEYANISSETEKLRSALLSSVSHDLRSPLAAMIGAADTIATYK STMTEEDQLTLLETIGLEGERLDRYIQNLLDMTRLGYQGLKLTRDWIEVNELVDTA TRRLKRYKPVVEFNIQRLLQELKIYVHPALIEQALFNVLENAAKFNPEDQPIDIILSQP DTAHIQFDISDQGKGIDIADREKIFDMFYTMHGDRNPTGTGLGLAIVKAIISAHIGSIK AQIGLKNKGTNIQIVLPVHISQD	22~~KdpD (4.5633E-111) ~~229,250~~Usp (4.97552E-18) ~~378,401~~DUF4118 (0.0000169944) ~~500,580~~GAF (0.00176035) ~~640,657~~HisKA (0.000000000399039) ~~723,776~~HATPase_c (4.73976E-21) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.1E-87	302.2	1	1.7E-87	301.6	0.7	1.3	1	A0A022LVB6_9MICO	Histidine kinase (EC 2.7.13.3)	H489_0104365	Curtobacterium flaccumfaciens UCD-AKU	830	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Curtobacterium, Curtobacterium flaccumfaciens, Curtobacterium flaccumfaciens UCD-AKU	1292022	>tr|A0A022LVB6|A0A022LVB6_9MICO Histidine kinase OS=Curtobacterium flaccumfaciens UCD-AKU GN=H489_0104365 PE=4 SV=1 MKRGKLRVLLGAAPGVGKTYTMLEEGRRLLDEGRDVVVAVVETHERAATAALVN GLEVVPRRTVSHRGVDLDDLDLDAVIARAPEVALVDELAHTNAPGSPNEKRWQD VEALRDAGIDVISTVNVQHMQSLGDVVREITGTVQRETVPDAVVRAADQIEVVDLA PAALRERLSDGLVYPAARIDAALSNYFRLGNLTALREIALLWLADEVDDALKAYRAE HGIEHRWETRERVLVALTGGPEGETLLRRGARIAARSAGGELAAVHVTTNDGLRV RHPGALGKQRTLLEQLGGTYHQVVGDDVPSTLVRFARSIDATQIVIGVSRRSRLAA AMTGPGIGNTVIRESGDIDVHVVTHERAGGGITLPKLGGSLSRGRVIAGFVLSVLV GPLLTWVLSIGSDPDAITVDVLAYQLLVLVVALVGGMWPAVFAAVLSGLSLDYFFV QPLYMVTVQQPWHLFALVMYVISAVLVSFVVDRSARRSRAARRASAESGLLMGIA GSVLRGDDALQALLDRTREAFGFAGVRIRQGDEVPATSGEFGATPDASTTLASGA VLEFAGAPDDPTQRRLLRVVEQQLDAAVEHRELTRTAVGAERIAAADRVRSALLA AVGHDVRRPIAAASAAVQTLRAPDIDLSGPDREALLATADESLGQLAVLLADLLDV SRVQAGVLAVTPASIALETVVAPALDELELGPDDVDLDLPADLPPVLADPVLLQRV VVNLLANAARYAPDGTHVRVAASAFAGVVELRVADHGPGIPADRRDEVFQPFQRL GDTDNETGLGLGLALARGFTEGMGGTIEVDDTPGGGLTVVVRLPIAGHVGVEIR	1~~KdpD (8.19836E-108) ~~211,233~~Usp (9.92023E-30) ~~356,424~~DUF4118 (0.0000763709) ~~476,X,601~~HisKA (5.79e-03)~~654, 718~~HATPase_c (6.11434E-27) ~~819	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.1E-87	302.2	0	1.7E-87	301.7	0	1.2	1	I0XR10_9LEPT	Histidine kinase (EC 2.7.13.3)	LEP1GSC185_3490	Leptospira licerasiae serovar Varillal str. VAR 010	891	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira licerasiae, Leptospira licerasiae serovar Varillal, Leptospira licerasiae serovar Varillal str. VAR 010	1049972	>tr|I0XR10|I0XR10_9LEPT Histidine kinase OS=Leptospira licerasiae serovar Varillal str. VAR 010 GN=LEP1GSC185_3490 PE=4 SV=1 MRPAEENRPDPDELLSRIGGEETNTRGKLKIFFGMAAGVGKTFEMLRDAQKAKSE GIDVWIGYLETHNRKETEAQAEGLPVIPRKRFKYKSVDLEEMDLDTILEKKPDLVLV DELAHTNVPGSRHPKRYQDVLEILDQGINVYSTLNVQHLESRAGIVEEISGAPVSE RVPDSILEIADEVELVDLVPDDLIKRLKEGKVYPSDKVPQALHSFFKVPNLTALREL SLNFTSKLVDRELSRLEPTKDSKLSDKILVAVSSSPQAANLIRYAKRIAFGLKCPWV AVYVDDGNILAPDQKRLLRENLGLARELGAEILNFSDRDPVLGILRAINRSKATHVVI GRSGKSKFSRILRGGSFVDKLSEQSGDFQILLAPTEVSKEKPKIRFGFFTKGTRSK PIQYFISFLALLGVTSFNLLLNIITGYWSIGLVYLFFIMFVSLFAGRGPVLITASLSAIF WNFLFIPPKFTFYIEKVEDWMMFGTYFVLALVLGALTTRLRDREEALQAGEEALSG LYRLSVALSKTHSLDEIASVAVETIGDTFQSSVLILLADQDSLLSRTPHPKSGFKPD MKESALAAWTFQNRKPSGKDTDTVPMSKGLYLPLLTPGGCFGVVGLDREYKESL ELEEETLLFSMLNQIALALERIHLLGIRANAKLVEESEKFYSALFNSVSHDFRTPLTVI RASLDLLESGCVKNEKEKSGLFSEIRIAYKKLDRLVGDLLDMSRLESGRLMLDLQW EDPVDLVNETIRIAEYEKGEHTLTVQTDESMPLVRMDRRLMIQVLIHLLQNAFLHTE KDSTVIVRASVPKDHLLLTVEDNGPGIPYGQEKRIFEKFTKVSGSMQGTGLGLSIC KGLVEAQGGKIWAENRQEGGARFLIRIPVLTFPPLEDAIV	26~~KdpD (2.15472E-112) ~~234,252~~Usp (5.44807E-29) ~~374,399~~DUF4118 (1.65456E-15) ~~499,525~~GAF (0.0000000756192) ~~644,661~~HisKA (0.00000000240015) ~~726,781~~HATPase_c (7.48417E-28) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.1E-87	302.2	1.2	2.1E-87	301.3	0.9	1.5	1	G7W7P5_DESOD	Histidine kinase (EC 2.7.13.3)	Desor_0406	Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	917	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus orientis, Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	768706	>tr|G7W7P5|G7W7P5_DESOD Histidine kinase OS=Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) GN=Desor_0406 PE=4 SV=1 MLENNNDDVLENDEGDVFLAKGKLTIFLGAASGVGKTYAMLEAALGRVSEGMDVI VGLVETHGRADTEAMLQELTVVPPKARDVSGRIAHELDLDAILARHPQLVLIDELAH SNIEGSRHQKRYMDVKELLAAGINVYTTLNIQDLETLNDIVTQITGVKVRETVPDQIL ETAAQIQLIDIPPEELIQRIKDGKVHVPEEETDSLKNFFRPGNINALRELALRYTAQR VDRQLESYRRDHGINGPWRTGEKILVCISASPFSAQLIRIAKRMTEKVQGELLAVH VETLRRFPSNEAEKDSMAKNLRLAEEMGAEVIGLTGNSVAEAIVELARKRNVSEIII GKPEHTRFWELIHGSVVDKVIRQSQGISIHVIPGSQQDAGTTRIHAGWSWNDDKD EVPWWKSPQVIPYLASSLLVILLTFSISLVSSFLGLVNISLIYILPILMIAARWGILPAIV TALMGTLAFDLFFVPPLFKFTVADLRYLISFAIFMLVGLITGTLSDRLKKQVSYSRQR ENSISALYSLSRDIAAVDNLEAVLECIVSNVSKTLEGQVMLLLPNENAQLVLKKDSGI NNLFDDREFQVASWVYERGLKAGRGTESWGKAKALFLPLSTEQGTQGVLGIYSN ARNYQLASEQIGLLEAFAGLAAMAINRIKLAEQARVSLSLVESERLRTALFNSLSHD LRTPLASIIGASTGLLEDQNVYSPEVRKELLKTILHGAERMNRFISNLLDMARLESG MLRLNKEWCDLQDIIGVAINRLGELLTRRPLEINIPEGLPLVQADGILIEQVLINLLDN ALKYSEVGSKIIISIRQNEKSLEIVVANRGHSIPEADLSKVFDKFYRLSSPLQVSGSG LGLAICKGLIEAHGGEIWADNNKLGGVTITFTLPLNDQFFGMVPEMLKESLEFRER NDS	20~~KdpD (8.59164E-106) ~~229,251~~Usp (1.96981E-37) ~~374,408~~DUF4118 (7.09616E-18) ~~508,534~~GAF (0.0000000155456) ~~654,671~~HisKA (0.0000000000020542) ~~737,790~~HATPase_c (1.65055E-27) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.2E-87	302.1	0.6	1.7E-87	301.6	0.4	1.2	1	Q1IUD7_KORVE	Osmosensitive K+ channel, histidine kinase sensor	Acid345_05108	Koribacter versatilis (strain Ellin345)	373	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Candidatus Koribacter, Candidatus Koribacter versatilis, Koribacter versatilis (strain Ellin345)	204669	>tr|Q1IUD7|Q1IUD7_KORVE Osmosensitive K+ channel, histidine kinase sensor OS=Koribacter versatilis (strain Ellin345) GN=Acid345_0508 PE=4 SV=1 MQKTPDQWLDEVSPEKKVGLLKLFLGYAPGVGKTYSMLSEAIRRMSRGEDVVIG VIETHGRRATAELSSKLDIIPKKQLEYKGTVFQEMDVDAILARKPQVVLVDELAHTN IDGSKHRKRYEDVLELVDANIDVLTTMNVQHIESLGPSVLQFTGIQVRETVPDWLM QRVDEIVLADVTPQALEKRMKRGDVYPTDRAERALSHFFRPGNLIALRELALRQVT QVVDRSLDAYLAKENVEQAPAVRERIAVCVSSNPAAQYLVARASRMAHAIGGEFY VIYVDVGRDTDPKDQKSLAENIRFAENLDAKVLRTKGKSVAEEVAKVVKENHITQII FGRSARTGYQKYLYLSAIHKFLRDAPSVDVHIVTQEAR	16~~KdpD (1.71949E-110) ~~226,248~~Usp (5.57085E-30) ~~369	non-kinase	KdpD;Usp
	1.2E-87	302.1	0	1.9E-87	301.5	0	1.3	1	K0CGR3_ALCDB	Histidine kinase (EC 2.7.13.3)	B5T_02498	Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	880	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Alcanivorax, Alcanivorax dieselolei, Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	930169	>tr|K0CGR3|K0CGR3_ALCDB Histidine kinase OS=Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5) GN=B5T_02498 PE=4 SV=1 MKDPTTPDPDALLAVNDDTGRGRLKIFIGAAPGVGKTYAMLQAARELARQGQPVL LGVIESHGRGETEALCANLPRLPLRPIQYRGHSFHEFDLQEALQQRPSLILVDELA HRNIPGSLHPRRYQDIEDLLAAGIDVWTTVNVQHLESLNDHIARITGVRMRETVPD ALVQSARDLILVDLPPDQLLERLRQGKVYVPEQARAAMDHFFNRSNLTALRELALQ TVANRIDHDVFTSMASQGVDGPWPVPRPLLVLVDGRGNDKAVVRAAARMAQRR RAPWTTLWVDTGQAPPDTQKQNLAAVFRLTEQLGGDTVTLHGHDVVGMALDHA RHHNVTGIVFGRSRHRPLAGLFGRTLSQKLMRRGQDFELTCIASAPPHHRRRWR APGWPPARQLWLALSVVAASVLAAAVADHFLALPNLSLIFLTGVLLVASRTGMRA ATFAAVLSLLTYNFFFTEPFFSLAMYHTQDILTVAFFLVIALVTGRLASRLRNQVVNL RRVGDHNRSLLRLSRKLGGATGIQDVQREAGEYLSREFATVVKVVPSQDLDQDK GLTGSLRTAAQWALESGKQAGRGTDTLGDLPQRIFPLRFRDQSLGVLLLSADKLE GLDTAVLSHMETLANQVALALWRVQLSATLEASRVAEETERLRSALLSSISHDLRT PLSSMIGAASSLRDQASLLSEEHRRELLDAILNEGHRLNSYIQNLLDMTRLGHGTL KLARDWIAPADLIAAALKRTAPLTANLTLHRQVEADLPLLFVHPALIEQALVNLIENA AKFSPTGGEITLVARADTDRIVVEISDQGPGIPEDQREKVFDMFFTGGDGRGPGY GSGLGLAICRGMVGAHGGTIEALPPVNGSGAHIVITLPLMEQQPDGPNHV	20~~KdpD (3.80141E-114) ~~229,279~~Usp (3.9345E-21) ~~372,421~~DUF4118 (2.96587E-16) ~~492,542~~GAF (0.000000887666) ~~626,645~~HisKA (0.000000000000083371) ~~711,764~~HATPase_c (2.17409E-26) ~~867	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.3E-87	302.1	0.1	2.1E-87	301.4	0.1	1.4	1	B8H6X0_ARTCA	Histidine kinase (EC 2.7.13.3)	Achl_1707	Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	849	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter chlorophenolicus, Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	452863	>tr|B8H6X0|B8H6X0_ARTCA Histidine kinase OS=Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6) GN=Achl_1707 PE=4 SV=1 MDRGTLRIFLGAAPGVGKTYAMLEEAHRMVADGDDLVVAVVVDHGRVRTAALTE GLEQIPLCSVEYRGTHVPEMDLDAVLARKPHTALVDEYAHTNAPGGRHAKRWED VEELLSAGINVLTTVNVQHLASLNDVVASITGTRQQEVIPDAIVRKADQIELADIPPE LLRQRLSSGLVYAPEKIDAALANYFRLGNLSALREIALIWLADRVEEGLAKYRQQH RIDEAWPARERVVVALTGGAEGEALLRRAARILSRVSGGDLLAVHVRRPDGLAEG SEHSLASQRQLVEDLGGSYHQLAGDNVAMSLLDFARSVNATQIVVGVSRHTRMQ QLFGAGGVGLSVVRDSGDIDVHMVTHPLAGRRPKLRLRPVLGRARTLTGYALALA APAMMTAALLPFPGLNLTTQALAHLCAVVAVAFVGGLWPAAVAAIVDSVLLNYFFT PPVGTLTINDPQNVFALLVFLAVAVAFSLLIGVSTRRSQDAAAARAEAGTLSDLAR GSLARDQTPEEFLDQLRDEFQLTAVSVLAPDADNGDTRGVGVKTWTVRARAGS GAPATADEADGTDRLTAGLILAWKGRPLSGGERRLLAAFEAHLTALIERQQLTSTL RETVRLGEANRIRTSILRAVSHDLRTPLAGIRLAVTALGRQRDKTTAEEQTEMIDTI DSYSGRLENLVGNLLDMSRIDSDALSILHEPVTWLDVVTTVLRELPPNSVRIDLAPN LPALDCDRGLLERALANIVENAVKYAQGSDIVIVATTGGLLAPGAGDRPTSELRVID HGTGVPSERVLAMFQPFQRLGDESNRAGIGLGLAVAKGFIEAMDGELTAEQTPG GGLTMVLRVPLYVGPRD	3~~KdpD (4.11709E-103) ~~211,233~~Usp (2.52564E-28) ~~356,413~~DUF4118 (0.000000134576) ~~479,X,617~~HisKA (0.0000000000900739) ~~683,732~~HATPase_c (4.38512E-20) ~~841	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.4E-87	301.9	1.6	2.4E-87	301.2	1.1	1.4	1	M4V6P6_9DELT	Histidine kinase (EC 2.7.13.3)	A11Q_658	Bdellovibrio exovorus JSS	896	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio, Bdellovibrio exovorus, Bdellovibrio exovorus JSS	1184267	>tr|M4V6P6|M4V6P6_9DELT Histidine kinase OS=Bdellovibrio exovorus JSS GN=A11Q_658 PE=4 SV=1 MTDESRLDPDALLKVIDDEAKLRSQGKLRVFLGMSAGVGKTYAMLKAAHRAQSE GHSVLVGVVETHGRSETAELLTGLEILPRKIIQHRGIDLEELDLDAILIKKPDIVIDEL PHSNVPGSRHEKRYQDVLEILRAGIDVFTALNVQHLESRKDAVESITGIRIRETVPD SILDQATLVEVVDIAPSELLKRLADGKVYLKDKATEAAAKFFKEDKLTALREIALRMT AERVDQDLQRFSVKRNDSPWQTNERLLVAVSHSPYSEKLLRATRRLAYNLESPWI AVHIDTGIKLSDEDQAQLVKNLHLARELSAEVITTTDTSIASAIKRIARQKNVTQVVV GRPTRRWFRDVIEGGSLLSRLVNESHDVDVHVIRMENLKHRRPSFWAELALYRTK TGIIKYWNTLCFLVGVTFFSALFQDYIGYRAIGFIFLLAVLIVGMFGSIGAVLFAAAFS ALFWDFLFIAPRFTFTIASPEDIILCISYFAVALITGFLTNRIRFQEKLMREREERMEV LYRILKDISESYDKKEFIQKVRARVGQLFDGECGVLLKAKESVLDFSNSDEYPLPLN DKERAVALWTFQNQKAAGWSTETLSQAQALYLPLNGMNETVGVFVFRPEKKIRK FGLDQETLLYTIVGQLGFSIERHFLRKRIIEAQRVEDSEKLQQTILASISHELRTPLTA ILGSAAALDSDLISNPLAKDIVKDIEFNSERLNRVIENLLDMSRLSSGSLALNLEWQD ISDLIGVVLKKHAKPLQSHRVEVGLQSELPLVRMDFRLFEHALANLILNAAQYSQPD TKIIIRAYTHEKQLVLEVKDHGAGIPVEFIGQIFEKFYRVPGTLPGGTGLGLSIVKNIV ELHRGTILYHKNEPQGSRFIIYLPLEPQPTLPIEENA	26~~KdpD (8.39929E-106) ~~233,254~~Usp (4.81031E-35) ~~375,406~~DUF4118 (1.87136E-15) ~~502,528~~GAF (0.00000821033) ~~648,665~~HisKA (0.000000000000306781) ~~729,782~~HATPase_c (7.12197E-18) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.6E-87	301.8	0.1	3.1E-87	300.8	0.1	1.5	1	H6LIZ9_ACEWD	Histidine kinase (EC 2.7.13.3)	kdpDAwo_c05630	Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	903	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Acetobacterium, Acetobacterium woodii, Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	931626	>tr|H6LIZ9|H6LIZ9_ACEWD Histidine kinase OS=Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655) GN=kdpD PE=4 SV=1 MAIFSDTRPNPDDISAGLFIKEQNKKGRLEIFFGYAAGVGKTYAMLDDAQEQIKCG VDVLVGYVEEHTHPETVQLISGLPALPPKIVEYRKIRLKEFDLDAALERKPDLILVDE LAHTNAPGTRNKKRYQDIEELLNAGIDVFTTVNVQHLESLNDVVQKITWVDVKETI PDYIFNQADKIRLIDIEPDELLRRFEGGKIYRTERTQKSQDDFFIRENLRLLREIAMR KAANRISTDNQNEPRLSKKMANTKLMVCISASPSSARCIRWTNRTAEAFRAPWTA VYVEAMDSDVMTDAEKDAVRDNLVLAERLGAEIVTLNGHDVATVIAEYAKLSGITNI VIGKSRNKKSLLSYLKASLEEKLIAMLPSIEIHIIPGDPGKNNSALYQQRRLRISGSLF FTWQDGLKTLLIIVIATAISLILQALNISDQNIIMVYILSVLIVSRVTTGYVYGILTSCLT VLVFNYFFTIPYYTLHAIQPGYPITFVIMLLVALITSALTVRIKTQAHLAVEREHRTEV LYEINKKLLASRDLKETIQLINVYMVKIFGRSAIFYHQDPKDLESETFQQSALDSDAS FLMSESERAVAHWVFMNKKCAGAGTDTLMGAGAFYMPIVSQSKVLGIIGLSCAD GVLNQNNRLFLRMIASQVEMALERHYLSNEQRRMIVEAEKEKMRSNLLRGISHDL RTPLTGILGSSSAILENGQTMDQDTQDTLLFNIREDSQWLIRMVENLLSVTRINEGP MNVTKTPEAVEEIVAEAISRIRKRFVNRKIKVKVPEQLLIVPMDGTLIEQVLINLLENA IKYSPEDSVIEVEVKKNENAAEFEVKDQGKGISDQDFPYLFETAVPDGKRSSDSSR GMGIGLSICNSIVKAHHGEMAAQNRLSGGSIFQFTLPLEEESKNG	25~~KdpD (9.54261E-111) ~~234,252~~Usp (3.67505E-39) ~~376,406~~DUF4118 (8.83403E-17) ~~506,532~~GAF (0.00000171635) ~~655,672~~HisKA (0.0000000000363933) ~~738,791~~HATPase_c (2.65656E-26) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.7E-87	301.7	2	2.1E-87	301.3	1.4	1.1	1	I4Z9Z0_9BACT	Osmosensitive K+ channel His kinase	PrebiDRAFT_1321	Prevotella bivia DSM 20514	378	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella bivia, Prevotella bivia DSM 20514	868129	>tr|I4Z9Z0|I4Z9Z0_9BACT Osmosensitive K+ channel His kinase OS=Prevotella bivia DSM 20514 GN=PrebiDRAFT_1321 PE=4 SV=1 MNKTDTHSAEYFLQLIKRQRRGKFKIYIGMIAGVGKSYRMLCDAHEMQQQGVDV QIGYIETHGRPGTKALIDGLTVIPRKQVYYKGKLVEEMDVDAIVARHPEVVIVDELA HSNIDGSRNAKRWQDVMNLLDAGINVISAVNIQHIESLNEEVHHIVGIDVGERIPDT VLREADEVVNIDLTAEELLDRLKAGKIYRKENIQQALDHFFQTDHILRLRELALKEVA FRVEKKVLSESSAETQQSPTKRGPLLACISSHPTSPRHIIRRVSRLAEQYDCSFLVL YVQTPHENTDNIPLADQRHLLDHFKLVAELGGKVVERTSPHVLEAIIDLCHEQPIST VCLGQPAFRMPRILWDIKKYRTFLDALKQLNTDLIILS	20~~KdpD (5.45174E-118) ~~229,251~~Usp (1.96366E-24) ~~378	non-kinase	KdpD;Usp

	1.9E-87	301.5	3.2	2.7E-87	301	2.2	1.2	1	Q5LHU3_BACFN	Putative osmosensitive potassium transport sensor protein (EC 2.7.3.-)	kdpD BF9343_05108	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides fragilis, Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	272559	>tr|Q5LHU3|Q5LHU3_BACFN Putative osmosensitive potassium transport sensor protein OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) GN=kdpD PE=4 SV=1 MDREESVQHFLDLIKKSRRGKFKVYIGMIAGVGKSYRMLQEAHDLIDNGVDVRIGY IETHGRAGTEALLKGLPVIRRRKLFYKGKELEEMDLEAIIRIHPEIVIVDELAHTNVEG SLNEKRWQDVMTLLDEGINVISAVNIQHIESVNEEVQDIAGIEVKERIPDSVLQEAD EVVNIDLTAEELITRLKAGKIYKPEKIQTALNNFFKTENILQLRELALKEVALRVEKKV ENEVVMGIGLGVRHEKFMACISSQEKTPRRIIRKVARLATRYNTSFVALYVQVPKE SMERIDLASQRHLLNHFKLVTELGGEVVQVQSKDILGSIVQVCKEKQISTVCMGSP GLRLPGALCSVLKYRRFLNNLAQANIDLIILA	17~~KdpD (1.40916E-124) ~~227,247~~Usp (2.76189E-24) ~~375	non-kinase	KdpD;Usp
	2E-87	301.4	0	2.9E-87	300.9	0	1.2	1	A0A0F0HZX5_9PSEU	Uncharacterized protein	UK12_05550	Saccharothrix sp. ST-888	839	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix sp. ST-888	1427391	>tr|A0A0F0HZX5|A0A0F0HZX5_9PSEU Uncharacterized protein OS=Saccharothrix sp. ST-888 GN=UK12_05550 PE=4 SV=1 MAGGGGTLRVYLGAAPGVGKTFAMLAEGRRLSAGGLDVAVGLVETYGRRGTEE QLGGLPVVPRRAVRYRGAALTELDLDALLARRPALALVDELAHTNVPGSRNTKRW QDVRELLGAGIDVATTLNIQHLESLTDVVEQITGIVQHEQIPDAVVRAADRIELVDLS PEALRARMAQGDVYPSDRIDVALDNYFRAGNLGALRELALLWLADRVEEELADYR ARHGIRAPWETKERIVVALNGAPQGEHLLRRGARTAARVHGDLIGVHVRADDGTL QPEPPELTAQRALLRELHGSYVELSGTDAARTLVDFARTESATQILLGPTSRSRLR ELLTGSVINRVIRLAGPIDIRVLPPPSPGQVALPGGPRPRRPARVPARRRAGWLL GPLGAVALAGALSPLRASLGLSGVLLWLLLLVAGVAGLGGLAPAAGTTLAAALAAD YFFTVPWHSLVIRHGADIAPLLVFLCVAGIISHLIDGLTRRSQEAARARAEAHALTRL AGETVRGEGRTLRSLLAELRRVFGLEAAGILAPTGDGWRPVAASGGPLPARPED APFAAELDQGTVLVLLGPVIDEENTRLLGPFVTQLRLAEEHERLTREAAAAHSLAR SDALHTTLLEAVAHDLRGPLAAIKAAAAQLDSPEPAAEADRRACAGTITAETGRLD HSVANLLALSRLRAGRAPVALRPTAVAEVLCAAVASLPATGAELALGRTEDLPPVQ ADPGLLERALANVLANARAWSPPGAAVRIDAGAVADRVDVRVVDRGPGIAPEERE RLFQPLRGHRVQPGGARGTGTGFGLAVAKGFVEAMHGELSVEDTPGGGATFVF SLRRADH	3~~KdpD (8.51294E-110) ~~213,235~~Usp (2.90181E-26) ~~356,X,618~~HisKA (0.11)~~683,730~~HATPase_c (4.61501E-16) ~~834	kinase	KdpD;Usp;X;HisKA;HATPase_c

	2.2E-87	301.3	0.6	3.9E-87	300.5	0.4	1.4	1	Q6F8D1_ACIAD	Histidine kinase (EC 2.7.13.3)	kdpDACIAD2975	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	881	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	62977	>tr|Q6F8D1|Q6F8D1_ACIAD Histidine kinase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) GN=kdpD PE=4 SV=1 MMQIDRNEKADAWLAHTQREQSGRLTIFLGAAPGVGKTYAMLTRAHELMQQGK QVVVGVVETHGRADTARLIAGLNVIPRRVVEYQDRKLEEMDLDQILHIKPEIVLVDE LAHRNVPGSRHEYRWQDVNEILDAGINVYSTLNIQHLESLNDVVYQITGIRVTETV PDALLKRLKDIRLVDLPVPELLERMKHGKIYLDDMAPHALQGFFKPAHLTALRDLAI QTVAGQVEIDYREKSVAQGRIVPIQNHVMLAIDGSVFAEDLVRRAHRIAERRNAT WSVISIQKSKTSSAQSLAVSKAFNLARKLGADTYLLYSHQIAPTILQAAYDYGASNI LLGKSPKKTLLERIRSEHIADQLLDKQHPFEITFVQPLKATSYSAQAAVPDQTWLQ QYTHFQARELIESVLIVLAGFIIAVISDHFIGYTELALIFVVTVLVVAMRARMLMTLLS VFVCFLLYNYFFIEPRFTFRISAERGVITIVIFILSALLVGRLANQLRAQVLSLRVANS VSLQLQELERKLSTCVDIAQVLSVSKQHLESALKATAWLRVSELEAGDRSQLNHK DHIAADWTQKNGQPCGRFTNTLTQSEWWFNPLNLAGEHGVIALRFHPDLDVISF EQQRLAELMIEDIAQTLARVLLSFQLENSRVVAETEKLRSALLSSVSHDLRSPLAAM IGSADTLKYYSVQLSDTDRDSLLDTIHIEGERLDRYIQNLLDMTRLGHQGLTLSRA WISIDELIGSATQRLKRYQPNIQIDTHIAPNLPALYVHPALIEQALFNVLENAAKFSP DAVPIQVKISAVDEQFQIDIIIDLGIGIPEQEREQIFDMFYTMQRGDRGKTGTGLGLAI VKAIIGAHMGSIEAMAGPYGQGTQIRIRLPQHQE	23~~KdpD (1.77243E-103) ~~230,250~~Usp (6.35116E-28) ~~370,401~~DUF4118 (0.000000000667026) ~~500,X,654~~HisKA (0.000000000166456) ~~720,773~~HATPase_c (0.00000000000255192) ~~876	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2.3E-87	301.2	1.6	3.1E-87	300.8	1.1	1.2	1	F4KRA6_HALH1	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Halhy_6477	Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	397	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Saprospiraceae, Haliscomenobacter, Haliscomenobacter hydrossis, Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	760192	>tr|F4KRA6|F4KRA6_HALH1 Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O) GN=Halhy_6477 PE=4 SV=1 MDNERNQVADRYLAQLRQAGRGKLKIYIGMSAGVGKTYRMLQEARQMLDQGIHV VLGLVVTHGRKETEALLEGLPMVAQREVFYKGKKMSELDINALLVLHPTWVVVDE LAHSNIPGSKNPKRWQDVMELLAAGINVITAVNIQHIESINDEVQRITGVQVQERVP DDFLQKADEVVNIDLSAEDLITRLKEGKIYDPAKVETALRNFFQPEKILQLRELALKE VATQVERKVEQEVPRTVQSRHERFLACISSNEATARKIIRKTARLSRYYQSKWYVL YVQTPNESLDKIPLDKQRHLINNFQLAVELGAEVLQAQAANRLSKWLVPVAIPLKLI NVSVPDIGNAILEVVKEKQITTICIGKPHLSFWQIVLHTGIFNQLLRALKENEVDVVIL S	19~~KdpD (4.12064E-115) ~~229,247~~Usp (1.88033E-27) ~~397	non-kinase	KdpD;Usp

	2.3E-87	301.2	2.3	3.2E-87	300.8	1.6	1.2	1	A6LIV0_PARD8	Osmosensitive K+ channel histidine kinase	BDI_3934	Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides distasonis, Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	435591	>tr|A6LIV0|A6LIV0_PARD8 Osmosensitive K+ channel histidine kinase OS=Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152) GN=BDI_3934 PE=4 SV=1 MDREQSVQHFLDLLKKSRRGNFKIYIGMIAGVGKSYRMLSDAHQLLESGIDVKIGYI ETHGRVETEALVEGLPIIPRRKIFYKGKEIEEMDLQSILSIHPEVVIVDELAHTNVEG SKNEKRWQDVMDILDAGISVITAVNIQHIEGLNEMVQDVVGIEVKERIPDIVLEQAD EVVNIDLTADELLARLKAGKIYKPDKIQTALNNFFKAEHILQLRELALKEVALRVEKK VENTIPENLGVRHERFMACISSNEKTPRKIIRKVARLATRYNSKFFVLYVQTPRESS DRIPLASQRHLLNHFKLATELGGEIIQVQSPHITDAIVQACKEKQISTLCIGRPALKY PSAILAMVHYRNMLEELAQLGIDLIILA	17~~KdpD (5.08099E-120) ~~227,245~~Usp (4.75161E-28) ~~373	non-kinase	KdpD;Usp

	2.7E-87	301	0.3	4.2E-87	300.4	0.2	1.3	1	A0LLJ3_SYNFM	Osmosensitive K+ channel His kinase sensor	Sfum_2617	Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	388	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophobacteraceae, Syntrophobacter, Syntrophobacter fumaroxidans, Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	335543	>tr|A0LLJ3|A0LLJ3_SYNFM Osmosensitive K+ channel His kinase sensor OS=Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB) GN=Sfum_2617 PE=4 SV=1 MSTDKALSFLHLIRRSQRGRLKVYLGYGPGVGKTWQMLLEGHRLKQEGIDVVAG LVETHGRADTARLAEGLEIIPRRQVRYHGIAIEEMDLEALLARKPGVALVDELAHSN VPGSPNAKRYQDVLDILAAGIHVITTLNVQHLESLYNTVETLVGVKVHERLPDSMLA EADEIVNVDLAPEDLQQRLREGKVYPTERMAVALENFFRRSNLDELRELTLRELAS QIDLKRRSAPDEPCTTAPDQVMVCLSSRGPNSPALLRYGSRLAGRLNRNWYAVY VQTPREAPAIIDSATQRLVSDTLTLANVLGAIVFTYKGEDIVDTILHFAREYRVGHIVI GRPGPLPLWKRLLGGKTLAERLIVKARGLTVVVVDAKAEAREDDRESISPA	16~~KdpD (5.45009E-113) ~~226,245~~Usp (3.45572E-27) ~~371	non-kinase	KdpD;Usp
	2.9E-87	300.9	0.2	6.1E-87	299.8	0.1	1.6	1	B3E0Q9_METI4	Histidine kinase (EC 2.7.13.3)	kdpD Minf_0758	Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	902	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, unclassified Verrucomicrobia, Methylacidiphilales, Methylacidiphilaceae, Methylacidiphilum, Methylacidiphilum infernorum, Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	481448	>tr|B3E0Q9|B3E0Q9_METI4 Histidine kinase OS=Methylacidiphilum infernorum (isolate V4) GN=kdpD PE=4 SV=1 MQEQIDNRPNPDALLEVVQKEEGEKNRGSLKIFLGMCPGVGKTYAMLQAAQVEL TNGKDVVIGYVETHGRKETEQLTRGIPIIPRKIVHYRDMVLEEMDLDAILERKPQLVI VDELAHTNAPGMRHLKRYQDVLEILDAGIDVFTTLNVQHIESRTDTVSYITGAPIYE KVPDSIVDIAEIELVDLSPEDLLKRLAEGKVYIPDQARAAALNFFREGNLRALREIVL RLAAEKAGKDVQEYMQIMHIQGPWKISHRLLVAISASPSSETLIRWTRRNAESLKC PWYAVYVETSRVLSEEDQQRLSKNMELAKHLGAEIITTADEDIVRGILRIARQWNIT QIVFGKPRGRGLLEWFKSRSLLHRLVRESGQIDIHIVGEDEKEEKRKKRKFLLIPES GLSQYGLTCLVIFVITLFCLWANRWIGSRSIGMIYLLGIVIIALFVGRGPVIVAALLSAI IWDFLFLSPKFSLGIQGIENSFVVFSYFVVALVLGQFIARLRAQEKAERRREARISAL YMLSQELSQAAGLDEIVIKVIEQLSHFFQAEVAVFLVNPYDNKLSGLPHWASTLKV TEKEAGVAAWAFEHGKAAGRFTENLPLSKAYYVPLSTHKGSVGVLGINIPGIQSLS FDQKSLIQAFANQIALVIDRQRLAELAEHARVVAESERLSRTLLNSISHEMKTPIAVI TTAIESLSKEDQSIKTADRAQLIEEIRSATLRLNRIVRNLLDMARIESGRFKLKKEWT DIHDLFNLSLKETAKELAGREVKVDIQRDIPLIRIDFSLMLEALNNLLLNAALHTPASS PVELSASVKKNSLVIRVADRGPGIDPEILNRIFEKFYRGTGAPPGGTGLGLSIVKGV VDAHGGKVLVQNRPEGGAVFSIILPLESVPEVHPMPLEESAKK	25~~KdpD (2.62035E-112) ~~232,256~~Usp (4.27128E-41) ~~378,401~~DUF4118 (0.00000000000101674) ~~501,528~~GAF (6.33053E-16) ~~647,668~~HisKA (0.0000000000961383) ~~730,797~~HATPase_c (2.11018E-18) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	3.4E-87	300.7	0.1	5E-87	300.1	0.1	1.2	1	Q1J2K3_DEIGD	Potassium-transporting ATPase, D subunit	Dgeo_2852	Deinococcus geothermalis (strain DSM 11300)	365	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus geothermalis, Deinococcus geothermalis (strain DSM 11300)	319795	>tr|Q1J2K3|Q1J2K3_DEIGD Potassium-transporting ATPase, D subunit OS=Deinococcus geothermalis (strain DSM 11300) GN=Dgeo_2852 PE=4 SV=1 MPGPTRLNPPCRHGPAPTRRGTHRIFIGMAAGVGKTYRALHELRERLERGEDALI GLLETHGRRETLEAAKGLPVFPRREVQHGNVTLGELDVEGLLRRRPQVVLVDELA HTNAPGSPRAKRWQDVEALLDAGIDVLSTMNVQHLESLNDTVARLTGVRVRERV PDHVLHDADELVLIDLPPEDLRERLRAGKIYGPDKIEQALGNFFTVPNLTALREIALR HVAQAVELEVPEGQPAAHEVIVVAVAAEGTAARLIRRGGQLAERLHGELHVVSVR SARLTQEQSRLLDTCREITQALGGTFELLENTGGVGPTLVAYARRVNATQIVLGET SRSRWAELLRGDIIKDVLRQTQGVDVYVISRD	19~~KdpD (9.88835E-120) ~~228,243~~Usp (1.32287E-33) ~~363	non-kinase	KdpD;Usp

	3.4E-87	300.6	2.5	4.7E-87	300.2	1.7	1.2	1	A6H082_FLAPJ	Probable two-component system sensory protein	FP1688	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium psychrophilum, Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	402612	>tr|A6H082|A6H082_FLAPJ Probable two-component system sensory protein OS=Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511) GN=FP1688 PE=4 SV=1 MENEKENNVKHFLDLIQKSRRGKFKIYIGMSAGVGKTFRMLQEAHTLLKNGIDVKI GYIETHNRKETQELIDGLPIIPRRTLFYKGKQLEEMNLQAIINLRPEVAIVDELAHTNI EGSKNEKRWQDVLEILEAGINVISAVNIQHIESLNKNVKLITNIEVQERIPDSVLKLAD EVVNIDLTADELIARLKEGKIYTADKIPTALNNFFKSDQILQLRELALKEVASQVVRK VENEVPKNLALKHDKFLACISSNDTMAKIVIRKTARLASYYNSKWYVLYVEIPSENS DKIALDKQRHLINNFKLATQLGGEVIKVQNKKITDAILEVVKQKEVTTVCIGKPHLSL FKVILSTTIFNKLLHNLSSSNIDLIILS	19~~KdpD (1.22434E-117) ~~229,247~~Usp (6.13607E-30) ~~375	non-kinase	KdpD;Usp
	3.9E-87	300.5	0.3	7.1E-87	299.6	0.2	1.4	1	N9GJ29_ACIHA	Histidine kinase (EC 2.7.13.3)	F927_02454	Acinetobacter haemolyticus CIP 64.3	878	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter haemolyticus, Acinetobacter haemolyticus CIP 64.3	1217659	>tr|N9GJ29|N9GJ29_ACIHA Histidine kinase OS=Acinetobacter haemolyticus CIP 64.3 GN=F927_02454 PE=4 SV=1 MQIDRNNKADAWLAHSQREQSGRLTIFLGAAPGVGKTYAMLTRAHELMQQGHH VVVGVVETHGRADTQALIHGLNVIPRKSVEYQGRFLDEMDLDQILKLKPEIVLVDEL AHRNVPTSRHEYRWQDVNELLDAGINVYSTLNIQHLESLNDVVYQITGIRVTETVP DVLLKRLKDIRLVDLPVPELLERMNHGKIYLADVAPHALQGFFKPANLTALRDLAIQ TVAGQVDIDYREKFVAQGQIIPIQNHIMLAIDGTEFSEDLVRRAHRIAERRNATWSV ISIQKSKIENTQTFAVSKAFNLARKLGADTHLLYSNHIAATILQAAYDCGASNILLGK SPQKSFWQRLFSDHIADQLLEKQHPFEITFVQPLKTKQQDRKKSLDDLSERGLDL HQREVIESSLIILAGFIVAAISDRFIGYSDLALIFIITVLLVAIRAKMLITIASVLICFLLYN YFFIEPRYTFLISAERGVITIITFIISALLVGRLANQLRAQVLSLRAANSVSLQLQELER KLSTCVDIEQVLNIAKQHLEGSLNATVWLRVGGQSVGDASILNEKDQIAADWTQK NAKPCGRFTNTLTNSEWWFNPVNLVADFGVVAIRFNRNLQSIHFEQQRLAELMID DIAQTLSRIQLSLQLENSRVVAETEKLRSALLSSVSHDLRSPLAAMIGSADTLKYYG EQIPESDRHELLDTIHIEGERLDRYIQNLLDMTRLGHQGLTLSRAWIGVDELIGSAT ERLKRYQPQVKIQVQLAEDLPQLYVHPALIEQAIFNVLENAAKFSPEDIPIEVIIQQQ DAFLQIEIEDQGVGIPENEREQIFDMFYTMQRGDRGKTGKGLGLSIVKAIIGAHMG SIEALSGKHGQGTLIRIRLPLHQD	22~~KdpD (1.91235E-102) ~~229,249~~Usp (4.01278E-26) ~~369,399~~DUF4118 (0.0000000767007) ~~497,X,651~~HisKA (0.000000000208945) ~~717,770~~HATPase_c (3.23826E-24) ~~873	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	4.3E-87	300.3	0	6.7E-87	299.7	0	1.2	1	A0A0F3L059_9GAMM	Histidine kinase	VI08_04320	Luteibacter yeojuensis	888	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Luteibacter, Luteibacter yeojuensis	345309	>tr|A0A0F3L059|A0A0F3L059_9GAMM Histidine kinase OS=Luteibacter yeojuensis GN=VI08_04320 PE=4 SV=1 MTDTRDARADALLNTVNGDVGQRLKIFLGAAPGVGKTYAMLSAARDLRRQGVDV VVGFVETHGRAETSALLEGIEVLPTRTVPYAGRDFQEFDLDAALARKPAVLIVDEL PHTNLPGGRHARRWQDIADLLDAGIEVYTALNVQHLESLNDQVRRITNVAVRETV PDAFLDRARDIVLIDLPPRELITRLKQGKVYVPETAAVALDAFFSPTNLAALRELAVE TVAHHVDSDLREHMLARGGAMPVRRRTMAAIDGHAQSEYLVRMTRRIAERRGGP WSVLFVDTGHVDGERRERVDAAMRLARRLGGEPVILRGHAIADELLAWADREGV GQIVVGRTRERPIARRMGFSLTQQLLRRGAHLELTIVATPAERARARRKLRSGVG AAGGTRRDYAFATAATAVAMGLSFVADRFLSVANLSLIFLTAVLVVAVRTRMAVAV YTAILCFFGYNFFFAPPRYTLAIANADDVLAVVLFLVAALVCSRLATRLAGQVQSLR AAQVRGRALVTLGQQLATSADAEGIRTAGARALARALEAEVAMLARNAGGELALA VSSPDAFALSTQDRAAADWCDKHAEPAGRYTDTLHGASCWMLPLGTEHHRAGV VALRFPLGAREPDADRRGLAQAMAEDIAQALERARLAVELESARVQGETERLRSA LLSSVSHDLRSPLASMIGSAGTLLSYDAQLPNDERHALLQAILGEGQRLDRYIQNLL DMTRLGHGTLQLHRDWVDAGEIVAAAVARLRKLMPDTHVDVHLPRDTVLLHVHP ALIEQALFNILENAASFSPAGEPVRVLVRTEAGRLLFDVSDRGPGIPEEERARIFDM FYSVSRGDRGKQGTGLGLAICRGMVGAHGGTVEALPHAGQGTTIRVSLPLPPPP DEPA	23~~KdpD (1.23155E-111) ~~229,249~~Usp (1.34507E-28) ~~369,407~~DUF4118 (0.000000000116719) ~~494,557~~GAF (0.000959609) ~~651,657~~HisKA (0.0000000000159398) ~~723,776~~HATPase_c (1.94307E-25) ~~877	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.6E-87	300.2	0.3	7.2E-87	299.6	0.2	1.3	1	A0A0F0KJB4_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpDRN50_02064	Microbacterium foliorum	845	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium foliorum	104336	>tr|A0A0F0KJB4|A0A0F0KJB4_9MICO Sensor protein KdpD OS=Microbacterium foliorum GN=kdpD PE=4 SV=1 MTAERMPRRGRLRVLLGAAPGVGKTFEMLVEGRRLIDEGRDVVIAIVETHDRAAT AAQTIGIPEVPRRTDLHRGVPLSEMDLEAVLARRPEIALVDELAHTNTPGSAHPKR WQDVDALLDAGIDVVTTVNVQHIESLNAVVEKITGIAQQETIPDAVVRAADEIEVVD LAPQSLRDRLSAGLVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALRSY RADHGIEGTWQARERVVVALTGGTEGETLLRRGARIAARSAGGELLAVHVATQD GLRDQTPGALAAQRALVESLGGSFHQIVGDDIPGTLVSFAQGADATQLVIGVSRR GRVAAALTGPGIGSEVIRRSGDIDVHIVTHAAAGGRVALPRITGGALGWRRQVLGL AVALVFGPLLSWLMFTFRSPESITSEVLAYQLLVVVVALIGGIRPAVFAAVLSGITLD LLFVAPLFTITIAHPLHVLALALYVVIAILVSIIVDQAARRARTAQRAVAEAELLAAVAG NVLRGDNAVLALVSRTREAFGLSGVRLLAPDGEVLASDGEPVPDGRATTVPVGS GGSAPALLELHGEPLDTPARRLLDAIVAQLAAAIEHTDLRATAREVAALAETDQVR SALLSAVSHDLRRPLASAVAAIGGLRGAHGLSASDRDELLATADESLATLSSLVTD LLDVSRVQAGVLAVSSMPLDVAGPVLAAVDELGLGPADVELVLDGELPAVSADPV LLQRVLVNVIANAHRHAPTDTRVIVSTSSLADRVEIRIIDRGRGVPAEQRDRIFQPF QRMGDTDNTTGLGLGLALSRGFAEGMGGTLTPEDTPGGGLTMVVSLPRAEDPD PLQEETE	7~~KdpD (2.27054E-112) ~~217,239~~Usp (3.47319E-28) ~~362,389~~DUF4118 (0.0000000115587) ~~483,X,614~~HisKA (0.00000000851059) ~~679,730~~HATPase_c (2.53815E-24) ~~831	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	5.9E-87	299.9	0	9.9E-87	299.2	0	1.4	1	K0I504_9BURK	Histidine kinase (EC 2.7.13.3)	C380_12765	Acidovorax sp. KKS102	910	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax sp. KKS102	358220	>tr|K0I504|K0I504_9BURK Histidine kinase OS=Acidovorax sp. KKS102 GN=C380_12765 PE=4 SV=1 MPMQDRPDPDALLQRIQQEQAQQQRGRLKVFFGACAGVGKTFAMLSAARAAQA QGLPVTIGVVETHGRTDTEALTAHLPRLPLRALPYKDRTLPEFDLDAALAWGAANP EGLVLLDELAHSNVAGSRHPKRWQDAEELLAAGIDVWSTMNVQHLESLNDIVSGI TGIRVWETVPDQFFDAADEVVVVDLPPDELLARLKAGKVYLPQQAERAAANFFRK GNLLALRELALRRTADRVDDEMRAYRRASTTTPEAVWPNREALLACVGTGDNAE KVVRSCARLAAQLDLPWHAVHVETPEQQGQSATLHPQVERTLKIAQQLGAAACA VLPAAQPAQALVRYAREHNLVRVVMGRSTRRWPWQATLAEQIGQSASDLDLLQV GTLPGRDAATDRKAPRTSTAAPRAAFWPGYIAAALACCIAAVIATPLANVLELTNIV MLFLLVVVGVALRFGRGPAIMAAFLGVGFFDFFFVPPRFNFAVSDAQYVVTFAVM LVVALVVGQLTAGLKVQAEAATDREHRVRSLYDMARDLSAALLPEQVAEIGARFIT GEFSAGSTLVVADDDNRLQVLPGGTAPVDMAVAQWAFERGEPAGRGTDTLHSS PTLVLPLKAPMRIRGVLVVAMPQGQVPGVEPRRLLQTCASLLAISLERIHYIDVAQK STVQIESERLRNSLLSAISHDLRTPLASLVGLAESLAMVQPPLPAHQQELTGAIQQS AQRMSALVNNLLDMARLEAGAVQLNKAWQPLEEVVGSALAASAPAIAAHRVEVTL PDDLPLLQIDAVLMERVLVNLLENAAKYTPADTTIHISAQPQSDAVALTLTDEGPGL PKGREELLFEKFERGTRESATPGVGLGLAICRAIVQAHGGSIRGDTIHNAQGQPA GARFTLLLPRGTPPTDLGTDADTTSEV	28~~KdpD (3.97277E-101) ~~237,262~~Usp (5.12789E-25) ~~382,434~~DUF4118 (0.00172509) ~~490,537~~GAF (1.53964E-14) ~~650,667~~HisKA (7.78624E-15) ~~732,785~~HATPase_c (7.2271E-27) ~~891	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.2E-87	299.8	5.2	8.4E-87	299.4	3.6	1.2	1	G8TDF4_NIAKG	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Niako_4128	Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10)	377	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Niastella, Niastella koreensis, Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10)	700598	>tr|G8TDF4|G8TDF4_NIAKG Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10) GN=Niako_4128 PE=4 SV=1 MSVSNDKEDQVQHYLDLANQSVRGKLKIYIGMSAGVGKTYRMLQEAHDLLRKNV NVKVGYVETHNRKETHALIEGLPLIPRRQVFYKGKQLDELDVQAVLLLHPEVVIVDE LAHSNIPGSKNEKRWQDVVDILDAGIDVITAVNIQHIESINVEVKQITGVEVKERVPD KLLQMADEVVNIDLTARELITRLQEGKIYDHHKVQQALTNFFQPEKILQLRELALKE VAGQVERKVDYTVTKNKTWQHERFLACISTSHEAAQRIIRKTGRLASYYNANWYV LYVQTPHEELDKIPLAAQRHLINNLKLATELGGEVVQVKSKHVANEIIQTAIDKKITTI CIGKPHLNLFQVILRTSLFNQLLKTLSEKDIDIIILS	23~~KdpD (3.81909E-115) ~~231,249~~Usp (4.96541E-34) ~~377	non-kinase	KdpD;Usp
	6.9E-87	299.7	0.2	9.6E-87	299.2	0.1	1.2	1	B2UQC5_AKKM8	Histidine kinase (EC 2.7.13.3)	Amuc_0827	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	892	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales, Akkermansiaceae, Akkermansia, Akkermansia muciniphila, Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	349741	>tr|B2UQC5|B2UQC5_AKKM8 Histidine kinase OS=Akkermansia muciniphila (strain ATCC BAA-835 / Muc) GN=Amuc_0827 PE=4 SV=1 MFSETHSDSQRADRILASIRREEARPGRGLLKIFFGMAPGVGKTCAMLEAAIQAAD KGVRVIIGVAESHGREDTMRLIGRLPRLPMKKMVYRGVEMEEFDLEEALRVKPQLI LVDELAHTNVPGMRHRKRYQDVEDLLAAGIDVYTTLNVQHLESRSDTVHDITAAPV QETVPDSVLAEADCIQLVDITPDQLRTRLREGKVYSAPQASAALDHFFKESNLTAL RELALRIVAEKVDHELTEVRTISGDRSIWRSGERLMVAVGPSPFSARLVRWTRRM AYALNAPWIALSVDTGVPLPPEQQQRLDANLELARRLGAEVVVMPGSDLAETLLR MAFLRNVSQIVVGKPQESYLWGLVRPISLVDKLVKGSDQIDIYVVPAASGPGRNR WKSWHRKTEKDGRDYWLAAGVTAAVTGAGLLVSAFTGYFAPGFLYLAGVVGLG FFIRSRWAMLLAAALSVLLWNLLFIPPVMTFKIERLEDALMCFFFLVALSTGRLTS RLRIREREEREREKKTNALFLYSRAIGSASDVPSLISVAAGQISQIMGVRLAVMTPE GGGGKLRLWETGGEYAMDEKEWSVAVWCMEHRRPAGRFTDTIPVAEGFYLPM MSGERCMGVLGVRPEEGECLTAGQKDLLESMGAQLAMALEREELRAERARTRTL MEESEKLHRSLLDSVSHEFKTPLAVIEGGCEKLAGRAASAPEEREEYGEILLAARR LRRLVKNLLDVSRLESGALKPKLDWCDLGDVIEGALAATREARRNHPVSVSLPPD YPLVKADFSLMEQVLVNLLLNACVHTPEGTSVTLQGGADSVRGQVWLDIHDMGP GIPPERAETIFERFRTTRPGGLGLGLPIVRGFMEAQRGAVSLVPVSAGTCFRLVLP LVEHDSVPEE	26~~KdpD (1.23403E-106) ~~236,258~~Usp (2.37258E-33) ~~380,405~~DUF4118 (0.00353548) ~~501,530~~GAF (0.00000000000541835) ~~649,666~~HisKA (0.00094028) ~~730,783~~HATPase_c (1.91343E-19) ~~881	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.9E-87	299.7	1.3	9.7E-87	299.2	0.9	1.2	1	H8KMI4_SOLCM	Osmosensitive K+ channel His kinase sensor	Solca_3779	Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) (Flexibacter canadensis)	368	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Solitalea, Solitalea canadensis (Flexibacter canadensis), Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) (Flexibacter canadensis)	929556	>tr|H8KMI4|H8KMI4_SOLCM Osmosensitive K+ channel His kinase sensor OS=Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) GN=Solca_3779 PE=4 SV=1 MNYNFLDLIQRSKRGKFKIYIGMSAGVGKTYRMLQEAHSLLKNGIDVKIGYIETHNR KETHALLDGLPTIPRRSLFYKGKELNEMDLNAILTIHPEVVIVDELAHTNIEGSKNEK RWQDVVDILNAGINVISAVNIQHIESINEEAQKISGAEIKERVPDSVLLMADEVVNID LTADELISRLKEGKIYDANKVPTALSNFFQSDKILQLRELALKEVARQVVRKIDTEIP KTIRQRQEVFLACISTRDTSAKMIIRKTARLAAYYNSKWILLYVQTPNESMEKIKLDL QRHLINNFKLATELGAEVIKLKHDDVAEAMLETIEKYNITTLCLGKPEFSWWKLFM GKALFENLLQKIENKDVDIVILS	12~~KdpD (5.477E-116) ~~222,241~~Usp (6.4898E-29) ~~368	non-kinase	KdpD;Usp
	7E-87	299.7	0.1	1.6E-86	298.5	0.1	1.6	1	I4B150_TURPD	Histidine kinase (EC 2.7.13.3)	Turpa_0348	Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) (Leptospira parva)	893	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Turneriella, Turneriella parva, Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) (Leptospira parva)	869212	>tr|I4B150|I4B150_TURPD Histidine kinase OS=Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) GN=Turpa_0348 PE=4 SV=1 MSYQRKGHFRPDADLLLSAVNKTETERRGRLRIFFGMAAGVGKTCAMLRAAHRL KDEGVDVVLGFVETHGRKDTAVLMEDLELIPRVSLPYQNVLLEEFDLEGALRRKPH TIVVDELPHTNAPGSRHPKRYQDILELLDAGINVMTAFNVQHLESVADSVEAITSVH VQERVPDSFVDMASDIELVDLVPEELIRRLEEGKIYAADKAVLAANNFFRKGNLTAL REMALHFTASFVDNELQHYRTLKNIGETWKTAERILVAVSPSANGENLIRLARQRA FELKARWIAVYIDSGASLKSEAQKSLAQNMSLARELGAEVISVRDTDVVTGILRLAR QKNITQVIVGKPPDTLWQRLTGRSILDRLVRSSGNLEIHAAGVAVRSKSAADFLSL QNLTSSRRQYLAAIATTCATTLICMPFLETIGYSAVSLIYLTVVIVLGLFVGRGPLVLA AAISALGWDYFFIPPKYTLHVAQLEDYLTLIIYFAVALAMGTLMARLRQRERALMAR EERVAAVYSFSRLLSRSTSLDETLQNCIEFIAQFFGARVSINLREKSGKLALEPAAA STRRISAKEASVAFWVFEHKKPAGRYTDTLPLAAATYYPLISTGGIVGVLGLRLPAK ARLTPDKEEILFAFVNHAAITIERDFLASERRRLRVAEESEKLHEAILNSISHELRTPI AVILGAVSAMQLKSTENNFAVQSELLSEVDIAARKLNVLVSNLLDMSRIEANKMRL NRQSYDLRNTITEATERLRSEIRNASLSVDFQGDDFTCECDNTLLQQAIMNIVVNS VLHNENGVAIQLTCSATEPGNLTVVISDDGVGLPPELIDSVFDKFVRSAQANSGGT GLGLPIAKAIVELHGGSITASNLPTGGACFRLTLPRCIPTGEK	>tr|I4B150|I4B150_TURPD Histidine kinase OS=Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) GN=Turpa_0348 PE=4 SV=1 MSYQRKGHFRPDADLLLSAVNKTETERRGRLRIFFGMAAGVGKTCAMLRAAHRL KDEGVDVVLGFVETHGRKDTAVLMEDLELIPRVSLPYQNVLLEEFDLEGALRRKPH TIVVDELPHTNAPGSRHPKRYQDILELLDAGINVMTAFNVQHLESVADSVEAITSVH VQERVPDSFVDMASDIELVDLVPEELIRRLEEGKIYAADKAVLAANNFFRKGNLTAL REMALHFTASFVDNELQHYRTLKNIGETWKTAERILVAVSPSANGENLIRLARQRA FELKARWIAVYIDSGASLKSEAQKSLAQNMSLARELGAEVISVRDTDVVTGILRLAR QKNITQVIVGKPPDTLWQRLTGRSILDRLVRSSGNLEIHAAGVAVRSKSAADFLSL QNLTSSRRQYLAAIATTCATTLICMPFLETIGYSAVSLIYLTVVIVLGLFVGRGPLVLA AAISALGWDYFFIPPKYTLHVAQLEDYLTLIIYFAVALAMGTLMARLRQRERALMAR EERVAAVYSFSRLLSRSTSLDETLQNCIEFIAQFFGARVSINLREKSGKLALEPAAA STRRISAKEASVAFWVFEHKKPAGRYTDTLPLAAATYYPLISTGGIVGVLGLRLPAK ARLTPDKEEILFAFVNHAAITIERDFLASERRRLRVAEESEKLHEAILNSISHELRTPI AVILGAVSAMQLKSTENNFAVQSELLSEVDIAARKLNVLVSNLLDMSRIEANKMRL NRQSYDLRNTITEATERLRSEIRNASLSVDFQGDDFTCECDNTLLQQAIMNIVVNS VLHNENGVAIQLTCSATEPGNLTVVISDDGVGLPPELIDSVFDKFVRSAQANSGGT GLGLPIAKAIVELHGGSITASNLPTGGACFRLTLPRCIPTGEK	26~~KdpD (2.88884E-111) ~~233,258~~Usp (1.16754E-35) ~~376,431~~DUF4118 (0.0000000000102661) ~~502,528~~GAF (0.000000000000104408) ~~647,671~~HisKA (0.0000000301524) ~~730,783~~HATPase_c (2.10368E-25) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	7.8E-87	299.5	0.1	1.3E-86	298.8	0.1	1.4	1	Q4JUR7_CORJK	Histidine kinase (EC 2.7.13.3)	kdpDjk1272	Corynebacterium jeikeium (strain K411)	898	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium jeikeium, Corynebacterium jeikeium (strain K411)	306537	>tr|Q4JUR7|Q4JUR7_CORJK Histidine kinase OS=Corynebacterium jeikeium (strain K411) GN=kdpD PE=4 SV=1 MTKRGTLKVYLGFAPGVGKTYAMLSEAHDLYDRGRDVLIGIVEDHGRERTRKLTE GLPTLPRKSVPYRGGHYEELDLEAALEAHPEIVLVDELAHTVVGENNADSSRPAEA IKRWHDVYALLDAGIDVISTMNIQHLESLNDVVSAVTGTRQLETVPDQVLRDADEIE LVDLSPDALRIRLARGEVYRQQQAETALNNYFRVGNLTALRELSLLWLADKVDEG LAKYREDKKIEENWPTRERVVVAVRGDEVSEALIRRGARITQRVAGREMLVVYVS GADEALGVDLPERLRRLQELTESLDGQWRVIEGDDIANTLLEFARTVNASQLVIGL GTRMSRLFSSTAHKIIDGSGRIDVHIVSTSSVSSDDGATKMSKRALRKASQLMGLT RDRGTGLDTSKQLSPTRRWIGWLLAVPGPILLTLLVLPFFRENGALGSILLGYLTIA VFAALAGGFGPAIVAVIIGSVMANWFFTHPYHTLTVTEPANLVQIILFFVISAAVAVV VDIAERRRAIANRRLGQAVVLSDLARGALDEGDDIRSLLARLRETFNLERVDLQQY SKERKKWVTMATTDPGGIGVPWPSKKAPSHVGAGDGMRFVLDGRDLTPAEDAM IEAHGARITAIYDREEIDAMRRATAALEAGNRVGTALLTAVSHDLRTPLAGIKAAVS ALNMDDMELDEESRSLLMETIESSTDRLETVIGNLLDMSRVNSNTVAVHRAKVHY NTVVEAVLAELPEATQHVDSFIDATVPPVLGDAGLVQRIIANIVVNARTYAPNSRIEL HAQQVPAGADDKTGAEASTVELAIVDHGPGFPSEHLNDVFTPFQRLGDQSANQN GLGLGLAVAHGFAEAMNGTLEARNTPGGGATLVLSLPTATGESEDGEERGVQKK VQGEAP	3~~KdpD (9.46941E-103) ~~220,242~~Usp (1.93077E-20) ~~360,412~~DUF4118 (0.00000000193721) ~~499,X,649~~HisKA (0.0000000000514061) ~~711,763~~HATPase_c (1.13233E-17) ~~874	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.4E-87	299.4	0.2	8.4E-87	299.4	0.2	1.6	1	U5VTG1_9ACTN	Histidine kinase (EC 2.7.13.3)	AFR_03310	Actinoplanes friuliensis DSM 7358	816	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	1246995	>tr|U5VTG1|U5VTG1_9ACTN Histidine kinase OS=Actinoplanes friuliensis DSM 7358 GN=AFR_03310 PE=4 SV=1 MPRGRLRIYLGAAPGVGKTYTMLGEAHRRAQRGTDVVVALVETHDRTHTTAMID GLEVLAPTPRGELDLDAVLARKPELAVVDELAHTNGPGSRHAQRWEDVDELLDA GIDVLSTVNVQHLESLNDVVAQITGVAQRETVPDAVVRAAEQVELVDMTPEALRR RVAHGNVYGPDEIDAALGNYFRAGNLTALRELALLWLADTVEDQLGRYRAEQDIS ATWETRERVVVALTGGPEGDTLVRRAARIANRTRGADLQAVHVMRNDGLTGADP AVLARQRVLVENLGGSYHQVAGPDIARALLDFARAVNATQIVLGASSRGRFAQLLT AGVGVTTTALAGAIDVHLVPHERAGKGTRAQRMPAALSRGRRLAGLALTLAGLPA LTGLLLTLAPSLTTDILLFLMVVVAVALIGGLWPALLAAVAGSLLLNWFFTPPYGRFL IAEGDNLLALVIFVVVAVAVSWVVDQAARKTRLAAEAGADAQTLATVAGSVLRGT RPLPALLERLRETFQLTSVTLLERGEVVANVGDSACTDVAGADGAVQVDDELVML LCGRSPAASDRRIVEAFAAQAAVALRQERLAAEAATARPLAETDRMRTALLAAVS HDLRTPLASAKAAVASLRSTEVHFDEDDRSELLETADESLERLDRLVTNLLDMSRL QAGALGVTIIGVGAEEVVPRVLDDLGPDGRAVITRIPDDLPALLTDPGLLERVLVNL VGNALRYSPADRPPVITASALGDRIELRVIDHGPGIPPDRHDDVFLPFQRLGDRDN HSGVGLGLALSRGLAEAMGGTVTPEETPGGGLTMVVTLPAG	3~~KdpD (2.05407E-106) ~~204,226~~Usp (2.37689E-28) ~~348,399~~DUF4118 (0.000000578277) ~~449,X,595~~HisKA (0.000000000000355887) ~~661,712~~HATPase_c (3.38517E-28) ~~813	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	8.8E-87	299.3	1.6	1.3E-86	298.8	1.1	1.2	1	D2QBF8_SPILD	Osmosensitive K channel His kinase sensor	Slin_0067	Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896)	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Spirosoma, Spirosoma linguale, Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896)	504472	>tr|D2QBF8|D2QBF8_SPILD Osmosensitive K channel His kinase sensor OS=Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896) GN=Slin_0067 PE=4 SV=1 MNPNDQNAEHFLDLLRQSRRGKFKVYIGMSAGVGKSYRMLQEAHTLLRAGIDVKI GFIETHNRTETQALVDGLPVIPRRRLFYKGRELDELDLQAILNLHPELVIVDELAHTN IPGSKNEKRWQDVVEIVEAGINVISAVNIQHIESLYQAVRAITGIDVTERVPDRVLQ MADEVVNIDLTADELITRLKDGKIYDTAKVSTALNNFFQPERILQLRELALREVATAV ERKIETSVPTSVKAKPERFLAAISSNHEIARRVIRKTARLAAYYNSRWFVLYVQTPA ESSDRIKLDVQRHLINNLKLATELGAEVIRVKDSNIVNSIMAEVEKRNITTVCIGKPH LTLIQIILRTNAFNQLLTKLSGSDTDLIILS	18~~KdpD (2.86999E-111) ~~228,246~~Usp (3.04737E-25) ~~374	non-kinase	KdpD;Usp
	1E-86	299.1	1.1	1.8E-86	298.3	0.8	1.4	1	I4D558_DESAJ	Histidine kinase (EC 2.7.13.3)	Desaci_1955	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	891	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	646529	>tr|I4D558|I4D558_DESAJ Histidine kinase OS=Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4) GN=Desaci_1955 PE=4 SV=1 MKNQGKLTVFLGAVAGVGKTYAMLEAAKERLSEGTDVVIGFVETHGSLETETVLK GIPYISSKTQEFLGKLVQEMDLEVLLERHPQLVVVDELAHTNIPGSRHRKRYQDVE ELLASGIDVYTTLNIQHLESLNDVVAQITGVTVSETVPDRILEIASQIQMVDITPDELI QRLKEGKVNVPGVAAEAIEKFFRPGNINALREMSLRYTAKRVDCQMESYMRNHGI AGPWPSGEKVMVCVSGNPFSTKLIRTAKRMAARQNAEWLAVHVVLPGEMQKNE NEKDLMEENLRMAEKLGAEIVTPHGDDIVEELLTLARKRNVSQIIIGKPERARFQEL FHGSVVDKVIRRSHGISVHVISGRKNAADRKRETIAEDNNTSLGHLSRRQRYSATP YLMSVLMMSALTVAVSPIETFLGPVNIPMLYLLPVLLTAARWGRLPALITAGMGVIIF DYFFVPPFYTLHVDDFRYVISFVILMIAGIVTGTLSGRLTDQINYSRQREQQVSALY SLSRDLTAVDKLERILDSIARKIGETLDGQVVLLLPDERNNLVLSQSSSTDHFMTES EMNVASWVYERGQKAGRGTETLRSAKALYLPLITEQGTHGVLGICFFHQNDIVSP QQIRFLDAFAGLAALAINRIKLADEARQAHALAESERLRTALFNSLSHDLRTPLSSII GAATGLLEDEDVVYSPDARHDLLQTILQGAERMNRFVNNLLDMARLESGMLKLHK DWCDIQDIIGVAINRLDIVLAKRLLDINIPAGLPLVQADYALIEQVIVNLLDNAVKYSE PVSKIVISVKQVGQNLEISVANRGNPIPETDLSKVFDKFYRLTSPLQVSGSGLGLSI CKGIIESHNGDIWAENNELGGVTIIFTLPLEYELSDKLPIEGGD	2~~KdpD (1.05578E-105) ~~212,234~~Usp (2.11613E-41) ~~357,396~~DUF4118 (2.44603E-15) ~~491,518~~GAF (0.00000000000425106) ~~637,654~~HisKA (0.00000000000209321) ~~721,774~~HATPase_c (1.97571E-27) ~~875	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.1E-86	299.1	0.1	1.4E-86	298.7	0.1	1.1	1	G8P0S1_GRAMM	Osmosensitive K channel His kinase sensor	AciX8_0324	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	380	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	682795	>tr|G8P0S1|G8P0S1_GRAMM Osmosensitive K channel His kinase sensor OS=Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8) GN=AciX8_0324 PE=4 SV=1 MGACDTPRKRPEDWLESAENVEKKRGRFKVFLGYAPGVGKTFSMLSEGIRRQG RGEDVVIGIVETHGRIGTSEVAAKIETVPRREIDYKGTLFSEMDVDAILARQPQVALI DELAHTNVEGSRFQKRYEDVFALLDAGIDVVTTVNIQHVESITPRVQSLTGITVRET VPDWVLDRADEIVISDLTPEALATRMRRGDIYPMERVERALSNFFRRGNLIALREM ALQRVTRAVDRTLDDYVKRKQLGGHWTVAEKVAVCISASPAARDLIARGARLSQG MDAEFYVLHLDTERDREPEAARALDDNLQFARNLGATIVRLKGSSVASATAEFAQ QNRITQVLFGRSALTGIKKYLYFLAIQQFAAAAPHTDLHIITQKSQ	23~~KdpD (5.26022E-110) ~~233,255~~Usp (5.52697E-25) ~~376	non-kinase	KdpD;Usp

	1.1E-86	299	2	1.5E-86	298.5	1.4	1.2	1	W8EUK8_9BACT	Osmosensitive K+ channel histidine kinase (EC 2.7.13.3)	Hsw_0623	Hymenobacter swuensis DY53	391	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Hymenobacter, Hymenobacter swuensis, Hymenobacter swuensis DY53	1227739	>tr|W8EUK8|W8EUK8_9BACT Osmosensitive K+ channel histidine kinase OS=Hymenobacter swuensis DY53 GN=Hsw_0623 PE=4 SV=1 MSTPANDDQQRDQSAERFLRLVQQRRRGRLKVYLGLAAGVGKTYRLLQEAHDLR AHGVDVVLGYVETHGRPGTVAQLRDLPTVPRKHIFYKGRMLEELDVQGILQRRPS VVVVDELAHTNVPGSENEKRWQDVEQLVRAGISVLTAVNIQHLESLHDQVLRITGT DVTERVPDQVLKQADEVVNVDLTVGELRARLEEGKIYDAAKVPTALQNFFQAENL LQLRQLAVRETANLISRQIETDGGGAAPVAPERRNQDRLLACINANAPAAREIIRKT SRLADRLSAASWAVLYVQTPRESADRINLATQRHLLNNLQLTTELGGQILRVKATD AVPEILRVAQEKGVTLLICGVTSEKSWWQRLLRPGVTRRLIRAVARSPLDVDVFLV SY	26~~KdpD (4.8669E-108) ~~235,258~~Usp (1.44936E-26) ~~390	non-kinase	KdpD;Usp

	1.2E-86	298.9	1.6	1.2E-86	298.9	1.1	1.6	1	Q81UW4_BACAN	Putative sensor protein KdpD (Sensor histidine kinase KdpD) (EC 2.7.13.3)	kdpD GBAA_0742 BASH2_05075	Bacillus anthracis	384	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus anthracis	1392	>tr|Q81UW4|Q81UW4_BACAN Putative sensor protein KdpD OS=Bacillus anthracis GN=kdpD PE=4 SV=1 MCVLYADDYKPTFQRRTPEEYLEYIRQQNRGKLKLYVGAAPGVGKSYKMLYDAR EMKKDGMDIVIGLIETHGRKETEEAIADLEKVPLKEIQYKGKVFYELDVEGIIKRAPQ VVVVDELAHSNVPGSKNKKRYMDVQELIDAGISVLSAFNIQHLESVHDIVAQITNVK VRERIPDFILQKANEIQLVDATPEVLRKRLIDGKIYKEEKIQQSLQNFFTLNNLGALR ELSLREVADDMDEKISQTVIEPIGVKEKILVCVQYSSTAEKLIRRGWRMADRLNAEL YVLNVEREKIDSLSAGKKQTIEEWKSLTNQFDASFVLEEANGRKPADVIIEVAKRL QVTQILLGQSARTRWDEIRKGSIVNEIMRETKYIDIHIVADQRA	29~~KdpD (8.00965E-113) ~~238,255~~Usp (7.77947E-45) ~~380	non-kinase	KdpD;Usp

	1.2E-86	298.8	1.4	1.6E-86	298.4	0.9	1.2	1	C6XZL2_PEDHD	Osmosensitive K channel His kinase sensor	Phep_2504	Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290)	376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Pedobacter, Pedobacter heparinus (Flavobacterium heparinum), Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290)	485917	>tr|C6XZL2|C6XZL2_PEDHD Osmosensitive K channel His kinase sensor OS=Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290) GN=Phep_2504 PE=4 SV=1 MEEENKASSVRKFLDLVKKSRRGKFKVYIGMSAGVGKTYRMLQEAHALLKNGIDI HIGYIETHNRAETQALLAGIPLIPRRKLFYKGKELEEMDVNTIINLHPEVVIVDELAHT NVEGSKNGKRWQDVVDILEAGISVISAVNIQHLESMNEEIEKITGIPITERIPDRILEL ADEIVNIDLTADELIDRLKAGKIYDHTKIERALANFFQSDRILQLRELALKEVAHHLER KISIEIPKQIKLRPERFMACISTNKETARIVIRKTARLASYYHSSWIVLYVQNNRERG DKVKLDLQRHLINNFKLATELGAEVIKIKSNQITQTILKIAEEKEVTTICIGKPHLNLFQ IIMRTAIFNQLLRSISATETDLVILS	20~~KdpD (1.13123E-110) ~~227,248~~Usp (8.08843E-28) ~~376	non-kinase	KdpD;Usp

	1.2E-86	298.8	3.1	1.6E-86	298.4	2.2	1.2	1	C7PUS6_CHIPD	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Cpin_3612	Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Chitinophaga, Chitinophaga pinensis, Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)	485918	>tr|C7PUS6|C7PUS6_CHIPD Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034) GN=Cpin_3612 PE=4 SV=1 MSDKDNNAQHFLDLIRQSRRGKFKIYIGMSAGVGKTYRMLQEARTLLRNGVDIKIA YIETHNRAETHALLDGLPIIPRRELFYKGKALEELDMQAVLNLHPEVVVIDELAHTNI EGSKNEKRWQDVMEILEAGINVISAVNIQHIEGLQDEVKNITGVDVAERIPDLVLQQ ADEVVNIDLTADELVTRLKEGKIYTPDKIAVAMKNFFQPERILQLRELALKEVATQV ERKIESSLPRTAHPRNERFLACVSSNHVIAKKVIRKTARLAAYYQSKWYVLYVQTP KEDGDKIGLAEQRHLINNFKLAMELGGEVIKVKNSNIAKSIMQTADEKKVTTICLGK PHLNVMGMLLNTAVFSQLLGKLSESDIDIIILS	18~~KdpD (2.56769E-115) ~~228,246~~Usp (1.93492E-28) ~~374	non-kinase	KdpD;Usp
	1.4E-86	298.7	0.4	2.9E-86	297.6	0.3	1.6	1	R7RTY1_CARML	Histidine kinase (EC 2.7.13.3)	kdpDBN424_665	Carnobacterium maltaromaticum LMA28	897	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium maltaromaticum (Carnobacterium piscicola), Carnobacterium maltaromaticum LMA28	1234679	>tr|R7RTY1|R7RTY1_CARML Histidine kinase OS=Carnobacterium maltaromaticum LMA28 GN=kdpD PE=4 SV=1 MQEEDIRPDPDQLLLQVGQDEETTMGKLRVFFGYAAGVGKTYGMLKEAIEQQET GKVVLAGYVEPHARPETMALLDHLNQLPSKKIPYKNMMLEEFDLDEALRLQPEIILV DELAHTNALGSRNKKRYQDIEELLQAGIDVYTTVNVQHIESLNDIVEDITHVRVHET VPDSFFDEALIKLIDVEPDELLGRLKEGKIYRPEHAKKAMNHFFTKENLKLLREIAIR RAADHIGMDNRIEEAYTEKRAHVKLLTCIDSEHQTGAEKCIRWTARLANAFRAEW VVLHVDESGDNEKSEAELALLKRNNELAERLGAEVVTLSGHNPVTTIAQYAKLTGV TDIIIGKHRRKLDYQRLLKDDIEDRLIKHLSNVELHIVPFIEKYPRIKNRFFSKERLIPK NLTIADSLKTMVLLLMATLLSEIFSFLGIGDQNVIVVYLLFILIISQVTTGYFYGVLSSII SVIFFNWFFVDPLFSLTVYKAGYPITLLIMLMVALFTSNMMIRVKSQARESIKKEHQ MGVLYDFNKKLLATRNLNGIINLTNDYLVSTMNHSVIFYTEQGKNLLNHKALAFENK QDIEVLTGSDEEAVANWVFNNQKVAGYGTDTLMGAKGFYLPVLSQGRVLAVIGVL LSKENPLTHENLNFLKLIASQLSLALERQYLVTEQQQIMLETEKEKMRSNLLRAISH DLRTPLTGILGASSAILENKDKFDEELKLSLIKDIKEDSEWLIRMVENLLSVTRIDEGT MKVKKMPEAVEEIVAGAVRRIRKRFKEQELIVKVPDEFLLVPMDGTLIEQVLINLME NAIKHSGSKGAISVIVKRNRNKAIFEVTDNGIGIPEKKLASLFDQFGKESDTPIDATR GMGIGLSICKTIVAAHSGTIEVTNKQQGGAVFRFTLPID	26~~KdpD (2.88189E-111) ~~232,250~~Usp (2.98447E-36) ~~376,405~~DUF4118 (7.18311E-15) ~~505,551~~GAF (0.00000000280051) ~~655,672~~HisKA (0.0000000000518188) ~~738,791~~HATPase_c (1.95015E-29) ~~894	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.4E-86	298.7	2.6	2.4E-86	297.9	1.8	1.4	1	I4C4T7_DESTA	Universal stress family protein,osmosensitive K+ channel His kinase	Desti_1870	Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	551	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfomonile, Desulfomonile tiedjei, Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	706587	>tr|I4C4T7|I4C4T7_DESTA Universal stress family protein,osmosensitive K+ channel His kinase OS=Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1) GN=Desti_1870 PE=4 SV=1 MTTAEDRANSFLRMIRRSRRGKLKIYLGYCAGVGKTYQMLQEGYRLMKEGVDVAI GLLETHGRQDIVDLSQGIEVLPRIRQEYRGHVLEEMDVDAIIARRPEVALIDELAHT NVPGTKNAKRYQDVQQILAAGIHVITTLNVQHLESLYDTVEKTVHVKVRERLPDSV VAEADEIVNVDLTTNDLKERLREGKIYPAERIETALSNFFQTSNLENLRELTLRELAS QIDLRMREGSQDDAEPTPDQVMVCLSSRGPNSEMLLRYASRLAGRLNRNWYAV YVQTPSEEPTVIDAYTQRILSGALTLAKQLGAMVFTYKGEDIPDTILRFAREYRVGH IVIGHPGEIPFWKKLFGKKTLVEELIRKARGITFVVLDTRGAEPTFASEGNGRNESS LQLRKEKVSLSDLISSRRIVIWNQPVEKEYVIRTLVEVAAKDFETCDAEDTIKAVLDR EKLGSTFFANEAAAIPHARIKGLSSPIISLGLTKQGILQDEAISPIGLVFLILTPAEIPSS QVEILALVSRATKDGHLYDRVAESDNPEELLSILRELRV	18~~KdpD (4.37476E-110) ~~228,247~~Usp (3.2764E-28) ~~373,403~~PTS_IIA_fru (1.13785E-14) ~~546	non-kinase	KdpD;Usp;PTS_IIA_fru

	1.5E-86	298.6	0.3	2.3E-86	298	0.2	1.3	1	T0VE02_9ENTE	Osmosensitive K+ channel histidine kinase Kdp (EC 2.7.3.-)	HSIEG1_1767	Enterococcus sp. HSIEG1	492	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	1316414	>tr|T0VE02|T0VE02_9ENTE Osmosensitive K+ channel histidine kinase Kdp OS=Enterococcus sp. HSIEG1 GN=HSIEG1_1767 PE=4 SV=1 MDRPTSVDTLKAENRKKGRLRVYFGFAAGVGKTYAMLLEAQELKALGKDVVIGYI EPHDRPDTNSLLAGLPQIPLKEIQYKGITLTEPDIDAIIQQQPAIVLIDELAHTNAEGS RNRKRYQDIEELLNAGIDVHTTVNVQHIESLNDIVEEVTGIEVKETVPDTFFQQATL KVIDVEPDELIDRLAQGKIYANENAKRALQNFFIPKKLEQLRGLAIQRASDHINRISG RTNGIQSKLITIVQDAFPKMAEKSIRWTARLAQGLGAEWTVLYIRSEEKNEATTLA EKLGAEVVVIEEDNYFETIIEYAKLVGATDIIMGKNLAKPWYEKLFVEELDVRLLKRL PDTEIHLIPYKEERASIFSLSKKVIEGGGKDLAIALISVFLATVTTEVMQYLHFGDQN LMLVYIFFILLVARLTSGYFWSALSSILSVLAFNWFFVEPLYSLTVYKQGYPITLVIML LVALMISNLMVRLKNKLFIQWKKNSRWKYFMS	16~~KdpD (9.28329E-124) ~~224,247~~Usp (2.57026E-27) ~~352,375~~DUF4118 (6.33329E-14) ~~476	non-kinase	KdpD;Usp;DUF4118

	1.6E-86	298.5	0	2.7E-86	297.8	0	1.3	1	A0A0A8UNS1_LEGHA	Sensor protein KdpD	kdpD LHA_1369	Legionella hackeliae	648	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella hackeliae	449	>tr|A0A0A8UNS1|A0A0A8UNS1_LEGHA Sensor protein KdpD OS=Legionella hackeliae GN=kdpD PE=4 SV=1 MVERRPNPDALLHSVQEEERQQKHGKLKIYLGAAPGVGKTHEMLHDALELLNKGL DVVVGIAESHGRQEINSLLTHFNVLPKKTIDYHGKQLSEFDLDGALKRYPGLILVDE MAHTNVPGSRHKKRWQDIKELLDRGIDVYTTLNVQHIESLNDDVSQIVHAPIKETIP DSIIEIADTIELVDLPPEELLKRLQDGKVYFPAQAKLATESFFRKGNLSALRELALRT AAKCVSAQVLLYRQGLGIRKIWPTKEKILVCVGPGISSLTLIRAAKRTARNLQAPWI AIYVDIPYGSQSEEKRQKAVENLRLAKQLGAETRILTGFNVVKTVLDFAHDQNITQI MIWKHIRTRWRDLFLRSLADEILRYSEEIDVYIMTGDRQVKKQEKKYKKRSPWVIY LASLVIVTLTTMINYLLYPVLSASNLIMVYLLGVTGIALFGRVGPSILGSVLSIFAYDY FFSPPLYTFSIPNLNYSFTLLVMLIVTQVISQLIIITRRQMAAARLHARQTSALYELSK QLSNTRGKNKLLNIGINYISKIFNSEVAVFLPQNKRLIAHAKKGLRPILDAEESEIIQW VYELGQRAGLGTDTFPTAEALYLPLPGIRKVVGVLRLQSPKGEDLDSPEKIQLLEA CASQFALALEIENLNSIV	449	>tr|A0A0A8UNS1|A0A0A8UNS1_LEGHA Sensor protein KdpD OS=Legionella hackeliae GN=kdpD PE=4 SV=1 MVERRPNPDALLHSVQEEERQQKHGKLKIYLGAAPGVGKTHEMLHDALELLNKGL DVVVGIAESHGRQEINSLLTHFNVLPKKTIDYHGKQLSEFDLDGALKRYPGLILVDE MAHTNVPGSRHKKRWQDIKELLDRGIDVYTTLNVQHIESLNDDVSQIVHAPIKETIP DSIIEIADTIELVDLPPEELLKRLQDGKVYFPAQAKLATESFFRKGNLSALRELALRT AAKCVSAQVLLYRQGLGIRKIWPTKEKILVCVGPGISSLTLIRAAKRTARNLQAPWI AIYVDIPYGSQSEEKRQKAVENLRLAKQLGAETRILTGFNVVKTVLDFAHDQNITQI MIWKHIRTRWRDLFLRSLADEILRYSEEIDVYIMTGDRQVKKQEKKYKKRSPWVIY LASLVIVTLTTMINYLLYPVLSASNLIMVYLLGVTGIALFGRVGPSILGSVLSIFAYDY FFSPPLYTFSIPNLNYSFTLLVMLIVTQVISQLIIITRRQMAAARLHARQTSALYELSK QLSNTRGKNKLLNIGINYISKIFNSEVAVFLPQNKRLIAHAKKGLRPILDAEESEIIQW VYELGQRAGLGTDTFPTAEALYLPLPGIRKVVGVLRLQSPKGEDLDSPEKIQLLEA CASQFALALEIENLNSIV	23~~KdpD (4.24452E-107) ~~229,254~~Usp (1.82225E-36) ~~376,397~~DUF4118 (5.92764E-14) ~~496,524~~GAF (0.0000000000121863) ~~640	non-kinase	KdpD;Usp;DUF4118;GAF

	2E-86	298.2	0	3.7E-86	297.3	0	1.5	1	A0A059W9N7_STRA9	Histidine kinase (EC 2.7.13.3)	DC74_7756	Streptomyces albulus	917	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	68570	>tr|A0A059W9N7|A0A059W9N7_STRA9 Histidine kinase OS=Streptomyces albulus GN=DC74_7756 PE=4 SV=1 MRWATEGTGAAEEPRPGRLKVFLGAAPGVGKTYRMLDEGRRRAARGTDVLVAF AECHGRPATEAMLDGLTVLPRLIRRHRDAERAELDLDRVLERRPAVALIDELAHTN APGGRRTKRWQDVEELLAAGIDVVATLNIQHLESLTDVVEKITGVPQFETVPDEVV RRAHEIELVDLPAEGLRRRMAHGNVYPPEKVDAALSHYFRLGNLNALRELALLWV AGRVGEALCAYRHDHRIGPVWETRERVVVALTGGPEGTTLIRRAARIVNLPRSRH PDRAAETALSAGDLLAVHIARSDGPAGSSAAALAGQRQLVESLGGSYHAVVADDV PAALLDFARAQNATQLVVGASRRGRLRRFLAPRGVGETVVELSGDIDVHTVSHER AGQGRGWPVAGSGLPRSRRVAGPIAGLVLPLLLTLVLRAVSGPLSLNLTSEALLFL LTVLGVACIGGVVSALLASVTTSLLLNYYFLPPVGEFTFAGANVVVAQAAFTTVAVT VAAIVDRSLRLGRRAARATAEAETLTSLAGGILRGDRAVPALLERTRETFGMDRIEL RPRVQTGEPSWPSCVADTVATGAMGAADPVRGPAAADGAGADHRTEVAIGDDG VLVLTGRRLPASEHRVLTAFAAHLTAAVERARLAEAAAEVEVVKAANRMRTALLAA VGHDLRTPLAGSWAAISSLRSRDVEFSAEDRDELLATAEESLAKLSRLVDNLLDMS RLQAGALTPHREPVALADVLAAALDTLPDSPPQASGRVVARGLEEAPDALADPPL LERVIANLVSNAVRHSPAGRPVTIGASALAGRVELRIIDRGPGIQLLDRERAFEPFQ RLGDTDNTTGLGLGLALSRGLTEAMGGTLVPEETPGGGLTMVVSLPAAPAPIVTA APAVPGSGALPVAGVGAGATELGLRRHRGR	14~~KdpD (2.56845E-103) ~~224,246~~Usp (4.35759E-22) ~~382,426~~DUF4118 (0.000299254) ~~505,X,655~~HisKA (0.00000000158146) ~~721,776~~HATPase_c (5.84232E-25) ~~877	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	2E-86	298.2	0.3	2E-86	298.2	0.2	1.9	1	I4D2C8_DESAJ	Histidine kinase (EC 2.7.13.3)	Desaci_0905	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	901	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	646529	>tr|I4D2C8|I4D2C8_DESAJ Histidine kinase OS=Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4) GN=Desaci_0905 PE=4 SV=1 MSEKKRVSPDELLADIEDEAKGKLTVFLGAAAGVGKTYAMLEVARERLSEGIKLSA GWVEPHARPETMALMEGIPQIAPKEIEYHGKVLKEMDLDEILSIHPQIVLVDELAHT NVPSSRHLKRYQDVEELLAAGIDVYTTVNIQHVESFNDIVAKITGVTVRETVPDSIL EHARIQLIDISTEALIQRLEEGKIYVPNQAKHALDKFFRPGNINALRELSMRFAAQRV DRQLESYMRVHGIEGPWPASERVMVCISSSPFGERLIRMGKRIAVGMKAELLVVY IDTPSNPLKNENQKDQLSKSLHLAQELDAETISLSGNDVVEELLEVAQKRNVTQIIIG KPGQLKIRERFSSSIVEKVLRQSQNISVHVIPGDGPKTKEERENKKTGVKKTNDLV PYLTTFVSLAVITVVAWLGSSELGLVNTAMLYLLPVLLSAGRYGKRVGIFTSIVSVIT YDFFTIPPVLTFTVADLRYLVSFAIMILIGYYLGNLSTRLRIQLINSRQRESQTAALYS LSREIAAVSDLDFVLESVVKKVSDIIRGEVVILVPETNGQLSLRSCSNLETAFEENER AVATWVFENNQTAGKGTDTLGGAKGFYLPLVSEQGICGVLGVQQSSSERYLSAE KRRLLDAFASLTALAIARISLVEKAREAQLLNESEKLRTALLNSISHDLRTPLASMIG AVTSLIENDKLFDVTSRQDLLETIKIGAMRMNKLVNNLLDMARLESDMLKLNKEWC EIDEIIKEAIKHIDEGLENKREIICEISNKELLVNVDFILIKQVLTNLLDNAMKYSKPDSR ICIIVRNNEKQVEVSVRDWGLPIPPEDLEHIFDKFYRVRSPRQISGTGLGLAISKGIV ELHGGKIQAENNSEIGGVTISFTIPLSKIPPRIPVEVGDDNE	19~~KdpD (1.66082E-111) ~~228,250~~Usp (4.79868E-40) ~~373,398~~DUF4118 (7.41053E-17) ~~496,524~~GAF (0.0000000000622464) ~~644,661~~HisKA (0.00000000000526607) ~~727,781~~HATPase_c (2.48232E-27) ~~883	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2E-86	298.1	0.9	2.9E-86	297.6	0.6	1.2	1	I0K509_9BACT	Osmosensitive K channel His kinase sensor	FAES_1202	Fibrella aestuarina BUZ 2	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Fibrella, Fibrella aestuarina, Fibrella aestuarina BUZ 2	1166018	>tr|I0K509|I0K509_9BACT Osmosensitive K channel His kinase sensor OS=Fibrella aestuarina BUZ 2 GN=FAES_1202 PE=4 SV=1 MNPNDQTAERFLNLIRESRRGKFKIYIGMSAGVGKSYRMLQEAHSLLRSGVDVRI GFIETHNRAETVALVEGLPLIPRRTLFYKGRQLEEMDVQAIINSHPELVIVDELAHTN IPGSKNDKRWQDVADVLDAGINVISAVNIQHIESLYDEVRAITGIDVTERVPDRMLQ LADEVVNIDLTADELIARLRLDGKLYDQAKVQTALAHFFQPEKILQLRELALKEVAGQ VERKVDQTLPPASVSRHERFLVAISTNADVARRVIRKTARLASYYNSRWYVLYVQ TPAEAPDRIRLDVQRHLINNLKLATELGAEVIRVKGQNIVDGIMGEVERRHITTVCIG KPHLNLLQIIIQTNAFNRLLNKLSASDVDLIILS	18~~KdpD (1.44758E-110) ~~228,246~~Usp (2.15632E-28) ~~374	non-kinase	KdpD;Usp

	2.1E-86	298.1	1.6	2.1E-86	298.1	1.1	1.7	1	Q81HP8_BACCR	Sensor protein kdpD (EC 2.7.3.-)	BC_0756	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	381	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	226900	>tr|Q81HP8|Q81HP8_BACCR Sensor protein kdpD OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) GN=BC_0756 PE=4 SV=1 MYADDYEPKFQRRTPEEYLEYIRQQNRGKLKLYVGAAPGVGKSYKMLFDAREMK KDGIDIVIGLIETHGRKETEEAIADLEKVPLKEIQYKGKVFYELDVEGIKKRAPQVVV VDELAHSNVPGSKHKKRYMDVQELLEAGISVLSAFNIQHLESVHDIVAQITNVKVR ERVPDFILQKANEIQLVDATPEVLRKRLIDGKIYKEEKIQQSLQNFFTLNNLGALREL SLREVADDMDEKISQTVIEPIGVKEKILVCVQYSSTAEKLIRRGWRMADRLNAELY VLNVERENIDSLSAGKKQTIEEWKTLTNQFDASFVLEEAKGRKPADVIIEVAKRLQV TQILLGQSARTRWEEIRKGSIVNEIMRQTKYIDIHIVADQRG	26~~KdpD (4.78423E-112) ~~235,252~~Usp (5.12353E-45) ~~377	non-kinase	KdpD;Usp

	2.2E-86	298	1	2.2E-86	298	0.7	1.6	1	C2WYK0_BACCE	Sensor histidine kinase KdpD	bcere0024_6410	Bacillus cereus Rock4-18	384	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock4-18	526988	>tr|C2WYK0|C2WYK0_BACCE Sensor histidine kinase KdpD OS=Bacillus cereus Rock4-18 GN=bcere0024_6410 PE=4 SV=1 MSVLYADDYKPTFQRRTPEEYLEYIRQQNRGKLKLYVGAAPGVGKSYKMLFDAR EMKKDGIDIVIGLIETHGRKETEEAIADLEKVPLKEIEYKGKVFYELDVEGIIKRGPQV VVVDELAHSNIPGSTNKKRYMDVQELLDAGISVLSAFNIQHLESVHDIVAQITNVKV RERIPDFILQKANEIQLVDATPEVLRKRLIDGKIYKEEKIQQSLQNFFTLNNLGALRE LSLREVADDMDEKISQTVIEPIGVKEKILVCVQYSSTAEKLIRRGWRMADRLNAELY VLNVERENIDSISAGKKQTIEEWKSLTNQFDASFVLEEAKGRKPADVIIEVAKRLQV TQILLGQSARTRWEEIRKGSIVNEIMRQTKYIDIHIVADQRG	29~~KdpD (4.5536E-113) ~~238,255~~Usp (8.72934E-45) ~~380	non-kinase	KdpD;Usp
	2.5E-86	297.8	0.1	5E-86	296.8	0.1	1.5	1	A0R377_MYCS2	Sensor protein KdpD (EC 2.7.13.3)	MSMEG_5372	Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	831	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	246196	>tr|A0R377|A0R377_MYCS2 Sensor protein KdpD OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=MSMEG_5372 PE=4 SV=1 MGLLSRKVGDLRIYLGAAPGVGKTYSMLAEAHRRMERGTDVVAAMVDTHGRRKV GQLLASIDVIPPLIVEHEGTEYQEIDVPALLMRRPKVVLVDDLAHTNAPGSRNPKR WQDVEELLNAGITVISTVNIQNLESVADLAGQITGVDEPDRIPDEVVRAADQIELVDI TPEALRRRLAHGNIYPRERVDAALSNYFRPENLTALRQLALLWLADQVDAALEKYR SANKIPDTWKPRERVVVGVTGGPGSETQVRRASLIASRTGADLKVVHVVRGDGL TVTSAQQKRVLRDLAASLGATLHTVIGDDVAATLIDFARDVNATQLVVGTSRRSRL ARFFDEGITATVVQRSGPLDVHVVTHEEAGTGISKPRVGPGASVTGWLAAVALPP AICALLLAVPPLGVGTQTALFVAGVLMIALLGGIARAALSAVLSGVLITYFLIEPRNSF AVAGADSALTTGVLLGLAIAVAGLVDQTARHSRAARRASQNAELLALFADGVLRD ADPGALLERVRETYAQRSVSLLRGRTGEVLAHAGANPCTDIDEADTTIEIGDDEY WLLLAGPDLTSHDRRVLNAVAEQAVSLVKKRRQADEAIKFDTEAEKLRSSIQSAIT HNLRTPLVTAKAAIAGAAHDNPPPDDTVELLAAAEKSVDELSVLVVNLLDSSCLAT GAIRPELRPVDLRDAVEHVLRDIGPDARRVHVDVDGTPVLADGELLGRVLGNLLTN SLRYGDPDGDSAGDSGVVRVTAGQVDDRVLIAVVDSGPGIPRGSEHEAFAPFQR LGRDDANIGVGLGLPVASGLVEAMGGKISMTETPGGGLTVEIDLPAARRSE	7~~KdpD (5.15205E-101) ~~216,249~~Usp (5.15367E-29) ~~359,381~~DUF4118 (0.00000316907) ~~474,X,603~~HisKA (0.14)~~666,716~~HATPase_c (1.83818E-22) ~~824	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.1E-86	297.5	0	5.4E-86	296.8	0	1.4	1	H2JYA4_STRHJ	Histidine kinase (EC 2.7.13.3)	SHJG_2400	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	831	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	1133850	>tr|H2JYA4|H2JYA4_STRHJ Histidine kinase OS=Streptomyces hygroscopicus subsp. jinggangensis (strain 5008) GN=SHJG_2400 PE=4 SV=1 MSDVRPGRLKVYLGAAPGVGKTYRMLDEGRRRAARGADVVVGFAECHGRPHTE AMLDGLESVPRASCAYRGGRFEEMDLAALLARRPQVAIVDEFAHGNVPGDGRNP NRRQDIEMLLDAGIDVITALNIQHLESLNDVVEKITGIPHHETVPDEVVRRARQIELV DMEPEGLRRRMAHGDIYAPEKIDAALANYFRPGNLTALRQLALLWVADRVDEALQ EYRTRHGIGGVWETRERVVVALTGGPEGDTLVRRAARIADRSAGGDLLAVHVAR SDGLASGVSHASLARQRRLVEDLGGSYHSVVGDDVPTTLVEFARGENATQLVLG TSRRGRLTRFLTGPGTGETVTELSGDIDVHRVTHERAGRGTLLPSRRRTLSPARLI AGPVTGLVLPVLLTVVLARTRGPLNLTSEALLFLLAVVGVACIGGVASAVIASVTAS LLLNYWFIPPIGAFTLDDPNALLALAVFAVVAAVVAAVVDRSLRLSRRSARATAEAE TMSSLAGSIVRGEATIPALLERTRETFGMESAELVDEAPEEAGVTAVPAGPGAWL ALRGRTLSSSERRVLAAFAAHAGSAVERARLAEAAAEVEPVKAGDRLRTALLRAV GHDLRTPLAAGWAAVTSLRSRDIEFPPEDRDELLATADESMAKLNRLVENLFDLS RLEAGALTLDLRATSLEEVLPTALADVPDVDVVDLEEIPAVLADPPLLERVIANLAG NAARHTPDGRKVLVTASVLADQVELRVVDRGPGLPAEGRDRLFEPFQRLGDTDN ATGLGLGLALARGLTEAMNGTLSPEDTPGGGLTMVVSLPFAQRTSSAVPTKASRR PE	5~~KdpD (5.45443E-106) ~~215,237~~Usp (1.07918E-28) ~~361,415~~DUF4118 (0.0000607328) ~~461,X,598~~HisKA (0.000000611921) ~~664,711~~HATPase_c (5.37033E-24) ~~812	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.2E-86	297.5	0.1	4.9E-86	296.9	0.1	1.3	1	M4WUS5_PSEDE	Histidine kinase (EC 2.7.13.3)	H681_10020	Pseudomonas denitrificans ATCC 13867	885	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas pertucinogena group, Pseudomonas denitrificans, Pseudomonas denitrificans ATCC 13867	1294143	>tr|M4WUS5|M4WUS5_PSEDE Histidine kinase OS=Pseudomonas denitrificans ATCC 13867 GN=H681_10020 PE=4 SV=1 MTDPNRADALLADLPGMGRGRLKVFLGAAPGVGKTYAMLLAAQGQLRQGVNLR VGIVETHGRAETEALLAGLPQQALKRSVYRGITLEEMDLDGLLADPPQLALVDELA HSNAPGSRHAKRWQDIQELLSAGIDVYTTVNVQHLESLNDQVRDITGVQVRETVP DWVLQEAYDLLLVDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELTM QTAAARVDADLAHRYRQQGGEAPAVRGRMLVGVDGEHNAERLVRHACRVAERR HLPWSLVHVDTGDARSEESRMQLQNAQQLAERLGGDVVELRGGEVARTLVEHA KERRATLLLVGRSRQRWHRRLFGGGLAARLLRLGDGLEVSVLDSEADLAPPKAR PQSPWPWGSYLLAALAAAGASALAWAVASVLELPNISLVFLAAVLLVAVRSSLGP ALACAVLSFLAYDFLFIPPHFSFSIQREEDVLTLLFFLLMAGLTGNLAARQRRQLQA LRETQEETSQMLELSRKLTAATDRKAVMAAAAQQLGGWEGLDICLLGQAHGEWK VEGGLSRPLDDQERAAADWAWQHDQPAGLGTGTLPGGRWWWWPLSGEEGPL ALLGVSPRDRQPLPGSRRRLLAALGQPLGQALARARLAEDLEAARLHGETEQLRS ALLASVSHDLRTPLTSMRGAIDSLLALGDAIPPDDRRRELLESTRDEAERLDRYIQNL LDMTRLGHGGLKLSRDWVSPGDIVGSALNRLRAVVAPYRVETRVPPELPLLYVHA ALIEQALVNVLENAARFSPPQGRLRVAVEANEEELRFSVSDEGPGIPPAEREKIFD MFYTAARGDRGGQGTGLGLAICQGMVGAHGGRITVEDGIDGRGTTLVLHLPLQQ QPDLEQLDAAV	17~~KdpD (1.78584E-117) ~~227,248~~Usp (1.22304E-31) ~~365,415~~DUF4118 (3.01385E-15) ~~489,X,648~~HisKA (2.92303E-14) ~~714,767~~HATPase_c (3.04539E-28) ~~870	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.4E-86	297.4	0.3	6.5E-86	296.5	0.2	1.5	1	A0A098G9H5_9GAMM	Histidine kinase (EC 2.7.13.3)	LFA_2760	Legionella fallonii LLAP-10	891	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella fallonii, Legionella fallonii LLAP-10	1212491	>tr|A0A098G9H5|A0A098G9H5_9GAMM Histidine kinase OS=Legionella fallonii LLAP-10 GN=LFA_2760 PE=4 SV=1 MGESRPDPEKILRKVHDEERRERQGKLKIYLGAAPGVGKTYEMLRDAFAERNKGL DVVIGVVESHGREEIKHMMMDFEVLPRQVIYYHENKLEDFDIDAALKRNPGLILIDE MAHTNAPGQRHSKRWQDIKELLDRGVNVYTTLNVQHIESLNDDVAQIIQAPIKETV PDFMIDRADTIELVDIPPEDLLKRLHEGKVYFAQQAEIAAENFFRIGNLIALRALALR VTAERVGAEVISYRHDKHITKIWPTKEKILVCVGPGNESLKLIRAARRMATNLHAT WMAVYVDIPRLRSSEEIKNKAIQNLRFAQQLGAETRFLSGTDIVKEIMNFAHEQNV TQIMVWKTIRTRPRDLFFRHLADEIVRYSGEIDVFIMTGTREQTKLAKEFRTEPEVF WSTYVSAISIVAVATLINSLLSPYVPMLNLIMVYLLSIIIVSLYGQQGPSLVASLLSVL AFDFFFVSPTYSFAVSDLAYIFTFVIMFFMAQVVSSLTIMIQRQAEAARFSEQQASA LYKLTRDLASTRGTDKLLETGLHFISQQFANKVVIFFAENGHLVFRDKAHNYEPPSL KEQSIAQWVYDLGQPAGLGTNTLSSAEALYLPLTGAENSIGVLRLGPIKQKRLLTP EQMHLLEACTSHLALAIEAERTHEQKGKSALSRDKNFMDNALLRSIAHQLRAPLAA IMVAANNQIELANKLSTNKIRSLGKDIYFESEQLSRLINNFLQITYLESRAARVNKQL NSLNDTLNTVLELSRLKLGGRTININIPDDFPVLYYDNALIQDVLINLIDNVVQLTPKD YPLDITAVQKDALVEISVEDNGAGIMPDEMHKVFEKFYRGRMITSERGLGLGLTIC HRIIKAHGGTIWAENRKQGGAAFRFTLPLKINHDLPEV	22~~KdpD (1.59127E-102) ~~232,254~~Usp (3.8197E-34) ~~376,399~~DUF4118 (1.894E-16) ~~498,525~~GAF (0.000000000000207981) ~~642,664~~HisKA (0.0000872407) ~~725,779~~HATPase_c (3.25887E-26) ~~880	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.5E-86	297.4	0.4	7.1E-86	296.4	0.1	1.7	1	A0A088QFP9_9CORY	Histidine kinase (EC 2.7.13.3)	DR71_936	Corynebacterium sp. ATCC 6931	867	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium sp. ATCC 6931	1487956	>tr|A0A088QFP9|A0A088QFP9_9CORY Histidine kinase OS=Corynebacterium sp. ATCC 6931 GN=DR71_936 PE=4 SV=1 MAKRGKLKVYLGFAPGVGKTCAMLSEGHDLYSRGHEVVIGLVEHHGRERTKKLIE GLPVLDCRKVSYRGNTYRELDVDAIIEMRPEVALVDELAHTVVTDEPDNEFVQQR KRWHDVYQLLDAGIDVISTMNIQHLESLNDVVAAVTGVRQMETVPDRVLRDADEI ELIDLSPDALRIRLSRGEIYRKEQAELALRKYFRPGNLSALRELALLWLADKVEEVL DAYREDEEIDDHWTTRERVVVAVRDDENAESMIRRGARMTGRVAGREMIVVHIT GEDDGLDRGYLRRLRKLQDLTESLGGQWRTIVGDDVPGILLEFSRTVNASQLVIG SERGLRRYVGLSTSQRIIDQAGPIDVHIISSSSEKKAKRRKKLRSRFSKERRITGWL LALVGPVLLTLLLYQLDTGPEFLGVLLLTYLMPIVFAAMAAGLVPALAAVVVSSILAN WYFTAPVNTLTITEPASLAQILLFGVIAAAVATVVERSERRREMADRSLHQAVVMS ELAHGVVHDGDNMSNLVHSLADTFSMERVDVQRYSSERKKWLTIVTTAEHGLSE PWPTELPMTKVSSGDDLRFVLSGRELTAAETAMIAAHGSRIRALMDMEEIAAMRR ATAALEAGNRVGSAVLTAVSHDLRTPLASIKAAISSMNMEDVELDDETRLILMETIE SSADRLEVVIGNLLDASRIDSSTKRVESVPVSVSDVVDAVCAELPEAAGHIDRDIDH DACMVEGDPGLIQRIVSNIVINGRQYAPESSLTIRTRPSERGVRGPADMPVMGSL GAIAASACIDILIIDHGKGIPEDKLEEIFQPFQRLGDYSAQSQGLGLGLAAASRFADA MGGAIRAEQTPGGGATFVLTLPRAMGERK	2~~KdpD (5.41434E-100) ~~218,240~~Usp (2.40254E-23) ~~361,418~~DUF4118 (0.0000103198) ~~470,X,627~~HisKA (0.0000000682077) ~~686,737~~HATPase_c (9.19647E-20) ~~859	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.6E-86	297.3	0.3	4.8E-86	296.9	0.2	1.2	1	E8V6Y1_TERSS	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	AciPR4_4262	Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	382	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus saanensis, Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	401053	>tr|E8V6Y1|E8V6Y1_TERSS Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4) GN=AciPR4_4262 PE=4 SV=1 MSDEKRKSAEDWLLATETEKKRGRFKIFLGYAPGVGKTFSMLSEGNRRRSRGED VVVGIVETHGRSGTAEQAVKLEQVPRREIDYKGTLFDEMDVDAILARAPHVVLVDE LAHTNVVGSRFAKRYEDVLLLLENNIDVLSTVNIQHVESLTPRVQALTGITVRETVP DWVLDRADEIIINDVTPEALATRMRRGDIYPMERVERALSNFFRRGNLIALREMAL QRVTRAVDRTLNDYVKRKRLGAQWSVIERVAVCISANPEARDLIARGARLAEGLN GELYVLHLTNERDNEPERRKTLDAHLQFAMNLGANIVHLTGKSVASATAAYVTEH RITQAIFGRSALHGLKKYLYYLAIQKFMSEAPHVDLHIITQDTQAGARK	20~~KdpD (5.98867E-108) ~~230,252~~Usp (6.80042E-27) ~~373	non-kinase	KdpD;Usp
	3.6E-86	297.3	0	6.9E-86	296.4	0	1.5	1	H8GH08_METAL	Histidine kinase (EC 2.7.13.3)	Metal_3636	Methylomicrobium album BG8	903	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomicrobium, Methylomicrobium album (Methylobacter albus), Methylomicrobium album BG8	686340	>tr|H8GH08|H8GH08_METAL Histidine kinase OS=Methylomicrobium album BG8 GN=Metal_3636 PE=4 SV=1 MRELDPEFFSAHANRTEIRKRRGRLKIFFGAVAGVGKTFTMLEVARAHQAEGCEV VAGLVETRGRADTAAQLQGLELLPPQIRYHQGTRRAEFDLDAALARHPDLILVDDL AHTNLPGSRHPKRWQDIRELLDGGIDVYTTLNVQHLESLHEDVGRFAGIRVWETV PDTVFEEADEVELVDLPPDDILARLHEGKIYPPEKAERALLNLFRKGNLIALRELALR RTAEWVSTQLREYRQAYAIREVWNVDERILVCVAPDARAKRLVRAAKRLAASLHA DWLALYVETPALQRLSARRRDGVLKALRLAERLGAETVTLSAPDMAEAILTFAHEH NVNKLVLGKPGRKGWRRWFLGSVVDSLISQAHDLNFYLLGDEETPRLQSSAPSP SKSFDRQLVEHKYGHWLWSLAIPLLLTAIEWPFRDLLTPANILMFYLLGVFFVAIRF GFWPSILASLANAAAFAYFFAPPIFSFAIAEPENLAGLAVTLVIGAVTGNLAENVRH QARVAESRERRASALHRLSKGLAEARSEREITEIGVYHIHAQFGGRNTFLFPDRNG RLHYPNEPPLAISLRGADLDVARWVFEHGQLAGRGTDTLPDAPAVYLPLNGSTGT IGVLALEPVELRRIFLPEPYQLLNTFVNQIVHTLERANMAEHAKEATLKMQAEALRN SLLSSISHDLRTPLATIVGAASTLETDAARLEESSKRKLVSAISEEARRMSDLTSKIL EMARLEAGEVRLNRQWYAPEEIVGSALRRLDKKLKARRINVRMADGPALIHVDAV LLQQVLVNLLDNADKYSPPELPIDITIESAPSGVSIAVADRGPGIPEGLEQKIFDKFF RVHAESAQSGVGLGLSICRAVVEAHGGTIRASQRSGGGTVVQLHLPMLERPPTID LEEKTL	20~~KdpD (5.17967E-107) ~~230,252~~Usp (7.11079E-42) ~~375,404~~DUF4118 (0.00000000000244501) ~~504,530~~GAF (0.0000000000366227) ~~650,667~~HisKA (0.0000000000116804) ~~733,795~~HATPase_c (2.58078E-23) ~~887	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5.6E-86	296.7	0.1	8.4E-86	296.1	0.1	1.3	1	A0A0A7FZ16_9CLOT	Osmosensitive K+ channel His kinase sensor domain protein	U729_174	Clostridium baratii str. Sullivan	376	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium baratii, Clostridium baratii str. Sullivan	1415775	>tr|A0A0A7FZ16|A0A0A7FZ16_9CLOT Osmosensitive K+ channel His kinase sensor domain protein OS=Clostridium baratii str. Sullivan GN=U729_174 PE=4 SV=1 MNKTRISPDTALKICATEEKGKLKIFLGYAPGVGKTYTMLNEANRRYNRGEDVVIG YFESHGRLDTINQIKSLPELPLKEIHYNSITFKELNVPLIIDRRPKLVLVDELAHTNAP GSKNKKRYEDVIEILNSGINVYATVNIQHLESLNDVITQITGVTINETIPDSIIATAEVV VIDIPPDSLRKRLKRGNVYKNDLIQRALKNFFRIGNLNALRELTLRQIADEVDCTLNE YKENHNIYDNWHTAEKVMVSISSNPKSKRLIRFGARIAKKYKCPLYVVYVDCTHSIY PKDTPEILKSLNENIDLAKKFDAIVINLKGKSISNELIKFSKEKNITKLIIGHSKRTKLQK FFRGSTVNKLLEGSKNIEIIVVPYD	18~~KdpD (1.63698E-111) ~~227,249~~Usp (3.60018E-35) ~~374	non-kinase	KdpD;Usp

	5.8E-86	296.6	0.2	7.9E-86	296.2	0.1	1.2	1	I3ZHZ0_TERRK	Osmosensitive K+ channel His kinase sensor	Terro_2254 Terro_2618	Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63)	377	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus roseus, Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63)	926566	>tr|I3ZHZ0|I3ZHZ0_TERRK Osmosensitive K+ channel His kinase sensor OS=Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63) GN=Terro_2254 PE=4 SV=1 MVEAERKTPEDWLASSDQEKKTGRLKIFLGYAPGVGKTFSMLSEGIRRRSRGED VVVGVVETHGRRGTAELSTKLEEVPPRELNYRGTVFREMDVDAILARAPQVVLVD ELAHTNVEGSRFAKRFEDVLLLLENNIDVLSTINIQHIESLTPRVQSLTGISVREQVP DWVLDRADEIVIADLTPEALATRMRRGDVYPMERVERALANFFRKGNLIALREMAL QKVTRAVDRNLDAYVRRKRLGAHWTVTERVAVCISSNPQSRDLIARGARLAEGLG GELYVLHVASDRDTEGQRKLTLDSHIQFAQNLGANIVQLAGSSVATATAAYVKEQ RITQAIFGRSALRGFRKYLYYLAIGKFMSEAPHVDLHIITQDPE	20~~KdpD (4.75761E-102) ~~230,252~~Usp (3.93584E-28) ~~373	non-kinase	KdpD;Usp
	6.7E-86	296.4	0	1.2E-85	295.6	0	1.4	1	X4ZL98_9BACL	Histidine kinase (EC 2.7.13.3)	PSAB_12660	Paenibacillus sabinae T27	885	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	1268072	>tr|X4ZL98|X4ZL98_9BACL Histidine kinase OS=Paenibacillus sabinae T27 GN=PSAB_12660 PE=4 SV=1 MEGIPAEKKRGKLNIFIGYAPGVGKTYAMLSAGKEEQKDGIDVVAGFIESHDRPDT MALLEGLELMPPLTISGAGAAIEEFDLDLALQRKPDLILLDDLGHTNAAGCRHKKRY RDVEELLRAGIHVYTTINIQQIESLTDIVASITGISVHERIPDSVFDSADQVKLVDIEP DDLIDRLHKGKIYRNDEAEEAQAQLFTREKLTALREIALRSTASQLNRIAIQISEQAK RDEYNTKDHILVCLSSAASNKKVIRTAARMAEAFHGRFTALFVETPETMALASKNK EELRGNLRLAEQLGAQIATVYGEDIPGQIAEYVKTSGVSKIVLGRSENKKRGLAKS NVVDKLTALVPNIETYIIPYSQPPSPRKFHLNAKPLHLSASDIAKTTAIIAGCTIIGLCF QYFGLKEANIVTVYILGVLLNAMITRGRLYSVFSSVLSVLVFNFCFTEPYFSLRVYD SGYPVTFLVMLAASFLTSTLTMRVRDQASQSAQKAYRTEVLLETSRKLQQAQDFP AIIDETARQMVKLLNRTVIFYSVQQKGLSAPIIFPKKDSGSTPAVYMDENEQAVAD WVYKNNKRAGATTDTFFGAHCLYHAVRGGETVFAVAAIVMDQEEPLDVFEKSLV FAMLGECGLALEKEKLNGQQQEIFMQIRQEQLRANLLRAISHDLRTPLTSISGNAGI LIGNSNVLSEEQKKGLYTDIYDDSMWLINLVENLLSISRIENGSINLNLQAELIEEVIS EALQHVNRNSVKHSIQSIVDDDLLMARVDSRLIVQVLINLVDNAIKYTQEGSCITLSA IRDGQMVLIEVSDDGPGISDESKTRLFEMFYTGDNIRGDGRRGLGLGLALCKSIVN AHGGTIGVRDHFPRGTVFYFTLQAAEVSVYE	8~~KdpD (5.72652E-106) ~~218,239~~Usp (9.46295E-35) ~~361,385~~DUF4118 (5.18793E-15) ~~486,X,654~~HisKA (0.000000000617172) ~~720,773~~HATPase_c (3.74462E-22) ~~876	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	7.6E-86	296.3	0	1.2E-85	295.6	0	1.3	1	A0A0D4DGQ0_9ACTN	Histidine kinase (EC 2.7.13.3)	T261_1310	Streptomyces lydicus A02	892	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	1403539	>tr|A0A0D4DGQ0|A0A0D4DGQ0_9ACTN Histidine kinase OS=Streptomyces lydicus A02 GN=T261_1310 PE=4 SV=1 MEEYMRARGTGTTDAPGPRPGRLKVFLGAAPGVGKTYRMLDEGRRRAARGRNV VVAFAECHGRPATEAMLEGLAVLPRVTRRHRGCDFTELDLDRVLELRPEVALIDEL AHTNAGGGRNAKRWQDIEELLGAGIDVVATLNIQHLESLSDVVEKITGVPQYETVP DEVVRRADQIELVDLPAEGLRRRMAHGNIFPPEKVDAALAHYFRIGNLTALRELALL WVAGRVDEALRKYRYEHGIGRVWATRERVVVALTGGPEGATLIRRAARIVDLPRA LRSSPTLGPARAAGPPCAEGRPFSGGTPLSGGDLLAVHITRSDGLSGASPAALAE QRQLTESLGGSYHSVVGDDVPAALLDFARAQNATQLVIGASRRGRLRRVLMPRG VGETVVELSGDIDVHTVTHEHAGRGRRWPAAGSVLPRSRRVAGPVAGLVLPVLL TLALRGVSGPLALNLTSEALLFLLTVLGVACIGGVVSALLASVTTSLLLNYYFIPPIGH FTFAEANIVVAQAAFTTVAVTVAAIVDRSLRLSRRAARATAAAETLTSLAGGILRGD RAVPVLLERTRETFGMDGIALRPRGAGPHDHDDEDDHAPDSDHDHETKVAIGDD SVLVLTGRRLPASEHRVLTAFAAHLTAAVERARLAEAAAEVEPVKAANRMRTALLA AVGHDLRTPLAGSWAAVSSLRSRDVDFSPEDREELLATAEESLAKLSRLVDNLLD MSRLQAGALTLRLEPVALTEVLPPALDTLPDSPPQALVHVVTQGLETAPDVLADPP LLERVIANLVSNAVRHSPAGRPVTIGASALAGRVELRIIDRGPGIQLTDWERAFVPF QRLGDTDNTTGLGLGLALSRGLTEAMGGTLTPEDTPGGGLTMVVSLPAAPVPVA GRLS	18~~KdpD (5.20211E-101) ~~228,250~~Usp (1.71847E-25) ~~404,434~~DUF4118 (0.000019932) ~~526,X,658~~HisKA (0.000000000188029) ~~724,779~~HATPase_c (1.87075E-24) ~~880	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	7.8E-86	296.2	0.7	1.2E-85	295.6	0.5	1.3	1	F2NIP5_DESAR	Osmosensitive K channel His kinase sensor	Desac_2706	Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	383	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfobacca, Desulfobacca acetoxidans, Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	880072	>tr|F2NIP5|F2NIP5_DESAR Osmosensitive K channel His kinase sensor OS=Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2) GN=Desac_2706 PE=4 SV=1 MNPTTNRAQDFLDLLERAKRGRLKIYLGFAAGVGKTVRMLKEAHALKLRGVDVVL AYIEPHGRAETAELIGDLEVIPRKQFVYRGITVEEMDLDAVLARRPEIAIVDEVAHTN VPLCRHRKRYQDILEITEAGINVICAFNIQHLESLNDLIERVTGVVVRETIPDTFVKEA DQVVTVDLSVDDLMERLKSGKIYTRDKIPWALEHFFRIANLSTLRELALLEVAESLG RRQPSGPEELKLQDRVSLRTLGRVMVCMASASPRAKTLLRKGSRMAGRLNTHW FVVYVETPGEAPTQIEAETQRHLLENFQKARELGAEVIRLQAKDPVPAILDFARSH GVGHIVIGRSQQPWWRKLLGRSVSHRIIDEAAGFDVHVISFEEEE	18~~KdpD (1.7293E-113) ~~228,252~~Usp (1.85572E-40) ~~378	non-kinase	KdpD;Usp

	8.4E-86	296.1	1.2	4.3E-85	293.8	0.1	2.1	1	A0A089M9Z7_9BACL	Histidine kinase (EC 2.7.13.3)	PGRAT_25575	Paenibacillus graminis	899	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus graminis	189425	>tr|A0A089M9Z7|A0A089M9Z7_9BACL Histidine kinase OS=Paenibacillus graminis GN=PGRAT_25575 PE=4 SV=1 MEINQTGDGSILEQLTGMKAGKRRGRLKIFIGYAPGVGKTCAMLNAAHEEQKEGT DVVGGYIETHARPDTQAMLEGLELVPPMKVSYEDSVIPEFDLDRAIQRSPELILLDD LAHANTAGCRHKKRYQDVEELLRAGIHVYTTINVQQIESLTDIVYSITGMTVQERIP DSVFDSADQVELVDIEPNDLIDRLNKGKIQRENADEQGIEQLFTKEKLTALREIALR NTASQLNRIAVQISEQAKKNDYDTKDHILVCLSSAASNKKVIRAAARMAEAFHGQF TALFVETPQTQKLTPKNKTELRDNLRLAEQMGANIATVYGEDVPGQIAEYVKTSRV SKIVLGRSPFKKRGYAKSNLVDKLTTLLPNIEIYIIPYTHPSFYKRLPLYVRYPKLSLA DTNKTIAILLVCTLIGIWFRYLGFLESNIITVYILGVLLSAIVTKGRVYSAVSSVMSVLV FNYFFTEPYYSLNAYDSGYPVTFLVMLTASFITSTLTMRVSEQARQSAQKAYRTEV LLETSRKLQQAKDSPAIIDEMAHQMVKLLDRTVIFYAVQEGALTEPLIFPKEGSEAD PHMYTGSNERAVADWVFKNNKRAGATTDTFFGANCLYHAVRGGDTVFAVAAIVM EQEEPLEVFEKGLMIAMLGECALALEKELNEKQKEISLQIQQEHLRANLLRSISHD LRTPLTSISGNAGILVGNSGVLSEEQKKGLYTDIYDDSIWLIHLVENLLSISRIENGTL NLNFQAELLEEVISEALLHVNRNSEKHVIQTELADELLMARMDSRLIVQVLINIVDNA IKYTQQGSHITVSAKQDGQRVIVEISDDGPGISEEAKARLFEMFYTVDNIRGDGRR GLGLGLSLCKSIVNAHGGTIGVMDNVPKGTVFYFTLHAEEVNIHE	22~~KdpD (1.2419E-104) ~~232,253~~Usp (4.11289E-34) ~~375,402~~DUF4118 (8.29466E-20) ~~500,X,668~~HisKA (0.00000000103348) ~~734,787~~HATPase_c (9.51555E-23) ~~890	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	8.5E-86	296.1	0.2	1.6E-85	295.2	0.1	1.5	1	S0LFX1_ENTAV	Sensor histidine kinase KdpD	OMU_00613	Enterococcus avium ATCC 14025	853	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus avium (Streptococcus avium), Enterococcus avium ATCC 14025	1140002	>tr|S0LFX1|S0LFX1_ENTAV Sensor histidine kinase KdpD OS=Enterococcus avium ATCC 14025 GN=OMU_00613 PE=4 SV=1 MEKKQMGDGRRGRLRVFFGFAAGVGKTYSMLSEAHELLLMGKDIIVGYIEPHDRP DTNRLLEGLPQIPPKKILYKQMLLTEPDIDQIIQQKPEIVLIDELAHTNAEGSRNRKR YQDVDELLNAGIDVFTTVNVQHIESLNDIVEEVTGVEVKETVPDTFLQQATIKVVDV EPEELIDRLEQGKIYASESAKRALQNFFIPQKLDQLRGLAIQRASDHINRISAKTIRIQ SKLLTVVNDAFPKMTEKSIRWTARLAQGLGAEWTVIQVRTQENTLTNIPLAEKLGA EVISIEEDNSFETIVEFAKMTGVTDIIMGKNLRQPWYEKIFIEAFDDRLLKRLNDTEL HLIPFKEEKQSLFLRTRKIIEGGGKDLVIALGGVFLATIVTELMQYIHIGDQNLMLIYIF FILLVARTTSGYFWSSLASILSVLSFNWFFVEPLYSLTVYKQGYPITLLIMCLVAILIS NLMVRLKKQAESSMEKEHQMELLYELNKQYVLADNRNQILDISATYLSRLLEREVIL FDSQAKVESIHCISGKPSILSTKDEAAVAFWTAKNQKEAGNGTDTLIGAKGFYLPII ASGKTLAVLGIERNAGLDLENNQLNYLKLVLTQLAVILEQTELKSEKERVEMENER EKVRSNLLRAVSHDLRTPLTVISGIAETLGNSSDLKENTRQKLLADIQDESQWLIRM VENLLSITRINMDTMKVNKTAEPIEEIIEAVYQHLKKVYPEGQVEISLPSEVTFIQAD PILIEQALFNIVENAFRHGEEKQPVKLTVYQKNDQTVFEIENDGEIPLKQFEKIQTNL SSTSEVPVDSKNGLGIGLSIVKTIIHAHNGKMEMMVGEGKTLVRIYLK	9~~KdpD (4.64306E-120) ~~218,231~~Usp (1.85692E-31) ~~347,370~~DUF4118 (0.00000000000171188) ~~471,499~~GAF (0.0000310285) ~~615,633~~HisKA (0.00000000000589629) ~~698,751~~HATPase_c (7.82971E-14) ~~852	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.7E-86	296.1	0.1	1.5E-85	295.3	0.1	1.4	1	R4LG40_9ACTN	Histidine kinase (EC 2.7.13.3)	L083_0730	Actinoplanes sp. N902-109	812	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	649831	>tr|R4LG40|R4LG40_9ACTN Histidine kinase OS=Actinoplanes sp. N902-109 GN=L083_0730 PE=4 SV=1 MARGELRIYLGAAPGVGKTYTMLAEAHRRAGRGTDVVVALVETHGRQHTEAMVG DLEVLPRRGGELDLDAVLARRPRLAVVDELAHTNGPGARHGKRWQDVQELLAAG IDVLTTVDVRHLESLNDVVTRITGVPQRETVPDAVVRSAGQVELVDMTPEALRRRL AHGNIFRPSQVDAALGSYFRAGNLTALRELALLWLADEVEAQLGRYRADHDIDAI WETRERVVVGLTGGPEGETLIRRAARIAARTRGTDVLAVHVARNDGLAGADPAGL ARQRVLVERLGGSYHQVVGADVAQALLDFARAVNATQIVLGASSRGRLARLLSAG VGAATTALSGTIDVHLVPHERVAPGRRARMPAALSRGRRLAGAAAAVAGLPGLTA LLKLSAGLSLTNDILFFLTATVGIALIGGLWPALLAAVGGFLLLNWFFTPPYGRFLIA EADNLLALAIFVVVALAVSWVVDTAARSTRRAAQAGAEAQTLAAVAGSVLRGERP LTALLERLRETFSLESVELRQGGATVAAVGTSELPAEQVRVDDDLVMVLRGRPLA ASDRRIAEAFAAQAAVALRQEQLSAEAATAKPLAEADRLRTALLAAVSHDLRTPLA AAKTAVASLRSADVEFGEQDRAELLETADESLDRLHRLVSNLLDMSRLQAGVLGV TLLPVGAEEVVPRALDDLGDAGRTVTAHIPDDLPALSADPGLLEQVLVNLLANALR YSPADRPPVVTASTLGDAVELRIVDHGPGIPKDRWDDVFLPFQRLGDRDNHTGV GLGLALARGLTEAMGGTLVPEETPGGGLTMVLALPHHTG	1~~KdpD (2.7459E-104) ~~203,225~~Usp (8.19514E-20) ~~347,394~~DUF4118 (0.0000000659303) ~~469,X,589~~HisKA (0.00000000000191203) ~~655,706~~HATPase_c (2.43292E-23) ~~807	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1E-85	295.8	0	1.3E-85	295.5	0	1	1	E7GKG0_CLOSY	Uncharacterized protein	HMPREF9474_01405	[Clostridium] symbiosum WAL-14163	231	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	742740	>tr|E7GKG0|E7GKG0_CLOSY Uncharacterized protein OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_01405 PE=4 SV=1 MEERRSSPEEFLRRCENENQAKGRGSLKIFFGYAAGVGKTYSMLKAAHAARRRGIDVVAGYVEPHARPQTSQLLNGLEMIPAKEIRHGNVVLHEFDLDGAIARKPQLILVDELAHTNGKGCRHQKRYQDINELLNNGIDVYTTVNVQHIESLNDLVASITGITVRERIPDSVFDNADQVELVDIEPRELIERLQEGKIYRKPQAEKALGNFFQSRISLRCVRSRSGAARTG	22~~KdpD (2.53521E-117) ~~213	non-kinase	KdpD
	1.1E-85	295.7	3.7	1.4E-85	295.4	2.6	1.1	1	F4C639_SPHS2	Osmosensitive K channel His kinase sensor	Sph21_4258	Sphingobacterium sp. (strain 21)	374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. (strain 21)	743722	>tr|F4C639|F4C639_SPHS2 Osmosensitive K channel His kinase sensor OS=Sphingobacterium sp. (strain 21) GN=Sph21_4258 PE=4 SV=1 MEEENQQAAHFLDLIKKSRQGKFKVYIGMSAGVGKTYRMLQEAHMLLRNGIDVKIAYVETHNRTETQALLAGLPIIQRRKLFYRGKELEELDVQGVLNLRPEVVIIDELAHTNIEGSKNEKRWQDVLEIIESGINVISAVNIQHIESLNDDIRKITGIEVKERIPDKIITLADEVVNIDLTADELIDRLKEGKIYTADKIETALQNFFRNDHILQLRELALKEVAGHVERKVDAVVPPLEALRSERFLACISSNEQKAKTVIRKTARLASYYNGQWYVLYVQTPKEATVKIPLDKQRYLINNLKLATELGGTVLQIQHKNVPLAISELAIKYKVTTVCIGKPRLNLFRIILATGIFNQLLRKLSDNDIDLIILS	18~~KdpD (3.16297E-113) ~~228,246~~Usp (2.53333E-29) ~~374	non-kinase	KdpD;Usp

	1.8E-85	295.1	1.4	2.4E-85	294.6	1	1.2	1	H1YB16_9SPHI	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Mucpa_5990	Mucilaginibacter paludis DSM 18603	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Mucilaginibacter, Mucilaginibacter paludis, Mucilaginibacter paludis DSM 18603	714943	>tr|H1YB16|H1YB16_9SPHI Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Mucilaginibacter paludis DSM 18603 GN=Mucpa_5990 PE=4 SV=1 MEKEESVQHFLELIKKSRRGKFKIYIGMSAGVGKTYRMLLEAQALLRNGIDVKIGYI ETHNRKETLAQLEGLPLIPRRHLFYKGKDLEEMDLQAIINLRPEVVIVDELAHTNIEG SKNDKRWQDVVDILNAGINVISAVNIQHIESLNEDIEKITGTAIRERIPDSVLQLADEV VNIDLTADELIDRLKEGKIYDEKKVPLALGNFFQTERILQLRELALKEVAHLLERKIDI EIPKTIKLRPELLLACISTNEASAKIIIRKTARLASYYRSKWFVMYVQTDTESSDKIRL SSQRYLINNFKLATELGAEVIKVKSNNVAKAIWETAEKYEITTICIGKPHFKFYQLVIK TAVFTQLLNKLSKSDVDLVILS	17~~KdpD (8.65563E-115) ~~224,246~~Usp (6.70394E-28) ~~373	non-kinase	KdpD;Usp

	1.8E-85	295	2.9	2.3E-85	294.7	2	1.1	1	A0A0C3NCU2_9PORP	Histidine kinase	BA92_10910	Sanguibacteroides justesenii	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Sanguibacteroides, Sanguibacteroides justesenii	1547597	>tr|A0A0C3NCU2|A0A0C3NCU2_9PORP Histidine kinase OS=Sanguibacteroides justesenii GN=BA92_10910 PE=4 SV=1 MDKEQNVQHFLNLIRKSRRGHFKVYIGMIAGVGKTYRMLQEAHELLRNRIDVQIGY IETHGRVDTEVLLKGLPVIPRRKIYYKGKEIEEMDLQSILQIRPEAVIVDELAHTNAE GSVNEKRWQDVFDLLDAGINVISAINIQHIESLNEEIQDIAGIEVKERVPDRVFEEAD EVVNIDLTAEELVARLKAGKIYKPEKIDIALNHFFKVENILQLRELALKEVALRVEKKV ENEVVENVGLRHERFMACISSHEKTPRKLIRKVARLATRYNSRFSVLYVQTRRESP DRIPLANQRYLINHFKLASELGGEVIQIQSDDIIGSIIRVCRERQISTLCVGKPDIRLFS FVRTALRYKKLLNNLAALNVDLIVLA	17~~KdpD (9.7547E-115) ~~227,245~~Usp (3.20966E-25) ~~341	non-kinase	KdpD;Usp

	2E-85	294.9	0.2	3.3E-85	294.2	0.2	1.4	1	C4KYL1_EXISA	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	EAT1b_1247	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	359	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	360911	>tr|C4KYL1|C4KYL1_EXISA Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b) GN=EAT1b_1247 PE=4 SV=1 MRGKLRLYIGAAPGVGKTYKMLADARAHQQEGVSVMIGLIETHGRKETEAMIGDL PIVPLLSIPYKGHELQELDVETILSLHPDIVLVDELAHTNAPGSVRTKRYQDVQVLLE NGIDVYAAVNIQHFESLLLTVKGITGVEVRERIPDLFLNRADEILLVDVTPQTLQERM RQGKIYRPDKIEQSLSSFFTLTNLSSLREIALRQVADEVDDQVYRTRKNVVSDPTLL QERIMVCIQLNDNARHLIYRGFRMASRLKAKLYILSVLHGEERKLTPEQTAILKEVR EQGASFQAEVIVLNVPRKELTKNLTTTAREKRITQLILGQSARTRWQEVMRGSIVN VIMRELKQVDIHIVSDQS	2~~KdpD (2.82524E-109) ~~210,231~~Usp (2.02404E-30) ~~356	non-kinase	KdpD;Usp
	2.1E-85	294.8	0	3.3E-85	294.2	0	1.3	1	I4MR07_9BURK	Histidine kinase (EC 2.7.13.3)	Q5W_1528	Hydrogenophaga sp. PBC	907	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Hydrogenophaga, Hydrogenophaga sp. PBC	795665	>tr|I4MR07|I4MR07_9BURK Histidine kinase OS=Hydrogenophaga sp. PBC GN=Q5W_1528 PE=4 SV=1 MNDTPQRPDPDILLAQVQADEDRARRGRLKIFFGASAGVGKTYAMLSAARAAQA EGTAVTIGVVETHGRPETQALTQGLPRLPLRSVPHKGHALHEFDLDAALAFGAAH PGALVLLDELAHSNAPGSRHPKRWQDAEELLATGVDVWTTMNVQHLESLNDVVS GITGVRVWETVPDRLFDEADEVVVVDLPPDELLERLHSGKVYLPTREGDDQRAER AAANFFRKGNLLALRELALRRTADRVDDEVRAFRQAGAVRPVWPNRESLLACVG PGASADKVVRSAARMAAQLDVPWHAVHVQALSHEPDAATQKALDLAESLGASVS SFSDRDPAAALVRHAREHNLTRLVLGRSRRAWPWARPMAERIAAQAGELELLHV AEPHGQRERSEPAHAPGEVPRGPRWPGYVAATVACGLTALLATPLIPVLELSNIV MIFLLVVVGIALRFGRGPAVLAAFLGVALFDFFFVPPRFTLAVSDVEYLVTFAVMLV VALAIGQLTAVLRQQADAATRRERRVRALHDMSRDLSAALLPEQVADIGARFVQA EFGMRSTLLAADEHDRLQALPGGQAPVDMAVTQWAFERGEPAGRGTDTLPASA TLVVPLKAPMRTRGALVIDPGATVAPGTGQRQALDTEQRRALQACASLLAISLERI HYIEVAQHSTVQIESERLRNSLLAAISHDLRTPLASLVGLGDALRLTPPPLAPAQAE LAEAIAQSARRMAALVTNLLDMARLQAGAVPLQRAWQPLEEVVGSALAACGDAL HGRAIDVHLPADLPLLQFDAVLMERVLVNLLENAAKYTPAGSAIRLWAAADAESVR LCVDDHGPGLPRGQEARIFEKFERGARESATPGVGLGLAIGRAIVEAHGGRIEGR NRERDGRVEGARIEITLPRGTPPADNSTQ	24~~KdpD (7.2088E-102) ~~244,267~~Usp (5.32913E-27) ~~381,408~~DUF4118 (6.57787E-24) ~~507,534~~GAF (0.000000000000752615) ~~655,672~~HisKA (0.000000000000653236) ~~737,790~~HATPase_c (7.85769E-26) ~~895	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	2.7E-85	294.5	1.4	3.9E-85	293.9	0.5	1.6	1	C1ABQ9_GEMAT	Sensor protein	GAU_2894	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	381	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	379066	>tr|C1ABQ9|C1ABQ9_GEMAT Sensor protein OS=Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505) GN=GAU_2894 PE=4 SV=1 MASPTPIDPRDQALLSLLPRNGRGHFKVYLGSAAGVGKTVRMLQEAHDLRQRGV DVVVGFIETHGRAETAALVRDLDIVPRTSMTYRDVTLEEMDLCAVLARAPQVALVD ELAHNNVPGSVHRKRWEDVLDLLEAGISVVSAMNVQHVESIAPIVQQALGVVVRE TVPDWVLGRADQVVNIDIPADELRRRLIDGKIYALDKVPTALDHFFTAENLTTLREL ALREAASSVDRERMELVRRETGRSATVHASADRLMVAMASHPPRTAALLHKARRI AGRLNSDWYCVYVQTPSERADRIDTSIQRALVSNIQLAQRMGAEVVKLEGDDVAA AIIQFAQREGVSLVLVGRSERSWWHRIRHGSVVDRLLSRDLGLDVLIVS	22-~-KdpD (3.75106E-108) ~~231,255~~Usp (2.89543E-32) ~~381	non-kinase	KdpD;Usp
	3.2E-85	294.2	0.1	5.5E-85	293.4	0.1	1.4	1	F8DYL4_CORRG	Histidine kinase (EC 2.7.13.3)	kdpD_CRES_1323	Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	972	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium resistens, Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	662755	>tr|F8DYL4|F8DYL4_CORRG Histidine kinase OS=Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026) GN=kdpD PE=4 SV=1 MATMTKRGTLKVYLGFAPGVGKTCAMLSEAHDLVDRGYDVLVGIVEDHGRARTK KLTEGLPILPRKSVAHRGGSYDELDLEAALEAHPQIILVDELAHTVVGTQETDGDR PVEGAKRWHDVYALLDAGIDVISTMNIQHLESLNDVVSAVTGTRQRETVPDQVLR DADEIELVDLSPDALRIRLARGEVYRQQQAETALNSYFRVGNLTALRELSLLWLAD KVDEVLEKYREDEKIQENWPARERVVVAVQGDEVSEALIRRGARITERVAGREML VVYVFSADAALEGDLPQRLQRLQELTESLDGQWRVLEGDDVANTLLEFARTVNA SQLVIGLGTRMSRLFSSTAHKIIDGSGRIDVHIVSTTNASLSAKGSKDSEQGGAGS GSRVQRSGFSNIPALLRRAVAYALGGSRRRASALDTSKQLSPGRKLAGWALALLG PIALTMLMMPLDHEEGALGSILLGYLTIAVFSALAGGFGPAIVAVLFGSILANWFFT HPYRTLTVTEPTNLVQILLFFVISVAMAAVVDIAERRRAVSNRRLGQAVVLSDLARG ALDEGDDIRSLLERLRETFNLRRVDLQQYSKERKKWVTMETTDPGGIGVPWPGK KAPAHVGAGDGMRFVLGGRDLSPAESAMIEAHGARITAIIDREQIDAMRRATAALE AGNRVGTALLTAVSHDLRTPLAGIKAAISGLTMDDVELDDDSRALLMETIESSTDRL ETVIGNLLDMGRVNSNTVTVRNMPVQYADVIDAVCAELPEAAQHIDNLVEETTQPV IGDAGLVQRIVANIVINARIYAPHSRIEIRAQVMPDSKAIQLRVIDHGPGFPPEKFND VFVPFQRLGDHSANTNGLGLGLAVARGFAEAMGGTLEAENTPGGGATLVLTLPA ADTEPMAAHSAPHALGSAESRPADSAPEPHPDTSAPAPHPQGTSAPEPHPQGTS APEPHPDTSTHNPQDTHANTPPAHEETR	6-~-KdpD (3.00783E-101) ~~223,245~~Usp (7.37738E-22) ~~365,435~~DUF4118 (0.00000000000651075) ~~535,X,672~~HisKA (0.000000000311886) ~~734,786~~HATPase_c (1.52912E-24) ~~888	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.6E-85	294.1	0.1	7.4E-85	293	0.1	1.6	1	Q838F4_ENTFA	Sensor histidine kinase KdpD	kdpD EF_0570	Enterococcus faecalis (strain ATCC 700802 / V583)	850	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus faecalis (Streptococcus faecalis), Enterococcus faecalis (strain ATCC 700802 / V583)	226185	>tr|Q838F4|Q838F4_ENTFA Sensor histidine kinase KdpD OS=Enterococcus faecalis (strain ATCC 700802 / V583) GN=kdpD PE=4 SV=1 MQSGDGRRGRLRIFFGFAAGVGKTYGMLTEAHELLMMGKHVVVGYIEPHDRPDT NRLLEGLPQIPPKNIFYKQMVLTEPDIDQIIQQKPEIVLIDELAHSNAEGSRNRKRYQ DIDELLNAGIDVFTTVNVQHIESLNDIVEEVTGIEVKETVPDTFLRQATIRVIDVEPDE LIERLEQGKIYANENAKRALKNFFIPQKLDQLRGLAIQRASDHINRISGKTIGIQSKLL TVVNDAFPKMTEKCIRWTARLAQGLVVDWTVIQVRTQENTPTNIPLADKLGAEVIS IEEDDSFETIVEFAKMTGVTDIIMGKNLRQPWYEKIFIEAFDDRLLKRLKDTELHLIP FNEEKRSLFFKTRKVIEGGGKDLVIAIGGVFLATVVTELMQYIHVGDQNLMLIYISFV LLVARTTSGYFWSSLSSILSVLSFNWFFVEPLYSLTVYKQGYPFTLLLMLVVALMS SNLMIRLKKQADTSMKKEHQMEILYELNKRYVLVESRKQILDISATYLSRLLEREVII FDRQVKTESVHCINEKKSILNNEDEAAVAFWAAKNQKEAGNGTDTLNGAKGFYLP IAAGRKTLAVLGIERNADLDLENDQLNYLKLVLTQIAVILEQTELKDEKEQVELENER EKVRSNLLRAVSHDLRTPLTVISGIAETLGIGNDLKEETQRKLLKDIQEESQWLIRM VENLLSITRINMDTMKVNKTAEPVEEVIEAVYKHLRKVYPDGQVDIHLPEEVIFIQAD PILIEQALFNLIENAFRHGENDLPVKLNVYQEKEQTVFEIENHGEIPLKQFQKIQSNL SGTNEVPVDSKNGLGIGLSIVKTIVHAHNGKMEMTIGRGKTLVRIYLK	6~~KdpD (1.70682E-121) ~~215,228~~Usp (6.15568E-31) ~~344,X,497~~GAF (0.00000363306) ~~612,630~~HisKA (0.000000000000197056) ~~695,748~~HATPase_c (0.00000000000048093) ~~849	kinase	KdpD;Usp;X;GAF;HisKA;HATPase_c
	3.9E-85	294	0.4	7E-85	293.1	0.3	1.4	1	R2QA65_9ENTE	Histidine kinase (EC 2.7.13.3)	UAW_02560	Enterococcus haemoperoxidus ATCC BAA-382	890	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus haemoperoxidus, Enterococcus haemoperoxidus ATCC BAA-382	1158608	>tr|R2QA65|R2QA65_9ENTE Histidine kinase OS=Enterococcus haemoperoxidus ATCC BAA-382 GN=UAW_02560 PE=4 SV=1 MERQVEEERLDPEQLLAKWKKNEQSLRSGRLKVFFGYAAGVGKTYAMLKEAHE QQAEGKNVLIGYVEPHARPETQTLVNGLPTLSTKTYEYKGIQINEFDVDAALKEKP DIILVDELAHTNAIGARNRKRYQDIEELLKAGIDVYTTVNVQHIESLNDVVEQVTGIHI SETVPDTFFETSSLKVVDIETDELLDRLKQGKIYHSENARKAMANFFTSDNLTLLRG LAIRKASDHINTTNQQETQKSTGIHSKLLTIIDEKNPDMTKKCLRWTARLAQALGAE WIALEILEDTSEHTESENSKLATKLGGEVVTLESDNQRETIIQYVKMRGVTDLVMG KIIKRSRFLRLYRPDLEDELVAFIPDVDIHLVPYQSSKYLLNKYATKKKNLKSIFTWQ DFYMTCGLLTVATILSEFGSYFHIGDQNLILIYILFVLLVARLTTGYLWAALASIASVL MFNWFFVEPLYSLTVYKQGYPVTLIFMLLVALLVSNLMMQIKKQAFYAMKREHQL EILYELNKKYLVTHDQKEILATTAEYLSNMLDREVVLYGEEELKNPTGAPIKGPLRS LEELAVANWVFVNQKEAGYGTDTLMGAKALYLPVLSNGVTLAVIGIEKSKEDPITD EIITFIELISTQLSLAIEQNNLTLERQQILFENEKERMRGNLLRAISHDLRTPLTGISGS VETVLDDHEATKLPEETKRKLLVGIKEDADWLIRMVENLLSITRINEETMKVAKSKE AAEEVVSSAIQRIKKSYPESEISVTLPDEFILVPMDSILIEQVLFNLMENAIRHSNCHS PIFVSVTATAKEVTFEVADQGKGLTGEQIKLLFDGMSKQNTPVDSKSGMGIGLSIV KTIIMAHDGTLNAGNRPQGGAVFTFTLPLERKEQK	27~~KdpD (3.87747E-108) ~~235,262~~Usp (3.96288E-25) ~~371,405~~DUF4118 (0.000000000000453902) ~~499,525~~GAF (0.00000000123694) ~~641,659~~HisKA (0.0000000000115544) ~~727,780~~HATPase_c (5.70492E-23) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	4E-85	293.9	0.5	6.6E-85	293.2	0.3	1.4	1	B1YM39_EXIS2	Osmosensitive K channel His kinase sensor	Exig_2548	Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	361	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sibiricum, Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	262543	>tr|B1YM39|B1YM39_EXIS2 Osmosensitive K channel His kinase sensor OS=Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15) GN=Exig_2548 PE=4 SV=1 MTRGKLKLYIGSAPGVGKTYKMLADAHALVREGKDVVIGLIETHGRRDTAEMIGGLEQVPLLEVHYKEKVFLEVNVEAIIARKPDIVLIDELAHTNAPGLIRKKRYQDVSVLLEAGINVYSAVNIQHFESLLFKVKEMTGVEVRERIPDPFLGEADEILLVDVTPQTLRERLEHGKIYKKEKIEQSLNSFFSLQNLASLRELSLRQVADEVDDQVYQARLLIEKDPTLLQERILVCVQLNENARKLIYRGFRMASRMKADLYILTILPKPENQLTASQKEVLAMLRESGALFDAEVLIRIQGERSIAETITAAAKHHRITQIVLGQSARTRWQEIRRGSIVNQIMRQNRGIDLQIVADDQV	3~~KdpD (4.42688E-109) ~~211,232~~Usp (2.55099E-39) ~~357	non-kinase	KdpD;Usp

	4.3E-85	293.8	0.3	6.3E-85	293.2	0.2	1.3	1	F8I8U7_SULAT	Osmosensitive K channel His kinase sensor	TPY_3242	Sulfobacillus acidophilus (strain TPY)	371	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiales incertae sedis, Clostridiales Family XVII. Incertae Sedis, Sulfobacillus, Sulfobacillus acidophilus, Sulfobacillus acidophilus (strain TPY)	1051632	>tr|F8I8U7|F8I8U7_SULAT Osmosensitive K channel His kinase sensor OS=Sulfobacillus acidophilus (strain TPY) GN=TPY_3242 PE=4 SV=1 MGFHVSGELGQLKIFLGMAPGVGKTYTMLREARLLKARGVDVVVGYVDTHERPD TARQLDGLEVVERLAIEWQGRMFEEVNLEAILARRPEVVVIDELAHSNVPGSRFPK RYMDVEFLLDHGIDVLTAVNVQHLEPVQSEAEAITKVPVREIIPATFLARAQEIEVID VTPETLRQRLLDGGIYPPEKVDQALKHFFRAENLAALRELMLRRVAEDVDERLQH SFERRLIPGPVGARETIMVCVSYLERSRPLLERAKRMADRMKADLIMLTVTDEEVE LLDQRERRHVDQLEALAQQYRAKFIAEPRRDRRLGEVILQVAERENVTQIVIGQPH ERGWRSWVKDSPVPFLLKNLRYVDLRIVGWRDQHAQ	10~~KdpD (1.86476E-93) ~~217,240~~Usp (1.53949E-27) ~~364	non-kinase	KdpD;Usp
	5.2E-85	293.5	0.4	1.3E-84	292.2	0.3	1.7	1	R2SE20_9ENTE	Sensor histidine kinase KdpD	UAU_02476	Enterococcus pallens ATCC BAA-351	863	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus pallens, Enterococcus pallens ATCC BAA-351	1158607	>tr|R2SE20|R2SE20_9ENTE Sensor histidine kinase KdpD OS=Enterococcus pallens ATCC BAA-351 GN=UAU_02476 PE=4 SV=1 MAVTNSSEIQQPFTQRGKLRVFFGFAAGVGKTYAMLAEAHELLALGKDVVVGYVE PHDRPETNQLLEGLPQMPLKAVTYKQLTLYEPDIDRIIERQPDVVIIDELAHSNAAG SRNRKRYQDVDELLNAGISVMTTVNVQHIESLNDIVEEVTGIEVKETVPDTFFQQA LLKVIDVEPDELIERLEQGKIYSNENAKRALQNFFIPQKLEQLRGLAIQRASDHINRV GGKNTGVQVKLLTIIHDTLPKMAEKCIRWSSRLAQGLGAEWVVIQIRSLDTKSTGV PLAEKLGAQVISIEEDDSFETIVEYAKMIGVTDIIMGKNLSRRWYHALFSEEFEDRLL RRLSATEVHLIPYKEAQPSIFAYPKKVIEGGAKDFGIALSGVVAATLVTELMQYLHV GDQNLMLIYIFFILLVARLTSGYFWSALSSILSVLSFNWFFVEPLYSLTVYKQGYPIT LVIMLIVALMISNLMVRLKAQAVRSKEKEHQMEILYELNKQYVLAENSQQIFEITTTY LSRLLNREVIFYDPAGEKKSVSVPENKTSKLSGAEEAAVAFWSAKNQKEAGNGTD TLVGSKGFYLPILSGGQSLGVLGIQRNRSQVLENSQLNYLRLVLTQIAVVLEQANL KSEKEKIEIENEREKVRSNLLRAVSHDLRTPLTAISGLAETMEKNPEIKPATREKLLA DIQEESQWLIRMVENLLSITRINMDTMKVDKTEESLEEIVEAVYKHIKKVYPQRAIQ VTLPEDFILLKVDPILMEQALFNLIENALRHGDGKLPVQLTAYQNEQRTIFEIENAGE IPLAQFQRIQNNLISDQEVPVDSKNGLGIGLSIVKTIVHAHGGQLEIETKPGRTIFRL ALRRENHG	15~~KdpD (3.09428E-115) ~~223,244~~Usp (1.04666E-25) ~~352,382~~DUF4118 (9.17845E-15) ~~476,504~~GAF (0.00000159629) ~~620,638~~HisKA (0.000000000000701565) ~~703,756~~HATPase_c (1.53396E-15) ~~857	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5.7E-85	293.4	0.1	1.4E-84	292.2	0.1	1.7	1	V5XQE6_ENTMU	Sensor histidine kinase KdpD	kdpD EMQU_1741	Enterococcus mundtii QU 25	873	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus mundtii, Enterococcus mundtii QU 25	1300150	>tr|V5XQE6|V5XQE6_ENTMU Sensor histidine kinase KdpD OS=Enterococcus mundtii QU 25 GN=kdpD PE=4 SV=1 MERQDVSEMLHQREKSRGRLRVYFGFAAGVGKTYAMLAEAQELSVLGKDIVVGY IEPHDRPDTNQLLEGLPQIPLKEVTYKGLTLSEPNIDAIIKRQPEIVLIDELAHSNAPG SRNRKRYQDIEELLNAGINVHTTINVQHIESLNDIVEEVTGIEVKETVPDTFFQQATL KVIDVEPDELIDRLAQGKIYADENAKRALQHFFIPKKLEQLRGLAIQRASDHINRVIG KTNGVQSKLITIVQDAFPKMAEKSIRWTARLAQGLGAEWIVLYIRSDDRLQGTNDL AEKLGAEVVVIEEDHSFETIVEYAKLVGATDLIIGKNLAKPWTERLFSEELDVRLLKR LPETELHLIPYKEKRSTILSHSKKLVEGGGKDFAISLICVFVATLLTEVMQYLHFGEQ NLMLVYIFFILLVARLTSGYFWSALSSILSVLAFNWFFVEPLYSLTVYKQGYPITLVI MLIVALMISNLMVRLKKQAVHAREKEQQMEILYELNKQFVLAEDQQQIVELSATYL GRLLDREVIFFDKHAIKLSQYTPKDAPFLLDHPEEAAVAYWTAKNQKDSGYGTDTL SGAKGFYLPIVANGKTLAVLGIRRSRGLPIEDSQLNYLRLVLTQLAVILEQTELKNEK EQIELENEREKVRSNLLRAISHDLRTPLTAISGIAETLLQTDEELKQATRQKLLTDIQ TESQWLIRMVENLLSITRINMDTMQVKKTTEPIEEIIEAVYEHVTKVYPDKELLVHLP TAVLFVEVDPILIEQAMFNLVENAFRHGSTQGQVEVSVFQEGQQVICEVKNDGEIS LKQYEKIQMNLSNEEVPIDSKNGLGIGLSIVKTIIHAHNGKLEMAVSEGKTVVRIYLN KSEEVTLHEESTID	15~~KdpD (1.71436E-114) ~~224,247~~Usp (3.77604E-26) ~~353,376~~DUF4118 (7.67496E-17) ~~477,503~~GAF (0.00000115656) ~~621,639~~HisKA (0.00000000000257611) ~~705,758~~HATPase_c (4.13154E-15) ~~858	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	6.2E-85	293.3	0	2.4E-84	291.3	0	2	1	A0A0F5PSN8_9RHIZ	Histidine kinase	WH91_19475	Devosia psychrophila	886	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia psychrophila	728005	>tr|A0A0F5PSN8|A0A0F5PSN8_9RHIZ Histidine kinase OS=Devosia psychrophila GN=WH91_19475 PE=4 SV=1 MARHTEKERPDPTALLQLAAREGRGKLTVFLGAAPGVGKTYAMLERARGLKAQG VDVVIGLVETHGRGETARLAEGLETLPRQGEGDAYREFDLDAALARRPALLIVDEL AHSNAPGSRHPKRHQDIAELIHAGINVWTALNIQHLESLSDLVARIAGIPVRETVPDI VLKTADEVILVDLPPAELIARLNEGKVYLPDNAARALDGFFKPATLTALRELALRRA ADRVDDQMVEFLRQSAVEGPWATGERLLVCVGPDTMSEKVVRTASRLASGLNA RWLVVSLNRPDAALPSPADAVRLEEVLRLAERFGAETRRESASDFVDAILRIARRE HITQIVIGRPTTTRWLRRSLPDALLRQAGEIGVHVVPGATSSAGRKPRRRLTLPEW ALTLGLPLVSVGATTIFGLGLTALVALQNLSMLYLAAVLVSAVIAGRGSALVAAALS FAAYNFFFIEPTGALTVAQPQEVLSLVIFVAVAFAAGQLAARLREQADLSRQQARQ SQALLDFSRKLSGAHGQDSVFDAIASHLHTSLGRPAVVLVPDDSGDLDPAAAWPP EQALDGTELTAARWAFDKKEPAGFLTGTLPQVRYLFRPIIAAQRILGVAGLGMGP RDVPLAADEERTLIALLDQAAIAMDRARLNRESAMASVAREGEKVQAALLSSLSHD LRTPLASITGAVTTLRQLGEKLPVETREDLLLSIEEESVRLNRFVANLFDMTRIEAG MMKARREAIDLNTVVASSVARAKRLHPDLLIDISLAPNLPSALGDGTLLEQVLFNLL DNARKYGAAEQPVSIFAKAEDGHATISVTDQGKGIPEADLEKIFEKFYRRAKSDGR PAGTGLGLSIARGLMTAMGGTIKATSPAVRKRGTRFTLRLPLATKEE	22~~KdpD (2.67749E-109) ~~229,251~~Usp (1.1208E-34) ~~371,398~~DUF4118 (8.13058E-15) ~~493,521~~GAF (0.000000266413) ~~639,656~~HisKA (0.0000000189619) ~~722,775~~HATPase_c (1.25867E-29) ~~879	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	6.8E-85	293.1	1.5	9.1E-85	292.7	1	1.2	1	K9PJF7_9CYAN	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	Cal7507_2475	Calothrix sp. PCC 7507	350	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix sp. PCC 7507	99598	>tr|K9PJF7|K9PJF7_9CYAN Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Calothrix sp. PCC 7507 GN=Cal7507_2475 PE=4 SV=1 MAPGVGKTFRMLEEGHALKQEGIDVVIGLLETHGRKETMEKAEGWEIVPRQQIPR GGLTLTEMDTEAILKRSPQLALIDELAHTNVPGSLREKRYEDVQLILAAGIDVYSTM NIQHLESLNDLVARITGVVVRERVPDRILEEADEVVVIDVTPETLQERLLEGKIYATE KIQQSLDNFFQRRNLIALRELALREVADNIEEDAIASSPNGKFCNVHERVLVCVSTY PNSVQLLRRGARLANYMNAPLYVLFVADPERFLTKEESLHIHTCEKLCKEFSGTFI RVTNSQIAKAIAEVAEKYHITQIVIGESQRSRWQMFLKGSLTQRLVRLLLKNVDLHIIS SEKASSSKR	1~~KdpD (4.60856E-121) ~~200,219~~Usp (1.44753E-45) ~~341	non-kinase	KdpD;Usp
	7.4E-85	293	2.2	9.9E-85	292.6	1.5	1.2	1	A0A088EZ71_9SPHI	Histidine kinase	KO02_07000	Sphingobacterium sp. ML3W	373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. ML3W	1538644	>tr|A0A088EZ71|A0A088EZ71_9SPHI Histidine kinase OS=Sphingobacterium sp. ML3W GN=KO02_07000 PE=4 SV=1 MEERKDAEYFLNLIKKSRKGKFKLYIGMSAGVGKTYRMLQEAHTLLHNGIAVKIGY VETHNRKETEALLDGLPVIPRRKLFYKGKELEDLDVQAIINLHPEIVIIDELAHSNME GSLNEKRWQDVVDILDSGINVISAVNIQHIESLHDEVKEITGIDVQERIPDRVLGLAD EVVNIDLTAEELIDRLKEGKIYDAAKIEMALANFFNTNHILQLRELALKEVASQVQRK VEAEVIHSKYVKKEQLLACISSNEKTAKIVIRKTARLANYYNSKWFVLYVQTPKESV SKIALDKQRHLINNFKLATELGAEIIKINHRNVSKAIIDQCETRQITTVCIGKPHLRLIKI IWATNTFNTLLTKLSNEKIDLIILS	17~~KdpD (8.12761E-111) ~~227,246~~Usp (2.14067E-28) ~~373	non-kinase	KdpD;Usp

	8.7E-85	292.8	0.3	1.1E-84	292.4	0.2	1.1	1	L0A4X7_DEIPD	Osmosensitive K+ channel His kinase sensor	Deipe_3483	Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	367	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus peraridilitoris, Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	937777	>tr|L0A4X7|L0A4X7_DEIPD Osmosensitive K+ channel His kinase sensor OS=Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200) GN=Deipe_3483 PE=4 SV=1 MAEPDEASPLTQQTPDENAARPRGRHKIYVGMASGVGKTYRALQDLHELLAAGR RVMIGVLETHGRRETQDVAYALPSFPRREVEFKGAVLSEMDLGGLLHLRPEVVLV DDLAHTNAPGSAHARRYEDVEDLLAAGIDVVSTVNIQHLESLNDLIARLTGVRVKD RLPDKVLQEADEVVLVDVSPQTLQHRLRAGKIYSPDKVDAALKNFFTESTLTTLRE LALRQVADAVQGEDQDNGGVKERILVACALEPESGRLIRRGGRIASRLGGELDVV FVSSGKPDAQGEQLLQFFQDTTEALGGHFKVIPSQGNIGRTLVQYVEANHITQVVI GESSRSRWEEFLRGSIVHTVLRHTRNVDVYVLTRE	23~~KdpD (1.54277E-108) ~~231,244~~Usp (1.14636E-29) ~~365	non-kinase	KdpD;Usp
	1.2E-84	292.4	0.5	2.5E-84	291.3	0.4	1.6	1	A0A0F2J2H6_9BACT	Osmosensitive K+ channel Signal transduction histidine kinase	MCHI_002510	Candidatus Magnetoovum chiemensis	896	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Candidatus Magnetoovum, Candidatus Magnetoovum chiemensis	1609970	>tr|A0A0F2J2H6|A0A0F2J2H6_9BACT Osmosensitive K+ channel Signal transduction histidine kinase OS=Candidatus Magnetoovum chiemensis GN=MCHI_002510 PE=4 SV=1 MSDNDLDKLISPDNLLEAVRKKESRTLEGKLKIFIGMAAGVGKTYAMVSEALAHHK NGIDIAVGLVETHKRKETQNLLRGLPVIKQKEYLYKGMKVSEIDIDAIIKRKPKIALID ELAHTNISECRHNKRYQDVLEILSHGIDVHTCVNIQHIESLNDQIRRITGVRVLETVP DSFFDRADEIVIIDLPPVDLLQRLREGKIYLGDNIARSLENFFKEDKLSLLRETALRFA AERVNIETQDFRLLNSITGAEQVKRKLMVGIFSSPYSEMLIRCTRRLAQALSTNWIG VYVDTDRELSDEEKELLEKNMNFVRQLGGEVVIAKDNDVVNGILRAARRQNVTQII VGKSRRNLFSSIFAGKSLIDRLFRESREIDIYMVCTDANTCAKKPSIPPKRRLPKFN KLSLGLLFVSILTAASFLIIPQSGYRIMGYIYIIFVTLSATYFPLDVVIVLSILCGVLWNF FFIPPRFTFTIAKNEDWMLVLVVLITASIAGILTSKLKKKQKLIIEREEKTNALYQFTK QLSVSKNLAEIIENAAEILSKVFQTKIGIFVKNDNDELTFTNRQKITLSEKDKTTALW VYHNRKHAGKFTDTLPVSDFYFTPLNTAQNDLGVLCTDLSGSKVFTHQQQALLSN FANQLTLTIEKEILHLRLNKTKLEKQSELIFKTLMDSVSHELKTPLSTIHGCASALLEP SISSNPNTVAELANEIVVGSRRMNSMVQNLLDMSRIESGQMRIVLSPVDLSDLIGV SIEKVSKIAQNRKITVYIDSDTPLMNLDFVLFEQAVTNILTNACLYTQQDGIIKITVKS MTDAVSMIIEDNGLGIPLEYKDKVFDKFFRANASKTGGTGLGLTIARSIIELHKAGIT AQSVKGEGAKFIITLPKEVFFINENTSNR	29~~KdpD (2.169E-111) ~~236,258~~Usp (6.81175E-33) ~~379,408~~DUF4118 (0.0000000301924) ~~498,529~~GAF (0.0000000390091) ~~646,667~~HisKA (0.0000000103081) ~~729,782~~HATPase_c (2.22492E-24) ~~882	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.5E-84	292	1.2	2.3E-84	291.4	0.5	1.6	1	D3HKC7_LEGLN	Putative osmosensitive K+ channel His-kinase sensor (EC 2.7.13.3)	LLO_2471	Legionella longbeachae serogroup 1 (strain NSW150)	653	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella longbeachae, Legionella longbeachae serogroup 1 (strain NSW150)	661367	>tr|D3HKC7|D3HKC7_LEGLN Putative osmosensitive K+ channel His-kinase sensor OS=Legionella longbeachae serogroup 1 (strain NSW150) GN=LLO_2471 PE=4 SV=1 MNDSRPNPNALLQQVLEEEKQQQRGKLKIFLGAAPGVGKTHSMLHEALEEQAKG LDIIVGIVESHGRSEIVEILKNFVILPKVTIDYHGKKLQEFDLDAALKRNPGLIIMDEM AHTNVTGVRHKKRWQDIKELLDRGIDVYTTLNVQHIESLNNDVSQIIHAPVQETVP DFMIESANTIELVDLAPEDLLKRLAEGKVYVPKQAQLAAEFYFRKGNLMALRELAL RTLAKRVNTQVLLYRQGQGIKSIWHIMEKILVCVGPGPESHKLIRSAKKIATSFQAD WMAVYVDSPRTQLSRTQRNQAIKNLFFAEQLGAETHILMGYDLVKEILNFAREQN VTLIMINKRIQTRWRNFFARSLADEVLRYSSDIDVYTITEMAKKPQKKALNKPLTSW FPYFLSISIVSVTTLFNFLLYSLVPDANLIMVYLIGMIAIASLGRTGPTISGIFLSLLAYD FFFVPPYYSFLPNDADYIFNLVMMLVIAVIICQLTLVTRRQSEIARLAEYQTSTLYTL SRRLSRTRGIVRLLRTGINYISEIFHCEIIALLPKDTRLVIRARSKSHQELDDKEYSIA QWVYELGQKAGLGTDTLSFSTAIFIPLLGSRGTIGVLRIQPFNSDEWATPEKIQLLE SCANQMALAIEVDSLQEESHKNKA	23~~KdpD (4.50543E-104) ~~232,254~~Usp (5.74687E-34) ~~376,396~~DUF4118 (0.00000000352323) ~~496,526~~GAF (2.94309E-14) ~~640	non-kinase	KdpD;Usp;DUF4118;GAF

	2E-84	291.6	0.1	2.9E-84	291.1	0.1	1.2	1	Q9RZN5_DEIRA	KdpD-related protein	DR_B0088	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	365	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus radiodurans, Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	243230	>tr|Q9RZN5|Q9RZN5_DEIRA KdpD-related protein OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) GN=DR_B0088 PE=4 SV=1 MSEPIRLTLPRDSQSPQPERGTHRIFIGMAAGVGKTYRALNELRERLERGEDALV GVLETHGRRETLQAAEGLPVFPRREIVHGNVTLSELDVEGLIARNPFIVLIDELAHT NAPGSPHEKRWQDVEALRDAGIHVLSTMNVQHLESLNDTVARLTGVRVRERVPD FVLHDADELVLIDLPPEDLRERLRAGKIYAPEKVEQALGNFFTLPNLTALREIALRHV AQAVELEVPEGQPAAHEVVVVAMAAEGTAARLIRRGGQLAERLRGELHVVTVRP ARLTPEASRMLDTCREITEALGGGFRVLDNVGTVGATLVAYARAVHATQIVMGET SRSRWAELLRGDIIKYVLRGTQGMDVHVISRD	18~~KdpD (1.59463E-122) ~~228,243~~Usp (4.84692E-33) ~~363	non-kinase	KdpD;Usp
	2.1E-84	291.5	0.5	3.2E-84	290.9	0.4	1.3	1	A9WQL7_RENSM	Histidine kinase (EC 2.7.13.3)	kdpDRSal3209_0916	Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	892	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Renibacterium, Renibacterium salmoninarum, Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	288705	>tr|A9WQL7|A9WQL7_RENSM Histidine kinase OS=Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235) GN=kdpD PE=4 SV=1 MWLICTVQTSHNSTLDGGWRGITTAEKAGIGEDGIMARGTLRILLGAAPGVGKTF AMLEEAHLKIGQGVDTVVAIALHHGRKDTQALLAGLEVIPTKQVEYRGSHFEEMDV DAVLERAPQLALVDEYAHTVVSEHGTKASRKRWEDVELLLDAGIDVISTLNIQHLA SLGDVVSQITETKQGETVPDDIVRRADQIELIDISPELLRQRLSAGNIYSADKVDAAL ASYFRMGNLSALRELALLWLADQVEDGLSAYRADHSIEASWPTRERVVVGLTGG PEGEVLIRRAARILARVSGGELLGVHVRASDGVLAESPRELETQRQLLKDLGGSY HSVTGEDQAQALLDFARRVNATQLVVGTSRRRPLARLVRGAGVGSKVVRGSGDI DVHMVSHPLGGRGVVFRKAGALGRRRLMLGFALAIVIPVILEWALVQWVPDSFTT ETLIQLTGCVVVAVIGGLWPALLAAVFSSLLLNFFTAAPIGTLTIADPENLLALIIFLIV SAVVAVVVDLATRRTRDALRAGAEAATLSELARGAVAGEDSLQTFLDQGREAFRV DSVSLLLKDPMTTSTPVWRFEAASGLNPPDNPETSDNIEEVQNELVLALNGRVLN VSDRRLLAAFGAHLLALRQRIQLDASRRDNVRLAEGNTMRTSILRAVSHDLRTPLA AIKLSVSSLRQDGVRFPPEDEAELLASVETSADRLDALVGNLLDMSRISSDAVNPL LGPVRWTDAIDAALQGLPEEQLRLELPANMPAIEADPGMLERVIANVVENALKYAP NSDLVLLGTVSGTPTIAGQPASELRIVDHGRGVAAKDVVAMFRPFQRLDDVPDGS GVGLGLAVAKGFTEAMGGVLTAEQTPGGGLTMVMRLPLSSGAAEAVRATQVER SVK	36~~KdpD (2.6879E-99) ~~249,271~~Usp (7.74525E-29) ~~394,416~~DUF4118 (0.0000000278921) ~~502,X,650~~HisKA (0.00000000000665736) ~~716,765~~HATPase_c (3.37334E-19) ~~872	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	2.2E-84	291.5	0.3	2.9E-84	291.1	0.2	1.1	1	Q725T9_DESVH	Potassium channel histidine kinase domain protein/universal stress protein	DVU_3336	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	379	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	882	>tr|Q725T9|Q725T9_DESVH Potassium channel histidine kinase domain protein/universal stress protein OS=Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303) GN=DVU_3336 PE=4 SV=1 MDDFSEILARKRQGSLKVYLGYAAGVGKTYAMLQEAHRLAREGLDVVIGYVEPHD RADTLALVEGLEQVAPRKVAIAGSDFTEMDVPGIIARRPQVVLVDELAHTNAAGSE NGKRYQDVLKVLEAGINVITTLNVQHLESVAERVESVAGVRVQERLPDAILRRADQ VVNVDLTKEDLRERLRQGRIYSPEQAERALGGFFSYRNLSFLRELCLREASGDQV RKIEEQEHFPRHSAGDVIEGVMVALSSSPTDAETLIRRGVRIAHQMGSPCYVVYV QRPSENPTRIDSGLQRVLQGNLRLATQLGAEVVQLAGGDIAETLANFASERNVRH AVFGKSRLSPLLERVRGSFILEFLHDAVGVDVHIVNTTPRQPGQERA	11~~KdpD (1.34359E-106) ~~222,243~~Usp (8.37802E-39) ~~368	non-kinase	KdpD;Usp
	8.2E-84	289.6	0	1.6E-83	288.6	0	1.5	1	A0A0F5FJ97_9RHIZ	Histidine kinase	VE26_00560	Devosia chinhatensis	886	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia chinhatensis	429727	>tr|A0A0F5FJ97|A0A0F5FJ97_9RHIZ Histidine kinase OS=Devosia chinhatensis GN=VE26_00560 PE=4 SV=1 MDRLDDERRPDPAALLQLAARERRGKLTIFLGMAPGVGKTYAMLERANALAANGT DVVVGLAETHGRNETAVLAEGLETLPRVEGARPYGEFDLDAALLRRPQLLIVDELA HTNSPSARHPKRYQDIAELIDAGIDVWTALNIQHVESLSELVGHITGIPVRETVPDV VLKKADEVVLVDLPPAELIERLKAGKVYLPDNAERALDGFFKPATLTALRELSLRRA ADRVDDQMVDFLRQGAIEGPWATGERLLVCVGYDDMSERLIRDASRLASGLNAR WTVLSLSHPHRLAPHQEAIDRLEATLRQAERFGAEIRRETASDYVKAILRLARRGN FTQIVIGQNRKNAFWRRSLPDALLRQAGEIGVHVVSGQGARAPVRAVRRRTLPE WTLTLGLPVLAVSATTLLGLGLSAIIALQNLSMMYLAAVLLSAMLAGRFSALLASLL SFLAYNFFFIDPTGRLTIAQPEEVLSLAIFVAVALVSGQLAARLRLSMDRTSQRARQ AQALLDFARKMSAAFGQDQVLDTMASHLHGALGRPAVVLASDDGGELTLMTAWP PDQNLNDAAMTAARWALEKREAAGFLTGTLPQVSYLFLPVQSGQRVLGVVGLGM RHEDGPVSDAEQRTINALLEQSAIALDRARLTQDSTRASVTRESAKVQSALLSSLS HDLRTPLASITGAVTSLRELGDRMPAAARADLLASIEEEAGRLNRFVTNLFEMTRIE AGIVRAKRDPLDVAMVIKAAVNRALRLHPHLQVDVSVADRMPLATGDQVMLEQVL FNLLDNARKYAGDAPVTIYARREGSDVSIAVTDQGKGIPEGDLERIFEKFYRRAEG DGRQAGTGLGLAIARGLVAAMGGTIKAESPALRRRGTRFIIRLPRAGEESA	22~~KdpD (1.22161E-108) ~~229,251~~Usp (2.57129E-29) ~~371,398~~DUF4118 (0.00000266871) ~~491,521~~GAF (0.0000000000470106) ~~639,659~~HisKA (0.000000014829) ~~722,775~~HATPase_c (1.54661E-28) ~~878	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.3E-83	288.9	0	2.1E-83	288.3	0	1.3	1	L8EQV5_STRRM	Histidine kinase (EC 2.7.13.3)	SRIM_19694	Streptomyces rimosus subsp. rimosus ATCC 10970	865	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rimosus, Streptomyces rimosus subsp. rimosus, Streptomyces rimosus subsp. rimosus ATCC 10970	1265868	>tr|L8EQV5|L8EQV5_STRRM Histidine kinase OS=Streptomyces rimosus subsp. rimosus ATCC 10970 GN=SRIM_19694 PE=4 SV=1 MEEYVMERGGDVTCGAGRRVGRLKVFLGAAPGVGKTYRMLDEGRRRAARGTR VVAFAECHGRASTEAMLDGLDVLPRPTRGDGGAEFTAADLDRVLELRPHVVLIDE LAHTNAPGSRHAKRWQDVEELLAAGIDVVATLNIQHLDSLSDVVEKITGVPQDETV PDAFVRRADQIELVDLPAEGLRRRMAHGNIYPPEKVDAALSHYFRLGNLTALRELA LLWVAGRVDEALRKYRDEHRIGRVWETRERVVVALTGGAEGATLIRRAARIVSRS SGDLLAVHITRSHDLVGSSPAALAGQRQLTESLGGSYHSVVGDDVPTALLDFARS QNATQLVIGASRRGRLRRLLTRRGVGETVVERSGDIDVHTVTHEHAGQGRRWAA PGSGLPRSRRVAGPVAGLVLPLLLTLVLRAVSGPLALNLTSEALLFLLTVLGVACIG GVVSALLASVTTSLLLNLYFIPPIGHFTYAEANIVVAQAALTTVAVTVAAIVDRSLRL NRRAARATAEAESLISLAGGILRGDRAVPVLLERTRETFGMDSIALRPRDGEADSGG AAGGLPSEGGDDRETRVAIGEDSVLVLKGRRLPASEHRVLTAFAAHLTAAVERAR LAEAAAEVEPVKAADRMRTALLAAVGHDLRTPLSGCWAAISSLRSRDVDFSAEDR EELLATAEESLAKLSRLVDNLLDMSRLQAGALTLRLEPVALTEVLPAALDTLPGSPP AAVAHVATLGLETAPDVLADPPLLERVLANLVSNAVRHSPAGRPVTIGASALAGRV ELRITDRGPGIRPPDRERAFEPFQRLGDTDNTTGLGLGLALSRGLTEAMGGTLTP EDTPGGGLTMVVSLPAAPVPEAVPGAAVSARTP	19~~KdpD (2.00166E-98) ~~227,249~~Usp (9.84938E-24) ~~371,427~~DUF4118 (0.00309634) ~~494,X,624~~HisKA (0.00000000115292) ~~690,745~~HATPase_c (3.40812E-27) ~~846	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.8E-83	287.4	0.2	1.2E-82	285.8	0.1	1.8	1	B8GEQ9_METPE	Osmosensitive K channel His kinase sensor	Mpal_2485	Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	637	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanosphaerula, Methanosphaerula palustris, Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	521011	>tr|B8GEQ9|B8GEQ9_METPE Osmosensitive K channel His kinase sensor OS=Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c) GN=Mpal_2485 PE=4 SV=1 MTGDDGRPLPDDLLSLAREDDRRRTEGKLTVYLGYASGVGKTYTMLADALGWRT AGTDVVIGYVETHGRPETDALAARLEAVQPKVVDYLGIHLNEMDLDAVLARNPAV VLVDELAHTMAPGQRHTKRYQEIEELLRAGISVCTTVNIQHIESEHDAVARITGIQV HETVPDTFLELAGDLRLIDLPPDQLVERLHAGKVYIQDMAALAVARFFTPANLIALR QLALRFVAGSTDRELVGLMHSQAIAGPWPAAERVLVGVRTGPYADQMVRAGYR VASRLQAEWIVLSVETEDDLGAPVKDQAHLREALETARRLGGRVVRYRAEDVAG EIIRHAKRNNVTTILLGKPRGLGLFLSPVYRVMRHTQGIALHLVDPIERTRIPIRRQL PIPSIPDAGIALVLIGGVAAVNVTLRDTLSPSNLLIIQLIPVVIAALFLGRAASVFAVAV SILLFDILFVPPYYTIAISDWQYFISFIGYLVVALVISNLASRLRYLLPQIRESEATVAA MSGLSKDLDVATTRQEVFERLVDHLHQVTGGPVTVLIPKGGELARTAGDPTYPLD EKEEAIAAWVYENRRPAGQGMETLPAGHGRYLPLVVSGRALGVVGVMPEEHGG PADEVLEGMVRLGSLVLDRLA	27~~KdpD (1.93624E-97) ~~231,256~~Usp (8.30027E-29) ~~374,399~~DUF4118 (3.42679E-14) ~~494,523~~GAF (0.00072878) ~~635	non-kinase	KdpD;Usp;DUF4118;GAF

	3.9E-83	287.4	0.3	7.4E-83	286.5	0.2	1.5	1	S0PGB6_9ENTE	Sensor histidine kinase KdpD	I573_00527	Enterococcus sulfureus ATCC 49903	858	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sulfureus, Enterococcus sulfureus ATCC 49903	1140003	>tr|S0PGB6|S0PGB6_9ENTE Sensor histidine kinase KdpD OS=Enterococcus sulfureus ATCC 49903 GN=I573_00527 PE=4 SV=1 MEENEYIHIDKGEGKFGKLRIFFGFAAGVGKTYAMLVEAHELQEIGKNIVIGYIEPH DRPETNRLIAGLPNIPTKKIHYKTLELNEPDVDQIIKQKPDIVLIDELAHTNAYGSRNK KRYQDVEEILKAGIDVFTTMNVQHIESLHDIVAQVTGIDVQETVPDTCLQQALIKVV DVEPEELIDRLEQGKIYADHAIKQALANFFIPEKLEKLRGLAIQRASDHINRINSKTLG IQSNLLTIVYDDFPKMSEKCIRWTARLAQGFHAEWTVITIKTQEEIEPSSTLAEKLG AKVIVIEEENSFETIIEFSKMTGVTDIIMGKNIKQHWYENVFAESFENRLLKRLQDTE LHLIPFHESKKVWRFNYQEMLTDSGRNASIAVGGVICATLITEGMKFLHVGDQNLM LVYILFVLLIARATSGYVWSAISSIISVLAFNWFFVEPLYSLTVYKQGYPITLLIMFAV ALMVSNLMVRLKKQAQTAIAKEKQMEILYELSKKFILTENRAQILAISTTYLSRLLDR EIAIFDAKGQVEHVHCVEEQTSVLSEKAEAAVAYWTAKNQKEAGHKTDTLIGAKG YYLPILTRGNTLAVLGIKTIDEPPLTNDQFNYIKLVLAQIAIVLEQNELKQEKNAIQIEN AQEKVRSNLLRAVSHDLRTPLTVISGIAQMLEQGNKLDPEMQKRFLQDIQVEAQW LIRMVENLLSITRIDSTTMDVEKTAEPVEEIMEAVYQHIKKVYPKAQLNIDLPEEMLF VQVDPILIEQALFNLVENALRHGQPQELIRISIYQDLDQTVFEIENKGEVPFKQFQKL QANLTQTYEVPVDSKNGLGIGLSIVKTIVHAHHGRINMTVNNGKTCVQIFLK	14~~KdpD (2.25389E-106) ~~223,246~~Usp (1.89935E-28) ~~352,377~~DUF4118 (0.000000000000410087) ~~476,505~~GAF (0.000000391001) ~~620,638~~HisKA (2.68369E-14) ~~703,756~~HATPase_c (6.72213E-14) ~~857	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4E-83	287.4	0.1	7.3E-83	286.5	0.1	1.4	1	R3WCP8_9ENTE	Sensor histidine kinase KdpD	UC3_01132	Enterococcus phoeniculicola ATCC BAA-412	854	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus phoeniculicola, Enterococcus phoeniculicola ATCC BAA-412	1158610	>tr|R3WCP8|R3WCP8_9ENTE Sensor histidine kinase KdpD OS=Enterococcus phoeniculicola ATCC BAA-412 GN=UC3_01132 PE=4 SV=1 MQGTEELGDERRGRLRVFFGFAAGVGKTYGMLAEAHELLLMGKHVAIGYIEPHD RPDTNRLLEGLPNIPPKIFTYKQLVLTEPDIDRIIQEKPEVILIDELAHTNATGSRNRK RYQDVDELLNAGIDVFTTVNVQHIESLNDIVEEVTGIEVKETVPDTFLQQATIKVIDV EPDELIERLEQGKIYANENAKRALQNFFIPKKLDQLRGLAIQRASDHINRISGKTVGI QSKLLTVVTDVFPKMTEKCIRWTARLAQGLGAEWTVIQIRTQEETPTNIPLADKLG AEVISIEEDGSFETIVEFAKMTGVTDIIMGKNLRQPWYEKIFVEAYDDRLLRRLNDT ELHLIPFKEEKQTLFSKTRKIIEGGGKDLSIALGGVFLATVITELMQYIHVGDQNLML MYIFFILLVARTTSGYFWSALSSILSVLSFNWFFVEPLYSLTVYKQGYPITLLIMLVV ALMISNLMVRLKKQADSSMEKEHQMEILYELNKKYMLAESRKQILEISVTYLSRLLE REVIIFDQQANMQSVHCVEDKSSVLNQKDEAAVAFWAAKNQKEAGNGTDTLIGA KGFYLPIIASGKTLAVLGVERNATLDLENDQLNYLKLVLTQIASILEQTELKTEKEQV ELENEREKVRSNLLRAVSHDLRTPLTVISGIAETLGLGTDLKEETRQKLVKDIQEES QWLIRMVENLLSITRINMDTMKVTKTSEPVEEIIEAVYKHLKKVYPEGQVRIQLPET VIFIQADPILIEQALFNLIENAFRHGDKNQLVNLIVYQENGQTVFEIENYGEIPLKQFQ KIQSNLSSTNEVPVDSKNGLGIGLSIVKTIIHAHNGKMEMKVGEGKTVVKIYLK	10~~KdpD (3.30464E-115) ~~219,232~~Usp (7.90412E-30) ~~348,378~~DUF4118 (2.33902E-14) ~~472,501~~GAF (0.0000716288) ~~616,634~~HisKA (0.000000000000548768) ~~699,752~~HATPase_c (0.00000000000149252) ~~853	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	4.9E-83	287.1	0.5	6.2E-83	286.8	0.4	1.1	1	A0A0F7FRR0_9ACTN	Turgor pressure sensor	SXIM_13900	Streptomyces xiamenensis	351	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces xiamenensis	408015	>tr|A0A0F7FRR0|A0A0F7FRR0_9ACTN Turgor pressure sensor OS=Streptomyces xiamenensis GN=SXIM_13900 PE=4 SV=1 MGKTYDMLADGRRRAALGGDVVIGFMEDHGREPTRRMAEGLETVPRREMTYRG ARFTEMDLDAVLARHPEVALVDELAHTNVPGSRNAKRWQDIDELLRAGVHVVSTV NIQHLESLNEVVENITGVVQRETVPDEVVRRADQIELVDLSAQALRRRMEYGDIYP RHKVADALTHYFREGNLTALRELALLWVADRVEEALQRYRGEQGIQTPWATRER VVVALSGGAEGTTLIRRGNRIAQRGAGGELLAIHVRRDDGLREAPSETIARQRALV ERLGGTFELVTSDDPAAAVLEFARGVNATQLVIGASRRGRVKSLLAGKGVGTSIVE GSGDYLDVYIVTHEEAAHGRL	2~~KdpD (2.95133E-101) ~~196,218~~Usp (4.88072E-25) ~~342	non-kinase	KdpD;Usp

	6.1E-83	286.8	0.1	1.8E-82	285.3	0	1.7	1	G1UPR9_9DELT	Uncharacterized protein	HMPREF1022_00592	Desulfovibrio sp. 6_1_46AFAA	374	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio sp. 6_1_46AFAA	665942	>tr|G1UPR9|G1UPR9_9DELT Uncharacterized protein OS=Desulfovibrio sp. 6_1_46AFAA GN=HMPREF1022_00592 PE=4 SV=1 MREFSDVLARKREGSLKIYLGYAAGVGKTCAMLQEAHNLLRQGFDVVAAYVEPH ERPDTLALLEGIETLPPLRVSQGGAAFPEMDAEALIRRAPQIALVDELAHTNAPGS QREKRYQDVLEILSHGINVIGTLNVQHLESVAERVQEATGVAVRERLPDAFLARAD QVVTVDVSKEDLRERLRQGKIYKPEQAERALRNFFSYENLSFLRELCLREASGDQ MRKIEAQALLSPEAEGHAAEAVMVAISSNPTDAETLIRKAMRLASQMGSRCYVVY VQRQRESPERINAAVQRGLQNNLQLAVRLGAEVVELEGEDVAETLVNFASARNV RHAFFGKSRLTPLRERLRGSFILNFLYDAVGVDVHIVNLTPREV	11~~KdpD (1.71715E-107) ~~218,243~~Usp (1.77831E-32) ~~368	non-kinase	KdpD;Usp
	1.2E-82	285.8	0.3	1.2E-82	285.8	0.2	1.6	1	R5C281_9FIRM	Histidine kinase (EC 2.7.13.3)	BN499_02256	Blautia hydrogenotrophica CAG:147	895	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	1263061	>tr|R5C281|R5C281_9FIRM Histidine kinase OS=Blautia hydrogenotrophica CAG:147 GN=BN499_02256 PE=4 SV=1 MERCPDTDVSVSDMKPQQTRSRGSLKIFFGYASGVGKTYSMLRAAHEAKSRGID VVAGFVDTHGRAQTTQLLHGLESLRTRKMDFESGLKREFDLDAALRRSPRLILVD ELAHTNVPGCRHTNRYQDVEELLRAGIDVYSTVNVENIESLNDMVAAITGEAAKDR ILDSVFDEAAQVELVDVEPEELIERLQAGEIYQDEKEKEEAAELFTLDKLTALREIAL RRCADRINKMTELVQAKSRRGYFTDEHILVCLSSAPSNAKIIRTAARMAKAFHGEF TALFVETSDFSVMEEEDKERIRVHMRLAQQMGAKIETVFGEDVAFQISEFARLFGV SKIVVGRAGAKRNRLFGKPTLTEKLISYASGIDIYIIPDKYAAVYRARRAKRESEAFS LADMSKGAAALVAATLAGMVIEKLGFSEANIITVYILSVLATSVIVSKRMYSLIFSAIN VVVFNFFFVTPKYSLTAYDSGYPITFLVMFLAAFITSSLAVRLKNHVKQSAQTAFRT QILFDTNQLLQQEKEKEGIVNITANQLIKLLSRDIVYYPVEKEQLREPKVFLTLNGKT DEKCVTQKEREVAAWVLKNNKHAGATTDTLSEAKCLYLAVRVNHVVYGIIGILLGE KPLDAFENSIVLSILGECALALENERTARENEEAAVLAKNEQLRADLLRAISHDLRT PLTSISGNASNLLFNSEDFDKETKKGLYKDIYEDSLWLINLVENLLSVSRIEEGRMN LRLSAELMDEVISEALQHVNRRSIEHVIVVENSDDILLARIDARLIVQVVINIVDNAIKY TPRGSHITISTVQTGQIITVKISDDGPGMDDEVKSHVFDMFYTGSNKVADSRRSLG LGLSLCRSIIHAHGGEITVKDNQPQGTVFSFTLPAGEVQLHE	22~~KdpD (5.64643E-97) ~~230,250~~Usp (4.53375E-32) ~~373,411~~DUF4118 (0.000142) ~~498,X,664~~HisKA (0.000000000367847) ~~730,783~~HATPase_c (3.18567E-28) ~~886	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.9E-82	285.2	0	2.6E-82	284.7	0	1.2	1	D3DFQ0_HYDTT	Osmosensitive K+ channel histidine kinase	kdpD HTH_0185	Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6)	408	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Aquificaceae, Hydrogenobacter, Hydrogenobacter thermophilus, Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6)	608538	>tr|D3DFQ0|D3DFQ0_HYDTT Osmosensitive K+ channel histidine kinase OS=Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6) GN=kdpD PE=4 SV=1 MEDLEERPSPEELLELVESVENVEFDVGKGYLTVYFGYAPGVGKTYSMLYDAHLL LEKGIDIVVGYVETHGRAETEALLKDLEIIEPVIYDYKGLKLREVNYEKIIQRKPQIVII DELPHTNPPGFSEEKRYQSIKRVLQAGIDVFTAMNVQHLESLKDLIYQITGVEVRE SVPDPFIKDAKEIKLIDLPPEELLVRLSEGKVYVKDMAEEARRRFFKIGNLIALRTLA LRVVADQLDQKLKNYLRRRGITTPLGLKEKILVGVYASPYASQLVRATYRIASELGG VEWIALFVETEKSKDFTEEEKKWLEKALDLARRLGGRVECIKGKNVAQEIISYAKR EGITKIVLGKPRREGALTGSIYKNLILETEGIDIYLIAPRVKAELPKSIEKKGFDRYLDI LRRYFG	28~~KdpD (3.4511E-101) ~~237,259~~Usp (8.35537E-30) ~~380	non-kinase	KdpD;Usp

	2.7E-82	284.7	0	5.2E-82	283.7	0	1.4	1	C7LZE9_ACIFD	Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD	Afer_1175	Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)	389	cellular organisms, Bacteria, Actinobacteria, Acidimicrobiia, Acidimicrobiales, Acidimicrobiaceae, Acidimicrobium, Acidimicrobium ferrooxidans, Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)	525909	>tr|C7LZE9|C7LZE9_ACIFD Osmosensitive K channel signal transduction histidine kinase, sensor subunit KdpD OS=Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP) GN=Afer_1175 PE=4 SV=1 MDAIDTEDADQLVATPEVEPVGRFRIYLGAMPGVGKTCAMLDEGFRRFHRGADV VVGFVETHGRDYTASLVRDLPVLARRRGTYRGRPAEEFDLEAALARKPEVILVDEL AHTNVPGLGAHAKRYEDVATLLEAGISVITTLNVQHIESVAALVEDLLGVPVRERVP DAVVRAADQIELIDSSPQALRRRLLHGHVYPPDRIEWALEHYFTTRNLTVLRELAL RFVADSQVPTPTLAVASRARWQAILETKERYLAGVTLSAASPRVLRRAARMALRS HADLYALFVHPDEYDPTRDAPRLDALRTLAADLGAILIERDGSDIATLLVDEARARQ VTQIVVGASRRRRIDEILHGSVLNRLLRLAGPVGIDVHVIGVRDYDPSPDEFNG	22~~KdpD (2.78663E-97) ~~228,253~~Usp (1.12582E-27) ~~376	non-kinase	KdpD;Usp
	3.1E-82	284.5	0.2	5.9E-82	283.6	0.1	1.5	1	F5YTX1_MYCSD	Histidine kinase (EC 2.7.13.3)	kdpD JDM601_0994	Mycobacterium sinense (strain JDM601)	832	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sinense (strain JDM601)	875328	>tr|F5YTX1|F5YTX1_MYCSD Histidine kinase OS=Mycobacterium sinense (strain JDM601) GN=kdpD PE=4 SV=1 MSVLSQRGELRIYLGASPGVGKTYAMLGEAHRRAERGTDVVAAAIETHGRSKTAE LLRGIETVGDPSAELDVAAVLARRPRVVLVDDLAHTNAAGSRNPKRWQDIEELLD AGITVISTVNVQQLESLSDVVTKITGTTEHDTVPDAIVRQAAQIELIDVAPEALRRRL SHGNVYPPEKVDAALANYFRGETLTALRELALLWLAGQVDAALTKYRADKKITQT WEARERIVAAVTGGPESETLVRRASRIASKAGGELLVLHVLGDGDSGAPAPRVGK IRQLAISLGASLHTVIGDDVPAALLEFARDVNATQLVIGSSRRSRWARILDEGVGAA VVQQSGDIDVHIVTDEDTKPNFRSVSISPRERRAVSWLAAVAVPCVMCAIVVGWL DRYLDTGQSALFVVGVLVVALLGGIAPAVLSALLSGVLLNYFLLAPRRGFTIAEHDA AVTEVVLLLVAVAVAVLVDSAAKRAREAGRASREAELMTLFAGSVLRGADLDTLLE RVRETYAQRAVSLVRIPAGTARPEVVASVGEQPCTSVDLADTTIDVGDDEFWML MVGRQLASRDRRVLSVVARQAAGLVRQEELAAEASRADAVMRTDELRRSLLSAV SHDLRTPLAAAKAAVSSLRADDVAFSPDDTAELLATVEESVDQLTDLVGNLLDSSR LAAGVIRPALTKVYLEEVVQRALIGIGRRSNVFGRGRLDQVKVEVGPTVAMADAGL LERVLANVIDNALRYASDSVVRVTAGRVGDRVLVNIADEGRGLPPGGELHAFDPF QRLGDRDNTSGVGLGLSVARGFVEAMGGTLSATETPGGGLTMVVDLAAPAGEG G	5~~KdpD (5.80259E-96) ~~207,229~~Usp (5.91313E-33) ~~349,X,601~~HisKA (0.00000000000962624) ~~667,724~~HATPase_c (2.84019E-24) ~~824	kinase	KdpD;Usp;X;HisKA;HATPase_c

	4.1E-82	284.1	0.1	7.4E-82	283.2	0	1.4	1	E3EJM1_PAEPS	Histidine kinase (EC 2.7.13.3)	kdpD3 PPSC2_12225	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	898	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus polymyxa (Bacillus polymyxa), Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	886882	>tr|E3EJM1|E3EJM1_PAEPS Histidine kinase OS=Paenibacillus polymyxa (strain SC2) GN=kdpD3 PE=4 SV=1 MAAKQNDAGSILNRITDMSVRKRRGRLKIFIGYAPGVGKTCAMLNAAYEEQKEGM DIVVGCVEHDARPYTAALLEGLELLPYIKISSEEESSTKEFDVDQALQRSPELILLDDL AHANAAGCRHRKRYQDVEELLRAGIHVYTTMDIQQIESLTDIVYSITGISVEERIPDS VFNRADQVELVDIEPDDLIERFYRGKIYRENENIQAHLFTKEKLTALREIALRNTASQ LNRIALQISDQTKTNECNTKEHILVCLSSADSNKKVIRTAARMAAAFHGHFTALFVE TQEARELTTKNKSELRENLRLAEQMGAQIATMYGDDIPGQIAEYVKTSHVSKIVLG RSPYKKRGLAKSNVMDKLTTLLPNIEIYIIPSTVPSFYKKMNYYAKYPNLSLADTIKTI AILAVCTVIGLWFKYLEFREANIITVYILGVLLNAIVTKGRMYSAISSIMSVLVFNYFFT EPYYSLQAYDSGYPVTFLVMLAASFMTSTMTMRIREQARQSAHKAYRTEVLLETS RKLQQAKDSPGIINEMAYQLVKLLDRTVIFYSVHQGALLAPQVFSKKESACDPGVYY TGGNERAVAEWVYKNNKRAGATTDTFFGAKCLYHAVRGGDQVLAVAAIVMDQE EPLEVFDNSLMLAMLGECALALEKEKLNEKQQEISMQIQQEQLRASLLRSISHDLR TPLTSISGNAGILLGNSEVLNDEQKKGLYTDIYDDSMWLINLVENLLSISRIENGTLN LNFQAELMEEVISEALLHVNRNSVKHVIQTELDDELMMARMDSRLIVQVLINMIDNA IKYTQDGSHITISARRERHRVVVEISDDGPGISSEEVKDRLFDMFYTADNIHGDGR RGLGLGLSLCKSIVNAHGGNIGVKNDVPKGAVFYFTLQAEEVNVHE	22~~KdpD (9.66339E-90) ~~230,251~~Usp (1.37296E-31) ~~373,398~~DUF4118 (8.26775E-16) ~~498,X,666~~HisKA (0.000000000133389) ~~732,785~~HATPase_c (4.11605E-20) ~~889	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.8E-82	283.9	0	6.9E-82	283.3	0	1.2	1	B8DR35_DESVM	Osmosensitive K channel His kinase sensor	DvMF_2574	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	375	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	883	>tr|B8DR35|B8DR35_DESVM Osmosensitive K channel His kinase sensor OS=Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637) GN=DvMF_2574 PE=4 SV=1 MEGFAELLARKRQGSLKVYLGYAAGVGKTYAMLQEGHRLRQAGFDVAIGYVEPH RRPETTALMDGLEVVPPRMCRVGDALFPEVDVPAVLARRPQVALVDELAHSNAA GSPNPKRYRDVLEIMEAGINVITTLNVQHLESVAERVETVTGIPVRERLPDAVLHRA DQVVNVDVTKEELRERLRLGKIYGAEQAERALMGFFTYQNLSLLRELCLREASGD QVRKITEQGLLSREAAGDAVEAVMVALSSDPTDAETLIRRGMRMASQFGSPCYVV YVRRPSETPVRIDAGLQRVLQNNLRLAALLGAEVVQLEGHDVPEALVNFASERNV RHAVFGKSRLSPLRERLRGSFILDFLHEAVGVDVHIVNTTPREAP	11~~KdpD (3.02387E-103) ~~222,243~~Usp (4.34454E-38) ~~368	non-kinase	KdpD;Usp

	2.3E-81	281.6	3.3	3.1E-81	281.2	2.3	1.2	1	R6XE34_9PORP	Osmosensitive K+ channel His kinase sensor domain protein	BN675_02911	Parabacteroides merdae CAG:48	346	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides merdae CAG:48	1263094	>tr|R6XE34|R6XE34_9PORP Osmosensitive K+ channel His kinase sensor domain protein OS=Parabacteroides merdae CAG:48 GN=BN675_02911 PE=4 SV=1 MIAGVGKSYRMLSDAHQLLESGIDVKIGYIETHGRVETEALVEGLPVIPRRKIFYKG KEIEEMDLQSILSIHPEVVIVDELAHTNVEGSKNEKRWQDVMDILDAGISVITAVNIQ HIEGLNEMVQDVVGIEVKERIPDIVLEQADEVVNIDLTADELLARLKAGKIYKPDKIQ TALNNFFKAEHILQLRELALKEVALRVEKKVESTIPENLGVRHERFMACISSNEKTP RKIIRKVARLATRYNTKFFVLYVQTPRESSDRISLASQRHLLNHFKLATELGGEVIQ VQSPHITDAIVQACKEKQISTLCIGRPTLKYPSVILAMVHYRNMLEELAQLGIDLIILA	1~~KdpD (3.90493E-113) ~~200,218~~Usp (7.79875E-28) ~~314	non-kinase	KdpD;Usp
	2.9E-81	281.3	0.1	4.5E-81	280.7	0.1	1.3	1	K8WAH7_PRORE	Histidine kinase (EC 2.7.13.3)	OOC_07093	Providencia rettgeri Dmel1	854	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia rettgeri, Providencia rettgeri Dmel1	1141663	>tr|K8WAH7|K8WAH7_PRORE Histidine kinase OS=Providencia rettgeri Dmel1 GN=OOC_07093 PE=4 SV=1 MLQEAQRLRAQGLDVLIGVVETHEREETAALLDGLSLLPPRRITHHGRRLNGFDID AAIARHPAIILMDELAFSNPHGSRHPKRWQDVEELLDAGIDVLTTINVQHIESLNDIV GSITGIRVRETVPDHIFDAADEVVLVDLPPDDLRQRLKEGKVYIPGQAERAIEHFFR KGNLIALRELALRRTADRVDDQMREFRDGKGQAPVWHTRDGLLLCIGHNTGNEK LVRTAARLAAKFGSVWHAVYVETPSLHQLPETQRRAILKALRLAQDLGAETATLSD PSEEKAILRYAREHNLGKILIGRRNKVNKWFKLNLRPGFADRLGKLGPDLDLVIVAL EEKSEWDKEPERKPFSEKWRSDMNGYLMAIVMCAAITLFSRTFLLALDKANLVTL YLLGVVLIALFYGRRPSVFAALVNVISFDLFFVQPHFSLAIMDMQYLVTFTVMLIVGV VVGNLTAGMRYQARIARYREQRTRHLYEMTKELGQAITTDDIGRTGYHFLNNAFQ AKSCLLLPDENDQLSPLKCEGHSEMLIDKAIAKWCFDKRQPAGAGTDTLPSVPYQ LQPITTADQTLAVLAIEPRNMRQLLIPEQQRMLQTFTGLIASALARLQLTKQAESAK LDIEREQLRNSLLAALSHDLKTPLTVLFGQTEILMLNLSAEKSPLTEQVNQMRQQV LSTSRLVNNLLDMARLQSGSIQPNLAWESLQEITSSAVRTLDYTLHSHPLEIDIPAD LLLYCDANLIERVLINLLENAVKYSHDDTPIGIRATVEGQKIHIEIWDASNAIPNGQEK TIFDKFSRAQKESAIPGVGLGLAICRAIIQLHEGEIWAQNNNKGGASFHFVLPLKQL PDIEVET	1~~KdpD (1.32117E-108) ~~190,213~~Usp (1.15841E-36) ~~337,364~~DUF4118 (1.6219E-20) ~~463,489~~GAF (3.75348E-16) ~~607,624~~HisKA (0.000000000293357) ~~689,741~~HATPase_c (1.57077E-23) ~~842	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	3.2E-81	281.2	0	5.5E-81	280.4	0	1.4	1	A0A089N5N8_9BACL	Histidine kinase (EC 2.7.13.3)	PSTEL_14205	Paenibacillus stellifer	888	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus stellifer	169760	>tr|A0A089N5N8|A0A089N5N8_9BACL Histidine kinase OS=Paenibacillus stellifer GN=PSTEL_14205 PE=4 SV=1 MRLDDQPAAAKGRGKLSIFIGYAPGVGKTSAMLSAAQEEHKDGIDVVAGFVDAHS RPDTTALVEGLEQLTPRILSGQGSPVHEFDLDRALSRGPEILLLDDLAHSNAAGCR HKKRYLDVEELLRAGIDVYTTLNVQQIESLADIVAAITGFPVQERIPDSVFDSADQV KLVDIEPDDLIDRLNKGKIYPDIEAQRAAEVLFTREKLTALREIALRSTASQLNRIAIQI SEQASRNEYDTKDHILVCLSSAESNKKVIRTAARMAEAFHGRFTALFVETPETMAL SAKNKEELRSNLRLAEQLGAQIATVYGEDIPAQIAEYVKTSQVSKIVLGRSPNKKR GFAKASVVDKLTALVPGVETYIIPYQQPAGSGKLSRHSKPLRLSPADLGKTAVIIAG CTLIGLDFQYLEVKEANIITVYILGVLLNAMITKGRLYSVVSSLLSVLVFNYFFTKPYY SLRVYDSGYPVTFLVMLAASFLTSTLTMRVRDQARQSAQKAYRTEVLLETSRNLQ QAQDFQAIVGETARQMVKLLDRTVIFYTASDVGLSKPMIYLKNDLSSLPDIYIDENE RAVADWVYTNNKRAGATTDTFFGARCLYHAVRGGETVFAVAGVVMEQEEPLDV FEKSLLIAMLGECALALEKDRLNEKQQEISMQIRQEQLRANLLRGISHDLRTPLTSIT GNAGILIGNSGVLSDEQKTSLYTDIYDDSMWLINLVENLLSISRIENDSIHLNLQAEL VDEVISEALLHLNRNREKHIIETDVEDELLMARMDPRLIIQVLINLVDNAITYTQVGSR IRISARREGRWVNIEVADDGPGITDDTKTRLFEMFYTANNIRGDGRRGLGLGLSLC KSIVNAHGGTINVRDQVPRGAVFYFTLQAAEVNVYE	11~~KdpD (3.71086E-98) ~~221,242~~Usp (6.65956E-35) ~~364,388~~DUF4118 (0.00000159068) ~~489,X,657~~HisKA (0.00000000472978) ~~723,776~~HATPase_c (2.99476E-20) ~~879	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	6.9E-81	280.1	0.1	1.5E-80	279	0.1	1.6	1	C9A6Y8_ENTCA	Sensor histidine kinase	ECBG_00518	Enterococcus casseliflavus EC20	866	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus casseliflavus (Enterococcus flavescens), Enterococcus casseliflavus EC20	565655	>tr|C9A6Y8|C9A6Y8_ENTCA Sensor histidine kinase OS=Enterococcus casseliflavus EC20 GN=ECBG_00518 PE=4 SV=1 MSENNQQTIPEEMLLQAGFGPKRGKLRVFFGFAAGVGKTYTMLTEAHECLLMGK NVVIGYIEPHKRPDTNRLLEGLPQVPLKQYQHKQLTLYEPDIDRLIQLKPDIVLIDEL AHTNPIGARNKKRYQDVDELLNAGITVYTTINVQHIESLNDIVEKVTEVEVRETVPD TFFQHASLRVVDVEPDELIDRLEQGKIYADENAKRALKNFFTPEKLDHLRGLAIQKA SNHINQMNGGRKRVQSKLLTIIDDRLPKMAEKCIRWTARLAQGVGAEWTVIQVRS LDDTPTEVPLAERLGAEVINIEADDSFETIVEYAKMTGASDIIMGKQVSQKWFQKLF VEDLEDRLIRRLDDIEIHLIPFKEKMQRPRLTFSQLFEGGGRDFTLTFGLIMLATLVT EGMQYLHFGEQNLMLVYIFFVLLVARYTSGYLWSAMASIISVLSYNWFFVEPLYSL TVYKAGYPITLVIMLIVALMISNLMVRLKTQAENAKEKEHQMEILYELNKQYMETRN EQEIYESTTTYLARLLQREVALYDREGHLRSLHSSRETLSQLTGKDEKAVAFWVV KNQKEAGRGTDTLIGANGFYLPIVLNGKPLGALGVERNEEHQLANSQLNYLRLVIT QIATVLEQVSLASEKEQIQLENEREKVRSNLLRAVSHDLRTPLTTISGIAETLSETEG VIKKETKQKLLGDIQSESQWLIRMVENLLSVTRINLTNMAVKRSEEPIEEIIEAVLTH LKKVYPQQKIIVKMPDQLIFVQVDPILIEQALFNLIENGVRHGTADTPIFLRVSQEQE VVIEIENQGEIPLGQYQKIQANLTNDTEVPVDSKNGLGIGLSIVKTIIHAHEGKLAIET KSGSTIFRIYLKQ	21~~KdpD (7.75715E-108) ~~230,243~~Usp (3.56898E-26) ~~359,385~~DUF4118 (4.26578E-15) ~~483,509~~GAF (0.00000000350628) ~~627,645~~HisKA (0.0000000000243371) ~~711,764~~HATPase_c (0.000000000000756934) ~~864	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.8E-80	278.7	0.6	1.8E-80	278.7	0.4	2.2	1	E8SI99_STAPH	Histidine kinase (EC 2.7.13.3)	SPSINT_0108	Staphylococcus pseudintermedius (strain HKU10-03)	874	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus pseudintermedius, Staphylococcus pseudintermedius (strain HKU10-03)	937773	>tr|E8SI99|E8SI99_STAPH Histidine kinase OS=Staphylococcus pseudintermedius (strain HKU10-03) GN=SPSINT_0108 PE=4 SV=1 MERHLTIKRGALTIYLGYSPGVGKTYEMLSNAIDAYHEGADIKIGYIEPHQRKETQA LAEQLPVIQTKSKNHGSHTFHYLDVDQIIEDDPDVVLIDELAHTNISKERHEKRYMDI EEILSHGIDVHTTLNIQHIESLSEQVALLTGVKIKERVPDQFIMSSDAIEVIDISPKQLI NRLKAGKVYKKERLDTAFSHFFTYENLTELRELTLRTAADMMSQKEHLYKKNTDIT PHVAVAISGSISNETVIREARRIANREHAQFTAVYIDVFDHEGKQYANNSQVHQNL MLAQSLGASVKVIYDNQIASGLDDWCKSQKVTKLVIGQHMNDKWHTRLKRPLIDQ LLDLKHHYKIEIVPIKHIQMKAKPERQHQHMQQKRWTVDIFKMIAIQAICVLLGLWIY STGKGEQDTIILLLFLLGIVVLSMWTQSYLIGFFAAILNVLVFNFFFTVPRFTFEVYR FDYPITFTISIIVSIVTSGLLKQIKHQYIVTKHQLYRTDILLQFNDSIKQTYTIPDLLVNA RHQIQHLLKQEVTIYLVEDEKISKTIPVEGPQTNDSRHQQALSWIIKNQKRAGATTD TFPGIHYLLIPIGTKPVKAIVSIHFSEAQIIDSYDNSILESMLNEMSLAVENLSLLRQTR ESMLRAEREVARAHFLRSISHDIRTPLTSIIGNLDVLLLNGKEMPRAEQQQLVSRSF DEAQYLHMLVSNILSLTRLEHSNMKLNRQLYLIEELVEEIESVLERRRLNKQVKVSA LHEICFVDIDSQLILQAVFNLIENALKHTPPETPITLRINKNEPHILFEVIDRGPGLSDE EQQTIFQPFEKHQLFKDNKKDSMGLGLYLVQAILQKHDSQLKYRQNEPHGSIFYF NLPFEKNTN	8~~KdpD (5.14653E-107) ~~215,233~~Usp (4.46822E-32) ~~356,432~~DUF4118 (0.00000672646) ~~476,X,645~~HisKA (0.000000000102214) ~~711,764~~HATPase_c (6.87918E-23) ~~867	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.9E-80	278.6	3.1	2.6E-80	278.2	2.2	1.2	1	A0A077EBR1_9FLAO	Osmosensitive K+ channel histidine kinase KdpD	BD94_1137	Elizabethkingia anophelis NUHP1	345	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Elizabethkingia, Elizabethkingia anophelis, Elizabethkingia anophelis NUHP1	1338011	>tr|A0A077EBR1|A0A077EBR1_9FLAO Osmosensitive K+ channel histidine kinase KdpD OS=Elizabethkingia anophelis NUHP1 GN=BD94_1137 PE=4 SV=1 MSAGVGKTFRMLQEAHTLLRNGIDVKAGFIETHGREETDALAIGIPTIERRSIFYKG KYLEEMDLQAIINDHPEIVLVDELAHTNVEGSKNKKRWQDVLEILENGINVISAMNI QHIESLNEDVKNITGIEVSERVPDKVLALADEVVNIDLTADELLTRLKEGKIYKKEKIE TALANFFQSNHILQLRELALKEVATHVEKKVEAEIKTENFKPVKFLACISSNEKVAK TIIRKTARLASYYSSPWTVLYIQKPSESPEKIALDKQRYLINNFNLAQELGAKVVRM KESSVHQGILEYVNQHNITTVCIGKPRHKLWQRISGYSWIYTLMNRLNEKHIDIIILS	1~~KdpD (1.36614E-110) ~~200,217~~Usp (5.5713E-31) ~~345	non-kinase	KdpD;Usp

	7.2E-80	276.7	0.5	1.2E-79	276	0.3	1.4	1	Q5NEA7_FRATT	Two component sensor protein kdpD (EC 2.7.3.-) (Universal stress family protein)	kdpD FTT_1736c BZ14_978	Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4)	893	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Francisellaceae, Francisella, Francisella tularensis, Francisella tularensis subsp. tularensis, Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4)	177416	>tr|Q5NEA7|Q5NEA7_FRATT Two component sensor protein kdpD OS=Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4) GN=kdpD PE=4 SV=1 MDNQQKVDALLNLANKSQESKKGKLKIFLGYAPGVGKSYAMLNNARALQKDNKD VVVGLLVSHGRADTQALLEGLEIMPLKKVNYRGRVFEELDIDAIKARKPDVVIVDEL PHSNLPTSRNKKRYIDIEELLDEGISVYTAINIQHIASLSYEVTQLTQANVNEIVPNDF IQSVDELVVVDVSPEELIKRLKQGKVYKSDAIDRALERYFQYANLTILRDYTFRMAA NHVGQDIQQYRKLYQHGSAIPTSPYVLVCCGYDEATPSLLRKGKLLATTLNARLIA VFVQKPNKVATKLNFGVIRRYKMLASSLGYNIDHILGDRLSDSILEYAKSIGATDLVI GKSIRPKWKDKLFGSVVYDIIRNNNNGMQVHIVSINKKEHKLQKQPRHSKIKTKGLI IDVIKSALIAAVSGVFIFFSLSIAGLVSQTLCFLMVLAACAYRYGLIPSIISSLVGLFLYI YLYLEPNFVFHISSLAGIITFAFFMTIVIFSSHVILRTKRAFTLLKERENNISVLYRFTKI FNEKSLDKDLRSVFLHALEEYFKCDFVFLSVSDGELDSAAFPQHPNFNQKELAAA KWSFKYKDSCGKGTNTFAGLDWAVEPLVIENRVLGVIAIYLSSETAVERITTDSVIL SSMLSHISHILLKRNLEKEEKKSLLLDEQRRLQKSMLSSVSHDLKTPLASIMGALSSI KSYKDSFNPEQQVEMLDLALTESKRLDSYIDNIIQMLKVDSGKLSLNIQNVNSNFFL TEIQETCARVYNKQKFRFIMPKEPFEIELDPVLFQQVILNLIDNAVKFTCDFEKEIIIS LKRKKAAFCLFEVQDKGIGLRESDMEKIFTIFHRIEKRDSYTHGNGLGLAICKGIVTA HNGKIRVYSDGEGKGSVFKITLPLKSSTN	20~~KdpD (1.2372E-100) ~~230,253~~Usp (1.90374E-19) ~~375,405~~DUF4118 (0.0000013599) ~~500,X,663~~HisKA (0.000000000103314) ~~728,781~~HATPase_c (2.3859E-25) ~~886	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	3.4E-79	274.5	2.2	6.6E-79	273.6	1.5	1.5	1	M1MSZ4_9CLOT	Histidine kinase (EC 2.7.13.3)	kdpD Cspa_c09110	Clostridium saccharoperbutylacetonicum N1-4(HMT)	857	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium saccharoperbutylacetonicum, Clostridium saccharoperbutylacetonicum N1-4, Clostridium saccharoperbutylacetonicum N1-4(HMT)	931276	>tr|M1MSZ4|M1MSZ4_9CLOT Histidine kinase OS=Clostridium saccharoperbutylacetonicum N1-4(HMT) GN=kdpD PE=4 SV=1 MLMEAHDMKKMGKDIVIGYIEPHARPETMALVNGIEDIGVKVIEYKGITLKEFDLDK AIARKPQIILVDELAHTNASTERHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDIVE SITHIAVRETIPDKVFDEADKVELIDIEPTELLNRFSEGKVYSKEQTRKAFDNFFTKN NLFALREIALRRTADRVNYEVESVRLAKGQVTVIPTSDVVLACISSSPSSLRVIRTAT RMAEAHHSKWIALYVETTKSQNLSKEDRERLNSHFNLAEQLGGEVVTAYGDNTV EQIIQYAKFRNATKIIIGKNHKKPNNLFHFYAKDIVDKLMESNSYIDVYVVPNSSSDK QKKFNIKKNRQKFNISSREILISIFIMIITTIISLFIDYFGFSDANVIMLFILGVIIVNIKTRG YILGFICSIISIFLFNYLFTEPRYSLEVYDKSNLATFPIMLIVTFIIGTLTNKIQREAINSS QRENRTRNLYRVSKKLLSATGTVDVVGIGIKYLSRLLEKTVICYLVQDNKLSTPFIYT ATRGEKDRTLLNKDEEAVAHWTFLNDKESGAGTNTFHGAKAYYMPLKSHGKILG VLGVSCVNGSLEPEQKYVFETVASQIYIALDREILAETQKKSSLEIESERLRSNLLRS ISHDLRSPLAGIKGSVSTIIETGEFLSEKTKGELLQSVYEDTEWLIRLVENLLSMTRL DGGGLKIKKEMEIVEEVVYEAVQRTSKHFKEHKIKVMVPDEVIMVPMDGSLIEQVL LNLLDNAIKFTPKDSLIEIKVYEENNNIMFEVIDNGPGIAEDILPHIFDIFFTDGYKISD SRRGVGLGLAICKSIVEAHGGEICAYNENGAVFKFNIPKEEEKL	1~~KdpD (2.33087E-110) ~~190,213~~Usp (4.47989E-42) ~~337,378~~DUF4118 (0.00000000000639622) ~~464,493~~GAF (0.000000780412) ~~613,630~~HisKA (0.000000000137537) ~~696,749~~HATPase_c (1.56358E-27) ~~850	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1E-78	273	0.1	1.4E-78	272.6	0	1.2	1	H8GX33_DEIGI	Potassium-transporting ATPase, D subunit	kdpD DGo_CA0646	Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	339	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus gobiensis, Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	745776	>tr|H8GX33|H8GX33_DEIGI Potassium-transporting ATPase, D subunit OS=Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0) GN=kdpD PE=4 SV=1 MGMAAGVGKTTRALNELRERLERGEDALIGVLETHGRRGTVQAAEGLPVFPRRV LAHGGVTLGELDVDGLIARRPGVVLVDELAHTNAPGSPREKRWQDVETLLDAGID VLSTVNVQHLESLNDTVARLTGVRVRERLPDAVLHGADELVFVDLPPDDLRARLR AGHIYGPEKIEQSLTNFFTVANLTALREIALRQVANAVEMDAPEGQPGVQERVVVA IAAEETGSRLIRRGGQLAERLHGELHVVTIRPARLSAEQSRMLGTFRAITAALGGQ FHVLDAQGSVAPVLVRFVQEIHATQVVMGETSRSRLTEFLRGDIIKTVLRETRNVD VYVISRD	2~~KdpD (1.21385E-107) ~~202,216~~Usp (4.09603E-28) ~~337	non-kinase	KdpD;Usp
	1.2E-78	272.8	0	2.4E-78	271.7	0	1.5	1	Q5HK61_STAEQ	Sensor histidine kinase KdpD (EC 2.7.3.-)	kdpD SERP2489	Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	889	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus epidermidis, Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	176279	>tr|Q5HK61|Q5HK61_STAEQ Sensor histidine kinase KdpD OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) GN=kdpD PE=4 SV=1 MESTYKKRGKLTIYLGYSPGVGKTYEMLSNGIDQYQEGADIKIGYIEPHQRPETNA LVQQLPEISTSSRKFGSHTFHYIDVSKIIEANPDVVLIDELAHTNISKERHLKRYKDIE EILSHGIDVWTTLNIQHIESLSGQIALMTGIQVTERVPDQFITSADAFEVVDISPNMLI QRLKAGKVYKKERLETAFSNFFTYENLTELRELTLRTVADIMSQKGQQYKTKHTDI TPHIAVAISGSIYNERVIREARRAAYKEHAKFTAVYIDVFETPSESRKQDHYVHKNL MLAKALGAEIKVLYAQDIAKALTDWCDLAFVTKLVLGQSEQPRWKDYFKQSLIEQI NHVPHHFKLEIVPIHYIHSDKPTNTPKQAQKSSRLTVEIMKMLVIQTICVLLGIWVYN LDKSESSAIILLMFFIGIIVLSIWTQSYLIGFFASILNVFVFNYFFTVPRFTLEMYRFEY PITFATSIFASIFTSAILKNLKHQHSLTERQLYRTNIMLQFNQSIKESYSIERLLNIAGD QIHQLLNQDVTVFLIQSKKVAASNSFGNRSISSSDKTHDAETLSWVIENESRAGKL TDTFPGSKFLCIPIGTNPVKGVISIRFTDETYIDTYDNSILDSMLNDITLAIENVDLLKQ TRQSILKAEREATRSNFLHSISHDIRTPLTSIMGNLDMLKYHNEHLNDQQQAELLTA SYGEAQYLHTLVTNILSLTKLESSDIQIQRTPYLVEELLEEFEEGLIRRHQANHVIIEN EDDASLINIDSKLILQVLFNLIDNALKHAESHSEIKLHVQHETNKIKFEMIDCGKGIPE EERQLIFNPYYSGDNFKDNKKDSLGLGLYLVQLILKQHNSELEYQPNTPQGSIFYF YLTVNPIEMEGAMDENNIIGR	6~~KdpD (8.28875E-104) ~~214,233~~Usp (9.52772E-41) ~~356,382~~DUF4118 (0.00000874199) ~~485,511~~GAF (0.0000818887) ~~631,648~~HisKA (0.00000000000159193) ~~714,767~~HATPase_c (1.77889E-22) ~~870	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	1.2E-78	272.7	0	2.4E-78	271.7	0	1.5	1	Q4LAI4_STAHJ	Staphylococcus haemolyticus JCSC1435 DNA, complete genome	SH0032	Staphylococcus haemolyticus (strain JCSC1435)	889	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus haemolyticus, Staphylococcus haemolyticus (strain JCSC1435)	279808	>tr|Q4LAI4|Q4LAI4_STAHJ Staphylococcus haemolyticus JCSC1435 DNA, complete genome OS=Staphylococcus haemolyticus (strain JCSC1435) GN=SH0032 PE=4 SV=1 MESTYKKRGKLTIYLGYSPGVGKTYEMLSNGIDQYQEGADIKIGYIEPHQRPETNA LVQQLPEISTSSRKFGSHTFHYIDVSKIIEANPDVVLIDELAHTNISKERHLKRYKDIE EILSHGIDVWTTLNIQHIESLSGQIALMTGIQVTERVPDQFITSADAFEVVDISPNMLI QRLKAGKVYKKERLETAFSNFFTYENLTELRELTLRTVADIMSQKGQQYKTKHTDI TPHIAVAISGSIYNERVIREARRAAYKEHAKFTAVYIDVFETPSESRKQDHYVHKNL MLAKALGAEIKVLYAQDIAKALTDWCNLAFVTKLVLGQSEQPRWKDYFKQSLIEQI NHVPHHFKLEIVPIHYIHSDKPTNTPKQAQKSSRLTVEIMKMLVIQTICVLLGIWVYN LDKSESSAIILLMFFIGIIVLSIWTQSYLIGFFASILNVFVFNYFFTVPRFTLEMYRFEY PITFATSIFASIFTSAILKNLKHQHSLTERQLYRTNIMLQFNQSIKESYSIERLLNIAGE QIHQLLNQDVTVFLIQSKKVAASNSFGNRSISSSDKTHDAETLSWVIENESRAGKL TDTFPGSKFLCIPIGTNPVKGVISIRFTDETYIDTYDNSILDSMLNDITLAIENVDLLKQ TRQSILKAEREATRSNFLHSISHDIRTPLTSIMGNLDMLKYHNEHLNDQQQAELLTA SYGEAQYLHTLVTNILSLTKLESSDIQIQRTPYLVEELLEEFEEGLIRRHQANHVIIEN EDDASLINIDSKLILQVLFNLIDNALKHAESHSEIKLHVQHETNKIKFEMIDCGKGIPE EERQLIFNLYYSGDNFKDNKKDSLGLGLYLVQLILKQHNSELEYQPNTPQGSIFYF YLTVNPIEMEGAMDENNIIGR	6~~KdpD (9.50084E-104) ~~214,233~~Usp (1.00072E-40) ~~356,382~~DUF4118 (0.00000964424) ~~485,511~~GAF (0.0000696545) ~~631,648~~HisKA (0.00000000000183784) ~~714,767~~HATPase_c (1.26104E-21) ~~870	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	1.5E-78	272.5	0.2	2.2E-78	271.9	0.1	1.3	1	A0A0F7JPZ3_9DEIO	Histidine kinase	SY84_13275	'Deinococcus soli' Cha et al. 2014	360	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, 'Deinococcus soli' Cha et al. 2014	1309411	>tr|A0A0F7JPZ3|A0A0F7JPZ3_9DEIO Histidine kinase OS='Deinococcus soli' Cha et al. 2014 GN=SY84_13275 PE=4 SV=1 MPGAPRPARGRHRVFVGMAAGVGKTTRALNELRDRLERGEDALIGVLETHGRAF TQAAAAGLPVFPRLEVVRGGVTLGELDVAGLIARRPDVVLVDELAHSNAPGSARE KRWMDVEALLDAGVNVLSTVNVQHLESLHDTVARLTGVRVRERIPDAVLGGADEL VLVDLTPADLRERVRSGAVYGAERAEHALTNFFTLPNLTALRELALRQVAHVVEQ GAADLGAGQGTGLGVQERVVVAVAAEETGARLIRRGGQLAQRLHADLQVVTVRS GRISAERARLLDTFRAVTVALGGEFIVLDPAGGVAATLIRHVQAAQATQVVLGESS RSRWEEVLRGDIIRSVLRQTRNVDVYVITRE	7~~KdpD (1.15587E-103) ~~214,237~~Usp (9.49576E-27) ~~358	non-kinase	KdpD;Usp

	3E-77	268.2	0	5.7E-77	267.3	0	1.5	1	A0A089KU75_9BACL	Histidine kinase (EC 2.7.13.3)	R70331_15305	Paenibacillus sp. FSL R7-0331	893	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. FSL R7-0331	1536773	>tr|A0A089KU75|A0A089KU75_9BACL Histidine kinase OS=Paenibacillus sp. FSL R7-0331 GN=R70331_15305 PE=4 SV=1 MAQHSIQTKKRGRLKIFFGYAEGVGKTSAMLNAAHDELRDGTDVVAGFIESHGRP ETGVLLNGLEQLPVLELRSNPSSRQELEFNLDQALRRRPELILVDELAHYNAAGCR HKKRYQDIEELLRAGINVYTTINVQHIESLHDVVTAITGITVHERIPDSVFDGADQIEL VDLPPDDLLERLNKGKLASEGLAEPGGPAAYLPVFVRTKLIALREIALRYTADQQE RITRESGSRSGKDTYSTADHILVCLSSAASSKKVIRTAARMAEAFRGSFTALYVET PKSKELTAKSKAELRDNLRLAEQLGAQPATVYGDDVAGQIAEYAVSSRVTKIVIGR SRSGKKRWIAKGNLIDKLTELAPNIDIHIIPDNQPARHKRPFLFVRPQRFSLPDTLKT LGILAVCTLIGLWFQYLGFREANMIIVYILGVLLNAIVTSGRLYSAANSVLSVLVFNYL FTEPYYSLWAADSGYPVTFLVMLTASFISSTLTTRIKEQARQNAQKAYRTEVLLET SRILQQAEDAEAIINETAVQMVKLVDRTVIFYPAGQEGLADPLVYPKPEADLDPSKY TGMNEWAVADWVYKNNKRAGATTDTFSAASCLYHAVRAGETVFAVAAVVMDQE EPLGIFEKSLLIAMLGECALALEKEQLSNTQKEISIQIRQEQLRANLLRGISHDLRTPL TSISGNAGILMANSNVLSDAQLRGLYTDIYDDSMWLINLVENLLSITRIDNGSLNLNF QAELLDEVIAEALLHVNRSSVEHNIQVKLEDELLMARMDSRLIIQVLINLVDNAIKYT QTRSTITITAGQEQQTVRVSVADDGPGISEEAKAKLFEMFYTADNLRGDGRRGLG LGLSLCKSIVHAHGGTIEVMDNNPQGAVFTFTLQAEEVNVLE	9~~KdpD (1.94657E-96) ~~224,246~~Usp (2.57694E-42) ~~369,394~~DUF4118 (0.0000000000203887) ~~494,X,662~~HisKA (0.000000000648977) ~~728,781~~HATPase_c (2.54355E-20) ~~884	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.9E-76	265.5	2.7	3.6E-76	264.7	1.9	1.5	1	A6LV16_CLOB8	Histidine kinase (EC 2.7.13.3)	Cbei_2027	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) (Clostridium acetobutylicum)	861	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium beijerinckii (Clostridium MP), Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) (Clostridium acetobutylicum)	290402	>tr|A6LV16|A6LV16_CLOB8 Histidine kinase OS=Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) GN=Cbei_2027 PE=4 SV=1 MLMEAHDMKKLGHDIVIGYIEPYARQETMALVNGLENLDNKIVEYKGINLKEFDLDK ALIRKPEIILVDELAHTNVITQRHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDIVESI THISVRETIPDKIFDEANKVELIDIEPDELLKRFSDGKVYSKGQARNDVNNFFTKNN LYALREIALRRTADRVNYEVESVRLSKGQITVMPTSDAILACISPSPSSSRVIRTATR MAEAHHSKWIAFYVETTKSQNLSKEDRKRLSEHFNLAEQLGGEVITVYSDNIVEQII EYAKFRNVTKIIVGKNRKKPNVFFRFYARDIVDKIMESNSYIDVYVIPNSTAIKRNEN HIKKNKTKFIISFKEILISSLIMLISALATLFIDKLGYGEANVIMIFILGVIIVNIKTRGYILG FICSTISVILFNYLFTKPRYSLQFYDKSYLVTFPIMLIVAFTIGTLTNKIRREAENSLAR ENTTQILYRVSRKLLSATGTSDVIGIGIKYLSRLLERTVICYLAQENKLSTPFIYTVIK GGKDRSLLNKDEEAAAYWTFVNDKESGAGTNTFYGAKGYYIPLKSHGKILGVLGI SCINGTLKPKQKFIFETVASQIYIALDREILAETQKKSNLEIESERLRSNLLRSISHDL RSPLAGIKGAVSTIIETGNLISEETKGELLQGIYDDTEWLIRLVENLLSMTRFDGGNL KVRKSIEIVEEVVYEAVQRTAKRFRDYKMEVTVPEEVIMVPMDGSLIEQVLINLFDN AVKFTPKGSLIEVKIYENNKNVIFEVIDNGMGISEEILPHIFERFFTNGDKISDSRRG VGLGLAICKSIVEAHGGTISAHNKDEGGAVFRFNIPKEEMSDGQ	1~~KdpD (1.04655E-102) ~~190,213~~Usp (3.40546E-44) ~~337,363~~DUF4118 (0.00000000000183672) ~~464,491~~GAF (0.00946855) ~~613,630~~HisKA (0.0000000000371005) ~~696,749~~HATPase_c (4.45353E-29) ~~852	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	6.7E-76	263.8	0.2	1.5E-75	262.6	0.2	1.6	1	Q2FWH7_STAA8	Histidine kinase (EC 2.7.13.3)	SAOUHSC_02314	Staphylococcus aureus (strain NCTC 8325)	885	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus aureus, Staphylococcus aureus subsp. aureus, Staphylococcus aureus (strain NCTC 8325)	93061	>tr|Q2FWH7|Q2FWH7_STAA8 Histidine kinase OS=Staphylococcus aureus (strain NCTC 8325) GN=SAOUHSC_02314 PE=4 SV=1 MSNTESLNIGKKRGSLTIYIGYSPGVGKTFEMLSNAIELFQSNVDIKIGYIEPHQRDE TNALAEQLPKITTNFTKHGSHHFQYLDVDRIIEESPTIVLIDELAHTNISRDRHEKRY MDIEEILNHGIDVHTTLNIQHIESLSSQIELMTGVHVKERVPDYFIMSADVLEVVDIS PEQLIKRLKAGKVYKKDRLDVAFSNFFTYAHLSELRTLTLRTVADLMSDKEKVRHN HKTSLKPHIAVAISGSIYNEAVIKEAFHIAQKEHAKFTAIYIDVFEKNRQYKDSQKQV HQHLMLAKSLGAKVKVVYSQTVALGLDEWCKNQDVTKLIIGQHIRNKWRDFFNTP LIDHLMSFEHSYKIEIVPIKQIPVELKMNKSPYRPKGKRFAIDMLKMILIQIICVMMGL WIYQLDKHESSTIILMIFLIGIILLSIWTRSFIIGFLAAIINVFVFNYFFTEPRYTFEVYRF DYPITFIVSILTSILTSALLKQIKFQYSITKKQLYRTDLLFQFNDSIKQTYTVENLLINA GYQINQLLQQSITIYVINQSKVIKTIPLQNHIDNTTQQHEQALSWVIKNERQAGATT DTFPGINKWLIPIGTSPIKGILAIDYQSSQVINPYDASILESMLNELSLAVENVTLLKQ TRESMLQAERQLTHSNFLRSISHDIRTPLTTIMGNLDILVSHSKDMSIIEKEQLLVHS FQESQYLYLLVTNILSLTKLQSSNVQIKLQPYLVSELVEEIDMILERRHLKKRITVSSS VNLQFIHIDSKLILQALFNLIENAVKHTSTDTKINLSIRYASYEQIEFAVIDEGPGISLE EQQKIFEPFYTGSNKYFKDNQKESMGLGLYLVQTILHKHQSNLQYKPNQPHGSIF YFNIYTDFNEGDV	11~~KdpD (6.57295E-117) ~~221,238~~Usp (9.03504E-37) ~~361,387~~DUF4118 (0.00000000171542) ~~483,X,655~~HisKA (0.000000102517) ~~717,770~~HATPase_c (6.12635E-20) ~~876	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.9E-75	262.3	4.9	2.6E-75	261.9	3.4	1.2	1	A0A077KDX1_9FLAO	Sensor histidine kinase KdpD	kdpDCHSO_1293	Chryseobacterium sp. StRB126	335	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Chryseobacterium, Chryseobacterium sp. StRB126	878220	>tr|A0A077KDX1|A0A077KDX1_9FLAO Sensor histidine kinase KdpD OS=Chryseobacterium sp. StRB126 GN=kdpD PE=4 SV=1 MLQEAHSLLRNGIDVKIGYIETHDREETVALAEGIPEIGRKSVFYKGKNLEEMDLQA IINEHPEVVLVDELAHTNVEGSKNKKRWQDVLEILDNGINVISAMNIQHIESLNEEVK KITGVEVAERVPDKILALADEVVNIDLTADELLTRLKEGKIYKKDKIQTALSNFFQSG HILQLRELALKEVATHVERKVETEIKTENFKPIKFLACISSNEKIAKTIIRKTARLASYY NSPWTVLYIQKPSETPEKIALDKQRYLINNFNLAQELGAKVVRIKENSVHNGILEYVI AHNITTVCIGKPHAKLWQRLSGYSWIYTLMNGLNERQVDIIILS	1~~KdpD (9.39232E-105) ~~190,207~~Usp (5.80053E-29) ~~335	non-kinase	KdpD;Usp
	3.1E-75	261.6	0	5.6E-75	260.8	0	1.4	1	R5XDF0_9FIRM	Histidine kinase (EC 2.7.13.3)	BN568_00631	Blautia sp. CAG:257	893	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	1262756	>tr|R5XDF0|R5XDF0_9FIRM Histidine kinase OS=Blautia sp. CAG:257 GN=BN568_00631 PE=4 SV=1 MEKQNQSADILPAASDQMSSTERGHLKIFFGYAAGVGKTYAMLEAAHMEKKHGT DVAVGYIKSNAHPQTRARLNGLKLLPPLYSKHNGTPVEEFDLDKAIKTKPGLILIDEL AHTNADGCRHHKRYLDIYELLKAGIDVYTTANVENIESLNDMVTAITGNRILERIPDS VFDNADQVKLVDIEPQELLERLAAEKDSDSSETDSFTFTLETLTALRELALRRCAD RVNKRTESARIRNKSDYYTDEHILVCLSSSPSNAKIIRTAARMANAFRGAFTALFVE TSQFSAMTEEDRQRLRSNIYLAQQLGATIETVYGDDVPLQIAEFAKLSGVSKIVIGR STVTGKRLFGRPSLTEQLIANVPNMDVHIIPDQSPNRTPPVHNQKNHIIFSASDILK SIFILSAASCLGYLFQQLGFDEANIITVYVLAVLVTSIVTVNRVYSLITSIVSVLVFNFL FTDPKFTLMAYDRGYLVTFVVMFISAFLTGTLTTRMKTIASQSARAAFRTKILFDTS QILQQATDRDAILTSTAHQLTKLLNRDIVIYPAEKNTLAAPMTFSAGEEDTASDYLT RNESAVAEWVFKNNRHAGATTQTLSNAKCLYLAIRVNDSVYGVVGIAAGKQPLDA SENNILLSILGECALAMENEKNAHEKEEAAILAKNEQLRANLLRTISHDLRTPLTSIS GNASNLLSNSSSFDENTKRTLYQDIYDDSMWLINLVENLLSVTRLEEGRLNLRISA ELADEVVTEALRHVNRLSVEHHITVNHQDDLLLAKMDAKLIVQVIINLVDNAIKYTPQ GSEIQISTFREENWAVISVADNGPGIPDENKKQIFDMFYTGSNRVADSRRSLGLGL SLCKSIINAHGGSISVSDNVPHGTVFTFTLPAEEVQLHE	22~~KdpD (5.81954E-88) ~~228,248~~Usp (1.63279E-38) ~~371,395~~DUF4118 (1.37566E-14) ~~494,522~~GAF (0.00000145709) ~~645,662~~HisKA (0.000000952866) ~~728,781~~HATPase_c (1.45643E-31) ~~884	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	9.1E-75	260.1	0	1.8E-74	259.1	0	1.5	1	A0A0F5MVL6_9MYCO	Histidine kinase	WR43_16120	Mycobacterium arupense	835	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium terrae complex, Mycobacterium arupense	342002	>tr|A0A0F5MVL6|A0A0F5MVL6_9MYCO Histidine kinase OS=Mycobacterium arupense GN=WR43_16120 PE=4 SV=1 MSVVTQHGQRGELRIYLGAAPGVGKTCAMLSEAHRCAGRGTDVVAAAVDTHGR SQTAELLAGIETLGGPGDPLDVAAVVARRPEVALIDDLAATNPSASGNTHRWQDIE ELLAAGITVISTVNVQQLESLSDVVAKIIGTTQHDTVPDAVVRQAAQIELIDIDPEALR RRLSHGHIYPPETVDAALANYFRSETLTALRELALLWLAGHVDATLTRYRADKKIT GTWEARERIVAAVTGGPESEALVRRASRIASKAGGDLLVLHVLGDDGTSRAPAPR VGKIRQLSISLGASLHTVIGDDVPTALLDFARDVNATQLVIGSSRRSRWARILDEGV GAAVVQQSGDIDVHIVTSSDAKPTRRALSISPRERRAVSWLAAVAVPCAMCAIMV GWLNRYFDAGQSALFFVGVLVVALLGGIAPAVLSAVLSGVLLNYFVLAPRRDFAIA EHDIAVTEIVLLLLAVAVAALVDGAAKRTREAGRASREAELMTLFAGSVLRGADLD TLLERVRETYAQRAVSLVRVPHSTATPHVVASVGEDPCTSVDLADTSIDVGDDEF WMLMAGRQLASRDRRVLSVVARQATGLVRQEELAAEADRADAVMRTDELRRSSL LSAVSHDLRTPLAAAKAAVSSLRADDVDFSPGDTAELLATVEESVDQLTALVGNLL DSSRLAAGVVRPALSKVYLEEVVQRALIGIGKRSNTFGSGGVDRVKVEVGPAVAM ADAGLLERVLANVIDNALRYASDSVVRVTAGRVGERVMINVADEGRGLPPGGEVH VFDPFQRLGDRDNTSGVGLGLSVARGFAEAMGGTISATQTPGGGLTMVVDLAAP AGEN	8~~KdpD (4.36664E-83) ~~210,232~~Usp (5.32418E-32) ~~353,376~~DUF4118 (0.000120857) ~~441,X,605~~HisKA (0.00000000000887826) ~~671,728~~HATPase_c (2.24625E-24) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.1E-73	256.5	0.7	3E-73	255.1	0	1.9	1	D7AV88_NOCDD	Histidine kinase (EC 2.7.13.3)	Ndas_0300	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	850	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	446468	>tr|D7AV88|D7AV88_NOCDD Histidine kinase OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_0300 PE=4 SV=1 MDPVARGKLRIYLGSAPGVGTTHNALAEARSRAERGTDVVVAAAHTHRRARTSAL LEGLERIPPLPSGSVDTAAVIARAPGTALVDDLARANPPGSPNATRWQDVEELLEA GVDVLSTVGIHHLESLNDVVHQITGVRPRQTVPDHVVRRAAEVELVDVTPQELRR RMARGDIHPAESVDAALADYYREGNLAALRELALLWTADRVEESLARYRGEHEIR RTWEARERVVVALTGGPEGETLIRRAARVAARSRGGHPQPSHLLAVHVVPPNGM AQAPTDDLLRQRRLLVELGGTYHQVVGNDVPTGLLEFARGVQATQIVLGSSRRRT WQYVFGPGVGAIVARDSGDIDVHIVTHERVGSGRWPLPPPGRGLGEHRRVTGW SLALLAPTLLSLVMALPLFEDVGAASDAMLLLLATVATAAVGGLRPALVSALWSAV LLTVLLSPLHGRPSVSLDNILALTAFALVGALVAIVVEMAARRSAQAARARAEADAV TLLASSVLAGKEPLQALLRRIRETFGQRSATLLERLDDERWRAAHSVGAPACESP EEADVLVSISDNLALALRGRVLPAADRGVLRAFAAHIGIALEHQRLEWDAAEARGQ VAGNRIRTALLAAVSHDLRTPLTSIKASLSSLRATDITLTEEDREDLLETVEESTDRL NRLIDNLLDMSRVHTDNVRPKLRAVGLEEVVPVTLLGLPHEAVVVDVPDRLPRVRA DAGLLERAVANVVSNAVRYNPDPRLPVLVSASAHGDSVQLRVVDRGPGVSDEGK QRMFEAFQRLGDAPQGTGVGLGLAVARGFVEAMHGRLDPEDTPGGGLTMVFTL RAVEKSETDTGDGEGTDACPGR	5~~KdpD (6.7253E-75) ~~207,229~~Usp (8.30735E-22) ~~356,385~~DUF4118 (0.00260834) ~~473,X,611~~HisKA (1.08297E-15) ~~677,726~~HATPase_c (2.53462E-25) ~~828	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	6.2E-73	254.1	0.1	7.2E-73	253.9	0	1	1	R5E231_9FIRM	ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	BN462_00740	Ruminococcus sp. CAG:108	188	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:108	1262950	>tr|R5E231|R5E231_9FIRM ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein OS=Ruminococcus sp. CAG:108 GN=BN462_00740 PE=4 SV=1 MDEIRHSPEHFLKEIEKEKQNLNRGHLKIFFGYAAGVGKTYAMLKAAHSVKRHGID VVAGYIEPHARLQTSALVNGLECLPNLVSEYNGITLSEFNLDAALARHPQLILVDEL AHTNAPVCRHTKRYQDIEELLNAGIDVYTTVNVQHIESLNDTVTSITGIMVHERIPD SVFDNASQVELVDIEPQE	23~~KdpD (5.43995E-97) ~~188	non-kinase	KdpD
	1.6E-71	249.5	3	3.8E-71	248.2	0.1	2.2	1	J7L7K9_NOCAA	Histidine kinase (EC 2.7.13.3)	B005_3174	Nocardiopsis alba (strain ATCC BAA-2165 / BE74)	847	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis alba, Nocardiopsis alba (strain ATCC BAA-2165 / BE74)	1205910	>tr|J7L7K9|J7L7K9_NOCAA Histidine kinase OS=Nocardiopsis alba (strain ATCC BAA-2165 / BE74) GN=B005_3174 PE=4 SV=1 MGDVKGRLRIHLGSAPGVGTTHHALDEARRRVERGADVVVGAVHTHRRVHTSAL LQGLEVVPAHPSGSVDTAAVISRAPELVVVDDLARPNPHGAPNPTRWQDVEELLD AGIDVLSTVGIHHLESLYDVVHQITGVRPEYTVPDRVVHAAAEVELVDVTPQELRR RMAHGDLHPAERVDAALAAYYREGNLAALRELALLWTADRVEEGLSRYRGEHEIR QTWEARERVVVALTGGPEGETLIRRAARVASRSRGGRPQPSDLLAVHVLPPNGI GERPSGDLLRQRRLLAELGGTYHQVVGTDVPSSLLEFARGAHATQIVLGSSRRRA WQYVFGPGVGTIVARESGDIDVHIVTHEEVGGGRWLLPAPGRGLNHHRRIWGW TLSLLAPLLVSLILTLPFFDGVGPASDPLFLLLITVATAAVGGLRPALVSALWSAVLL TVLLSPLHGRPSMSSDNFLAMTVFVLVGSLVAVMVEMAARRSSQAVRGRAEADA VALLAASVLSGNEPLQALLRRIRETFGQRSATLLERLEDDRWHPVHSVGAPACET PEEADALVTVSDTVALALRGRMLPAADRGVLSAFATHVGIAMEHQRLAWDAAEA RGQAAGNRIRTALLAAVSHDLRTPLTSIKASVSSLRATDIALSEEDRSELLETVEES TDRLDRLIGNLLDMSRVQTDSVVPRIRSVGLDEILPSTLLGVPREAVVVDVPEDLPR VRVDVGLLDRAVDNVVANAVRYNPDPGTPVLVSASAHGDNVQLRVVDRGPGVSD EAKQRMFEAFQRLGDAPQGTGVGLGLAVARGFVEAMHGTLDPEDTPGGGLTMV FTLRAVTPEDEEEERRVDAGPGR	5~~KdpD (2.38406E-72) ~~206,228~~Usp (3.19183E-30) ~~355,382~~DUF4118 (0.00011759) ~~481,X,610~~HisKA (2.39568E-15) ~~676,725~~HATPase_c (4.72412E-25) ~~827	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	6E-70	244.3	0.1	1E-69	243.6	0	1.4	1	R6RPX4_9CLOT	Histidine kinase (EC 2.7.13.3)	BN719_02218	Clostridium sp. CAG:58	876	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	1262824	>tr|R6RPX4|R6RPX4_9CLOT Histidine kinase OS=Clostridium sp. CAG:58 GN=BN719_02218 PE=4 SV=1 MTEERQNAGEGGKSGQLKIFFGYAAGVGKTYAMLQAALTAEERGMDVVIGSIAP YRSLEDTALAERLRAMERLEEFDLDQAIRRKPDLILMDDLACENPKGSRHSRRYQ DIRELLKAGISVYTTVSAQNIESLNDIVTAITRVPVKDRIPDSVFDHADQVELVDLEP RELLERLRNGALAEKEGEHSPGTAYFTVANLTALREVALRRCADRINMLTRGDGA AHGDEHVLVCLSASPSNAKIVRTAARMANAFRGAFTALFVKTPDLAYMDEEDRKR LQSHMRLAEQLGARIEILYSDDIPFQIAEFARISGVSKIVIGRSAATRDHIFSKPALTE KLISNAPDLDVYIIPDADPGSSFYRKRHFGTRRHLVFSAGDILKSIGILLAASCIGFFF YNLGVNEANIITIYVLGVLVTALVTKNQIYSLISSAVSVLVFNFLFTEPRYTLQAYAPG YPLTFSVMFLSAFITGSLVMRLKSHAKQSAEVAFRTRILFDTNRLLQQARGQEEITS VSAGQLVKLLKKDIVVYPAENGVLGEPQIFQAGETEPDAGCISARE REVAAWTLK NNKHAGATTDTFSDAGCLYLAIRVGENVYGVLGIVMEGGELDAMENSILLSVLGE WAFALENEKSTREKEEAAVLAKNEQLRANLLRAISHDLRTPLTSISGNASNLLAMG QDFDEETRKQLYTDIYENSMWLINLVENLLSITRLVEGRLNLNITEDLVDDVVAEAL RHVNKKSAEHTIVTESGEEFLLARMDPRLIVQVIINIVNNAIEYTPAGSHITIRSEKKD GTIILSIADDGPGIPDQEKPRVFDMFYSGGNPIADSRRNCGIGLSLCRSIIDAHGGE LTVSDNAPHGAVFTFTLPAGEVQLHE	12~~KdpD (5.33455E-78) ~~213,228~~Usp (3.8871E-38) ~~351,378~~DUF4118 (0.000000000000194506) ~~477,X,645~~HisKA (0.0000000000762938) ~~711,764~~HATPase_c (4.38387E-27) ~~867	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	6.9E-70	244.1	0.3	2.5E-69	242.3	0.2	2	1	K4L432_9FIRM	Histidine kinase (EC 2.7.13.3)	DCF50_p2267	Dehalobacter sp. CF	894	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Dehalobacter, Dehalobacter sp. CF	1131462	>tr|K4L432|K4L432_9FIRM Histidine kinase OS=Dehalobacter sp. CF GN=DCF50_p2267 PE=4 SV=1 MKSQGGGGVQDIRARAAKKTGKLKIFFGYAPGVGKTYAMLDDARSQLKSRVDVV VGYLEPHTGSETIQLLDGLPALPPKTVNHKNRYRKEFDLDAALQRKPELLLVDVLA HNNADGMRNKKRYQDIEELLNAGIDVYTTVNVQHIESLRDLVQDITKVNEQDTIPD YMFDSADKVELIDIEPDELMKRYAEKKCPLSLESLRLLRETAMRKVTDRIVNENQN EQLLSAKTAGIKLLVCISSSPSTAKCIRWTARSAEAFHAPWTALYIEDMESRYFTEE EKKNVQENLDLAELLGAKIVTLNGQGLASIIAEYARLTGITNIVIGKSRNKKTLKTLFD PALEDKLIGLLPNIEIHIIPSSGPRRSYREPRRKRISKDLFLSWPDIWKTIGVLTGATL LSFGLRALEFGNQNIIMVYILSVFFISRLTMGYVYGITASVLSVLVFNFFFVSPLFSF YAIQTGYPVTFVIMLVVALITSTTTVRIQTQARLAAEREGRTELLYEINKRLLTTRGL QHIVTLTNEYIVKLFKCSAVFYTRDQYGSANLHRSSNHHGSSGILTQSSAEPDASF LLSERESKVVQWVFANQKQAGVGTDTHTEAGAYYMPIISQGDVLGVVGISCLKGR LSRNNRLLLKMIISQVAMALERQYLSDEQRQILIESEKEKMRSNLLRAISHDLRTPLT GILGASSAILENGDHLDKETHIQLVSNIKEDSQWLIRMVENLLSVTRIKEGTMNVAK TFEAAEEIVAEAISRTRHRYPDRKITVQVPEDLLLVPMDGKLIEQVLINLLENAVKHS PDDAVTAVRVTKAGAQAVFEVSDNGPGVAEEDFPYLFESYVPCGKRSSDSARGM GIGLSICMSIIKAHNGKMEAANKEQGGAVFRFTLPLEEENIYE	18~~KdpD (9.99358E-88) ~~193,234~~Usp (1.31829E-37) ~~358,388~~DUF4118 (1.08277E-15) ~~486,513~~GAF (0.00000362756) ~~646,663~~HisKA (0.00000000000491767) ~~729,782~~HATPase_c (2.79539E-27) ~~885	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	2.1E-69	242.6	0	3.9E-69	241.7	0	1.5	1	A0A0A8EBL8_9ACTN	Histidine kinase (EC 2.7.13.3)	GZL_00906	Streptomyces sp. 769	892	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	1262452	>tr|A0A0A8EBL8|A0A0A8EBL8_9ACTN Histidine kinase OS=Streptomyces sp. 769 GN=GZL_00906 PE=4 SV=1 MAYAECHGRPATEAMLDGLAVLPRAVRSHRGTEFGELDLDLVLERRPEVVLIDEL AHTNAPGCRHTKRWQDVEELLGAGIDVVATLNIQHLESLTDVVEKITGVPQYETVP DEVVRRADQIELVDLPAEGLRRRMAHGNIYPPEKIDAALSRYFRLGNLSALRELALL WVAGRVDEALRKYRHEHRIGPVWETRERVVVALSGGLEGTTLIRRAARIVNLSRA LSSSPTLNCVRAGGPPCAGGTPIPAGDLLAVHITRSDGLAGSSPAALADQRQLTE SLGGTYHAVVGDDVPAALLDFARAQNATQLVVGASRRGRLRRFLAPRGVGETVV ELSGDIDVHTVGHEYAGQGRTWVIPGSGLPHTRRVAGPIAGLVLPLLLTLVLRGVS GPLSLNLTSEALLFLLTVLGVACIGGVVSALLASVTTSLLLNYYFIPPVGQFTFAEAN IVVAQAAFTTVAVTVAAIVDRSLRLGRRAARATAEAETLSSLAGGILRGDRAVPDLL ERTRETFGMDRIELCPRDDVPEPWPSTTGRTAMGSARAVHTAGTAGDVGTDHR TEVAIGDDSVLVLIGRRLPASEHRVLTAFAAHLTAAVERARLAEAAAEVESVKAAN RMRTALLAAVGHDLRTPLAGSWAAISSLRSREVDFSPEDREELLATAEESLAKLSR LVDNLLDMSRLQAGALTLHLEPVALADVLPAALDTLPGSPPQAPGRVVARALDTAP DVLADPPLLERVVANLVSNAVRHSPAGRPVTIGASALGGRVEVRIIDRGPGIQLPD RERAFEPFQRLGDTDNTTGLGLGLALSRGLTEAMGGTLTPEETPGGGLTMVVSL PAAPEPHLPESEEVPPPPATGVAVPPTAVRAEKVAAAPHAVIARTVGAAGTAGTA DEA	2~~KdpD (2.28458E-87) ~~174,196~~Usp (9.69748E-24) ~~344,388~~DUF4118 (0.0000420399) ~~467,X,612~~HisKA (0.000000000162991) ~~678,733~~HATPase_c (2.05128E-26) ~~834	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	1.2E-67	236.8	0	1.6E-67	236.4	0	1.1	1	D7DKJ9_METV0	Osmosensitive K channel His kinase sensor	M301_2076	Methylotenera versatilis (strain 301)	176	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylotenera, Methylotenera versatilis, Methylotenera versatilis (strain 301)	666681	>tr|D7DKJ9|D7DKJ9_METV0 Osmosensitive K channel His kinase sensor OS=Methylotenera versatilis (strain 301) GN=M301_2076 PE=4 SV=1 MVDTRPDPDQLLDKINKEAEKQKNGRLKIFFGACAGVGKTFAMLAAARSLRLQGV DVIVGIVETHGRNETASQISGLDVLPLKKLEYRGRELSEFDLDAALLRKPRLILVDEL AHSNVEGSRHPKRWQDIEELLSVGIDVYTTLNVQHLESLNDVVGQITGIRVNETIP DKVVELH	23~~KdpD (5.35182E-90) ~~174	non-kinase	KdpD
	2.5E-63	222.7	0.2	5.4E-39	143.2	0	2	2	H2JY98_STRHJ	Two-component system sensor kinase	SHJG_2394	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	166	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	1133850	>tr|H2JY98|H2JY98_STRHJ Two-component system sensor kinase OS=Streptomyces hygroscopicus subsp. jinggangensis (strain 5008) GN=SHJG_2394 PE=4 SV=1 MARGMLRIYLGAAPGVGKTYAMLSEAHRRTERGTDCVVAFVEHHHRPRTEVMPH GLEQVPRRRLLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADDI ELVDMSPQALRRRMAHGNIYQPDKVDAALANYFRPGNLTALRELAELPDLSAVAA S	1~~KdpD (1.79526E-79) ~~155	non-kinase	KdpD
	4.2E-63	222	0	7.1E-63	221.2	0	1.4	1	E8N3E5_ANATU	Histidine kinase (EC 2.7.13.3)	ANT_09250	Anaerolinea thermophila (strain DSM 14523 / JCM 11388 / NBRC 100420 / UNI-1)	853	cellular organisms, Bacteria, Chloroflexi, Anaerolineae, Anaerolineales, Anaerolineaceae, Anaerolinea, Anaerolinea thermophila, Anaerolinea thermophila (strain DSM 14523 / JCM 11388 / NBRC 100420 / UNI-1)	926569	>tr|E8N3E5|E8N3E5_ANATU Histidine kinase OS=Anaerolinea thermophila (strain DSM 14523 / JCM 11388 / NBRC 100420 / UNI-1) GN=ANT_09250 PE=4 SV=1 MSNSRLKIFLSYADGAGKTSAMLSDAFQQKARGVDVLVAWVKLPENSETRQLLEE LEVLPPSSHGVDLDEVLRRRPQLVLVDELEGVNPAGSRHLYRWQDVEELLNAGIS VYTTLNILHVESLKDTVEEITGLPVEQTVPDRLLDRADELEVVDLPPEELLERLHPH SPAPPAGTLRQKSNLLALRQLTMRRAAMRVEDQARALLGTARAPLGTERVCVGIS NRPEAERLVREGRMLADALNAEWFVLYVETPTAAGERAEERANLLKAMRIAEENG ANTLLIPAETIAEGIESFCRQQGITRLVLGKPRDPLWRMRLGVSPVEHLLRSGLPV DVILVDTPHKPLVRAGTPPRWWVYLRNGGAVFLAVLLVTLLGWSLRQRPGAMGM EGIYLLLVIALSFWLGRSAGVLAAGLSTLAFAWFFFGASMGLDGADLPLLLTFLGW ATAGWVTASLARAVRRQTRAMRWRQVQSAVLNTLSRELAGALDMPAVLSIIVRHI VGVFNRAVMVLLLEEGQLKVAHSEGNVSLSERDWKISRWVLEHRRPAGLDTDTF ADSPMRFIPLMAHDLPVGVLVVVPDPASHTLLPEQREIRDGIAGLASLAIERVRLNQ QAQQAAVLQMTEKLQTALLNSISHDLRTPLSAVEGSLSSLLEAETNGLQMDRETR LDLLENATEEAERLNRLVGNLLDMTRIEAGALRIRRRPCDVQDLIGTALTQFQRRL QDRKVSTHIASDIPEVEMDFVLIEQVLERLLDNAVKYSPPGSEINVEAKVRDGALYI SVADRGEGIPPEDLERIFGKFYRVQRPDGVSGTGLGLSICKGIVEIHGGRIWAENR PDGGAKFTFTIPIKASGESK	5~~KdpD (1.29568E-68) ~~197,216~~Usp (6.87714E-30) ~~338,363~~DUF4118 (0.00000000000641311) ~~460,486~~GAF (0.00109897) ~~604,621~~HisKA (0.000000000160683) ~~690,743~~HATPase_c (7.0547E-34) ~~844	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	5E-63	221.7	0.2	9E-63	220.9	0.1	1.4	1	B0RCI0_CLAMS	Histidine kinase (EC 2.7.13.3)	CMS0459	Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	798	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Clavibacter, Clavibacter michiganensis, Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	31964	>tr|B0RCI0|B0RCI0_CLAMS Histidine kinase OS=Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) GN=CMS0459 PE=4 SV=1 MLEGLEILPRREVSHRGVEITDLDVDAVIARRPTIALVDELAHTNAPGGRYKKRWQ DVDLIRDAGIDVISTVNIQHIASLNDVVEKITGVPQRETIPDRVLREAHQIEVIDLAPK ALRDRLAGGRVYPAERIDAALSHYFRLGNLTALRELALLWLADEVDTALAAYRDEK GIDARWEARERVVVALTGGPEGETLLRRGARIAARSAGGELMAVHVSSQDGLRS GSPEALASQRALVDSLGGSYHQVVGDDIPRALVEFARASNATQLVLGVSRRSRLA AAATGPGIGATVIRESGDIDVHIVTHAAAGGRFRLPRVRGGALSMRRRILGGVLAL GGGPLLTWLLSATRSDDSITSDVLSYQLLVVLVALVGGIWPALFAAVLSGFTLDYF FIDPLYTITVDEPLHLLALVLYVVIALLVSWIVDQATRRTRLARLAVAEAELLATVSG SVLRGEGAVHALVSRTREAFGLQGVKLVDRDETIAWDGVVTGAAATDVPVGSRG VLTLYGDDLEASGRRLLRVIAAQLDAALEHRDLSDTAREVGPLAQTDRVRTALLSA VSHDLRRPLSAATAAVSALRSPGMTWADGDREELLATAEESLGTLADLVTDLLDV SRVQAGVLGVRLMDVDLDDVVLAALDELDLGPADAVLDLAPDLPGAVADPGLLER VVVNLLSNAVRHAPDGVPVRLSTSAFADAVEIRVVDHGPGVAPERRDDMFVPFQ RLGDTDNASGLGLGLALSKGFTEGMGGTLTAEDTPGGGLTMVVALPACRADAPV PEPAEPALADPDTDSEQVSA	1~~KdpD (2.75422E-83) ~~160,182~~Usp (1.10163E-31) ~~305,374~~DUF4118 (0.00000238363) ~~431,X,551~~HisKA (0.00000000304836) ~~617,668~~HATPase_c (4.29213E-26) ~~769	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	4.1E-62	218.7	0.4	5.8E-62	218.2	0.3	1.2	1	A0A068NUV8_9BACT	Osmosensitive K channel His kinase sensor	OP10G_3863	Fimbriimonas ginsengisoli Gsoil 348	331	cellular organisms, Bacteria, Armatimonadetes, Fimbriimonadia, Fimbriimonadales, Fimbriimonadaceae, Fimbriimonas, Fimbriimonas ginsengisoli, Fimbriimonas ginsengisoli Gsoil 348	661478	>tr|A0A068NUV8|A0A068NUV8_9BACT Osmosensitive K channel His kinase sensor OS=Fimbriimonas ginsengisoli Gsoil 348 GN=OP10G_3863 PE=4 SV=1 MLDEAHRRQRRGQETVIGVIDTQDRAPVGDLLHDFEQVPPGSEELNVDAILARKP DLVIVDELEHKNAPTSRNERRWQDVEELLAAGINVLSTLNVSSLESLNDHVADITG VKVEDTVPDRILGEAYEVELVDLTPRALINRLERGDIYPGRTVTGQESAFFREGNL AALREMAMREAASHVDEDLVAYRKEKRIEKPWAAQDRVMICLSPTRSSLRLIRRG WRMGQRMHGDVIAVHVEDGPIGEKERKILADDFKLAEKLGIETVSLKGELAPTLID FAKERNVTQLIIGHPERSRIQEIMKASVLSELVRSLKTVDILVVASENAPVGH	1~~KdpD (7.62921E-75) ~~182,204~~Usp (1.08454E-32) ~~323	non-kinase	KdpD;Usp

	5.9E-61	214.9	0	9.5E-61	214.3	0	1.3	1	U2RI82_9FIRM	Histidine kinase (EC 2.7.13.3)	HMPREF1546_00017	Oscillibacter sp. KLE 1745	881	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	1226323	>tr|U2RI82|U2RI82_9FIRM Histidine kinase OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_00017 PE=4 SV=1 METSAQVGRGERRRKGSLTIFAGYFSGTGKTYRMLEAAGRAVRAGEDVAVGLLS CSQWPQTQILADGFETLPLKAFSEAGKTVYELDVDTCLKRGPRLLLIDELSHENAG GSRHRKRCQDIEELLQAGIDIYTTLDVQHIESIQDTVSEILGAPAEERIPDRVFDQAA RVEFVDCEPEDLRERLIRQDRTDLLSEYSQPKLSALRELALRRCADRTALDTQKSR GGERYRTREHVLVCLSAAPSNERVIRTAARMADAFRCGFTALFVETKNFQSIPQP DRNRLRANLRLAQQLGASVETVYGDDVAYQIAEFSRLSGVTKIVLGRGETSNRILF WKPSLTERLVELTPELDIHIIPDTGTARRFASHYKKELYAPAVPLLDLLKSTLLLVLS TLVGLIFYYLGLSEANIITVYILGVMLTSIFTKSAVCSFLNSVVGVLAFNFFFTEPRFS LHIYASDYMVTFLVMFLASLLTGSLAAKLKSLAKHSAQLAWRTKLLFETNQELQKA GTQDEILSVTARQLLKIFQRDIVTYRSDQGQLDAPKIFPVDDAFSESKYSAASEHQ AAQWVLTNNKRAGAGTETFSDACCTYLAVRTAEQVYGVIGVAASGEEMDSFEGG LLLSILGECALAMENQKNLEEKEAAAVLAKNEQLRANLLRSISHDLRTPLTSISGNA SNLLSNGDMFDAKTKHQMYYDIYDDAMWLINLVENLLSVSRLEGGQMNLHLSTEL IGEVVAEALRHINRRSAEHHLHIQSGDEYLLAQMDAHLIVQVIINIVDNAIKYTPPGS DIEISWERQGRFAALSVADNGPGIPDSAKPRVFDMFYSASNRIADSRRSMGLGLA LCKSIITAHGGEITVADHAPHGTVFTFTIPIEEVELHE	14~~KdpD (1.94904E-72) ~~215,234~~Usp (6.78806E-38) ~~357,397~~DUF4118 (0.000000000915133) ~~482,510~~GAF (0.0000671087) ~~633,650~~HisKA (0.000000000905809) ~~716,769~~HATPase_c (1.74529E-29) ~~872	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c
	8.3E-58	204.7	0	1.2E-57	204.1	0	1.2	1	K7S831_PROA4	Histidine kinase (EC 2.7.13.3)	PACID_29820	Propionibacterium acidipropionici (strain ATCC 4875 / DSM 20272 / JCM 6432 / NBRC 12425 / NCIMB 8070)	840	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Propionibacterium, Propionibacterium acidipropionici, Propionibacterium acidipropionici (strain ATCC 4875 / DSM 20272 / JCM 6432 / NBRC 12425 / NCIMB 8070)	1171373	>tr|K7S831|K7S831_PROA4 Histidine kinase OS=Propionibacterium acidipropionici (strain ATCC 4875 / DSM 20272 / JCM 6432 / NBRC 12425 / NCIMB 8070) GN=PACID_29820 PE=4 SV=1 MMTARGRLRVLLGAAHGVGTTCAMLEEGRRLRDEGRDVVIAAAQAHSRSATDPG AWGLDVVPETAGRLDTDAVLTRRPDVALVDELAAADPPGSRHLRRWEDVEDLLA GGVDVISTLTIDRVESLSEVAWAITGVPPGGTVPDAVLRAADAVEVVDLAPAALQA RLAAGLIGDPRSGGRAFQLDSLIALRELTLMWVADDADQELRRYRDRHGAARSR QIRERVVVALGDEGSAPSLLRRAARLVSGSAGAGPIGVHVSGQRNRPLEDPPALR RLAERLGGSLHEVVGDDVPGAIIDFARSVDATQIVVATAGRGPVGRVLRPGVGER VARRADGPDVHLVTGSGEPGGRLPRPAGMLGGSLRGAPGGALGGVRRLAGFAL AVVAGPLLTWFLLADPAQDSTAVVALAFQLLVVVVALVGGIWPALCSAVGLGVTL DYFFTAPLRTFSISSISHLSTVVLCVAIAALVSLIVDRAARQTRAARRSAAESQLLQS VSGRVLGGQDAVRALVDQIRESFGMTRARLIRDGEEVASSSAALAGTASGRARA GQWRRSSLPVGEGARLELDGPALDASGQKLLPVITAQLATALDRADLSRAAASGK VRTALLSALGHDLRRPLASATAAVTGLRSAAGELTGTDRAELLETAAESLSALSGLI EDLVDVRRLETGALAVTMAAVDVEDVIGDALDEAGAGPDQVSLDVEPDLPVLGAD AALLRRVLVNLLTNALRHSPGGVELSARRAGGTRVVGEGEGEDVGDVVELSVAD HGPGIDPGRRAEIFMPFQRLGDDDNTTGLGLGLALSKGFVEGMGGTLEPEDTPG GGLTMVVSLYRWPGEDG	4~~KdpD (1.58667E-61) ~~199,223~~Usp (6.52397E-19) ~~342,X,605~~HisKA (0.00000718753) ~~668,728~~HATPase_c (7.66503E-18) ~~832	kinase	KdpD;Usp;X;HisKA;HATPase_c
	1.4E-55	197.3	0	2.5E-55	196.6	0	1.3	1	R7DGT7_9PORP	Histidine kinase (EC 2.7.13.3)	BN686_01930	Tannerella sp. CAG:51	879	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:51	1262979	>tr|R7DGT7|R7DGT7_9PORP Histidine kinase OS=Tannerella sp. CAG:51 GN=BN686_01930 PE=4 SV=1 MNKVFRFKPQKRLSLLNPERKTKGQLTLFFGMCMGIGKTHLMLQEGIHLIKDGFD VVLANYNSHGNKEIERLAAQIEQIPLKKNGEINLDYIIKRDPQIVLIDEMAHQNPNGS RHKHRHQDIEELLDDGIHVYTTLSVLQLESKAYSVQENTEYYTTCTVPDILFELAEK VHYIDASPQEIAKRFLDKSIYLDQHLGEHYRKAFFSIKNLHLLQRLCKQMMAFRRN EKQRQYLYEHHMQEDTITGVKLLISINESPHMESFIRRSKNLSYTLGVPLYAVYFDS TGQLTNKEQEQLNKNISMAYRLGVFVIRSTGENWVSSMLDVIRIEKITHLIFERLPN EKYIKKIFRRSELDRLISKCKNLDIYILSNESILERKKKFFQINTSGFKTSIWNYIKSATI TLSAVAILSPFIGMVSEVSSGYIFLIILALQSIYFSTGPILLSALLSAGVYDIFFTIPYGT PSLSSPDDWLQFFMFLAIPFINIMLATRLRKQEQQSRKRERISNTMFNFSKHLSTA SGINSILEISAKAINDSFKLKCAFILKNNKGGLSNSTSPHSNFTLTSNEFKVAQWVF DKGKQAGKSTENYMHEERTFYPLNSLKMKMGVVVLEFKKLFDAEEELLWLTLKR QISNALEREYLNDMARQASILSESDRLYKTLFNSISHELRIPVTSILSASETLKEIEQG ISKDIGEEIYMAAQRLHRLIENLLSMSRLDSGRLSPRFDWYDVHDLVNSVTGLLKN ELKEYDLSINIPDDMPLVRIDFGLIEQVLYNLLYNITVYVPSHTLIELDFQHDGTNFCI SITDYGKGFADKDLPYIFNKFYRGESGITGGSGLGLSIVKGYIDIHKGQVEASNVTG KGANIFIRIPSMLPLIENF	23~~KdpD (3.98497E-51) ~~216,247~~Usp (0.000000000000743362) ~~369,394~~DUF4118 (0.000000268587) ~~494,521~~GAF (0.00077288) ~~637,654~~HisKA (0.0000000545504) ~~716,769~~HATPase_c (3.6208E-19) ~~869	kinase	KdpD;Usp;DUF4118;GAF;HisKA;HATPase_c

	9.2E-51	181.6	0.2	1E-50	181.5	0.1	1	1	A0A0F5VIN1_9ACTN	Uncharacterized protein (Fragment)	TN53_42855	Streptomyces sp. WM6386	124	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	1415558	>tr|A0A0F5VIN1|A0A0F5VIN1_9ACTN Uncharacterized protein (Fragment) OS=Streptomyces sp. WM6386 GN=TN53_42855 PE=4 SV=1 MLSEAHLRVERGTDCVCAFLKHHNRSRTEVLLHGLEQIPRKELEYRGSTFTEMDV DAVLARHPEVALVDELPHTNIPGSRNTKRWQDVEELLAAGIDVISTVNIQHLESLG DVVESITGIRQQE	1~~KdpD (1.04605E-69) ~~124	non-kinase	KdpD
	8E-50	178.6	0	1.3E-48	174.6	0	2.2	1	C1DIF6_AZOVD	Histidine kinase (EC 2.7.13.3)	kdpDAvin_24520	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	874	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Azotobacter group, Azotobacter, Azotobacter vinelandii, Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	322710	>tr|C1DIF6|C1DIF6_AZOVD Histidine kinase OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) GN=kdpD PE=4 SV=1 MTHAMNEARDVPERTAAQSSHGEGGGRLRRGRLRIYLGAAPGVGKTLAMLQAA TELLRQGVDLRVGSLDCADDAARGELRMRLAALPGGREAAGELDLDALLARPPAL LLVDRLARANPPGSRHAQRWQDVQELLAAGIDVHATLDVSHLESLKNRVEALTGQ PVTETLPDWLLEEAHEVLLIDCLPGELRDFAPTTLAALRALALQVVAGRADSEVQR RYRPSGREAPAVLGRLLVAVDGDEQSEQLVRHASQVARRRQLPWTLVHVDDGR ARGEESRRLLQAAQRLAERLGGEVVGLLGDEVADTLLRHARERRASVLLVGGHR RRWFGRGVVERLLRRARGLEIGVLAAEEAVSVPSFAVRGFVAGPLDYALALLATL LASAVAWGFSRMLALQNISLVFLAAVLLVAVRSGFGPALCCALLSFFAYDLLFIAPT FSLIVAHRVDVLGLLFFLLMAALTGNLATRQRRQMQALRETQAETAALLDLTRKLS AATDRRAVLAAAVEQFAAWRDLDVRLLGPDGAGALRVEAGVAGDLGKSERAAAE WVWQHELPAGLGTDTLPDGRWWWWPLSGERGPLALLGIAPRDGRPLPASRRH RLVALCQPLAQALARAQLAEELQAARLRGETEQLRSALLASVSHDLRTPLTVMHG AIDSLLTLDGQIAAADRRELLESTRDEAERLDRYIQNLLDMTRLGHGGLKLERDWV APADIVASSLQRLRPVLASFRLETRIAGELPLLHVHAALIEQALVNVLENAARFSPP GGRLRVAVDSDGGELRLSVSDQGPGIPPAEREKIFDMFYTAARGDRGGPGTGLG LAICQGILGAHGGRVTVGEGLDGQGATLTLHLPLQPQPPGESERDDEAPVLP	35~~KdpD (1.32951E-42) ~~192,234~~Usp (1.61452E-25) ~~351,388~~DUF4118 (0.000000181966) ~~472,X,632~~HisKA (0.000000000000268729) ~~698,751~~HATPase_c (2.9579E-27) ~~854	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	9.1E-47	168.6	0.9	9.3E-46	165.3	0	2.2	1	Q02CX4_SOLUE	Osmosensitive K+ channel His kinase sensor domain	Acid_0076	Solibacter usitatus (strain Ellin6076)	346	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Solibacteres, Solibacterales, Solibacteraceae, Candidatus Solibacter, Solibacter usitatus, Solibacter usitatus (strain Ellin6076)	234267	>tr|Q02CX4|Q02CX4_SOLUE Osmosensitive K+ channel His kinase sensor domain OS=Solibacter usitatus (strain Ellin6076) GN=Acid_0076 PE=4 SV=1 MRSAPQRRLDPDELLRRVQAEERRERRGRLKVFLGYAPRVGKSLRMFDEGRRR KERGQDVVVAAVQEKSTEAVREIIVRLEQLPTVDGAIDLPAVFRRRPSVCLVDELA FDNPPGSANACRWQDVDAILNQGIAVMSAINVQHIREQQPAVEAITGKRATRSIPQ EFLREADEIEVVDAPPDLSMGDARALAELRELALLLAADVVDHQLQAYLDSHGVSV HWGAQERILVCLTPRSNALDMLHSGQRNARRFHGALLVAYVAQVNLSPADQQRL DDNLALARELGAEVHCLPAGDFVDSLLAFAREHRITQLFLGHSQRERSPIERLIDAA EDFDIRLFPHGEGK	30~~KdpD (4.00455E-44) ~~182,228~~Usp (1.65258E-24) ~~341	non-kinase	KdpD;Usp
	3E-44	160.3	0	3.9E-44	160	0	1.1	1	R6FM65_9FIRM	Conserved domain protein	BN525_01006	Eubacterium sp. CAG:192	208	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:192	1262883	>tr|R6FM65|R6FM65_9FIRM Conserved domain protein OS=Eubacterium sp. CAG:192 GN=BN525_01006 PE=4 SV=1 MLKIFTSYTPGAGKSYAMLEKAMAEQAKGKKVLIGFLNGGHRNIELIKEKNHIDSAI YNGKGFSYKQILEEKPDIVVLDEMGMRSKNHGYIYEIIELLLDNDIDVFTSINIKRFD SINPEFKKISGIGVKNMVPSKFLDMADEIYFIDRRPELMIRDFKNGNLFNKRYMKSG IMKKNFRRDILESYRKVSLEILKKYGDKVTVVERNE	2~~KdpD (1.29702E-29) ~~164	non-kinase	KdpD

	7.5E-44	159.1	0	1.5E-43	158.1	0	1.5	1	R5IQN6_9PORP	Histidine kinase (EC 2.7.13.3)	BN472_00372	Tannerella sp. CAG:118	874	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:118	1262978	>tr|R5IQN6|R5IQN6_9PORP Histidine kinase OS=Tannerella sp. CAG:118 GN=BN472_00372 PE=4 SV=1 MLTNTSLYAEKVSREMLISDSQKKHGDLTIFFGTCMGEGKTQAMLEKAYLHRQKG LDVVLGNFHPDSLSRRHAVMECILPNQFGEIDIEAILHRSPGLVIIDELAHNNSSGSR HKFRYQDIEELLDNGINVYTTLSVIQLESNSYMMSNRIGIKAPYIVPDIFFEQAAQIIPI DCKIEEIIRRYNSGEITTSFLTPEQETVFFSLDNLTLLKKSFKKLISFRKNESLRQRIE ANKLEDISREGLRLLVHIDEKPKTERIIQRAKELSYTMGAPLFAVYVYTSDSLSNTE QDQLNKNIRLAYRLGAYVIRMTGDNWISEMSSVIKKEKITHLILEREPYKKWYQLRT PYPFEKLTKKCEDIDIYILSKESSIKRKRKISTAIKRPNFTASLTNYVTSILITISFTILLY PLISWVHPQAVIYLCMIILAIQSLFFTTGPILTSAIVVALIIDYFFTLPFGTFTLYRINNL AMFGLFLSIPLINSIFANRLKRQELMSRKREQATNTLLHLSKHMAFVSGIEEVLKVA DKAVKESFDLDCTIILKDQNDSLNKVPTFIQHLPINEEEYEVAKWVFSNRKSAGRST ETFMSEEKTFYPLNSVRMRMGVIAVKLKRPFSPHEELIWLTLKRQISNTLEREYLN ELATQTLLLQESDKLYKTLFNSISHELRIPVATILTASETLSTIGNDMIKEINNEIYTAG KRLHRLIEELLSMSRVDSGRLSPRCEYYDIQDLIGPVLQQMKIELSDYKLNIDIEEDT PLINMDLVLMQQILTNLLYNIINYVPKHSQINIKTHYENSLFSMEVSDNGPGFNEEDL PHIFDKFYRGAHVPTGGSGLGLAIVKGYAEAMKGTATACNIPGACITITIPSEILIIKE	23~~KdpD (2.01417E-43) ~~212,245~~Usp (2.50396E-15) ~~366,392~~DUF4118 (0.000000030884) ~~492,X,652~~HisKA (0.000000141568) ~~714,767~~HATPase_c (2.60854E-22) ~~865	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.1E-42	155.3	0	1.4E-42	154.9	0	1.1	1	R5KT34_9FIRM	Conserved domain protein	BN508_00513	Eubacterium sp. CAG:161	207	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:161	1262881	>tr|R5KT34|R5KT34_9FIRM Conserved domain protein OS=Eubacterium sp. CAG:161 GN=BN508_00513 PE=4 SV=1 MLKIFTSYTPGAGKSYAMMEEAMNESRNGKKVVIAFINKQHRDSSKMPFECNENV TIHPLKGRESIEEIIEMKPDIVVLDELGMRIGKHTFLYNVAESFIKNNISVLTSANLKR FEEVNPIFRSETGVGIKTTIPNRFIKGADEIVFIDREPELMIKDFKEGKLFGERYMNS RIMNKNFEENTLKTYREISLDYLEKYNNVRIIQRD	2~~KdpD (1.13859E-27) ~~192	non-kinase	KdpD

	8.7E-37	136	1.2	1.7E-36	135	0.2	2	1	I3UFD2_ADVKW	Osmosensitive K+ channel histidine kinase kdpD	TKWG_19630	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	634	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella kashmirensis, Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	1036672	>tr|I3UFD2|I3UFD2_ADVKW Osmosensitive K+ channel histidine kinase kdpD OS=Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) GN=TKWG_19630 PE=4 SV=1 MLGAGIDVWTTLNVQHLESLNDVISGITDIRVTETVPDQVFDDADEVILVDITTEALL ARLQAGKVYMAEQVPLARQHFFRKGNLIALREIALRRTAERIHKDVRQYRHETYVE AIWRTAEGILVVVDTALTPNAAQALIRHGSRLSGQMSCPMHVMFLREAANSRGPA RSNGDWQLLLQQAEQLQATTTEHYCNGDVMPDIVAYCRSQNLSRLLLDRSVLRR YWWRLSPLVRVGQLGPDIDVIIYGGVSNRQRQAAARAQDHAFARREPVDWGKV GLALMFVCATTALLWPFSSILAITNIAMLYLALTMVVALRLGRWPGLVCAVSSVALF DFSFIPPLLSFSVADIQYLITLLVMLAVSTLISQLAAQQRFQGRLALQQTQRVHSLFE LAKRLSGSLQKEQIVQESQKLLLSDLGEDVFVILPDAHESLLLPEAEAGHEAAGLD MVAAQWAFDNEDKAGFGADTLSANAFRYFPLHAPVRIRGVLAVRMQGAPHLLSP EWQQQLEIYAHVIAIALERIHFVEVANEFLRQVESEKLRVTMLNIISHDLRTPLTVLI GEAEVLAAESNDNHVRQKAAIILDRARCMHDMMSKLLDMARIDSGQQHISKSWQ SIEELVGAPSGTRMCPPGVMS	1~~KdpD (5.64947E-48) ~~100,123~~Usp (0.00000175388) ~~245,279~~DUF4118 (1.20446E-15) ~~375,403~~GAF (0.00000023488) ~~520,537~~HisKA (0.0000000870569) ~~600	dysfunctional kinase	KdpD;Usp;DUF4118;GAF;HisKA

	4.4E-32	120.6	0.1	9.9E-32	119.5	0.1	1.7	1	R5HD40_9FIRM	Histidine kinase (EC 2.7.13.3)	BN469_02101	Firmicutes bacterium CAG:114	755	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:114	1263001	>tr|R5HD40|R5HD40_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:114 GN=BN469_02101 PE=4 SV=1 MYTTVNVQHLESLNDVVASITGISVSERVPDNVFDSAYQVEVVDLEPADLLERLRE GKIYRGPQAAQALDHFFSLKNLASLREIALRRTADQLESSPRFQGEVKPKAGEHILI CLSGAPSNAKVIRTAARMAKAFHGAFTALFVETSDFASQSEQDRKRLRDHVHLAE ELGARIATAYGDDPAVQIAEYARISGISKVVLGRSPRKRGFTSPKNLVDRLNELAPD LDLYIIPDQTARQSKRLRRLRQSQEKFSPKDLAKMLGILLLCTLGGALFSHWGFAN SNVIMLYILGVLGIAMVTTGRSYSVAASVLSVLIFNFFFTHPYFTFMSDPSYIATFGV MFVVAFLGSSLTTRMKRQARLNAEKAYRTAILLETSQKLQKAEGSQAILALTAHQL NKLLDRDLVIYQREENGELSPTLFPVSPGTDLSEFLTESERGVAEWVFKNNKHAG ATTNTLPSAKCLYMSIRGTGGALAVAAIVTKNREKPEAFEKNFMVAILDECGLALEK EMTVREKQAVEERAHQETLRANLLRAISHDLRTPLTSISGNANILMEGRGQLCQEK LQALYTAIYDDSMWLIDLVENLLSITRIEDDKLGLKTQPELLEEIFQEALQHLDRNAS QHQISVELEDDLLMANVDARLLVQVVINIVNNAIKYTPEGSHITLSAHREGDQVEVE IADDGPGIDQDAKDRIFDMFYTADKKRGDSRRGLGLGLSLCKSIINAHGGTIQAVD NHPQGTIFRFTLGAVEETNHE	2~~KdpD (9.59517E-44) ~~93,110~~Usp (1.54991E-34) ~~232,257~~DUF4118 (7.11021E-17) ~~357,X,524~~HisKA (0.00000000466702) ~~590,643~~HATPase_c (5.85488E-32) ~~746	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c
	1.6E-29	112.3	0	3.3E-29	111.2	0	1.5	1	A9B064_HERA2	UspA domain protein	Haur_2535	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	351	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Herpetosiphonales, Herpetosiphonaceae, Herpetosiphon, Herpetosiphon aurantiacus (Herpetosiphon giganteus), Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	316274	>tr|A9B064|A9B064_HERA2 UspA domain protein OS=Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785) GN=Haur_2535 PE=4 SV=1 MRSDSASYRYGEHRIYLSLAPGIGCTRRLMADAQLLAAQGYDVGIAFNASSDYLC DFARGLRPLPLIYERQNNQRIEALDLATILNDPPQIIVLGNLAHQHGLSNQPIEPLQL VEQLRMAGIAVWSTIYAYNLTTIAPIYTRLTNITPSPIIPESALEQASELVLIDPEPTDII RQLDEGILLAPPDAEQARQTALRLDVLNQLRAATHALLEIRRPLSDSAERPRWLVG IGFNPSAMYLLQRAADLAYGMGALLIGVHIRPPGGGSSGYRLAAREHLDYAEELC HEVVIIEEKDVAAAMLQVAHEQHATGIFIGRPVRSRWDELRGGSLLTKLINSDRDL DIFVLADAPQ	9~~KdpD (1.82684E-24) ~~205,226~~Usp (1.64015E-20) ~~347	non-kinase	KdpD;Usp

	5.9E-24	94.1	0.4	3.1E-23	91.7	0.3	1.8	1	A0A0F2RLL4_9PROT	Uncharacterized protein (Fragment)	VR70_07975	Rhodospirillaceae bacterium BRH_c57	173	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), unclassified Rhodospirillaceae, Rhodospirillaceae bacterium BRH_c57	1629718	>tr|A0A0F2RLL4|A0A0F2RLL4_9PROT Uncharacterized protein (Fragment) OS=Rhodospirillaceae bacterium BRH_c57 GN=VR70_07975 PE=4 SV=1 MPAASVAPESESLRGRLTLVLGVVPGVATAPTLATTAAQAAPDVGLAALMVPSGD VEGQVREALSAEGWDGAFVMSGDLDAIVAAAPDVVLVEDLLETNPSGSRHLSRR QDVEELLGRGLSVRAAVSVTQLRAAREVVRRYTGILPRNTLPDDLLDSADAVELLD VSPATLLE	78~~KdpD (1.48522E-24) ~~173	non-kinase	KdpD
	2.2E-23	92.2	0	2.7E-23	91.9	0	1.1	1	I3UFD3_ADVKW	Osmosensitive K channel His kinase sensor	TKWG_19635	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	144	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella kashmirensis, Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	1036672	>tr|I3UFD3|I3UFD3_ADVKW Osmosensitive K channel His kinase sensor OS=Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) GN=TKWG_19635 PE=4 SV=1 MVTPYRKDPDQLLEALAREESRQARGKLRIYFGASAGVGKTFSMLTAAHQELAAG HDVVIGVIETHDREDTRQLALSVPAIPLDIIHYRDRVIRELDLDAMLTRRRRLRSSMN WPIPMRRDCDIANAGRILMNCWAQGSMSGPR	24~~KdpD (4.99459E-31) ~~102	non-kinase	KdpD

	3.5E-21	85	0.4	5.7E-21	84.3	0.3	1.4	1	R5C547_9FIRM	Uncharacterized protein	BN499_00280	Blautia hydrogenotrophica CAG:147	516	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	1263061	>tr|R5C547|R5C547_9FIRM Uncharacterized protein OS=Blautia hydrogenotrophica CAG:147 GN=BN499_00280 PE=4 SV=1 MKERVPDTVFDSADQVKIIDIEPETLIQRLQEGKIYKSIQAERALNNFFAKEKLISLR EIALRRTADRVNRIAIEESKMYRDKKYYTGEHVLTCISPSPTCAKVIRSASRLAYAF HANFTALYVETPDLQNADRKVKKMVEENMHLAEALGAKIATVFGEDIPFQIAEYAKI CSASKLVLGRTNHKIWLGQKKGTLTDQITQYIPNMDIYIIPDTSNRAERWAVPKDV AKHKKEEKNGSLFLDLIRGVATLGIATVVSLGVEQVGFMSANIIIIYLFAILMLSLYSR RRWVSAVAALLSVFLFNFFFVPPIYSFAVHAPAYYTTFVFMFLFAFIISTIITSERKQ AKESAKFAYRTELLLENSKRMRRVHTVRALLKELSNQVLKLMNLSVIFFVKKDNKM TGPWLFPRVGMDKAQLRDMLDDQERAVVQWVLENKKRAGCCTHTLPGAQAMY LPIKSGDEIYAVMGIVLEEKREIPPFEYGLLTAMLNEAALVFARIYMTNNNVEEQKG DQKTVR	2~~KdpD (3.14363E-30) ~~69,90~~Usp (6.57176E-34) ~~213,248~~DUF4118 (0.000000000000663217) ~~345,371~~GAF (0.000000184807) ~~497	non-kinase	KdpD;Usp;DUF4118;GAF
	2.4E-20	82.3	0.1	2.4E-20	82.3	0.1	2.7	1	U4KQI1_9MOLU	Histidine kinase (EC 2.7.13.3)	kdpDBN8541043 0	Acholeplasma palmae	833	cellular organisms, Bacteria, Tenericutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Acholeplasma, Acholeplasma palmae	38986	>tr|U4KQI1|U4KQI1_9MOLU Histidine kinase OS=Acholeplasma palmae GN=kdpD PE=4 SV=1 MIGGMCMQRGKLKIFFSYFYKTAKTKAMLSEIIEKYHLKYRVLIIDAQCDDTQMNQ EIIHMNHIVIDDQLSFNINSILKMNPEIVVIDQIENFDLYSIEKLLEVGINIYATLNVFNIL SMNQYLSEKFNILTHEKTVPDYFFNQADEVEFIDIPPKELLLRLEPYEQYQWVTEE NLKYFRTIALDKLIDHNKYSHKKLIESNLQFLVCISPSPSAIRSIEWTARNAQAFYAS WKALYITTNKHKNNIQDIKKIEEYENKVHELGGEFVRITANNIDAAIIEYAKLTGVTN MVIGKSRTVNYRFPFRLTTLESKIINAIKGIELHIIPNYDYGTKKYEYKPKKTSSRVW KDILLSVLITLFATAICFLINFNTDEFNEGLIYLMAVLLISRFTKGYIYGIATSFISFLIFL YLFVQPNFTFNVSQVDSWVTFGIIFITSIMTSMITSQIKSDKESNVSAITELEKLYTF NQELLKVDDKLEIINLMKAFFKNEFGGESTFYDIDNNQIVNEPAQNDHIEAVQWMII NHQEVGNATKLFSNIDTTYFPIIISKKIIGAVSITGLNLQTFKDYDYLIRVILYQTGLAIE KETLKIHRQKLSEIASQEIVRSNLLRSVSHDLRTPLTSIYGMITTIIEQETITRDEIVNN LASARDDIQWLIRMIENLLSITRINQETQKVMKNLEVVEEIVSESVIRVRKRFPKAKI KVKIPNDVLLVPMDGTLIEQVIINLLENTIKHGKNVQNIILSVDDEQDKVIFKVSDDGK YIDLNKIENLLKDTQTIEYGDKGTKHSGIGLLICKTIIQAHQGQFSFYKNQENGITFY FTLPKGDHDEFK	7~~KdpD (2.65117E-22) ~~190,205~~Usp (3.01923E-22) ~~327,351~~DUF4118 (0.00000000000806508) ~~449,X,607~~HisKA (0.000000000469423) ~~669,722~~HATPase_c (1.67044E-16) ~~824	kinase	KdpD;Usp;DUF4118;X;HisKA;HATPase_c

	3.1E-15	65.5	0	5E-15	64.9	0	1.3	1	A0A0F5VLI6_9ACTN	Histidine kinase (Fragment)	TN53_41240	Streptomyces sp. WM6386	279	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	1415558	>tr|A0A0F5VLI6|A0A0F5VLI6_9ACTN Histidine kinase (Fragment) OS=Streptomyces sp. WM6386 GN=TN53_41240 PE=4 SV=1 IELVDMSPPALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVD EYLTEYRSEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAVRLAEKGAGGEVLAVYI ARSDGLTSASPKELAVQRTLVEDLGGTFHHVIGDDIPAALLDFSRGVNATQIVLGV SRRKGWQYVFGPGVGATVARESGPDLDVHLITHDEAGKGRGLPVARSARLGRP RVIWGWLTGIGGPAVLALLLSEAAPGLGLANDMLLFLSLTVAAGLLGGLCPALASA AFG	1~~KdpD (2.39862E-24) ~~54,76~~Usp (3.92925E-33) ~~199	non-kinase	KdpD;Usp
	4.8E-11	51.9	0.1	1E-10	50.8	0	1.6	1	R6MS94_9FIRM	ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	BN531_00832	Eubacterium sp. CAG:202	391	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:202	1262884	>tr|R6MS94|R6MS94_9FIRM ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein OS=Eubacterium sp. CAG:202 GN=BN531_00832 PE=4 SV=1 MPQELIERLQAGKVYSPTQAERATENFFTVENLTVLREIALRRCADRVNLLTETVR TKSHSDYHTDEHILVCLSSSPSNAKIIRTAARMANAFKGAFTALFVETPDYQVMSE EDVKRLRSNMRLAEQLGAKIETVYGEDVSYQIAEFARLSGVSKIVIGRSSATRKSIF SKPTLTEKLIANAPNLDVHIIPDTDGKNTAYRAKKARKRNGIVFSVSDLLKSIAILILA SCIGMLFRQLGFAEANIITVYVLGVLVTSVVTRHRVYSLISSIVSVLVFNFFFTDPQF TLRAYNQGYPVTFLIMFLAALLTSSLAVKLKEHAKQSAKAAYRTKVLFDTNQLLQQ AKDKNEIVSATANQLIKLLGKDIVFYLTEGETLGEPIFLQFREIKQTKK	2~~KdpD (9.80695E-19) ~~48,68~~Usp (4.15249E-42) ~~191,218~~DUF4118 (1.68135E-14) ~~319	non-kinase	KdpD;Usp;DUF4118

Disagreement between HMMER and CDD prediction	0.000014	34	0	0.039	22.7	0	2.2	2	A0A0C5VG59_9GAMM	ABC-type multidrug transport system, ATPase component	YC6258_00348	Gynuella sunshinyii YC6258	577	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, unclassified Oceanospirillales, Gynuella, Gynuella sunshinyii, Gynuella sunshinyii YC6258	1445510	>tr|A0A0C5VG59|A0A0C5VG59_9GAMM ABC-type multidrug transport system, ATPase component OS=Gynuella sunshinyii YC6258 GN=YC6258_00348 PE=3 SV=1 MSTPVVVIDHLCKHFKGMDRPALEDISTEIFPGRMTGLVGPDGAGKTTLLRHLVGL MQADTGRITVAGLDTVRQAGEVHEVTGYMPQKFGLYEDLTVLENLKLYADLRQVT GQARADKFARLLHFTALESFQQRLAGKLSGGMKQKLGLACALLGDPQLLLLDEPS VGVDPISRRELWAMVRELLSAGMAVVWSTAYLDEAEKCDTVILLNDGKKLYDGVP AQLFQQVSGRVVWQIQGIPAETRRRVLSGMLRQPEVIDGVIQGHHVRVVLGAGQA RPKLERGQWQSVTPGFEDAFIDILGGGPGGQSALAAEMTDKPANDQPVIDARRL TKQFGQFTAVADNTFQIHRGEVFGLLGPNGAGKSTTFKMMCGLLQPSSGEAFVT GLNLKTATSKARARIGYMAQSFSLYTNLSVLQNLRFFAGLYGLSGKRRRHQIELMT DIFNFAPYLKMTAGSLPLGYKQRLALACAVMHQPDVLFLDEPTSGVDPITRREFW MHINAMVEKGVTVMVTTHFMDEAEYCDRIGLIYRGHNIATGSPDDLKLKASNLSGV ESSTLEEAFITLVRDYDNNPVVEEGAA	6~~P-loop_NTPase (2.16162E-56) ~~214,324~~P-loop_NTPase (1.35628E-75) ~~530		

Disagreement between HMMER and CDD prediction	0.00011	31.1	0.2	0.00017	30.5	0.1	1.3	1	R5UAA6_9FIRM	Cobalt ABC transporter ATP-binding protein	BN481_00926	Ruminococcus gnavus CAG:126	278	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	1263106	>tr|R5UAA6|R5UAA6_9FIRM Cobalt ABC transporter ATP-binding protein OS=Ruminococcus gnavus CAG:126 GN=BN481_00926 PE=4 SV=1 MSEEIILEARDIWHSYEENDRFSLQGLDLKVKKGSKVAFMGANGSGKSTFFLCCN GILRPQKGDILFHGKPVSYKRKELLALRAKVGIVFQDPDKQLFSASVEQEISFGILN LGVAKEQARTEVEQVMEELEIVPFRKRPVHALSGGQKKQVSIADILVMRPEIIILDE PAAALDPKHTRMVNEMVDKLTEQGITVLMATHDMDYAYAWADEIVLMKDGKVLC QGAPEAVCRETEKLKETNLEEPALLRLFDRLKARKIIEATGKAPRTWKELEQLIG	8~~P-loop_NTPase (2.80843E-91) ~~220		

Disagreement between HMMER and CDD prediction	0.00014	30.8	0	0.42	19.4	0	2.3	2	F8KV38_PARAV	Uncharacterized ABC transporter ATP-binding protein YbhF	ybhFPUV_01640	Parachlamydia acanthamoebae (strain UV7)	575	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Parachlamydiaceae, Parachlamydia, Parachlamydia acanthamoebae, Parachlamydia acanthamoebae (strain UV7)	765952	>tr|F8KV38|F8KV38_PARAV Uncharacterized ABC transporter ATP-binding protein YbhF OS=Parachlamydia acanthamoebae (strain UV7) GN=ybhF PE=3 SV=1 MSDLVQINQLTKIFEKGSAPALDCIQASVPKGKIVGLVGPDGAGKTTLIRLMAGLLL PTKGNISVAGFDTVNDAEEIHLLLGYMPQKFGLYEDLSVQQNLDLYASLRGVPKNE RKETFEKLLKFTSLEPFTERLAGALSGGMKQKLGLACALIRTPQLLLLDEPSVGVD PVSRRELWKMVHQLIDEGVSVLWSTAYLDEAEQCDSVLLLNEGKMLFNGIPQDLT KRVQGQTFKIEHITGRKRVVLVKALSSEDVIDGVIQGRDVRIVFKGKSHRLDLNTLG AGPEAKLEETPPRFEDAFIDILGGGPSGESELAKITKPIKPEETPVVEAIGLTKRFGE FTAADDITFKIKSGEIFGLLGPNGAGKSTTFKMMCGLLKPTAGESFVTGLNLQDAP GEARAQIGYMAQKFSLYGNLSVMQNLQFFSGIYNLTGTYRAEAVQKMVDTFDLKP YLNVSADELPLGFKQRLALSCAVMHNPTVLFLDEPTSGVDPITRREFWNHINGLVE KGVTVMVTTHFMDEAEYCDRIGMVYRSRLIRLGSPDELKDIVKTDHNPSPTLEDAF IELINRYDQEHAK	5~~P-loop_NTPase (2.12249E-66) ~~214,328~~P-loop_NTPase (2.30315E-74) ~~535		

Disagreement between HMMER and CDD prediction	0.0005	28.9	0.6	0.2	20.5	0.1	2.3	2	A0JVZ5_ARTS2	Monosaccharide ABC transporter ATP-binding protein, CUT2 family	Arth_1825	Arthrobacter sp. (strain FB24)	505	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. (strain FB24)	290399	>tr|A0JVZ5|A0JVZ5_ARTS2 Monosaccharide ABC transporter ATP-binding protein, CUT2 family OS=Arthrobacter sp. (strain FB24) GN=Arth_1825 PE=3 SV=1 MTDMLAPRVVARLRGVTKSFDGTTVVRNVDLDFRSGEVHVLAGENGAGKSTLTK LLAGIHQPDHGTVEINGQMGPFDVKSSRTAGVTLVHQELLIAPNLTVADNLAMGQ ENRNRFRGLDRTATLENARAQLAHIGATFPVTMRAEELTVADHQQIEIARALAQKP KILILDEPTSALSSAETERLLRIVDELRRNGTSVIYITHRMEEIEALADIVSIMRDGSLV ETMPKAEATPDAIVLRMVGRKIDSLFTAERPEPGRVVLRVEQLTNGKDIGPIDLDV RAGEVVGIGGLIGSGRSEFVRLIFGADRASSGTVSVDGSPVNVTGPGSAVRAGIA LLPESRKTQGLVLDQSIAANIVLASLGHISSAGVVTPAAVKRVASKAQKRLGIKSAS LGQEVTTLSGGNQQKVLFAKWLETKPKVLILDEPTRGVDVGAKAEIYQIINECAHA GVAVLVISSELPELIGLSSRVHVMREGRLVAEIDAQSLTEEAVMNHAFGIAQATQA	12~~P-loop_NTPase (9.07309E-63) ~~227,259~~P-loop_NTPase (3.45043E-84) ~~478		

Disagreement between HMMER and CDD prediction	0.00084	28.2	0	0.0014	27.5	0	1.3	1	Q6A7G4_PROAC	ABC transporter ATP-binding protein	PPA1557	Propionibacterium acnes (strain KPA171202 / DSM 16379)	249	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Propionibacterium, Propionibacterium acnes, Propionibacterium acnes (strain KPA171202 / DSM 16379)	267747	>tr|Q6A7G4|Q6A7G4_PROAC ABC transporter ATP-binding protein OS=Propionibacterium acnes (strain KPA171202 / DSM 16379) GN=PPA1557 PE=3 SV=1 MPETPLTLDPHAPTEVLLLEDVRVTFGHVIALDALSLTAVTGAITAVLGPNGAGKTT MMRCCTSLISPDSGRIDVLGHAPGSPEAAAATGLMPQSSGAWSGIRAGELLHYM AGLHANPIDPDLLIEALAITPFAHTTYRRLSGGQQQAVNLAAALVGRPKLVFLDEPT SGMDPHARHHTWDIVEQMRHDGVSVVLTTHNMDEAQRLADHVWIVDRGRVATH GTVPELTAESSLEDVFLTHTSDRAAGRN	19~~P-loop_NTPase (4.72056E-60) ~~218		
Disagreement between HMMER and CDD prediction	0.0011	27.9	0	0.0018	27.1	0	1.3	1	D7C130_STRBB	ABC transporter ATP-binding protein	SBI_04811	Streptomyces bingchenggensis (strain BCW-1)	322	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7C130|D7C130_STRBB ABC transporter ATP-binding protein OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_04811 PE=3 SV=1 MTDLAIAANGLRKSYGDKTVLDGIDLAVPEGTIFSLLGPNGAGKTTAVKILSTLISPD PASGQIRVGGHDLATSPQAVRAAIGVTGQFSAVDGLITGEENMLLMADLHRLPKR EGRQVTAELLERFDLVDAAKKPASTYSGGMKRRLDIAMTLVGSPRIIFLDEPTTGL DPRSRHNMWQIIRELVSDGVTVFLTTQYLEEADELADRIAVLNDGKIAAEGTADEL KRLIPGGHIQLRFTDPAAYQNAATTLREANRDDEALSLQIPSDGSQRELRSILDWL DSAGIEADELTVHTPDLDDVFFALTATSQPAQPTQPKETVR	6~~P-loop_NTPase (6.34639E-95) ~~226		

Disagreement between HMMER and CDD prediction	0.0011	27.8	0	0.0039	26	0	1.8	1	A0A0C5XC33_NOCSI	ABC transporter, ATP-binding component	KR76_27340	Nocardioides simplex (Arthrobacter simplex)	250	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Pimelobacter, Nocardioides simplex (Arthrobacter simplex)	2045	>tr|A0A0C5XC33|A0A0C5XC33_NOCSI ABC transporter, ATP-binding component OS=Nocardioides simplex GN=KR76_27340 PE=3 SV=1 MNLTTPAIEVAALRKAYGDQVVLDGLDLTVPAGTVYALLGPNGAGKTTTVNICSTL LAPDAGTVAVAGHDVRTRSDAVRRSIGLTGQFSAIDELLTGRENLRLMADLAHLSR PDARARVDEQLARFGLTEAADRRAATYSGGMKRRLDLAMTLVSRPQVIFLDEPTT GLDPRSRRDLWQIVRELVADGVTILLTTQYLEEADQLAHTVGLLDGGRLVAEGTP AELKAQSGGETLDDVFLALTGHAAEVVR	8~~P-loop_NTPase (1.40804E-96) ~~226		
Disagreement between HMMER and CDD prediction	0.0013	27.6	0.1	0.002	27	0.1	1.3	1	R5BXN1_9FIRM	Uncharacterized protein	BN499_00019	Blautia hydrogenotrophica CAG:147	281	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	1263061	>tr|R5BXN1|R5BXN1_9FIRM Uncharacterized protein OS=Blautia hydrogenotrophica CAG:147 GN=BN499_00019 PE=4 SV=1 MKDIILKAQELYFSYDDENTHSLNGLSLEIQRGKKVAFMGANGSGKSTFFLCCNGI HRPSSGTLFVDGKPIDYSKKGLLDLRQKVGIVFQDPDNQLFSASVYQEISFGILNL GISEEEAQKEVEKVIADLEITPFRHKPTHALSGGQKKQVSIADILVMHPQIIILDEPAA ALDPKHTQKVNHIVDEMTQQGITVLMSTHDVDYAYQWADQIFLFKDGRVLSQGTP TEVFADQNALEETNLHQPTVMKLYFRLCEKGILDPSFPVPKNLQELEQYIENIHL	11~~P-loop_NTPase (2.45248E-89) ~~219		

Disagreement between HMMER and CDD prediction	0.0018	27.1	0	0.0031	26.4	0	1.3	1	A0A0F7N9U9_9ACTN	ABC transporter	AA958_20875	Streptomyces sp. CNQ-509	317	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. CNQ-509	444103	>tr|A0A0F7N9U9|A0A0F7N9U9_9ACTN ABC transporter OS=Streptomyces sp. CNQ-509 GN=AA958_20875 PE=3 SV=1 MTTTTDSPAIAATGLRKSYGDKTVLDGIDLHVPEGTVFSLLGPNGAGKTTAVKILST LITADAGAIRVAGHDPATHADAVRAAIGVTGQFSAVDNLITGEENMRLMADLHHLP RAEGRRITAELLERFDLTDAAARPAATYSGGMRRRLDIAMTLVGSPRIIFLDEPTTG LDPRSRHDMWQIIRELLTDGVTVFLTTQYLEEADELADRIAVLHGGRIAAQGTAAE LKRLVPGGHVRLRFEDPGAYERAAGELRETVRDDQALTLQIPSDGTQRELRAILD WLEAADVHADTLTVHTPDLDDVFFALTAAPEKEAAR	10~~P-loop_NTPase (2.3089E-91) ~~228		
Disagreement between HMMER and CDD prediction	0.0018	27.1	0	0.0038	26	0	1.5	1	A0A0F5W392_9ACTN	ABC transporter	TN53_09930	Streptomyces sp. WM6386	325	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	1415558	>tr|A0A0F5W392|A0A0F5W392_9ACTN ABC transporter OS=Streptomyces sp. WM6386 GN=TN53_09930 PE=3 SV=1 MPTPRQDGGHTPPAAVSTVDLRKSYGDKVVLDGIDLHIPAGSVFALLGPNGAGKT TAVKILSTLITADGGQAQVAGHDVAMSPDGVRAAIGVTGQFSAVDGLITGEENMLL MADLHHLPKQEGRRVTAELLERFDLTEAAKKPASTYSGGMKRRLDIAMTLVGNPR IIFLDEPTTGLDPRSRHNMWQIIRELVTDGVTVFLTTQYLEEADQLADRIAVLNDGKI AAEGSAEELKRLIPGGHVRLRFTAPDAYRSAADALREVTRDDEALALQIPSDGSQ RELRSLLDWLDAAGIEADELTVHTPDLDDVFFALTGDTDKPKESVR	16~~P-loop_NTPase (1.44823E-96) ~~234		

Disagreement between HMMER and CDD prediction	0.0019	27.1	0	0.0032	26.3	0	1.3	1	D7BTW9_STRBB	ABC transporter ATP-binding protein	SBI_06418	Streptomyces bingchenggensis (strain BCW-1)	329	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7BTW9|D7BTW9_STRBB ABC transporter ATP-binding protein OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_06418 PE=3 SV=1 MPTSRRGGGTQPPSAAISTVGLRKSYGDKTVLDGIDLHIPAGSVFALLGPNGAGK TTAVKILSTLISADGGQSQVAGHDVATSPDGVRAAIGVTGQFSAVDGLITGEENML LMADLHHLSKREGRQVTAELLERFDLTEVAKKPASTYSGGMKRRLDIAMTLVGNP RIIFLDEPTTGLDPRSRHNMWGIIRELVSGGVTVFLTTQHLEEADELADRIAVLNDG KIAAEGTAEELKRLIPGGHIRLRFTDPAAYQNAATTLREANRDDEALSLQIPSDGSQ RELRSILDWLDSAGVEADELTVHTPDLDDVFFALTGPAGVPNQPKETAR	17~~P-loop_NTPase (3.2652E-94) ~~235		
Disagreement between HMMER and CDD prediction	0.0025	26.7	0	0.0043	25.9	0	1.3	1	F8JLH7_STREN	ABC transporter ATP-binding protein	SCATT_p01160	Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	323	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cattleya, Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	1003195	>tr|F8JLH7|F8JLH7_STREN ABC transporter ATP-binding protein OS=Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057) GN=SCATT_p01160 PE=4 SV=1 MSTTNHDSPFAVSAVGLRKSYGDKTVLDGIDLRIPAGSVFALLGPNGAGKTTTVKI LSTLVTADGGRAQVAGHDVATSPDGVRAAIGVTGQFSAVDGLITGEENMLLMADL HHLSRREGRRVTARLLERFDLVDAARKPAQSYSGGMKRRLDIAMTLVGDPRIIFLD EPTTGLDPRSRHNMWQIIRELVSDGVTVFLTTQYLEEADELADRIAVLNDGGIAAE GTADELKRLVPGGHVRLRFSDPAAYRSAAGALRGAARQDEALALQIPSDGSQREL RAILDRLDSSGIEADELTVHTPDLDDVFFALTGSGRPNRPMETAR	16~~P-loop_NTPase (8.33767E-95) ~~230		

Disagreement between HMMER and CDD prediction	0.0036	26.1	0	0.0083	24.9	0	1.6	1	C7MRY6_SACVD	Daunorubicin resistance ABC transporter ATP-binding subunit	Svir_39000	Saccharomonospora viridis (strain ATCC 15386 / DSM 43017 / JCM 3036 / NBRC 12207 / P101)	322	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharomonospora, Saccharomonospora viridis, Saccharomonospora viridis (strain ATCC 15386 / DSM 43017 / JCM 3036 / NBRC 12207 / P101)	471857	>tr|C7MRY6|C7MRY6_SACVD Daunorubicin resistance ABC transporter ATP-binding subunit OS=Saccharomonospora viridis (strain ATCC 15386 / DSM 43017 / JCM 3036 / NBRC 12207 / P101) GN=Svir_39000 PE=3 SV=1 MDEQVAVRARGLVKSYGSTQALNGVDLDVLSGRVLGLLGPNGAGKTTVVRILTTL LRPDAGEASVAGHDVLTEPDAVRAAIGVSGQYAAVDENLTGFENLYMIGRLYGLS KRHAKQRSRELLKRFQLAEAADRTARGYSGGMRRRLDLAGALVAEPKVVVLDEP TTGLDPRGRLEMWQVIEQLVATGATVLLTTQYLEEADRLADSIVVIDKGVVIARGT AEELKQRIGGERLELVLEDAADVPRAVRILEEVGTSEPVVEEPIRTVTVSVDAGAK ALVQALRKLDAQHLALQDVALRRPTLDDVFLALTGRATATDEETTS	7~~P-loop_NTPase (1.62933E-98) ~~225		

Disagreement between HMMER and CDD prediction	0.0038	26.1	0	7.1	15.4	0	2.4	2	W0TRN1_9GAMM	Thiolapillus brandeum DNA, complete genome	TBH_C2792	Thiolapillus brandeum	578	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, Thiolapillus, Thiolapillus brandeum	1076588	>tr|W0TRN1|W0TRN1_9GAMM Thiolapillus brandeum DNA, complete genome OS=Thiolapillus brandeum GN=TBH_C2792 PE=3 SV=1 MGRPALILRDVHKVFRRGEASLCALDGVSVQVARGSVTGLIGPDGAGKTTLMRLC CGLLKLDGGMIETLGLDAAADPAAVQATVGYMPQRFGLYEDLSVQENLDLYADLQ GVPRNERPARYARLMEMTNLAKFTKRLAGKLSGGMKQKLGLACALVRPPQLLLLD EPTVGVDPVSRRELWEIVYSQVQDSGMSVLLSTAYLDEAERCDEVILLHKGKVLG QAAPDSFSRNLVGRTWEVSTGDISPRRLQARLIRQGGINDAIINGDRVRIITRKGFH PDAKMLLSGTETLTVEAVPPHFEDAFIDRLGGARNGQHATPAIRQVNPGKYPGDP IEVQQLERRFGNFVAVKKVSFSVKRGEIFGLLGANGAGKTTTFRMLCGLLPLSSG RVSVAGHDLRTASARARSRIGYMAQKFSLYANLTVAQNLEFFSAAYNLRGRRQRE RIQWALEGFELGPYAGVNAGTLPLGYKQRLAFAAALMHEPEILFLDEPTSGVDPLA RREFWARTNALAEAGVTVLVTTHFMEEADYCDRLVIMAEGSVLAEGSPHEIRALA RTQDHPQPSMEDAFIGLIQSREEAA	6~~P-loop_NTPase (6.37519E-64) ~~218,333~~P-loop_NTPase (1.40877E-77) ~~550		

Disagreement between HMMER and CDD prediction	0.0038	26.1	0	0.0064	25.3	0	1.3	1	A0A0F0HLI3_9PSEU	ABC transporter	UK12_26820	Saccharothrix sp. ST-888	325	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix sp. ST-888	1427391	>tr|A0A0F0HLI3|A0A0F0HLI3_9PSEU ABC transporter OS=Saccharothrix sp. ST-888 GN=UK12_26820 PE=3 SV=1 MPTPRRADGHASPAAVSTVGLRKSYGDKTVLDGIDLRIPAGSVFALLGPNGAGKT TTVQILSTLITADGGQAQVAGHDIATSPDGVRAAIGVTGQFSAVDGLITGEENMLL MADLHHLSRREGRRTAAELLQRFDLVEAAKKPASTYSGGMKRRLDIAMTLVGNPR IIFLDEPTTGLDPRSRHNMWQIIRELVSDGVTVFLTTQYLEEADQLADRIAVLDDGR IAAEGTAAELKRLIPGGHVRLRFSDPSAYQSAALALREVTRDDEALSLQIPSDGSQ RELRSILDRLDSAGIEADELTVHTPDLDDVFFALTGGTDQPKEAVR	16~~P-loop_NTPase (5.5146E-97) ~~234		
Disagreement between HMMER and CDD prediction	0.0046	25.8	0	0.0086	24.9	0	1.5	1	A0A0F4K8N5_9ACTN	ABC transporter	VR46_23065	Streptomyces sp. NRRL S-444	336	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-444	1609134	>tr|A0A0F4K8N5|A0A0F4K8N5_9ACTN ABC transporter OS=Streptomyces sp. NRRL S-444 GN=VR46_23065 PE=3 SV=1 MTSHSGLPAITATGLRKAYGDKTVLDGIDLHVPTGTIFSLLGPNGAGKTTTVQILST LIGTDAGHVRIAGYDLATHPDAVRAAIGVTGQFSAVDKLLTAEENLLLMADLRHLG KAEGRRRAAELLEAFDLVDVARKVALTFSGGMLRRLDLAMTLMGSPQVIFLDEPT TGLDPRSRRAMWQIIRELVADGVTIFLTTQYLEEADQLADRIAVLDHGKLVAEGTA YELKRLVPGGNINLRFAERGGYERAARSFGEASRDAEALTLQIPSDGGVQSLRALI DRLDAESIEVSGLTVHTPDLDDVFLALTGRPVTPVAPGTSTAPVVAPVQTAKESAR	10~~P-loop_NTPase (1.40754E-91) ~~228		

Disagreement between HMMER and CDD prediction	0.0048	25.7	0	0.0089	24.9	0	1.4	1	D7CAV3_STRBB	ABC transporter ATP-binding protein	SBI_05550	Streptomyces bingchenggensis (strain BCW-1)	336	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7CAV3|D7CAV3_STRBB ABC transporter ATP-binding protein OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_05550 PE=3 SV=1 MNPAARTLLGMTTSRSPRAITATGLRKAYGEQVVLDGIDLDIAEGTVFSLLGPNGA GKTTMVQILSTLIGADGGDIRVAGHDPAKDPDAVRSAIGVTGQFSAVDHLLTGEEN LLLMADLNYLGRREGRRRAAELLERFDLVDAAKRTPATYSGGMQRRLDIAMTLVG QPRIIFLDEPTSGLDPRSRHTMWQIVRDLVAGGVTVFLTTQYLDEADQLADRIAVL NGGKLVAEGTAEELKRRIPGGHVRLRFAVPGDLERAARAFGEVSRDDEALTLQVP SDGSVRELRSLLDWLDAESVDAEELSVHTPDLDDVFFALTEKPGNPTAQVTTAQK VNA	20~~P-loop_NTPase (4.16731E-86) ~~238		
Disagreement between HMMER and CDD prediction	0.0052	25.6	0	0.008	25	0	1.3	1	F2R8D9_STRVP	Putative ABC transporter ATP-binding protein	SVEN_0570	Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	268	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces venezuelae, Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	953739	>tr|F2R8D9|F2R8D9_STRVP Putative ABC transporter ATP-binding protein OS=Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745) GN=SVEN_0570 PE=3 SV=1 MKILSTLVSADGGHARVAGHDLAAEPQKVRAAIGVTGQFSAVDGLITGEENMLLM ADLHHLSKREGRRVAAELLERFDLVEAAKKPASTYSGGMKRRLDIAMTLVGDPRII FLDEPTTGLDPRSRHNMWQIIRELVAGGVTVFLTTQYLEEADELADRIAVLNDGKI AAHGTAEELKRLIPGGHVRLRFTDPAAYRNAASALGEVTRDDEALALQLPSDGTQ RELRSILDWLDSAGIEADELTVHTPDLDDVFFALTGGTDQPKEAVR	2~~P-loop_NTPase (7.5233E-73) ~~177		

Disagreement between HMMER and CDD prediction	0.0053	25.6	0	0.012	24.4	0	1.6	1	H6R377_NOCCG	ABC transporter ATP-binding protein	NOCYR_4924	Nocardia cyriacigeorgica (strain GUH-2)	314	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia cyriacigeorgica, Nocardia cyriacigeorgica (strain GUH-2)	1127134	>tr|H6R377|H6R377_NOCCG ABC transporter ATP-binding protein OS=Nocardia cyriacigeorgica (strain GUH-2) GN=NOCYR_4924 PE=3 SV=1 MNTTAIAASGLRKSYGDKTVLDGIDLTVGAGTIFALLGPNGAGKTTTVNVLTTLLKS DGGTARVAGHDLDTETKAVRAAIGVTGQFAAVDGLLTGAENLRLMADLHRLRGK DGKRVIAELLERFDLVESANKPAASYSGGMRRKLDLAMTLVTKPQIIFLDEPTTGLD PRSRRTMWEIVRELTDEGVTIFLTTQYLEEADQLADRIAVLDQGRIVAEGTAEELK RRVPGGHIRLRFADAAQLATAAQILPEATADHDALTLDVPGDGDSTTLRALLDRLA AHTIEAAQVSIHTPDLDDVFLALTGHATTEAEAR	6~~P-loop_NTPase (6.02086E-87) ~~224		

Disagreement between HMMER and CDD prediction	0.0053	25.6	0	4.5	16	0	2.2	2	Q6M9Y7_PARUW	Uncharacterized protein	pc1888	Protochlamydia amoebophila (strain UWE25)	576	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Parachlamydiaceae, Candidatus Protochlamydia, Candidatus Protochlamydia amoebophila, Protochlamydia amoebophila (strain UWE25)	264201	>tr|Q6M9Y7|Q6M9Y7_PARUW Uncharacterized protein OS=Protochlamydia amoebophila (strain UWE25) GN=pc1888 PE=3 SV=1 MTEALVFLQNVSKIFDPSHPPALCSLSAKLMPGKMIGIAGPDGAGKTTLLRLIAGLL LPSSGSITVAKYDTVLQAKHIHSLIGYMPQKFGLYEDLTVDQNLALYADLKGLEKEE RKEIFDKLLDFTGLKPFTKRLARALSGGMKQKLGLACTLLRKPQLLLLDEPNVGVD PISRRELWRMVQDLITNGITVLWSTAYLDEAEKCDSVILLNEGQLLYHGSPYEFAE RVRGRTFKLTHLQGNRREILTHILNQPFVKDGIIQGNDIRLVTENPNVELNPLSLPA GLSATVIPILPRFEDAFVDILGGGPKGPSPLAVQIPQISSCQKEIIQARDLVKKFGSF TAADHINFTVEEGEIFGLLGPNGAGKSTTFKMMCGLLKPTAGSAIVNGLNLQLAPG KVRSQIGYMAQKFSLYGNLSVSQNLNFFSGIYNLRGKHRQKMIDQMIVIFGLQDYL NESAETLPLGLKQRLALSCSLMHYPKVLFLDEPTSGVDPITRREFWNHINGLVKKG VTVMVTTHFMEEAEYCDRIGLIYRSRLIQVGTPENLKSIAKTVQNPYPTLEDAFIHLI EEYEKENPT	8~~P-loop_NTPase (1.38862E-46) ~~221,329~~P-loop_NTPase (8.41833E-81) ~~546		

Disagreement between HMMER and CDD prediction	0.0057	25.5	0	0.01	24.7	0	1.3	1	A0A0F4IQH3_9ACTN	ABC transporter	VR46_42675	Streptomyces sp. NRRL S-444	320	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-444	1609134	>tr|A0A0F4IQH3|A0A0F4IQH3_9ACTN ABC transporter OS=Streptomyces sp. NRRL S-444 GN=VR46_42675 PE=3 SV=1 MTNLAIAANGLRKSYGDKSVLDGIDLNVPEGTIFSLLGPNGAGKTTAVKILSTLISAD AGEIRVAGHDLAADPQAVRAAIGVTGQFSAVDGLITGEENMLLMADLHHLSKSEG QRVTAELLQRFDLVEAAKKPAASYSGGMKRRLDIAMTLVGNPRIIFLDEPTTGLDP RSRHNMWQIIRELVTGGVTVFLTTQYLEEADQLADRIAVLNNGKIAAEGTAEELKR LIPGGHVRLRFSDPAAYQAAAAVLGDVARDDEALALQIASDGSQRDLRSVLDRLD SAGVEADELTVHTPDLDDVFFALTGATVPSQTNEAKEAVR	6~~P-loop_NTPase (6.87318E-94) ~~224		
Disagreement between HMMER and CDD prediction	0.0064	25.3	0	0.017	23.9	0	1.7	1	H5X7V6_9PSEU	Daunorubicin resistance ABC transporter ATP-binding subunit	SacmaDRAFT_4268	Saccharomonospora marina XMU15	320	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharomonospora, Saccharomonospora marina, Saccharomonospora marina XMU15	882083	>tr|H5X7V6|H5X7V6_9PSEU Daunorubicin resistance ABC transporter ATP-binding subunit OS=Saccharomonospora marina XMU15 GN=SacmaDRAFT_4268 PE=3 SV=1 MTNKTARPAIAVSGLRKAFGDKVVLDGIDLTVAQGTIFSLLGANGAGKTTMVKILST LLAATGGHAEVAGHDVASDPDSVRAAIGVTGQFSAVDNLLTGEENLRLMADLNHL SKADGRRKAAELLERLELTEAARKPVATYSGGMRRRLDLAMTLVGNPRLIFLDEPT TGLDPRSRRGMWRIVRELVDGGVTVFLTTQYLEEADELADRIAVLEGGRLVAQGT SEELKRRIPGGHVELRFDEPEIFRAAQRVLGRAAYRDGDAMSLRVGNDGSVRQL KALLDLLDSEAIEVEGLSVHTPDLDDVFLALTGDPDDKKVTAR	10~~P-loop_NTPase (2.5037E-86) ~~228		

Disagreement between HMMER and CDD prediction	0.0064	25.3	0	0.012	24.4	0	1.4	1	Q82Q26_STRAW	Putative ABC transporter ATP-binding protein	SAV_695	Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	321	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces avermitilis, Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	227882	>tr|Q82Q26|Q82Q26_STRAW Putative ABC transporter ATP-binding protein OS=Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680) GN=SAV_695 PE=3 SV=1 MTNLAIAANGLRKSYGDKTVLDGIDLSIPAGSVFALLGPNGAGKTTAVKILSTLITAD GGQAQVAGHDLAAEAHAVRAAIGVTGQFSAVDGLITGEENMLLMADLHHLPKSE GQRVTAELLERFDLVEAAKKPASTYSGGMKRRLDIAMTLVGSPRIIFLDEPTTGLD PRSRHNMWQIIRELVTGGVTVFLTTQYLEEADELADRIAVLSDGKIAAQGTADELK RIVPGGHVRLRFTDPAAYQSAASALREGTRDDEALSLQIPSDGSQRALRSLLDQL DAAGIEADELTVHTPDLDDVFFALTGSTTVPAQPNQPKEAVR	6~~P-loop_NTPase (1.71518E-91) ~~224		

Disagreement between HMMER and CDD prediction	0.0066	25.3	0.6	0.024	23.4	0	2.1	1	V9W9R8_9BACL	Daunorubicin/doxorubicin resistance ATP-binding protein DrrA (EC 3.6.3.-)	drrA ERIC2_c31670	Paenibacillus larvae subsp. larvae DSM 25430	312	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus larvae, Paenibacillus larvae subsp. larvae, Paenibacillus larvae subsp. larvae DSM 25430	697284	>tr|V9W9R8|V9W9R8_9BACL Daunorubicin/doxorubicin resistance ATP-binding protein DrrA OS=Paenibacillus larvae subsp. larvae DSM 25430 GN=drrA PE=3 SV=1 MIVAEKLSKTFTVGKQTVEAVSSISFSIQKGEIYCLLGSNGAGKSTTVLMLSTLLRP SGGTAKIAGYDLLQNANAIRSIMGIVNQETGLDPLLTGKNIVTLHAKLWGYSRKEA KKRTNELLERYHLLEAADRPLKTYSGGMRRRLDLALALVRTPKVLFLDEPTTGLDP VSRRIIWEEVKMLRDQGVTVLLTTQYLDEADVLADRIGIVMNGTIAIENTPSALKKQ YGQEYITILLDNAGQAKQVAQLYPDAVIDQAEVKLKVADCTNEAPQILSVLHEQHIK ITSISITQPTLEDIYLSTTGYQVRGESNA	2~~P-loop_NTPase (9.47699E-94) ~~224		
Disagreement between HMMER and CDD prediction	0.0076	25.1	0	0.014	24.2	0	1.5	1	C0ZMQ9_RHOE4	Putative ABC transporter ATP-binding protein	RER_46090	Rhodococcus erythropolis (strain PR4 / NBRC 100887)	317	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus erythropolis (Arthrobacter picolinophilus), Rhodococcus erythropolis (strain PR4 / NBRC 100887)	234621	>tr|C0ZMQ9|C0ZMQ9_RHOE4 Putative ABC transporter ATP-binding protein OS=Rhodococcus erythropolis (strain PR4 / NBRC 100887) GN=RER_46090 PE=3 SV=1 MSGTIPAISVRGLRKRYGDQQVLGGLDLSVPAGSVYALLGANGAGKTTAVRILTTL IPFDGGEVTVAGHSLPGDPQNVRRRISVTGQYAAVDTLLTGFENLTLLGELNHLG RKNSRRRAEELLDQFDLKDFGDKRAGDYSGGMLRRLDIAMSLVARPDVVFLDEPT TGLDPRSRHEMWSIVRGLTASGVTIFLTTQYLDEADELADTVGVLSGGRLVAEGT PDELKHLVPGGHVALQFENLAQLELAAASLPQAHSNTETLTLHIPSDGAVPSIKAIL DSIDDPSITVEKFSVHTPDLDDVFFALTGSGQPEIASVR	8~~P-loop_NTPase (8.09092E-96) ~~226		

Disagreement between HMMER and CDD prediction	0.0083	25	2.5	0.047	22.5	0.8	2.1	1	F7YVE9_9THEM	ABC transporter related protein	Theth_0357	Pseudothermotoga thermarum DSM 5069	303	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Thermotogaceae, Pseudothermotoga, Pseudothermotoga thermarum, Pseudothermotoga thermarum DSM 5069	688269	>tr|F7YVE9|F7YVE9_9THEM ABC transporter related protein OS=Pseudothermotoga thermarum DSM 5069 GN=Theth_0357 PE=3 SV=1 MKVIAVKELKKYYGQVKAVDGISFEVEEGTVVAMLGPNGAGKTTTIEILEGLRKKD SGEIYYFGKKVEEIDETIKQMIGVQLQKTAFFEYLTVYETLELFAALYNKKVDKQRIK SLIELVALEEKAKAKIKELSGGQLQRLSLAVALVNDPKIVFLDEPTTGLDPQARRHV WQIVEDLRKSGKTIFLTTHYMEEAEKLADHVLIMDHGKIIAEGTVDQLINSLDMESY VEFWTDQPEKLLEKLEGTVLLNHDKLQIPAKNVEEVLHKLFDLSKTLQLKIDNIVIRR SNLEDVFLKLTGRLLRD	6~~P-loop_NTPase (5.30566E-81) ~~219		
Disagreement between HMMER and CDD prediction	0.0086	24.9	0	0.013	24.3	0	1.2	1	F6FT61_ISOV2	ABC transporter related protein	Isova_1365	Isoptericola variabilis (strain 225)	324	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Promicromonosporaceae, Isoptericola, Isoptericola variabilis, Isoptericola variabilis (strain 225)	743718	>tr|F6FT61|F6FT61_ISOV2 ABC transporter related protein OS=Isoptericola variabilis (strain 225) GN=Isova_1365 PE=3 SV=1 MPTSLAPHGAAVVVRGLVKRYGGTAVVDGLDLEARAGAVTAVLGPNGAGKTTTV ECCEGLRTPDGGTVRVLGLDPVADARLLRPRVGVMLQDGGLPSGVRAGEMLRH VAAMYAAPRDLGELAERLGLDSFARTTVRRLSGGQRQRLALAAAVVGRPEVVFL DEPSAGMDPQSRLAVWALVRELRDEGVAVVLTTHLMDEAEDLADVVHVVDHGRV IASGTVPELLTAEAAGARTVRLDAPPGLDVAALAAALDGRGAGGDDPTERWVVTE PEPGSYVATGPADARAVARLTAWLADGDVLASRLTVGRRTLEDVFLDLTGRHLR	12~~P-loop_NTPase (2.22013E-69) ~~215		

Disagreement between HMMER and CDD prediction	0.0086	24.9	0.3	0.025	23.4	0.1	1.7	1	D6DI17_CLOSC	Cobalt transport protein ATP-binding subunit	CLS_18030	[Clostridium] cf. saccharolyticum K10	308	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, [Clostridium] cf. saccharolyticum K10	717608	>tr|D6DI17|D6DI17_CLOSC Cobalt transport protein ATP-binding subunit OS=[Clostridium] cf. saccharolyticum K10 GN=CLS_18030 PE=4 SV=1 MKQTELTGTCRVCCRDMTQKETEAPARPVCPESEVILQADHLFFSYDQGRSCALRDLSLKIRRGSKTAFLGANGSGKSTFFLCCNGIHRPTSGTLSFAGKLVGYSRKELLSLRQKVGIVFQDPDSQLFSSSVYQEISFGVMNLGFPEEKARQAVERILDEMELTSLKSRPVHTLSGGQKKQVSIADILVMEPELVILDEPASALDPRHTKLVQEAVKRMTDKGITVMMATHNVDFALAWADEAVVLKDGCVLRQGTPEEIFTDRELLSQANLSVPAALRLFDSLCRKGILDPSLPIPRNLDELESYLA	38~~P-loop_NTPase (2.37115E-86) ~~249		
Disagreement between HMMER and CDD prediction	0.0089	24.9	0	0.02	23.7	0	1.7	1	W5W733_9PSEU	Daunorubicin/doxorubicin resistance ATP-binding protein DrrA (EC 3.6.3.-)	KALB_3193	Kutzneria albida DSM 43870	318	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Kutzneria, Kutzneria albida, Kutzneria albida DSM 43870	1449976	>tr|W5W733|W5W733_9PSEU Daunorubicin/doxorubicin resistance ATP-binding protein DrrA OS=Kutzneria albida DSM 43870 GN=KALB_3193 PE=3 SV=1 MTTRQSSAIAVTGLRKSFGDQVVLDGLDLTVRRGTVFSLLGANGAGKTTTVKILSTLLSADAGEVQVAGHDLAREPDAVRAAIGVTGQFSAVDNLLTGEENLLLMADLHHLARGEGRRRAAQLLEQFDLVEASRKPASTYSGGMRRRLDLAMTLVGSPQVIFLDEPTTGLDPRSRRNMWQIIRDLVAGGVTIFLTTQYLEEADELADRIAVLDHGRVVAEGTAEELKRRIPGGHVRLRFAAPQGLDAAMGLLGQASRDNDALALRVPSDGSLRSLKTLIDRLDDRAIEVDELSVHTPDLDDVFLALTGDSTNEKVTTR	9~~P-loop_NTPase (3.89144E-98) ~~227		

Disagreement between HMMER and CDD prediction	0.0097	24.7	0	0.017	24	0	1.3	1	B5HLD9_9ACTN	Nodulation ABC transporter NodI	SSEG_08323	Streptomyces sviceus ATCC 29083	319	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sviceus, Streptomyces sviceus ATCC 29083	463191	>tr|B5HLD9|B5HLD9_9ACTN Nodulation ABC transporter NodI OS=Streptomyces sviceus ATCC 29083 GN=SSEG_08323 PE=3 SV=1 MTDLAIAANGLRKSYGDKTVLDGIDIQVPAGTIFALLGPNGAGKTTAVKILSTLITAD GGQARVGGHDLTAEAQAVRASIGVTGQFSAVDGLITGEENMLLMADLHHLSRSE GRRVSAELLERFDLTEAAKKPASTYSGGMKRRLDIAMTLVGDPRIIFLDEPTTGLD PRSRHTMWQIIRELVSDGVTVFLTTQYLEEADELADRIAVLHNGTIAAEGSAEQLK RLVPGGHVRLRFTDPDAYRGAARALREGTRDDESLTLRLPNGGSQSELRALLDQL DAAGIEADELTVHTPDLDDVFFALTGGSADVTDQTKETVR	6~~P-loop_NTPase (4.84927E-94) ~~224		
Disagreement between HMMER and CDD prediction	0.0097	24.7	0	0.017	23.9	0	1.3	1	V6KLC2_STRRC	ABC transporter	M878_19750	Streptomyces roseochromogenus subsp. oscitans DS 12.976	326	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	1352936	>tr|V6KLC2|V6KLC2_STRRC ABC transporter OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_19750 PE=3 SV=1 MTTTEHALAIAATGLRKAYGDKTVLDGIDIQVPAGTIFSLLGPNGAGKTTAVNILSTL ISADAGEARVAGHHLTAEAQAVRAAIGVTGQFSAVDGLITGEENMLLMADLHHLS RREGRRATVELLERFDLVEAAKKPASTYSGGMKRRLDIAMTLVGNPRIIFLDEPTT GLDPRSRHTMWQIIRELVAGGATVFLTTQYLEEADQLADRIAVLNGGKLVAEGSA DELKRLVPGGHIRLRFSEPVAYERAATALRETTRDDESLALQIPSDGSQRELRAVL DWLDAAGIEADELSVHTPDLDDVFFALTGSPVPAQPANSVAKETTR	10~~P-loop_NTPase (8.00335E-92) ~~228		

Sheet 4

All KdpA proteins retrieved from the RFP														
HMMER search output														
Whole protein prediction			**KdpA domain prediction**					**Uniprot entry name**	**Protein name**	**Gene name**	**Organism (and Synonym)**	**Protein length**	**Taxonomic lineage (ALL)**	**Organism ID**	**Protein sequence**
E-value	**score**	**bias**	**E-value**	**score**	**bias**	**exp**	**KdpA domain number per protein**								
4E-250	840.1	34	5E-250	839.8	23.6	1	1	I4D2C5_DESAJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Desaci_0902	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	565	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	646529	>tr|I4D2C5|I4D2C5_DESAJ Potassium-transporting ATPase potassium-binding subunit OS=Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4) GN=kdpA PE=3 SV=1 MRTMDIVQILFYVLILTVLAIPLGRYMAKVFSQENTWVDPLFRPLEKLIYRLTGTDEQSEMDW KSYAGALLIFNFCGFFVLFLLQLLQKYLPLNPQGFGAVSPDLAFNTAASFVTNTNWQAYSGE STMSYMVQMAGFTVQNFVSAATGIVVVIALTRGLARKTASTIGNFWVDLTRSILWILLPLSVI GALVLTQQGVIQNFSSYLHLATLDGGKQTLAMGPVASQEAIKMFGTNGGGFFNANSAHPFE NPTPLSNFLEMLFILLIPAALPFTFGHMVGNPKQGRVIFVTMLVLFLIFVGATYSSEMYGNPN VTALGISGPSAMEGKEVRFGVANSALFATITTAASCGAVNAMHDSLTPLGGMIPMLQMMLG EVVFGGVGAGLYGMLIFVILTVFIVGLMVGRTPEYLGKKIESWEIKMATIAILVPAVTILVGSAL ASVTKAGTSSILNPGPHGLSEILYAFTSAGANNGSAFAGLNANTPFYNIAIGIAILLGRFGIILP VLAIAGGMVKKKAIPEGPGTFQTTGLLFGGLLAGIVIIVSALTFFPALALGPIVEHLIMIGK
1E-248	835.4	31.1	1E-248	835.2	21.5		1	KDPA_RHILO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA mll3133	Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium, Rhizobium loti (Mesorhizobium loti), Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	266835	[illegible] OS=Rhizobium loti (strain MAFF303099) GN=kdpA PE=3 SV=1 MTLNGWIQILVFCGIIGLLTKPLGFYMHRVFNGDRTPLSPIFGPLERGLYRICGTSEREEQH WTAYAVALLLFNLAGFLVLYALQRLQGSLPYNPAGMGAVDPALAFNTAASFVTNTNWQNY GGESTMSYLLQMAGLTVQNFVSAATGIAIAIALIRGFARASGKSIGNFWVDMTRCTLYVLLPL CIVLTLVYVWLGIPQTLGPYVDATTLEGAKQTIALGPVASQVAIKMLGTNGGGFFNANAAHP FENPDAISNLIQMVTIFALGAALTNVFGRMVGNQRQGWAILASMGALFIAGVAVCYWAEAA GNPLVHALGLDGGNMEGKETRFGIALSALFAVITTAASCGAVNAMHDSFTALGGMIPLINMQ LGEVIVGGVGAGFYGILMFIVVAVFVAGLMVGRTPEYLGKKIEAKEVKMAMLAILCLPLAMLIF TAIAVVLPSAVASIANGGPHGFSEVLYAYTSAAANNGSAFGGLSGNTPWYNITIGIGMLMGR FLVIIPALAIAGSLAAKKTVPASAGTFPTDGPLFVGLLIGVIVIVGGLTFFPALAVGPIIEHLAMIH GQTF

5E-248	833.3	28.6	6E-248	833	19.8	1	1	E8V6X7_TERSS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AciPR4_4258	Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	587	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus saanensis, Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	401053	>tr|E8V6X7|E8V6X7_TERSS Potassium-transporting ATPase potassium-binding subunit OS=Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4) GN=kdpA PE=3 SV=1 MSLNGWLQIVLFIAAVLLLAKPMGSYLTRVFERRRTFLDPLLAPCERLLYRLTGVKPEEEMR WTEYAVAMLAFSTATLVLTYAIERLQHLLPLNPQHLTGVEPALALNTAISFTTNTNWQSYVP ESTMSYLTQMVGLATHNFWSAAVGLALAVAFVRGIARREAKTLGNFWVDLTRGTLWVLLPI SIVFALALVSQGVVQNFRAYDTAKLVEPQHSVGTDGKTTTITTQTIAQGPVASQEAIKMLGT NGGGFFNANSAHPFENPTPLTNFLQMLSIFLIPAGLTVMLGQMVGSPKHGWAILAAMVVLW FAGTATCYWAESQANPLLHGVDQHASLTQSGGNMEGKEVRFGIANSALFAAVTTDASCGA VNGMHDSFTPLGGMVPMVNILLGEVVFGGVGAGLYGMLVFVIMAVFIAGLMVGRTPEYLGK KIEAYDIQMAMLYLLIFPLLILGFAAVAVRMPNLGLGSLANRGPHGLSEILYAYTSATGNNGSA FAGLNANTHWWNYSLAVAMFFGRFMMIVPMLAIAGNLAGKKITPASAGTFPVTTPLFTLLLT GVIVIVGALTFFPALSLGPVLEHLLLRAGHTF
9E-248	832.3	37.9	1E-247	832.1	26.3	1	1	J7J1Q1_DESMD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Desmer_2982	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	568	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	768704	>tr|J7J1Q1|J7J1Q1_DESMD Potassium-transporting ATPase potassium-binding subunit OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=kdpA PE=3 SV=1 MMSNDFIQLIVFFVVLFALAIPLGLYMAKVFQGEKTFLDPIMGPLEAFIYRICGIDAQKEMNW WEYALSLLVFSFVGLFTLFILQLGQGYLPLNPQGFGGLKWDLAWNTAVSFTTNTNWQAYG GESTMSYLSQMAGLTVHNFVSAAAGIAVVVALIRGLSRHQAKTIGNFWVDLTRTILWILLPIS LVGGMLLVSQGVIQNLSPYLTVKTLQGANQTLAMGPVASQEAIKMLGTNGGGFMNANSAH PFENPTPFSNLVEMLLLLLIPVGLTFSFGKMLKDAKQGKVIFGAMLILLVLTLGTTYSTEIAGN PLVSKIGITGSSVMEGKEVRFGVVNSALWATITTATSCGAVNAMHDSLTPLGGLSPMLQMM LGEVVFGGVGSGLYAMLLFVILTVFIIGLMVGRTPEYVGKKIESFEMKMAILAVLIPSACILLGS ALAVLITAGTSSILNPGPHGLSEILYAFSSATGNNGSAFAGLNVNTVFYNIILSVCMLIGRFSPI VLVLAIAGSMAGKKITPAGAGTFQTTGGLFSGLLAGVVLIVGALTFFPALALGPIVEHLLMLAG KAF
1E-247	831.9	32.6	2E-247	831.7	22.6	1	1	E8RRM4_ASTEC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Astex_0658	Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Asticcacaulis, Asticcacaulis excentricus, Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	573065	>tr|E8RRM4|E8RRM4_ASTEC Potassium-transporting ATPase potassium-binding subunit OS=Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48) GN=kdpA PE=3 SV=1 MFLGIPSAGWLQLVLFMAALTALAVPLGDYVARVLSGQRTWLSPVFTPVEGLIYSMGDVRP DQDMRWTDYATAVILFSFGGFALLFGLLLTQGVLPFNPQHLPNLTPDLAFNTAVSFVTNTN WQSYAGETTLSYFSQMVGLTVQNFVSAAVGIAVLAAVIRGLTGQTTDKLGNFWVDLVRIQL YILLPLALIVAIALSSQGVIQTFASYVTAHTLEGASQTIAMGPVASQEAIKMLGTNGGGFFNTN SAHPFENPTPLSNLIEMLSILLIPAALCFTFGKMIGDRRQGIAIFVAMTLIFVPLTATCIGLEQAG NPHLVAAGAQAGGNMEGKDTRFGIANSAIWATATTAASNGSVNAMHDSFTPLGGLIPMILM QFGEVIYGGAGSGLYGMLVFVILTVFIAGLMVGRTPEYLGKKIGAFEIKMASIAVLLPCALVLI CTAVAVLTPWGQAGIYNPGAQGFSEVLYAFTSAANNNGSAFAGLSANSPFYNSLLGLCMLF GRFFVLLPVLAIAGSLAAKRTVPTSAGTLATHTPLFVVFLMGVIIIVGVLTYAPALALGPVIEHL NLIKG
2E-247	831.5	27.9	2E-247	831.2	19.3	1	1	D3P2B6_AZOS1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AZL_b02730	Azospirillum sp. (strain B510)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum sp. (strain B510)	137722	>tr|D3P2B6|D3P2B6_AZOS1 Potassium-transporting ATPase potassium-binding subunit OS=Azospirillum sp. (strain B510) GN=kdpA PE=3 SV=1 MNAADSLQIIVFCVLLVALTPLAGGYMARVFTGERVPLDRLLGPVERGIYRLCGIRADQEQH WTAYALAMLAFNLLGFLLLYALLRAQSWLPLNPAGMAPVSPDLAFNTAVSFMSNTNWQAY GGESTLSYLSQMAGLTVQNFVSAATGIAVLVALIRGFVRRSARTVGNFYVDMTRATLYVLLP LSIVTALFLVSQGVPQNLDSYAVATTVEGGQQVIAQGPVASQEAIKQLGSNGGGFFSVNSA HPYENPTPLANFVEMVFLLMLAAGLTDTFGRMVGDRRQGWAIFAAMGILFLAGLGVACWA ELQANPAAIAAGLDPAAGNMEGKEVRFGIINSALWAVATTAASNGSVNAMHDSFMPLGGMI PMVNIMLGEVVFGGVGAGLYGMLIFVVLAVFIAGLMVGRTPEYLGKKIEAKEIKLAMIATLTLP LGVLGFSALTLVLPAGLAGIQDPGPHGLSEVLYAYSSATGNNGSAFAGFAANSLYHNTTIAL AMLLGRFLVILPVLAIAGGLAAKRAVPASAGTFPTHGGLFIGLLVGIVLIVGGLTFFPALALGPI VEHLMLGTGTFF
3E-247	830.6	18.5	4E-247	830.4	12.8	1	1	D5MJC7_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DAMO_0410	Candidatus Methylomirabilis oxyfera	601	cellular organisms, Bacteria, unclassified Bacteria, candidate division NC10, Candidatus Methylomirabilis, Candidatus Methylomirabilis oxyfera	671143	>tr|D5MJC7|D5MJC7_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Candidatus Methylomirabilis oxyfera GN=kdpA PE=3 SV=1 MTANGYAQLGLYMVVLLALAKPLGAYMARVYEGRPFGLDRLLGPFERWIYRLSGIRADDEM RWQTYARAMLLFNLTGVLMVYALQRMQGLLPLNPQSLGPVSPDSAFNTAVSFATNTNWQ GYGGETTMSYLTQMLGLTVQNFLSAATGMAVLVAFIRGLARRSAQTIGSFWVDLTRTTLYIL LPLSLVLALALASQGVVQTFGPYAKASVVQPTTYDEPVTDKDGTPVLDEKGRPVTKKARLTE QVIALGPVASQVAIKQLGTNGGGFFNVNSAHPYENSTPLSNFLELLAILLPAALCHTFGVMV KDTRQGWAILAAMTIMFVGLLALCVGAEQGGNPLLTGLGIDQHAGELQAGGNMEGKEVRF GIVNSALWATATTAASNGSVNAMHDSFTPLGGLAPIWLIQLGEVVYGGVGSGLYGMLVFAII AVFVAGLMVGRTPEYLGKKIEAYEMKMASLVILIPPALVLLGTAVAVVTSGGKAGISNPGPH GFSEILYAFSSAGNNNGSAFAGLGANTPFYNISLGVAMFFARYWLAIPTLAIAGSLAGKKPVP PGPGTLPTHTPLFVALLISVVVIVGALTFFPALALGPIVEHLIMMSS

1E-246	828.6	27.1	1E-246	828.4	18.8	1	1	KDPA_SORC5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA sce1352	Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	580	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Sorangiineae, Polyangiaceae, Sorangium, Sorangium cellulosum (Polyangium cellulosum), Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	448385	>sp|A9F773|KDPA_SORC5 Potassium-transporting ATPase potassium-binding subunit OS=Sorangium cellulosum (strain So ce56) GN=kdpA PE=3 SV=1 MTASGALQPALYLAVLIGLSVPLGTYMARVYQGERGLMASVLGPLERLAYRAAGVRPDQE MRWKDYAFAVLAFNLAGLLVLYALQRLQGVLPLNPEGMAAVPPDLAFNTAASFASNTNWQ AYGGESTLSYLTQMAGLGVQNFVSAATGMAVLVALIRGITRKTADTVGSFWVDLVRSTLYIL LPLSLLLAVLLVSQGVVQGFGGHQSASLLQAVKDQGGSAVVEQVIPMGPAASQIAIKQLGTN GGGFFNVNSAHPLENPTALSNFLEMLAILLIPAALCHTFGRMVGDRRQGWAVLAAMTAIFAV LLVACVASEQAGNPALSALGVDQAASALQAGGNMEGKEARFGITSSALWATATTAASNGS VNAMHDSFTPLGGLVPLWLMQLGEVVFGGVGSGLYGMLMFVVIAVFVAGLMVGRTPEYLG KKIEAFEMKMASLVVLFPAITVLVGTAIAVTTEGGQKGVFNPGPHGFSEVLYAFSSGANNNG SAFGGLGANSPFYNTAIGVAMLVGRYAVIVPVLALAGSLARKKLVPAGPGTLPTHTPLFVGL LTGTVLLVGALTFVPALALGPVVEHLEMTR
2E-246	827.7	26.5	3E-246	827.5	18.4	1	1	D5SYH3_PLAL2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Plim_1871	Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	582	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Planctopirus, Planctopirus limnophila (Planctomyces limnophilus), Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	521674	>tr|D5SYH3|D5SYH3_PLAL2 Potassium-transporting ATPase potassium-binding subunit OS=Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) GN=kdpA PE=3 SV=1 MTSNGLVQLAIYLGVLLACVKPLGFYMARVYSGSATFLDRFIGPLERLLYRLCGIDKSAEMT WRQYSVAAMSFSLVSFLAVYAFQRTQGWLPLNPESLPAVSPDSSFNTAVSFTTNTNWQG YGGETTMSYLTQMLALTVQNFVSAAAGMAVLVALIRGFTRHTTETIGNFWVDLVRGTLYILL PLSLFLAVALVSQGVVQTFNSYHEVAFLEPTVDAEGHAVTTQSIAVGPAASQIAIKQLGTNG GGFFNVNSAHPLENPTPLSNFLQLLAILLIPAALCYTFGEMIGDRRQGWAVLAAMLVIFVPLL AATTITEQSGNPILARLGADQSASDSQPGGNMEGKESRFGIVNSSLWAVATTAASNGSVNS MHDSFTPLGGLVPMWLMQLGEVIFGGVGSGLYGLLMFAIVAVFLSGLMVGRTPEYLGKKIG AFEMKMAALAILFPCAMVLVGTAVSVVSASGRATIFNPGPHGFSEVLYAFSSAGNNNGSAF AGLGANTPFYNGLLGLAMLVGRFWVMLPVLAIAGSLAAKKTVPAGPGTLPTHTPLFVVLLVA VVIVVGALSFFPALALGPIVEHLLTANQE
3E-246	827.4	35.4	3E-246	827.1	24.5	1	1	E8TDR1_MESCW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mesci_1800	Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium, Mesorhizobium ciceri, Mesorhizobium ciceri biovar biserrulae, Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)	765698	[illegible] OS=Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271) GN=kdpA PE=3 SV=1 MTLNGWIQILVYCGIVILLVKPLGGYMHRVFDGDRTLLSPLFGPLERGLYRVCGTSEREEQH WTTYAVALLLFNLAGFLVLYALQRLQGSLPYNPAGMTAVEPGLAFNTAASFMTNTNWQNY GGESTMSYLVQMAGLTVQNFVSAATGIAIAIALIRGFARASGKSIGNFWVDMTRSTLYLLLPF CVVLTLAYVWLGMPQTLGAYVNATTLEGAQQTIAVGPVASQVAIKMLGTNGGGFFNANAA HPFENPDAISNLIQMVSIFAIGAALTNVFGRMIGNQRQGWAILSAMGVMFIAGVAICYWAEA AGNPLVHALGIDGGNMEGKETRFGIALSALFAVITTAASCGAVNAMHGSFTALGGMIPIINM QLGEVIVGGVGAGLYGILMYIVVAVFVAGLMAGRTPEYLGKKIEAKEVKMAMLAILCLPLAML IFTAIAVVLPTGVASMGNAGPHGFSEVLYAYTSAAANNGSAFGGLSGNTPWYNITIGIGMLM GRFLVIIPALAIAGSLVAKKTVPASAGTFPTDGPLFVGLLIGVILIVGGLTFFPALAVGPIIEHLA MAHGQTF
4E-246	827.1	32.4	4E-246	826.8	22.5	1	1	A0A0C1PZ83_9ACTN	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LK07_41650	Streptomyces pluripotens	590	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pluripotens	1355015	>tr|A0A0C1PZ83|A0A0C1PZ83_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces pluripotens GN=kdpA PE=3 SV=1 MNAFLLQLAIYLVVLLVLAKPLGAYMTGVFGDKPSRTHWLGPVERLFYRVAGVNPKAEMG WKHYALAVIVVNVLGALAVYALQRAQQWLPLNPQGFGAVTPDSSFNTAVSFVTNTNWQGY SGESTMSYLTQMLGLAVQNFLSAATGIAVVIALIRGFARHSANTIGNFWVDFTRSTVYVLLPL SIIVSVFFVSQGVIQNFDGYKEVTTVTATTYDNPKMDASGQPIKDAQGNPVTEKATTQTQTL PMGPIASQEAIKMIGTNGGGPFNANSAHPYENPNALTNFVQMLCIFIIPAALCFTFGGMVGD GRQGWAVLAAMTVLFVVLAVFLAWAELHANPMLTNLGIDQTVGNMEGKETRFGIVASSLFA TITTAASCGAVNAMHDSLTALGGFVPMFLMQLGEVVFGGVGSGLYGMLVYAILAVFIAGLMI GRTPEYLGKKIEVFEMKMTSIAILVTPLLVLVGTAVAVVVTQGKAGIFNPGTHGFSEVLYAFS SAANNNGSAFAGLSANTPFYNVALGICMWLGRFWIIVPVLAMAGTFAAKKRLPVTAGTLPT HGPLFVVLLIGSVLLVGALTYIPALALGPIAEHLAR
5E-246	826.8	31.7	5E-246	826.5	22	1	1	KDPA_RALPJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Rpic_3589	Ralstonia pickettii (strain 12J)	590	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia pickettii (Burkholderia pickettii), Ralstonia pickettii (strain 12J)	402626	>sp|B2UH25|KDPA_RALPJ Potassium-transporting ATPase potassium-binding subunit OS=Ralstonia pickettii (strain 12J) GN=kdpA PE=3 SV=1 MNAFLLQLAIYLVVLLVLAKPLGAYMTGVFGDKPSRAHWLGPVERLFYRVAGVNPQAEMG WKHYALAVIVVNVLGALAVYALQRAQQWLPLNPQGFGAVTPDSSFNTAVSFVTNTNWQGY SGESTMSYLTQMLGLAVQNFLSAATGIAVVIALIRGFARHSANTIGNFWVDFTRSTVYVLLPL SIIVSVFFVSQGVIQNFDGYKEVTTVTATTYDNPKMDASGQPIKDAQGNPVTEKATTQTQTL PMGPIASQEAIKMIGTNGGGPFNANSAHPYENPNALTNFVQMLAIFIIPAALCFTFGGMVGD GRQGWAVLAAMTVLFVVLAVFLAWAELHPNPMLANLGIDEAVGNMEGKETRFGIVASSLFA TITTAASCGAVNAMHDSLTALGGFVPMFLMQLGEVVFGGVGSGLYGMLVYAILAVFIAGLMI GRTPEYLGKKIEVFEMKMTSIAILVTPLLVLVGTAVAVVVTQGKAGIFNPGTHGFSEVLYAFS SAANNNGSAFAGLSANTPFYNLALGICMWLGRFWIIVPVLAMAGTFAAKKRLPVTAGTLPTH GPLFVVLLIGSVLLVGALTYIPALALGPIAEHLAR

5E-246	826.5	37.9	6E-246	826.3	26.3	1	1	C3KRJ0_RHISN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NGR_b12460	Rhizobium sp. (strain NGR234)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Sinorhizobium fredii group, Rhizobium fredii (Sinorhizobium fredii), Rhizobium sp. (strain NGR234)	394	>tr|C3KRJ0|C3KRJ0_RHISN Potassium-transporting ATPase potassium-binding subunit OS=Rhizobium sp. (strain NGR234) GN=kdpA PE=3 SV=1 MTINGWIQILVFCGIVTLLVKPLGGYMTRVFNGERTLLSWIFAPVERGLYAVAGTSEREEQH WTTYAAALLFFNLAGFLLLYFLQRFQGALPFNPAGMAAVPPELAFNTAVSFMTNTNWQNY GGESTMSYLVQMAGLTVQNFVSAATGIAIAIALIRGFSRASVKSIGNFWVDMTRATLYVLLPL SVVLTLIYVYLGMPQTLGAYVEATTLEGAQQTIAVGPVASQIAIKMLGTNGGGFFNANAAHP FENPDAISNLIQMVSIFAIGAALTNVFGRMVGNQRQGWAIFATMGVLFLAGVVVCYWAEAA GNPLVHALGLEGGNMEGKEVRFGISLSALFAVITTAASCGAVNAMHDSFTALGGLIPLINMEL GEIIVGGVGAGFYGILLFVVLAIFVAGLMVGRTPEYLGKKIEAKEVKMAVLAILCLPLAMLVFT AIAVVLPDAVASIANPGPRGFSEILYAYTSAAANNGSAFGGLTGNTVWYNLTLGIAMLMGRF LVIIPALAIAGSLVAKKTVPASAGTFPTDGALFVGLLSGVILIVGGLTFFPALAVGPIVEHLAMLL GQTF
6E-246	826.4	31.1	7E-246	826.2	21.6	1	1	E3I291_RHOVT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Rvan_3287	Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Rhodomicrobium, Rhodomicrobium vannielii, Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	648757	>tr|E3I291|E3I291_RHOVT Potassium-transporting ATPase potassium-binding subunit OS=Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299) GN=kdpA PE=3 SV=1 MTLAGWAQILVFCAIVVASAKPLGAYMTHVFAGERTFLSFILSPVERIFYALAGVDPKAEQR WSAYALSMLAFNFAGFLLLYAILRLQDLLPLNPQGMGGMPPDLALNTAASFVTNTNWQNYG GESTLGYFAQMAGLTVQNFVSAATGIALAVALIRGFTRRSAAGIGNFWADLTRCTLYILLPLS LVIALTLVWQGMPQNLNPYVETTTLEGGKQVIAQGPVASQVAIKMLGTNGGGFFNANAAHP YENPTPLSNMIQMIAIFALSAGLTNVFGRLAGDQRQGWAIFGAMGALFLVGVSLAYWAEAN GNPLLTALGLDGAPGNIEGKETRFGIAASALFATITTAASCGAVNAMHASLTPLGGLVPLVN MELGEVVIGGVGAGLYGMLLFAILSVFVAGLMVGRTPEYLGKKIEAREVKLTMLALLCLPLM MLGFTALAVVVPNGLSSISSAGPHGFSEVLYAYTSAAGNNGSAFAGLSGNTVFYNTTLAIAM LVGRFFVIIPMLAIAGSLAAKKIVPPSSGTFPTNGPLFAGLLIGVVVLVGGLTLFPALALGPIVE HLAMIAGQTF
6E-246	826.4	36.6	7E-246	826.2	25.4	1	1	G7ZDN7_AZOL4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AZOLI_p20514	Azospirillum lipoferum (strain 4B)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum lipoferum (strain 4B)	862719	>tr|G7ZDN7|G7ZDN7_AZOL4 Potassium-transporting ATPase potassium-binding subunit OS=Azospirillum lipoferum (strain 4B) GN=kdpA PE=3 SV=1 MTVNGWIQILVFLALVVAVTRPLGGFMTRVFTGERTLLSPIVGPVERGLYRLAGVDERTEQH WVSYAVSMLLFSAAGMLLLYALQRLQAVLPLNPQGMAAVPADLAFNTAASFTTNTNWQNY GGETTMGHLVQMAGLTFHNYVSAAVGIALAVALVRGFARASSRTVGNFWVDLTRATLYVLL PLCLVYALFLVWQGVPQTLAGSVDATTLEGARQTIALGPVASQEAIKMLGTNGGGFFNANS AHPFENPNALTNLVQMLSIFALGAGLTNLFGRMVGDERQGWAILAAMGLLFVAGVTIAYWA EAQGNPAFAALGIDGSAGNMEGKETRFGIAASALFATVTTAASCGAVNAMHDSFMPLGGM VPMINMMLGEIIVGGVGAGLYGMLLFAIVALFVAGLMVGRTPEYLGKKLEAKEVKMTMLAILC LPLMMLGFTAAAVVLDTGTASMANAGPHGFSEALYAYVSGAANNGSAFGGLSGNTPWYN VTLAIAMLVGRFLVIVPMMAIAGSLAAKTRATASAGTFPTHDGLFVGLLVGVILIVGGLTFFPA LALGPVVEHLAMSAGTLF
7E-246	826.2	25.6	8E-246	826	17.7	1	1	V5U8L9_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA X636_00795	Pandoraea sp. RB-44	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Pandoraea, Pandoraea sp. RB-44	1380774	>tr|V5U8L9|V5U8L9_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Pandoraea sp. RB-44 GN=kdpA PE=3 SV=1 MTLNAWIQLGVFLAALLVLARPLGRFMADVLAGESRVNRWFAPLERTLYRLCGIDPDKEMH WRAYAVALLGFNALGALAVYALQRWQVWLPLNPQGFGAVTPDSSLNTAVSFVANTNWQG YAGESTMSYLTQMLGLAVQNFLSAATGIAVVIALIRGFARHTAQTIGNFWVDMTRITLYILMP LCVVLAAALMSQGVIQNFDAYKDVTTLQVTHYDNPVLGADGQPKTDAAGKPVTVPALTHTQ TLPMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPLSNFLEILAIFLIPAALCHTFGRMVG DRRQGLAILAAMTIAFSIAAVATVSAEQAGNPVLAPLGVDQQASATQPGGNMEGKETRFGI VASGIFATVTTAASCGAVNAMHDSLTPLGGLVPMLLMQLGEVIFGGVGSGLYGMLVFAMLA VFVAGLMIGRTPEYLGKKIEAFEMKMVAVAVLMTPLLVLCGTALAVLLPMGQAGVANPATH GFSEILYAYSSAANNGSAFAGLSANTPFYNTTLAIAMWFGRFWVIVPVLAIAGGLARKKRIA ATSGTLPTHGPLFVVLLLGTVLLVGALTYVPALALGPVAEHLAMIGAH
9E-246	825.7	25.8	1E-245	825.5	17.9	1	1	KDPA_RHOCS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RC1_0436	Rhodospirillum centenum (strain ATCC 51521 / SW)	573	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum centenum (Rhodocista centenaria), Rhodospirillum centenum (strain ATCC 51521 / SW)	414684	>sp|B8IQY9|KDPA_RHOCS Potassium-transporting ATPase potassium-binding subunit OS=Rhodospirillum centenum (strain ATCC 51521 / SW) GN=kdpA PE=3 SV=1 MTAEGLLQILLYLGLLAAVTPLLGRYMARVFEGERTLPGIVLGPLERGLYRIAGIDPAREQHW TGYTLALLSFNLLGLLLLYALLRFQALLPLNPAELGPVGPDLAFNTAVSFTTNTNWQSYGGE TTLSYLSQMLGLTVQNFVSAATGIAVAVALIRGFARRAGKTVGNFWADLVRATLYVLLPLAFL GALVLVWQGVPQNFDAYVTATTLEGGNQVLAQGPAASQIAIKQLGSNGGGFFNVNSAHPY ENPTALTNLLESFYLLMIAAALIYSFGRMVGDTRQGRALWTAVFILFVAGLAVTWWAEAQG NPAVTALGVETTDGNMEGKEVRYGTALSALWAVATTAASNGSVNAMHDSFMPLGGMVPM LNMMLGEVIYGGVGAGLYGLLVFVILAVFIAGLMVGRTPEYLGKKIEAREIKLAVIAVLVFPLGI LGGAALTTVVPQMLASVQDPGPHGLSEILYAYTSATGNNGSAFAGFGANTPWHNTGLGLA MLLGRFAVIVPTLAIAGSLVAKRAAPAGPGTLPTHGTLFITLLIATILFVGGLTFFPALALGPIAE HLSLTAGTLFGAVP

1E-245	825.6	30.2	1E-245	825.4	20.9	1	1	A0A0F3L053_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VI08_04295	Luteibacter yeojuensis	573	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Luteibacter, Luteibacter yeojuensis	345309	subunit OS=Luteibacter yeojuensis GN=kdpA PE=3 SV=1 MTTNDFLQLGLYLAVLMALVKPLGAYMALVFADAPNRVTRVGAPVERLLYRLAGVRADEDM GWKRYALAMLVFNVAGVAAVYLLQRTQQWLPLNPQHLGTITPDSAMNTAISFATNTNWQG YAGESTMSYLTQMLGLAVQNFLSAATGIAVLIAVVRGFARRGAGAVGNFWVDVTRTTVYILV PFSLLIAVLLLSQGVVQTLSPYVDVATLQHGTQSLPLGPVASQEAIKMLGTNGGGFFNANSA HPFENPTPFSNFIEMLAIFAIPASLCYTFGSMVGDRRQGWAILATMLLIFVPLTVGLVAAEQA GNPALHGLAIDAQASAMQAGGNMEGKETRFGIASSGLFAAITTAASCGAVNAMHDSLTPLG GLVPMWLMQLGEVIFGGVGSGLYGMLAFAVVAVFIAGLMVGRTPEYLGKKIEAHEMKMASL AVLIPCALVVVCTAIAVMVPGGKAGIANPGAHGFSEMLYAVSSAANNNGSAFAGLSANTPF WNTLLAICMFLARFPLAIAMLAMAGSLAAKRHVPPSAGTLPTHTPLFIALLACVVIVVGALTFL PALALGPIVEHLTSITGH
1E-245	825.4	27.8	1E-245	825.2	19.2	1	1	KDPA_RALSO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RSc3382 RS02656	Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	590	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia solanacearum (Pseudomonas solanacearum), Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	267608	>sp|Q8XU12|KDPA_RALSO Potassium-transporting ATPase potassium-binding subunit OS=Ralstonia solanacearum (strain GMI1000) GN=kdpA PE=3 SV=1 MNAFLLQLAIYLAVLLVLARPLGTYMARVFGDAPSRAHWLRSVERLLYRVAGVDPRAEMGW KHYALAVIAVNVLGALAVYALQRLQPWLPLNPQGFGAVTPDSSFNTAVSFVTNTNWQGYS GESTMSYLTQMLGLAVQNFLSAATGIAVVIALIRGFARHSARTIGNFWVDFTRGTLYVLLPLS VIVAVFFVSQGAIQNFDAYKEVTTVAATTYDNPKTDAQGNPIKDAQGNPVTEKATTQKQTLP MGPIASQEAIKMLGTNGGGPFNANSAHPYENPTPLANFVQMLSIFLIPAALCFTFGAMVGDR RQGWAVLASMTILFVVLAVFEMWAELHANPMLAHLGVDQAVGNMEGKETRFGVVASSLFV TITTAASCGAVNAMHDSLTALGGFVPMFLIQLGEVVFGGVGSGLYGMLVYAILAVFIAGLMIG RTPEYLGKKIEVFEMKMTSIAILVTPLLVLVGTAVAVLASGGRAGIFNPGTHGFSEVLYAFSS AANNNGSAFAGLSANTPFYNVALGIVMWLGRFWIIVPVLAMAGTFAAKKRLPVTVGTLPTH GPLFVVLLIGSVLLVGALTYIPALALGPIAEHLAR
2E-245	824.7	31	2E-245	824.5	21.5	1	1	KDPA_HERA2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Haur_2275	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	579	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Herpetosiphonales, Herpetosiphonaceae, Herpetosiphon, Herpetosiphon aurantiacus (Herpetosiphon giganteus), Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	316274	>sp|A9AXU9|KDPA_HERA2 Potassium-transporting ATPase potassium-binding subunit OS=Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785) GN=kdpA PE=3 SV=1 MISNSVIQIGIFLVVLMACVVPLGRYMAKVYGENPPLQGFFGPIERLIYRLLGIDAKSEMHWK HYALALLGFNAMGMLLLYGLQRMQAWLPLNPQQLPAVSADSAFNTAASFVSNTNWQGYA GETTMSYLTQMLGLTVQNFVSAATGMAVLIGLIRGIARRSTSTIGNFWVDLTRSTIYILLPLAL VLSVTLVSQGVVQTFSPSQTVELIQPIVNADGTTISQQTIALGPAASQIAIKQLGTNGGGFFN VNSAHPLENPTPLSNFLELLSILLIPAALCYTFGLMVGDKRQGWAILATMTIILLGFTVLAVSAE QAGNPLYQKLGVDDQASALQAGGNLEGKETRFGIVNSALWATVTTAASNGSVNSMHDSYT PLGGLAPMVLMQLGEVVFGGVGSGLYGMLIFAIIAVFVAGLMVGRTPEYLGKKIEAFEMKMA ALIILIPCVMTLLITAIAVSSESGRATVFNSGAHGFSEVLYAATSAANNNGSAFAGLGANTPFY NTWLGIAMLVSRFWLIVPTLAIAGSLAGKKLIPQSAGTLPTHTPLFVSLLIGVVLIVGALTFIPA LALGPIVEHLLLSL
3E-245	823.9	28.9	4E-245	823.6	20	1	1	E8X5C7_GRATM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AciX9_2439	Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9)	595	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella tundricola, Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9)	1198114	>tr|E8X5C7|E8X5C7_GRATM Potassium-transporting ATPase potassium-binding subunit OS=Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9) GN=kdpA PE=3 SV=1 MTANGWFQILFFFALVLVSAKPVGVYMARVFERERTLVDILFRPVERALYKLSGIDESYEMR WTEYAISMLLFSLVTLLLTYMIERLQQWLPLNPQHLANVSPDLALNTAVSFTTNTNWQSYVP EATMSYLTQMLTLAYHNFFSAAAGMALAIALIRGIARKETKTLGNFWVDTTRASLWILLPGCF IYALLLVSQGVVQNFRPYDQAKLIQPMTVTTTGADGKSVTQTITEQSIAQGPVASQEAIKML GTNGGGFFNTNSAHPFENPTPLSNLLQMFSIFLIPAGLTVTLGHMTKKPAHGWAVFAAMAT LFFVGVFVTYYAEAQPNPLLHTASMHIDQQVSATQSGGNMEGKEVRFGIANSALFATITTDA SCGAVNAMHDSFMPLGGLVPLVNIMLGEVIFGGVGAGLYGMLIFVILAVFIAGLMVGRTPEY LGKKIESFDVKMAMLYILIFPLSILGFSAVSLMMPNLGISALGNGGPHGLSEILYAFTSATGNN GSAFAGISANTHWYNLSLGAAMLIGRFLMIVPMLAIAGNLAQKKLAPPSQGTFPVDTPLFTVL LIGTIIIVGALTFFPALSLGPILEHLLLNAGKVY
4E-245	823.8	36.4	4E-245	823.6	25.2	1	1	KDPA_OCHA4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Oant_3776	Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Ochrobactrum, Ochrobactrum anthropi, Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	439375	OS=Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168) GN=kdpA PE=3 SV=1 MTINGWIQILVFCGIIILLVKPLGGYMTRVFGGERTLLSPVLVPVERGLYRLAGTTEREEQHW TTYAASLLLFNLAGFLLLYMLQRFQGSLPFNPMGMSDVPADLAFNTTASFVTNTNWQNYGG ESTMSYLTQMAGLTVQNFVSAATGVAIAIALIRAFSRKSMKTLGNFWVDLTRCTLYVLLPLCII LTLAFVSLGVPQTIGVYAEATTLEGARQVIALGPVASQLAIKMLGTNGGGFFNANSAHPFEN PDAISNMIQMVAIFAIGASLTNVFGRMVGNERQGWAIFAAMGILFVAGVAICYWAEAAGNPL IHALSVDGGNMEGKETRFGIAMSALFAVVTTAASCGAVIAMHDSMMALGGMIPMINMMLGE IIIGGVGAGFYGIVLFVVVAVFVAGLMVGRTPEYLGKKIEAKEVKMAMLAVLCLPLSILGFTAIA SVIPTGLASIANPGPHGFSEILYAYTSGTANNGSAFGGLSGNTPWYNITIGLAMLMGRFLVIL PAMAIAGSLVAKKAAPQSAGTFPTTGPLFVGLLIGVILVVGGLIFFPALALGPIAEHLAMIKGQ MF

6E-245	823.1	36.1	7E-245	822.9	25	1	1	D7DK K2_M ETV0	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA M301_207 9	Methylotenera versatilis (strain 301)	590	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylotenera, Methylotenera versatilis, Methylotenera versatilis (strain 301)	666681	>tr|D7DKK2|D7DKK2_METV0 Potassium-transporting ATPase potassium-binding subunit OS=Methylotenera versatilis (strain 301) GN=kdpA PE=3 SV=1 MLSNTFIQVGLYLTVLLLLTKPMGLWIAKVMNGESVIANKLGGPIERIIYRALGIKPETEMGWK HYAVALLLFNVIGIVFVYVLQRLQVWLPLNPQSFPAVSVDSSLNTAISFVTNTNWQGYSGES TMSYLTQMLALTVQNFLSAATGIAVVIALIRGFARHTVQTIGNFWVDITRSTLYILLPLSFIFAIA LMGQGVIQNFDAYKEVTTLQPTTYSVTDSAGKQTTEVTSTQTLAMGPVASQEAIKMIGTNG GGFFNANSAHPYENPTPLSNFLQMLAIFIVPAGLCFTFGLMVGDRRQGWAVFSAMAIVFVL MAGVAIWAEQAGNPVLTASGADQTVSVLQSGGNMEGKETRFGIVSSALFTTITTAASCGAV NAMHDSLTPLGGLVPMWLMQLGEVIFGGVGSGLYTMLIYAVLAVFIAGLMIGRTPEYLGKKI EIFDMKMTALIILVTPLIVLVGTAIAVVADPGKAGIANPGAHGFSEILYALSSAANNNGSAFAGL SANTPFYNTLLAFAMFLGRFGIILPVLAIAGSMAAKKRIPVSLGTMPTHGPLFITLLIGAVILVG ALTYVPAIALGPVIEQLLMTATH
1E-244	822.2	28.7	1E-244	822	19.9	1	1	D5W U10_ KYRT 2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Btus_056 5	Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	571	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Kyrpidia, Kyrpidia tusciae, Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	562970	>tr|D5WU10|D5WU10_KYRT2 Potassium-transporting ATPase potassium-binding subunit OS=Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) GN=kdpA PE=3 SV=1 MSGVASDVLQMVLLLAAVLLAAWPLGRYMARVFQGERTFLDPVLRPLERGLYRLFGLNASR EMSWKTYAWAVIAFNAVGMAVLFVLQLVQGWLPFNPQHFSAVRWDTALNTAASFITNTN WQSYSGESTMSYFTQMAGLTVQNFLSGATGVAVLIALIRGLVRRRASAIGNFWVDMTRCTL WVLLPLSLVVSLVLVSQGVIQNLHPYVTVQTVEGVNQTLAMGPVASQEAIKMLGTNGGGFF GANSAHPFENPTPLSDLVEIWSIIVIPAALVFTFGRMIGKPRQGAAILGAMLFLLVVALAGNYI SERMGNPLLAQMGVQAPTAMEGKEVRFGLGQSSLFSVVTTAVACGAVNNMHDSLTPLGG MVPMLLMMLGEVVFGGEGSGLYGMLVFAILAVFLVGLMVGRTPEFLGKKIESREVKLATLA GVIIPSATILIGAAISVVTPAGLASLGNPGPHGLSEVLYGFASGVGNNGSAFAGLNANTPYYN LMIAAAMLIGRFGVIVPVLGIAGSLAEKNKVPEGPGTFRTDTPLFSVLLSVTIVLVVALTFFPSL ALGPIVEHIMMWQGMAA
2E-244	821.7	24.4	2E-244	821.4	16.9	1	1	KDPA _MET CA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MCA2217	Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	595	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylococcus, Methylococcus capsulatus, Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	243233	>sp|Q605R1|KDPA_METCA Potassium-transporting ATPase potassium-binding subunit OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) GN=kdpA PE=3 SV=1 MTANGLLQICGYLGVLLALAKPLGSYMAAVYEGRSATVRVLASVERFIYRITGIDPEAEMRW TGYASAFLVFNLLGVLAVYALQRCQGFLPLNPQGLPAVAPDSAFNTAISFATNTNWQGYGG EMTLSHLTQMLGLTVQNFVSAASGMAVLVALIRGFVRRNADTLGNFWVDLTRSILHILLPLSF LLALLLIGQGVVQTFEPYRNVTLVEATGYDRPKQDEGGHPLVDADGNPVTEHVTVSEQTLA LGPAASQVAIKQLGTNGGGFFSVNSAHPFENPTPFSNFLEMLAILVISGALCHTFGVMVGDT RQGWVILAAMTLIFVPLLFVTVLCEQGGNPAFAALGVDPAGGNMEGKETRFGIVNSALWAT ATTAASNGSVNAMHDSFTPLGGLVPMWLMQLGEVVFGGVGSGLYGMLVFAIVAVFVAGLM IGRTPEYLGKKIEAYEMKMAAIVILVPPLMVLGGTAVAVMLDAGKSSVFNPGAHGFSEILYAF SSAGNNNGSAFAGLAANTPFYNLMLGLAMWFSRYWLAVPVLAIAGALAAKNYVPPGAGTL PTHTPMFVGLLVGVVIIVGALTFIPALALGPIVEHLMMIGAR
2E-244	821.5	38.1	2E-244	821.2	26.4	1	1	Q186 E7_P EPD6	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CD630_1 5910	Peptoclostridium difficile (strain 630) (Clostridium difficile)	564	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptoclostridium, Peptoclostridium difficile (Clostridium difficile), Peptoclostridium difficile (strain 630) (Clostridium difficile)	272563	>tr|Q186E7|Q186E7_PEPD6 Potassium-transporting ATPase potassium-binding subunit OS=Peptoclostridium difficile (strain 630) GN=kdpA PE=3 SV=1 MGGTIFMVQIVILVAIFMILVIPMGKYLYHIATNQKTFGDRLFDKVDNFIYKVCSIDKKKEMNW KQYALALLFTNAVMVFIGYIILRTQSMHIFNPSGIKSMEQGLSFNTIISFMTNTNLQHYSGESG LSYFSQMTVIIYMMFTSAATGYAAAMAFVRGLVGKKKTLGNFYVDLIRITTRVLLPGALIIGLIL VTQGVPQTFAGTETVTTIEGKLQDIARGPVAALESIKHLGTNGGGFFGSNSSHPFENPTIISN IVEILSMMILPGACVVAFGHMIKNKKQGWVVFGAMSIIFLIGLVVCFKAESAGNPILSQLGLNQ SMGSMEGKEVRFGIAQSSLFTTVTTSFTTGTVNNMHDTLTPLGGLVPLLNMMLNVVFGGK GVGLMNMLMYAIIAVFLCGLMVGRTPEFLTKKIEGKEMKLIALLIILHPLLILMFSGLSVAIPAGL EGISNPGFHGLSQVLYEFASSAANNGSGFEGLGDNTMFWNITTGVVMFFGRYVSIIVLLAIS SLLASKKAVNESIGTLRTDNFTFTIVLVLVVLIVGALTFFPALALGPISEHLVLWH
4E-244	820.2	32.7	5E-244	820	22.6	1	1	KDPA _MET NO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mnod_019 3	Methylobacterium nodulans (strain ORS2060 / LMG 21967)	571	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium nodulans, Methylobacterium nodulans (strain ORS2060 / LMG 21967)	460265	>sp|B8IJ53|KDPA_METNO Potassium-transporting ATPase potassium-binding subunit OS=Methylobacterium nodulans (strain ORS2060 / LMG 21967) GN=kdpA PE=3 SV=1 MTLNGWTQITLYGAVVLALVKPLGWYMTRVFTGERTLLSPVLAPIERGLYRAAGIDARQEQ TWLGYAGALLLFHVFGFLVLYAILRLQAALPLNPADQAAVAPDLAFNTSASFITNTNWQNYG GESTLSYLSQMLGLTHQNFLSAATGIAVAVALIRGFARASTRTLGSFWVDLTRAILYVLLPICI LYTLFLVWQGIPQTLGAYIDATTLEGGKQTIALGPVASQVAIKMLGTNGGGFFNANAAHPFE NPTALSNFVQMVSIFAIGAALTNVFGRMVGDERQGWAILAAMGALFLAGVAVAYWAEANG SPVLASFGLSGGNLEGKEVRFDIAASALFAVVTTAASCGAVNAMHDSFTALGGMIPLVNMQ LGEVIIGGVGAGLYGMLIFVVVAIFVAGLMVGRTPEYLGKKIETKEVKMAMLGILCLPLMMLG FTALATVLPTGLAGPANAGPHGFSEILYAYTSAAANNGSAFAGLSGNTPFYNATLAVGMLV GRFFVIIPALAIAGALAAKKTVPASAGTFPTDGALFVGLLVGVILIIGGLTFFPALALGPVVEHL AGAAGQTFAMGD

6E-244	819.7	37.6	8E-244	819.4	26.1	1	1	G8AUX8_AZOBR	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AZOBR_p230078	Azospirillum brasilense Sp245	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum brasilense, Azospirillum brasilense Sp245	1064539	>tr|G8AUX8|G8AUX8_AZOBR Potassium-transporting ATPase potassium-binding subunit OS=Azospirillum brasilense Sp245 GN=kdpA PE=3 SV=1 MTVSGWINILLFAALVAAVARPLGGYMTRLFNGERTLLSPLLGPVERGLYRLAGVDVKAEQH WVTYAVAMLLFNVAGLLLLYALQRLQGVLPLNPTGMAAVPADLAFNTAASFVTNTNWQNY GGESTMSHLVQMAGLTVQNFVSAATGIALAVALVRGFTRTGARTVGNFWTDLTRGTLYLLL PLSLLYALFLVWQGVPQTLAGTVDATTLEGARQTIALGPVASQEAIKMLGTNGGGFFNANS AHPFENPNALTNLVQMLSIFAIGAGLTNLFGRMAGDERQGWAILAAMGLLFFIGVAAVYWA EAQGNPAFAALGLDNAAGNMEGKETRFGIAMSALFAAVTTAASCGAVNAMHDSFMPLGG MVPMVNMMLGEIIVGGVGAGLYGMLLFAIVTMFVAGLMVGRTPEYLGKKLEAKEVKMTMLA VLCLPLMMLGGTAFAVVLDSGLASLANAGPHGFSEALYAYVSAAANNGSAFGGLSGNTLW YNLTLAAGMLVGRFLVIVPMLAVAGSLAAKTRSAASAGTFPTHGGLFVGLLAGVILIVGGLTF FPALALGPVAEHLAMRAGLLF
7E-244	819.5	31	8E-244	819.3	21.5	1	1	G8M758_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BYI23_A008890	Burkholderia sp. YI23	585	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. YI23	1097668	>tr|G8M758|G8M758_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia sp. YI23 GN=kdpA PE=3 SV=1 MNANTFTQTAIFIVVLIALALPLGRYMANVFEGTSVVVRRIGRPVESVFYRLAGVDPESEMS WKQYALAVLLFNALGALVLYAILRLQGMLPLNPQGMSGMTPDAAFNTAVSFVANTNWQDY GGESTLGYLAQMLGLTVQNFLSAATGIAVVIALIRGFKRHSAQTIGNFWVDLTRSTLYVLMPL AVVFALVFVSQGVIQNFKAYEDVPTLEVTQYKTQTETVKVDKQTLPMGPVASQESIKMLGT NGGGFFNANSAHPFENPTPFSNFMQMLAILIIPAGLCMTFGRMVGDRRQGYAVLAAMTIAL TVACVAEISAEQAGNPLFASLHVDTHASALQAGGNMEGKETRLGIAQSGIFTVVTTAASCGA VADMHDSLTPLGGLVPMLLIQLGEVIFGGVGSGLYGMLAFALLAVFVAGLMIGRTPEYIGKKI EAFDMKMVSIVILLTPLLVLVGTSIAVLTEAGKAGIANPGAHGFSEILYAFSSAANNNGSAFAG LSVNTPFYNSMLAIAMWFGRFGTIVPILAIAGSLAAKKRLAVNAGTLPTHGPLFVVLLLGTLLL VGALTYVPALALGPIVEHLTMIAGH
8E-244	819.4	26.6	1E-243	819	18.4	1.1	1	D8IRD1_HERSS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Hsero_3779	Herbaspirillum seropedicae (strain SmR1)	593	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herbaspirillum, Herbaspirillum seropedicae, Herbaspirillum seropedicae (strain SmR1)	757424	>tr|D8IRD1|D8IRD1_HERSS Potassium-transporting ATPase potassium-binding subunit OS=Herbaspirillum seropedicae (strain SmR1) GN=kdpA PE=3 SV=1 MDSNNYYQLGLYLAVLLLLSLPLGWYMARVMEGKSRVNRLFGGIERVFYRLCGISREHEMD WKQYAIAVVLFNFIGAIAVYLLQRLQQWLPLNPAALASVSPDSSFNTALSFVTNTNWQGYA GESTMSYLTQMAALALQNFLSAATGIAIAFALIRGFARHSSKGIGNFWVDMTRSTLYVLLPLS VVLALVLVQQGSIQNFRAYQDVKTLEVTHYTVPKLDAAGQPLKDAKGEPVTEAQSTDKQTL PMGPVASQEAIKMIGTNGGGFFNANSAHPYENPTPLSNFLQMLAILIIPAALCTSFGVLVGDR RQGWAILAAMTLLFVVMTLVLMYAESQPNPMLASLHASGPGMMEGKETRFGIPASALFASI TTAASCGAVNAMHDSLSPLGGLVPMLQMQLGEVVFGGVGSGLYGMLIFAVLAVFIAGLMIG RTPEYLGKKIGVFDMKMMSIAILMTPALVLIFTALSVMVEAGLAGIANPGAHGFSEILYAFSSA ANNNGSAFAGLSANTPYYNITTGICTWLGRFGIIVPVLAMAGSLAGKKRLAATSGTLPTHGP LFVALLIGAVILVGALTYVPALALGPVVEHLQMMAM
1E-243	818.6	32.3	2E-243	818.4	22.4	1	1	I3ZH04_TERRK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Terro_2258 Terro_2622	Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63)	586	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus roseus, Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63)	926566	>tr|I3ZH04|I3ZH04_TERRK Potassium-transporting ATPase potassium-binding subunit OS=Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63) GN=kdpA PE=3 SV=1 MSLNGWLQIAVFIAAVLVLAKPMGSFMTSVFERRRTFLDPVLVPCERLLYRVTGVNPDEEM NWMQYGVAMLIFSAASLALTYVVQRLQNVLPLNTQHLPGVPADLAFNTAVSFTTNTNWQS YVPETTMSYLTQMLGLATHNFWSAAAGLALAIAFIRGIARREAKTLGNFWVDLTRGTFWVLL PLSVIFAMVLVSQGVVQNLKSYDTVKLLEPQKVTGTDGKTSTVTTQTIAQGPVASQEAIKML GTNGGGFFNANSAHPFENPTPLTNFLQMLSIFLIPAGLTVTLGQMVGSPKHGWAVLAAMTV LWFAGVFTVFWAEAKGNPQFANVDQHVSMQQAGGNMEGKEVRFGIANSALFATVTTDAS CGAVNSMHDSFTPLGGLVPLTNILLGEIVFGGVGAGMYGMLVFVIVAVFIAGLMVGRTPEYL GKKIESYDVQMAMLYLLIFPLIILGLAAIGLRTPAGLAGLANHGPHGLSEVLYAYTSATGNNGS AFAGLSANTHWYNFTLGIAMFAGRFLMIVPMLAIAGNLAAKKITPATAGTFPVTTPLFTVLLT GLIVIVGALTFFPVLSLGPILEHLLLRAGHLF
2E-243	818	36.2	2E-243	817.8	25.1	1	1	A0A075K867_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UFO1_0779	Pelosinus sp. UFO1	568	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Pelosinus, Pelosinus sp. UFO1	484770	>tr|A0A075K867|A0A075K867_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Pelosinus sp. UFO1 GN=kdpA PE=3 SV=1 MINDIMMFAFYIVVLLLLALPLGKYMAKVFSQEKTIFDFVLKPIEKVIYRITGVKETEEMNWKQ YAATLIIFNLFGMILVFMIQVWQDILPFNPEQLAGVDPWHLALNTAVSFMTNTNWQSYSPEA TMSYFTQMTVLTVQNFLSAATGLTVAVALIRGLTRKNAKTIGNFWVDMVRSIMWVLLPLAIIC STILVEQGVLQNLSPYVTVQTLDGADQKLAMGPVASQEAIKMLGTNGGGFFNANSAHPFEN PTPVSNFIEMLSIFLIPAGLVFTFGHMVGNKRQGYAIIASMILLFIIMLGTLYTSELNGNPILSSI GVSSPTSMEGKEVRFGIGGSALFATITTAASCGAVNSMHDSFTPLGGLITMLQIKLGEVIFG GVGAGFYGMMMFVIITVFIVGLMVGRTPEYLGKKIEAWETKMATIAILIPSVIILIGSGIASVIDQ GTSALTNSGPHGLSEILYAFASAAGNNGSAFAGLSANTPFYNLMLAFNMVVGRFGVIIPTLAI AGSMAAKKISPPGPGTFPTTGWLFVVLLVGVVLIVGALTFLPVLSLGPIIEHLLMLKGTTF

2E-243	817.9	29	3E-243	817.7	20.1	1	1	KDPA_CHRVO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CV_1599	Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Chromobacterium group, Chromobacterium, Chromobacterium violaceum, Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	243365	>sp|Q7NXM7|KDPA_CHRVO Potassium-transporting ATPase potassium-binding subunit OS=Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) GN=kdpA PE=3 SV=1 MSTPAMLQLGLFLVVLIALAWPLGAYMTRVMQGENIGPARWCAPLERGFYRLAGIKQEEEM GWRGYAVALILFNVLGVAAVYALQRLQGMLPFNPQAMAAVSPDSSFNTAISFVTNTNWQG YGGETTMSYLTQMLGLTVQNFVSAATGAAVVIALIRGFARHSSAKIGNFWVDVTRMTLYVLL PLAVVFALVFTQQGAIQNLSAYQDVHTVETVKYQQPKQDAKGNPVLGKDGKPVMEDKTSQ TQTLPMGPVASQEAIKMLGTNGGGFFNANSAHPFENPTPLANFLQDIAIFLIPAALCFLFGRM VGDRRQGWAILAAMTIMFATAVVVETRAEQAGVPQYSSLGIDQRASQLQSGGNMEGKEAR FGIIDTSLFVAVTTSASCGAVNAMHDSLTPIGGLVPMFLMQLGEVVFGGVGSGLYGMLIFAIL AVFIAGLMVGRTPEYLGKKIETYEMKMTAITILVTPTLVLALTAIAVSLAAGKAGIANPAAHGF SEILYAFTSAANNNGSAFAGLSANTPFYNIMTGLAMFFGRFFMIVPILAIAGSLAAKKRLAVTG GTLPTHGPLFVTLLIGTVLLVGALNYVPALALGPVVEHLQMLAAR
2E-243	817.7	32.9	3E-243	817.5	22.8	1	1	KDPA_ACIC5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ACP_0429	Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	590	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Acidobacterium, Acidobacterium capsulatum, Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	240015	>sp|C1FA47|KDPA_ACIC5 Potassium-transporting ATPase potassium-binding subunit OS=Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161) GN=kdpA PE=3 SV=1 MTVNGWLQIGIFIAAVLLGAKPLGVYMAAVFERRHTWLDPVLVPVEKLLYRLTAVKAEEEMH WTAYCASMLIFSAATMLLTYLIERVQQFLPLNPQHLGGVPAQLAWNTAISFTTNTNWQAYT PESTMSYLTQMVGLATHNFWSAAVGIALAIAFIRGIARKEMKTLGNFWVDMTRAILWVLLPI CVVFALVLTSQGVIQNLKSYTVAHVVQPQSQTQTVNGKTVTTTDSTQTIAQGPVASQEAIK MLGTNGGGFFNANSSHPFENPTPLSNMLEMISIFLIPAGLTVTLGQMTGSPRHGWAVLGAM LILWFAGVATCYWAEAQPNPLFHGVNQQATALQAGGNMEGKEVRFGIADSALFATVTTDA SCGAVNAMHDSFMPLGGMVPLTNIMLGEIVFGGVGAGLYGMLVFVIVAVFIAGLMVGRTPE YLGNKIQAYDVQMAMLYLLIFPLIILGFSAVAVLTPHLGLPSISNPGPHGLTQILYAYSSATGN NGSAFAGLNANTSWYNLSLGFAMFIGRFLMIVPMLALAGNLAQKKNVPETLGTFPVTTPLFT VLLTSVIIVVGALTFLPALSLGPILEHLLLQAGRTF
3E-243	817.3	31.5	4E-243	817.1	21.8	1	1	KDPA_GRABC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GbCGDNIH1_0182	Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	568	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Granulibacter, Granulibacter bethesdensis, Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	391165	>sp|Q0BVS2|KDPA_GRABC Potassium-transporting ATPase potassium-binding subunit OS=Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1) GN=kdpA PE=3 SV=1 MSMAGWITIGIFFLCVLALTRPLGGFLVSVLEGRRTFLSPILGPVERALYRFSGVRPEEEQS WSHYALALLSFKIVCFVAVYAILRLQAYLPLNPAGQGSVAPDLAYNTAVSFVTNTNWQSYG GETTMSYLSQMLGLTVQNFVSAAAGIAVAAAIIRGFARRESKAIGNFWVDMVRATLYVLLPIS VVLSLFYVFEGIPQTFSGSVVATTYEGIHQTIALGPVASQEAIKMLGTNGGGFFNVNSAHPF ENPDALTNFVEMISIFAIGAGLTNVFGRMVGNERQGWAVFSAMSVLFFVGVTAVYWAEAH GNPAFSAFGIDQSLGNMEGKETRFGVAASALFAAVTTDASCGAVNAMHESFLPLGGMVPLI NMMLGEVIIGGVGAGLYGFILFAIIAVFMAGLMVGRTPEYLGKKIEAREIKMTMLAVLCLPLVM LGFTAVAVVVKPGLAALSATGPHGFTEALYAYTSAAANNGSAFAGLTANPYWNITLGIGMMI GRFFVIVPALAIAGSMAAKKIVPPSSGTFPTDTGLFIGLVAGVIIIVGGLTFLPALALGPIVEHLS MLRGTLY
4E-243	817.1	32.2	4E-243	816.9	22.3	1	1	C6D691_PAESJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Pjdr2_5990	Paenibacillus sp. (strain JDR-2)	559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. (strain JDR-2)	324057	>tr|C6D691|C6D691_PAESJ Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus sp. (strain JDR-2) GN=kdpA PE=3 SV=1 MDILQLIIVVGVLILLVKPLGTYVYHVYSDQPNRTDRLFGGIERFIYKVIGLKSREGMTWKKYA LSFLLTNIVLVALSYLILRLQGSLSGNPNGIGAMEETLSFNTVISFITNTNLQHYSGETGLSYFS QMAVIMMMMFTSAATGFSVAIAFIRGLTSRGSTIGNFFSDFVKSHTRIFLPLATLITLVLVALH VPQTLQPNVTATTLEGAAQSIAIGPVASLESIKHLGTNGGGFFGVNSAHPFENPNPLTNVIEI LSMWALPASLPYVYGRFAGNRKQGWVVFGAMMSLFLVFLATVYTAELHGNPVMNNLGVD ASQGSMEGKEVRFGIAQSSLFTAVTTAATTGSVNNMHDTLTPIGGLVPLAEMMLNVVFGGK GVGLVNMLMYAILAVFIAGLMVGRTPEFLGRKIEPKEMKLIAIAILVHPFIILAPTAIAFLTDLGQ GAITNPGFHGISQVLYEYTSSAANNGSGFEGLADNTPFWNITTGLVMLLGRYVSMIAMLAVA GSLVRKKPVPETIGTFRTDNVLFGGILVGTVVIVGALTFLPAVVLGPIAEHLTIR
4E-243	817.1	31	4E-243	816.9	21.5	1	1	KDPA_RHORT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Rru_A1155	Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum rubrum, Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	269796	[illegible] OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1) GN=kdpA PE=3 SV=1 MDANAILQVVLFCAIILGLTPLLGGYMARVFSGERVLLSVVFGPLERGLYRLSGVRPKEEQH WAAYALSMLVFNLAGLLGLYLILRVQGWLPLNPAGLGAVAPDLAFNTAVSFVTNTNWQAYG GESTLSYFSQMVGLTVQNFVSAATGIAVLVALIRGFARRSARTLGNFWVDLTRTVLYLLLPL AFVTALVLVWQGAPQTLGDYVQAAPLEGGSQVIALGPVASQEAIKQLGSNGGGFFSVNSA HPFENPTPLSNLIEMVLLLAVAAGLTNTFGRMVGDTRQGWALFAAMSLMFVVGLGVTLWQ ESAANPAMVVAGIEAGGGNMEGKEVRLGVANSAIWAVATTAASNGSVNAMHDSFMPLAG MVPMINMMLGEVIFGGVGAGLYGMLIFVMVTVFIAGLMVGRTPEYLGKKIEAREMKLAVISLL VPPLCILGFGAVALTWPQAAASVQDPGPHGLTEALYAYVSGTANNGSAFAGFAANVFPHNL MIGLAMLIGRFLVILPVLAIAGSLGAKKIVPVSAGTFPTHGGLFIGLLVGVIVVVGGLTYFPVLA LGPILEQLMLRSGSLF

4E-243	817.1	23.5	5E-243	816.8	16.3	1	1	Q09AH8_STIAD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA STAUR_0217 STIAU_2789	Stigmatella aurantiaca (strain DW4/3-1)	571	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Cystobacteraceae, Stigmatella, Stigmatella aurantiaca, Stigmatella aurantiaca (strain DW4/3-1)	378806	[illegible] OS=Stigmatella aurantiaca (strain DW4/3-1) GN=kdpA PE=3 SV=1 MTLTGWLQILVFFALVLALTKPLGGYLYRVFEGRPPLPQVLGPVERGLFRLCGVDPSREQT WGQYTRALLAFSLFGVLLLDALQRLQHVLPLNPQGLPAVGPALAFNTAASFTANTNWQSYA GESTMSHFSQMVGLTWQNFVSAAAGLGVALALARGFTRRLGPEGPKTLGNFWGDLVRGV LYVLLPLCVVYALFLVSQGVLQNLDAARELTTLEGAKQTLAMGPVASQEAIKMLGTNGGGFF NANSAHPFENPTPLTNLVQMLSIFAIPAALTHAYGRMAGDTRQGWALFAAMSVLFFVGVAA AYAAESQGNPALAAAQVAQAGNMEGKEVRFGIAASTLFATVTTDASCGAVNAMHDSFTPL GGLVPMVNMQLGEVIFGGVGAGLYGMLVMGVLAVFIAGLMVGRTPEYLGKKIEAREMKLV MLYVLIFPLLILGLSGGAAVLPQGTSSLNNAGPHGLSELLYAFTSGTSNNGSAFAGLNANTPF WNISLGLAMLAGRFLMIVPVLAIAGSMVGKKGVPVGPGTFPTHGLLFTGLLVSVVVIVGALTF FPALSLSPLVEHFLAGAGKVF
5E-243	816.6	30.2	6E-243	816.4	21	1	1	KDPA_SOLUE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Acid_0073	Solibacter usitatus (strain Ellin6076)	568	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Solibacteres, Solibacterales, Solibacteraceae, Candidatus Solibacter, Solibacter usitatus, Solibacter usitatus (strain Ellin6076)	234267	[illegible] OS=Solibacter usitatus (strain Ellin6076) GN=kdpA PE=3 SV=1 MTTNGILQILAFTAIIWALAKPIGGFMAKVFAGERTWLHRILRPVEVAIYKLCGVDEAAEQRW TGYAGSLLAFSLVSLLFTYLIQRVQQWLPLNPQGLANVAADLGWNTAASFTTNTNWQAYTP ETTMSYITQMIALATHNFFSAAAGIAVAIAFVRGFSRHSANTLGNFWVDFTRATLYILLPMSLL AALFFCSQGVIQNLDPYTKVTTLEGAVQTIPQGPVASQEAIKMLGTNGGGFFNANSAHPYE NPTPLANLAQMVLIFLIPAGLTYTFGKMIKDTRQGWALLAAMTVLFLAGVCVVYPAEQAGNP VITRLGVAGGNMEGKEVRFGIANSALFTVVTTDASCGAVNNVHDSLTPLGGLVPLVNIELGE VVFGGVGSGLYGMLLFAILAVFIAGLMVGRTPEYLGKKIEQKEVKMVMLSVLVLALCILGFSA AGIGQQTVANSMTNHGPHGLTEVLYGYTSAAGNNGSAFAGLSANTMYLNTTLGIAMLCGR FLMLIPLLAAAGSLAQKKLVPVSAGTFPTHGPLFVTLLVGVVVIVGALTFFPALSLGPIVEHFL MHQGRLWS
6E-243	816.4	35.1	7E-243	816.2	24.3	1	1	C5APA7_METEA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MexAM1_META1p0128	Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	571	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium extorquens group, Methylobacterium extorquens (Methylobacterium dichloromethanicum) (Protomonas extorquens), Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	272630	[illegible] OS=Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1) GN=kdpA PE=3 SV=1 MTLNGWMQIALYGAVVLALVRPLGGYMTRVFDGERTLLSPALAPIERGLYRVSGIDARQEQ TWLGYAGAMVLFNVAGFVLLYALLRLQALLPFNPAEQAAVAPDLAFNTATSFVTNTNWQSY GGETTLSYLSQMLGLTHQNFVSAASGMAVAVALIRGFARASTKTLGSFWVDMTRATLYVLL PLCTVLALFYVSQGMPQTLSPYVEATTLEGAKQTIAVGPVASQVAIKMLGTNGGGFFNANA AHPFENPTALSNFMQMLSIFVIGAALTNVFGRMVGDERQGWAILTAMGLLFIAGVTVTYWA EANAHGVLSNFGLTGGNMEGKEVRFGIAASALFAVITTAASCGAVNAMHDSFTALGGLIPLL NMQLGEVIIGGVGAGLYGMLIFVVVAIFVAGLMVGRTPEYLGKKIEAREVKMAMLGILCLPLM MLGFTAFATVVPDGLAGPANAGPHGFSEILYAYTSAAANNGSAFGGLTANTLFYNTTLAIGM LVGRFFVKIPVLAIAGSLAAKKRLPASAGTFPTHGGLFVGLLVGVVLIIGGLTFFPSLALGPVV EHFVGAAGQTFATGG
7E-243	816.2	35.8	8E-243	816	24.8	1	1	A0A090AID4_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA THII_0845	Thioploca ingrica	570	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Thiotrichaceae, Thioploca, Thioploca ingrica	40754	[illegible] subunit OS=Thioploca ingrica GN=kdpA PE=3 SV=1 MNTNAYLQLGLFMGILLLTVKPLGGYIAQLMADKPARLNRFGQSIERAIYRLCGIQADVEMN WKQYAGAVILFNLLGVLAVYALQRLQGLLPLNPQAFGAVKPDTAFNTAISFVTNTNWQSYA GESTMSYLTQMLGLTVQNFLSAATGLAVGITLIRGFARHNALTLGNFWVDLTRSILYLLLPLA LLLAVLLMSQGVIQNFEGYRKIHTLQATTQTLAMGPVASQEAIKMLGVNGGGFFNANSAHP YENPTPLTNFWQMLAIFLIPAALCYTFGQMVGDTRQGWAILTAMSLVFVIMATATIWAEQQ GNPSFTASGVDQMSSAMQAGGNMEGKETRFGIVASALFAAITTAASCGAVNAMHDSFTPL GGLAPLWLMQLGEVIFGGIGAGLYGMLIFVLLAVFIAGLMIGRTPEYLGKKIEAFEIKMISLSILI TPLLILVGTALALIVGKASIFNSGPHGFSEVLYALSSAANNNGSAFAGLAADTPFYNVLLAVT MWIGRFGVIVLVLAMAGSFARKQRLAVTVGTLPTHGPLFVTLLISVVIVVGALTYLPALVLGP VVEHLLMLGH
1E-242	815.2	37.6	2E-242	815	26.1	1	1	Q20XR4_RHOPB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RPC_4550	Rhodopseudomonas palustris (strain BisB18)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Rhodopseudomonas, Rhodopseudomonas palustris, Rhodopseudomonas palustris (strain BisB18)	316056	[illegible] OS=Rhodopseudomonas palustris (strain BisB18) GN=kdpA PE=3 SV=1 MTLIGWIQIALYCAIVVALAKPLGWYMTRVFTGEWTPLSPLLRPVEAGLYWLGGVDAKREQ HWLTYTVAMLLFHVGGFLILYAVLRLQAVLPFNPQEQSAVAPDLAFNTAISFLTNTNWQNYG GESTLSYLSQMLGLTTQNFLSAATGIALAVALIRGFARSSMRTIGNFWVDVTRCVLYVLLPIC VVYALFLVWQGMPQTLNAYVDATTLEGAKQTIAVGPVASQVAIKMLGTNGGGFFNANASH PFENPTALSNFVQMLSIFALGAGFTNVFGRMVGNQRQGWAILGVMGVLFIAGVAITYWAEA SGTTGLNALRLAGGNMEGKEVRFGIVASSLFAVITTAASCGAVNAMHDSFTALGGMIPLNM QLGEIIVGGVGAGLYGMLLFVVLAIFVAGLMVGRTPEYVGKKIEAREVKMAMLAILVLPLMYL GWTAVAVVLPSAVASIANPGPHGFSEVLYAFTSATGNNGSAFGGLTGNTLFYNLTLATSML VGRFFMIVPAMALAGSLAAKKSIPASAGTLPTTGGLFIGLVVGVILIIGGLTFFPALALGPIVEH LAMTANTLF

3E-242	814.4	29.1	3E-242	814.2	20.1	1	1	G8P1E5_GRAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AciX8_0329	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	595	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	682795	>tr|G8P1E5|G8P1E5_GRAMM Potassium-transporting ATPase potassium-binding subunit OS=Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8) GN=kdpA PE=3 SV=1 MTANGWFQILLFFALVLVCAKPVGVYMARVFEREKTFLDVVFRPLERLVYKLTGIDETREMR WTEYSIAMLVFSLVTLIATYAIERLQHILPLNPQHLAAVPSDLAWNTAVSFTTNTNWQSYVPE TTMSYLTQMLTLAYHNFFSAAVGMALAVALLRGISRRESKTLGNFWVDTTRASLWVLLPAC FVYALLLVSQGVVQNFRPYDQAKLVQPMTVTTTGADGKATTQTVTTQSIAQGPVASQEAIK MLGTNGGGFFNTNSAHPFENPTPFSNFLEMFSIFVIPAGFTVMLGKMTKSPAHGWAVFAA MSALFFAGVLVAYYAEAQPNPLLHSAAMHIDQHTTAMQPGGNMEGKEVRFGIANSALFATV TTDASCGAVNAMHDSFMPLGGLVPLVNIMLGEVIFGGVGAGMYGMLIFVVLAVFIAGLMVG RTPEYLGKKIESYDVKMAMLYTLIFPLSILGFSAVTLMMPSLGLSALANGGPHGLSEILYAFTS ATGNNGSAFAGLSANTHWYNLSLGFAMLIGRFLMAIPVLAIAGNLARKKLVPPSPGTFPVHT PLFTILLIGTILIVGALTFFPALSLGPVLEHLLLHAGKAY
4E-242	813.8	31	5E-242	813.5	21.5	1.1	1	C6XCN2_METGS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Msip34_1060	Methylovorus glucosetrophus (strain SIP3-4)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylovorus, Methylovorus glucosotrophus, Methylovorus glucosetrophus (strain SIP3-4)	582744	>tr|C6XCN2|C6XCN2_METGS Potassium-transporting ATPase potassium-binding subunit OS=Methylovorus glucosetrophus (strain SIP3-4) GN=kdpA PE=3 SV=1 MSANALLQVAIYLAALLLLTKPMGLYLHRAMEGRLPVLGKLLGPLERLLYRISGVNPQQEMG WKSYTVALLLFNAIGVLTVFCLQRWQDSLPLNPAGMGEINLDSAFNTAVSFVTNTNWQGYA GESTMSYLTQMLALAVQNFLSAATGIAVVIALIRGFARHSVATIGNFWVDMTRSTLYVLLPLS VLLAVLLMGQGVIQNFSAYQLVNTLESVTYSQPALDAQGQPKLDSDGKPAQETITSHTQTLA MGPVASQEAIKMLGTNGGGFFNANSAHPFENPTPFSNFLQMLAIFLIPAGLCYAFGLMVGD RRQGWAIWTAMALLFVTMTAVSLWAEQDGNPILTTLGVDQTSSALQSGGNMEGKETRFGI TTSALFATITTAASCGAVNAMHDSLTPLGGLVPLWLMQLGEVVFGGVGSGLYTMLIYAVIAV FVAGLMIGRTPEYLGKKIEIFEMKMSAVILLVTPILVLVGTAIAVMLPAGLAGIANPGAHGFTEI LYAVSSAANNNGSAFAGLSANTPFYNLLLAVAMAVGRFGIIIPILAIAGALAAKKRITPGLGTLP THGPLFIALLIGTVVLVGALTYVPALALGPVIEHLQMVAGH
5E-242	813.5	19.9	6E-242	813.2	13.8	1	1	KDPA_PSEAE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PA1633	Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	208964	[illegible] OS=Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228) GN=kdpA PE=3 SV=1 MNSHEILLILAFFALVLVPAPFLGRYCFKVMEGQRNLLSAPLAPLERVCYRLFGVDPASEQD WKTYTLALLAFNLAGLVLLFSILMLQGSLPLNPQHLPGLEWTLAFNTAVSFVTNTNWQAYSG EASLSYFSQMVGLTVQNFVSAAVGLCVLVALARGISRRSTRQLGNFWVDLTRGTLYVLLPL CLLLALLLVWQGVPQTFFDYVHATTLQGAEQTIPLGPAASQIAIKQLGTNGGGFFGVNSTHP FENPSAWSNLFEVASIILIPAALVFTFGHYVKDLRQSRAILGCMLLLFCLGLGLSLWAEYQPN PALAQLPIEQGAPMEGKESRFGTAASMLWAITTTAASNGSVNAMHDSLSPLGGMLPLLNM MLGEVIFGGVGAGLYGMLLFVLIAVFLAGLMVGRTPEYLGKKLEAKEVRLLVFTLLVMPVGV LVLGAIAASLPGPASAVTNPGPHGFSQLLYAYTSGSANNGSAFAGFGANTPFHNLMIGLAM LIGRFGYILPILAIAGSLAAKKASPVGPNSFPTHGPLFVSLLTVTILLVGGLTFLPTLALGPIAEQ LSLGF
5E-242	813.3	39.5	6E-242	813.1	27.4	1	1	M1ME79_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cspa_c09070	Clostridium saccharoperbutylacetonicum N1-4(HMT)	559	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium saccharoperbutylacetonicum, Clostridium saccharoperbutylacetonicum N1-4, Clostridium saccharoperbutylacetonicum N1-4(HMT)	931276	>tr|M1ME79|M1ME79_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium saccharoperbutylacetonicum N1-4(HMT) GN=kdpA PE=3 SV=1 MEWLQIIISLLLFMLIIVPLGKYLYYVSTGEKTFADKLFNPIDNLIYKICRINKDEEMNWKEYVF SIIAVNAVMVFIGYIILRAQGGLFLNPNKIDGMEQSLSFNTIISFMTNTNLQDYSGESGLSHLS QMIVIIFMMFTSAATGFAAALAFMRGIIGKKGMGNFFVDITRITTRVLLPFSIVIGLLLVSQGVP QTLSGTKTVTTIEGKMQDIAMGPVAALEAIKHIGTNGGGFFGANSAHPFENPTPLSNLIELLS MMMLPGALVYTFGLMLKNKKQGWTIFAAMAGIFIIALPICYFAEKAGNPALAHVGLSQAMGN MEGKEVRFGIAQSSLFTTVTTAFTTGTVNNMHDSLTPLGGAVALMNMMLNVIFGGKGVGF MNMIMYAILTVFLCGLMVGRTPEFLSKKLEGKEIKLIALAIIIHPFLILMFSALALITPQGLAGISN PGFHGLSQIVYQFTSSAANNGSGFEGMADNTLFWNTATGIVMFLGRYLSIIILLSVAGSLAG KRTIPQTTGTFRTDNTMFAVTLIAIVLIIGALTFLPALALGPVAEHLTLWH
6E-242	813	28.7	8E-242	812.7	19.9	1.1	1	S0EVD3_CHTCT	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CCALI_01554	Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	597	cellular organisms, Bacteria, Armatimonadetes, Chthonomonadetes, Chthonomonadales, Chthonomonadaceae, Chthonomonas, Chthonomonas calidirosea, Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	1303518	>tr|S0EVD3|S0EVD3_CHTCT Potassium-transporting ATPase potassium-binding subunit OS=Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49) GN=kdpA PE=3 SV=1 MTPNGVAQILLFFLLILVFTKPLGSYMARVFQGERTLLHPILRPLEVGLYRLFGIEEEVEMPW TTYALAFVLFSVVGLLLTYILLRLQGHLPWNPQKFGADQMTPDLAFNTAVSFTTNTNWQSY TPESTVSYFSNMVALAMHNWMSAAAGIAVAVAFIRGFARRTVHEIGNFWVDTTRATLYILLP LTFILALLLVWQGVPQNFSPYTKVATVEGSTQLIPQGPVASQEAIKELGTNGGGFFNANSAH PYENPTPLTNLLEMLAIFLIPAALTYTFGKMVGNTRQGWALFAAMSAMFFMGVFVCYQQEQ RGIALLQSGPLRLDLKPSSLQPGGNMEGKEMRFGIAATALFATVTTDTSCGAVNAMHDSFT PIGGLVPLVNMMTGEVIFGGVGAGLTGMLIIAVIAVFIAGLMVGRTPEYLGKKIEKYEITMAVL VMLIHAASVLTFTAIASDLPLSAHSSWNRVNGSTTYLGATYNNVNNPGPHGFSEILYAFTSTT NNNGSAFAGLNANTPIYNLLLGLAMWVGRFFMLIPSIAIAGSLARKKLVPATAGTFPTDSSTF VFLLVGTTIIIGALTFFPALALGPFAEQFQLHIGKLF

7E-242	813	39.7	8E-242	812.8	27.5	1	1	KDPA_AGRFC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Atu3790 AGR_L_2088	Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Agrobacterium fabrum, Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	176299	[illegible] OS=Agrobacterium fabrum (strain C58 / ATCC 33970) GN=kdpA PE=3 SV=1 MTLNGWFQVLLFCGIVFALVKPLGFYMARVFNGERTLLSPVLAPVERGLYALAGTSEREEQ HWTTYAFSMLLFNLFGFALLYALMRFQAVMPYNPQAMPAVGPELSFNTAVSFVTNTNWQN YGGESTLSYLTQMSGLTVQNFVSAATGMAIAIGLIRAFSRASGKAIGNFWVDMVRSTLYVLL PLCIVLTLVYVWLGVPQTLGPYITAQTLEGAQQTIAVGPVASQLAIKMLGTNGGGFFNANSA HPFENPDAISNMIQMVSIFAIGAAFTNVFGRMVGNQRQGWAILAAMGVLFIAGVAVTYWAE AAGNPLMHGFGLAGGNMEGKEVRFGVALSSLFAVITTAASCGAVNAMHGSFTALGGLVPLI NMQLGEVIVGGVGAGFYGILLFIVIAIFVAGLMVGRTPEYLGKKIEAKEMKMAVLAILCLPLAM LAFTATATVLPSAVASIGTAGPHGFSEILYAYTSAAANNGSAFGGLTGNTTWYNITLGFGML MGRFLVIIPALAIAGSLVTKKTVPASAGTFPTDGPLFVGLLVGTILIVGGLTFLPALALGPVAEH LVMAAGQLF
7E-242	812.9	41.1	8E-242	812.7	28.5	1	1	G7M3P7_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CDLVIII_3976	Clostridium sp. DL-VIII	559	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. DL-VIII	641107	>tr|G7M3P7|G7M3P7_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium sp. DL-VIII GN=kdpA PE=3 SV=1 MEWLQIIITLLLFMLIVVPLGKYLYYVSTGEKTVVDKVFNPIDNFIYKICGINKEEKMNWKEYVF SIIAVNAVMVFIGYIILRAQGLLFLNPNKIDGMEQSLSFNTIISFMTNTNLQDYSGESGLSNLSQ MIVIIFMMFTSAATGFAAALAFMRGIIGKKSTGNFFVDITRITTRVLLPFSIVIGILLVSQGVPQT LSGTKTVTTIEGKMQDIAMGPVAALEAIKHVGTNGGGFFGANSAHPFENPTPLTNLIELLSM MMLPGALVYTFGLMLKNKKQGWAIFGAMAGLFIVALPICYFAEKAGNPALAHIGLSQAMGN MEGKEVRFGIGQSSLFTTVTTAFTTGTVNNMHDSLTPLGGAVALMNMMLNVIFGGKGVGF MNMIMYAILTVFLCGLMVGRTPEFLSKKLEGREIKLIALAIIIHPFLILMFSALALVMPEGLAGIS NPGFHGLSQIVYQFASSAANNGSGFEGLGDNTMFWNTTAGIVMFYGRYLSIIILLSVAGSLA AKRSIPATAGTFRTDNTMFAVTLMAIVLIIGALTFLPAIALGPVAEHLTLWH
1E-241	812.3	37.9	1E-241	812	26.3	1	1	Q2K0Q6_RHIEC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RHE_PE00266	Rhizobium etli (strain CFN 42 / ATCC 51251)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium etli, Rhizobium etli (strain CFN 42 / ATCC 51251)	347834	[illegible] OS=Rhizobium etli (strain CFN 42 / ATCC 51251) GN=kdpA PE=3 SV=1 MTLNGWLQILLYCGIVLALVQPLGGYMMRVFSGERTFLSPVLVPIERGLYRVAGTSEGEEQ HWTSYAFAMLTFNLLGVIALYALLRLQAGLPYNPAGMAAVPPELSFNTAVSFVSNTNWQNY GGESTMSYLTQMAGFTVQNFVSAATGIAIALAFIRAFSRASGKAIGNFWVDMTRATFYVLLPI SIVLTLVYVYLGVPQTLGPYVTATTLEGAQQTIAVGPVASQLAIKMLGTNGGGFFNANSAHP FENPDAISNLIQMVSIFAIGAALTNVFGRMVGNQRQGWAILATMGVLFLAGVTVTYWAEAA GNPLMHAFGLGGGNMEGKEVRFGVALSSLFAVITTAASCGAVNAMHGSFTALGGLIPLINM QLGEIIVGGVGAGFYGILLFIIVAVFVAGLMVGRTPEYLGKKIEAKEMKMAVLAILCLPLAMLV FTAIATVLPSAVASIGTAGPHGFSEILYAYTSAAANNGSAFGGLTGNTPWYNVTLGIGMLAG RFLVIIPALAIAGSLIAKKRVPASAGTFPTDGPLFVGLLVGTILIVGGLTFFPALALGPVVEHLV GLAGQTF
1E-241	812.1	33.6	2E-241	811.8	23.3	1.1	1	Q1LSF2_CUPMC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Rmet_0038	Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	610	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus metallidurans, Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	266264	>tr|Q1LSF2|Q1LSF2_CUPMC Potassium-transporting ATPase potassium-binding subunit OS=Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) GN=kdpA PE=3 SV=1 MSTPHFTQFLGLLVLFLAILFVVGPFLGRYMRRAVEEGNFSLTAWGRPIERVLYRVAGVRAD AEMGWKQYAIAVLVFNVIGVIAVYALQRVQGLLPLNPQAFGAVSPDSSFNTAISFVTNTNWQ GYSGESTMSYLTQMLALTVQNFVSAATGIAVVFVLIRGFARHTSATIGNFWVDITRTTLYVLL PLSVITALLLVSQGVIQNFDGYKDANLVTAVEYTQPKVDAAGQPVLDPQGKPVTEAMKTTTQ TLAMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPLSNFIEMLAIFLIPAALCFTFGEMV RDRRQGVAVLASMTVIFVVMAVAAMASEQHITAALSSLSIDHAASALQAGGNMEGKEVRFG ISATSLFATITTAASCGAVNAMHDSFTAIGGLVPMLLMQLGEVVFGGVGSGLYGMLVYAVLA VFIAGLMIGRTPEYLGKKIEAYEMKMTAVAILVTPLLVLVGTAIAVMLEPGRAGVFNPGTHGF SEILYALSSASNNNGSAFAGLSANTPFYNTLLAAAMWFGRFWIIVPVLAMAGSLAAKRRTPV TAGTMPTHGPLFIVLLVGSVLLVGALTYVPALALGPVAEQLQPAAVTAAAK
1E-241	812	31.3	2E-241	811.8	21.7	1	1	A0A0B4Y2B2_9PROT	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TH3_16315	Thalassospira xiamenensis M-5 = DSM 17429	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Thalassospira, Thalassospira xiamenensis, Thalassospira xiamenensis M-5 = DSM 17429	1123366	[illegible] subunit OS=Thalassospira xiamenensis M-5 = DSM 17429 GN=kdpA PE=3 SV=1 MTTDLGQFALYCAILLACAPLLGGYMYRVYSGQAVLLSPVFKPVEKVIYRICGIDAQASQHW SRYAVALLAFNAAGWVLLFAILRLQHLLPWNPAGLAPMSSDLAFNTAVSFVTNTNWQAYGG ETSLSYFSQMVGLTMQNFVSASTGMAVGVAVIRGFAGRKVRDLGNFHVDMTRGVLYVLLP LSIVAGIFLMSQGVPQNLNSYVDATTLEGTKQVLAQGPAASQIAIKQLGTNGGGFFNVNSSH PYENPTPLSNLLQMVYILLIPAAFCFLFGKMVNDKRQGIAIFAVMALLFVGGFAATYSAEKAG NALLTNSSTIIADPGNMEGKETRFGILNSTLWATATTAASNGSVNAMHDSLTPLGGMVTMLN MQLGEIVYGGVGAGFYGMLLFVVLTVFIAGLMVGRTPEYLGKKIEAREIKLAVLAILTMPIGIL VFGALSATVPVAMTAVQDAGPHGLSEILYAYSSATGNNGSAFAGFGAGMPFHTTLQGIAML LGRYGFIIPILAIAGSLGTKNVVPVSGGTFPTHGPLFVTLLIAVILIVGGLTFFPALALGPIAEHF AMLAGIAY

2E-241	811.8	31.1	2E-241	811.5	21.5	1	1	F5LL25_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HMPREF9413_0625	Paenibacillus sp. HGF7	559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. HGF7	944559	>tr|F5LL25|F5LL25_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus sp. HGF7 GN=kdpA PE=3 SV=1 MEIVQIVIVIAALCLLVKPLGTYIYHVFSNERNRTDKWFGWLERPIYKLAGIRSENGMTWKKY AGSLVLTNIVLVAVGYLILRLQRALPLNPNGIDNMEATLSFNTIISFMTNTNLQHYSGETGLSY FSQMAVIMMMMFTSAVTGIVVAIAFIRGLTSKGNTIGNFFTDFVKGHTRLLLPLAIVVTLVLVG LKVPQTLDPTVAAKTLEGGEQQIAIGPVASLVSIKHLGTNGGGFFGVNSSHPFENPSPLTNVI EMLSMWCIPASLTYTFGRFAKNRKQGWVIFTAMMTLFLVFLSVAFFSEKAGNPALNALGAD SSIGSMEGKEVRFGIAQSALFTTVTTAATTGTVNNMHDTLTPLGGMVPLAQMMLNCVFGG DGVGLVNMLMYAILAVFLAGLMVGRTPEFLGRKIESREMKLIAVAILAHPLIILAPTAIAFMTEL GKGAVTNPGFHGISQVLYEFTSSAANNGSGFEGLADNTPFWNISTGIVMLLGRYVSIIALLG AAGSLGRKQWVPETIGTFRTDNALFTGIVVGTVVIIGALTFLPVIALGPVAEYLTLR
2E-241	811.6	30.5	2E-241	811.3	21.2	1	1	R6BHA4_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN513_00393	Clostridium sp. CAG:169	587	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:169	1262778	>tr|R6BHA4|R6BHA4_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium sp. CAG:169 GN=kdpA PE=3 SV=1 MLQLVLTILIYLIMVIPVGSYLYHIAAGKHTFADPVLNRVDDVIYKISGIDPHKKMDWKKYALAL LGTNAVMILLGYMILRIQSIPIFNPNGVGSMEESLSFNTIISFMTNTNLQHYSGESGLSYLSQM LVITFMMFVSAASGYAACVAFIRGLAGKSKNNVGNFYSDLVRIITRVLLPFSIIGGLLLVWQGV PQNFSGNVIVDTIEGAKQIIAQGPVAALEIIKHLGTNGGGFIGANSATPIENPTILTNLIELYSM MLLPGACVITFGKMVRDRKCEAQAGSTAFTVRSGVDSRSFTARFFGREGRTIFAAMSILFVI GLGVCFWAESQGNPALAEAGLSQSMGSMEGKEVRFGIAQSAMFTTTTTSFTTGTVNNMH DTLTPLGGMIPLLHMMLNVVFGGKGVGLMNMIIYAILAVFICGLMIGRTPEYLGKKIEGREMK LTALCIIIHPFLILAFSALAVGTQAGLEGITNPGFHGLSQVLYEFTSSAANNGSGFEGLADNTM FWNITTGLAMFFGRYLSIVIQLAIAGSFMKKKKFVNDSVGSLHTDTAAFPIILVVVVYIFAALTFF PVLALGPIAEHLTLWA
2E-241	811.6	37.6	2E-241	811.3	26.1	1	1	A0A0B4XEH2_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RGR602_PC00992	Rhizobium gallicum bv. gallicum R602	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium gallicum, Rhizobium gallicum bv. gallicum, Rhizobium gallicum bv. gallicum R602	1418105	>tr|A0A0B4XEH2|A0A0B4XEH2_9RHIZ Potassium-transporting ATPase potassium-binding subunit OS=Rhizobium gallicum bv. gallicum R602 GN=kdpA PE=3 SV=1 MTLNGWLQILLYCGILITLVKPLGGYMTRVFNGERTFLSPVLVPIERGLYGIAGTGEREEQH WTSYAFAMLLFNFMGVLVLYALMRLQAGLPYNPAGMAAVPPELSFNTAVSFVTNTNWQNY GGESTMSYLTQMAGLTVQNFVSAATGIAIAVGLIRAFARASGKAIGNFWVDMVRSTLYVLLP LCIVLTLVYVYLGVPQTLGPYVEATTLEGAKQTIAVGPVASQLAIKMLGTNGGGFFNANSAH PFENPDAISNLVQMLSIFAIGAALTNVFGRMVGNQRQGWAILATMGILFVVGVGVTYWAEA AGNPLMHAFGLNGGNMEGKEVRFGVALSSLFAVITTAASCGAVNAMHGSFTALGGLIPLIN MQLGEVIVGGVGAGFYGILLFVIIAIFVAGLMVGRTPEYLGKKIEAKEMKMAVLAILCLPLAML VFTAIASVIPSAVASIGTAGPHGFSEILYAYTSAAANNGSAFGGLTGNTPWYNITLGIGMLMG RFLVIIPALAIAGSLVTKKTVPASAGTFPTDGPLFVGLLSGTILIVGGLTFFPTLALGPVIEHLM MIAGQTF
2E-241	811.5	35.1	2E-241	811.3	24.3	1	1	A0A0D3VB21_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UB51_10580	Paenibacillus sp. IHBB 10380	559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. IHBB 10380	1566358	>tr|A0A0D3VB21|A0A0D3VB21_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus sp. IHBB 10380 GN=kdpA PE=3 SV=1 MGILQIAIVILVLVLLVKPLGTYLYNVFQNESNKTDKWFSFVERPIFSLIGLKERKGMTWKRYA FSFILTNIVLVIVSYLILRMQKFLPFNPNNIDNMEPTLTFNTVISFMTNTNLQHYSGESGLSYFS QMAVIMMMMFTSAATGLCVAIAFIRAITSKGETIGNFFEDFVKAIIRVFLPIAFVVTMLLVALQV PQTLQPMLSVTGLDGQGQQIAIGPVASLESIKHLGTNGGGFFGVNSAHPFENPNPLTNVVEI LSMWSLAAALPYTFGLFAKNKKQGWVIFSAMMILFMVFLSLVYVSESNGNPALNRLGTDSS QGSMEGKEVRFGVAQSALFTTVTTAATTGSVNNMHDTLTPLGGITPLALMMLNCVFGGKG VGIVNMLMYAILAVFLAGLMVGRTPEFLGRKIEAREMKLIAIAILAHPLIILAPTAIALMTEVGKV AITNPSFHGISQVLYEYTSSAANNGSGFEGLGDNTAFWNISTGVVMLLGRYISMIALLAVAG SLSRKKWVPETIGTLRTDNGLFVGILIGTVLIIGALTFLPAIVLGPIAEHLTNR
2E-241	811.2	33.1	3E-241	811	23	1	1	KDPA_METRJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mrad2831_0209	Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	571	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium radiotolerans, Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	426355	>sp|D1MVD1|KDPA_METRJ Potassium-transporting ATPase potassium-binding subunit OS=Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831) GN=kdpA PE=3 SV=1 MTLNGWIQIALYGAIVLALVKPLGSYMTRVFTGERTFLSPVLGPIERGLYRVSGIDDRQEQH WLAYTGAVILFHVLGFAVLYAILRLQAVLPLNPADQTAVAPDLAFNTSTSFITNTNWQSYGG ETTLSYLSQMLGLTHQNFLSAATGIAVAVALIRGFARASSGTIGSFWVDVTRATLYVLLPICV PYTLFLVWQGIPQTLGAYADATTLEGAKQTIALGPVASQVAIKMLGTNGGGFFNANAAHPF ENPTALSNLVQMVSIFAIGAALTNVFGRMVGDERQGWAILGAMGILFLAGVLVTYWAEAHG SSVLNSFGLTGGNMEGKETRFGIAASALFAVITTAASCGAVNAMHDSFTALGGLIPLLNMQL GEIIIGGVGAGLYGMLIFVIVAIFVAGLMVGRTPEYLGKKIEAKEVKMAMLGILCLPLMMLGFT ALATVVPAGLAGPANAGPHGFTEILYAYTSAAANNGSAFGGLTANTLFYNSTLAIGMLVGRF FVKIPVLAIAGSLAAKKTVPASAGTFPTHGGLFVGLLVGVILIIGGLTFFPSLALGPVVEHLAGA AGQTFATGG

3E-241	811.1	40.7	3E-241	810.9	28.2	1	1	C6WWR2_METML	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mmol_1455	Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540)	595	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylotenera, Methylotenera mobilis, Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540)	583345	>tr|C6WWR2|C6WWR2_METML Potassium-transporting ATPase potassium-binding subunit OS=Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540) GN=kdpA PE=3 SV=1 MFSNTLVQVGLFLTVLLLVTKPMGLWIVNVMNGNCKIINRLSAPFERLIYRTLGTSPDTEMG WKQYAIALLLFNLVGVAFVYILQRWQVWLPLNPQHFSAVSVDSSFNTAISFVTNTNWQGYS GETTMSYLSQMLGLTVQNFLSAATGIAVVFALIRGFARHTSKTIGNFWVDMTRSTLYILLPLS FVFAIALMGQGVIQNFDAYKEVSTLQPTTYSTANEAGQLINQTANTQTLAMGPVASQEAIKM IGTNGGGFFNTNSAHPFENPTPLSNFLQMLAIFLIPAGLCFAFGMMVGDRRQGWAVFSAMA IVFVVMAAVAISAEQAGNPILTASGADQTVSVSQSGMALQSGGNMEGKETRFGIVSSALFAT VTTAASCGAVNTMHDSLTPIGGLVPMWLIQLGEVIFGGVGSGLYTMLIYAVLAVFIAGLMIGR TPEYLGKKIEIFDMKMTAIIILVTPLLVLIGTAIAVSVTSGTVGVANPGAHGFSEMLYALSSAAN NNGSAFAGLSANTPFYNTLLAFAMFFGRFGIILPVLAIAGSMAAKKRIPVSLGTMPTHGALFV TLLIGAVILVGALTYIPALALGPVIEHLLLMVGV
3E-241	811	34.9	3E-241	810.8	24.2	1	1	C0ZIZ1_BREBN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BBR47_03820	Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	557	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus brevis (Bacillus brevis), Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	358681	>tr|C0ZIZ1|C0ZIZ1_BREBN Potassium-transporting ATPase potassium-binding subunit OS=Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599) GN=kdpA PE=3 SV=1 MDFIQIALVLVVLFVLAIPMGRYLARSFSLETTRLDRVFGGLEKAIYKLSGIRVADMTWKQYA MAVLVSNISMVAIAYLLLRLQGMLPGNPSGIAAMEPLLSFNTAVSFLTNTNLQHYSGESGLS YLSQMLVIIYLMFTTPATGIAVVMAFMRGLTGQRSIGNYYVDLVRAHTRVLIPLAIVVTLLLVS QGVPQTMEPTATATTISGTEQQIARGPVASLVSIKHLGTNGGGFFGVNSSHPFENPTPLTN VIEILSMFLIPAALPFAFGFLAKSRKQGWVIFGAMFVMFLAFLITAYANEGIGNPALERAGLSQ EMGSMEGKEVRFGIAQSALFTAVTTAATTGTVNNMHDTLTPLGGLVPLGEMMLNCVFGGD GVGTINILMYAILAVFLAGLMVGRTPEFLGRKIEGKEMKLIAIAILVHPLILAPTAIALATEMGSS AVSNPGFHGISQVLYEYTSSAANNGSGFEGLGDNTPFWNISTGLVMLFGRYVSIITMLAVAG SLLAKTPVPETMGTLRTDNSVFTVILIATVVIVGALTFLPVLALGPIAEWLTIR
4E-241	810.6	35.2	4E-241	810.3	24.4	1	1	I3VXZ2_THESW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Tsac_2385	Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	568	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family III. Incertae Sedis, Thermoanaerobacterium, Thermoanaerobacterium saccharolyticum, Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	1094508	>tr|I3VXZ2|I3VXZ2_THESW Potassium-transporting ATPase potassium-binding subunit OS=Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485) GN=kdpA PE=3 SV=1 MIYDILQMLIFICLLVIITIPLGSYIAKVFTNQHTFFDFVAKPIEKFVYKITGIDESHEMNWKEYAL SLVIFNFLGMIFLFILLVSQGKLPLNPQKLPGISSWHLALNTAVSFVTNTNWQAYNGETTVSY LTQMLGFTVQNFLSAATGLSVAIALIRGIMRHSTKDIGNFWVDITRSIIWIFLPLSLILSLILAQQ GVIQNFSSYIRVHTLEGLKQVIAMGPVASQEAIKMLGTNGGGFFGANSAHPFENPTPLTNML EMLAILAIPASLPYAFGKMVKNTRQGWAIFSAMLILFVIMLGTTYYSEKTGNPIISHINITGPSA MEGKEVRFGIAGSSLFSTVTTAASCGAVNSSLDSMTPLGGLIPMLQIMLGEVIFGGVGSGLY SMLIDAFLAVFIVGLMVGRTPEYIGKKIESYEMKMSILAIIIPASTILIGSAIASVTKTGTSVLLNH GPHGLSEILYAFASTTGNNGSAFAGLNSNTLFYNLITSIAMIIGRFGVIIPALAIAGSLANKKVV PVSVGTFPTDNALFSVLLVGIVLIIGALTFFPALSLGPIIEQLLMNAGKLF
4E-241	810.5	38.1	5E-241	810.3	26.4	1	1	KDPA_AGRRK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Arad_9462	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Rhizobium radiobacter (Agrobacterium tumefaciens) (Agrobacterium radiobacter), Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	311403	>sp|B9JKQ7|KDPA_AGRRK Potassium-transporting ATPase potassium-binding subunit OS=Agrobacterium radiobacter (strain K84 / ATCC BAA-868) GN=kdpA PE=3 SV=1 MTFNGWLQILIYIGILLLLVKPLGGYMTRVFTGERTLLSYVLGPLERGLYRIAGTDEREEQHW TTYSISMLLFSLAGFLMLYFLQRFQASLPYNPAGMTSIGPELSFNNAASFVTNTNWQNYGG ESTMSYLVQMAGFTVQNFVSAATGIALAIALIRAFSRASGKAIGNFWVDLTRATLYVLLPACI VMTLVFVYLGVPQTLGPYVNATTLEGAQQTIAVGPVASQLAIKMLGTNGGGFFNANSAHPF ENPDAISNLIQMLAIFAIGAALTNVFGRMVGNQRQGWAILAAMGTLFIAGVIVTYWAEAAGN PLVHALGVQGGNMEGKEVRFGITMSSLFAVITTAASCGAVNGMLGSFTAIGGMIPLINLQLG EVIVGGVGAGFYGILMFVIIAIFVSGLMVGRTPEYLGKKIEAKEVKMAMLAVLCLPAGMLIFTA ISVVLPSAVASIGNPGPHGFSEILYAYSSAAANNGSAFAGLSANTTWYNITLGVVMLIGRFLVI VPALAIAGSLIAKKTVPASAGTFPTDGPLFVGLLVGTILIVGGLTFFPALALGPIVEHLSMIAGQ AF
5E-241	810.2	19.7	6E-241	809.9	13.7	1	1	A6V7F9_PSEA7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA2 kdpA PSPA7_3640	Pseudomonas aeruginosa (strain PA7)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	381754	>tr|A6V7F9|A6V7F9_PSEA7 Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas aeruginosa (strain PA7) GN=kdpA2 PE=3 SV=1 MNSHEILLILAFFALVLVPAPFLGRYCFKVMEGQRNLLSAPLAPLERACYRLFGVDPASEQD WKTYTLALLAFNLAGLVLLFAILVLQGSLPLNPQHLPGLEWTLAFNTAVSFVTNTNWQAYSG EASLSYFSQMLGLTVQNFVSAAVGLCVLVALARGISRRSTRQLGNFWVDLTRATLYVLLPLC LPLALLLVWQGVPQTFFDYVHATTLQGAEQTIPLGPAASQIAIKQLGTNGGGFFGVNSTHPF ENPSAWSNLFEVASIILIPAALVFTFGHYVKDLRQSRAILGCMLLLFCLVLGLSLWAEYQPNP ALAQLPVEQGAPMEGKESRFGTAASMLWAITTTAASNGSVNAMHDSLSPLGGMLPLLNMM LGEVIFGGVGAGLYGMLLFVLIAVFLAGLMVGRTPEYLGKKLEAKEVRLLVFTLLVMPVGVLV LGAIAASLPGPASAVTNPGPHGFSQLLYAYTSGTANNGSAFAGFGANTPFHNLMIGLAMLIG RFGYILPILAIAGSLAAKKASPVGPNSFPTHGPLFVSLLTVTILLVGGLTFLPTLALGPIAEQLSL GF

5E-241	810	28.7	6E-241	809.8	19.9	1	1	KDPA_KORVE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Acid345_0510	Koribacter versatilis (strain Ellin345)	591	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Candidatus Koribacter, Candidatus Koribacter versatilis, Koribacter versatilis (strain Ellin345)	204669	>sp|Q1IUD5|KDPA_KORVE Potassium-transporting ATPase potassium-binding subunit OS=Koribacter versatilis (strain Ellin345) GN=kdpA PE=3 SV=1 MSANGWFQILLFLGLILAVTKPLGVFMARVFNRERTFLDPVLRPIERLIYRCTAVDESQEMK WTEYAIAMLLFSAVSMLMLYIMQRVQLHLPFNPQKFGAVDPAHLAFNTAASFTTNTNWQAY SGEAVMSYFTQMAGLAYHNFMSAAVGIAIAIAFIRGIARRQSETIGNFWVDMTRAVLWVLLP FCIMGALALVSQGVVQNLKPYDTVKLVEPQQVTTTGADGKSSTQTITTQTIAQGPVASQEIIK EWGTNGGGFFNANSSHPYENPTPLSNLIEMFSIFAISAGLTYTLGRMTGSQRHGWAVWGA MAALFLVGVSVVYWAEASGNPLLAGVDQHTSAMQAGGNMEGKEVRFGIANTALFATITTD ASCGAINGWHDSFTPLGGMVPLVNIMLSEVIFGGVGAGMYGMLIYIVLAVFIAGLMVGRTPE YLGKKIEAYDVKMAMLVALIFPLIILVFSAISSVKTFGTGSILNPGPHGLSEILYAFVSGTGNNG SAFGGLTVNTPWYDVAIGIAMLGGRFLMIIPMLAIAGNLAKKKYVPASAGTFPVTTPLFSVLLI GTIIIIGALTFFPALSLGPILEHLQMHAGKAF
5E-241	810	27.5	6E-241	809.8	19.1	1	1	KDPA_DECAR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Daro_1087	Dechloromonas aromatica (strain RCB)	592	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Dechloromonas, Dechloromonas aromatica, Dechloromonas aromatica (strain RCB)	159087	>sp|Q47H38|KDPA_DECAR Potassium-transporting ATPase potassium-binding subunit OS=Dechloromonas aromatica (strain RCB) GN=kdpA PE=3 SV=1 MSNHAWILLGIFLVVLLLTVKPLGTYIANVMEGRFRLAGKIESPIYRLCGIRPDEEMGWLKYA CAILLFNVLGVLAVYALQRLQAELPLNPQVFPAVSPDSAFNTAISFATNTNWQGYVGEATMS YLTQMLALAVQNFFSAATGIVVVIALIRGFARHTAKTFGNAWVDLTRITLHVLLPISIIYAVFLT GQGVIQNFNAYKDVTTLEVTSFDNPKLDDAGQPLKDDKGAVVTEPAQTQTQTLAMGPVAS QEAIKMLGTNGGGFMNANSAHPYENPTPLSNFIQMLSIFLIPAALCFTFGRIVGDTRQGWAV LAAMTLMFVALAYTAMHFEQQANPLLTQLGVDPASGNMEGKETRFGIGDSGLFATITTLAS CGAVNAMHDSFTPLGGLVPLIDMQLGEVVFGGVGTGLYGMLVFAIMAVFIAGLMIGRTPEYL GKKIEAFEMKMVSIAILVTPLLVLVGTAIAVMLADGKAGIANPGAHGFSEILYAFTSAANNNGS AFAGLSANTPFYNVMLGIAMWFGRFGVIVPVLAIAGSLAAKKRIAVGAGTLPTHGPLFVTLLI GTVLLVGLLNYVPALALGPVIEHLVLWAAH
7E-241	809.7	38.1	8E-241	809.5	26.4	1	1	A9HGI8_GLUDA	Potassium-transporting ATPase A chain (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GDI1563	Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5)	582	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Gluconacetobacter, Gluconacetobacter diazotrophicus (Acetobacter diazotrophicus), Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5)	272568	>tr|A9HGI8|A9HGI8_GLUDA Potassium-transporting ATPase A chain OS=Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5) GN=kdpA PE=3 SV=1 MSFSRWYGRKGSEKMTIAGWTLIAAFLFATVLLAPVAGNAMTRVMGGARGAIGRFFGPFE AGLYRLAGIDAAREQSWWGYAVAMLVFKLLCFLTVYALLRFQVHLPLNPVGMGTITPDLAY NTAISFMTNTNWQSYAGETTMSYLSQMLALTVQNFTSAAAGIAIAFAVFRGFSRESAKTIGN FWVDLTRITLYVLVPGSVILALFLVWQGVPQTFSNSIAVTTLEGARQTIAVGPVASQEAIKML GTNGGGFFNTNSAHPFENPTPLTNLVEMLAIFVIGAGLTSAFGRMVNDRRQGWAVFSAMA VLFVVGVAVTYWSEAHANPAFAALGVDPGLGNMEGKETRFGIVASSLFATVTTDASCGAVN AMHESFLPLGGMVPLVNMMLGEVIFGGVGSGMYGFLLFAIVAVFIAGLMVGRTPEYLGKKIE AREIKMTMLGILVPPMLVLTLTAIAIVVSSGTSAMSASGPHGFTEVLYEYTSAAANNGSAFSG LTANSFWNVTLGIAMMIGRFFVIIPSLALAGSLAGKKTVAPSAGTFPTHGGLFIGLVIGVILIVG GLTFLPALALGPIVEHLAMGAGKLY
7E-241	809.6	35.4	8E-241	809.4	24.5	1	1	B8ETA2_METSB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Msil_2826	Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Methylocella, Methylocella silvestris, Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	395965	>tr|B8ETA2|B8ETA2_METSB Potassium-transporting ATPase potassium-binding subunit OS=Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906) GN=kdpA PE=3 SV=1 MTFIGWIQILIFFALVLVAVKPLGFYMTRVFTGEKTFLSLGLGPVEHAFYRLSGVRKDDEQH WLIYAVALLAFNAAGFMLLYALQRLQASLPFNPAEMSAVDPALAFNTAGSFISNTDWQNYG GESTMSYLTQMAGLAVQNFMSAATGIAVAIVLIRGFSRHTSRTVGNFWVDMTRATLYVLLPI CVVFTLVLVWQGVPQTLGPYVDATTLEGGKQTLALGPVASQIAIKMLGTNGGGFFNANAAQ PFENPTALSNMIQMASIFIIGAALTNVFGRMVNDQRQGWAILAAMLTLCFIGVVIVYWAEAAG NPLIHALGVNGPNMEGKEVRFGAAMSSLFAVVTTDASCGAVNAMHDSFTAIGGMIPLINMM LGEIIIGGVGSGFYGMILFIVIALFVAGLMVGRTPEYLGKKIEAKEVKMTMLGVLCLPLAMLGF TAAAVVLPAAVASIANPGPHGFSEILYAYTSVAANNGSAFGGLTGNTPWYNVTLALGMLMG RYFVIIPAIAIAGSLAAKKTAPPSLGTFPTHGGLFVGLLIGTILIVGGLTFFPAVALGPIVEQLSA LAGQSFGG
7E-241	809.6	35.3	8E-241	809.4	24.4	1	1	I3Y5A2_THIV6	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Thivi_0083	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	574	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiocystis, Thiocystis violascens, Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	765911	>tr|I3Y5A2|I3Y5A2_THIV6 Potassium-transporting ATPase potassium-binding subunit OS=Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) GN=kdpA PE=3 SV=1 MTPHAWMLLGLYLLVLLLAAKPLGSYIAAVMEGRPILALRLGGGLESLLYRLCGVRQNKEMG WLHYALAILLFNLLGALAVYALQRLQVWLPLNPQQLANVSPDSAFNTAISFATNTNWQGYA GESTMGHLTQMLGLAVQNFLSAATGIAVAVALMRGFARHSASTIGNAWVDLTRVTLYLLLPI ALVYAVFLVSQGTIQTLDGYQEVTTLESGPATAAPQTQTLPTGPVASQEAIKMLGTNGGGF FNANSAHPYENPTPLTNIIQMLSIFLIPAALCLTFGRIVGDVRQGWAVLAAMTVLFVVMAVVA MSVEQQSNPLLTSLGIDGSAGNLEGKETRFGSAESGLFATITTLASCGAVNAMHDSFMPLG GFVTLWNMMLGEVVFGGVGTGLYGMLVFAVMAVFLAGLMIGRTPEYLGKKIEAHDIKMVSL AILVTPLLVLTGTALAVTLPAGVAGVANPGAHGFAEILYAFTSAANNGSAFAGLSANTPFYN VLLGIAMWFGRFIVIVSVLALAGNLAAKKRIAANAGTMPTHGPLFVMLLIGTVVLVGALNYVP ALALGPVVEQLMLQSAH

8E-241	809.5	31.3	1E-240	809.1	21.7	1.2	1	A0A023NTT9_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CH75_16350	Dyella jiangningensis	600	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Dyella, Dyella jiangningensis	1379159	>tr|A0A023NTT9|A0A023NTT9_9GAMM Potassium-transporting ATPase potassium-binding subunit OS=Dyella jiangningensis GN=kdpA PE=3 SV=1 MTTNDFLQVAIYLVVLLLLVKPVGSYMALVFAETSNGVLRVGRHVENLLYRLSGVRAEEQM GWRRYAIAMLIFNMAGLVVVYVLQRFQQWLPLNPQHFGAVTPDSAINTAISFVSNTNWQGY AGESTMSYLTQMLGLAVQNFLSAATGIAVLVAVVRGFVRRSTDSIGNFWVDMTRSTLYILVP FSLVIALLLASQGVVQNFRSYVDVPLVEHTTAVETVKDAAGNIVKDAAGKDVTKVTTVTTQTL PMGPAASQIAIKQLGTNGGGFFNANSAHPYENPTPFSNFIEMLAIFLIPAGLCFTFGSMVGD RRQGWAILATMLLIFVPLALGAVAAEQAGNPALHGLAVDQQASTLQSGGNMEGKETRFGV ASSSLFTAITTAASCGAVNNMHDSLTPLGGLVPMWLMQLGEVIFGGVGSGLYGMLAFAVVA VFIAGLMVGRTPEYLGKKIEAHEMKMASLAVLVPCALVVICTAIAVASPAGVAGVANPGAHG FSEMLYAVTSASNNNGSAFGGLSANTPFWNVLLGVCMYFSRFLLAIAMLAMAGSLAAKRHV PPSAGTLPTHTPLFVTLLACVVIVVGALTFLPALALGPIAEFLMSAH
1E-240	809	28.2	1E-240	808.8	19.6	1	1	L7TYC2_MYXSD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MYSTI_00152	Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	572	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus stipitatus, Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	1278073	>tr|L7TYC2|L7TYC2_MYXSD Potassium-transporting ATPase potassium-binding subunit OS=Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8) GN=kdpA PE=3 SV=1 MTIIGWLQILLFFALLLVLTKPLGVYLFRVFESDARPLPRVLGPVERVLLELTGASERREQTW VEYCGALLAFSAVSLLILYALQRMQHVLPLNPQGLGAVGPELSFNTAASFVANTNWQSYAG ESTLSYLTQMVGLAWQNFVSAAAGLGVALALARGFTRRPGPEGAKTLGNFWVDVVRGTLY VLLPISFVVALFFVSQGMLQNFSPYPELTTLEGAKQTLAMGPVASQEVIKMLGTNGGGFFNA NSAHPFENPTPLTNLVQMLLIFAIPSALTYTYGRMTGDSKQGWALFAAMSVLFFAGVTAAYA AESQPNAAVAASGVAQGGNMEGKEVRYGITASALFATVTTDASCGAVNSMHDSYNPLGGL VPLVNMQLGEVIFGGVGAGLYGILIMVVLSVFIAGLMVGRTPEYLGKKIEAKEMKLAMLYVLIF PLFILGLSAVAAVIPQGVSSLNNAGPHGLTEMLYAFTSATANNGSAFAGLNANTPFWNISLG MAMLGGRFLMIVPALAIAGSMVGKKVVPTGPGTFPTNGALFTGLLVSVVLIVGALTFFPALSL SPIVEHFLAGAGKVY
1E-240	808.9	32.1	1E-240	808.7	22.2	1	1	A0A0C4YAH4_9BURK	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RR42_m0091	Cupriavidus basilensis	606	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus basilensis	68895	>tr|A0A0C4YAH4|A0A0C4YAH4_9BURK Potassium-transporting ATPase A chain OS=Cupriavidus basilensis GN=kdpA PE=3 SV=1 MSTEFLGLLVLYLAILLALAPFVGRYIRRAMEDDRYLATAWGRPLERVLYRVAGVRANAEMG WKQYAIAVIAFNMLGVVVVYALQRMQAWLPLNPQGFGAVSPDSAFNTAVSFVANTNWQG YAGESTMSYLTQMLALTVQNFFSAATGIAVVFALIRGFARQSAATIGNFWVDMTRCTLYVLV PISAAIALALVSQGVIQNFDSYKEVSLVTPVEYSQPKVDAAGQPVLDAKGAPVMEAMKTDKQ TLAMGPVASQEAIKMLGTNGGGFFNANSAHPFENPTELANLIEMLAIFLIPAALCFTFGEMVK DRRQGVAILASMAVIFVVMACVAAASEQQANAALAGLPIDHAASALQAGGNMEGKETRFGI AATALFATITTAASCGAVNAMHDSFTAIGGLVPMLLMQLGEVVFGGVGSGLYGMLVYAVLA VFIAGLMIGRTPEYLGKKIETYEMKMTAVAILVTPLLVLLGTAVAVMVEPGRAGVFNPGTHGF SEILYALSSAANNGSAFAGLSANTPFYNVLLAAAMWFGRFWIIVPILAMAGSLAAKRRLPVT GGTMPTHGPLFVVLLVGSVLMVGALTYIPALALGPVAEQLQAPVVSAASK
1E-240	808.9	38.5	1E-240	808.7	26.7	1	1	A4Z018_BRASO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BRADO5830	Bradyrhizobium sp. (strain ORS278)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium sp. (strain ORS278)	114615	[illegible] OS=Bradyrhizobium sp. (strain ORS278) GN=kdpA PE=3 SV=1 MTVIGWIQILLYCAVVVALAKPLGWYMTRIFNGERTFLSPVLRPVEAAIYWAGGVDERREQH WLTYTVAMLLFHVGGFLIIYGVMRLQAVLPFNPAGQSAVAEDLSFNTAISFLTNTNWQNYG GESTLSYLVQMLGLTHQNFLSAATGIVLAIALIRGFSRASARTVGNFWVDITRCTLYILLPLCIV YTLFLVWQGIPQTLGPYVEATTLEGAKQTIAVGPVASQVAIKMLGTNGGGFFNANAAHPFE NPTALSNFIQMISIFALGAALTNVFGRMVGNQRQGWAILAVMGVLFIAGVAVTYWAEASGS NVLNALGLTGGNMEGKEVRFGIVASSLFAVITTAASCGAVNAMHDSFTALGGMIPLINMQLG EIIVGGVGAGLYGMLLFVVLAIFVAGLMVGRTPEYVGKKIEAREVKMAMLAILVLPLMYLGWT AVAVVLPSAVASMANAGPHGFTEVLYAFTSATANNGSAFGGLTGNTFFYNLTLASSMFVGR FFMIIPAMAIAGSLAEKKSIPPSAGTLPTTGGLFVGLVVGVILIIGGLTFFPALALGPIVEHLAMT AGTVF
2E-240	808.5	37.5	2E-240	808.2	26	1	1	W6RET0_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LPU83_4158	Rhizobium sp. LPU83	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium sp. LPU83	348824	[illegible] OS=Rhizobium sp. LPU83 GN=kdpA PE=3 SV=1 MTLNGWLQILLYCGIIIVLVKPLGGYMTRVFSGERTFLSPVLAPIERGLYALAGTSEREDQHW TSYAFAMLMFNLLGVVVLYALLRLQAVLPYNPAGMAAVGPELSFNTATSFVSNTNWQNYG GESTMSYLSQMAGLTVQNFVSAATGMAIAIGLIRAFSRASGKAIGNFWVDMVRSTLYVLLPI CIGLTLVYVYLGVPQTLGPYVDATTLEGAKQTIALGPVASQLAIKMLGTNGGGFFNVNSAHP FENPDNISNMIQMVSIFAIGAAFTNVFGRMVGNQRQGWAILATMGILFIAGVAVTYWAEAAG NPLMHAFGLQGGNMEGKEVRFGVAMSSLFAVITTAASCGAVNAMHGSFTALGGLIPLINMQ LGEVIVGGVGAGFYGIILFIIVAVFVAGLMVGRTPEYLGKKIEAKEMKMAVLAILCLPLAMLVF TAIASVLPSAVASIGTAGPHGFSEILYAYTSAAANNGSAFGGLTGNTPWYNITLGIGMLMGR FLVIVPALAIAGSLVTKKTVPASAGTFPTDGPLFVGLLSGTILIVGGLTFFPALALGPVIEHLVMI AGQTF

2E-240	808.3	29	2E-240	808.1	20.1	1	1	Q1DFX6_MYXXD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MXAN_0164	Myxococcus xanthus (strain DK 1622)	573	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus xanthus, Myxococcus xanthus (strain DK 1622)	246197	>tr|Q1DFX6|Q1DFX6_MYXXD Potassium-transporting ATPase potassium-binding subunit OS=Myxococcus xanthus (strain DK 1622) GN=kdpA PE=3 SV=1 MSFIGWSQILLFFALVLAVTKPLGAYLFRVLEGDTRPLPRVLGPLERLLLRLCGAADRHEQT WVAYASSLLAFSLFSVLIVYGLQRVQHLLPLNPQGLGAVGPELAFNTAVSFTANTNWQSYA GESTLSYLTQMVALAWQNFVSAAAGIGVALALARGFTRRPGPDGQKTLGNFWVDVMNATL YVLLPLSLLYALFLVSQGVLQNFAPYAQVVTLEGASQTLAQGPVASQEAIKTLGTNGGGFFN ANSAHPFENPTPFTNLVQMLSIFAIPAALTYTYGKMAGDTRQGWALLSAMSVLFLVGVAAV YAAESQANPALSVAGQVAQAGNMEGKEVRYGIAASSLFAAVTTAASCGAVNAMHDSFTPL GGLVPMVNMQLGEVVFGGVGAGLYGILVMVVLSVFIAGLMVGRTPEYLGKKIEAREMKLAM LYVLVFPLFTLGFSGLAAVLPQGVSSLNNAGPHGLSEILYAYTSGTANNGSAFAGLNANTPF WNITLGVAMLGGRFLMMVPALAIAGSMVGKKVVPAGPGTFPTHGVLFTGLLVSVIVIVGALT FFPALSLSPIVEHFLAGAGKRY
2E-240	808.1	37	2E-240	807.9	25.6	1	1	A0A0A2UBB6_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA P364_0106850	Paenibacillus sp. MAEPY2	559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. MAEPY2	1395587	>tr|A0A0A2UBB6|A0A0A2UBB6_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus sp. MAEPY2 GN=kdpA PE=3 SV=1 MSSGLLQVAVTLLIIILLVKPVGSYLVKVFDGKRTGLDRIFGGPERLLYRLMGVKENESMDW KKYLSAVLLSNFVMLLLMFLVLRLQQYLPLNPDGIANMPAAQAFNTAASFMTNTNWQSYTG ENALSYLSQMLAVTFPMFTSAATGFAVAIAFIRGLVGRRDGLGNFYVDMVRSITRIFLPLSFIV ALFLVFQGVPQTLAGAVNATTLEGAQQTISRGLVASLESIKHLGTNGGGWFGTNAAHPFEN PTSLSNLVHIVCMMLLPTSLVYAFGIMVNNRKQGWALFAAMSFLFLIMLTTVFVSEYRGVPA LEAVGIQGNMEGKEVRFGISESALFTAVTTAATTGSVNNMHESLTPLGGMVALAEMMLNNV FGGKGVGLLNGLLYVILAVFICGLMVGRTPEFMGKKIEGKEVKLASIALLIHPLIILGPTALALM RPEAVASISNSGMHGLTEVLYAFASGAANNGSAFAGLNANTDFYNIAIGVVMLLGRYISMIA MLAIAGSLATKRVVPVTTGTLRTHTPLFAGILVMMIVVVGALTFFPSLALGPIAEHLAMIR
2E-240	808	23.1	3E-240	807.7	16	1	1	S6AI28_PSERE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PCA10_22330	Pseudomonas resinovorans NBRC 106553	566	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas resinovorans, Pseudomonas resinovorans NBRC 106553	1245471	>tr|S6AI28|S6AI28_PSERE Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas resinovorans NBRC 106553 GN=kdpA PE=3 SV=1 MQLQDIGLILAFFVLVLAPAPLLGRFYYRVMEGQRTFLSPVFAPVERFCYRIAGVDAEREQD WKGYCVALLAFNLAGFALLFAILMLQGALPLNPQNLPGLEWSLAFNTAVSFVTNTNWQAYS GEASLSYFSQMVGLGVQNFVSAAVGLCVLVAFARGISRRSTDRLGNFWVDLTRGTLYGLLP LGLLLALFLVWQGVPQTLTDYAHAVTLQGTEQSIPLGPAASQIAIKQLGTNGGGFFGVNSAH PFENPTAWSNLLEMASIILIPAALLFTFGHYVKDLRQSRALLACMLLLFVIGLGVTLYSEYQPN PALAALPIEQSGSLEGKESRFGIAASALWAVTTTAASNGSVNAMHDSFSALGGMVPMFNM MLGEVIFGGVGAGLYGMLLFVLIAVFLAGLMIGRTPEYLGKKLEAREVRLLVATLLVMPVGVL VFCGLAISLAGPAASITNPGAHGFSQALYAYTSGTANNGSAFAGFGANTPFHNVLIGLAMIL GRFGYILPVLAIAGSLAMKNRAPLGANSFPTHGPLFVTLLTLTILLVGGLTFLPALALGPIAEHL MQIQGF
3E-240	807.4	38.9	4E-240	807.2	27	1	1	A7IKC6_XANP2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Xaut_3240	Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	571	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Xanthobacter, Xanthobacter autotrophicus, Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	78245	>tr|A7IKC6|A7IKC6_XANP2 Potassium-transporting ATPase potassium-binding subunit OS=Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2) GN=kdpA PE=3 SV=1 MTPNGLIQIALFCLVVLVLTRPLGGYMTRVFAGERTLLSPVLAPVEKLVYRLGGVDAGREQH WLTYTIAMLLFHVGGFLLLYALMRVQDLLPFNPQGMAAVAPDLAFNTAISFITNTNWQNYGG ESTMGYLVQMLGLTHQNFLSAATGIVLGMALIRGFSRASAQTVGNFWVDITRCTLYVLLPIC VVFTLALVWQGIPQTLGPYVDAATLDGGKQTIALGPVASQVAIKMLGTNGGGFFNANAAHP FENPTALSNFLQMVSIFALGAALTNVFGRMVGNEKQGWAILAAMGVLFVAGVGVTYWAEA SGTPALNALGLSGGNMEGKELRFGIVASALFAVITTAASCGAVNAMHDSFTALGGMIPLINM ELGEIIVGGVGAGLYGMLLFVVITMFVAGLMVGRTPEYVGKKIEAKEVKMAMLAILILPLMML GWTAVATVLPSAVASINNPGPHGFSEILYAFTSATANNGSAFGGLTGNTFFYNLTLASSMFV GRFLMIVPAMALAGALAAKKTVPASAGTFPTTGGLFVGLLVGVILIVGGLTFFPALSLGPIVEH LAAAAGQSFGAGG
3E-240	807.3	34.1	4E-240	807.1	23.6	1	1	G9Z516_9ENTR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HMPREF0880_02600	Yokenella regensburgei ATCC 43003	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yokenella, Yokenella regensburgei, Yokenella regensburgei ATCC 43003	1002368	>tr|G9Z516|G9Z516_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Yokenella regensburgei ATCC 43003 GN=kdpA PE=3 SV=1 MAAQGFLLIAGFLLVLFVLARPLGTVLARMIGDSPLPGVAGIERGLWRVLGIRTDEMGWCQY LMALLLLNLFGLVILFAMLMLQGILPLNPQNYPGLSWDLALNTAVSFVANTNWQSYGGETTM SYLSQMAGLTVQNFLSAATGIAVVFALIRAFSRHSVKTLGNAWVDLTRITLWVLLPISLVIALF FIQQGVLQNFHPYQAFTSLEGAKQLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPTA LTNFVQMLSIFLIPAALCFAFGEAVGDRRQGRTLLWTMTLIFIVAAAVVMWAETQGNPHLMA LGADSNINMEGKESRFGILASSLFAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGAGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPTLVLLGTALA MMTDAGRSAMLNPGTHGFSEVLYAVSSAANNNGSAFAGLSANTPFWNCLLAFCMFFGRF AVIVPVMAIAGSLVTKKSQPASIGTLPTHGPLFIGLLIGTILLVGALTFIPALALGPVAEHLSLL

4E-240	807.2	40.6	4E-240	807	28.2	1	1	KDPA_BRADU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA bll6779	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium diazoefficiens, Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	224911	[illegible] OS=Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110) GN=kdpA PE=3 SV=1 MTMIGWLQIILFCVIIVALTKPLGWYMTRVFNGERTFLSPVLRPIEAGIYWISGVDERREQHW LTYTVAMLLFHVGGFLVIYGVMRLQAVLPFNPAGQSAVAQDLSFNTAISFITNTNWQNYGGE STLSYLVQMLGLTHQNFLSAATGIALAMALIRGFSRASVRTVGNFWVDVTRCTLYVLLPICVV YTLFLVWQGIPQTLGDYVEATTLEGAKQTIAVGPVASQVAIKMLGTNGGGFFNANAAHPFE NPTALSNFVQMLSIFALGAALTNVFGRMVGNQRQGWAILAVMGVLFVAGVAVTYWAEANG TSTMHALGLTGGNMEGKEVRFGLVASSLFAVITTAASCGAVNAMHDSFTALGGMIPLINMQ LGEIIVGGVGAGLYGMLLFVVLAIFVAGLMVGRTPEYVGKKIEAREVKMAMLAILVLPLMYLG WTAVGVVYPAAVASMANAGPHGFTEVLYAFTSATGNNGSAFAGLTGNTLFYNLTLASAMF VGRFFMIVPAMAIAGSLAAKKSIPPSAGTFPTTGGLFVGLVVGVILIIGGLTFFPALALGPIVEH LAMNAGQVF
5E-240	806.8	38.3	6E-240	806.6	26.5	1	1	R6NNJ3_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN627_01446	Lachnospiraceae bacterium CAG:364	569	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	1262983	[illegible] OS=Lachnospiraceae bacterium CAG:364 GN=kdpA PE=3 SV=1 MLQIVLTLAIFMILVIPMGTYMYHIATKQKTFADKIFNPLDNTIYKICHIGREGMNWKQYALHLL TTNAVMVFIGYLVLRLQGILFANPNGIEAMEPTLSFNTIISFMTNTNLQHYSGESGLSYLSQM LVIIFMMFVSAASGYAACMAFCRGLAGKQKDVGNFYEDMVRITTRILIPVSFIAGLLLIWQGV PQTLEANQTVQTIEGQFQDLAMGPVASLESIKHLGTNGGGFFGANSTTPFENPTIISNLIELF SMMILPGACVITFGKMTMKRKKQENKKVLFGNQGRTIFAAMSILFIVGLTICFTSEMAGNPAL EQAGLNQDMGSMEGKEVRFGIAQSTLFTTTTTSFTTGTVNNMHDTLTPLGGMVPMLHMML NCVFGGKGVGLMNMIMYVILAVFLCGLMIGRTPEYLGKKIEGKEMKLVALVLIVHPLLILGFSA LAVMTGAGQAGITNEGFHGLSQVLYEYASSAANNGSGFEGLADNSYFWNITTGLAMFFGR YIAIVAQLAIAGSMLAKRKVNETVGTLRTDNVIFIAILVVVVYIFAALTFFPALALGPIAEHLTLW MP
6E-240	806.6	26.8	7E-240	806.4	18.6	1	1	A0A0A7PLI9_9SPHN	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SKP52_16060	Sphingopyxis fribergensis	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingopyxis, Sphingopyxis fribergensis	1515612	[illegible] OS=Sphingopyxis fribergensis GN=kdpA PE=3 SV=1 MTFQGWFLIIAFVAILLVLTKPMGRWLFALYEGRRTPLHRLLGPVERGFYRLSGIDPDEEQG WRRYAVHMLIFNAMLLLFTYAVLRLQGVLPLNPLGYDAVGADGAFNTAISFTTNTNWQWYS GEATLSNLSQMLGLTIQNFLSAATGIALAFALFRGFARRSAATIGNFWADMTRVTLYLLLPLC FVYAIFLIANGVPQTLAASIDISTLEGVKQTLALGPVASQEAIKMLGTNGGGFFNANSAHPFE NPNALTNLVQMLSIFAIGFGLTWTFGKAVGNQRQGWAILAAMLTIFLAGVSITYWQEAAGNP ILHQLGAAGGNMEGKEVRFGIAASALFSVVTTAASCGAVNAMHDSFTALGGMIPLLNIQLGE VVIGGVGAGIYGFLLFAILAVFVAGLMVGRTPEYVGKKIEAREVKLAVLAIAVLPLIILGGTAIAS VTEAGLAGPLNKGPHGFSEILYGFTSAVGNNGSAFAGLSAGTPFYNGMLGVAMWLGRFFIII PMLAIAGGLAAKKYTPESAGSFPTTGPLWTGLLVGIVLIVGGLTFLPSLALGPIADHLAMING QLF
6E-240	806.6	34.1	7E-240	806.4	23.6	1	1	A0A089UIQ7_9ENTR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LH23_11620	Cedecea neteri	561	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cedecea, Cedecea neteri	158822	>tr|A0A089UIQ7|A0A089UIQ7_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Cedecea neteri GN=kdpA PE=3 SV=1 MAASGFLLIASFLLVLFALAKPLGAVLARLIDGEPLPIVGRIEPFLWSLMGSKGEEMGWKRYL MAILAFNVFGLILLFAMLLFQDSLPLNPQHLPGLSWHLALNTAVSFVSNTNWQSYGGETTLS YFSQMVGLTVQNFVSAATGIAVVFALIRGFSRHSTSTLGNAWVDLTRVTLYILLPISLVMALF FISQGSLQNFSAYQPYTTIEGVQHLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPTA LTNFVQMVSIFLIPAALCFAFGEAVGDRRQGRALLWAMTIIFVVCVVVVMWAELQGNPHFIQ LGANSSINMEGKESRFGILNSSLFAVITTAASCGAVNAMHDSFTALGGMVPMWLMQIGEVV FGGVGAGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVPEMKMTSLAILILTPALVLLGTALAM MTEAGRSGMANPGIHGFSEVLYAVSSAANNNGSAFAGLSTNTPFWNMLLAVCMWIGRFG VIIPVMAIAGSLAAKKSQAVSIGTLPTHGPLFIGLLIGTVLLVGALTFIPALALGPVAEHLSLVNF
7E-240	806.3	35.2	8E-240	806.1	24.4	1	1	KDPA_CROS8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ESA_02641	Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	560	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cronobacter, Cronobacter sakazakii (Enterobacter sakazakii), Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	290339	[illegible] OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=kdpA PE=3 SV=1 MAASAFLLIASFLLVLMALAKPLGSLLARLINGEALPGVGGVERALWAVLGIRQEEMDWKRY LLAILLFNTLGLVLLFAILMCQGVLPLNPQNLPGLSWHLALNTAVSFVANTNWQSYAGESTV SYFSQMAGLAVQNFLSAATGIAVAFALIRAFARQSATTLGNAWQDLTRVTLWVLMPISLIIAL FFIQQGAIQNFSAYQPFTTLEGARQMLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPT ALTNVVQMLAIFLIPAALCFAFGDAVGDARQGRAILWTMTVIFVVCVALVMWAETTGNPHFL TLGADSAANMEGKESRFGILASSLFAVVTTAASCGAVNAMHDTFTALGGMIPMWLMQIGEV VFGGVGSGLYGMLLFVLLGVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPALVLLGTAL AMMTDAGRAGMFNPGIHGFSEVLYAVSSAANNNGSAFGGLSANTPFWNLLLAFCMWFGR FLVIIPVMAIAGSLAAKKAQPASPGTLPTHGALFIGLLTGTVLLVGALTFIPALALGPVAEHLSL VK

7E-240	806.3	31.1	8E-240	806.1	21.6	1	1	R6RMK4_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN583_01047	Anaerostipes sp. CAG:276	576	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, environmental samples, Anaerostipes sp. CAG:276	1262699	>tr|R6RMK4|R6RMK4_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Anaerostipes sp. CAG:276 GN=kdpA PE=3 SV=1 MGTILQYVLYLVILAALAIPLGKYIGKIMDGEKVFLSRLLRPVEHGIYKIMHVKEEEEMGWKRY AGSVFMFSITALIVLMLIHMFQGVLPWNPQGQKGISWDLAFNNAVSFVTNTNWQAYSGESA LSYFTQAMGLTVQNFLSAAVGIAVLFALIRGFIKVKSKGLGNFWVDLTRITLYLLIPLCIVSSLV LVSQGVVQNFSAYETVDLVEPITMEDGTEVTQQIVPQGPAASQIAIKQAGTNGGGFFGVNS AHPLENPTALSNMVEMISLLLIPAALCFTFGRQVKNKKQGFAIFMAMFLMLAVSLGVVGYNE QKGTPQLANEQTVDLSTDNQPGGNMEGKESRFGIATSATWAAFTTAASNGSVNSMHDSY TPIGGMVPMLLMQLGEVVFGGTGCGLYGMLGFAILTVFIAGLMVGRTPEFLGKKIEPFEMK MAVLVCLATPVAILVGSGIAALLPQVADSLNNPGAHGFSEILYAYSSAGGNNGSAFAGFGAD TVFLNVSLGLVMLFVRFLPIFAVLAIAGSLAQKKKVAQTAGTLSTTNAMFVFLLILVVLIVGALS FFPALSLGPIAEFFQM
7E-240	806.3	37.7	8E-240	806.1	26.1	1	1	A0A075R0Q8_BRELA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BRLA_c003530	Brevibacillus laterosporus LMG 15441	557	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus laterosporus (Bacillus laterosporus), Brevibacillus laterosporus LMG 15441	1042163	>tr|A0A075R0Q8|A0A075R0Q8_BRELA Potassium-transporting ATPase potassium-binding subunit OS=Brevibacillus laterosporus LMG 15441 GN=kdpA PE=3 SV=1 MDLLQIAAVLGMLLILAILFGRYLAQAFSWEATKVDRIFGRFERIIYKASGIQVRAMTWKQYA GAVLLSNLVMFIIGYLIVRLQGFLPGNPSRIDGMEPLLAFNTVASFLTNTNLQHYSGESGLSY LSQMTVIIYLMFTTPATGIAVVMAFMRGITGQKQIGNFYVDLIRAHTRVLLPLAVVVTLLLVAQ GVPQTMSPTVTATTLQGAEQQIARGPVASMESIKHLGTNGGGFFGVNSSHPFENPTPLTNV IEILCMFLIPASLPFTFSAMARNKKQGLMIFSAMFLMFLTFLTIVYVAESNGNPALAQAGLSQE NGSMEGKEVRFGIAQSALFTAVTTAATTGTVNNMHDTLTPLGGMVPLAQMMLNCVFGGDG VGTMNILMYAIMAVFLAGLMVGRTPEYLGRKIESKEMKLIAIAILIHPLIILAPSAIALASELGTSS ISNAGFHGISQVVYEFTSSAANNGSGFEGLSDNTPFWNISTGLVMLFGRYFSIVLMLAVAGS LMMKKPVPETIGTFRTDNTVFMSILLATVLIVGALTFFPVIALGPVAEWLSIR
8E-240	806.2	41.3	9E-240	806	28.6	1	1	F7QKE7_9BRAD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CSIRO_2042	Bradyrhizobiaceae bacterium SG-6C	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, unclassified Bradyrhizobiaceae, Bradyrhizobiaceae bacterium SG-6C	709797	>tr|F7QKE7|F7QKE7_9BRAD Potassium-transporting ATPase potassium-binding subunit OS=Bradyrhizobiaceae bacterium SG-6C GN=kdpA PE=3 SV=1 MTLIGWAQIFVFCAIIVALTPVVGGYMTRVVFAGERTFLSPILRPVEAVLYRLGGVDEKHEQH WLTYTVAMLLFHVGGFVLLYTLIRLQGVLPFNPAGQSAAAPDLTFNTAISFLTNTNWQNYGG ESTMSYLVQMLGLTPQNFLSAATGIVLALALIRGFARTSMQTVGNFWVDMTRCTLYVLLPIC VLFTLFLVWQGIPQTLGPYIEATTLEGAKQTIAVGPVASQVAIKMLGTNGGGFFNANASHPF ENPTALSNFIQMLSIFVLGAALTNVFGRMVGNQRQGWAILAAMGVLFIAGVAVCYSAEAHG TTLLQSLGLTGGNMEGKEVRFGIVASALFVVITTAASCGAVNAMHDSFTALGGMIPLINMEL GEIVVGGVGAGLYGMLLFVIVTVFVAGLMVGRTPEYVGKKIEAREVKMAMLAILILPLMMLG WTAIAVVYEPAVASMANAGPHGFSEVLYAFTSQAANNGSAFAGLTGNTPFYNLAGAIAMFI GRFWVIVPAMAIAGALAAKKTVAASSGTFPTTGGLFVGLLVGVILIVGGLTFFPALALGPIAEH LAMLAGGSF
8E-240	806.1	33.6	1E-239	805.9	23.3	1	1	C7JIB0_ACEP3	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA APA01_40500 APA01_43100	Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)	568	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acetobacter, Acetobacter pasteurianus (Acetobacter turbidans), Acetobacter pasteurianus subsp. pasteurianus, Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)	634452	>tr|C7JIB0|C7JIB0_ACEP3 Potassium-transporting ATPase potassium-binding subunit OS=Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153) GN=kdpA PE=3 SV=1 MSFYGWVAIMAFLICVIAMTRPLGGFLKRVLEGEQHVLGRIFGPVERGIYRIAGIHKDREQS WSQYAIAVIVFKVICFIAVYTLLRVQGVLPLNPNGMGGVAPDLAYNTAISFLTNTNWQSYGG ETTMSHLTQMLGLTVQNFVSAAAGIAIAAAVIRGFARRSATSIGNFWADLVRTTLYVLLPICV VLALFFVLEGVPQTLLGSVTVSTLEGARQTIAFGPVASQEAIKMLGTNGGGFFNVNSAHPFE NPNALTNFVQMLAIFALGAGLTNMFGRMVGRERQGWAIFSAMALLFLIGTGVAYWSEAHA NPLITALGADPSAGNMEGKETRFGIIGSALFATVTTDASCGAVNSMHESFLPLGGMVPLLNI MLGEIIFGGVGSGLYGFLLFAIIAVFMAGLMVGRTPEYLGKKIEAREIKMTMLAVLCLPLVMLG FTALAVVVSPGLSALSASGPHGFTEALYAYTSAAGNNGSAFGGLTANTFWNVTLGIGMMA GRFFVIIPVLAIAGAMAAKKTATPTPGTFPTDTGLFIALVTGVILIVGGLTFLPALALGPIVEHLA MLGGTLF
8E-240	806.1	38.9	1E-239	805.8	27	1	1	A0A097R067_HAFAL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AT03_06765	Hafnia alvei FB1	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Hafnia, Hafnia alvei, Hafnia alvei FB1	1453496	>tr|A0A097R067|A0A097R067_HAFAL Potassium-transporting ATPase potassium-binding subunit OS=Hafnia alvei FB1 GN=kdpA PE=3 SV=1 MAASAFLMIAVFLLVLFALALPLSRVLARLIDGEPFVALRGIENGFWRCCGIQPQPEMSWLQY LLAIIAFNLLGILLLFVLLMAQGILPLNPQQMPGMSWHLALNTAVSFVTNTNWQAYSGENTLS YFSQMVGLSVQNFLSAATGIAVVFALIRGFARHSASTLGNAWVDLFRVTLYVLLPLSLILALF FVSQGVLQNLHSYITVHTLEGGTQLLPMGPVASQEAIKLLGTNGGGFFGANSAHPFENPTA LSNMVQMLAIFLIPAALCFAFGQAVGENRQGHTLLWAMSLIFVVAIVVMYAELQGNPHLSD FGAASNFNMEGKETRFGILATAMYSVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGSGLYGMLLFVLLTVFIAGLMIGRTPEYLGKKIEVFDMKMTAVAILVTPALVLIGSAVA LMTDAGRAGILNPGAHGFSEVLYALSSAANNGSAFAGLSVNTPFYNVLLAIAMFLGRFGVII PVMAIAGSLVAKKRQPAGNGTLPTQGALFIGLLVGTILLVGALTFIPALALGPVAEHLQVWLT R

8E-240	806.1	36	1E-239	805.8	25	1	1	E1SHL0_PANVC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Pvag_3068	Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea vagans, Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	712898	[illegible] OS=Pantoea vagans (strain C9-1) GN=kdpA PE=3 SV=1 MAANAFLLIAFYLVLLMVLAQPLGRGLAALVADKPVFARFEAPLWRLLGAQQSEMRWPHYL LAILLFNALGFVVLLAILLLQGSLPLNPQQLPGLSWHLALNTAVSFVTNTNWQSYSGESTLSY FSQMVGLTVQNFLSAATGIAVAFALIRGFANRSSASLGNAWRDLTRITLYVLLPISLLMALFFV SQGSIQNFAPYHSFTTLEGVQQTLSMGPVASQEAIKMLGTNGGGFFNANSAHPFENPTVLT NLVQMLSIFLIPAALCFAFGESVRDRRQGHMLLWAMTLMFVAAVAVVMWAELQGNPHFLQ LGADSAVNMEGKETRFGILNSSLFAVITTAASCGAVNAMHDSFTALGGMVPMWLMQLGEV VFGGVGAGLYGMLLFVLLAVFIAGLMIGRTPEFLGKKVDVWEMKMTALAILVTPALVLIGTAL AMMTDAGRSAMANPGIHGFSEVLYAVSSAANNNGSAFAGLSANTPFWNLLLAVCMLLGRF GIIIPVMAIAGAMAVKKVQPVGNGTLPTHGPLFIALLIGTVLLVGALTFIPALALGPVAEHLQLV QGQSS
1E-239	805.8	35.6	1E-239	805.6	24.7	1	1	E6WH85_PANSA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Pat9b_3783	Pantoea sp. (strain At-9b)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. (strain At-9b)	592316	[illegible] OS=Pantoea sp. (strain At-9b) GN=kdpA PE=3 SV=1 MAANAFLLIAVFLLVLMVLAQPLGRFLALMIADKPLLPRTERALWRLAGVDGDAMRWPHYLL AILLFNALGVVLLLVMLMMQGALPLNPQHLPGLSWDLALNTAISFVTNTNWQAYSGESSLSY FSQMAGLTVQNFLSAATGIAVAFALIRGFANRSLATLGNAWRDLTRITVYLLLPISLLMALFFV SQGSIQTFEPYHVLTTLEGAQQTLPLGPVASQEAIKMLGTNGGGFFNANSAHPFENPNALT NFVQMLSIFLIPAALCFAFGQQVGDRRQGHMLLWAMTLMFVLAVVTVMWAELRGNPHFLT LGADSAINMEGKETRFGILNSSMFAVITTAASCGAVNAMHDSLTALGGMVPMWLMQLGEV VFGGVGAGLYGMLLFVLLAVFIAGLMIGRTPEFLGKKIDVWEMKMTALAILVTPTLVLLGTAL AMMTEAGRAGMANPGTHGFSEVLYAVSSAANNNGSAFAGLSANTPFWNLLLAVCMFVGR FGIIIPVMAIAGSLAVKKVQPVGNGTLPTHGPLFVALLIGTVLLVGALTFIPALALGPVAEHLQLI QG
1E-239	805.7	26.1	1E-239	805.4	18.1	1	1	A0A0D5VLE9_9BURK	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OI25_4643	Burkholderia fungorum	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia fungorum	134537	>tr|A0A0D5VLE9|A0A0D5VLE9_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia fungorum GN=kdpA PE=3 SV=1 MNLNNLVQPGVFIVVLIALAIPLGRYMTGVVDGSSVVVRRFGRPIETAFYKLAGVDPSAEMS WKRYALAVLAFNTLGVAAVYGFLRLQQWLPANPQGFGPMTPDAAFNTAVSFVTNTNWQD YTPESTVSYLTQMAALTVQNFLSAATGIAVVVALIRGFARHTTATIGNFWVDLTRITLYILAPL ATVIALVLISQGVIQNFKSYEDVPTLQVTTYQTPKTDAQGNPVKDAKGTPVMVDNKADKQTL AMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPFSNFVQMIAMLVIPAALCVVFGRMVG DPRQGYAVLAAMTIAFALACWGEISSEQNGNPLYASLHVDQTASATQPGGNMEGKETRFG IAQSGIFTVATTAASCGAVNNTHDSLTPMGGFVPLLLIELGEVIFGGVGSGLYGMLVFALLAV FVAGLMIGRTPEYIGKKIESYEMKMVSIAVLLTPLLVLVGASIAVLTAAGAAGIANPGPHGFSE ILYAYSSAANNNGSAFAGLSVNTPFYNSTLAFVMWFGRFGSIVPVLAIAGSLAAKKRISATAG TLPTHGPLFVVLLLGTVVLVGALTYVPALALGPVVEHLIMVAGH
2E-239	805.2	39.4	2E-239	805	27.3	1	1	H2IX76_RAHAC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Rahaq2_3197	Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Rahnella, Rahnella aquatilis, Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	745277	[illegible] OS=Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65) GN=kdpA PE=3 SV=1 MAATGFLLIASFMLVLLLAKPLGNFIAQLIEGQPGAFIQRIENGVLRTSGSSNAEMNWWQY ALAIMVFNILGIVVLMALLMAQGALPMNPQHFGGLSWDLAFNTAVSFVTNTNWQAYSGEST LSYLSQMVGLTVQNFLSAATGIAVAFALIRAFARPSAQTIGNAWTDLWRITLYLLLPVAFLLAL FFVSQGVLQNFEAYQHITTLEGLQQTLPMGPVASQEAIKMLGTNGGGFFGANSAHPFENPT ALTNMVQMLAIFIIPCALCFAFGRVVGDNRQGHALVWAMSVIFVVSVVVVMYAELKGNPHL MALGASSNFNMEGKESRFGILASSLYAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIG EVVFGGVGSGLYGMLLFVLLTVFIAGLMIGRTPEYLGKKIDVYDMKMTALAILVTPTLVLLGT ALALVTDAGRAGILNPGAHGFSEVLYAVSSAANNNGSAFAGLSVNTPFYNLLLAVCMFFGR FGVIIPVLAIAGSLVMKKRQQAGNGTLPTSGPLFIGLLVGTVLLVGALTFIPALALGPVAEHLQ VWSAQ
2E-239	805.1	26.9	2E-239	804.8	18.6	1	1	G8QNA4_DECSP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Dsui_0279	Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azospira, Azospira oryzae, Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	640081	>tr|G8QNA4|G8QNA4_DECSP Potassium-transporting ATPase potassium-binding subunit OS=Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) GN=kdpA PE=3 SV=1 MSANLLLQYGFFFAVLFLLAWPLGLYMARIYRGDLPAFVAWLRPLENFCYRLAGVRHGDDM GWRRYAGAVLAFSLLGVLAVYALQRLQLWLPFNPQAMANTTPDLAFNTAVSFVTNTNWQA YGGETTMSYLTQMLGLAVQNFLSAATGMAVVVALMRGFQRKEAGGIGNFWIDLVRSTLYV LLPLSLILALALVGQGVVQSVAPYASVPLTQAVDYEQPKVGADGQPVLDAAGKPVLEAATAR EQTLALGPAASQIAIKHLGTNGGGFFNANSSHPYENPTPVSNLLQMLAIVLIPAALCFTFGRR VGDLRQGLAILAAMTAILVALLAVEVWAEQAGNPLFERLGMATQGSELMAGGNMEGKEAR FGISATSLFVTVTTAVSCGAVNAMHDSLTPLGGLVPMWLMQLGEVVFGGVGSGLYGMLVF AIVGVFVAGLMIGRTPEYLGKKIEAYEMKMAAVAILATPLAVLLGTALSLMLEAGTAGVFNPG AHGFSEVLYAFSSAANNGSAFAGLGANTPYYNTALGLAMLFGRFTIIAAVLAIAGSLAAKKR IPPSAGTLPTHTPLFVVLLIGTVIVVGALTFLPSLALGPVVEHLQMVGVR

2E-239	804.8	30.6	2E-239	804.6	21.2	1	1	KDPA_SALG2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SG0703	Salmonella gallinarum (strain 287/91 / NCTC 13346)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella gallinarum, Salmonella gallinarum (strain 287/91 / NCTC 13346)	550538	OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=kdpA PE=3 SV=1 MAAQGFLLIASFLLILLVLAKPLGSGLARLIAAVPLPGVAGVERILWRTLGITDHEMNWRQYLL ALLTLNLLGLGILFCLLFWQEWLPLNPQRLPGLSWDLALNTAVSFVTNTNWQAYSGESTLS YFSQMAGLTVQNFLSAATGIAVVFALIRAFTRQNVHTLGNAWQDLVRITLWILFPVALIIALFFI QQGVPQNLSAYQPITTLEGAKQLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPTALT NLAQMLAIFLIPAALCFAFGEAAGDRRQGRALLWAMSFIFVVCVAVVMWAEVQGNPHLLAA GADSSVNMEGKETRFGVLASSLFAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPMLVLLGSAL AMMTDAGRSAMLNPGPHGFSEVLYAVSSAANNNGSAFAGLSANSPFWNCLLAFCMFVGR FGVIIPVMAIAGSLVSKKVQPASQGTLATHGALFIGLLIGTVLLVGALTFIPALALGPVAEHFSL P
2E-239	804.7	31.6	3E-239	804.5	21.9	1	1	KDPA_ERWT9	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ETA_33650	Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	561	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Erwinia, Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	338565	OS=Erwinia tasmaniensis (strain DSM 17950 / Et1/99) GN=kdpA PE=3 SV=1 MMASASLLIGSYLLLLMLLARPLGKGLAHLVADRPLHGFATAERGLWRVSGVENQGMRWQ RYLLAILLFNAAGLLLLLLILMNQASLPLNPQQMPNLSWDLALNTAVSFITNTDWQAYAGEST LSYFSQMAGLTVQNFLSAATGIAVAFALMRGFVNREQGELGNAWRDITRITLYVLLPLSLLM ALFLVSQGTLQNLHGYLDLTTLEGAKQTLPMGPVASQEAIKMLGTNGGGFFNANSAHPFEN PTALSNFVQMLAIFLIPAALCFAFGDVVRDRRQGHALLWSMSLMFVAAVVVVMWAEVKGN PHFLTLGADSAANMEGKETRFGILNSSLFAVITTAASCGAVNAMHDSFTALGGMVPMWLM QIGEVVFGGVGSGLYGMLLFVLLAVFIAGLMIGRSPEYLGKKIDVWEMKMTALAILVTPVLVL LGAALAMMTDAGRSAMLNPGTHGFSEVLYALSSAANNNGSAFAGLNANTPFWNMLLAFCM LVGRFGIIVPVLAIAGSLAMKKVQPAGNGTLPTHGTLFIALLIGTVMLVGALTFIPALALGPVAE HLHMSGH
3E-239	804.4	37.2	3E-239	804.2	25.8	1	1	A0A068SK25_RHIGA	Potassium-transporting ATPase A chain (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RG540_CH02680	Rhizobium galegae	571	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Neorhizobium, Rhizobium galegae	399	OS=Rhizobium galegae GN=kdpA PE=3 SV=1 MTLNGWLQILLFCGIIIALVKPLGGYMTRVFSGERTFLSPVLVPIERGLYAMAGTSEREDQH WTSYAFSLLMFNLFGVIVLYAMMRLQAGLPYNPAGMSAVPPELSFNTAVSFVSNTNWQNY GGESTMSYLTQMVGLNVQNFLSAATGMAIAVGLIRAFSRASGPGARKTIGNFWVDMTRATL YILLPICIVLTLVYVYLGVPQTLGPYVEATTLEGAKQTIALGPVASQLAIKMLGTNGGGFFNAN SAHPFENPDNISNMIQMLSIFAIGAAFTNVFGRMVGNQRQGWAILASMGILFIAGVGITYWA EAAGNPLMHAFGLEGGNMEGKEVRFGVAMSSLFAVITTAASCGAVNAMHGSFTALGGLIPL INMQLGEVIVGGVGAGFYGIILFIIAVFVAGLMVGRTPEYLGKKIEAKEMKMAVLAILCLPLA MLVFTAIATVLPSAVASIGTAGPHGFSEILYAYTSAAANNGSAFGGLTGNTPWYNVTLGIGM LMGRFLVIIPALAIAGSLVAKKTVPASAGTFPTDGPLFVGLLVGTILIVGGLTFMPALALGPVV EHLVMIAGQTF
3E-239	804.2	31.9	4E-239	804	22.1	1	1	A0A0A6CYC5_9SPHN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NI18_17415	Sphingomonas sp. Ant20	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. Ant20	104605	subunit OS=Sphingomonas sp. Ant20 GN=kdpA PE=3 SV=1 MTFQGWILILGFVAILLALTKPVGVWLFTLYEGRRTPLHIVLGPVERGFYKLAGIDPNAEQG WRRYALHMLLFNVMLMAFTYAVLRLQGVLPGNPQGLAGLSPNLAFNTAISFTTNTNWQSY GGESTMSNLSQMLGLTIHNFLSAATGIALAFALFRGFARRESKAIGNFWADMTRVTLYVLLPI SIVYALFLIASGVPQTMAGVVDVQTLEGAKQSLLLGPVASQEAIKMLGTNGGGFFNANSAHP FENPTALTNLVQMLSIFLIGFGLTWTFGKAVGNTKQGWAILSAMLILFLAGVTVTYWQEAAG NPVLQRLGVAGGNMEGKEVRFGIAASALFSVVTTAASCGAVNSMHDSFTALGGMIPLFNM QLGEVVIGGVGAGIYGFLLFAILAVFVAGLMVGRTPEYVGKKIESREVKLAVLAIAVLPLMILG LTALSSVLQQGLAGPLNKGPHGFSEILYAFTSAVANNGSAFAGLTANTPYYNGLLGVAMWV GRFFIIVPMLAIAGSLAAKKYTPESAGSFPTTGGLWVGLLVGIILILGGLTFLPGLALGPIADHL AMISGTLS
3E-239	804.2	36.2	4E-239	803.9	25.1	1	1	R6PVD9_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN618_00207	Clostridium nexile CAG:348	575	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	1263069	OS=Clostridium nexile CAG:348 GN=kdpA PE=3 SV=1 MLQIIATLAIFLILVIPMGKYMYHIATYQKTFADKVFNPIDHFIYKICGIKDEEMGWKKYALTLV MVNAVMVFVGYLILRIQNVLFLNPNGIEGMDASLSFNTIISFMTNTNLQHYAGESGLSYASQ MCVIIFMMFTSAASGYAACMAFCRGLSGRKMGNFYKDMVRIITRILIPVSLILGLVLVSQGVP QTLMGNVTVNTIEGKFQDLAMGPVAALESIKHLGTNGGGFFGANSTTPFENPTIISNMVELIS MMILPGACVVTFGHMLHDRKKEKKEMQAVMPTKKRILMGRQGAVIFGAMAILFAVGLTLCY HSEMAGNPVISDMGVDQTAGNMEGKEVRFGVAQSSLFTTVTTSFTTGTVNNMHDSLTPLG GLVPLLHMMLNCVFGGKGVGLMNMVVYVILAVFICGLMVGRTPEYLNKKIEGKEMKLVAIVIL IHPLLVLGFSALAVSVTGGTDGITNPGFHGFTQVLYEYASSAANNGSGFEGLADNSTFWNV TTGLAMFFGRYIAIIAQLAIAGSLLAKKKVNETIGTLRTDNVTFMIILVFIVYIFAALTFFPALALG PIAEHLSMWM

4E-239	803.7	27.3	5E-239	803.5	19	1	1	A0A0F3K4U7_9NEIS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VI06_17100	Aquitalea magnusonii	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Aquitalea, Aquitalea magnusonii	332411	>tr|A0A0F3K4U7|A0A0F3K4U7_9NEIS Potassium-transporting ATPase potassium-binding subunit OS=Aquitalea magnusonii GN=kdpA PE=3 SV=1 MSTPAFLQLGLFLLVLLALAWPLSSYITRVMQGENPGVLRFVAPLERGVYRLAGIRPDEDMG WRGYAVALLLFNLLGALAVYGLQRLQGILPLNPQALAGVAPDSSFNTAISFITNTNWQGYGG ETTMSYLTQMLGLTVQNFLSAATGAAVVIALIRGFARHNSARIGNFWVDVSRFTLYILLPLSL VLALVFTQQGVIQNLLPYQTAHTVEVTQFQQPKLDAKGSPLIGKDGKPVMVDSQTRLQTLP MGPVASQEAIKMLGTNGGGFFNANSAHPFENPTPLSNLLQELAIFLIPAALCLVFGRMVGDR RQGWAILAAMLLMFATAVVVETGAEQAGIPQLSAMGVDQQASSMQAGGNMEGKESRFGII DTSLFTVITTAASCGGVVAMHDSLTPVGGLVPTFLMQLGEVVFGGVGSGLYGMLVFAILAVF IAGLMVGRTPEYLGKKIETYEMKMTAITILVTPILVLVLTAIAVSLDAGKAGIANPGAHGFSEIL YAFTSAANNNGSAFAGLSANTPFYNIMTAIAMFFGRFLMIVPILAIAGSLSAKKRLAVTSGTLP THGPLFVVLLIGTVLLVGALNYVPALALGPVVEHLQMVSGH
5E-239	803.7	32.9	5E-239	803.4	22.8	1	1	KDPA_KLEP7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KPN78578_06990 KPN_00717	Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Klebsiella, Klebsiella pneumoniae, Klebsiella pneumoniae subsp. pneumoniae, Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	272620	>sp|A6T6D9|KDPA_KLEP7 Potassium-transporting ATPase potassium-binding subunit OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=kdpA PE=3 SV=1 MAAQGFLLLASYLLVLLVLARPLGMCLARMVNDIPLPGLAGVERVLWRVAGIRAEEMGWLQ YLLAILFNALGGLALFALLMLQGVLPFNPQHLPGLSWDLALNTAISFISNTNWQAYAGESTM SYLSQMVGLTVQNFLSAATGIAVVFALTRAFARQKMSTLGNAWVDLTRITLWLLLPLSLLVA LFFIQQGVPQNLQAYQPFITLEGVHQLLPMGPVASQEAIKLLGTNGGGFFNANSAHPFENPT ALTNLVQMLAIFLIPTALCFAFGEVVSDRRQGRAILWAMTLIFILCVAVVMWAETRGNPHLLT LGADSSLNMEGKESRFGILASSLFAVITTAASCGAVNAMHDSFTALGGMVPMWLMQIGEVV FGGVGSGLYGMLLFVMLAVFIAGLMVGRTPEYLGKKIDVREMKMIALAILVTPTLVLLGTALA MMTDAGRAGMFNPGPHGFSEVLYAVTSAANNNGSAFAGLGAATPFWNLLLAFCMLVGRF AVIIPVMAIAGSLVAKKIQPASPGTLATHDALFIGLLIGTVLLVGALTFIPALALGPLAEHFSLL
5E-239	803.6	31.2	5E-239	803.4	21.6	1	1	J7QUT1_METSZ	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN69_2489	Methylocystis sp. (strain SC2)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylocystaceae, Methylocystis, Methylocystis sp. (strain SC2)	187303	>tr|J7QUT1|J7QUT1_METSZ Potassium-transporting ATPase A chain OS=Methylocystis sp. (strain SC2) GN=kdpA PE=3 SV=1 MTPIGLAQIAIVLVAVIVAAIPLGGYVARVLAGEQNLLTPALAPIERVFYRLAGVDPAREQNWL AYTMAMLAFSVIGFVSLYALQRLQAYLPLNPQGFGGVPADLAFNTSISFVTNTNWQNYGGE STMSHLTQMLGLTVHNFVSAATGLAMAFALVRGFSRAESPTIGNFWVDLTRSTLYVLLPMSI VVALALVALGVPQTLQGSIEATTLEGAKQTLAIGPVASQEAIKELGTNGGGFFNANSAHPFE SPNALSNMLEIWALLVIPFATAFAFGRAVFDYRQGRAIAVTMMIVLVAGVLVAYWAEAGGNP LLTEIGVDPSPGNMEGKEVRFGPAMSALFAASTTGTSCGAVNAMHDSFMPLGGLVPLFNM LMGSIAPGGVGAGLYGFLVLAIIAVFIAGLMVGRTPEYLGKKIETREMKLAMLAVLIYPLSVLV FTGVSVMLQTGLASLNNAGPHGLSEILYAFASTTDNNGSAFAGLTGNTPWYNTTLGVAMLL GRFAFVIPVLAIAGAFAAKKKGVASVGTFPTHGPLFIGLLLGVIVILYLLQYFPALALGPIVEHF ALLAGKTF
5E-239	803.6	40	5E-239	803.4	27.7	1	1	KDPA_RHOPA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RPA3004	Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Rhodopseudomonas, Rhodopseudomonas palustris, Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	258594	>sp|Q6N5H0|KDPA_RHOPA Potassium-transporting ATPase potassium-binding subunit OS=Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009) GN=kdpA PE=3 SV=1 MTFIGWCQIALFGAVVVALVKPLGWYMTRVFAGEWTPLTPVLRPVETMLYRAAGVDPKQE QHWLTFTLAMLLFHIGGFAIIYAVLRLQALLPFNPAEQGAVAPDLAFNTAISFLTNTNWQNYG GESTLSYLSQMLALTHQNFLSAATGIVLAMALIRGFSRASVRTIGNFWVDITRCTLYVLLPICI PYALFLVWQGMPQTLGSYVDATTLEGAKQTIAVGPVASQVAIKMLGTNGGGFFNANAAHP FENPTALSNFVQMLSIFVLGAALTNVFGRMIGNQRQGWAILGVMGVLFVVGIAVAYWAEAS GTATLDALGITGGNMEGKEVRFGIVASALFAVVTTAASCGAVNAMHDSFTALGGMIPLINMQ LGEIIVGGVGAGLYGMLLFVVLAIFVAGLMVGRTPEYVGKKIEAREVKMAMLAILVLPLMYLG WTAIAVVLPSAVASMGNAGPHGFSEVLYAFTSATANNGSAFGGLTGNTFFYNLTLATAMFV GRFMMIVPTMAIAGSLAGKKLVPPSAGTLPTTGGLFVGLVVGVILIIGGLTFFPALALGPIVEQ VSMSAKTLF
5E-239	803.4	34.7	6E-239	803.2	24	1	1	A0A0F5PRY6_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA WH91_19460	Devosia psychrophila	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia psychrophila	728005	>tr|A0A0F5PRY6|A0A0F5PRY6_9RHIZ Potassium-transporting ATPase potassium-binding subunit OS=Devosia psychrophila GN=kdpA PE=3 SV=1 MSLSGWLQIGFVLIVVLLLVKPLGLYMARVFTGERTFLSPVLGPVERGFYALAGVRTDKEQG WLGYTMGVLAFSLAGFVVLYSMLRLQNFLPLNPQGFAGLSPDLAFNTAASFVTNTNWQSY GGETTMSHLSQMLGLTVQNFVSAATGIAVAIALTRAFVRSGVNELGNFWVDLTRATLYVLLP LAIVVALAFVAMGLPQNLDANFVATTIEGVQQTIATGPVASQEAIKQLGTNGGGFFNVNAAH PFENPTAFSNYLNIIAMLAISAALVYTFGQMVGNRRQGWALISVTVIMLVIGTGAIYWAESFG NPLLTAVGVDPSMGNFEGKEVRFGQAMSALYSAVTTGLSNGGVNAMHGSLTPLGGLVPM FLMQLGEVLPGGVGSGLYALLVFAILAVFVAGLMVGRTPEFLGKKVEAREMKFAMLAVLILP LVILGFTAISVVADFGTSSILTPGPHGLSEILYAYTSAAANNGSAFGGLTANTPWYNTTLGIA MLLGRFAYLVPVLAIAGSLVAKPRAAASSGTFPTDKPLFVGLLIGVIIILGGLQFFPALALGPIV EHFVMLAGQSF

5E-239	803.4	24.5	8E-239	802.9	17	1.2	1	KDPA_BORPE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BP2480	Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	594	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella pertussis, Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	257313	>sp|Q7VVZ9|KDPA_BORPE Potassium-transporting ATPase potassium-binding subunit OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) GN=kdpA PE=3 SV=1 MNADFLGLLLLYLAILLCAAPLLGRHIRQAINGERTWLTAWGQPLERGLYRLAGVDPAAEMD WRRYAVAMLVFNVLGVLAVYALQRLQGWLPLNPAGLPGVAPDSALNTAISFVTNTNWQGY AGESTMSYLTQMLALTVQNFVSAATGIAVLIALVRGLARHSAATLGNFWADLVRATLYVLLP LSFILALALVSQGVVQNLDPYVEAQTVQAQQYETARLDAQGQPMTGPAGQPLTDTVVTRV QTLPMGPVASQEAIKLLGTNGGGFFNANSAHPYENPNAWSNLLEMLAILLIPAALCWTFGE MVGSRRQGVAILAAMTVLFAGFAASAAYFEQQPTPALRQAEAALLADGGNLEGKEARFGV AATALFATVTTAASCGAVNGMHDSFSALGGVTPLLQMQLGEVIYGGVGSGLYGMLAFAILA VFIAGLMIGRTPEYLGKKIEALDMQMVALVILATPALVLAGTAVAVLADAGRAGVLNPGAHGF SEILYAMSSAANNNGSAFAGLSANTPFYNVLLGLAMWFGRYTIIVAILALAGSLAAKPRLPAS VGGMPTTGPLFVALLVGAVLLVGALTYVPALALGPVAEHLQP
6E-239	803.2	24.5	9E-239	802.7	17	1.2	1	KDPA_BORBR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BB3917	Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	594	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella bronchiseptica (Alcaligenes bronchisepticus), Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	257310	>sp|Q7WCL8|KDPA_BORBR Potassium-transporting ATPase potassium-binding subunit OS=Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) GN=kdpA PE=3 SV=1 MNADFLGLLLLYLAILLCAAPLLGRHIRQAMNGERTWLTAWGQPLERGLYRLAGVDPAAEM DWRRYAVAMLVFNVLGVLAVYALQRLQGWLPLNPAGLPGVAPDSALNTAISFVTNTNWQG YAGESTMSYLTQMLALTVQNFVSAATGIAVLIALVRGLARHSAATLGNFWADLVRATLYVLL PLSFILALALVSQGVVQNLDPYVEAQTVQAQQYETARLDAQGQPMTGPAGQPLTDTVVTRV QNLPMGPVASQEAIKLLGTNGGGFFNANSAHPYENPNAWSNLLEMLAILLIPAALCWTFGE MVGSRRQGVAILAAMTVLFAGFSASAAYFEQQPTPALRQAEAALLADGGNLEGKEARFGV AATALFATVTTAASCGAVNGMHDSFSALGGVTPLLQMQLGEVIYGGVGSGLYGMLAFAILA VFIAGLMIGRTPEYLGKKIEALDMQMVALVILATPALVLAGTAVAVLADAGRAGVLNPGAHGF SEILYAMSSAANNNGSAFAGLSANTPFYNVLLGLAMWFGRYTIIVAILALAGSLAAKPRLPAS VGGMPTTGPLFVALLVGAVLLVGALTYVPALALGPVAEHLQP
7E-239	803	27.1	8E-239	802.8	18.8	1	1	A5V6B6_SPHWW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Swit_1468	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas wittichii, Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	392499	>tr|A5V6B6|A5V6B6_SPHWW Potassium-transporting ATPase potassium-binding subunit OS=Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273) GN=kdpA PE=3 SV=1 MSLAGWALILVFIAILLLLAKPMGAWMFALYEGRRTPLHRLLGPVETGFYRLSGIDPAAEQG WRRYAVHMILFNLGLLLLTYVILRTQAWLPFNPRGLPNVAPDLAFNTAVSFTTNTNWQSYA GEATMSQLSQMVALTVHNFTSAATGIALAFALFRGFARREAGTIGNFWADVTRITLYLLLPLS ILFAVFLIANGVPQTLAGSVDATTVEGARQSIALGPVASQEAIKLLGTNGGGFFNANSAHPFE NPNALTNLFQMLSIFLIAVGLTWTFGKAVGNPRQGWAILAAMLVLFLIGASVVYWQEAAGNP VLHGLGVPGGNMEGKEVRFGIAGSALYAAVTTAASCGAVNAMHDSFTALGGMIPLINMQLG EVVVGGVGAGVYGFLLFAILAVFVAGLMVGRSPEYVGKKIEAREVKLAVLAIAVLPLVILGFT ALSAVTPAGLAGPLAKGPHGFSEILYAFTSGVANNGSAFAGLTAATPWYDGLLGVAMWIGR FFVIIPMLAIAGSLAAKKYVPAGAGSFPTTGPLWIGLLVGIVLIVGGLTFLPSLALGPIADHLAM IRGQLF
7E-239	803	28.3	9E-239	802.7	19.6	1	1	A0A098G6L1_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LFA_2763	Legionella fallonii LLAP-10	605	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella fallonii, Legionella fallonii LLAP-10	1212491	>tr|A0A098G6L1|A0A098G6L1_9GAMM Potassium-transporting ATPase potassium-binding subunit OS=Legionella fallonii LLAP-10 GN=kdpA PE=3 SV=1 MTKISILQIAIYYLVLLALVKPLGWYMACVYEGKDCAIGRFISPIEHFLYRCCGIEPEREMNWK SYLSAMLIFNLIGFFVVYLIQRVQFYLPLNPQHFFATSSDLSFNTAISFVTNTNWQSYSGETT MSYFTQMIALTVQNFLSAATGMSLLVALIRGIARCESTNLGNFWVDTVRGILYILLPLSLFLAIV LTSQGVIQNFIPNQKISLLQEGSFSQAKLDGSGQIVKDEHGNPLMESKKITEQVIPMGPVAS QVAIKQLGTNGGGFFNSNSAHPFENPNPLTNFLEMLAILLIPAAFCYTYGMMVSDKRQGWA LFAAMCIILIPLTFLAVHIEIKGNPAFNALDVSQSSDHHLAAIGNMEGKETRFGAATSAIWATV TTAASNGSVNAMLDSFMPMGGFVPLFMMHLNEVVCGGVGSGLYGMLMLAIVTVFIAGLMV GRTPEYLGKKIEPFEMKMASLTVLVMPLIVLLFTAIASVSAAGTSSLANPGAHGFSEILYTFTS MGNNNGSAFAGLNANTYFYNVVGGLAMLISRYWIAIPTLAIAGSLVRKKRIPSSSGTLQTYTP LFIILLVSVIFIFGALSFIPALALGPIVEHLLLWGQYGH
7E-239	803	30.5	9E-239	802.7	21.1	1	1	A0A0F5K278_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA WM40_09835	Burkholderia andropogonis	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia andropogonis	28092	>tr|A0A0F5K278|A0A0F5K278_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia andropogonis GN=kdpA PE=3 SV=1 MNANNLGQATVLIVLLLVLAFPVGRYIASVMDGSSFVVRRIGRPVERLLYKLAGVDPGSEMS WKRYALCLLVFSGAGTLLLYAILRLQQWLPLNPQGMANMTPDAAFNTAISFVTNTNWQEYG GESTLGYFAQMVGLTVQNFLSAATGIAVAIALIRGFARHTTSTIGNFWVDLTRITLYILAPIAIV FAVFLTGQGVIQTFSPYRDVATLQTTTYQTPKLDAAGSPVKNAKGEPVMVDGTADKQTLAL GPVASQEAIKMLGTNGGGFFNANSAHPFENPTPLSNFMQVLVMLLIPAALCVTFGRMVGDK RQGRALLAAMTIAFVLAVGVELTSEQAGNPAFAALHVDQAATAMQSGGNAEGKETRFGIAQ TGIFTVATTAASAGATDATHDSLTPIGGLVPMLLMQLGEMIFGGVGAGLYSMIIFAVLAVFVA GLMIGRTPEYLGKKIESYEMKMVAITVLLTPFLVLVGTSIAVLADAGVAGILNPGPHGFSEILY AFTSASNNNGSAFAGLTVNTPFYNVLLGIAMWLGRFVWIIPVLAMAGALAAKKRLAQTAGTL PTHGPLFVVLILGTIVLVGALTYVPALALGPVVEQLIMLAPH

8E-239	802.8	31.9	1E-238	802.6	22.1	1	1	KDPA_SALAR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SARI_02235	Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica subsp. arizonae, Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	41514	[illegible] OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=kdpA PE=3 SV=1 MAAQGSLLIASFLLILLVLAKPLGSGLARLIAASPLPGVAGVERVLWRTLGITGHEMNWRQYL LALLTLNLLGLSILFCLLFWQEWLPLNPQRLPGLSWDLALNTAVSFVTNTNWQAYSGESTLS YFSQMAGLTVQNFLSAATGIAVVFALIRAFTRQNMHTLGNAWQDLVRITLWILFPVALIIALFF IQQGVLQNLSAYQPITTLEGAQQLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPTAL TNMVQMLAIFLIPAALCFAFGEAAGDRRQGRALLWAMSFIFVVCVAVVMWAEVQGNPHLLT AGADSSVNMEGKETRFGVLASSLFAVVTTAASCGAVDAMHDSFTALGGMVPMWLMQIGE VVFGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPMLVLLGSA LAMMTDAGRSAMLNPGPHGFSEVLYAVSSAANNNGSAFAGLSANSPFWNCLLAFCMFVG RFGVIIPVMAIAGSLVSKKAQPASQGTLATHGALFIGLLIGTVLLVGALTFIPALALGPVAEHFS LP
9E-239	802.6	22.6	1E-238	802.3	15.6	1.1	1	A0A0A1H5K4_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA E1O_24650	Burkholderiales bacterium GJ-E10	606	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, unclassified Burkholderiales (miscellaneous), Burkholderiales bacterium GJ-E10	1469502	>tr|A0A0A1H5K4|A0A0A1H5K4_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderiales bacterium GJ-E10 GN=kdpA PE=3 SV=1 MTSHAWTLLVLYGAVLIVVSYPLGTYLADCLDGGPSRVAAAARRIVGPIERILYRLCGIRAEE EMDWKRYALAILIFSVLGALTVYALQRLQAKLPLDPQALPAVGPDSSFNTAVSFATNTNWQ GYSGETTMSYLTQMLGLAVQNFLSAATGIVVAIALIRGIARHSAATIGNAWVDLTRTTFYVLL PISFVYAIFLIGQGAIQNFSAYKDVHTVEVTTYQTPKLDAAGQPVKDAHGNPVNVNAQTQTQ TLPMGPVASQESIKMLGTNGGGFFNANSAHPYENPTPLSDFVQMVSIFLIPAALCFSFGRM VGDRRQGWAIFAAMSLLFLISTVVVIVAEQHGNPAFTPLGVDQAASAMQAGGNMEGKETR FGIADSGLFASITTAASCGAVNAMHDSLMPMGGFVPLWNMMLGEVVFGGVGSGLYGMLVF ALTAVFIAGLMIGRTPEYLGKKIESFDMKMISLAILATPMLVLVCTAIAVASADGRAGIANPGP HGFSEILYAFTSAANNNGSAFAGLSADTPFYNVLTVVAMWFGRFAVIVPVLGIAGSLAAKKR LAATGGSMPTHGPLFVVLLIGTVVLVGALNYVPALALGPVVEQLTLPAAG
1E-238	802.3	28.6	1E-238	802	19.9	1	1	E3HLY1_ACHXA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AXYL_01194	Achromobacter xylosoxidans (strain A8)	600	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Achromobacter, Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans), Achromobacter xylosoxidans (strain A8)	762376	>tr|E3HLY1|E3HLY1_ACHXA Potassium-transporting ATPase potassium-binding subunit OS=Achromobacter xylosoxidans (strain A8) GN=kdpA PE=3 SV=1 MTAEFIGLLVVYLAVLLAIAPLLGRYIRIAMENGQSRLTAWGRPIERGIYRLAGIDPQAEMGW KRYAVAVLAFNIIGIAAVYALQRLQGVLPLNPAGMGAVSPDSALNTAISFVTNTNWQGYGGE STMSYLTQMLALTVQNFVSAATGIAVVFALIRGLSRHCSATVGNFWTDMVRSTLYVLLPLSL VLALALVSQGVVQNFSPYQEVQTVEAVHYDQPRMDAQGQPVLDAKGQAVTDPAVSKTQTL AMGPVASQESIKLLGTNGGGFFNANSAHPFENPTPLANFLEMLAILAIPAALCFSFGEMVGS RRQGIAILAAMTVLFAVFALSAAYFEQQPNPMAAQASADSTLSAFSPGGNMEGKETRFGIA ATSLFATVTTAASCGAVNGMHDSLNAMGGLTPMLLMQLGEVVFGGVGSGLYGMLAFAILG VFIAGLMIGRTPEYLGKKIEAYDMKMVSIVILATPLLVLCGTALAVSVAAGQAGVLNPGIHGFS EILYALTSAANNNGSAFAGLSANTPFYNVLLGIAMWFGRFAIIVAILAMAGSLAAKRRHPAGP GSMPTTGPLFVVLLIGAVLLVGALTYVPALALGPVAEHLQLKG
1E-238	802	38.2	2E-238	801.8	26.5	1	1	F8JAZ8_HYPSM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HYPMC_3102	Hyphomicrobium sp. (strain MC1)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium sp. (strain MC1)	717785	[illegible] OS=Hyphomicrobium sp. (strain MC1) GN=kdpA PE=3 SV=1 MTLIGWIQIALFCAIVLALVKPLGWYMTRVFSGEKTFLSPILSPVEAGLYKIAGVDARGEQDW LRYTVSMLLFHIGGFVILYAVLRLQGALPFNPQGMTALAPDLSFNTAISFITNTNWQNYGGET TMSYFTQMLGLTHQNFLSAATGIVLAIVLIRGFARASTRNLGNFWVDVTRCTLYILLPLCIPYT LFLVWQGIPQTIGAYVDATTLEGAKQTIAVGPVASQVAIKMLGTNGGGFFNANAAHPFENPT ALSNFVQMISIFALGAALTNVFGRMVGNQRQGWAILAVMGVLFIAGVAVCYWAEANGTTGL NALGLTGGNMEGKETRFGIVGSALFAVITTAASCGAVNAMHDSFTALGGMIPLVNIQLGEIIV GGVGAGLYGMLLFVVLAIFVAGLMVGRTPEYVGKKIEAKEVKMAMLAILILPLMILGWTAVAA VLPSALASIANPGPHGFSEILYLFSSSTGNNGSAFAGITGNTFFYNVTGAISMFVGRFLMIVP AMAIAGALAEKKTLAPSVGTFPTTGGLFVGLVVGVILIVGGLTFFPALALGPIVEHLAMTAGTL Y
2E-238	801.8	39.5	2E-238	801.6	27.4	1	1	E4T7V0_PALPW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Palpr_2664	Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	564	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Paludibacter, Paludibacter propionicigenes, Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	694427	>tr|E4T7V0|E4T7V0_PALPW Potassium-transporting ATPase potassium-binding subunit OS=Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4) GN=kdpA PE=3 SV=1 MFTTYDFLQIIIFLGLLIGLTPVLGNYMYKVFTGEKHLMSAPLGWLERLTYKLVGVDATEETN WKTYTFGLLLFNFIGFLFVFLLQLTQAYLPLNPANLPNVSWHSAFNTAVSFMTNTNWQGYG GETTLSYLVQMLALTVQNFVSAATGIAVLLALTKGLSRRTTDKLGNFWVDLTRSTLYVLLPLS IIFAVFLVGQGVIQNFETYQTAHTLQGAQQVIPMGPVASQEAIKQLGTNGGGFFNANSAHPF ENPTPLSNLLEMLAILLIPAGLTFTYGKMVGSKRQGWTIFIVMMILLLGGLAISLYGEYSANPIF GHSALMEGKETRFGITNSVLWSTSTSAASNGSVNAMHDSLSPLAGMVAMINIMLGEIVFGG VGAGIYGMVVFIILTVFIAGLMVGRSPEYLGKKVEAFEVTMAIIANLATSFVILLFTAWAAVSTL GLSSLNNAGPHGFSEILYAFSSAAGNNGSAFAGLNANTVFYNLLLGIGMLIGRFGVIIPILAIA GNMAKKKITPVSTGTFQTDNWLFVSLLIGVIIIVGGLTYFPALSLGPIVEHLLMNNGITF

2E-238	801.7	25.1	3E-238	801.1	17.4	1.2	1	X4ZK81_9BORD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA D560_0210	Bordetella holmesii ATCC 51541	594	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella holmesii, Bordetella holmesii ATCC 51541	1247649	>tr|X4ZK81|X4ZK81_9BORD Potassium-transporting ATPase potassium-binding subunit OS=Bordetella holmesii ATCC 51541 GN=kdpA PE=3 SV=1 MNADFLGLLLLYLASLLCAAPLLGRHIRQAINGERTWLTAWGQPLERGLYRLAGVDPAAEM NWRRYAVAMLVFNVLGVLAVYALQRLQGWLPLNPAGLPGVAPDSALNTAISFVTNTNWQG YAGESTMSYLTQMLALTVQNFVSAATGIAVLIALVRGLARHSTATLGNFWADLVRATLYVLL PLSFILALALVSQGVVQNLDPYVEAQTVQAQQYETARLDAQGQPMTGPAGQPLTDTVVTRV QTLPMGPVASQEAIKLLGTNGGGFFNANSAHPYENPNAWSNLLEMLAILLIPAALCWTFGE MVGSRRQGVAILAAMTVLFAGFAASAAYFEQQPTPALRQAEAALLADGGNLEGKEARFGV AATALFATVTTAASCGAVNGMHDSFSALGGVTPLLQMQLGEVIYGGVGSGLYGMLAFAILA VFIAGLMIGRTPEYLGKKIEALDMQMVALVILATPALVLAGTAVAVLADAGRAGVLNPGAHGF SEILYAMSSAANNNGSAFAGLSANTPFYNVLLGLAMWFGRYTIIVAILALAGSLAAKPRLPAS VGGMPTTGPLFVALLVGAVLLVGALTYVPALALGPVAEHLQP
2E-238	801.6	22.8	3E-238	801.1	15.8	1.1	1	E5AVA3_BURRH	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RBRH_02803	Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia rhizoxinica, Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454)	882378	>tr|E5AVA3|E5AVA3_BURRH Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454) GN=kdpA PE=3 SV=1 MNAHSLLQAVLFIIVLIALALPLGRYMCGVLDGSSVLVRKLGRPLEHGLYRVAGVDPQAEMS WKHYALAVLLFNALGAVVVYGLLRLQQWLPANPQGLGAMPPDAAFNTAVSFVTNTNWQN YSPESSVSYLTQLAGLAVQNFLSAATGIAVVVALIRGFARHTARTIGNFWVDLTRVTLYILAPL AIVVSLVLVSQGVLQNLKPYQQVSTLQVTTYPVPRTDAQGNPVKDAHGNVVMQDAKVDKQ TLAMGPVASQEAIKMLGTNGGGFFNANSAHPFENPTPLSNFVQILSILIIPAGLCVVFGRMVG DRRQGYAVLAAMTIAFAVACFAEISAEQSGNPLFASLHVDQQASALQAGGNAEGKEVRLGI AQSGIFTVATTAASCGAVDNTHDSLTPLGGFVPLLLMQLGEVIFGGVGSGLYGMLVFALLAV FVAGLMIGRTPEYVGKKIESFEIKMVALVVLLTPFLVLVGTSIGVLSPLGVAGIANPGPHGFSE VLYAFSSAANNNGSAFGGLSVNTPFYNVLLAIAMWFGRFGTIVPVLAVAGSLASKKRIATTP GTLPTHGPLFVVLLLGTLVLVGALTYVPSLALGPIVEQLMMIAGH
2E-238	801.3	33.1	3E-238	801.1	22.9	1	1	KDPA_YERPE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA YPO2692 YP_2495	Yersinia pestis	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia pseudotuberculosis complex, Yersinia pestis	632	>sp|Q8ZD96|KDPA_YERPE Potassium-transporting ATPase potassium-binding subunit OS=Yersinia pestis GN=kdpA PE=3 SV=1 MVASGFLLIASFMLVLFVLSRPLGGFLARLIEGEPFSALQKVEAGLWRCSGVKNAEMNGWQ YALAILCFNLLGIVLLFVLLMTQGSLPLNPEHLPGMSWHLALNTAVSFVTNTNWQAYSGENT LSYLSQMAGLTVQNFLSAATGIAVAFALIRAFARHSATTLGNAWVDLVRITLYVLLPIALIIALIF VSQGVLQNLDDYLHITTLEGVQQTLPMGPVASQEAIKVLGTNGGGFFGANSAHPFENPTAF SNFVQMLAIFLIPCALCFAFGQVVGDNRQGHALIWAMSLIFIVAVVVVMYAELAGNPHLSPLG ADSNSNMEGKESRFGILATSLYAVVTTAASCGAVNAMHDSFTALGGMIPLWLMQIGEVVFG GVGSGLYGMLLFVLLTVFIAGLMIGRTPEYLGKKIDVFDMKMTALAILVTPTIVLLGTALALCT EAGRAGILNPGAHGFSEVLYALSSAANNNGSAFAGLSVNTPFYNLLLAAAMFIGRFGVILPVL AIASSLVAKKRQPAGNGTLPTGGLLFIGLLIGTVLLVGALTFIPALALGPVAEHLQVWLAH
3E-238	801.2	38.8	3E-238	800.9	26.9	1	1	D4GD2_PANAM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PANA_3790	Pantoea ananatis (strain LMG 20103)	560	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea ananas (Erwinia uredovora), Pantoea ananatis (strain LMG 20103)	706191	>tr|D4GD2|D4GD2_PANAM Potassium-transporting ATPase potassium-binding subunit OS=Pantoea ananatis (strain LMG 20103) GN=kdpA PE=3 SV=1 MAANAFLLIAVYLLLLMVMAQPLGRGLAALVADKPLFARAEALLWRFSGVQEGGMRWQHY LLAILVFNLLGFVVLLAILMFQGALPLNPQHLPGLSWDLALNTAISFVTNTNWQSYAGESTLS YFSQMVGLTVQNFVSAATGIAVAFALIRGFANRSVATLGNAWRDLTRITLYVLLPISLLMALF FVSQGSIQNFLPYHNVTSLEGAQQTLAMGPVASQEAIKMLGTNGGGFFNVNSAHPFENPT ALSNFVQMLSIFLIPAALCFAFGESVKDRRQGSMLLWSMTLMFVVAAALVMWAELRGNPHF LTLGADSAINMEGKETRFGILNSSLFAVITTAASCGAVNAMHDSFTALGGMVPMLLMQLGEV VFGGVGAGLYGMLLFVLLAVFIAGLMIGRTPEFLGKKIDVWEMKMTALAILVTPALVLIGTAIA MMTDAGRAGMANPGTHGFSEVLYAVSSAANNNGSAFAGLSANTPFWNLLLAVCMFVGRF GIIIPVMAIAGAMAVKKVQPVGNGTLPTHGPLFIALLVGTVLLVGALTFIPALALGPVAEHLQLI QGQ
3E-238	801.2	27.2	3E-238	800.9	18.8	1	1	D2R317_PIRSD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Psta_4100	Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	596	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Pirellula, Pirellula staleyi, Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	530564	>tr|D2R317|D2R317_PIRSD Potassium-transporting ATPase potassium-binding subunit OS=Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) GN=kdpA PE=3 SV=1 MTSYSVLQIVLFLGVLLVCVAPLGRYMAKVYRGDQQLADRILGPLERLIYYASGIDPRASMT WQQYATSVVMLSLVSFVSVYAIQRLQSYLPLNPAGLADVSPDSSFNTAVSFTTNTNWQGY GGETTMSYLTQMLALGVQNFVSAATGMAVLVALIRGFMGHHDKTIGNFWVDTTRSLVYILL PLSLVLALLLVSQGVVQTLGSYASVPLLEQTISHTGQAAADQASGDQPTAAQPIAQTIALGPV ASQVAIKQLGTNGGGYFNVNSAHPFENPTPISNFLEMLSILLIPAALCYTFGEMVNDRRQGW TILAAMSVVLIPLLFAVYATEQRGSPVLANLGVDQVASDSQPGGNMEGKEVRFGIVSSTTW GVATTAASNGSVNSMHDSYLPVGGLFTMWLMQLGEVIFGGVGSGLYGMLVFAVVAVFLSG LMVGRTPEYLGKKIGAFEMKMASLAILLPCAMVLLGTAIAVSTTAGRASVFNPGAHGFSEVL YALSSAGNNNGSAMAGLGANTPFYNGLLGLAMLVGRFWVMLPVIAMAGSLANKKSLPGGE GTLPTHTPMFVVLLVAVVLVVGALSFFPALALGPIVEQLQLPSLR

3E-238	801.1	32.8	3E-238	800.9	22.7	1	1	KDPA_SERP5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Spro_1248	Serratia proteamaculans (strain 568)	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia proteamaculans, Serratia proteamaculans (strain 568)	399741	[illegible] OS=Serratia proteamaculans (strain 568) GN=kdpA PE=3 SV=1 MAASAFLLIASFMLVLLLARPLGSFLARLIEGEPLPALRRVEAAVWRCCGNTTAEMNWWQ YALAILWFNLLGLALLFALLMTQGSLPLNPQGFPGLSWDLAFNTAVSFVTNTNWQAYSGES TLSYLSQMAGLAVQNFLSAATGIAVAFALIRAFTRRSSATIGNAWIDVFRITLYVLLPISLLIALF FVSQGTLQNFLPYLHISTLEGAQQTLPMGPVASQEAIKMLGTNGGGFFGVNSAHPFENPTV LTNFVQMLAIFLIPCALCFSFGQVAGENRQGHALIWAMSLIFVVAVVVVMYAELAGNPHLSE LGSASNINMEGKESRFGILATSMFSVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGSGLYGMLLFVLLTVFIAGLMIGRTPEYLGKKIDVYDMKMTALAILVTPTLVLLGSALA ISTDVGRAGILNPGAHGFSEVLYALSSAANNNGSAFGGLSVNTPFYNLLLAFAMFVGRFGVI LPVLAIAGSLCAKKRQPAGNGTLPTYGPLFIGLLVGTVLLVGALTFVPALALGPVAEHLQLWL TK
3E-238	800.9	32.6	4E-238	800.7	22.6	1	1	R6S6M0_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN652_02352	Firmicutes bacterium CAG:424	574	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	1263022	[illegible] OS=Firmicutes bacterium CAG:424 GN=kdpA PE=3 SV=1 MLQIILTLAIFVILVIPMGKYMYHIATKQKTFADKVFNPIDRFFYKICGIKGEDMGWKKYALTLL LVNGVMVLVGYGILRLQDLLFLNPNGISDMEPTLSFNTIISFMTNTNLQHYSGESGLSYAAQ MCVIIFMMFTSAATGYAACMAFCRGLAGKKIGNFYEDMVRITTRILIPVSFLVGLLLVSQGTP QTLHANFTIETLEGNLQDIAVGPVAALESIKHLGTNGGGFFGANSTTPFENPTVITNIAEMISM MLLPGACVVTFGHMLHDKKKAKQAEKAAVGSKKLIFGRQGAVVFGAMAILFLVGLMICYNS ELAGNPVIQDMGVDQTQGSMEGKEVRFGIPQSALFTTVTTSFTTGTVNNMHDTLTPLGGLV PLLHMMLNCVFGGKGVGLMNMIMYVILAVFICGLMVGRTPEYLNKKIEGKEMKLVALCILIHP LLILGFSALAVAVPAGLEGITNPGFHGLTQVLYEYASSAANNGSGFEGLADNTAFWNVTAGL AMFFGRYIAIIAQLAIAGSMLAKKKVNESVGTLRTDNVTFMIILVFIVYIFAALTFFPALALGPIA EHLSIWM
4E-238	800.5	33.6	5E-238	800.1	23.3	1.1	1	R5A9S5_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN452_00249	Clostridium sp. CAG:1013	592	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:1013	1262769	[illegible] OS=Clostridium sp. CAG:1013 GN=kdpA PE=3 SV=1 MLQIILTIILYLIMVVPVGIYVYHIAAGKHTFADPVFDRVDGAIYKISGIKPQNGMNWKKYALALI STNGVMILLGYIILRMQSLPIFNPNGVGNMEETLSFNTIISFMTNTNLQHYSGESGLSYLSQM VVIIFMMFVSAASGYAACVAFIRGLAGKTRDNVGNFFADLVRITTRVLLPFSIVGGLLLVWQG VPQNFSGNVVVDTIEGAKQIIAMGPVAALEIIKHLGTNGGGFLGANSSTPIENPTIITNLIELYS MMLLPGACVITFGKMVHDRKQEMAQAKSGLDAEQAFESQGKVRKSFTVWMYGREGRSIF AAMGIIFLIGLSVCFWAESQGNPALADVGLSQSMGSMEGKEVRFGIAQSAMFTTTTTSFTT GTVNNMHDTLTPLGGMIPMLHMMLNVVFGGKGVGLMNMIMYAILAVFICGLMIGRTPEYLG KKIEGREMKLTALCIIIHPLLILAFSALAVGTQSGLEGITNPGFHGLSQVLYEYASSAANNGSG FEGLADNTMFWNITTGLAMFFGRYLSIVIQLAIAGSLMKKRFVNESAGTLHTDTFSFAVILVF VVYIFAALTFFPVLALGPIAEHLTLWA
4E-238	800.4	30.3	5E-238	800.2	21	1	1	H8MWC1_CORCM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA COCOR_07866	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	565	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, Corallococcus coralloides (Myxococcus coralloides), Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	1144275	[illegible] OS=Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) GN=kdpA PE=3 SV=1 MTLLGWLQTLLFFALVLALTKPVGLYLFRVFVADTQPLPRVLGPIERALLRLCGVRREQEQT WGQYTAALLAFSAVGLVVLYALQRFQHVLPLNPRGLPAVGPALAFNTAASFVANTNWQSY AGESTMSYATQMLGLTWQNFVSAATGLGVALALARGLTRRTLGNFWVDLVRGTLYVLLPL SFLAALFFVSQGVLQNLAPYPEHTTVEGAKQTLAFGPVASQEAIKMLGTNGGGFFNANSAH PFENPTPLTNLVQLLLIFVLPAGLTYTYGKMAGDTKQGWVLFAAMSVLFLVGAAASYAAEVQ PNPALTAANVLPSGNLEGKETRFGVAASALFATVTTDASCGAVNAMHDSFTALGGLVPLVN MQLGEVIFGGVGAGLYGILVMAVLAVFIAGLMVGRTPEFLGKKIEAREMTLAMLYVLVFPLVI LGLSAVGAVLPQGTSSLNNAGPHGLSEILYAFTSGVANNGSAFAGLNANTPFWNISLGVSM LAGRFLMMVPVLALAGSLVGKKTVAPGPGTFPTNGVLFTGLLVSVVVVVGALTFFPALSLGP IVEHFLGAAGKVF
5E-238	800.3	29.7	5E-238	800.1	20.6	1	1	W0A4I8_9SPHN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NX02_05685	Sphingomonas sanxanigenens DSM 19645 = NX02	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sanxanigenens, Sphingomonas sanxanigenens DSM 19645 = NX02	1123269	[illegible] OS=Sphingomonas sanxanigenens DSM 19645 = NX02 GN=kdpA PE=3 SV=1 MTPQGWTLILVFVAILIALAKPMGLWLHALYEGRRTPLHVVLGPVEAGFYRLAGIDPAAEQS WRRYAVHMLIFNVALLLLTYAVLRLQGLLPGNPLGYAGLSEHLAFNTAVSFTTNTNWQSYG GESTMSNLSQMLGLTIHNFLSAATGIALAFAFFRGFARRRAATIGNFWADCTRVTLYLLLPICI VYAVFLIASGVPQTLVGSVDVTTLEGAKQTLALGPVASQEAIKLLGTNGGGFFNVNSAHPFE NPTALTNFVQMLSIFIIGFGLTWTFGKAVGNPRQGWAILAAMVTIFMIGASVTYWQEAAGNP ILHQLGVAGANMEGKEVRFGVAASALFSVVTTAASCGAVNAMHDSFTALGGMIPLLNIQLG EVVVGGVGAGIYGFLLFAILAVFVAGLMVGRTPEYVGKKIEGREVKLAVLAIAVLPLVILGFTA LASVTDAGLAGPLNKGPHGFSEILYAFTSGAGNNGSAFAGLTANTPFYNGLLGVAMWIGRF FIIVPMLAIAGSLAAKKHTPETAGSFPTTGPLWTGLLIGIVLIVGGLTFLPSLALGPIADHLAMIN GRTF

5E-238	800.1	32.5	6E-238	799.9	22.5	1	1	R5BWD7_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN499_00283	Blautia hydrogenotrophica CAG:147	575	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	1263061	[illegible] OS=Blautia hydrogenotrophica CAG:147 GN=kdpA PE=3 SV=1 MLQILISLAIYMVLVIPMGTYMYHIATNKKTFADPVFNRIDNGIYKLCRINRQGMNWKQYALHL LMANAVMVFVGYLVLRFQGVLFNNPNGIEGMEPTLSFNTIISFMTNTNLQHYSGESGLSYLS QMLVIIYMMFTSAASGYAACMAFCRGLAGKRKDLGNFYEDMIRITTRILIPVSIIGGLILISQGT PENFLSNQTIHTIEGKLQDLAMGPVAALEIIKHLGTNGGGFFGANSTTPFENPTIISDLVEMYS MMILPGACVITFGKMVQERKRSENKTVEAAKKISIFGKQGRTVFAAMAIIFMVGVCVCFFSE KAGNPILADAGVSQAMGSMEGKEVRFGIDQSALFTTVTTSFTTGTVNNMHDTLTPLGGMVP LLHMMLNCVFGGKGVGLMNMVMYVILAVFLCGLMIGRTPEYLGKKIEGREMKLVALVLIVHP LLILGFSALAVSTTGGIEGITNPGFHGLSQVLYEYSSSAANNGSGFEGLADNSYFWNITAGLA MFFGRYIAIIAQLAIAGSMLAKKKVNETVGTLRTDNAIFVIILVVVVYIFAALTFFPALALGPIAE HLTLWM
5E-238	800.1	22	6E-238	799.9	15.2	1	1	D1CGX3_THET1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Tter_2091	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	572	cellular organisms, Bacteria, unclassified Bacteria, Thermobaculum, Thermobaculum terrenum, Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	525904	>tr|D1CGX3|D1CGX3_THET1 Potassium-transporting ATPase potassium-binding subunit OS=Thermobaculum terrenum (strain ATCC BAA-798 / YNP1) GN=kdpA PE=3 SV=1 MSWLQIPAFLLVLLAITKPLGSYMARVYQGERTFLSPALAPLERAIYRVARVDPDREQDWRG YALALLLFNLSGMLALYALQRLQAWLPLNPEHLPGVAPDLAFNTAASFVTNTNWQAYAGET TMSYLTQMAGLTVQNFLSAAVGLAAAVALARGLTRRSTRQLGNFWVDVTRSVLYVLLPLAIL GALLLVWQGVPQNLSPYVAAETVEGHRQILPQGPVASQEAIKLLGTNGGGFFNANSAHPYE NPTPLTNFLEALYIFVVPAALLYTFGKMTGDTRQGWALWVASALLFLAGLGVASWAERAGN PLLAGLHVGQGGLAGVSMEGKEIRLGLPGTLLFSVVTTAASCGAVNGMLSSLSPLAGGVAL FNMQLGEIIFGGVGSGLYGLVIYAMLAVFIAGLMVGRTPEYLGKKIEAFEIKMSVVYMLAFAAI ILLLSAWAAAASYGRGQVLNPGPHGLSEIVYAYSSATGNNGSAFAGLSANTAFYNLTLGLA MLGGRFLLLLPVLAIAGSMARKRAVPPSLGTFPTNGGTFVALLVGTILIVGALTFFLVLSLGPV AEQLIMAAGKAFGGR
6E-238	799.9	22.9	8E-238	799.6	15.9	1	1	M4XEY4_PSEDE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA H681_10005	Pseudomonas denitrificans ATCC 13867	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas pertucinogena group, Pseudomonas denitrificans, Pseudomonas denitrificans ATCC 13867	1294143	[illegible] OS=Pseudomonas denitrificans ATCC 13867 GN=kdpA PE=3 SV=1 MNSHDLLLIVVFLALVLVPAPFLGRFYYKVMEGQRTFFSPVFLPVERAIYRACGIDPDVQQD WKGYTLALLAFNLAGLLLLFSILLLQGLLPLNPQHLPGLEWTLAFNTAVSFVTNTNWQAYSG EASLSYLSQMLGLTVQNFVSAAVGLAVLVALARGIARKSTNSLGNFWVDLTRATLYGLIPLCL LLALLLVWQGVPQTFLDYAHALTVQGADQTIPLGPAASQIAIKQLGTNGGGFFGVNSAHPFE NPTIWSNLFEVASIILIPAALVFTFGHYVKDLRQSRAILGCMLVLFCLGLGTSLWAEYQPNPAL SALPVEQSAPMEGKESRFGTTASVLWSVTTTSASNGSVNAMHDSLNPLSGMVAMINMMLG EVIFGGVGAGLYGMLLFVLIAVFLAGLMVGRTPEYLGKKLEAREVRLLVATLLVMPVGVLVL GAIAASLPGPAAAVTNPGPHGFSQLLYAYTSGTANNGSAFAGFGANTPFHNLMIALAMLIGR FGYILPVLAIAGSLAAKKATPVGPNSFPTHGLLFVSLLTATILLVGGLNFLPTLVLGPVADHLTL GF
7E-238	799.8	37.1	8E-238	799.6	25.7	1	1	A0A0D1XA26_ANEMI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TS65_28120	Aneurinibacillus migulanus (Bacillus migulanus)	559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Aneurinibacillus group, Aneurinibacillus, Aneurinibacillus migulanus (Bacillus migulanus)	47500	>tr|A0A0D1XA26|A0A0D1XA26_ANEMI Potassium-transporting ATPase potassium-binding subunit OS=Aneurinibacillus migulanus GN=kdpA PE=3 SV=1 MSTGIVQIAITLLIIILLIKPAGSYLVNVFNYEKTKLDKVFGPIEKVLYRIMGVHENERMGWKQY VMALLLSNFVMTMLMYAVLRLQKYLPFNPDGIDNMPSALAFNTAASFITNTNWQAYSGENG LSYLSQMLAITFPMFTSAATGLVAAIAFIRGLTAQKDNLGNFYVDLIRSLTRVFLPLSLLVALFL VFQGAPQTLDGAQTATSMEGAQQVITRGLVASLESIKHIGTNGGGYFGMNASHPFENPTPL TNLVHILCMMFIPTALVYAFGVMIKNKRQGWTVFATMAAIFLIMLATVFFAEYKGTPALQTLGI SGNMEGKEVRFGYSESALFTTVTTAATTGSVNNMHDSLTPIGGLVPLAQMMLNNVFGGDG VGLMNGLLYVILTVFICGLMVGRTPEFLGKKIEGKEIKLASIALLAHPVIIMVPTAIAFLRPESMA SILNAGSHGISEVLYAFTSGAANNGSAFAGLSANTNFYNMAIGLVMLFGRYVSIIALLAVAGS LATKRMAPATIGTFRTDSPLFALILFVIIVVIGALTFFPALALGPIAEQLSMWK
7E-238	799.7	30.1	8E-238	799.5	20.9	1	1	A0A0F5FIL4_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VE26_00575	Devosia chinhatensis	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia chinhatensis	429727	[illegible] subunit OS=Devosia chinhatensis GN=kdpA PE=3 SV=1 MTIFGWLQIGLVLIAVLLLVKPLGLYMARVFSGDRTWLSPVLAPIETGLYRIAGIRADKEQGW LGYALAVLAFSLAGFLALYGMLRLQHLLPLNPQGFAGLPPDLAFNTAVSFVTNTNWQNYGG ESTMSHFSQMAGLTVQNFLSAATGMAVAIAVSRALVRSKVSELGNFWVDMTRATLYVLLPL SLVVTLAFIAMGLPQSLDASFVATTLEGAQQTIATGPVASQEAIKQLGTNGGGFFNVNAAHP FENPSAFSNYLNIIAMLSVSLALVYAFGQMVGSRRQGWALIAVTIVLLTTGIGLVYWAETGG NPVLHAVGVDALQGNMEGKEVRFGQAMSALYGTVTTGLSNGGVNAMHSSLTPLGGLVPM FLIQLGEVLPGGVGSGLYGMIVFAILAVFVAGLMVGRTPEFLGKKIEAREMKLAMLAVLILPLA ILGFTAVSAVAEFGVGSITTPGPHGLSEILYAFSSAAGNNGSAFGGLTGNTPWYNTTLALAM LLGRFAYIVPVLAIAGSLAAKPRAEASSGTFPTDRPLFVGLLIGIILIMGGLQFFPALALGPIAE HFAMLAGQSF

8E-238	799.5	31	1E-237	799.2	21.5	1	1	A8HY16_AZOC5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AZC_1565	Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Azorhizobium, Azorhizobium caulinodans, Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	438753	>tr|A8HY16|A8HY16_AZOC5 Potassium-transporting ATPase potassium-binding subunit OS=Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571) GN=kdpA PE=3 SV=1 MTANGWLQIIVLFAVVIATAIPLGRFMARVYAGERTFLSPVLGPVERGLYRVAGVDPKLDQS WIGYTLAMLAFNGAGAVLLYAILRFQDFLPWNPQGFAGLSPDLAFNTAVSFVTNTNWQAYA GETTMSNFSQMVGLTVQNFLSAATGLALAIALVRGFARSGAKGVGNFFVDTTRSTLYILLPL SLVTAIVLVAMGVPQTLDGSVVATTLDGAQQNISIGPVASQIAIKQLGTNGGGFFNANAAHP FENPSALANMLQVWQMLVISVGIVFAFGQLIGDKRQGHAILAAMMILLVTGVAVAYWAEAA GTPILHGAGLDPAGGNMEGKEVRFGLALSALWAAVTTGLSCGAVNAMHGSFTPIGGLVPLV LIKLGEILPGGVGSGLYGMLVMAIIAVFVAGLMVGRTPEYLGKKIEAKEVKMAVLASLVLPVF VLGFSAVAAVLPGPLAAVGNGGPHGLSEILYAYASGTGNNGSAFASLSANTPWWNSTLGL SMLAGRFAYIVPMMAIAGSLAAKTRLAASSGTFPTHGPLFVGLLIGTIVILGGLQFFPAFALGP IAEQVQMLAGKTF
9E-238	799.3	34.7	1E-237	799.1	24.1	1	1	W8UBF3_YERENN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LC20_01659	Yersinia enterocolitica LC20	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia enterocolitica, Yersinia enterocolitica LC20	1443113	>tr|W8UBF3|W8UBF3_YERENN Potassium-transporting ATPase potassium-binding subunit OS=Yersinia enterocolitica LC20 GN=kdpA PE=3 SV=1 MAASGFLLIASFMLVLLVLSRPLGSFLARLIEGEPFMPLQQIEAALWRCSGVKNEEMNGWQ YALAILLFNVLGIVLLFALLIMQGSLPLNPENMPGMSWHLALNTAVSFVTNTNWQAYSGENT LSYLSQMAGLTVQNFLSAATGIAVAFALIRAFSRHSANTLGNAWVDLVRITLYVLLPIALVIALI FVSQGVLQNLDGYLHITTLEGVKQTLPMGPVASQEAIKMLGTNGSGFFGANSAHPFENPTA FSNFVQMLAIFLIPCALCFAFGHVVGDNRQGHALIWAMSLIFVVAVVVVMYAELAGNPHLMP LGADSNINMEGKESRFGILASSMYAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGSGLYGMLLFVLLTVFIAGLMIGRTPEYLGKKIDVFDMKMTALAILVTPAIVLLGTALA LGTDAGRAGILNPGAHGFSEVLYALSSAANNNGSAFAGLSVNTPFYNLLLAAAMFLGRFGVI LPVLAIASSLVAKKRQPAGNGTLPTSGPLFIGLLVGTVLLVGALTFIPALALGPVAEHLQVWLT H
1E-237	799.1	29.6	1E-237	798.9	20.5	1	1	A0A089R6S7_PLUGE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ABW07_01250 LG71_21430	Pluralibacter gergoviae (Enterobacter gergoviae)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pluralibacter, Pluralibacter gergoviae (Enterobacter gergoviae)	61647	>tr|A0A089R6S7|A0A089R6S7_PLUGE Potassium-transporting ATPase potassium-binding subunit OS=Pluralibacter gergoviae GN=kdpA PE=3 SV=1 MAAQAFLLIGSFLLLLFIAARPLGGVLAKMIANQPLPGTAGIERGLWRLLGVGQQEMGWRR YLLAILALNAAGIVLLFALLMLQHLLPLNPQRLPGLSWDLALNTAISFVTNTNWQAYAGESTL SYFSQMVGLTVQNFLSAATGIAVAFALIRGFCRRGADTLGNAWVDLVRVTLWLLLPLALIAL VMVQQGTLQNLLPYQHFISLEGAKGVLPMGPVASQEAIKMLGTNGGGFFNANSAHPFENP TALTNFLQMLAIFLIPAALCFAFGEAVKEARQGRTLLWAMSVIFVVCAAAVMWAELRGNPHF LQLGADSSANMEGKESRFGILASSLFAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIG EVVFGGVGSGLYGMLLFVLLAVFIAGLMVGRTPEYLGKKIDVREMKMTALAILVTPALVLLGT ALAMMTDAGRAGIFNPGIHGFSEVLYAVSSAANNNGSAFAGLGASTPFWNCLLAVCMLLGR FAVIVPVMAIAGSLVVKKRQPAGPGTLPTSGPLFVGLLIGTVLLVGALTFIPALALGPVAEHLS LLQEQHL
1E-237	799.1	31.7	1E-237	798.8	21.9	1	1	R5HPY7_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN469_01458	Firmicutes bacterium CAG:114	583	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:114	1263001	>tr|R5HPY7|R5HPY7_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Firmicutes bacterium CAG:114 GN=kdpA PE=3 SV=1 MLQLILTIIIYLIIVIPVGVYLYHVAAGKRTLADPVFNRIDGAIYKISGINPNQGMNWKKYALCLL GTNAIMILIGYIILRIQSIGLFNPNGIGAMEETLSFNTIISFMTNTNLQHYSGESGLSYLSQMLVI TFMMFVSASTGYAACIAFIRGLAGKTKDNVGNFFVDLVRVTTRVLLPFSIVGGLLLVWQGVP QNLTGNLVVDTIEGTKQAIAMGPVAALEIIKHLGTNGGGFIGANSTTPIENPTIISDLIELYSMM LLPGACVITFGKMVRDRKKAMAESSEVKVDLRKSLTARIYGREGRSIFLAMGIIFLIGLSLCF WSESQGNPALADAGLSQSMGSMEGKEVRFGIAQSAMFTTTTSFTTGTVNNMHDTLTPLG GMVPLLHMMLNVVFGGKGVGLMNMIMYAILAVFICGLMIGRTPEYLGKKIEGREMKLTALCIII HPFLILAFSALAVGTAAGQEGITNPGFHGLSQVLYEYASSAANNGSGFEGLADNTYFWNITA GLAMFFGRYLSIVIQLAIAGSLMKKRFVNESAGTLHTDTFSFAVILVFVVYIFAALTFFPALALG PIAEHLTLWA
1E-237	798.9	23.9	2E-237	798.7	16.6	1	1	Q4K8P4_PSEF5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA_1 kdpA PFL_4297	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	220664	>tr|Q4K8P4|Q4K8P4_PSEF5 Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=kdpA_1 PE=3 SV=1 MHSYDYWLILAFFALVLLPAPWLGRFYYRVMEGQRTWLTPVLGPVERVCYRISGVDPQVE QSWQKYTLALLAFNLAGFVLLFAILLFQDHLPLNPQHLPGQEWTLAFNTAVSFMTNTNWQS YSGEASLSYLSQMVGLTVQNFVSAATGLAVLVALCRGIGRRSVRTLGNFWVDMTRATLYGL LPLCLLLALFLVWQGVPQTFAHYVDALTLQGNDQVIPLGPAASQIAIKQLGTNGGGFFGVNS AHPFENPTAWSNLFELVSIILIPVALVFTFGHYVKDLRQSRAIIACMFALFLIGGATSLWAEYQ PNPALQNAAVEQAAPMEGKEARFGTTATVLWSVTTTAASNGSVNGMHDSLNPLSGMVALI NMMVGEVIFGGVGAGLYGMLLNVLIAVFLAGLMIGRTPEYLGKKLQAKEVQLLVVTLMVMPI GVLVLGALAASLPGPAAAISNPGPHGFSQLLYAYTSASANNGSAFGGFSANTPFHNLMLGL GMLIGRFGYILPVLALAGSLAMKKTAPIGQNSFPTHGPLFVALLTVTILLVGGLTFLPTLALGPI AEHLSMGF

1E-237	798.8	30.8	2E-237	798.6	21.4	1	1	KDPA_VARPS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Vapar_4995	Variovorax paradoxus (strain S110)	575	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Variovorax, Variovorax paradoxus, Variovorax paradoxus (strain S110)	543728	>sp|[illegible] OS=Variovorax paradoxus (strain S110) GN=kdpA PE=3 SV=1 MTSSAWGLLALFLAALLVLAWPVGKFLAALCNERVPRWMQRVEAPLYKIAGTRPEQSMHW LRYAIALLAFNAVGAVFVYALQRLQGWLPLNPAGMGAVSPDSAFNTAVSFVSNTNWQGYA GESAMSYLTQMLGLAVQNFFSAATGIAVAFALIRGFARRGDGKARGLVGNFWADLTRITLW VLVPLSFVLAVFFVSQGVIQNFDAYKTVQTVEATAAGGQTLAMGPVASQEAIKMLGTNGGG FFNANSAHPYENPSALANLLQMIAVFLIPAALCFAFGRVAGDLRQGWAVLAAMTVMFVAAV MVVIPAEQDGNPLFGALGVDQLHGALQSGGNMEGKEVRFGIDASALFAAVTTAASCGAVIA MHDSFTPLGGMVPMVLMQLGEVVFGGVGSGLYGMLIFAMLAVFIAGLMIGRTPEYLGKKIE VREMKLISIAILVTPVLVLAGTAVAVLAGAGKAGIANPGAHGFSEILYALSSAANNNGSAFAGL SANTPFYNGLLGLAMWLGRFAVIVPVLAIAGSLAAKQRLPVTGGTLPTHGPLFVSLLIGTVLL VGLLNYVPALALGPVVEHLVLWK
1E-237	798.8	30.7	2E-237	798.6	21.3	1	1	A0A089MIP7_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PODO_02705	Paenibacillus odorifer	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus odorifer	189426	>tr|A0A089MIP7|A0A089MIP7_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus odorifer GN=kdpA PE=3 SV=1 MGILQIVVVIVILILLVKPMGTYLYHVFSNEPNRTDRWFAGTEKGIYKLIGLKKRDGMSWKKY ALSFVLTNIVLVAFSYIFLRLQRGLPLNPNGIADMEQTLSFNTVISFMTNTNLQHYSGETGLSY FSQMAVITMMMFTSAASGFSVAVAFVRGITGQKSVGNFFEDFVKAHIRVFIPLALLVSLVLVG LHVPQTLKPSLEVTTLEGQTQQIAIGPVASLESIKHLGTNGGGFFGANSAHPFENPNPLTNV LEILSMWMLPASLPYMYGLFAKNKRQGWVIFTAMMTLFVLLLGLNYYAETKGNPAINALGIE SSQGSMEGKEVRFGIPQSSLFTSVTTAATTGSVNNMHDTLTPLGGITPLALMMLNNVFGGK GVGLINMLMYAIMGVFLCGLMVGRTPEFLGRKIEAKEMKLIAIAILVHPFIILVPTAGAFLTDLG NGSITNPGFHGLSQVLYEYVSSAANNGSGFEGLADNTTFWNVTTGIVMLLGRYVSIIVMLAV AGSLIQKKPVPETIGTFRTDNGLFTGILIGTVVIIGALTFLPVIVLGPIAEYLTLR
1E-237	798.7	29.1	2E-237	798.5	20.2	1	1	KDPA_POLSQ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Pnuc_1670	Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1)	596	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Polynucleobacter, Polynucleobacter necessarius, Polynucleobacter necessarius subsp. asymbioticus, Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1)	312153	>sp|A4SZG9|KDPA_POLSQ Potassium-transporting ATPase potassium-binding subunit OS=Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1) GN=kdpA PE=3 SV=1 MSTHAILTIVLYVGVLLLLAYPLGGFIDAVMSGQSITSKKPFRFIENFIYKVCGIDPAIEMSWLS YAIGLIAFNILGVLFVFGLQLFQGILPLNPQGLVSVSPDSSFNTAISFATNTNWQAYVGEGTM SYLTQMLGLTTQNFLSAASGIVVVIALIRGFARNSIKTIGNLWVDLTRITLYVLVPISVVYAIFLV GQGSIQNFDAYKDVKTVEVAKFDAPKLDADGQPLKDEKGAVLTGPASTDQQTLPMGPVAS QEAIKMLGTNGGGFFNANSAHPYENPTPLSNFIQILSIFLIPAALCFTFGRMVRDKRQGWVV LVTMILIFLTVTFAAVHFESQANPVLTNLGVDGAMGNMEGKETRFGIDDSSIFASITTLASCG AVNSMHDSFMPMGGFVPLWNMMLGEVVFGGVGTGLYGMLVFAILAVFIAGLMIGRTPEYL GKKIESYEMKMVAIAILVTPILALVGTAIAVMSVDGVAGIANPGAHGFSEILYAFTSAANNNGS AFAGLSANTPFYNSMLAIAMWFGRFGVIVPVLALAGAFAAKKKIAVNEGTMPTHGPLFIVLLA GTVILVGALNYVPALALGPIVEQLMLPVIH
1E-237	798.7	30.4	2E-237	798.5	21.1	1	1	Q0K2T4_CUPNH	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA H16_B0898	Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	606	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus necator (Alcaligenes eutrophus) (Ralstonia eutropha), Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	381666	>tr|Q0K2T4|Q0K2T4_CUPNH Potassium-transporting ATPase potassium-binding subunit OS=Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) GN=kdpA PE=3 SV=1 MSSQFVGLLVLYLAILLACAPFLGRYIRRAVEDGNYSLTAWGRPLERLLYRLGGVRADAGM GWTQYAVAVLAFNLLGVVAVYALQRLQGMLPLNPQGFGAVSPDSAFNTAISFVANTNWQG YGGESTMGYLTQMLALTVQNFLSAATGIAVVFALMRGFARQSAATIGNFWVDMTRVTLYVL APIATVIALALVSQGVTQNFDAYKEASLVTPVEYSQPKLDAAGQPVLDAQGKPVTEDLKTDR QTLAMGPVASQEAIKMLGTNGGGFFNANSAHPFENPNGLANLLEMLAIFLIPAALCFTFGEM VGDRRQGVAVLASMTVIFVAMACVAAMSEQMATPALAGLPVDHAASLLQAGGNMEGKETR FGIAASALFATITTAASCGAVNAMHDSFTAIGGLVPMLLMQLGEVVFGGVGSGLYGMLVYA VLAVFIAGLMIGRTPEYLGKKIEVYEMKMTAVAILVTPLLVLLGTSVAVMTEAGRAGVFNPGT HGFSEILYALSSAANNNGSAFAGLSANTPFYNTLLAAAMWFGRFWIIIPVLALAGSLAAKKRV PVSGGTMPTHGPLFVVLLVGTVLLVGALTYVPALALGPVAEQLQGAVTATAAK
2E-237	798.6	33	2E-237	798.4	22.9	1	1	KDPA_GEOSL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GSU2480	Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	592	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter sulfurreducens, Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	243231	>sp|Q74AB0|KDPA_GEOSL Potassium-transporting ATPase potassium-binding subunit OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) GN=kdpA PE=3 SV=1 MNVYESLQTVLLFVVLLAMVKPLGTFMARVFQGERTILSPVLAPAESLLYGVCGVNSEEEM DWKRYARAMVLFNLVIFATLFAMLMLQHLLPLNPQKFPAFSWQLALNTAVSFTTNTNWQAY AGEQAASYFTQMVGLTVHNFVSAATGIAVAIAVIRGFARRTTSALGNFWVDLTRATLYILVPI SLIAALVLVSQGVIQNFSAYQAVSLVQPVTYDTPKRDGTGSPVKDPTGNPVTERVTAKEVTI PMGPVASQEAIKELGTNGGGFFNANSAHPFENPTPLSNMLEILILILPFSLTYTFGAMVGNT RQGWTLLGVMLLILLASFAVLQGVESGGNPLVTKLGVHGANMEGKDTRFGLAGSSLFTVAT TGTSCGAVNTMHDSLTPIGGMIPMSLMLLGELVPGGVGSGLYTMLAFAVIAVFVSGLMIGRT PEYLGKKIEVREMWMSVVTVLAAGVMVLILSGIAMISPSAVAAMANPGAHGLSEVLYAFASM ANNNGSAFAGLSANTTFYNILGALAMIVGRFAPAVAVLAMAGSLAAEKKYVPPSLGTLPTDKV PFALWLTLVILIVGALTFFPALSLGPIVEHLTMTM

2E-237	798.6	32.6	2E-237	798.3	22.6	1	1	R6N8V0_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN578_00324	Clostridium leptum CAG:27	591	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium leptum CAG:27	1263068	>tr|R6N8V0|R6N8V0_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium leptum CAG:27 GN=kdpA PE=3 SV=1 MVQLILTILIYLIMVIPVGIYVYHIAAGKHTFADPVFDHVDNVIYKVSGIKKDKGMNWKTYAIALL ATNGVMILLGYIILRIQSIPLFNPNGIGNMEESLSFNTIISFMTNTNLQHYSGESGLSYLSQMLV ITFMMFVSAASGYAACIAFIRGLAGKTKDNVGNFFVDLVRITTRVLIPFSIVGGLLLVWQGVP QNFSGNVVVDTIEGAKQIIAMGPVAALEIIKHLGTNGGGFLGANSSTPIENPTIISNLIELYSMM ILPGACVITFGKMVRDRKKAQQAENGELAEATTLRTRRSFTAWMYGREGRSIFAAMGIIFLI GLGVCFWSESQGNPALQEIGVSQSMGSMEGKEVRFGIAQSAMFTTTTTSFTTGTVNNMH DTLTPLGGMIPLLHMMLNVVFGGKGVGLMNMIMYAILAVFICGLMIGRTPEYLGKKIEGREM KLTALCIIIHPFLILSFSALAIALVNVLPDSNGITNPGFHGLSQVLYEYSSSAANNGSGFEGLAD NTMFWNITAGLAMFFGRYLSIVIQLAIAGSLMKKRFVSESVGTLHTDTASFAVILVFVVYIFAA LTFFPVLALGPIAEHLTLWA
2E-237	798.1	33.2	3E-237	797.8	23	1	1	A0A0A1B553_9ENTR	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PSNIH2_18250	Pantoea sp. PSNIH2	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH2	1484157	>tr|A0A0A1B553|A0A0A1B553_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Pantoea sp. PSNIH2 GN=kdpA PE=3 SV=1 MIASAFLLLASYLLVLMLLAQPLGRAMAGIVRDRPLLPTLEGALWRLCGAEKQSMGWQHYL LAILLFNGAGLALLLAILLTQQALPLNPLHLPNLSWHLALNTAVSFVTNTNWQSYGGESTLSP LSQMVGLTVQNFLSAATGIAVAFALMRGFANKSLATLGNAWRDLTRVTLYVLLPIGLIIALLLV SQGVVQTLSASVDVQTLEGAKQTLSLGPVASQEAIKMLGTNGGGFFNANSAHPFENPTALS NFIEMLAIFLIPAALCFTFGDVVGDHRQGHAQLWAMTLMFVVAVAAVMWAELRGNPHFLTL GADSAINMEGKETRFGILNSSLFAVITTAASCGAVNAMHDSFTALGGMVPMWLMQLGEVVF GGVGAGLYGMLLFVVLAVFIAGLMIGRTPEYLGKKIDVREMKLTALAILVTPTLVLLGTALAM MSEAGRAGMANPGVHGFSEVLYAVSSAANNGSAFAGLSANTPFWNLLLAFCMLVGRFGI IIPVMAIAGSLAAKKAQPVSSGTLPTHGALFVCLLIGTVLLVGALTFIPALALGPVAEHLQLISR
3E-237	797.8	26.1	3E-237	797.5	18.1	1	1	A0A024HFC5_PSEKB	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpa1 kdpA PKB_1847	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas knackmussii, Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	1301098	>tr|A0A024HFC5|A0A024HFC5_PSEKB Potassium-transporting ATPase A chain OS=Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13) GN=kdpa1 PE=3 SV=1 MNSHDVLLLVAFFVLVLAPAPLLGRFYYKVMEGQRTFLSPVLLPVERMIYRVCGVDPQAEQ NWKTYTLALLAFNLVGLAVLFAILVGQGALPLNPQHMPGLEWTLAFNTAVSFVTNTNWQAY SGEASLSYLSQMLGLTVQNFVSPAVGVAVLVVLARGIARKSTQNLGNFWVDLTRATLYGLL PLCLLMALFLVWQGVPQTFLDYVHASTLQGADQVIPLGPAASQIAIKQLGTNGGGFFGVNS AHPFENPSAWANLFEVASIILIPAALVFTFGHYVKDLRQSRAILGCMLLMLVIGLGVALWAEY QPNPTLAHLPITQGAPLEGKESRFGTTASVLWAVTTTAASNGSVNAMHDSLNPLSGLVAMF NMMLGEVIFGGVGSGLYGMLLFVLVAVFLAGLMIGRTPEYLGKKLEAREVRLLVATLLVMPV GVLVLGAIAASLPGPASAVTNPGAHGFSQLLYAYTSGTANNGSAFAGFGANTPFHNLMIALA MLIGRFGYIVPVLAIAGSLAAKKRVPVGPNSFPTHGLLFIGLLTATILLVGGLNFLPTLVLGPVA DHLALGF
3E-237	797.7	30.5	3E-237	797.5	21.1	1	1	Q1J2K5_DEIGD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Dgeo_2850	Deinococcus geothermalis (strain DSM 11300)	568	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus geothermalis, Deinococcus geothermalis (strain DSM 11300)	319795	>tr|Q1J2K5|Q1J2K5_DEIGD Potassium-transporting ATPase potassium-binding subunit OS=Deinococcus geothermalis (strain DSM 11300) GN=kdpA PE=3 SV=1 MSSALLQFTLLLAVMAALVIPVGNWLYGVLTSERHTAPERLTYRLLGVDPTERMTWKRYGL VLVVSNLVLLLFAYLLLRLQGLLPWNPAGLRAQAPDLAWNTVVSFMTNTNWQAYSGEQSL SYFSQMAVITTFMFTSAATGFAAAAAFMRGLAGRDGTNLGNFWVDLTRIIYRVFLPLSFVLA LVFVWQGMPQTLSPSVNATTLEGATQRIALGPVATLESIKHLGTNGGGFFGMNAAHPFENP TPLTNALHILSMLLLPSALTYTFGRMLGNLRQGWVIFGSMLVMFVGFLATVYSFEQAGNPIL SRLGADQTLSAMQAGGNMEGKEVRFGIAQTALFATTTTAATTGSVDSMHDSYTGLGGLVP MTQMMLNNVFGGKGVGFINFVQYLVLGVFIAGLMVGRTPEFLGKKIEAREIKLTMLALLAHP LSILGFTALAVTLPSALSSLNNPGPHGFSEILYAYTSGTANNGSAFAGLGANTPFYNLTIGLA MLIGRYLTLLPMLAVAGLLAAKRRVPVSSGTLPTDTALFGGLTVFVILIVGALTFLPALTLGPV ADHLQMLKGVVLK
3E-237	797.6	34.9	4E-237	797.4	24.2	1	1	D8ML43_ERWBE	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA EbC_43400	Erwinia billingiae (strain Eb661)	561	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Erwinia, Erwinia billingiae, Erwinia billingiae (strain Eb661)	634500	>tr|D8ML43|D8ML43_ERWBE Potassium-transporting ATPase potassium-binding subunit OS=Erwinia billingiae (strain Eb661) GN=kdpA PE=3 SV=1 MAASAFLLIASYLLLLMILARPLGSGLARLIDDRPLAGVAGFERLLWRASGVAAESMSWRSY LLAILLFNLGGLILLTVMLMTQASLPLNPQHLPNLSWHLALNTAVSFVTNTNWQAYAGESTLS YFSQMVGLTVQNFLSAATGIAVAFALIRGFANRSLGTLGNAWRDMTRITLYVLLPLSLLIALFF VSQGTLQNVNGYLDLTTLEGVKQTLPMGPVASQEAIKMLGTNGGGFFNANSAHPFENPTA LSNVVQMLAIFLIPAALCFAFGDVVKDRRQGHALLWAMSLMFIGAVVVVMWAELKGNPHFL SLGADSAINMEGKETRFGILNSSLFAVITTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGAGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVWEMKMTALAILITPTLVLLGTALA MMTDAGRSGMANPGIHGFSEVLYAVSSAANNGSAFAGLSANTPFWNLLLAFCMLVGRFG IIIPVMAIAGSLAMKKVQPVGNGTLPTHGVLFIALLIGTVLLVGALTFIPALALGPVAEHLIMFAH

3E-237	797.6	27.8	4E-237	797.4	19.3	1	1	R5SY62_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN544_02006	Clostridium hathewayi CAG:224	583	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	1263067	>tr|R5SY62|R5SY62_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium hathewayi CAG:224 GN=kdpA PE=3 SV=1 MTNTAIQMILYCAVLIVLAIPLGRYIGKVMNGEKTVLTRLLSPVENGIYKVLKINREEEMDWKK YAVCAGVFSVISLAVLWLILMLQNILPLNPEGQAGTSWHLGFNTAASFVTNTNWQAYSGES ALSYFSQMIGLGVQNFVTPAVGMAVLFALIRGFIRVKKKGIGNFYTDVTKSTVYVLIPLSLIVS VFIVSRGVPQTFRGHEEVQLLEPVTVENEDGTATVVDKQIVPLGPAASQISIKQLGTNGGGF YGVNSAHPLENPDPWSNLFEMISLLLIPAALCFTFGRNIKDKKQGVAVFLAMFIMLALALAVV GYTEQVSTPQIAQGGAVDISTAGQAGGNMEGKETRFGIATSGTWAAFTTAASNGSVNSMH DSYTPLGGMIPMLLMMLGEVVYGGVGCGLYGMLAFAILTVFIAGLMVGRTPEYLGKKIEPYE MKMAVLICLATPIGILVGSGITAVLPATADSLNNPGAHGLSEVLYTYASAGGNNGSAFAGFN ANTPFLNTSIGLVMLFVRFLPMFGALAIAGSMAQKKKVAVSAGTLPTHNAMFIFLLIVVVLLIG ALSFFPALALGPIAEFFEMIG
3E-237	797.5	28.3	4E-237	797.3	19.6	1	1	A0A0A8UNF8_LEGHA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LHA_1366	Legionella hackeliae	605	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella hackeliae	449	>tr|A0A0A8UNF8|A0A0A8UNF8_LEGHA Potassium-transporting ATPase potassium-binding subunit OS=Legionella hackeliae GN=kdpA PE=3 SV=1 MLEISILQVALYLVILLLLVKPLGWYMARVYEDKPCGLNRLGGFLERGIYRLCGINCAEQMN WKQYLFTMLFFNLLGLLVAYLIQRLQFYFPLNEQKFPGLSPELAFNTAASFATNTNWQAYS GEGTMSYFTQMLALTVQNFISAATGMSLLMALIRGIAKHEETGLGNFWVDTVRGVLYILLPL SFVFAVILTSQGVIQNFKPYEKVNLIQAVNYSKPVTDNLGKTILDEQGKPRNEIVQLTEQMIP MGPVASQIAIKQLGTNGGGFFNTNSAHPFENPTPLTNFLEMLAILLIPAALCYTFGLMVNDKR QGWAILIAMTLIFIPCASIAIIAEQQGNPAFASLGIDSTAGDNLYPAGNMEGKEIRNGIVSSAL WATATTAASNGSVNAMHDSFTPLGGLITVWMMQLGEIIFGGVGSGLYGMLMIVIITVFVAGL MVGRTPEYLGKKIEPYEMKMASFVVLLMPILVLITTAIGVVTPMGVKSIANPDAHGFTEILYAF TSMANNNGSAFAGLNANTPFYTIVGGISMLIGRFWVAIPVIAIAGSLARKKRISVTSGTLATHT PLFILLLIGVTLIVGALSFLPALSLGPIVEHLMLWSNHGH
3E-237	797.5	19.5	4E-237	797.3	13.5	1	1	KDPA_DESMR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DMR_09290	Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	582	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio magneticus, Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	573370	>tr|U4YWI6|KDPA_DESMR Potassium-transporting ATPase potassium-binding subunit OS=Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1) GN=kdpA PE=3 SV=1 MNPINLVQLLFFLSVLLVLSWPLGLYAARVYQGQPCVMDKILGPLERLLYRISGVDASREMD WKIYALVMLGLNAFGMVFVYVLERLQGGLPLNPLHLPGVDPFVAVNTAVSFATNTNWQAYA GESTMSILTQMLGLAVQNFLSAATGMAVAVALIRGLARRETTHLGNFWQDLTRSVLYILLPL SFVLALLLVWQGVPQTFTGQVEADWLDPAPHVAESISPDTPSTDQPPAKQTIVLGPVASQV AIKQLGTNGGGYFNVNSAHPLENPTPLTNLLEMLAILLIPAALCHTFGVMIGDRRQGLAILAA MTILFAGFAALTLAAESVPNPTLSGIGVPAVPSLEGKEVRFGTAGSALWAAATTAASNGSVN AMHDSFSPLGGMWPMLLMQLGEVVYGGVGSGLYGMLVFAVVTVFVAGLMVGRTPEYCG KKIEPFETKMAALVILIPPFLCLAGTALAAVIGPADAVSNPGPHGFSQMLYAFSSMGNNNGS AFAGLTATSPFWTIAGAVAMFVSRYWLIVPVLALAGSLAGKKRLAQGPGTLPTHGGIFVALLI IVVLVVGALTFVPALALGPIAEQLALFQ
3E-237	797.4	31.4	4E-237	797.2	21.8	1	1	E0SEX9_DICD3	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Dda3937_01549	Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	561	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Dickeya, Dickeya dadantii, Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	198628	>tr|E0SEX9|E0SEX9_DICD3 Potassium-transporting ATPase potassium-binding subunit OS=Dickeya dadantii (strain 3937) GN=kdpA PE=3 SV=1 MPSDAFLLIVSLFAILLVLAQPLGQFMARLVEGETGALRRYELGVARLCGFSTREMGWQHY AGAILVFNLLGIVLLFLMLAYQDRLPLNPQQMPGLSWHLALNTAISFVTNTNWQAYSGENTL SYFSQMVGLTVQNFLSAATGIAVAFVLMRAFARRTTHELGNAWLDLLRINLYLLLPMSLLLSL FFISQGSIQNFLPYQHLTTLEGASQVLPMGPLASQEAIKMLGTNGGGFFGANSAHPFENPN ALTNFVQMLSILLIPAALCFTFGRVVNDRHQGHTLLWAMSLMLIAATAVVMYAEVNGNPHLL SLGADSAQNMEGKESRFGMLSSAFFAAITTATSCGAVNAMHDSFTALGGLIPMWLMQIGEV IFGGVGSGFYGMLVFVLLTVFIAGLMIGRTPEYLGKKIEAWEMKMAALAILITPALVLLGTALA LGTEAGRAGILNPGAHGFSEVLYAYSSAANNNGSAFAGLSVNTPFYNLTLGIAMLLGRFSSLI PVLAIAGSLVAKKRQPETKGSLSTRGPLFIGLLIAIILLISALNFIPALALGPVAEHLQSSLVH
4E-237	797.1	34.7	5E-237	796.9	24.1	1	1	A0A0A0YZS0_9ENTR	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PSNIH1_04930	Pantoea sp. PSNIH1	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH1	1484158	>tr|A0A0A0YZS0|A0A0A0YZS0_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Pantoea sp. PSNIH1 GN=kdpA PE=3 SV=1 MAANAFLLIALFLLVLMALAQPLGRFLARLVADKPLLPRTEHLLWQLTGSGTAAMRWQHYLL ALLLFNAVGFVVLLAILMLQGALPLNPQQMPGLSWDLAFNTAVSFVTNTNWQAYGGESSLS YFSQMAGLTVQNFLSAATGIAVAFALMRGFANRSLATLGNAWRDLTRITLYVLLPLSLVIALF YVSQGTIQSFAAYHTLTTLEGAQQTLPLGPVASQEAIKMLGTNGGGFFNANSAHPFENPTA LTNFVQMLSIFLIPASLCFTFGQHLNDRRQGHMLLWSMSILFVLAASAVMWAEVRGNPHFL ALGADSALNMEGKETRFGILNSGLFAVITTAASCGAVNAMHDSFTALGGMVPMWLMQLGE VVFGGVGAGLYGMLLFVLLAVFIAGLMIGRTPEYRGKTIDVWEMKMTALAILVTPALVLLGTA LALMTDAGRAAMANPGIHGFSEILYAVSSAANNGSAFAGLSANTPFWNLLLGVCMLAGRF GIIIPVMAIAGSLAAKNVQPAGNGTLPTHGPLFIGLLTGTVLLVGALTFIPALALGPVAEHLQLI QE

5E-237	797	32	5E-237	796.8	22.2	1	1	A0A060QHW7_9PROT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ASAP_2238	Asaia platycodi SF2.1	568	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Asaia, Asaia platycodi, Asaia platycodi SF2.1	1382230	>tr|A0A060QHW7|A0A060QHW7_9PROT Potassium-transporting ATPase potassium-binding subunit OS=Asaia platycodi SF2.1 GN=kdpA PE=3 SV=1 MTLSGWITLAVFFLCVVAITRPLGGFLKRVLEGEKHLFQRPFGGLERLMYRLAGVDPKREQ SWSHYALAVILFKIFCFIAVYALLRLQGFLPFNPAGLGAVSPDLAYNTAVSFLTNTNWQSYG GETTLSPLSQMLALTVQNFVSAAAGIAVAAAIMRGFVRRSASTIGNFWVDLVRVTLYVLLPA CMLLTLFFVLEGVPQTLTGSASIFTLEGARQTIALGPVATQEAIKMLGTNGGGYFNVNSAHP FENPNALTNFVQMLCIFALGAGLTNMFGRMIGQEKQGWAIFSAMSALFLIGAGVLYWSEAH ANPLFASLGLDGTLGNMEGKETRFGIAASALFATVTTDASCGAVNAMHESFLPLGGMVPLIN MMLGEVIFGGVGSGLYGFLLFALIAVFMAGLMVGRTPEYLGKKIEAREIKMTMLAVLCLPLV MLGFTALAIVLPAGLSALSASGPHGFSEALYAYTSAAANNGSAFAGLTANSFWNVTLGIGM MIGRFFVIIPALAIAGSMAAKKVAAPTPGTFPTDNGLFIALVAGVIVIVGGLTFLPALALGPIVE HLAMLHGTTY
6E-237	796.6	27.4	8E-237	796.2	19	1.2	1	F8GKK3_NITSI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Nit79A3_1970	Nitrosomonas sp. (strain Is79A3)	595	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas sp. (strain Is79A3)	261292	>tr|F8GKK3|F8GKK3_NITSI Potassium-transporting ATPase potassium-binding subunit OS=Nitrosomonas sp. (strain Is79A3) GN=kdpA PE=3 SV=1 MNTSPWIQIGLFLTVLFVVAWPLGRYLASISDGQLTRRFIWLDKFEHGFCRFIGTNPAEDMP WQRYATAIVLFNVIGVVVVYGLQRFQSELPLNPQSLGDVSSDSAFNTAISFVTNTNWQGYG GESTMSYLTQMLALTVQNFASSATGIAVVIALIRGFTRKNAAGIGNAWLDLSRSIFYVLLPLSL VFALILVNQGVIQNFNAYQDVKLIEPLEYAAPKQDLNGQPLQDDHGNVIMETIKTDKQSIAMG PVASQEAIKLLGTNGGGFFNANSAHPFENPTPLTNFLEMISIFLIPTALCFAFGQMVGDQRQ GWTILAAMTVLFITMATVALWSESHSNPLITQLGVDGSMGNLEGKEIRFGIISSALFATVTTA ASCGAVNAMHDSFLPLGGLVPMGLMMLGEVVFGGVGAGLYGMLIFAMLAVFLSGLMIGRT PEYLGKKIGVFEMKMVSIAILVVPMLVLGGTAIAVVTEVGKASMANPGAHGLSEVLYAFTSA GNNNGSAFAGLSSNTPFYNILLAIAMWFGRFGVIIPVLAIAGKLAAQPKLAVTGGTLPTHGPL FVILLISTVLIFGALNYVPALALGPIIEHLQLFSH
6E-237	796.6	30.9	7E-237	796.4	21.4	1	1	KDPA_SALTY	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA STM0706	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella typhimurium, Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	99287	>sp|Q8ZQW2|KDPA_SALTY Potassium-transporting ATPase potassium-binding subunit OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=kdpA PE=3 SV=1 MAAQGFLLIASFLLILLVLAKPLGSGLARLIAAVPLPGVAGIERILWRTLGITDHEMNWRQYLL ALLTLNLLGLGILFCLLFWQEWLPLNPQRLPGLSGDLALNTAVSFVTNTNWQAYSGESTLSY FSQMAGLTVQNFLSAATGIAVVFALIRAFTRQNVHTLGNAWQDLVRITLWILFPVALIIALFFI QQGVPQNLSAYQPITTLEGAKQLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPTALT NLAQMLAIFLIPAALCFAFGEAAGDRCQGRALLWAMSFIFVVCVAVVMWAEVQGNPHLLAA GADSSVNMEGKETRFGVLASSLFAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPMLVLLGSAL AMMTDAGRSAMLNPGPHGFSEVLYAVSSAANNNGSAFAGLSANSPFWNCLLAFCMFVGR FGVIIPVMAIAGSLVSKKVQPASQGTLATHGALFIGLLIGTVLLVGALTFIPALALGPVAEHFSL P
7E-237	796.5	36.2	8E-237	796.3	25.1	1	1	B6JA58_OLICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OCA5_c03390	Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	565	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Oligotropha, Oligotropha carboxidovorans (Pseudomonas carboxydovorans), Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	504832	>tr|B6JA58|B6JA58_OLICO Potassium-transporting ATPase potassium-binding subunit OS=Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5) GN=kdpA PE=3 SV=1 MTINGWIQILVFLGIVIALVKPLGGYITRVMNGERTFLSPVLGPVERGLYGMAGTSEKEEQH WTTYLGAMLLFNLAGFALLYLLQRVQGGLPFNPAGMGAVSADSSFNTAVSFMTNTNWQG YGGETTMSYLTQMAGITVQNFVSAAVGVAGAMAIIRGFSRASAKTVGNFWVDLTRATLYIL MPICIVGSLVLVWQGVPQNLNPYTVATTVEGAQQTIAQGPVASQMIIKHLGTNGGGFFNAN SSHPFENPTALTNLIHILAIYSISFAMLNVFGRMTGNQKQGWALLAAVLTIVIAGIGVIYWAES AGNPLLHALGLEGGNMEGKETRFGIALSSLFAVVTTSASTGAVNTMHDSLMPLGGLVPLFN MQIPPLGGIGAGVYGTLIFAILAVFIAGLMVGRTPEYIGKKIEAKEVKMSILAMLGPSLAILALT AIAVVLPVGLSSIQDAGPHGLSEVLYAYTSGANNNGSAFAGLNANTPFFNITVGLAMLMGRF LLIVPLVLAIAGSLAAKKSVPASTGTLPTTGPLFIGLVVGVTLIVGGLTFFPVLALGPIVEHFAML AGQVF
7E-237	796.4	35.2	8E-237	796.2	24.4	1	1	KDPA_CLOAB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CA_C3682	Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	557	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium acetobutylicum, Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	272562	>sp|O32327|KDPA_CLOAB Potassium-transporting ATPase potassium-binding subunit OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) GN=kdpA PE=2 SV=2 MEILQIAIILIVFVLLCIPIGRYMYKVSEHKKTLLDPVLDKIDGFIYKLSGIQKEEEMNWKQYIFAL LMCNAVPAIIGYIILRIQAVGIFNPNHVKGMEQGLTFNTIISFLTNTNLQDYAGETGASYLSQMI VITFFMFFAAATGIAVALAFIRALSGKKKLGNFYVDLVRITTRILLPLSIIVAIFYIGQGVPQTLSA NKTVTTIEGKLQNIPLGPVASLEAIKLIGTNGGGFFSANSSHPFENPTPLTNSVQIITLLLLAGS MVVCFGHMIKKKKQAVAIFAAMMVLLLAGAAICFSAEKAGNPALSRIGLSQSMGNLEGKEER FGIAGSSLFTTVTTDTSCGAVNNMHDSLTPIGGAVPLINMMLNVIFGGVGVGFMNMIMYAILT VFLCGLMVGRTPEFLNKKIEGKEIKLVAFAIIVHPFLILMSSALALTTKQGLAGISNPGFHGLTQ VLYQFTSSAANNGSGFEGLIDNTMFWNVSAGVVMFLGRYLSIIILLAVASSFAAKRAVPATQ GTFKTDNTIFTVTLIVIIVIIGALTFLPAVALGPISEYLTL

7E-237	796.3	27.4	9E-237	796.1	19	1	1	M4S2C6_9SPHN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA G432_12245	Sphingomonas sp. MM-1	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. MM-1	745310	>tr|M4S2C6|M4S2C6_9SPHN Potassium-transporting ATPase potassium-binding subunit OS=Sphingomonas sp. MM-1 GN=kdpA PE=3 SV=1 MTLQGWILILGFVAILLALAKPVGAWLFALYEGRRTPLHLVLGPFERGFYRLSGIDPTQEQG WRRYAVHMLLFNAALMFFSYAVLRLQAFLPLNPQGLGPVSEHLSFNTAISFTSNTNWQSYG GEATMSNLSQMLGLTIHNFLSAATGIALAFALFRGFARREAKTVGNFWADVTRITLYLLLPLC VALTIFYIASGVPQTLGGVVDVTTLEGARQSILLGPVASQEAIKMLGTNGGGFFNANSAHPF ENPTALTNLVQMLSIFVVGVGLTWCFGKAVGNTRQGWAILSAMMILFLAGTTITYWQEAAG NPVLHSLGVEGGNMEGKEARFGIAASALFAVITTAASCGAVNAMHDSFTALGGMIPLFNMQ LGEVVIGGVGAGIYGFLLFAILAVFVAGLMVGRTPEYVGKKIEAREVKLAVLAIAVLPLIILGFT ALSSVADQGLAGPLNKGPHGFSEILYAFTSGVANNGSAFAGLTANTPWYNGLLGVAMWLG RFFIIVPMLAIAGSLAAKKYTPESAGSFPTTGGLWVGLLVGIILILGGLTFLPSLALGPIADHLA MIRGQLF
8E-237	796.3	34	9E-237	796.1	23.5	1	1	KDPA_GEOKA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GK3248	Geobacillus kaustophilus (strain HTA426)	560	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Geobacillus, Geobacillus kaustophilus, Geobacillus kaustophilus (strain HTA426)	235909	>sp|Q5KUV3|KDPA_GEOKA Potassium-transporting ATPase potassium-binding subunit OS=Geobacillus kaustophilus (strain HTA426) GN=kdpA PE=3 SV=1 MWHVFSQYTLIFLLLIVIAVPLGKYLYVAFFEKGKIDRFFSPIEAVIYRLSGIRSLEEMTWKSYC TALLIVNAALLGISYGLLRIQHYLPLNGAKVENMEPTLTFNTVVSFMTNTNLQHYSGESGLSIL SQMLFVTMMMFTSAATGLTVATALIRALSKKGKTIGNFYQDFVRANVRVLLPLSVIVTILLVAF GVPQTFLARMAVSTLEGGTQTLALGPVASLESIKHLGTNGGGFFGANSSHPFENPHPFTNV IEMLSMWCIPAALPFTYGHAVKNRKQGWVLFATMFVLFVMMLGVVYNAEQSGNPLVGKSG FAADQGNMEGKEVRFGIPLSSLFTAITTAATTGSVNNMHDSLTPIGGLVPLALMMLNNVFGG DGVGFVNIMMYAMIAVFLSGLMVGRTPEFLGRKIEPKEMKLIVIALLLHPLIILAPSAIALMTHM GTEAISNPGFHGISQVVYEYTSSAANNGSGFEGLKDNTAFWNISTGVVMLLGRYVSIAMLA VAGSLVGKQPVPETIGTFRTDTATFGVILFGTVFIIGALTFFPVLILGPVAEYLTIR
1E-236	795.9	22.2	1E-236	795.7	15.4	1	1	C9R8E6_AMMDK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Adeg_1479	Ammonifex degensii (strain DSM 10501 / KC4)	568	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Moorella group, Ammonifex, Ammonifex degensii, Ammonifex degensii (strain DSM 10501 / KC4)	429009	>tr|C9R8E6|C9R8E6_AMMDK Potassium-transporting ATPase potassium-binding subunit OS=Ammonifex degensii (strain DSM 10501 / KC4) GN=kdpA PE=3 SV=1 MTWRIILEVSFFAAVLTALAVPLGFYMARVFEGERTLLSPLLRPIEGVVYRLAGVNPYAEMS WTRYLGSLLLFNFWGLLAGYLLLRWQNHLSFNPLHLPGVPGVLAFNTIVSFVTNTNWQAYS GETTMSYFSQMFVLAVQNFLSAATGLAGAVALTRAFARKEKKTLGNVWVDLTRSVLYILLPI SLVVALVLVSQGVVQTLHPPVKAVTLEGREQTIPLGPVASREAIKLLGTNGGGFFNANSAHP FENPNPFTNFLEAMLITILPAALCFTFGRMVRNLRQGWVIYGVMMFLFLVGAFTCCWFEAQ GNPLFSRLGFSAGPNLEGKEWRFGAIDSALFATVTTAVSCGAVDSLHDSFTPLGGLVLLANI LTGEVIFGGIGSGLYGMIAYALLTVFLAGLMVGRSPEFLGKKIEKREVKLSLAVVLVPAFLVLF FSALAVILPAGREGITAAGPHGLSQVLYAFASTANNNGSAFGGLKADLPFYLWTTALAMLLG RFLPLAAVLALAGSLVEKKTIPPSPGTFPTTSWLFAVLLVGVIIIVGALTFLPGLALGPILEQLLL ARGRLF
1E-236	795.5	34	2E-236	795.3	23.6	1	1	A0A0F2RT00_9PROT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VR70_06040	Rhodospirillaceae bacterium BRH_c57	563	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), unclassified Rhodospirillaceae, Rhodospirillaceae bacterium BRH_c57	1629718	>tr|A0A0F2RT00|A0A0F2RT00_9PROT Potassium-transporting ATPase potassium-binding subunit OS=Rhodospirillaceae bacterium BRH_c57 GN=kdpA PE=3 SV=1 MDAAGILQILIYIAVITALTPLLGGYMAKVYEGQARFLGPAERGLYKVCGVDPAREQHWTGY ALSLLAFNLAGWALLFGIQRLQGMLPLNPAEMAAVPPDLAFNAAVSFMTNTNWQSYGGES TLSYLTQMIGLTVQNFVSAATGMAVVVALIRGFARTNAHTVGNFYVDLVRSTVYILLPLSFVA ALFLVWQGVPQNFDSYSAAATLEGANQVIAQGPVASQVAIKQLGSNGGGFFNVNSSHPFE NPTPLSNIIEMTFLLMLAAALTNTFGRMVKDQRQGWAIFAAMGLMLIVGLGVTYWSETNAN PAMVVAGMDGTHGNMEGKEVRFGIANSTIWATATSAASNGSVNSMHDSFMPLGGLVPMV NMLLGEVIFGGVGAGLYGMLIMVIVAVFIAGLMVGRTPEYLGKKIEAKEVKLAMLAILIFPVGV LGLGAASLLGAPGAIQDAGPHGLSEVLYGFASATGNNGSAFAGWTANTLLNNTLLGIAMLL GRFVVIIPALAIAGAVAAKKAVPPSAGTFPTHGGLFVVLLMGVILVVGGLTFFPVLALGPIVEH LMLGAGTLF
1E-236	795.4	26.6	2E-236	795.2	18.4	1	1	U7DIH3_PSEFL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA B723_08530	Pseudomonas fluorescens NCIMB 11764	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens NCIMB 11764	1221522	>tr|U7DIH3|U7DIH3_PSEFL Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas fluorescens NCIMB 11764 GN=kdpA PE=3 SV=1 MHSYDYWLILAFFAVVLIPAPFLGRFYYKVMEGQRTWLTPILGPVERGCYRVAGVDPQAEQ SWQKYTLALLAFNLAGFLLLFAILLFQDHLPLNPQNLPGQEWTLAFNTAVSFMTNTNWQAY SGEASLSYLSQMAGLTVQNFVSAATGLAVLVALCRGIGRKSTKTLGNFWVDMTRATLYGLL PLCLLLALYLVWQGVPQTFAQYVNAVTMQGVDQVIPLGPAASQIAIKQLGTNGGGFFGVNS AHPFENPTAWSNLFEVSSIILIPVALVFTFGHYVKDLRQSRAIIACMLALFLIGGATSLWAEYQ PNPSLNNVAVEQTAPLEGKEARFGTTATVLWSVTTTAASNGSVNGMHDSLNPLSGMVAMV NMMVGEVIFGGVGAGLYGMLLNVLIAVFLAGLMIGRTPEYLGKKLQAKEVQLLVVTLLVMPV GVLVLSAIAASLPGPVASVTNPGPHGFSQLLYAYTSASANNGSAFGGFGANTPFHNLMLGL GMLIGRFGYILPVLALAGSLAMKKTAPIGQNSFPTHGPLFVTLLTVTILLVGGLTFLPTLALGPI AEHLSMGF

2E-236	795.4	26	2E-236	795.1	18.1	1	1	KDPA_PSEPK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PP_4161	Pseudomonas putida (strain KT2440)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas putida (Arthrobacter siderocapsulatus), Pseudomonas putida (strain KT2440)	160488	>sp|Q88…|KDPA_PSEPK Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas putida (strain KT2440) GN=kdpA PE=3 SV=1 MHSYDFALLLAFFVIVLLPAPWLGRFYYKVMEGQRTWLTPVLGPVEQGCYRLAGVNASQE QNWRQYTLALLAFNLVGFLLLFAVLLLQGYLPLNPQNLPGQEWSLAFNTAVSFVTNTNWQA YSGEASVSYLSQMLGLTVQNFVSPATGLAVLVVLCRGIARRSATTLGNFWVDMTRATLYGL LPLCLLLALLLVWQGVPQTFADYAHALTLQGADQTIPLGPAASQIAIKQLGTNGGGFFGVNS AHPFENPTAWSNLFEVASIILIPVALVFTFGHYVKDLRQSRAILACMLALFLIGGSTALWSEH QPNPALESTQVQQTAPLEGKESRFGTTGSVLWAVTTTAASNGSVNAMHDSLNPLTGMVA MVNMMVGEVIFGGVGAGLYGMLLFVLIAVFLAGLMIGRTPEYLGKKLQAREVQLLVATLLVM PVGVLVLGAIAASLPGPAGAVTNPGAHGFSQLLYAYTSGSANNGSAFAGFGANTVYHNLMI GLAMLIGRFGYILPILALAGSLAAKKSAPLGQNSFPTHGPLFTGLLLVTILLVGGLTFLPTLALG PIAEHLSLGF	
2E-236	795.2	34.6	2E-236	795	24	1	1	L0M8Q7_ENTBF	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA D782_3152	Enterobacteriaceae bacterium (strain FGI 57)	555	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, unclassified Enterobacteriaceae (miscellaneous), Enterobacteriaceae bacterium (strain FGI 57)	693444	>tr|L0M8Q7|L0M8Q7_ENTBF Potassium-transporting ATPase potassium-binding subunit OS=Enterobacteriaceae bacterium (strain FGI 57) GN=kdpA PE=3 SV=1 MAAQGFLLIASFFVVLFILARPLGKMLAGMIANEPLRGETVLWRTLGISTDEMSWQRYALAIL LLNLCGLVALFAMLMLQGVLPFNPQGFPGLSWHLALNTAVSFVTNTNWQSYAGETTLSYFS QMAGLTVQNFLSAASGIAVLFALARAFARQRVTTLGNAWVDLVRITLWVLLPLSLLVALFFIQ QGTLQNLLPYQHITTLEGVSQQLPMGPVASQEAIKMIGTNGGGFFNANSSHPFENPTALTN FVQMLAIFLIPAALCFAFGEVVNDKRQGRAILWAMSFIFVICVAVVMWAETKGNPHLLALGA DSNLNLEGKESRFGILASSLYAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEVVFG GVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIEVPEMKMTALAILVTPTLVLLGTALAMM TDAGRSGMLNPGTHGFSEVLYAVSSAANNGSAFAGLSANTPFWNCLLAFCMLLGRFAVI VPVLAIAGSLVNKKIQPATPGTLATHDALFIGLLIGTVLLVGALTFIPALAIGPVAEHLSLF	
2E-236	795.1	40.1	2E-236	794.8	27.8	1	1	Q1QJ46_NITHX	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Nham_2994	Nitrobacter hamburgensis (strain X14 / DSM 10229)	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Nitrobacter, Nitrobacter hamburgensis, Nitrobacter hamburgensis (strain X14 / DSM 10229)	323097	>tr|Q1QJ46|Q1QJ46_NITHX Potassium-transporting ATPase potassium-binding subunit OS=Nitrobacter hamburgensis (strain X14 / DSM 10229) GN=kdpA PE=3 SV=1 MTVLGWAQILLFCAIVAALAPLFGGYMTRVFNGERTFLSPILRPVEAMLYRVAGVDETREQY WLTYVVSMLLFHAAGFLVLYGLMRLQALLPLNPAGQSAVAPDLSLNTAVSFITNTNWQNYG GESTMSYLVQMLGLTHQNFLSAATGIVLAVALIRGFARTSVRTVGNFWIDITRCTLYVLLPICI PLTLFLVWQGIPQTLGAYVDATTLEGARQTIAVGPVASQVAIKMLGTNGGGFFNANAAHPF ENPTALSNYVQMIAIFVLGAAMTNVFGRMVGNQRQGWAILAAMGVLFIAGVAVCYWAEAN GTTLLDGLGLAGGNMEGKEVRFGIVGSALFAVVTTAASCGAVNAMHDSFTALGGMIPLINM QLGEIVVGGVGAGLYGMLLFVIVTMFIAGLMVGRTPEYVGKKIEAREVKMAMLAILVLPLMM LGWTAVAVIYPPAAASMGNAGPHGFSEALYAFTSQTANNGSPFAGLSGNTLFYNLAGAVA MFVGRFWMIVPAMAVAGSLAAKKTVAVSSGTFPTTGGLFVGLLVGVILIVGGLTFFPALALG PIVEHLAMQSGSLF	
2E-236	794.9	38.7	3E-236	794.3	26.8	1.2	1	KDPA_HERAR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HEAR1626	Herminiimonas arsenicoxydans	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herminiimonas, Herminiimonas arsenicoxydans	204773	>sp|A4G5J9|KDPA_HERAR Potassium-transporting ATPase potassium-binding subunit OS=Herminiimonas arsenicoxydans GN=kdpA PE=3 SV=1 MTSQSIMLLVAFLGVLLALAYPLGLFMAKVGDGTAIRGLGWLLKMENALYRLAGLDTQSAM SWKSYAIALLVFNTLGALFVYAVQRLQAWLPLNPQAFGNVSPDSSFNTAVSFVSNTNWQG YGGESTMSYLTQMLALTGQNFFSAATGIAVAFALIRGFSSRSAKSIGNFWVDLTRSTLYILLP LAIVVSVALMGQGVIQNFSAYQDVALVDPVTYQQAKTTADGQPVVDAEGKPVMETLTAKM QTIAMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTVFSNFIEMLAIFLIPAGLCFTFGRM VGDMRQGWAVLGAMTLIFVVMTSIVMTSEQSAHPAMQALGVDQTTTALQSGGNMEGKET RFGISASALFTAVTTAASCGAVNNMHDSLMPMGGFVPLVLMQFGEVVFGGVGTGLYGMLI FAILSVFIAGLMIGRTPEYLGKKIQSYEMKMASIAILVTPTLVLVGTAIAVLVESGKVGIANPGA HGFSEILYAFTSAANNGSAFAGLSANTPFYNTMLAIAMWFGRFAMIVPILAIAGSLACKQRL AANAGTMPTHGPLFVALLVGVVVLVGVLNYVPALALGPIVEHLQLFSH	
2E-236	794.7	32.9	3E-236	794.4	22.8	1	1	D3EAK4_GEOS4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GYMC10_0432	Geobacillus sp. (strain Y412MC10)	559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Geobacillus sp. (strain Y412MC10)	481743	>tr|D3EAK4|D3EAK4_GEOS4 Potassium-transporting ATPase potassium-binding subunit OS=Geobacillus sp. (strain Y412MC10) GN=kdpA PE=3 SV=1 MGILQIAIVILVLVLLVKPLGTYLYQVFRYESNGTDRWFSWAEKRIFALIGLKERKGMTWKGY AVSFVLTNIVLVAAGYLILRLQKVLPLNPSGIGHMEPTLSFNTIISFMTNTNLQHYSGESGLSY LAQMAVITMMMFTSAATGLCVAIAFIRAVTSKGTTVGNFFEDFVKAHTRVFIPAAFIIAMVLVA LQVPQTLKPTLSVTTLEGSEQQIAVGPVAALESIKHLGTNGGGFMGANSAHPFENPSPLTNV IEILSMWSLGAALPYTFGLFAKSRKQGWIIFSVMMTLFIGFLSLNYAAETNGNPALNQLGIDA SQGSMEGKEVRFGIAQSSLFTTVTTAATTGSVNNMHDTLTPLGGITPLSLMMLNSVFGGKG VGLMNMLMYAILAVFLAGLMVGRTPEFLGRKIEAREMKLIAIVILVHPLIILAPTALALMTDAGQ PGIAHSGFHGISQVLYEYTSSAANNGSGFEGLADNTPFWNISTGLVMLIGRYISMIALLAVGG SLMRKQWVPETLGTFRTDNKLFAGILIAVVLIIGALTFLPVLVLGPIAEHLTIR	

3E-236	794.5	33.9	3E-236	794.3	23.5	1	1	R5R447_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN747_02088	Firmicutes bacterium CAG:646	569	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	1262995	>tr|R5R447_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Firmicutes bacterium CAG:646 GN=kdpA PE=3 SV=1 MLQIVLTLAIFLVLVIPMGRYMYHIATNQKTFADVVFNPIDKGIYKVCGIKGEDMGWKKYALSL LMANGVMVLVGYLILRIQGILFLNPNGIEGMEPSLSFNTIISFMTNTNLQHYSGESGLAYVSQ MCVIIFMMFTSAASGYAACMAFCRGLSGRKLGNFYQDMVRITTRILVPAAFLVGLLLVSQGT PQTLDGNFTVETVEGKYQDIAMGPVAALESIKHLGTNGGGFFGANSTTPFENPTVISNIAEMI SMMILPGACVVTFGLMLHERKKEKKKEQKKVLMGRQGAVVFGAMGILFLVGLLICFNAEKA GNPVIGEMGINQDMGSMEGKEVRFGIAQSSLFTTVTTSFTTGTVNNMHDTLTPLGGMVPM LHMMLNCVFGGKGVGLMNMVMYVILAVFICGLMVGRTPEYLNKKIEGKEMKLVAIVILIHPLLI LGFSALAVTMQAGLDGITNPGFHGLSQVLYEYASSAANNGSGFEGLADNSVFWNVTTGLA MFFGRYLAIVAQLAIAGSLLRKKRVNESIGTLRTDNVVFMIILVFIVYIFAALTFFPALALGPIAE HLSLWL
3E-236	794.5	29.4	3E-236	794.3	20.4	1	1	A0A097EJP3_9SPHN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MC45_17030	Sphingomonas taxi	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas taxi	1549858	>tr|A0A097EJP3_9SPHN Potassium-transporting ATPase potassium-binding subunit OS=Sphingomonas taxi GN=kdpA PE=3 SV=1 MTLQGWILILGFVGILLALTKPVGMWLFALYEGRRTPLHALLGPVETGFYKLAGVDPTAEQG WRRYAVHMLIFNVALMVFTYAVLRLQGMLPGNPQGLAGLSPDLAFNTAVSFTTNTNWQSY GGESTMSNLSQMLGLTIHNFLSAATGIALAFALFRGFARREAKAIGNFWADCTRVTLYLLLPL CVVYTVFLIASGVPQALAGVVDVTTLEGAKQSLLLGPVASQEAIKMLGTNGGGFYNANSAH PFENPTALTNMVQMLSIFLIGFGLTWTFGKAVGNTRQGWAILSAMVILFLAGVTVTYWQEA AGNPVLHHLGVGGGNMEGKEVRFGIAASSLFAVVTTAASCGAVDAMHDSFTALGGLVPLF NMQLGEVVIGGVGAGIYGFLLFAILAVFVAGLMVGRTPEYVGKKIESREVKLAVLAIAVLPLMI LGLTALSSVLAQGLAGPLNKGPHGFSEILYAFTSAVGNNGSAFAGLTANTPYYNGLLGLAM WVGRFFIIVPMLAIAGSLAAKKHTPESAGSFPTTGGLWVGLLVGIVLILGGLTFLPGLALGPIA DHLAMIHGQLS
3E-236	794.4	35.7	3E-236	794.2	24.8	1	1	R5WRK0_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN568_01732	Blautia sp. CAG:257	577	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	1262756	>tr|R5WRK0|R5WRK0_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Blautia sp. CAG:257 GN=kdpA PE=3 SV=1 MLQIILTLAIFLILVIPMGKYMYHIATEQKTFADKVFNPIDHLIYKICGIKNEDMGWKKYALTLVT ANAVMVFVGYLILRIQNLLFLNPNGIEGMESSLSFNTIISFMTNTNLQHYSGESGLSYAAQMC VIIFMMFTSAASGYAACMAFCRGLSGRKLGNFYRDMVRITTRILIPVSFIVGLILVSQGTPQTL MQNFTVETIEGKYQDFAMGPVAALESIKHLGTNGGGFFGANSTTPFENPTVISNIVELLSMM ILPGACIVTFGHMLHDRKKNKVKAAAVAVAPAKKKILMGRQGAVVFGAMAVIFMIGLLLCYNS EMAGNPVIAEMGIDQSAGSMEGKEVRFGTAQSSLFTTVTTSFTTGTVNNMHDTLTPLGGLV PMLHMMLNCVFGGKGVGLMNMVMYVILAVFICGLMVGRTPEYLNKKIEGKEMKLVAIVILIH PLLILGFSALAVAVPGGLDGITNPSFHGLSQVLYEYTSSAANNGSGFEGLADNSVFWNVTT GLAMFFGRYIAIVAQLAIAGSLLAKRRVNESIGTLRTDNVVFMIVLVFIVYIFAALTFFPALALG PIAEHLSLWM
3E-236	794.2	32.6	4E-236	794	22.6	1	1	W0LCN2_9ENTR	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Z042_19840	Serratia multitudinisentens RB-25	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia multitudinisentens, Serratia multitudinisentens RB-25	1441930	>tr|W0LCN2|W0LCN2_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Serratia multitudinisentens RB-25 GN=kdpA PE=3 SV=1 MATSAFLLIASFMLILLLLARPLGGFIARLIEGEPLPVLRHLEAAVWRCCGNHSAEMNGRQYA LAILWFNLFGLVLLFILLMAQGSLPLNPQKFAGLSWDLAFNTAVSFVTNTNWQAYSGENTLS YLSQMVGLTVQNFLSAATGIAVAFALIRAFARRSSATIGNAWADLLRITLYVLLPLSLITALFFV SQGSLQNLLPYLHLNTLEGVQQTLPMGPVASQEAIKMLGTNGGGFFGANSAHPFENPTALT NFVQMLAIFLIPCALCFAFGQVTGENRQGHALIWAMTLIFVVAVIVVMYAETAGNPHLSTLGS TSNINMEGKESRFGILDSSLFSVVTTAASNGAVNAMLDSFTPLGGLVPMWLMQIGEVVFGG VGSGLYGMLLFVLLTVFIAGLMIGRTPEYLGKKIDVYDMKMTALAILVTPALVLLGTALAIATE AGRAGILNPGAHGFSEVLYVLSSTANNNGSAFAGLSTNTPFYNLLLAFAMFVGRFGVILPVL AIAGSLCVKKRQPTGNGTLPTYGPLFIGLLIGTILLVGALTFIPALALGPVAEHLQLWLAN
3E-236	794.1	36.5	4E-236	793.9	25.3	1	1	F6D4T7_METPW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MSWAN_1127	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	568	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	868131	>tr|F6D4T7|F6D4T7_METPW Potassium-transporting ATPase potassium-binding subunit OS=Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1) GN=kdpA PE=3 SV=1 MDVNSLIYIILFFVVAILLAWPLGKYMSKVFSGEKNFMTPLVRPVEKFIYRICGVDEAEEMTW KGYAKALILFNILAILFVFIIQLIQGILPLNPEGFSGVRWDTALNTAISFVTNTNWQAYAGETTM SYLTQMVGLAVQNFLSAAVGMAAALVLIRGFIRKNTDKLGNFWVDITRMVLYILLPLSIILAILL VSQGVVQTFDSYATAQTIEGASQIIPLGPVASQEAIKMLGSNGGGFFNVNSAHPFENPNGF TNLLETLAIILIPMSLVFMFGYLVRNIKQGLALFAVMMVLLIMGLGVALWSEDHPNPVIEKMGV TGQNMEGKEVRLGTTNSVLWGVLTTDVSNGGVNSMHDSTMPLTGLVYMFNMGTGEVIFG GIGVGLAGLLFYVILTMFIAGLMIGRTPEFLGKKLGPYEMKLALIPLIGAPASVLILSALALSTPD GLAGISNPSAHGLSEILYAYFSTIANNGSAFGGLTVNTVFYNLTTGLAMLIGRFATIIPAIAIAG ALAQKGKVSMSSASFPTTGPLFVIMVVAVVIIIGALTFFPVFALGPGLEHLFLQAGKIFA

4E-236	794	33	4E-236	793.8	22.9	1	1	A0A089L4H0_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA R70331_28070	Paenibacillus sp. FSL R7-0331	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. FSL R7-0331	1536773	>tr|A0A089L4H0|A0A089L4H0_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus sp. FSL R7-0331 GN=kdpA PE=3 SV=1 MGILQIVIVIAILVLLVKPAGTYLYHVFSNEPNRTDRIFGGMERGIFRLGGLSKREGMSWKRY AVSFLTTNIVLVAFGYLILRLQGALPLNPGGIGKMEQTLAFNTVISFITNTNLQHYSGETGVSY FSQMAVMTMLMFTSAAGGFSVAVAFVRGITGRKSLGNFFEDFVKAHTRVFIPLALLVTLLLIG LQVPQTLKPTLEVTTLEGQTQQIAVGPVASLESIKHIGTNGGGFFGANSAHPFENPSPLTNVI EILSMWLLPASLPYMYGRFARNKRQGWMIFSAMMTLFVLLLSLNYYAESQGNLAINAMGID ASQGSMEGKEVRFGIAQSALFTTVTTAATTGSVNNMHDTLTPLGGITPLALMMLNNVFGGK GVGLINMLMYAILGVFLCGLMVGRTPEFLGRKIEAREMKLIAIAILIHPLIILVPTAGAFLTALGH GSISNPGFHGLTQVLYEYTSSAANNGSGFEGLADNTSFWNMTTGVVMLLGRYVSIIAMLAV AGSMIRKKAVPETIGTFRTDNGLFTGILIGTVLIIGALTFLPVIVLGPVAEYLTLR
4E-236	793.9	24.8	5E-236	793.6	17.2	1	1	D3HKC4_LEGLN	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LLO_2468	Legionella longbeachae serogroup 1 (strain NSW150)	605	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella longbeachae, Legionella longbeachae serogroup 1 (strain NSW150)	661367	>tr|D3HKC4|D3HKC4_LEGLN Potassium-transporting ATPase potassium-binding subunit OS=Legionella longbeachae serogroup 1 (strain NSW150) GN=kdpA PE=3 SV=1 MTKFGLLQISFYLLFLLLLVKPLGWYMARVYQGKSCLLDSLVKPLESFIYKLCGINPEEEMG WKTYLSTMLLVNFLGLLAVFLLQRVQYYLPLNPQNFTAPSSDLAFNTAISFATNTNWQAYSG ETTFSYLTQMFALTVQNFISAATGMSLLIALIRGLTKREGSGLGNFWVDTIRGILYILLPLSFIF SLILCSQGVIQNFKPYQKISLLHPFTYQQSVTNIKGQPLLDNQANPKVSPEKITEQIIPMGPAA SQIAIKQLGTNGGGFFNVNSAHPFENPTPLTNFLEMIALLLIPAAFCFTFGMMVRDKRQGWS VLIAMIILFIPPLILETIVEQKGNPAFQAMGIDMQPISGLYPAGNMEGKETRFGIVNSAIWATAT TAASNGSVNSMLDSFTPLGGLVPLWMMHLGEVCFGGVGSGLYGMLMMIIITVFVAGLMVG RSPEYLGKKIEPYEMKMASIAVLIMPLIVLISTAYASVTSSGISSIANPGSHGFTEILYAFTSMG NNNGSSFAGLNVNTPFYNILGGLLMLISRYWIAIPALAIAGSLVKKKHIPSSPGTLATHTPLFIIL LVCITIIIGALSFVPALALGPVVEQLILWGKYGY
5E-236	793.7	33.9	5E-236	793.6	23.5	1	1	KDPA_CLOBB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CLL_A0978	Clostridium botulinum (strain Eklund 17B / Type B)	579	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum B, Clostridium botulinum (strain Eklund 17B / Type B)	935198	>sp|B2TM61|KDPA_CLOBB Potassium-transporting ATPase potassium-binding subunit OS=Clostridium botulinum (strain Eklund 17B / Type B) GN=kdpA PE=3 SV=1 MMNLVLQYGLYILILVVLAIPLGNYIGKIMNGEKVFLSKILTPCENFIYKILHIDKDEDMSWKKY SFSVLAFSIISLIVLFLLHIFQGFLPLNPEKVSGTSWDLAFNNAISFVTNTNWQGYSGESSLSY FTQMMGLTVQNFVSAAVGISVLFALIRGFIRVKQKGIGNFWIDITRTVLYILIPLSIVVSLALVS QGVVQNFKQYETVSLLEPITLEDGTLVTEEVVPLGPAASQIAIKQLGTNGGGFMGTNSAHPI ENPTILSNLFEMISLLLIPVALCFTFGRNIKDRRQGIAIFVAMGIMLVVAMAIVGVNEQIGTPQM ALNGQVDLSTINQAGGNMEGKEARFGIATSSTWATFTTAASNGSVNSMHDSYTPIGGMIPM LLMQLGEVVFGGVGCGLYGMIGFAILAVFMAGLMVGRTPEYLGKKIEPFEMKMAVLVCLAT PIAILIGSGIASILPETVNSLNNSGAHGFSEVLYAYTSAGGNNGSAFAGFAANTPFINISIGLSM IFARFVPMMGTLAIAGSMVKKKKVAESVGTLPTHNAMFIGLLIFVVLLIGALSFFPALALGPIAE FFQMLG
5E-236	793.7	34.8	5E-236	793.5	24.1	1	1	R5TWB5_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN481_00428	Ruminococcus gnavus CAG:126	576	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	1263106	>tr|R5TWB5|R5TWB5_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Ruminococcus gnavus CAG:126 GN=kdpA PE=3 SV=1 MLQILTLAIFLILVIPMGKYMYHIATKQKTFADKVFNPIDNFLYKICGIKREDMGWKKYAMSLV LANAVMVFIGYLILRLQNLLFLNPNGADGMEASLSFNTIISFMTNTNLQHYAGESGLSYGSQL CVIIFMMFTSAASGYAACMAFCRGVSGRKMGNFYEDVIRVTTRILIPFSFVIGLLLVSQGVPQ TLQANETIQTIEGKMQDLALGPVAALEAIKHLGTNGGGFFGANSATPFENPTVISNIIETISMM ILPGSCVVAFGHMIHDNRKENAARKAVAPKQFGKPMLMGRQAAVIFGAMSILFVVGLVICYS AEMAGNPVTHSLGLAQAGNMEGKETRFGIAQSALFTTVTTSFTTGTVNNMHDSLTPLGGLV PMLHMMLNCVFGGKGVGLMNMVMYVILAVFICGLMVGRTPEYLNKKIEGREMKLVALVILIH PLLILGFSALGVATQTGTSGITNPGYHGLSQVLYEFASSAANNGSGFEGLADNSVFWNITTG LAMFFGRYFSIVAQLAVAGSLLAKKKVNESIGSLKTDNVTFMIILVFIVYIFAALTFFPALALGP VAEHLSLWQ
5E-236	793.7	29.1	5E-236	793.5	20.2	1	1	U2RJ08_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HMPREF1546_00025	Oscillibacter sp. KLE 1745	601	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	1226323	>tr|U2RJ08|U2RJ08_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Oscillibacter sp. KLE 1745 GN=kdpA PE=3 SV=1 MLQLALTIIIFLIIVIPVGRYMYHIATWNHTLADPVFDRLDGVIYKIGGVNPHQGMNWRQYALA LVGTNAVMVAIGYLILRIQSVGIFNPNSIGNMEPTLAFNTIISFMTNTNLQHYSGESGLSYLSQ MLVIIFMMFVSAASGYAACIAFIRGLTGKTKDDVGNFFADLTRITTRLLLPFSIVGGLLLVWQG VPQNFDANIVVNTLEGTFQTIAMGPIAALEIIKHLGTNGGGFLGANSTTPLENPTIISDMIELYS MMLFPGACVITFGKMVRGRKKKDAAGDKALAGSESAGQLSAGGAEQGPRLKDHSLTASIY GWEGRTIFLAMGIIFLVGLGVCYWSELQGNPALAKIGLDQSMGSMEGKEVRFGIAQSAMFT TTTTSFTTGTVNNMHDTLTPLGGMIPLLHMMLNVVFGGKGVGLMNMIMYAILAVFICGLMIG RTPEYLGKKIEGREMKLTALCIIIHPFLILFFSALAVSTSGGLEGITNPGFHGLSQVLYEYASSA ANNGSGFEGLADNSYFWNITAGLAMFFGRYLSIVIQLAIAGSLMRKRFVNETVGTLRTDTLS FAVILVFVVYIFAALTFFPALALGPIAEHLTLWA

5E-236	793.7	36.9	6E-236	793.5	25.6	1	1	W0V0F1_9BURK	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GJA_692	Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Janthinobacterium, Janthinobacterium agaricidamnosum, Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	1349767	>tr|W0V0F1|W0V0F1_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628 GN=kdpA PE=3 SV=1 MTTQSILLLVVFLVVLLALAYPLGLYMAKVAGDGPLRGLGWLQKIENVLYRWSGMSADRAM NWKTYAIALVVFNTVGAFFVYALQRLQGFLPLNPQGLGTITPDSSFNTAVSFVANTNWQGY SGEQTMSYLTQMLGLACQNFFSAATGIAVIFALVRGFSARSSKSIGNFWVDLTRSTLYVLVP LSLVLSVIFMGEGVIQNFSAYKEVPLLDQVAYSTPKTGADGQPVLDQAGQPVMEAQVAKTQ VIAMGPVASQESIKMLGTNGGGFFNANSAHPFENPTVMSNFLQMLAIFIIPAGLCFTFGRMV GDMRQGWAVLAAMTLIFVVMTAAVMGAEQQASPGLQALGVDQNVTLLQSGGNMEGKETR FGISSSSLFAAITTAASCGAVNSMHDSYMPLGGMVPLLLMQFGEVVFGGVGTGLYGMLMF AILAVFIAGLMIGRTPEYLGKKIQAYEMKMVSLAILVTPALVLTGTAIAVMVDAGKAGVANPGA HGFSEILYAFSSAANNGSAFAGLSANTPFYNIMLAIAMWFGRFAVIVPVLAVAGSLASKQR LSANAGTMPTHGAMFISLLIGVVILVGVLNYIPSVALGPIVEHLQLFTQ
5E-236	793.7	31.6	5E-236	793.5	21.9	1	1	C4IDW9_CLOBU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CLP_3549	Clostridium butyricum E4 str. BoNT E BL5262	579	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	632245	>tr|C4IDW9|C4IDW9_CLOBU Potassium-transporting ATPase potassium-binding subunit OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=kdpA PE=3 SV=1 MMSLILQYGVYLLILVVLAIPLGNYIGKVMNGERVFLSKILVPCESFIYKVLHVDKNEDMGWK KYSFSIIAFSLISLVILFFIHLCQGFLPLNPENIKGTSLDLAFNNAISFVTNTNWQAYSGESSLS YFTQMIGLTVQNFVSPAVGMCVLFALIRGFFRVNAKGIGNFWTDITRSILYVLIPLSVVLSLVL VSQGVVQNFKSYDKVSLVEPITLDDGTVVTEEIVPQGPAASQIAIKQLGTNGGGFFGVNSAH PLENPNVLTNLFEMISILLIPAALCFTFGRNIKDKRQGIAIFVAMGIMLVFAMGIIGVNEQNATP QLAMNGQVDISTINQPGGNMEGKESRFGIASSTTWAAFTTAASNGSVNSMHDSYTPIGGM MTMLQMQLGEVIFGGAGCGLYGMLAFAILTVFMAGLMVGRTPEYLGKKIEPFEMKMAVLVC LATPIAILIGSGIATLLPQTVHSLNNSGAHGFSEVLYAYSSAGGNNGSAFAGFGANTPFLNISI GIIMLFARFVPMLCTLAIAGSLVQKKKVAESSGTLPTHNMMFIGLLIFIVLLIGALSFFPALALG PIAEFFQMLG
7E-236	793.1	31.8	9E-236	792.8	22	1	1	A0A0F5FWH1_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VE25_03035	Devosia geojensis	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia geojensis	443610	>tr|A0A0F5FWH1|A0A0F5FWH1_9RHIZ Potassium-transporting ATPase potassium-binding subunit OS=Devosia geojensis GN=kdpA PE=3 SV=1 MTWQGWLQIGLVLLAVAVVAKPLGLYMARVFAGEGTFLSPVLRPIERGFYRLAGVDPKAEQ GWLGYTFGVLTFSFVGVLLLYALLRLQGILPLNPQGFEGVPPDLAFNTAASFVTNTNWQSY GGETTMSHFSQMAGLTVQNFVSAATGIAIAVAVSRAFVRSGAEAIGNFWVDLTRATLYVLLP AAIVVALLFVALGLPQTLAASAGATTLEGASQTIAMGPMASQEAIKQLGTNGGGFMNVNAA HPFENPNAFSNYLGIFSMLVISSGVFYAFGQIVGSRRQAWALLAAVGILLVVGTGAIYWAET FGNPIHLAAGVDPALGNMEGKEVRFGQAMTALYAAVTTGLSNGGVNAMHSSLTPLGGLVP LFLMQLGEVLPGGVGSGLYGMVVFAILAVFVAGLMVGRTPELLGKKIEAREMKLAMLAILILP LAILGFSAAAAVIPAGLAGLANAGPHGLSEILYAYTSAAANNGSAFAGLSANSPWYNTTLGLA MLAGRFAYIVPVLAIAGSLVKKQKVPASAGTFPTDGPLFVGLLIGIILIMGGLQFFPALALGPIL EHVLMLAGQTF
9E-236	792.7	27.2	1E-235	792.5	18.9	1	1	KDPA_EDWI9	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NT01EI_2888	Edwardsiella ictaluri (strain 93-146)	565	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Edwardsiella, Edwardsiella ictaluri, Edwardsiella ictaluri (strain 93-146)	634503	>sp|C5BC66|KDPA_EDWI9 Potassium-transporting ATPase potassium-binding subunit OS=Edwardsiella ictaluri (strain 93-146) GN=kdpA PE=3 SV=1 MFANALMLLGLLILLLLILAPLLGSLLSRLIDGEPYRAMARTENTLWRLCGVTPHEMDWRHYL LAILAFNLLGIVLLFALLMAQGLLPLNPQGFPGLRWDLALNTAVSFVTNTNWQAYSGESSLS YLSQMAGLGVQNFLSAASGIAVLFALIRAFARHADPSLGNAWVDLWRITLYVLLPLSLLLSLL FVSQGVIQNVSGYVSVTSLEGGSQLLPMGPVASQEAIKLLGTNGGGFFGANSAHPFENPTA LSNLLQMVAIFLLPTALCFAFGRSVGDSRQGHALLWTMSLIFIVAAGCVMYAELQGNPHLMA LGTDSNGNMEGKENRFGILASALYAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGAGSGLYGMLLFVLLTVFIAGLMIGRTPEYLGKKITVFEVKMTALAILIPPALVLTGSAIAL LCDAGRSAIHNPGAHGFSEVLYAFSSAANNGSAFGGLSVNTPFYNLLLALVMLIGRFGVIIP VMAIAGALALKKRQPAGNGTLASHGALFVSLLIGTILLVGALTFIPALALGPVAEQLQNTRAHI QP
9E-236	792.7	36.2	1E-235	792.5	25.1	1	1	E3GJV8_EUBLK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ELI_1132	Eubacterium limosum (strain KIST612)	561	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium limosum, Eubacterium limosum (strain KIST612)	903814	>tr|E3GJV8|E3GJV8_EUBLK Potassium-transporting ATPase potassium-binding subunit OS=Eubacterium limosum (strain KIST612) GN=kdpA PE=3 SV=1 MLQVALTLALFVIIIFPLGTYIYHIATNKKTFADPVFDRVDNAIYKVCGVDMDRQMNWKQYAV ALVVTNAFMIFIGYIILRIQFLPVFNPNGIEGMEASLSFNTIISFMTNTNLQHYSGESGLSYLSQ MLVIIYMMFVSAASGYGVCVAFIRGLAGGKDGRKAMGNFYADLIRITTRVLLPLSIILGTFLISQ GVPQTLLGTATVASLEGGLQDIARGPVAALEIIKHLGTNGGGFLGANSSTPIENPTILTNICEL LSMMIIPGALVVAFGLMIKDKKQGWMVFGAMAIIFVIGLGVCMTAEHAGNPALAEVGLNQSM GNFEGKEVRFGIDQSALFTTVTTSFTTGTVNNMHDSLTPLGGMVPLLHMMLNCVFGGEGV GLMNILTYAVLTVFICGLMVGRTPEFLTKKIESREVKLAALVIIIHPLLILGFSALAVSVQAGLDG ITNPGFHGLSQVLYEYASSAANNGSGFEGLADNSVFWNVTAGLAMFFGRYLAIILQLAFASS LMNKASVSVSAGTMKTNNVMFMILLVLIVYVVGALTFFPALALGPIAEHLTLWF

1E-235	792.6	34.4	1E-235	792.3	23.9	1	1	D7A9S5_STAND	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Snov_1542	Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Starkeya, Starkeya novella (Thiobacillus novellus), Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	639283	[illegible] OS=Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113) GN=kdpA PE=3 SV=1 MTVLGWLQIATILALVVAAAVPLGNYMARVYAGERTLLSTVLGPVERGFYRLAGVDETREQ GALAYTLGMLAFNAAGVVLLYAILRLQGFLPFNPLGFAGVSPDLAFNTATSFVSNTNWQSY GGETTMSLFSQMAGLTVQNFLSAATGLALAVALVRAFARSNASTVGNFFVDMTRSTLYVLL PLAIVTALVQVWMGVPQTLDATTAATTIEGAKQTLAMGPVASQIAIKQLGTNGGGFFNVNAA HPFENPSPISNALEIWQMLVVSAALVFAFGRLIGDRRQAWALIGAIAIILVAGIGIVYWAESAG TPSLLAAGLDPTGGNMEGKEVRFGLAASSMFAAVTTGLSDGAVNAMHDSFTPIGGLVPMFL IQLGEILPGGVGSGLYGLMVMAIIAVFVAGLMVGRTPEYLGKKIEVAEVKMAILAVLILPCTILG FSAISAVLPAGLAGLANAGPHGLSEIIYAYSSAAGNNGSAFAGLSANTPWWNTTLGLAMLLG RFAYIVPMMAIAGSLAAKTRLSASSGTFPTHGLLFVGLLVGVILILGGLQFFPALALGPIAEQV QMLAGKTF
1E-235	792.2	35.4	2E-235	792	24.5	1	1	KDPA_ENT38	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Ent638_1210	Enterobacter sp. (strain 638)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Enterobacter, Enterobacter sp. (strain 638)	399742	>sp|A4W861|KDPA_ENT38 Potassium-transporting ATPase potassium-binding subunit OS=Enterobacter sp. (strain 638) GN=kdpA PE=3 SV=1 MAAQGFLLIASFLLLLFLLARPLGNVLARMINGVPLPLVGGVENGVWRVLGIQNQEMNWRQ YLLAILLLNVFGLFVLFAMLMLQGILPLNPQQLPGLSWHLALNTAVSFVSNTNWQSYAGETT LSYFSQMVGLTVQNFLSAASGIAVIFALTRAFARQKVNTLGNAWVDLTRITLWVLLPISLVIAL FFIQQGTLQNLLPYASYTSLEGVKQMLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPT ALTNFVQMLAIFLIPAALCFAFGDVVNDRRQGRTLLWAMSLIFVVCAALVMWAEWHGNAHF MQLGVDSNINMEGKESRFGILASSLYAVVTTAASCGAVNAMHDSFTALGGMIPLWLMQIGE VVFGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKLTALAILVTPALVLMGTA LALMTDAGRSGIFNPGIHGFSEVLYAVSSAANNNGSAFAGLSANSPFWNCLLAFCMFVGRF GVIVPVMAIAGSLVSKNIQPTSSGTLPTHGALFVGLLIGTVLLVGALTFIPALALGPVAEHLSLR
1E-235	792.2	37.1	2E-235	792	25.7	1	1	A5N882_CLOK5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CKL_1471	Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	572	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium kluyveri, Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	431943	>tr|A5N882|A5N882_CLOK5 Potassium-transporting ATPase potassium-binding subunit OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=kdpA PE=3 SV=1 MLQIILTLAIFIVLVIPMGKYLYHIAARKHTFLDPVFDPIDGMIYRICGIDKKEMNWKQYITALLV TNAFMVLIGYFILRLQALHIFNPNGISGMEPTLSFNTIISFMTNTNLQHYSGESGLSYLSQMM VITFMMFTSAATGFSAAMAFIRGLAGKTKTMGNFYMDLIRIITRVLLPISILGGLLLVYLGVPQT LSANLTVGTIEGKFQDIAMGPIASLEIIKHLGTNGGGFLGANSSAPFENPNIFTNIIEIISMMILP GACVVAFGHMVHDGKKEEEKKNPKRIFFGSEGRTIFIVMSIIFIVGLVICFMSENAGNPLLAQ AGLSQSMGSMEGKEVRFGIAQSSLFTTVTTAFTTGSVNNMHDTLTPMGGFVALLFMMLNV VFGGKGVGLMNMILYAILAVFICGLMIGRTPEYLGKKIEGKEMKLTALGIIIHPLLILAFTALAIA VPAGLKGITNHGFHGLTQVVYEYASSAANNGSGFEGLTDNTYFWNITTGLAMFFGRYLSIII QIAIAGSLMLKRPVSESVGTLKTDTRTFAAALLMVVLIISALTFFPVLALGPIAERLTLWN
2E-235	791.8	35	2E-235	791.6	24.3	1	1	G0AB23_COLFT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CFU_1316	Collimonas fungivorans (strain Ter331)	605	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Collimonas, Collimonas fungivorans, Collimonas fungivorans (strain Ter331)	1005048	>tr|G0AB23|G0AB23_COLFT Potassium-transporting ATPase potassium-binding subunit OS=Collimonas fungivorans (strain Ter331) GN=kdpA PE=3 SV=1 MTSQSIMLLIAFLAVLLVLSYPLGKFIVQVAGGSSDHAPVPGFGWFNRVEQWLYRCAGIQAK SEMNWKHYALALLLFNTIGALATYALQRLQVWLPLNPQHFANVSPDSSFNTAVSFISNTNW QGYAGEGTMSYLTQMLVLAVQNFFSAATGIAVAFALIRGFSRHSAQSIGNFWTDITRSTVYI LLPLSVIFSVFLISQGVIQNFDSYKDANIVQSLDYQQPKIGADGQPVNDAAGKPVLEAANTKV QTLAMGPVASQEAIKMIGTNGGGFFNANSAHPYENPTPLSNFMQMLAIFLIPAALCFTFGFM VGDIRQGWAVLAAMTVIFVIMTAVVMYAEQQAHPGLTAMGIDQGQSLLQSGGNMEGKETR FGISASALFAAITTAASCGAVNAMHDSFTALGGLVPMALIQMGEVVFGGVGSGLYGMLVFAI MAVFIAGLMIGRTPEYLGKKIQSFEMKMTSIAILATPMLVLGGTAIAVMATAGVAGILNPGAH GFSEILYAFSSAANNNGSAFGGLSANTPFYNVMLAIAMWFGRFIIIVTILAMAGSFAAKKRLE PNSGTMPTHGPLFIVLLIGVVVLVGVLNYVPALALGPVVEHLQMFAH
2E-235	791.7	36.5	2E-235	791.5	25.3	1	1	I0DX89_PROSM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA S70_15710	Providencia stuartii (strain MRSN 2154)	567	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia stuartii, Providencia stuartii (strain MRSN 2154)	1157951	>tr|I0DX89|I0DX89_PROSM Potassium-transporting ATPase potassium-binding subunit OS=Providencia stuartii (strain MRSN 2154) GN=kdpA PE=3 SV=1 MATSALLLIASFLLVLFVLAKPLGLFIARLIEGDMPHFIAKTETIIWRFSGLKQPGREMAEMNW SRYAFAILLFNALGFALLFILLLFQGNLPLNPQKFQGMNWDLAFNTAISFVTNTNWQSYSGE SSLSYLSQMAGLTVQNFLSAATGIAVVFALIRAFARHSSKTLGNAWVDLTRITLYLLLPLAVIF ALFFVSQGVIQNFSPYVLSNNLDSSAQLIPMGPVASQEAIKLLGTNGGGFFAANSSHPFENP TALTNFVQMLAIFLIPTALCFAFGRSVGDNKQGNALLWVMAIIFVIAATTVIYAEYVGNPFLAD FAANSSINMEGKESRFGILGSALYAVVTTAASCGAVNAMHDSFTALGGMVPMWLMQIGEV VFGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIEVREMKMVAIAILVTPTLVLCGTTLA LMTDVGRAAIFNPGAHGFSEVLYAFSSAANNNGSAFAGLSANTPFYNVALAITMFLGRFGVI FPVLAIAGSLAMKKPQMASTASLPTYGPVFIGLLILTILLIGALTFVPALALGPIAEHLQIGLAA

2E-235	791.6	27.5	2E-235	791.4	19.1	1	1	A0A024HIE1_PSEKB	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpa3 kdpA PKB_3062	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	590	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas knackmussii, Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	1301098	>tr|A0A024HIE1|A0A024HIE1_PSEKB Potassium-transporting ATPase A chain OS=Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13) GN=kdpa3 PE=3 SV=1 MSLQAGTLLGAFLIALLVLSWPLGWFIDAVMAGRIRLLTRIEAPLYRIAGTRAEDEMGWLPYT LSVLLFNVLGVVAVYLLQRLQAMLPLNPQHFGAVTPDSAFNTAISFVTNTNWQGYSGEATM SYLTQMLALAVQNFFSAATGIVVAIALVRGFARHSAQSIGNAWIDLTRVTLWVLLPVSFLLAL FLVSQGAIQNLAPYQDVTTLEVSHYQLPKLDADGQPVRDAQGDALMEERSSPTQTIAMGPV ASQEAIKLLGTNGGGFFNANSAHPYENPTPLSNFAQMLAIFAIPAALCFVFGRMVGDARQG WAVLIAMTLMFVTGVIAANHYELLGNPQFQALGVDPAGGNMEGKETRFGIAASSLFATVTT SASCGAVIAMHDSFTPLGGAVALVMMQLGEVVFGGVGSGLYGMLVFALLAVFIAGLMIGRT PEYLGKKIEAFEMKMVAIAILVTPLLVLCGTAIAVMADAGRVGVANPGPHGFSEILYAFTSAA NNNGSAFAGLSANTPFYNSLLGIAMWFGRFGVLVPVLAIAGSLAAKKRLAATAGTMPTHGP LFVVLLIGTVLLVGLLNYVPALALGPGIEHLLLFK
3E-235	791.2	35.8	3E-235	790.9	24.8	1	1	M4V8V0_9DELT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA A11Q_655	Bdellovibrio exovorus JSS	563	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio, Bdellovibrio exovorus, Bdellovibrio exovorus JSS	1184267	>tr|M4V8V0|M4V8V0_9DELT Potassium-transporting ATPase potassium-binding subunit OS=Bdellovibrio exovorus JSS GN=kdpA PE=3 SV=1 MNIFDVLQLILFVGVLFLLTPPLGKFMAAVFKGETTWLHKPLGWLERLTYKISGIDSKKDMG WKEYALCLMAFNILGIVVLFLLQLIQGGLPFNPQAISGITWDSALNTAVSFVTNTNWQGYAG ETTMSYLTQMIGLAYQNFVSAAVGIAVAVAVTRGIARKSLEGIGNFWTDLTRSVIYILLPSSFV LAIVLVSQGVVQNFSPYLEALTLEGAKQMLPFGPAASQIAIKMLGTNGGGFFNSNSSHPFEN PTAFSNLLQMLAIFVIPAALTYMFGVMTNAKKHGWLIFGVMLALFLGLTGASLYSEYSHNPV VSQSAVMEGKETRFGTFNSVLFSTVTTSASCGAVNSMHSSLSPLSGGVALFNMMLGEIIFG GVGAGLYGMLLFVLLTVFLSGLMVGRTPEYLGKKIEGKEMTMVIVAILAPCTMILVGSAFSSV LPMGLSSLANKGPHGFTEILYAFSSAAGNNGSAFAGLNANTPYYNLFLALAMFVGRFAVIIPI LAVAGSLAKKKVSPPSSGTFEVDSLLFAVLLIGVILIVGALTFLPALSLGPIMEHILMLNGRTF
3E-235	790.9	31.5	4E-235	790.7	21.8	1	1	KDPA_METPP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mpe_A2507	Methylibium petroleiphilum (strain PM1)	576	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Methylibium, Methylibium petroleiphilum, Methylibium petroleiphilum (strain PM1)	420662	[illegible] OS=Methylibium petroleiphilum (strain PM1) GN=kdpA PE=3 SV=1 MNSQAWIQLAVFLALLMLLAWPLGRWLAAVAEGHLPQGLAPFCRVETALYRAAGIDAAVG MGWKAYALALLAFNALGALAVYALQRLQGGLPLNPQGLPGVGADSSLNTAVSFVSNTNWQ GYAGETTMSYLTQMLALGVQNFLSAATGIAVAFALIRGFAARSSSAIGNFWVDVTRITVYVLL PLSLVFAVFLVSQGVIQNVQPYQDVSTLEGAASTPQTLAMGPVASQEAIKMIGTNGGGFFN ANSAHPYENPTPLSNFAQMLAIFLIPAGLVFAFGRLVGDVRQGGALLAAMTVMFVLAVVTVT SLEQRGHPQLAALGVDPVASALQAGGNMEGKEARFGIAASALFAAITTAASCGAVNAMHDS FMPLGGAVPLLLIQLGEVVFGGVGSGLYGMLVFAILAVFIAGLMIGRTPEYLGKKIEPYEMKM TAVVILVTPLLALLGTAVALTAPTGPAGMGNPGPHGYTEILYALSSAANNNGSAFAGLSANT PFYNLLLAVAMWFGRFGVIVPVLAIAGSLAAKKRLPVTAGTLPTHGPLFVVLLIGAVLLVGLLN YVPALALGPVVEHLMQAAAR
3E-235	790.9	30.3	4E-235	790.7	21	1	1	A0A0C9NHK5_SPHPI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SP6_31_00050	Sphingomonas paucimobilis NBRC 13935	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas paucimobilis (Pseudomonas paucimobilis), Sphingomonas paucimobilis NBRC 13935	1219050	[illegible] subunit OS=Sphingomonas paucimobilis NBRC 13935 GN=kdpA PE=3 SV=1 MTLQGWALILGFVAILLALTKPVGAWLFALYEGRRTPLHVVLGPVERGFYKLSGIYPEVQQG WRRYALHMLIFNVALMVFTYAVLRLQFYLPGNPQGLAGLTPHLAFNTAISFTTNTNWQSYG GESTMSNLSQMLGLTIHNFLSAATGIALAFALFRGVAGRETKNLGNFWADVTRITLYLLLPLC IVYTIFLIASGVPQTMAGVVNIDTLEGVRQSILLGPVASQEAIKMLGTNGGGFFNANSAHPFE NPTALTNFVQMLSIFVIGFGLTWCFGKAVGNTRQGWAILSAMILLFLGGAAVCYWAEAAGN PVLHQLGVAGGNMEGKEVRFGVAASALFAAVTTAASCGAVNAMHDSFTALGGLIPLFNMQ LGEVVIGGVGAGIYGFLLFAILAVFVAGLMVGRTPEYVGKKIEAREVKLAVLAIAVLPLFILGLT ALSCVTQQGLAGPLNKGPHGFSEILYAFTSAVANNGSAFAGLTASTPWYDGLLGVAMWVG RFFIIVPMLAIAGSLAAKKHVPASAGSFPTTGVLWVGLLVGIVLVLGGLTFLPSLALGPIADHL AMIRGQLF
4E-235	790.8	33.1	4E-235	790.6	22.9	1	1	A0A0D6T8L4_9RHOB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SY26_17610	Paracoccus sp. 361	566	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 361	1603292	[illegible] subunit OS=Paracoccus sp. 361 GN=kdpA PE=3 SV=1 MSPFLVFALYGAVTVGLAWLLAGHMHRVFTGRRVWSSPLIAPVERAFLSAAGVTAGRGQT WSGYAMAVLVFNLAGFLLLYAILRLQGMLPWNPQGIGPMAPDLAFNTAISFVTNTNWQAYS GEVQLSYLSQMVGLTVQNFVSAATGMAVAVAIVRGFAARGDGRLGNFWVDATRAVLYILLP LSILAAVVLIWQGVPQSLSAYVRATTLEGAGQVIAQGPAAAQIAIKQLGTNGGGFFGVNSAH PLENPTILSNMIQSVYLLLIPVAFCFLFGRMVGDRRQGWAIFAAMGVLFVAGLLLMNAPEQA GNPALTQATGITGPNMEGKEVRFGATLSVLWAEATTAASNGSVNAMHDSFMPLSGLVMML NMQVGEVIFGGVGSGLYGMLLYVVLAVFLAGLMVGRTPEYLGKKIEGREVTLSVLAFLSMP LGILVFGALSVVIPAGLAAVQDAGPHGLSEVLYAYSSATGNNGSAFGGFGAAAPFHTTLQGI AMILGRYAIIVPMLAVAGSLALKSPVPATAGTFPTHGPLFVLLLVITVLILGALTFFPALVLGPIA EHVSMLGGQTF

4E-235	790.8	25.4	4E-235	790.6	17.6	1	1	A0A052IL53_9BORD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAL539_3536	Bordetella hinzii 5132	594	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella hinzii, Bordetella hinzii 5132	1331257	>tr|A0A052IL53|A0A052IL53_9BORD Potassium-transporting ATPase potassium-binding subunit OS=Bordetella hinzii 5132 GN=kdpA PE=3 SV=1 MDSQFFGLLALYLILLLGLAPVLGRYIRRAMEEGRYAATAWGRWAERLFYRAAGVDPDREM HWRQYAVAVLLFNVLGLAAVYALQRLQGSLPLNPAGMGAVSPDSAFNTAISFVANTNWQG YGGESTMSYLTQMLALTVQNFLSAATGICVLFALMRGLARHGSATVGNFWVDVTRSTLYVL LPLALALALALVSQGVIQNTSAYQEVATLQAQPYDAPRLDANGQALNDAAGKPLTDPAIART QTLAMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTALSNLLEMLAILIIPAALCFSFGEM VGNRRQGIAILAAMTLLFIAFAWLTQSSEQTLTPALAHLPADAGLGNMEGKESRFGVPASAL FAVVTTAASCGAVNAMHDSLSALGGLGPMLLMQLGEVVFGGVGSGLYGMLAFALLAVFIAG LMIGRTPEYLGKKIEAYDMKMVSIVVLATPFLVLMGTALAISLPAGLAGLLNPGAHGFSEALY ALSSAANNNGSAFAGLSANTPFYNVLLGLAMWFGRFAIIVAILALAGSLAAKKRLADSAGSM PTTGPLFVVLLIGAVLLVGALTYVPALALGPVAEHLQPRL
4E-235	790.8	28.9	4E-235	790.5	20.1	1.1	1	KDPA_GEOUR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAGura_1227	Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	592	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter uraniireducens, Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	351605	>sp|Q1GQA2|KDPA_GEOUR Potassium-transporting ATPase potassium-binding subunit OS=Geobacter uraniireducens (strain Rf4) GN=kdpA PE=3 SV=1 MNPYEWLETILFFVVLLALIKPFGTYMAKVFQGERTLLSPVFVPCENLLYRICGVDKDDEMG WKRYACAMLLFNLVFAVSLFAMLLLQGILPLNPQKLPAFSWPLALNTAISFTTNTNWQNYG GEAAASYFTQMFGFAVHNFTSAATGIVIAIAAIRGLVRRKSSALGNFWVDTTRCTLYILLPLSL IAAIFLVSQGVIQNFSPYKTVPLVQATSFEKPRLDAKGTPIKDAKGNPVTESVTVKEVTIPMG PVASQEAIKELGTNGGGFFNANSAHPFENPTPLSNIFEVFLILLISGGLTYTFGRMAGNTRQ GWALLAVMLAILILAIGVFYRAESSGNPLVAKLGVHGINMEGKETRFGLAGSALFATATTGTS CGAVNTMHDSLTPIGGMVPLSLILLSEVIFGGVGTGLYTMLAFVVIAVFVAGLMIGRTPEYLG KKIEVREMWMSITTVLASGILVLIFSGIAMILPAGVSSMNNSGAHGLSEVLYAFASMSNNNGS AFAGLNGNTLFYNLTGAVAMLLGRFVPAVAVLAMAGGLAEKKYVPPSLGTLPTDQAPFALW LTLVILIVGALTFFPALAMGPIAEQLIMMR
4E-235	790.8	31.1	4E-235	790.5	21.6	1	1	B3EAQ3_GEOLS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAGlov_3230	Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	574	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter lovleyi, Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	398767	>tr|B3EAQ3|B3EAQ3_GEOLS Potassium-transporting ATPase potassium-binding subunit OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) GN=kdpA PE=3 SV=1 MNQTLVELLQLLFLLLILLALVRPLGSFMARVYQGERNLFLPLLAPVERLIYRSCGVQPDEEM GWKRYAAAMLFFNLVFAGLFVLLMTQHLLPLNPRQMPSFSWQLALNTAVSFITNTNWQN YAGEQAVSYLTQMVGLTVHNFVSAATGMAIVIALIRGFARRRSDTIGNFWVDLTRGILYILLP LSLVAAILLVSQGVIQNFSPYKTVPLLQASQNSQGLAVESVTIPMGPVASQESIKLVGTNGG GVFNANSAHPFENPTPLSNFAEILLILLIPASLTYTFGLMVGNTRQGWMLLGVMLFLWLLCFS VLQGVEQAGNPLVAKLGVVGGNLEGKETRFGMVASNLFTVTTTATSCGAVNSMHDSLTPI GGMIPLSLILLGEIVFGGVGSGLYSMLAFAIIAVFVSGLMIGRTPEYLGKKIEVQEMWLSIITILI AGVVVLILSGIAMITPSAVASMANPGAHGLSEVLYGIASMANNNGSAFAGLNGNVPFYNLLG ALAMTIGRYIPAVAVLAMAGSLAEKKYIPPSLGTLPTDKLPFAIWLCLVILIVGALNFFPALALG PIVEHMTMRG
4E-235	790.7	34.2	4E-235	790.5	23.7	1	1	N0BB32_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAHYPDE_28253	Hyphomicrobium denitrificans 1NES1	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium denitrificans, Hyphomicrobium denitrificans 1NES1	670307	>tr|N0BB32|N0BB32_9RHIZ Potassium-transporting ATPase potassium-binding subunit OS=Hyphomicrobium denitrificans 1NES1 GN=kdpA PE=3 SV=1 MTLAGWFEIALVLGAVLAAAWPLGLYMARVFAGERTALSTVMRPVERGLYAFAHVQHGSE QNWLSYTLSMLIFNGAGFLFLYALMRLQHALPLDPQDFAAVEPSLAFNTAMSFVTNTNWQS YAGETTMGHLVQMAGLTVQNFLSAATGIALAIAVTRAFARSGAREIGNFWVDVTRATLYVLL PLAIFVAILYTASGVPQTLAANVSATTLEGAKQTIALGPVASQEAIKQLGTNGGGFFNANAAH PFENPSVWSNILSIWSMLLIPTAMTFTFGRMVGDRRQGYALLAVMGVLLIVGTAVVYASETA GNPLLTTAGVDPSSGNLEGKEIRFGQALTALYVAATTGISCGAVNAMHDSLTPLGGIVPLFMI ELGEILPGGVGSGLYGMIVMALLAVFVAGLMVGRTPEYLGKKVEAREMKLAMLALLVLPFCI LGFTAIAAVLPTALASLANSGPHGLTEILYAYSSATGNNGSAFAGLNANTPWFNTTLGLAMM FGRFAYVVPVMAIAGSIATKTKTAASAGTFPTDGMLFCGLLTGVILILGGLLYFPALALGPIVE HFLMLAGKTF
4E-235	790.6	24.4	5E-235	790.4	16.9	1	1	A0A077F628_9PSED	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAPSAKL28_17430	Pseudomonas alkylphenolia	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas alkylphenolia	237609	>tr|A0A077F628|A0A077F628_9PSED Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas alkylphenolia GN=kdpA PE=3 SV=1 MHSYDYALLLAFFALVLLPAPWLGRFYYKVMEGQRTWLTPVLGPVERGCYRLAGVDAGDE HNWRQYTLALLAFNLAGFVLVFAVLLLQGYLPLNPQRLPGQEWSLAFNTAVSFVTNTNWQ AYSGEASVSYLSQMIGLTVQNFVSAATGLAVLVALCRGIARRSAHTLGNFWVDMTRATLYG LLPLCLLLALLLVWQGVPQTFGHYVQALTLQGADQTIPLGPAASQIAIKQLGTNGGGFFGVN SAHPFENPTAWSNLFEVASIILIPAALVFTFGHYVKDLRQSRAIIACMLALFLIGGGTALWSEY QANPSLNNPQVAQSAPLEGKENRFGTTASVLWTVTTTAASNGSVNNMHDSLNPISSMVAL VNMMVGEVIFGGVGAGLYGMLLNVLIAVFLAGLMIGRTPEYLGKKLQAREVQLLVATLLVMP VGVLILSALAASLPGPAASVTNPGAHGFSQVLYAYTSASANNGSAFAGFGANTTFHNLMLG LGMLIGRFGYILPVLALAGSLALKKTAPLGENSFPTHGPLFATLLVVTILLIGGLTFLPALALGPI TEHLSLGF

5E-235	790.3	32	6E-235	790.1	22.2	1	1	D2TNK8_CITRI	Potassium-transporting ATPase A chain (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ROD_07041	Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter rodentium, Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	637910	[illegible] rodentium (strain ICC168) GN=kdpA PE=3 SV=1 MAAQGFLLIASFLSLLFLARPVGAGLTRLINTKPLPGTAGIERVLWRGLGISAQEMSWKQYL LAILSVNLLGLAALFMLLRFQHLLPLNPQQLPGLSWHLALNTAVSFVTNTNWQSYGGETTLS YFSQMAGLTVQNFLSAATGVAVAFALIRGFTRQSISTLGNAWVDLTRITLWILFPLALLIALFFI QQGVPQNLLPYQPYTTLEGVKQLLPMGPVASQEAIKMLGTNGGGFFNANSAHPFENPTAL TNMVQMLAIFLLPAALCFAFGDAAGDRRQGRMLLWAMSLMFIVCAAVVMWAEVQGNPHLL QYGADSSLNMEGKESRFGVVVSSLFAVVTTAASCGAVIAMHDSFTALGGMVPMWLMQIGE VVFGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPALVLSGSA LAMMSEAGRSAMLNPGAHGFSEVLYAVSSAANNGSAFAGLGANTPFWNCLLAFCMFVG RFGVIIPVMAIAGSLAVKKRQPTTAGTLATHDALFVGLLTGTVLLVGALTFIPALALGPVAEHL SLR
6E-235	790	27.9	7E-235	789.8	19.3	1	1	C5AAP3_BURGB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA bglu_1g26280	Burkholderia glumae (strain BGR1)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia glumae (Pseudomonas glumae), Burkholderia glumae (strain BGR1)	626418	>tr|C5AAP3|C5AAP3_BURGB Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia glumae (strain BGR1) GN=kdpA PE=3 SV=1 MNANNLLQAGIFIAVLLALAVPVAGYLSRVMDGSSRVVRVFGPLERALYRVAGVDPGAEMS WKHYALATIAFNVLGMFFLYLLLRIQQWLPGNPQQFPAMTVDGAFNTAVSFVTNTNWQDY SPEQTVSYLTQMLGLTVQNFLSAATGIVVVIALIRGFARHTAKTIGNFWVDITRVTLYVLLPMS VLVAALLMSQGVIQNFRAYTDVPTLQASSYAAPKLDAQGNPLKDAKGNPVTVATPLTSQTIA MGPVASQEAIKMLGTNGGGFFNGNSAHPYENPTPFANFIETLSILILPAALCLVFGRMIGDRR QGIAVLAAMTLAFVVAVGVEMGAEQRASPVFAALHVDQGASAQQAGGNMEGKETRFGIAQ TSLFVVATTAASCGAVDGAHDSLTPVGGLVPMLLIQLGEVIFGGVGSGLYGMLVFALLAVFV AGLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPLLVLVGTSIAVLSAAGRAGIANPGPHGFSEIL YAFSSAANNGSAFAGLTVSTPFYNWLTAIAMWFGRFGTIVPVLAIAGSLAAKKRIAATSGT LPTHGPLFVVLLLGSVLLVGALTYMPALALGPGVEHLMLFANAH
7E-235	789.9	34.3	7E-235	789.7	23.8	1	1	KDPA_LARHH	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LHK_01572	Laribacter hongkongensis (strain HLHK9)	567	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Laribacter, Laribacter hongkongensis, Laribacter hongkongensis (strain HLHK9)	557598	[illegible] OS=Laribacter hongkongensis (strain HLHK9) GN=kdpA PE=3 SV=1 MNHSAVAQTGLYLLVLLALAWPLGRYLAALLEGRLAQRFAWMGRIERGILWLMGAAPDEE MGWKRYAAAILLFNLAGVVLLFLLQRWQGMLPLNPAGLEGMSADSALNTAVSFVTNTNWQ GYSGETTMSLLTQMLGLAVQNFLSAATGIAVVVALVRGFVRSGGGAIGNAWLDLLRATLWL LLPLSIVVALVLVWQGVVQNWYAGLTISSLESHTTQLLASGPVASQEAIKLLGTNGGGFFNA NSAHPFENPTPFSNWVEMLSIFLVPAALVVMFGRMVGDLRQGVVLLAAMTVLFVGAFAVVY LAESQANPLLTALGAAGDSGNLEGKEVRFGVLASSLFATITTAASCGAVNAMHDSLMPLGG GMTMLLMQLGEVVFGGVGSGLYGMLLFAVLAVFMAGLMIGRTPEYLGKKIGAPEMKLVSVA ILVGPLLVLAGTAIAVLTEAGRAGMANPGAHGFSEVLYAFSSAANNGSAFAGLSANTPFYN LMLAVAMWFGRFAVIVPVLALAGSLAGKPRLAATAGTLPTHGPLFVVLLVLSVLLIGALTYIPA LALGPVIDHLQLFSR
7E-235	789.9	36.2	8E-235	789.7	25.1	1	1	U5RTG7_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CAETHG_1801	Clostridium autoethanogenum DSM 10061	557	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium autoethanogenum, Clostridium autoethanogenum DSM 10061	1341692	>tr|U5RTG7|U5RTG7_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium autoethanogenum DSM 10061 GN=kdpA PE=3 SV=1 MEILQIGIILVIFVLLCIPTGKYIYKVAEHEKTFLDPVLDKVDNFIYKISGITKEEMTWKQYIGALL LCNLVPAILAYIILRIQFMPVFNPNHIGGMEQGLTFNTVISFLTNTNLQGYSGESGLSYFSQMI VITFFMFLAASTGLSIALAFMRGLAGKKKTLGNFYVDYVRIITRILLPVCIVISIFYIQQGVPQTL SANKTITTIEGKLQDIPMGPVASLESVKLFGTNGGGFFGANSAHPFENPTPLTNAFEIISFLLF AGATVVCFGHMIKKKKQAICIFSAMSVLFIIGVVICYAAEKAGNPILGHLGLNQIMGNMEGKE VRFGIPMSALFTTATATSCGAVNMHDSLTPIGGLVALVNMMLNVIFGGKGVGFMNMIMY AILTVFLCGLMVGRTPEFLSKKIEGKEIKLIALAIIIHPFLILMVSALALVVPQGIAGISNPGFHGL TQILYQFSSSAANNGSGFEGLSDNTMFWNTTAGIVMFFGRYLSMIILLAVSTSLASKKAIPVT AGTFKTDNGVFTITLVFIVLIIGALTFFPALSLGPIAEQLTL
7E-235	789.8	24.6	8E-235	789.6	17.1	1	1	KDPA_ACIAC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Aave_0355	Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax citrulli (Acidovorax avenae subsp. citrulli), Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	397945	>sp|A1TJ24|KDPA_ACIAC Potassium-transporting ATPase potassium-binding subunit OS=Acidovorax citrulli (strain AAC00-1) GN=kdpA PE=3 SV=1 MTASAWGLLALFLSVLGLLAWPLGRGLAAVCDGRLPGWMHRAEAPLYRLAGVRPEAGMH WRHYALALLAFNALGVFAVYALQRLQGVLPLNPQGLPAVAGDSAFNTAVSFVSNTNWQGY AGESTMGYLVQMLGLSVQNFLSAATGIAVAFALARGFAARGGDGAGHVGNFWADIVRITA WVLVPLSFVLAVFLAGQGVIQNFTAYQDVATVEATVYQDPQSDAQGQPLKDASGNPLTRE VRTRTQTLPMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPLTNLAQMLAIFLVPAALC FAFGRVVGDWRQGVAILAAMTLMFVVAVVAVTAAEQAGNPALSALGADPVASALQAGGNM EGKEVRFGISASALFAAVTTAASCGAVNAMHDSFTPLGGMVPMVLMQLGEVVFGGAGSGL YGMLVFAILAVFIAGLMIGRTPEYLGKKIEVREMKLTSVAILVTPLLVLVGTAVAVLAPAGQAGI ANPGAHGFSEVLYALTSAANNNGSAFAGLSANTPFYNVLLALAMWFGRFGVIVPVLAIAGSL AAKKRLPPGPGTMPTHGPLFVALLVFTVLLVGLLNYVPSLALGPVVEHLVLQAR

7E-235	789.8	39.6	9E-235	789.5	27.5	1	1	V6F0K6_9PROT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MGMSRv2__1830	Magnetospirillum gryphiswaldense MSR-1 v2	566	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum gryphiswaldense, Magnetospirillum gryphiswaldense MSR-1, Magnetospirillum gryphiswaldense MSR-1 v2	1430440	>tr|V6F0K6|V6F0K6_9PROT Potassium-transporting ATPase potassium-binding subunit OS=Magnetospirillum gryphiswaldense MSR-1 v2 GN=kdpA PE=3 SV=1 MDSNGILQILIYILLIVAVTPLLGGFMARLFGGERVLLSPVLGPIERSLYKICGVNAAREQHWA AYALSLLMFNLAGVLVLYGLQRLQAHLPFNPAAMAAIAPDLAFNTAISFVTNTNWQAYGGET AMSYLVQMAGFTVQNFVSAATGIAVAVALIRGFARNGAKSIGNFYVDLTRAVLYLLLPLCVV GALVLVWQGVPQNLSTYVEATTLEGGAQVIAQGPVASQMMIKHLGTNGGGFFNANAAHPY ENPTALVNLLHMVAIFAIGAGLTNTFGRMVGDQRQGWAILGAMGVLFVIGVAMAYWAEAQA NPALVQAGAEAVGSLEGKEVRFGTALSALFAVITTAASCGAVNAMHDSLMPLAGMVPLVNM MLGEIVVGGVGAGFYGMMVFVILTVFIAGLMVGRTPEYLGKKIEAREVKLAIIAMLVFPLGVL GLGAVGLLAGSGSIPAGGPHGLSEVLYAYTSATANNGSAFGGFGANTLLHNVLLALAMWF GRFVVILALLAVAGSVAAKRTVPPSSGTFPTQGGLFVGLLVGVIVVVGGLTFFPVLALGPIVE HLLLGAGTLF
1E-234	789.3	24.2	1E-234	789	16.7	1	1	KDPA_PSEFS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PFLU_1676	Pseudomonas fluorescens (strain SBW25)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens (strain SBW25)	216595	>sp|Q3KRY6|KDPA_PSEFS Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas fluorescens (strain SBW25) GN=kdpA PE=3 SV=1 MHSYDYWLIIAFFAVVLVPAPFLGRFYYKVMEGQRTWLTPVLGPVERACYRLSGVDEQQE QSWQKYMLALLAFNLAGFLLLFAILLFQDYLPLNPQKLPGQEWTLAFNTAVSFMTNTNWQS YSGEASLSYLSQMAGLTVQNFVSAATGLAVLVALCRGIGRKSTKTLGNFWVDMTRATLYGL LPLCLVLALFLVWQGVPQTFAHYVDAVTMQGVDQVIPLGPAASQIAIKQLGTNGGGFFGVN SAHPFEDPTAWANLFELAAIILIPVALVFTFGHYYVKDLRQSRAILGCMLALFLIGGATSLWAEY QPNPTLNNPAVEQAAPLEGKEARFGTTGTVLWSVTTTAASNGSVNGMQDSLNPLSGMVAL VNMMVGEVIFGGVGAGMYGMLLNVLIAVFLAGLMIGRTPEYLGKKLQAKEVQLLVVTLLVM PVGVLVLGAIAASLPGPAGAISNPGPHGFSQLLYAYTSASANNGSAFGGFSANTPFHNLML GLGMLIGRFGYILPVLALAGSLAMKKTAPIGQNSFPTHGPLFVTLLTVTILLVGGLTFLPTLAL GPIAEHLSMGF
1E-234	789.2	26.3	1E-234	788.9	18.3	1	1	R5F2L1_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN723_02735	Clostridium bolteae CAG:59	583	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	1263064	>tr|R5F2L1|R5F2L1_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium bolteae CAG:59 GN=kdpA PE=3 SV=1 MMNVALQMIIYCVILVVLAIPLGSYMGKVMNGERVFLSRLLLPVENLIYRGLRIDKEEEMDWK KYSVCTAVFSVMSLAVLWAILCFQNLLPLNPQGMGKMSWHLGFNTASSFTTNTNWQAYSG ESSLSYFSQMIGLNFQNFVSAAVGIVVLFALIRGFVRVKERGLGNFYTDMTRTVLYILIPLSVV VSLAIASQGVPQTFKQYDEVQLVEPVVVEQEDGTAAEVTKGVVPLGPAASQIAIKQLGTNG GGFWGNNSAHPFENPTPLSNLFEMISLLLIPAGLCFTFGRNVKDKRQGVAVFLAMFIMLAAA LAIVGCSEQAGTPQIAQDGAVYMGTEGQAGGNMEGKETRFGIATSGTWAVFTTAASNGSV NSMHDSYTPFGGLVPMLLMQLGEVVFGGTGCGLYGMLGFAILTVFIAGLMVGRTPEYLCKK IEPFEMKMAVLVCLATPVAILVGSGIATLLPSTHDSLNNPGAHGLSEVLYAYSSAGGNNGSA FAGFNANTPFLNVSIGLIMLFVRFLPMFATLAIAGSLAAKKKVAVSSGTLPTHNAMFIFLLIFVV LLVGALSFFPALSLGPVAEFFQMIA
1E-234	788.8	24.7	2E-234	788.6	17.1	1	1	I4C4T4_DESTA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Desti_1867	Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	595	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfomonile, Desulfomonile tiedjei, Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	706587	>tr|I4C4T4|I4C4T4_DESTA Potassium-transporting ATPase potassium-binding subunit OS=Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1) GN=kdpA PE=3 SV=1 MEHLGYIQLALYIVILLALTKPMGLYLVQVLDINGRTFLHPVIGPLERLLYRILGIDSNTEQDWK QYTLSLLAFSLVGVLFTYCILRSQHILPLNPEGLQAVSDQLSFNTAVSFTTNTNWQNYGGES TMSYFSQMVGLVFHNFVSAAVGIAVAAALVRGIARHSAKTIGNFWVDLVRINLYLLLPVCLVY AVFLVSQGMIQNFKSYDTAQLIEPYTVTAKSSEGGESPDNSVPEQRKIETQRITQGPMASQ VAIKMLGTNGGGFTNANASHPFENPTPLSNFLQMLSIFLIPSGLTYYLGRIVKNQRHGWAV WAAMAIIFLAGVSVCWWAESAGNPRLHALGVDISSGNMEGKEVRFGIFNSALFATITTAASC GAVNSMHDSFTPLGGLIPLLNIELGEVVFGGVGAGLYGMLVFVVLAVFLAGLMIGRTPEYLG KKIESYDIKAAVLFVMAAVFGILGFTALASVSNWGLAGLNNAGPHGFSEMLYAFSSGTGNN GSAFAGLNGNTVPYNITLGLAMLVGRFFMIVPVLALAGHLAQKKIVPQSSGSFPVTGPIFVML LVGTVLIVGALTFFPALSLGPIVEHFLMTNSSVLF
2E-234	788.5	32.4	2E-234	788.3	22.5	1	1	V9W240_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ERIC2_c03120	Paenibacillus larvae subsp. larvae DSM 25430	559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus larvae, Paenibacillus larvae subsp. larvae, Paenibacillus larvae subsp. larvae DSM 25430	697284	>tr|V9W240|V9W240_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus larvae subsp. larvae DSM 25430 GN=kdpA PE=3 SV=1 MDFVQIAIVIVLLCLLVKPLGTYLYNVFSNEPNKTDRIYGPVERFLFKLGGIRPEASMSWKKY MLSILLTNAVLIGLGYLVLRLQNILPFNPNGIGRMEETLSFNTIISFMTNTNLQGYSGESGLSY FSQMIVIIMMMFTSAATGFSVAAAFIRGITGKGKGLGNFFQDFVKTHTRILLPFAFVITLILVAL HVPQTLEPTIKATTLEGAVQNISVGPVASLESIKHLGTNGGGFFGVNSSHPFENPNGITNVIEI LSMWWMFPAALTYTYGLFARNKRQGWVIFSAMLVLFLVFLGIEYAAESQGNPLLNNLGVSAE QGSPEGKEVRFGLAQSALFTTVTTSATTGTVNNMHDTLTPLGGMVPTVLMMLNSVFGGNG IGLVNMLMYAILAVFLAGLMIGRTPEFLVRKIEAKEMKLIAIVILLHPFIILVPTAIALVTDAGQAG ITNPGFHGITQVLYQYTSSAANNGSGFEGLADNTPFWDITTGIVMLLGRYISMIALLGVAGSL AAKHPVPETIGTFKTDNKLFMGLLIGTVLIIGALTFLPVLVLGPVAEYLTIR

2E-234	788.3	31.7	2E-234	788	22	1	1	A0A0F5LAB7_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VW29_17375	Devosia limi DSM 17137	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia limi, Devosia limi DSM 17137	1121477	[illegible] subunit OS=Devosia limi DSM 17137 GN=kdpA PE=3 SV=1 MTWQGWLQIAAVLLAVLVIIKPLGLYMARVFAGDRTPLSPVLAPVETGFYRLAGVDPRREQ GWFAYAIGVLAFSLAGFLLLYAMLRLQAYLPFNPQGFGALAPDLAFNTAASFVTNTNWQAY GGETTMSHFSQMAGLTVQNFVSGATGIAVAIAVTRAFARSGVKELGNFWVDLTRATLYVLL PMAIIVALAFVALGLPQTLDGAMAATTLEGASQTIALGPVASQEAIKQLGTNGGGFFNVNAA HPFENPNAFSNYLNIFSMLSISAALVYAFGQIVGSRRQAWALLSAMAILLVTGIGIVYWAETA GNPIHLALGVDPALGNMEGKEVRFGQAMTALYAGVTTGISNGGVNAMMSSLTPLGGLVPM FLMQLGEILPGGVGSGLYAMLVFSILAVFIAGLMVGRTPELLGKKIEAREIKLAMLAVLLLPTAI LGFSSVAAMLPAGLAGLASAGPHGLSEILYAYTSAAANNGSAFGGLSANSPWYNTTLGLAM LAGRFAYIVPVLAIAGALATKPRVAPSSGTFPTHGPLFVGLLIGIILILGGLQFFPALALGPILEH VLMLAGQTF
2E-234	788.1	26.8	3E-234	787.8	18.6	1	1	KDPA_PSESM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PSPTO_2242	Pseudomonas syringae pv. tomato (strain DC3000)	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas syringae group, Pseudomonas syringae group genomosp. 3, Pseudomonas syringae pv. tomato, Pseudomonas syringae pv. tomato (strain DC3000)	223283	[illegible] OS=Pseudomonas syringae pv. tomato (strain DC3000) GN=kdpA PE=3 SV=1 MHSYDYLLILAFLVLLLAPAPWLGRFFYRVMEGERTWLSPVLGPVERACYLISGVDPKTEQS WKQYAWALLAFNLAGFVVLFAMLMLQGLLPLNPQQLPGMEWSLAFNTAMSFVTNTNWQA YSGEASLSYLSQMVGLTVQNFVSAATGLAVLVALCRGISRRSSHSLGNFWADMTRATLYAL LPISIVLAVFLVWQGVPQNFAHYIDALTLQGADQSLPMGPAASQISIKQLGTNGGGFFGVNS AHPFENPTAWSNLFELVSILLIPAALVFTFGHYVKDMRQSRAILGCMLALLLIGGAVSLWAEY QPNPALNIAGVEQTAPLEGKETRFGTTGTVLWSVATTAASNGSVNGMHDSLNPLAGMVAL VNMMVGEVIFGGVGVGLNGMVLNVLIAVFLAGLMIGRTPEYLGKKLQAQEVRLLVATLLVMP VGVLVLGAIAASLPGPAGAISNPGPHGFSQLLYAYTSATANNGSAFGGFSANTVFHNLMLSL AIFIGRFGYILPVLALAGSLAMKKTAPQGQNSFPTHGLLFVTLLTVTILLVGGLTFLPTLALGPI AEHLSLGF
3E-234	787.9	29.7	3E-234	787.6	20.6	1	1	B4E5R1_BURCJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BCAL2383	Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) (Burkholderia cepacia (strain J2315))	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia cenocepacia, Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) (Burkholderia cepacia (strain J2315))	216591	>tr|B4E5R1|B4E5R1_BURCJ Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) GN=kdpA PE=3 SV=1 MNANNLLQTLLFIVVLLAAAVPVARYLSAVMDGSSRVVRVFGPLERALYRVAGVDAGTEMN WKQYAVATIAFNALGVLFLYGLLRLQGFLPGNPQQFGAMTPDGAFNTAVSFVANTNWQDY APEQTVSYLSQMLGLTVQNFLSAATGIVVVIALIRGFARHTAQTIGNFWVDLTRVTLYVLVPM AALVAALLMSQGVLQNMKAYQDVPVLQASTYAAPKLDAQGNPVKDDKGNAVTVPTLTKQ TLAMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPFANFIEIFAILIIPAALCLVFGRMIGD RRQGVAVLAAMTVAFTIAIGVEVSAEQAGNPTLAALHVDQSAGALQSGGNMEGKETRFGIA QTGIFTVATTAASCGAVDAMHDSLTPVGGLVPMLLMQLGEVVYGGVGSGLYGMLVFALLA VFVAGLMIGRTPEYVGKKIESYEMKMVSIVVLLTPLLVLVGTSIAVLADAGKAGIANPGPHGF SEILYAFSSAANNNGSAFAGLTVSTPFYNWMTAIAMWFGRFGTIVPVLAIAGSLAAKKRIAVT SGTLPTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLMMWLGA
3E-234	787.8	30.1	3E-234	787.6	20.9	1	1	KDPA_GEOMG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Gmet_2433	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	586	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter metallireducens, Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	269799	>sp|Q39SW6|KDPA_GEOMG Potassium-transporting ATPase potassium-binding subunit OS=Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) GN=kdpA PE=3 SV=1 MTQYEWLQTTLFLVLLLAVVKPMGAFMAKVFQGERTMLSPLLVPCENLLYRICGVNRDEEM DWKRYAVAVLLFNLALFVSLFAILMLQHLLPLNPQKFPAYTWQLALNTAISFVTNTNWQAYS GESAASYFTQTVGLAVHNFVSAATGIAVAIAVIRGFARRRTSMLGNFWVDMTRCTLYVLLPI SLIGALILVSQGVIQNFSDYKTVPLVQPITYDKPKADGKGNPVTGRVTVKDITIPMGPVASQE AIKELGTNGGGFFNANSAHPYENPTPISNMVEIFLILLIPFALTSTFGVMVGNTRQGWAILGV MLLMMAISFAVLQGVETSGNPLVAKLGVHGVNMEGKEVRFGLAGASLFTVATTGTSCGAV ATMHDSLTPLGGMIPLGLILLGEIAPGGVGSGLYTMLAFVVIAVFVAGLMIGRTPEFLGKKIEV REMWMSIITVLAAGVVVLILSGVAMITPQAVASKANPGAHGLSEVLYAFASMANNNGSAFA GLNANVDFYTILGSLAMLVGRFAPAVAVLAMAGSLAEKKYVPPSLGTLPTDKVPFALWLMLV ILIVGALTFFPALSLGPLVEHLTMLGGK
3E-234	787.6	28.5	4E-234	787.4	19.8	1	1	K9QN51_NOSS7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Nos7524_0589	Nostoc sp. (strain ATCC 29411 / PCC 7524)	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain ATCC 29411 / PCC 7524)	28072	>tr|K9QN51|K9QN51_NOSS7 Potassium-transporting ATPase potassium-binding subunit OS=Nostoc sp. (strain ATCC 29411 / PCC 7524) GN=kdpA PE=3 SV=1 MLQGWIQIALTLLIVIATTPLLGKYIFRVFMGEKTLLDAVINPLERVIYAFSGIRYQEEMTGWQ YAKAVLYSNLIMVILVYFILMVQGWLPLNPTNLNAPSWDLALHTTISFVTNTNQQHYSGETTF SYASQVFALGFLMFTSAATGLAVGIAFIRGLTGRPLGNFYTDLIRSITRILLPISIIGGLLLILAGV PETLASPATATTLEGATQVIARGPVAHFEIIKQLGENGGGFFGINSAHPYENPNGFSNLLEM WAMISIPAALIYAYGMFANNRKQAWLVFWMVFVIFVFLVGVAAVGEFQGNPLVNSLLGEQE PNLEGKEVRFGWAQTALWAVMTTATMCGAVNGMHDSLMPPGGFATLFNMFLQIIWGGQ GTGTAYLFIYLILAVFLTGLMVGRTPEFLGRKIEKKEIVLASVILLVHPFAILIPWAIVFGFPDTL SGITNPGFHGVSQVVYEYASAAANNGSGFEGLNDNTLWWNLSTSISILAGRYIPITALLLLAD SMSRKQLVPTTTGTLRTDTRLFTGVTGGVILILGALTFFPVLVLGPIAEAFLIARVG

4E-234	787.5	24	4E-234	787.3	16.6	1	1	KDPA_MYCTU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Rv1029 MTCY10G2.20c	Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)	571	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex, Mycobacterium tuberculosis, Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)	83332	>sp|P9WKF3|KDPA_MYCTU Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) GN=kdpA PE=1 SV=1 MSGTSWLQFAALIAVLLLTAPALGGYLAKIYGDEAKKPGDRVFGPIERVIYQVCRVDPGSEQ RWSTYALSVLAFSVMSFLLLYGIARFQGVLPFNPTDKPAVTDHVAFNAAVSFMTNTNWQSY SGEATMSHFTQMTGLAVQNFVSASAGMCVLAALIRGLARKRASTLGNFWVDLARTVLRIMF PLSFVVAILLVSQGVIQNLHGFIVANTLEGAPQLIPGGPVASQVAIKQLGTNGGGFFNVNSAH PFENYTPIGNFVENWAILIIPFALCFAFGKMVHDRRQGWAVLAIMGIIWIGMSVAAMSFEAK GNPRLDALGVTQQTTVDQSGGNLEGKEVRFGVGASGLWAASTTGTSNGSVNSMHDSYTP LGGMVPLAHMMLGEVSPGGTGVGLNGLLVMAILAVFIAGLMVGRTPEYLGKKIQATEMKLV TLYILAMPIALLSFAAASVLISSALASRNNPGPHGLSEILYAYTSGANNNGSAFAGLTASTWS YDTTIGVAMLIGRFFLIIPVLAIAGSLARKGTTPVTAATFPTHKPLFVGLVIGVVLIVGGLTFFPA LALGPIVEQLSTQ
6E-234	786.8	34	7E-234	786.5	23.6	1	1	KDPA_ECOLI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA b0698 JW0686	Escherichia coli (strain K12)	557	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli (strain K12)	83333	>sp|P03959|KDPA_ECOLI Potassium-transporting ATPase potassium-binding subunit OS=Escherichia coli (strain K12) GN=kdpA PE=1 SV=1 MAAQGFLLIATFLLVLMVLARPLGSGLARLINDIPLPGTTGVERVLFRALGVSDREMNWKQY LCAILGLNMLGLAVLFFMLLGQHYLPLNPQQLPGLSWDLALNTAVSFVTNTNWQSYSGETT LSYFSQMAGLTVQNFLSAASGIAVIFALIRAFTRQSMSTLGNAWVDLLRITLWVLVPVALLIAL FFIQQGALQNFLPYQAVNTVEGAQQLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENP TALTNFVQMLAIFLIPTALCFAFGEVMGDRRQGRMLLWAMSVIFVICVGVVMWAEVQGNPH LLALGTDSSINMEGKESRFGVLVSSLFAVVTTAASCGAVIAMHDSFTALGGMVPMWLMQIG EVVFGGVGSGLYGMMLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKLTALAILVTPTLVLMGA ALAMMTDAGRSAMLNPGPHGFSEVLYAVSSAANNNGSAFAGLSANSPFWNCLLAFCMFV GRFGVIIPVMAIAGSLVSKKSQAASSGTLPTHGPLFVGLLIGTVLLVGALTFIPALALGPVAEY LS
6E-234	786.7	31.1	7E-234	786.5	21.5	1	1	D5AKZ2_RHOCB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RCAP_rcc02252	Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter capsulatus (Rhodopseudomonas capsulata), Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)	272942	>tr|D5AKZ2|D5AKZ2_RHOCB Potassium-transporting ATPase potassium-binding subunit OS=Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003) GN=kdpA PE=3 SV=1 MTVFGWLQIAAVLLFTLATAVPLGRYMARLFSGERTFLHPLLHPVERGFYRLAGVTPEREQ GWLGYALAMLAFSAAGFAALYLILRAQGLMPFNPGQLPGLPADLAFNTAVSFLTNTNWQAY AGETTMSPFSQMAGLAVQNFLSAATGIALAMAVTRAFARAGTDRLGNFWADMTRATLYVL LPLSILVALALVALGVPQTLTGSVAAVTLEGAQQTIALGPVASQEAIKQLGTNGGGFFNANSA HPLENPSALSNGLVIWAMLAISAALPITFGRMTGSERQGWAILAAMGLLLIAATTTVYWAET AGTPHLAALGLDPLAGNMEGKEVRFGQAMSALFVAVTTGLSCGAVNAMHDSLTPMGGLVP MLLMQLGEVLPGGVGSGLYGMVVFCVLSVFVAGLMVGRSPAFLGKKIEAREIRLAVLAVLIL PLVILGFTSAAALLPSALASLNNAGPHGLSELLYAYSSAAGNNGSAFAGLNANTPWFNTTLG IAMMLGRFAYVLPVLAMAGALAAKPRLAASAGTFPTTSPLFVGLLVGVIVILGGLQFFPALAL GPIVEQVLMRDLVTF
8E-234	786.4	27.9	9E-234	786.2	19.4	1	1	A0A0C5L0M7_9SPHN	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TS85_00360	Sphingomonas sp. WHSC-8	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. WHSC-8	1609977	>tr|A0A0C5L0M7_9SPHN Potassium-transporting ATPase potassium-binding subunit OS=Sphingomonas sp. WHSC-8 GN=kdpA PE=3 SV=1 MTFAGWAMIAMFVAILVALARPVGGWLFALYEGRTTPLHRVLGPVERGFYRLAGIDPTAEQ GWRRYAVHLLVFQLALLLFTYAVLRLQGVLPMNPRGLAGLGADGAMNVAISFTTNTNWQW YSGEVALSNFSQMFGLVIHNFLSAATGIAVAFALFRGFARRQASGVGNFWADVTRVTLYLLL PVSIVYALYLIWSGVPQTFAWSADATTLEGARQTIALGPVASQEAIKMLGTNGGGFFNANSA HPFENPNAITNFVQMLSIFVLGVGLTNTFGRAVGNPRQGWAILSAMLVLFVAGVAVTYWQE AAGNPVLHHLGVAGGNMEGKEVRFGIAGSALFSVVTTAASCGAVNAMHDSFTALGGMIPLF NMQLGEVVVGGVGAGIYGFLLFAILAVFVAGLMVGRTPEYVGKKIEAREVKLAVLAIAALPLC ILGFTALASVLPQGLAGPLNKGPHGFTEILYAFSSAAANNGSAFAGISSGTPFYNGLLAVAM WIGRFFIIVPVLAVAGSLAAKTTHPESAGSFPTTGPLWIGLLVGIILIVGGLTFLPGLALGPIAD HVAMVRGQLF
8E-234	786.3	31.9	1E-233	786.1	22.1	1	1	R6RWK3_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN719_02212	Clostridium sp. CAG:58	587	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	1262824	>tr|R6RWK3|R6RWK3_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium sp. CAG:58 GN=kdpA PE=3 SV=1 MLQIMLTLTAFMVLVIPMGHYLYHIAVGQKTFADPVFDPVDRLIYKLCGLKGEDMGWKKYGL SLLMANAVMVLIGYAVLRLQGILFFNPNGIGAMEESLSFNTIISFMTNTNLQHYSGESGLSYG SQMGVIIFMMFTSAASGYAACMAFCRGLAGRQLGNFYTDMVRITTRVLVPAAFLVGLFLVS QGTPQTMIGNLTVKTVEGSYQDIALGPVAALESIKHLGTNGGGFFGANSATPFENPTVLSN MAEMLSMMLLPGACVVTFGLMLHDRKQAAGRETVRREREEQLAGSATDRKKCRAMIGGQ GAAVFGAMTVIFLVGLSICFFSERAGNPVIAQMGIDQSAGSMEGKEVRFGIPQSSLFTTVTT SFTTGTVNNMHDTLTPLGGMVPMLHMMLNCVFGGKGVGLMNMVMYVILAVFICGLMVGRT PEYLNKKIEGKEMKLVAMVLLIHPLLILGFSALAVSMQAGLDGITNPGFHGLSQVLYEYSSSA ANNGSGFEGLADNSLFWNMTTGLAMFFGRYLAIIAQLAIAGSLLGKRRINESAGTLRTDTVT FMVVLIFIVYIFAALTFFPALALGPIAEHLSLWL

8E-234	786.3	34.2	1E-233	786.1	23.7	1	1	D3UX96_XENBS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA XBJ1_1067	Xenorhabdus bovienii (strain SS-2004)	568	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus bovienii, Xenorhabdus bovienii (strain SS-2004)	406818	>tr|D3UX96|D3UX96_XENBS Potassium-transporting ATPase potassium-binding subunit OS=Xenorhabdus bovienii (strain SS-2004) GN=kdpA PE=3 SV=1 MVASAFLLITSFLVILFILSRPLGSLIANLVEGELPRWLTNAETSLWRCCGLQKPGGNVKEMN WWQYALAIITFNIMGLLLLFMLLISQEHLPLNPQHFAGMKWDLALNTAISFITNTNWQAYSGE NTLSYLSQMAGLTVQNFLSAATGIAVAFALMRAFSRQGVKTLGNAWIDITRITLYLLLPLSIIIA LIFVSQGVIQNFSPYVLVHTLEGQQQLIPMGPVASQEAIKLLGTNGGGFFGANSAHPFENPN ALSNFVQILTIFLIPCALCFAFGLVVGDNRQGHALLWAMTIVFIIAVTIVIYAEIMGNPHFIQAGA SSNLNMEGKESRFGILASSLYSVVTTAASCGAVNAMHDSFTALGGMIPLWLMQIGEVIFGG VGSGLYGMLLFVLLAVFIAGLMIGRAPEYLGKKIDVHDMKMVALAILVTPSLVLLGTALATSID AGRAAIMNPSAHGFTEVLYALSSAANNNGSAFAGLNANSVFYNLLLGAIMFLGRFGVIFPVL AIAGSMISKKRQPISSGTLPTHGSLFTGLLILVVLLMGALTFIPALALGPVAEHLQLWQAPR
8E-234	786.3	30.3	1E-233	786	21	1	1	A0A0D5EGF9_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BW23_2574	Burkholderia ubonensis MSMB22	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	1249668	>tr|A0A0D5EGF9|A0A0D5EGF9_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia ubonensis MSMB22 GN=kdpA PE=3 SV=1 MNANTIFQSVLFIVVLLAAAVPVARYLSAVMDGSSRVVRVFGPLERALYRIAGVDAGSEMN WKQYAIATIAFNALGALFLYGLLRLQGLLPGNPQQFGPMTVDGAFNTAVSFVTNTNWQDYT PEQTVSYLTQMLGLTVQNFLSAATGIVVVIALIRGFARHTAQTIGNFWVDLTRVTLYVLVPMA ALVAALLMSQGVIQNMKAYQDVPALQASTYAAPKLDAQGNPVKDDKGNPVTVATPLTKQTL AMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPFANFVQIFAILIIPAALCLVFGRMIGDR RQGIAVLAAMTVAFTVAVGVEVSAEQAGNPALAALHVDQSAGALQAGGNMEGKETRFGIA QTGIFTVATTAASCGAVDTMHDSLTPLGGLVPMLLMQLGEVVYGGVGSGLYGMLVFALLAV FVAGLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPLLVLVGTSIAVLADAGKAGILNPGPHGFS EILYAFSSAANNNGSAFAGLTVGTPFYNWMTAIAMWFGRFGTIVPVLAIAGSLAAKKRIATTS GTLPTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLMMWLGA
9E-234	786.2	34.8	1E-233	786	24.1	1	1	KDPA_ECO57	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Z0845 ECs0726	Escherichia coli O157:H7	557	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli O157:H7	83334	>sp|Q8X3F0|KDPA_ECO57 Potassium-transporting ATPase potassium-binding subunit OS=Escherichia coli O157:H7 GN=kdpA PE=3 SV=1 MAAQGFLLIATFLLVLMVLARPLGSGLAWLINDIPLPGTTGVERVLFSALGVSNHEMNWKQY LCAILGLNMLGLAVLFFMLLGQHYLPLNPQQLPGLSWDLALNTAVSFVTNTNWQSYSGETT LSYFSQMAGLTVQNFLSAASGIAVIFALIRAFTRQSMSTLGNAWVDLLRITLWVLVPVALVIAL FFIQQGALQNFLPYQAVNTVEGAQQLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENP TALTNFVQMLAIFLIPTALCFAFGEVTGDRRQGRMLLWAMSVIFVICVGVVMWAEVQGNPH LLALGADSSINMEGKESRFGVLVSSLFAVVTTAASCGAVIAMHDSFTALGGMVPMWLMQIG EVVFGGVGSGLYGMMLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKLTALAILVTPTLVLMGA ALAMMTDAGRSAMLNPGPHGFSEVLYAVSSAANNNGSAFAGLSANSPFWNCLLAFCMFV GRFGVIIPVMAIAGSLVSKKSQPASSGTLPTHGPLFVGLLIGTVLLVGALTFIPALALGPVAEY LS
1E-233	786.1	32.5	1E-233	785.9	22.5	1	1	K8WCL9_PRORE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OOC_07108	Providencia rettgeri Dmel1	567	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia rettgeri, Providencia rettgeri Dmel1	1141663	>tr|K8WCL9|K8WCL9_PRORE Potassium-transporting ATPase potassium-binding subunit OS=Providencia rettgeri Dmel1 GN=kdpA PE=3 SV=1 MTTTTLLFLGSFLLFLFILAKPLGNAIARLIDNDIPHRLASSESLLWRLTGVKQPGRDMAEMN WKQYALAIVLFNLLGFILLFVILICQGRLPLNPQHFEGMSWDLAFNTAVSFITNTNWQAYSGE NTLSYLSQMAGLTVQNFLSAATGIAVAFAIIRAFSHHGSKTVGNAWLDIYRITVYLLFPLAIIFA LFFVSQGVIQNYSSYLLIHPLDNSEQLLPMGPVASQEAIKLLGTNGGGFFGANSSHPFENPT ALSNFVQMFAIFLIPTALCFAFGRAVGNNKQGHTLLWVMGIVFVVAAIVVVKAEYVGNPFLT DLHATSTANMEGKESRFGIVGSALFAVVTTAASCGAVNAMHDSFTAMGGMVPMWLMQIG EVVFGGVGSGLYGMLLFVLLAVFLAGLMIGRTPEYLGKKIEVREMKMVALAILVTPTLVLLGT TLSLITEAGRAGILNPGAHGFSEVLYAFSSAANNNGSAFAGLSANTPFYNVLLAITMFIGRFG VILPVLAIAGSMANKKPQAKSHATLPTTGPLFIGLLVFTVLLIGALTFVPALALGPIAEQLHIGFA G
1E-233	786	33.3	1E-233	785.8	23.1	1	1	A0A089LT39_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PSTEL_14230	Paenibacillus stellifer	555	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus stellifer	169760	>tr|A0A089LT39|A0A089LT39_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus stellifer GN=kdpA PE=3 SV=1 MSYLAIAVTLLIAFLLARPAGLYMAKVFDYEATGLDRWFGWIEKPLYKIGGIRQENQTWKQY AIALVLSNTVMILLVYLIFRLQGVLPLNPSGIQSMEPTLAFNTAISFMTNTNLQHYSGESGLSY LSQMIAIVFMMFAAPASALAGAIAFIRGLSGKPLGNFFADMIRCITRILLPISFVLALVFVAMGV PQTLHGTAMATTLEGAAQEIARGPVASFLSIKELGNNGGGFFGVNSAHPFENPSGLSNFIQII LMLLLPASLPFTYGKMVGNKKQGRVLFVSMIVMLIVLLSTSLASENAGNPVINAMGVQHNQG SMEGKEVRFGVAESALYSVVTTASETGAVNTMHDSLTPLGGLVTLGNMMLNTVFGGVGAG FINVLMYAMIAVFLSGLMVGRTPEFLGKKIEGKEMKLIAVTLIINPLLILLPTALALYAHPDTISN PGYHGLSQALYEYTSAAANNGSGFEGLGDANPFWNISTGIVMFLGRYFSVITMLAVAGSLA SKKSVPETAGTFRTDNALFGTVFIGAVLIVGALTFFPAVALGPIAEYLTLKP

1E-233	785.8	25.1	1E-233	785.6	17.4	1	1	R5W702_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN505_00149	Alistipes sp. CAG:157	565	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes sp. CAG:157	1262692	>tr|R5W702|R5W702_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Alistipes sp. CAG:157 GN=kdpA PE=3 SV=1 MNTEILGVILQWVCLVVLCYPLGRHIAKVYKGEKNIMDFMAPVERFIYKVCGIDPEREMNWK QFLKALLTVNLFWFIWGMVLLVCQGWMPLNPDGNPGQTPDQAFNTCISFMVNCNLQHYS GETGLSYFTQLFVIMLFQFITAACGMAALAGIFKGMAAKTTKSIGNFWVYLTRSVTRILMPLS LLVGILLVINGTPMSFDGKQTLTTLEGATQEISQGPTAAIVPIKQLGTNGGGYFGVNSSHPLE NPNAFTNMLECWSILIIPMAMVFALGFYLKRRKLAACIFTVMLAAYTCGIVISVWQEMAGSP QIDEMGIAQDLGSMEGKEIRIGSAASAMWGMTTTVTSNGSVNSMHDSQTPLSGMLQMLNM QINCWFGGVGVGFMNYYAFLIIAVFISGLMVGRTPEFLGKKVEAREMKIATMVVLMHPFLILV GTGLASWLAARNPELASSWLNNPSFHGLSEMLYEYTSSAANNGSGFEGLSDNTPFWNITT GIVLIMGRYFPIVGQVAIAGLLAGKKFVPESAGTLKTDTATFSVMTFAVIIIVAALSFFPALALG PIADYLTF
1E-233	785.6	35.6	2E-233	785.4	24.7	1	1	A0A090UA85_9ENTR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CIFAM_08_00530	Citrobacter farmeri GTC 1319	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter farmeri, Citrobacter farmeri GTC 1319	1114922	>tr|A0A090UA85|A0A090UA85_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Citrobacter farmeri GTC 1319 GN=kdpA PE=3 SV=1 MAAQGFLLIASFLVILFVLARPLGAGLALLIGNNSLPGTAGIERLIWRGLGISSHEMNWKQYLL AILGLNVLGLVILFLMLMGQHLLPLNPQQLPGLSWHLALNTAVSFVANTNWQSYSGETTLSY FSQMAGLTVQNFLSAATGIAVVFALIRAFTRQSMSTLGNAWVDLVRITLWILFPIALVIALFFI QQGSLQNLLPYQPFTTLEGVRQLLPMGPVASQEAIKMLGTNGGGFFNANSAHPFENPTALT NMVQMLAIFLLPAALCFAFGDAAGDRRQGRMLLWAMSLIFIVCVAVVMWAEIQGNPHLLQF GADASLNMEGKESRFGVLVSSLFAVVTTAASCGAVIAMHDSMTALGGMVPMWLMQIGEVV FGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPALVLLGTALA MMTDAGRSAMLNPGPHGFSEVLYAVSSAANNNGSAFAGLSANTPFWNCLLAFCMFVGRF GVIIPVMAIAGSLVAKKSQPASPGTLATHGALFIGLLIGTVLLVGALTFIPALALGPVAEHLSLR
1E-233	785.5	32.6	2E-233	785.3	22.6	1	1	K9X7N8_9CHRO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Glo7428_0027	Gloeocapsa sp. PCC 7428	561	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	1173026	>tr|K9X7N8|K9X7N8_9CHRO Potassium-transporting ATPase potassium-binding subunit OS=Gloeocapsa sp. PCC 7428 GN=kdpA PE=3 SV=1 MLQGFFQIALTLVILVAITPIFGKYMARVFLEKSVLLNRVINPIERTIFAINGTRYKDNMTGRQYI QAVIISNLVMSIFVFSILMLQGVLPLNPTGLNPPSWDLALHTTISFITNTNQQHYSGETTYSYA SQMLALAFLMFTSAATGLAVGIAFIRGLTGRPIGNFYVDLTLAITRLLPISLIGALILLIAGVPET LASPATVTTLEGATQTIARGPVAHFEIIKQLGENGGGFFGINSAHPFENPNTFTNLLATIAMLS IPMALIFTYGVFANNMKQAWLLFWMVFIIFFILICITAIGEYQGNPLVNNAIFGGEQPNLEGKE VRFGWAQTALWAVSTTATMCGAVNGMHDSLMPNGGFSTLFNMFLQIVWGGQGTGTAYL FIYLILTVFITGLMVGRTPEFLGRKIEKREIVLASVVLLVHPIFVLIPSAIALSFPGTLAGISNPGF HGLSQVVYEYTSASANNGSGFEGLGDNTLWWNLSTSISLLGGRYIPIIALLLLADSMTRKQP VPETAGTLRTDTVLFTSVTAGVILILGVLTFFPVLALGPIAEGFQLLRN
2E-233	785.4	33.5	2E-233	785.2	23.2	1	1	KDPA_DEIRA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DR_B0086	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	568	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus radiodurans, Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	243230	>sp|Q9RZN7|KDPA_DEIRA Potassium-transporting ATPase potassium-binding subunit OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) GN=kdpA PE=3 SV=1 MSASLLQFVVLLGVMAALVVPVGNWLYGVATGQKDTALERLTYRVIGINPRERMDWKRYG LAIVVSNLVMLLLAYLLIRLQGALPWNPAGLAAQSPDLAWNTVVSFMTNTNWQAYSGEQSL SYFSQMAVITTFMFTSAATGFAAALAFMRGLAGRDGTNLGNFWVDVTRLIYRVLLPVCFGL ALVFVWQGMPQTLGAYANATTLEGAAQRIALGPVASLESIKHVGTNGGGFFSMNAAHPFE NPTPLTNALHILSMLLLPSALTYVFGRMLGNLKQGWVIFGGMLVMFVGFLGTVYSFEQAGN PILSKLGAEQAITATQAGGNMEGKEVRFGIAQTSLFATTTTAATTGSVDSMHDSYTGMGGF VPMLQMMLNNVFGGKGVGFINFVQYLVLGVFIAGLMVGRTPEFLGKKIEAKEVKLTMLAVLA HPLSILGFTALACVLPGALNSLNNPGPHGFSEILYAYTSGTANNGSAFAGLSANTFFYNLTIG LSMLMGRYLTLLPMLAVAGMLAAKRRVPAGSGTLPTDTALFGALTVFVILIVGALTFLPALTL GPVADHLQMLRGVVLK
2E-233	785.2	26	2E-233	785	18	1	1	B1WPS5_CYAA5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA cce_3892	Cyanothece sp. (strain ATCC 51142)	559	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain ATCC 51142)	43989	>tr|B1WPS5|B1WPS5_CYAA5 Potassium-transporting ATPase potassium-binding subunit OS=Cyanothece sp. (strain ATCC 51142) GN=kdpA PE=3 SV=1 MIQGLIQIGFTLLILIIIVPIFGNYMAKVYLREKTILDSLLSPIEKLIYALSGVRSQREMTGWQYA KNVIFSNLVMGIFVFLIFSFQAILPLNPTELAAPTWDLALHTAISFITNTNQQHYSGETTYSYAS QMLALGFLMFTSAGTGLAVAIAFIRGLTGRSLGNFYVDLTRSITRILLPISLISAIILLSQGVPET LAPPVSLTTLDGATQIIARGPVAHFESIKELGENGGGFFGINSSHPFENPNGLTNLIETLLMLS IPTSLIYTYGVIMGNKKQAWLLFWMVFIIYIFLVGITAIGEYQGNPLINNLLNTSQPNLEGKEIR FGWAQTALWAISTTGTMCGAVNGMHDSLMPLGGFSTLFNLFLQIIWGGQGTGTAYLFIFLIL TVFLTGLMVGRSPEFLGRKIEKREIVLASVILLVHPFAILIPGAITLAFPEILSGISNSGFHGISQ VIYEYASAAANNGSGFEGLGDNTLWWNLTTSVALLFGRYIPIIALLLLAESMRQKQPVPETR GTLRTDTGLFTGVTAGVILILGALTFLPVLASGPIAEALKLAS

2E-233	785	21.9	2E-233	784.8	15.2	1	1	A0A077LPP9_9PSED	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PSCI_3956	Pseudomonas sp. StFLB209	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. StFLB209	1028989	>tr|A0A077LPP9|A0A077LPP9_9PSED Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas sp. StFLB209 GN=kdpA PE=3 SV=1 MHSYDYLLIGAFVLLLLGSAPLLGRFWYRVMEGERTWLSPLLGPLERGCYRLGGVDPKAG QDWKTYALALLAFNAAGFVLLFALLMLQGALPLNPQQLPGLEWTLAFNTAMSFVANTNWQ AYSGEASLSYLSQMLGLTVQNFVSAATGIAVLAVLCRGIARRSTNDLGNFWTDLTRATLYGL LPISLLLALLLVWQGVPQNFAHYVDALTVQGSQQSLPMGPAASQIAIKQLGTNGGGFFGVN SAHPFENPTALSNLLELVAILLIPAALVFSFGHYVKDLRQSRAILACMLLLLAIGSALALWAEY QPNPTLALSGVEQAPSLEGKEARFGVTGTTLWAVATTAASNGSVNGMHDSLNPLTGMVAL INMMVGEVIFGGVGVGLNGMLLNVLIAVFLAGLMIGRTPEYLGKKLQAREVKLLVASLLVMPL GVLVLGAIAASVPGAASAVSNPGPHGFSQLLYAYTSATANNGSAFGGFSANTPFHNLMLSL AMFIGRFGYILPVLALAGSLALKQSAPQGSDSFPTHGPLFVALLTVTILLVGGLTFLPTLALGP LADHMSLGF
2E-233	784.9	30.9	3E-233	784.6	21.4	1	1	G2IMJ2_9SPHN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SLG_31060	Sphingobium sp. SYK-6	567	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingobium, Sphingobium sp. SYK-6	627192	>tr|G2IMJ2|G2IMJ2_9SPHN Potassium-transporting ATPase potassium-binding subunit OS=Sphingobium sp. SYK-6 GN=kdpA PE=3 SV=1 MTVQGWILILVFTALIVAIAKPMGLWLFALYEGRRTPLHMVFGPIERGFYALARIDPQAEQS WRRYALHMLLFQLVALLFTYAVLRLQGVLPMNPRGLAGIGADGAFNTAISFTTNTNWQWYS GEVALSNLSQMLGLALHNFLSAATGIAIAFALFRGFARRQSATIGNFWADMTRVTLYLLLPICI VYALFLIASGVPQTFASILDATTLEGATQHIVVGPVASQEAIKMLGTNGGGFFNANSAHPFEN PTALTNLVQMLSIFSIGVGLTWCFGKAVGNTRQGWAILAAMMALFLAGVGIVYWQEAVGNP VLHQLGLAGGNLEGKEVRFGIAASALFAVITTAASCGAVNAMHDSFTALGGMIPMFNIQLGEI VVGGVGAGIYGFLLFALLAVFVAGLMVGRTPEYVGKKIEGREVKLAVLAIAVLPLCILGFTALS AVMPQGLAGPLNKGPHGFSEILYAFSSATGNNGSAFAGITSGTPWYNGLLGMAMWIGRFF VIVPVLAIAGSLAAKKYTPETAGSFPTTGALWVGLLLTIILIVGGLTFLPSLALGPIADHLAMVR GQLF
3E-233	784.7	28.4	3E-233	784.5	19.7	1	1	K9U1Y8_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Chro_3173	Chroococcidiopsis thermalis PCC 7203	559	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Chroococcidiopsis, Chroococcidiopsis thermalis, Chroococcidiopsis thermalis PCC 7203	251229	>tr|K9U1Y8|K9U1Y8_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Chroococcidiopsis thermalis PCC 7203 GN=kdpA PE=3 SV=1 MWQGFLQIAITLIILVAITPSFSSYIASVFLEKKTFLDPVAKPIERVIYALGGIPTKSDMTGWQY AQAILYSNIVMGIFVYLIFMLQGILPLNPTNLQAPSWDLALHTTISFVTNTNQQHYSGETTFSY ASQMLALGFLMFTSAATGLSVGIAFIRGLTGRPLGNFYVDLVRSITRILLPISIIGAIALLMAGVP ETLAAPATVTTLEGTTQVIARGPVAHFEIIKQLGENGGGFFGINSAHPFENPNAFTNLVEILA MVSIPAALIITYGIFANNKKQGWLLFWMVFIIFVTLVVVTGVGEYQGNPLVNNLIGDSPNLEG KEVRFGWAETALWAVLTTGTMCGAVNGMHDSLMPNGGFSTLFNMFVQMVWGGQGTGT AYLFVYLILTVFLTGLMVGRTPEFLGRKIEKREIVLASVILLVHPIAILIPSAITLAFPDTLAGISNP GFHGISQVVYEYTSASANNGSGFEGLGDATLWWNLSACFSLLAGRYLPITALLLLADSMTR KQPVPETAGTLRTDTLLFTGVTAGVILILGVLTFFPVLALGPIAEGFQIGNW
3E-233	784.4	28.4	4E-233	784.2	19.7	1	1	A0A068R419_9ENTR	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA XPG1_2371	Xenorhabdus poinarii	565	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus poinarii	40577	>tr|A0A068R419|A0A068R419_9ENTR Potassium-transporting ATPase A chain OS=Xenorhabdus poinarii GN=kdpA PE=3 SV=1 MAASAFLLIASFLFILFLLSKPLSKLIARLVTGELPYWLTKAERILWRSCGQQKPGHDVREMN WWQYALAIFSFNLAGLLFLFILLISQGYLPLNPQHFAGMKWDLALNTAISFITNTNWQAYGG ENTLSYLSQMAGLTVQNFLSAATGIAVAFALMRAFSRQSAATVGNAWIDISRITLYLLLPLAII VALFFVSQGVIQNLSPYVLTHSLEGQPQWIPMGPVASQEAIKLLGTNGGGFFGANSAHPFE NPTSLSNFVQVLAIFLIPSALCFAFGQVVGDRRQGYALLGAISLVFIVAVSVVISAESAGNPHL LQSGISHPFNMEGKEARFGILGSALYGVVTTAASCGAVNAMHDSFTPLGGMIPLWLMQIGE VIFGGVGSGLYGILLFVLLAVFIAGLMIGRTPEYLGKKIDVYDMKMVALAILVTPSLVLLGTALA ISTDAGRSAMTNPGAHGFTEVLYAFSSTANNGSAFAGLNANTMFYNLLLGITMLLGRFGVI LPVLAIAGSMVNKKRQPLSSGTLPTHSVLFIGLFILVILLIGALTFIPALALGPIAEHLQLWL
4E-233	784.2	33.6	4E-233	783.9	23.3	1	1	KDPA_PECAS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ECA1342	Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	562	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pectobacterium, Pectobacterium atrosepticum (Erwinia carotovora subsp. atroseptica), Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	218491	>sp|Q6D7I3|KDPA_PECAS Potassium-transporting ATPase potassium-binding subunit OS=Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) GN=kdpA PE=3 SV=1 MAADAFLLIFGLLLTVLIVAQPLGSGLARLIEGETGTLLQKFETKTARFFALDTTEMRWQQYA AAILALNLIGIVVLFVLLMAQGNLPLNPENMPGLSWHLALNTAVSFVTNTNWQAYSGENTLS YLSQMVGLTVQNFLSAASGIAVAFALIRAFSRRCVDTLGNAWLDLLRITLYVLLPLSLLLALFF VSQGVLQNLLPYQHLTTLDGAAQTLPMGPVASQEAIKLLGTNGGGFFGANSAHPFENPTAL SNIVQMLAILLIPTALCFAFGKAVSDKRQGHALLWAMALIFIVAAAVVMKMEVTGNPHLLALG ADSAANLEGKETRFGVLTSSLYAVVTTATSTGAVNAMHDSFTALGGMVPLWLMQIGEVVF GGVGSGLYGMLLFVLLTVFIAGLMIGRSPEYLGKKIEVYEMKMTALAILIPPALVLLGTALALS TEAGRGGILNPGAHGFSEVLYAVSSAANNGSAFAGLSVNTPFYNVLLAVAMLLGRFAVMV PVLAIAGSLVVKKRQPESKGSLSTRSPLFIGMLIAIVLLIGALTFIPALALGPVAEHLQFGLTH

4E-233	784.2	26.8	4E-233	783.9	18.6	1	1	F2LE23_BURGS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA bgla_1g29650	Burkholderia gladioli (strain BSR3)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia gladioli (Pseudomonas marginata) (Phytomonas marginata), Burkholderia gladioli (strain BSR3)	999541	>tr|F2LE23|F2LE23_BURGS Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia gladioli (strain BSR3) GN=kdpA PE=3 SV=1 MNANNLLQAGIFLVVLLALAVPVAGYLTRVMDGSSRVLRVFGLLERALFRIAGVDAGAEMS WKQYALAAIAFNVLGVFFLYMLLRIQQWLPGNPQQFAPMTVDGAFNTAVSFVTNTNWQDY SPEQTVSYLTQMLGLTVQNFLSAATGIVVVVALIRGFARHTAKTIGNFWVDLTRVTLYVLVP MSMVVAGLLMSQGVIQNFRAYTDVPTLQASSYQAPKLDAQGNPVKDDKGNPVTVATPLKT QTIAMGPVASQEAIKMLGTNGGGFFNGNSAHPYENPTPFSNFVQILSILILPASLCLVFGRMI GDRRQGVAVLAAMTVAFAVAVGIEAGAEQRGNPSFSALHVDQSSGALQAGGNMEGKETR FGIAQTSLFVVATTAASCGAVDGAHDSLTPVGGLVPMLLIQLGEVIFGGVGSGLYGMLVFAL LAVFVAGLMIGRTPEYVGKKIESYEMKMVSIVVLLTPLLVLVGTSIAVLADAGRAGIANPGPH GFSEILYAFSSAANNNGSAFAGLTVSTPFYNWLTAIAMWFGRFGTIVPVLAIAGSLAAKKRIA ATSGTLPTHGPLFVVLLLGSVLLVGALTYVPALALGPGVEHLMLFSGSH
5E-233	783.8	26.1	6E-233	783.6	18.1	1	1	K9WM91_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mic7113_5921	Microcoleus sp. PCC 7113	562	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	1173027	>tr|K9WM91|K9WM91_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Microcoleus sp. PCC 7113 GN=kdpA PE=3 SV=1 MWQGFLQIAITLVILVAIVPFLGRYMARVFLGERTLLDPVMTPVEGIIYTATGVRHRENMTGW QYARAVLWSNLAMFILVYLIFMFQGFLPLNPTGLEAPSWDLALHTAISFVTNTNQQHYSGET TFTYASQMLALGYLMFTSAATGLAVAIAFIRGLTGRPLGNFYIDLTQSITRILLPISIVGAIALLIL GVPETLAGPEIVTTLEGAQQVIARGPVAHFEIIKELGENGGGFFGINSAHPYENPNGLANLIE TVIMVCIPASLIITYGIFAGNKKQGWLIFWMVFILYAILITISAIGEYQGNPLVNNILGSQQPNLE GKEVRFGWALTALWAVTTTGTMCGAVNGMHDSLMPPGGFSTLFNMFIQIVWGGQGTGTA YLFIYLILTVFLTGLMVGRTPEFLGRKIEKREIVLASVILLVHPIIILPSAITIAFPEALSGITNPLY HGVSQVVYEYDSAAANNGSGFEGLADGTLWWNLSASVSLLAGRYLPIIALLLLADSMYRKQ PVPETTGTLRTDTGLFTGITAGVILILGALTFFPVLALGPIAEAFLIGAGAT
6E-233	783.5	39.1	7E-233	783.3	27.1	1	1	R4KGK3_CLOPA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Clopa_3995	Clostridium pasteurianum BC1	557	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium pasteurianum, Clostridium pasteurianum BC1	86416	>tr|R4KGK3|R4KGK3_CLOPA Potassium-transporting ATPase potassium-binding subunit OS=Clostridium pasteurianum BC1 GN=kdpA PE=3 SV=1 MEILQIGIILLVFVLLCILVGKYIYKVSEHERTFLDPVLDRVDNFIYRISGIKKEDMSWKQYIFALI SCNAVAAFLAFLILRLQSIPILNPNHIGSMEQGLTFNTVIAFMTNTDIQDYSGEWGLSYFSQMI VITFFMFFAAATGLAITLAFIRAISGRKKEIGNFYVDLVRIITRILLPLSIIVAVFFIQQGVPQTLAS NKTVTTIEGKLQDIPMGPVASLEAIKMLGTNGGGFFGANSAHPFENPTPLTNAVQSVSILLLA GAVVVCFGYMLKKKKQAISIFAAMGVLLIIGITISYMAEKAGNPVLAGLGLNQLMGNMEGKEV RFGVGLSSLFTTLTTATSTGAVNNMHDSLTPIGGAVALMNMMLNVIFGGIGVGFMNMIMFAI LTVFLCGLMVGRTPEFLSKKIEGREIKLIALAIIIHPLLILMFSAAALIVPQGLAGISNPGFHGLTE ILYQFTSAAANNGSSFGGLNVNTMFWNTSTGIVMLAGRYISMIILIAVAASLASKRAIPVTSGT FRTDNAVFTVTLIFIVLVIGALTFFPALSLGPIAEQLTL
6E-233	783.4	31.1	7E-233	783.1	21.6	1	1	Q2SZS4_BURTA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BTH_I1021 DR63_2803	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, pseudomallei group, Burkholderia thailandensis, Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	271848	>tr|Q2SZS4|Q2SZS4_BURTA Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301) GN=kdpA PE=3 SV=1 MNANNLLQAAILIAVLIAAAVPVSRYLTRVMDGSSAVVRVFGPLERVLYRLAGIDPRAEMSW RQYAFATIAFNALGVLFLYALLRVQGGLPGNPQQFGPMTADGAFNTAVSFVTNTNWQDYT PEQTVSYLAQMLGLTVQNFLSAATGIVVVIALIRGFARHTAQTIGNFWVDVTRVTLYVLVPMA AIVAALLMSQGVIQNMKAYQDVPALQTTTYAAPKLDAHGNPVKDAQGNPVTVQTPVKAQTL AMGPVASQEAIKMLGTNGGGFFNGNSSHPYENPTPFSNVLEIFSILIIPAALCLVFGSMIGDR RQGIAVLAAMTVALAVAIGVEVSAEQGGTPVLASMNVDQTASPLQAGGNMEGKETRFGIAQ TGIFVVATTAASCGAVNAMHDSLTPVGGLVPMLLMQLGEVIFGGVGSGLYGMLVFALLAVF VAGLMIGRTPEYVGKKIESYEMKMVSIVVLLTPFLVLVGTSIAVLAAAGRAGIANPGPHGFSEI LYAFSSAANNNGSAFAGLSVNTPFYNWMTAIAMWFGRFGTIVPVLAIAGSLAAKKRIAATSG TLPTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLMLFVGAH
6E-233	783.4	28.9	7E-233	783.2	20	1	1	E0UCQ4_CYAP2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cyan7822_3298	Cyanothece sp. (strain PCC 7822)	560	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7822)	497965	>tr|E0UCQ4|E0UCQ4_CYAP2 Potassium-transporting ATPase potassium-binding subunit OS=Cyanothece sp. (strain PCC 7822) GN=kdpA PE=3 SV=1 MVQGLIQIVLTLIILVVIVPFLGNYLARVFLFKKTILDPILNPIERIIYAGIGTNPNKNMTAAQYIKA VLWSNLVMAILVYLIFMIQGSLPFNPTGLQAPSWDLALHTTISFITNTDQQHYSGETTLSYAS QMWAIGYLMFTSAATGLAVGIAFIRGLTGQPLGNFYVDLTLSITRVLLPFSLVAAIVLISLGVP ETLAPPVTLTTLEGATQTLAVGPVAHIEAIKQLGENGGGFFGINSAHPFENPNGFSNLIETILM VIIPAAMIYTYGIIAGNKKQGWLLFWMVFILFVITIFIAASGEFQGNPIINGLLGEQQPNLEGKEI RFGWAQTALWAITTTGTMCGAVNGMHDSLMPPGGGATLFNLFLQIIWGGQGTGTAYLFVF LILTVFLTGLMVGRTPEFLGRKIEKREIVLASVILLVHPIAILIPGAITLAFPEQIAGISNPGFHGIS QVIYEYASAAANNGSGFEGLGDNTLWWNLSTSVVLLAGRFIPIIALLLLAENMYRKQPVPET PGTLRTDSNLFTSVNAITILILGALTFFPVLALGPIAEAFQIAAK

6E-233	783.4	32.7	8E-233	783.1	22.7	1	1	KDPA_ALIAD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Aaci_0251	Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	562	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Alicyclobacillus, Alicyclobacillus acidocaldarius, Alicyclobacillus acidocaldarius (Bacillus acidocaldarius), Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	521098	>sp|Q9XE11|KDPA_ALIAD Potassium-transporting ATPase potassium-binding subunit OS=Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) GN=kdpA PE=3 SV=1 MTLSGILAIFLVVLALVACAWPLGGYIYRTFVGERVRPDAVMVPVERAIYRLIGVNPEVEMD WKAYLRAMMVSNLVMALFAYAVFRLQGVLPLNPAHIPAMPPYLAFNTAASFITNTNWQNYA GEQSLSYLSQMIGITFLQFTSAATGLAAAMAFLRGLSRQKTDALGNFWVDLVKAHTRLLLPI AAILAVLLLALGVPETLSGPAVVHTLAGSMQTIARGPVATLEAIKQLGTNGGGFFNANSAHPF ENPNAWTCILEIMGMGLIPTALVFTAGHFLRSRRLAIVLCTLLGAILLAGAYIVYAYEAAGNPIL AHALGIHGPNMEGKEVRFGLPLTSLFVAATTAYTTGAVNAMHDSLMPLSGMVPLLFMMFNL IFGGKGVGLLNILMFLIIAVFISGLMVGRTPEIFGKKIEAREMKLATAAMLVHPFVILVPTAIAMA LPSARASMGNPGLHGFTEVLYAFTSAAANNGSAFAGLNGNTPFYNISIGLVMLFGRYVSIIA MLAIAGSLAGKARIPETSGTLKVDTFAFGYVFVAVFIIVGALTFFPYLALGPIGEQLQLG
7E-233	783.3	29.7	8E-233	783.1	20.6	1	1	C6X587_FLAB3	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA FIC_01125	Flavobacteriaceae bacterium (strain 3519-10)	563	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, unclassified Flavobacteriaceae, Flavobacteriaceae bacterium (strain 3519-10)	531844	>tr|C6X587|C6X587_FLAB3 Potassium-transporting ATPase potassium-binding subunit OS=Flavobacteriaceae bacterium (strain 3519-10) GN=kdpA PE=3 SV=1 MNTEILGIIVMFAVSVALAIPFGKYIAKVYGGEKTLPDPLFNPIEKLFYKISGIVPTREMNWKEH MTALLTINLVWFLLGIGILMTQQWLPLNPDNNPNMSADLAFNTTISFVVNCNLQHYSGETGL SYLGQMWLMFLQFVSAGTGLAAAAVLFKAFREKTSVQLGNFYEFFIKSCTRILLPVSFVVAL LLVFNGTPMTFDGKDQITTLQGDTVDVSTGPAAAFIAIKHVGTNGGGFFGVNSAHPFENPS YFTNMVEMVAQLIIPLAIIFAFGYFIRRKKFSWMIFGVMTFGFLLLTLPNIHMEMNGNPAIAAM DIDNSTGAMEGKEIRLGAAASGFWSIVTTVISTGSVNSMHDSTMPLSGMNELLAMMVNAFY GGCGVGLLNFFIFIILAVFISGLMVGRTPEFMGKKIEAREMKIAMIIALLHPFLILVGTALATAFP EQGASTLNNPGYHGFSEILYEYTSSAANNGSGFEGLGDNNLWWNITTGFVLILGRFLPIIGPI AIAGLLAGKKYIPEGNGTLKTDTSTFGLMVFAVIAIIAALAFFPALTLGPIAEYFSMKQ
7E-233	783.3	31.1	8E-233	783.1	21.5	1	1	E7GKG6_CLOSY	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HMPREF9474_01411	[Clostridium] symbiosum WAL-14163	570	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	742740	>tr|E7GKG6|E7GKG6_CLOSY Potassium-transporting ATPase potassium-binding subunit OS=[Clostridium] symbiosum WAL-14163 GN=kdpA PE=3 SV=1 MFQILITLLIYMVLVIPIGIYLYHVATKQRTFADPVFDRIDGMIYRICRINREDMHWKTYALNLL MTNAVMILIGYLVLRLQGLLFLNPNGIASMEESLSFNTIISFMTNTNLQHYSGESGLSYLSQTA VIIFMMFTSAATGYAACMAFCRGMAGRPMGNFYEDMVRNTTRILIPLSFIAGMLLIWQGTPQ NFHANFTVSTLEGKWQDIAAGPIAALEAIKHVGTNGGGFLGANSSTPLENPTIISNLVELYSM MILPGACVIAFGNMIADKRKKEGKKSLFGRQGRTVFAAMAIIFLIGVAVCFAAESAGNPVLAG IGLNQDMGSYEGKEVRFGIAQSALFTTTTTSFTTGTVNNMHDSLTPLGGLVPLLHMMLNCV FGGKGVGLMNMVMYVILAVFICGLMIGRTPEYLGKKIEGKEMKLVAVCLIIHPLLILGFSALAV STAGGLAGITNPGFHGLSQVLYEYSSSAANNGSGFEGLADNSVFWNLTTGIAMYFGRFPAII LQLAIAGSIFAKRRVVNETVGTLRTDNVVFTLILVFVVYIFAALTFFPALALGPVAEHLTIWFPGL S
7E-233	783.2	31.5	8E-233	783.1	21.8	1	1	KDPA_CITK8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CKO_02463	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter koseri (Citrobacter diversus), Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	290338	>sp|A8AJB7|KDPA_CITK8 Potassium-transporting ATPase potassium-binding subunit OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=kdpA PE=3 SV=1 MAAQGFLLTASFLLILFVLARPLGVGLARLINDIPLPGTASVERLLWRGLGISTQEMDWKQYL LAILTLNLLGLTVLFLMLLGQNLLPLNPQQLPGLSWHLALNTAISFVTNTNWQSYGGETTLSY FSQMAGLTVQNFLSAATGIAVIFALIRAFTRQNIDTLGNAWMDLVRITLWILLPLALLIALLFIQ QGALQNLLPYQSFTSVEGVKQLLPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPSALT NMVQMLAIFLIPAALCFAFGDASGDRRQGQMLLWAMSIIFVVCVAVVMSAEVQGNPHLLKF GTDSSLNMEGKESRFGVLVSSLFAVVTTAASCGAVIAMHDSFTALGGMVPMWLMQIGEVV FGGVGSGLYGMLLFVLLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILITPTLVLLGTALAM MTETGRSGMLNPGPHGFSEVLYAVSSAANNGSAFAGLNANTPFWNCLLAFCMFVGRFG VIIPVMAIAGSLVGKKRQPASPGTLPTHGALFVGLLIGTVLLVGALTFIPALALGPVAEHLSLY
8E-233	783.1	31.7	9E-233	782.9	21.9	1	1	A0A077KG65_9FLAO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CHSO_1289	Chryseobacterium sp. StRB126	564	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Chryseobacterium, Chryseobacterium sp. StRB126	878220	>tr|A0A077KG65|A0A077KG65_9FLAO Potassium-transporting ATPase potassium-binding subunit OS=Chryseobacterium sp. StRB126 GN=kdpA PE=3 SV=1 MNTEILGIIAMFAITLVIGIFLGKYIANVYGYKKTFLDPVFQPIEKLIYKISGINPNRQMNWKQN MYAMLAINLVWFIIGFILLLTQAWLPLNPDGNPNMSPDLAFNTTISFLVNCNLQHYSGETGVS YLSQLYLMFLQFVTAATGMAAMAVLFKAFKEKTATELGNFYDYFTKSMIRILLPISVVVALILSI NGSPMTFEGKDHITTLEGQKIDVSRGPVAAFVAIKHLGTNGGGFFGANSAHPLENPNYITNM TEMVTQMIIPFALVFALGFYLKKRKLSWVIFTVMTIGFLALTVPNIVNETGGNPLITKMGTDSS IGAMEGKEIRFGSAASAYWSIATTVISTGSVNSMHDSTMPLSGMNELLAMMINCFYGGCGV GILNYFIFIILAVFISGLMVGRTPEFMGKKIEAKEMKIAMIVALFHPFLILVGTALTAYMPEFGAK TLNNPGFHGFSEMLYEFTSSSANNGSGFEGLGDNTPWWNISTGIVLLLSRFIPIIGPVAIAGL LAQKKFIPESSGTLKTDTATFGFMTLAVILLIAALSFFPALTLGPIAEQIQYFSK

8E-233	783.1	28.8	9E-233	782.8	20	1.1	1	KDPA_BURPS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BPSL1171	Burkholderia pseudomallei (strain K96243)	602	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, pseudomallei group, Burkholderia pseudomallei (Pseudomonas pseudomallei), Burkholderia pseudomallei (strain K96243)	272560	>sp|Q63VS3|KDPA_BURPS Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia pseudomallei (strain K96243) GN=kdpA PE=3 SV=1 MNANNLLQAAIFIVVLIAAAVPVARYLTRVMDGSSAVVRVFGPLERALYRFAGIDPRTEMSW KQYALATVAFNALGVLFLYALLRVQGWLPGNPQGFGPMTVDGALNTAVSFVTNTNWQDYT PEQTVSYLAQMLGLTVQNFLSAATGIVVVLALIRGFARHTAQTIGNFWVDVTRVTLYVLVPM AAIIAALLMSQGVIQNTKAYQDVPTLQTTSYAAPRLDAQGNPVKDAKGNPVTVQTSVKAQTL AMGPVASQEAIKMLGTNGGGFFNGNSSHPYENPTPFSNFLEIFAILIIPAALCLVFGNTIGDR RQGVAVLAAMTVALAAAIGIETSAEQGGTPVLASLNVDLAASPLQAGGNMEGKETRFGIAQ TGLFVVATTAASCGAVDAMHDSLTPVGGLVPMLLMQLGEVIFGGVGSGLYGMLVFALLAVF VAGLMIGRTPEYVGKKIESYEMKMVSIVVLLTPLLVLVGTSIAVLADAGRAGIANPGPHGFSEI LYAFSSAANNNGSAFGGLSVNTPFYNWMTAIAMWFGRFGTIVPVLAIAGSLAAKKRIAATSG TLPTHGPLFVVLLLGTVLLVGALTYMPALALGPGVEHLMLFVGAH
8E-233	783	32.7	1E-232	782.8	22.6	1	1	KDPA_AGRVS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Avi_6074	Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium vitis (Rhizobium vitis), Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	311402	>sp|B9K2I8|KDPA_AGRVS Potassium-transporting ATPase potassium-binding subunit OS=Agrobacterium vitis (strain S4 / ATCC BAA-846) GN=kdpA PE=3 SV=1 MSSNGWLQIGLLLALVFLTIKPLGLYIACVFEGQRTFLSPILGPLERLLLRISGVDARREQGW LAYTLAMLAFNAAGFLALYGILRLQAYLPYNPQGFAGMTPDLAFNTAISFVTNTNWQAYSGE QSASHFSQMAGLAVQNFLSAATGIAIALAVTRAFARSAANTLGNFWVDMTRSTLYLLLPMSI VLALVFVWMGIPQTLDASVTATTLDGAQQTIALGPIASQEAIKQLGTNGGGFFNANAAHPFE NPSAISDYFNILAMMSITMALIYAFGKMVGDLRQGWALIASVAVLLIAGIAAVYIAETAGNPIHL ALGLDPSFGNMEGKEVRFGQAMSAAYTAITTGISNGGVNTMHGSLTPLGGLVPLFLIQLGEI LPGGVGSGLYGLIVFCVLTVFVAGLMVGRTPEFLGKKIEAREMKFAMLAVLVLPFAILGFSAI AAVLPNALASLGNAGPHGLSEILYAYTSAAGNNGSAFAGLSANTAWYNTTLGISMALGRFA YAVPVLAIAGSLAAKTKGTASAGTFPTHTPLFVGLLVAIIIILGGLQYFPALALGPIAEHVGMLA GTLY
9E-233	782.8	27.7	1E-232	782.6	19.2	1	1	C7RUE6_ACCPU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CAP2UW1_1688	Accumulibacter phosphatis (strain UW-1)	603	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, unclassified Betaproteobacteria, Candidatus Accumulibacter, Candidatus Accumulibacter phosphatis, Accumulibacter phosphatis (strain UW-1)	522306	>tr|C7RUE6|C7RUE6_ACCPU Potassium-transporting ATPase potassium-binding subunit OS=Accumulibacter phosphatis (strain UW-1) GN=kdpA PE=3 SV=1 MNNHAWLLLGLFMAALLLVRPLGIYIARVMMMENHATLVSRFEVAVFRACGFQRDEDMG WLKYALALLLFNALGLLAVYSLQRLQLWLPLNPQGMVNVSPDSAFNTAVSFVTNTNWQGY GGESTMGYLVQMLGLTVQNFLSAATGIAVAIALIRGFARHSNAGIGNAWADLFRATTWILLP LSLVFALFLASQGVIQNLDAYQELTTLEVTKYDNPRLDTDGQPLKDDKGNAVTEPATTPTQT LPMGPVASQEAIKMLGTNGGGFFNANSSHPFENPTPLVNFLQMLSIFLIPGALCIAFGCIVGD ERQGWTLLAAMALLFVTFAIAAIGFEQEGNPLLAQVGVGETTSVSTTALTDGNMEGKETRF GIADSALFATITTAASCGAVNSMHDSFTPLGGAVPLVMIQLGEVVFGGVGSGLYGMLIFAVL AVFIAGLMIGRTPEYLGKKIESHEMKMTSIAILATPLLVLVGTAIAVMTEAGRAGIANPGAHGF AEILYALSSAANNNGSAFAGLSVNTPFYNGLLATAMWFGRFAVIVPVLAMAGSLAAKKRIFV TAGTLPTHGPLFVTLLIGVVLLVGLLNYVPALALGPLIEHLVLWSAH
1E-232	782.6	30.6	1E-232	782.3	21.2	1	1	A4JGG9_BURVG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bcep1808_2373	Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia vietnamiensis, Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))	269482	>tr|A4JGG9|A4JGG9_BURVG Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia vietnamiensis (strain G4 / LMG 22486) GN=kdpA PE=3 SV=1 MNANDVFQIALFIVVLLAAAVPVARYLTGVMDGSSRVVRVFGPLERALYRIAGVDAGTEMN WKQYALATIAFNALGALFLYGLLRLQGVLPGNPQQFGAMTADGAFNTAVSFVTNTNWQDY TPEQTVSYLTQMLGMTVQNFLSAATGIVVVIALIRGFARHTAQTIGNFWVDLTRVTLYVLVP MAALVAALLMSQGVIQNMKAYQDVPVLQASTYAAPKLDAQGNAVKDDHGNPVTVPTPLVK QTLAMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPFANFVQIFSILIIPAALALVFGHMI GDRRQGIAVLAAMTVAFAIALGVEVSAEQAGNPTLAALHVDQQASALQPGGNMEGKETRF GIAQTGIFTVATTAASCGAVDTMHDSLTPLGGLVPMLLMQLGEVIYGGVGSGLYGMLVFALL AVFVAGLMIGRTPEYVGKKIESYEMKMVSIVVLLTPLLVLVGTSIAVLADAGRAGIANPGPHG FSEILYAFSSAANNNGSAFAGLTVGTPFYNWTTAIAMWFGRFGTIVPVLAIAGSLAAKKRIAA TSGTLPTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLMMWLGA
1E-232	782.5	30.3	1E-232	782.3	21	1	1	A0A068QPW3_9ENTR	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA XDD1_1329	Xenorhabdus doucetiae	563	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus doucetiae	351671	>tr|A0A068QPW3|A0A068QPW3_9ENTR Potassium-transporting ATPase A chain OS=Xenorhabdus doucetiae GN=kdpA PE=3 SV=1 MAVSAFLLITSFLLILFLLSKPLGNLIARLVEGELPRWLTKTETILWRCCGLQKPGSNIKEMNW WQYALAICIFNIAGLLLLFTLLVSQDHLPLNPQHFAGMKWDLALNTAISFVTNTNWQAYSGE NTLSYLSQMAGLTVQNFLSAATGIAVAFALMRAFSRQGMKTVGNAWIDITRITLYLLLPLAIIIA LFFVSQGVIQNFSSYVLIHSLEGQPQWLPMGPVASQEAIKLLGTNGGGFFGANSAHPFENP TSLSNFVQVLAIFLIPCALCFAFGLVVGDNRQGYALLWTISIVFIIATSVVMYAETAGNSHLIHA NISDHVNMEGKESRFGILASSLYGVVTTAASCGAVNAMHDSFTALGGMILLWLMQIGEVIFG GVGSGLYGLLLFVLLAVFIAGLMIGRAPEYLGKKIDVYDMKMVALAILATPSLVLLGTALAIST DIGRSAIANPGAHGFTEVLYAFSSAANNNGSAFAGLNANNVFYNLVLGIIMFLGRFGVILPVL AIAGSMIHKKRQPISSGTLPTHGSLFIGLLILVILLIGALTFIPALALGPIAEHLQF

1E-232	782.4	29.9	2E-232	782	20.7	1.1	1	KDPA_POLNA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Pnap_3604	Polaromonas naphthalenivorans (strain CJ2)	599	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Polaromonas, Polaromonas naphthalenivorans, Polaromonas naphthalenivorans (strain CJ2)	365044	>sp|A1VTC2|KDPA_POLNA Potassium-transporting ATPase potassium-binding subunit OS=Polaromonas naphthalenivorans (strain CJ2) GN=kdpA PE=3 SV=1 MTASSWELLALYLGALLLAAWPLGIWLARISSGRLPGWMQRVEAPLLRLAGTSADQAMNW WQYALALLAFNALGLLAVYALQRLQAVLPLNPAGMAAISPDSAFNTAISFVSNTNWQGYGG EASMSYLTQMLALAVQNFLSAATGIAVVFALFRGFAARATGAIGNFWVDVTRITAWLLLPLS LVFALFLAGNGVIQNFDAYKDVATLEATSYQQPKTGLDGQPLKDAQGAAVMENVRTDKQTL AMGPVASQEAIKMLGTNGGGFFNANSAHPYENPNALTNFFQMLAIFLIPAALCFAFGREVG DLRQGWAVLAAMTVMFVIAVVAITPAEQAGNPLLTPLGVDQAASALQAGGNMEGKETRFGI NASSLFAVITTAASCGAVIAMHDSFTPLGGMVPMVMMQLGEVVFGGTGTGLYGMLIFAILAV FISGLMIGRTPEYLGKKIESHEMKLTSIAILVTPILVLAGTAVAVLAGAGRAGVANPGAHGFSE ILYALSSAGNNNGSAFAGLSANTPFYNTLLGLAMWLGRFGVIVPVLAIAGSLAAKKRLPVTP GTMPTHGPLFVLLLIGTVLLVGLLNYVPALALGPVVEHLMLWPAH
2E-232	782.1	33.9	2E-232	781.9	23.5	1	1	K9Y0M2_STAC7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Sta7437_4009	Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	561	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Stanieria, Stanieria cyanosphaera, Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	111780	>tr|K9Y0M2|K9Y0M2_STAC7 Potassium-transporting ATPase potassium-binding subunit OS=Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437) GN=kdpA PE=3 SV=1 MIQGFIQIALTLLIVVLIVPWFGNYMARIFLAQKTILEPIAQPLEKLIYTVGGINYQKNMTGWRY ARSVLISNLVMLVFVFLILIFQGLLPLNPTGLTAPSWDLALHTAISFVTNTNQQHYSGETTYSY ASQMFALGFMMFTSAATGIAVAIAFIRGLTGNPLGNFYVDLTKSITRILLPISIVGGIVLLILGVP ETLAPPAVANTLEGATQYIARGPVAHFEIIKQLGENGGGFFGINSAHPFENPNGFSNLIETVI MLVIPTSLIYTYGVIAGNKKQGWLIFGMVFIIYVILIVISAVGEYYGNPIINNFLGTNAPNLEGKE VRFGWAQTALWAVTTTGTMCGAVNGMHDSLMPTGGFATLFNMFLQIVWGGQGTGTAYL FVFLILTVFLTGLMVGRTPEFLGRKIEKQQIVLASVILLVHPIAVLIPSAITFINPDTLAGISNPGF HGVSQVVYEYTSAAANNGSGFEGLGDNTVWWNLTAAASMIIGRYIPIVALLLLADNMTRKQ PVPKTPGTLRTDTTLFTGVTAGVILILGALTFFPVLALGAIAEGFEIAKNL
2E-232	782	31	2E-232	781.8	21.5	1	1	K0IAK7_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA C380_12750	Acidovorax sp. KKS102	597	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax sp. KKS102	358220	>tr|K0IAK7|K0IAK7_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Acidovorax sp. KKS102 GN=kdpA PE=3 SV=1 MSTGAWLQLAVFIALLLALAWPLARYIDTVMAGRFALGRRLEGPLFRLAGVWPDEETGWLR YTQGLLVFNGLGVLAVYALQRWQAVLPLNPQGMAAVAPDSAFNTAISFVTNTNWQGYGGE STMSYLTQMLALTVQNFLSAATGLVVVIALVRGFSRHSAQSIGNVWADLTRATLWVLLPLSL VLAVVFAGQGVIQNLSPYTEVQTLEPVHYEAPKLDAAGQPVLDAQGAPVTEPATQTTQTLA MGPVASQLAIKMLGTNGGGFFNANSAHPFENPSAASNLLQMLAIFLIPAALCLVFGRMVGDE RQGWTILATMSLLFVVAVVAATAFEQQGNPLLASLGVDQTASALQAGGNMEGKETRFGIAT SALFAVITTAASCGAVIAMHDSFTPLGGMVPMVLMQIGEVVFGGVGSGLYGMLVFAIMAVFI AGLMIGRTPEYLGKKIETHEMKLVAIAILVTPLLVLLGTAVAAMSEAGRAGLSNPGAHGFSQV LYALSSAANNNGSAFAGLSANTPFFNVLLAVAMWLGRFGVIVPVLAMAGSLAAKKRATATD GTLPTHGPLFVALLAGVVLLVGLLNYVPALALGPVVEHLVLTTR
2E-232	782	24.1	2E-232	781.8	16.7	1	1	R4MBQ5_MYCTX	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA J113_07260	Mycobacterium tuberculosis CAS/NITR204	571	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex, Mycobacterium tuberculosis, Mycobacterium tuberculosis CAS, Mycobacterium tuberculosis CAS/NITR204	1310114	[illegible] OS=Mycobacterium tuberculosis CAS/NITR204 GN=kdpA PE=3 SV=1 MSGTSWLQFAALIAVLLLTAPALGGYLAKIYGDEAKKPGDRVFGPIERVIYQVCRVDPGSEQ RWSTYALSVLAFSVMSFLLLYGIARFQGVLPFNPTDKPAVTDHVAFNAAVSFMTNTNWQSY SGEATMSHFTQMTGLAVQNFVSASAGMCVLAALIRGLARKRASTLGNFWVDLARTVLRIMF PLSFVVAILLVSQGVIQNLHGFIVANTLEGAPQLIPGGPVASQVAIKQLGTNGGGFFNVNSAH PFENYTPIGNFVENWAIQIIPFALCFAFGKMVHDRRQGWAVLAIMGIIWIGMSVAAMSFEAK GNPRLDALGVTQQTTVDQSGGNLEGKEVRFGVGASGLWAASTTGTSNGSVNSMHDSYTP LGGMVPLAHMMLGEVSPGGTGVGLNGLLVMAILVVFIAGLMVGRTPEYLGKKIQATEMKLV TLYILAMPIALLSFAAASVLISSALASRNNPGPHGLSEILYAYTSGANNNGSAFAGLTASTWS YDTTIGVAMLIGRFFLIIPVLAIAGSLARKGTTPVTAATFPTQKPLFVGLVIGVVLIVGGLTFFPA LALGPIVEQLSTQ
2E-232	781.8	32.3	2E-232	781.6	22.4	1	1	X4ZCZ5_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PSAB_12640	Paenibacillus sabinae T27	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	1268072	>tr|X4ZCZ5|X4ZCZ5_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus sabinae T27 GN=kdpA PE=3 SV=1 MTTTSLLAIAVTVLIALLLARPAGLYIAEVFNYERTGLDRWFGWLEKPVYALGGIRKENQSW KEYALALLLSNSVMILLVYLIFRFQGVLPLNPTRIASMEPTLAFNTAISFMTNTNLQHYSGESG LSYLSQMIGIIFMMFTAPASALAGAIAFIRALSGKPLGNFFVDMIRCITRILLPVSFVLAFVFVA MGVPQTLEPAAVAHTLEGATQEIARGPVASFLSIKEFGNNGGGFFGVNSAHPFENPSGFSN FLQIVLMLLLPASLPFTYGKMVGNRKQGRVLFASMVMMFVVLLGISLASENTGNPVINALGIQ HAQGSMEGKEVRFGAAQSTLYSVVTTATETGAVNTMHDTLTPIGGLVALGNMMLNTVFGG VGAGFINVLMYAMIAVFLSGLMVGRTPEFLGKKIEGKEMKLIAVTLIISPLLILLPTAFALYAHP DTISNPGFHGLSQALYEFTSSAANNGSGFEGLGDATPFWNISTGIVMFLGRYFPVITMLAVA GSLAAKKSVPETAGTFRTDNILFGTVFIGAVLIVGALTFFPAVALGPIAEYLTLKP

2E-232	781.6	32.7	3E-232	781.1	22.6	1.2	1	KDPA_GEOBB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Gbem_2608	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	594	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	404380	>sp|B5EH80|KDPA_GEOBB Potassium-transporting ATPase potassium-binding subunit OS=Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622) GN=kdpA PE=3 SV=1 MNAYEWIQSVVLFAVLLLAIKPMGSFMAKIFQGDRTFLSRLLVPCESFIYRVCGIDKDEEMG WQQYAWALLLFNLICGVALFFILLLQGVLPLNPQKFPAFSWHLALNTAVSFMTNTNWQNYG GESTASYFTQTFGFAVHNFLSAATGIVVAIATIRGFVRRRVSKIGNFYVDIARCTLYLLLPVSL VFAVFLVSQGVIQNFSGYRTVPLVQATSYLKPKLDATGNALKDPKGNSITETIQVKEVTIPMG PVASQEAIKELGTNGGGFFNANSAHPYENPTPLANVVEVFLMLLIGGSLTYTFGVMAGNTR QGWAILAVMLAILVTAVGTLYWAETSGNPLVAKLGVHGVNMEGKETRFGVAGTSLFTSAAT GTSCGAVNAMHDSMTPIGGMIPLSLILLSEVVVGGVGTGLYTMIAFVVISVFIAGLMIGRTPEL LGKKIEVREMWMSIITVLTSGILVLIFSGLALVVPSAVSSMANPGAHGLSEVLYAFASMSNNN GSAFAGLNGNTIFYNVTGAIAMFLGRFAPIVASLAMAGSLAQKKFIPASLGTLPTDKIPFALW LTLVILIVGALTFFPALSLGPIVEHLIMLGGK
3E-232	781	27	4E-232	780.8	18.7	1	1	I2BB55_SHIBC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA EBL_c26800	Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	559	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Shimwellia, Shimwellia blattae (Escherichia blattae), Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	630626	>tr|I2BB55|I2BB55_SHIBC Potassium-transporting ATPase potassium-binding subunit OS=Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) GN=kdpA PE=3 SV=1 MISATALLLISYLALLLALAKPLGSLLARQIEGIPLPGTAWLERPLLRLVGADNREMDWRQYLL AIVLFNLLGLVVLFTLLTSQASLPLNPQHFPGLSWDLALNTAISFVTNTNWQAYAGESTLSYF SQMAGLTVQNFLSAATGIAVAYALIRAFTRQSVTTLGNAWSDLLRITLWILLPLSLIIALFFIQQ GVIQNVQPYTPALSLEGVNMLLPGGPVASQEAIKLLGTNGGGFFNANSAHPFENPTVLTNA VQMLAIFLIPAALCFAFGDVCGDPRQGRAILWTMGLIFAVCVVLVVWAEWRGNPHFLTLGA DSSVNMEGKESRFGILVSSLFAVITTAASCGAVNAMHDAFTAPGGMIPLWLMQIGEVVFGG VGSGLYGMMLFIMLAVFIAGLMIGRTPEYLGKKIDVREMKMTALAILVTPTLVLAGTALAMMT GAGPGAMLNPGPHGFSEVLYAVSSAANNNGSAFAGLSANTPLWNLLLALCMLLGRFAVIAP VLAIAGSMVTKRTQPTSAGTLPTHGPLFIGLLIGTILLVGALTFIPALALGPVAEYLVHR
4E-232	780.6	31.1	6E-232	780.2	21.5	1.1	1	KDPA_BORA1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BAV2701	Bordetella avium (strain 197N)	594	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella avium, Bordetella avium (strain 197N)	360910	>sp|Q2KWC8|KDPA_BORA1 Potassium-transporting ATPase potassium-binding subunit OS=Bordetella avium (strain 197N) GN=kdpA PE=3 SV=1 MDSQFFGLLVFYLAILLILAPFLGRYIRRAMEDEHYAATAWGRWLERLMYRLSGVNPAAEMT WRQYAVAVLIFSVLGFIAVYALQRLQGFLPLNPVGLGAVSPDSAFNTAISFVSNTNWQGYSP ESTMSYLTQMLALTVQNFLSAAVGMSVLFALIRGFARHGCATVGNFWVDATRATLYVLLPL ALALALALVSQGVIQNTAAYQEVTTLQAQSYEQARLDSTGQPMMDAAGKPLTETLVIQTQTL AMGPTASQEAIKLLGINGGGFFNANSAHPYENPTGLSNLLEMLAILIIPAALCFTFGEMVGDR RQGVAILAAMTLLFVGLAWLTQNAEQALTPALSHLSADGLLGNMEGKESRFGVAASALFAV VTTAASCGAVNTMHDSLSAMGGLGPMLLMQLGEVVFGGVGSGLYGMLAFALLGVFIAGLM IGRTPEYLGKKIEAFDMKMVSIAILVTPFLVLAGTALAVSVPQGLAGMLNPGAHGFSEVLYAL SSAANNNGSAFAGLSSNTPFYNSLLGLAMWFGRFLVIVAILALAGSLAGKRRLAQSPGSMP TTGPLFIVLLIGTVLLVGALTYVPALALGPVAEHLQARP
6E-232	780	27.4	8E-232	779.8	19	1	1	G8Q1U1_PSEFL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PSF113_1665	Pseudomonas fluorescens F113	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens F113	1114970	>tr|G8Q1U1|G8Q1U1_PSEFL Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas fluorescens F113 GN=kdpA PE=3 SV=1 MHGYDYGLILGFFALVLIPAPFLGRFYYRVMEGQRTWLSPILGPVERGCYRLAGVDATVEQ SWQKYTLALLAFNLAGFVLLFAILLLQGYLPLNTEQLPGMEWTQAFNTAVSFMTNTNWQSY SGEASLSYLSQMVGLTVQNFVSAATGLAVLVALCRGIGRKSAATLGNFWVDMTRATLYGLL PLCLLLALFLVWQGVPQTFAHYVHGVTMQGVDQVIPLGPAASQIAIKQLGTNGGGFFGVNS AHPFENPTAWSNLFEVASIILIPAALVFTFGHYVKDLRQSRAIIACMLALFLIGGATSLWAEYQ PNPALYNPAVEQAAPLEGKEARFGTTATVLWSVTTTVASNGSVNGMHDSLNPLSGMVSLV NMMVGEVIFGGVGAGLYGMLLNVLIAVFLAGLMIGRTPEYLGKKLGAREVQLLVATLLVMPV SVLVLGAVAASLPGPAAAVSNPGAHGFSQLLYAYTSAGANNGSAFAGFGANTPFHNLMLG VGMLIGRFGYILPVLALAGSLALKKTAPIGQNSFPTHGPLFVTLLTVTILLVGGLTFLPTLALGP IAEHLSLGF
7E-232	779.9	31.8	8E-232	779.7	22.1	1	1	R6QPM4_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN621_00570	Clostridium sp. CAG:352	603	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:352	1262798	>tr|R6QPM4|R6QPM4_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium sp. CAG:352 GN=kdpA PE=3 SV=1 MSAVIQYILYLAVLIVLAIPLGAYIKKVMNGEKTFLSKILTPCENAVYKVMRIKKDEQMNWKKY AVSVLIFSGIGLIFLFLLQILQGVLPGNPQGISGVKWDLSFNTAASFVTNTNWQAYSGESTLS YLTQALGLTVQNFVSAATGIAVLFALIRGFIKVKADGLGSFWVDITRIVIHILIPLNLVISLCLVG GGVIQNLKGAETVSLVEPIAVSADGEILENAEIDLDTNTVTVDGKKIEDAEIVTEQFVPMGPAA SQVAIKQTGTNGGGYMGVNSAHPLENPNAFTNLIEMLSILLIPAALCFTFGKAVKNKKQGVAI FMAMFICLALALGTIAVSEQVATPQLAQDGVNVSMTDQAGGNMEGKETRFGIATSSTWAAF TTAASNGSVNSMHDSYTPLGGMVTMLLMQLGEVIFGGVGCGLYGMLAFAILTVFIAGLMVG RTPEFLGKKIEPYEMKWSVLVCLATPIAILIGSGIAAVVPSVADSLNNGGAHGFSEILYAYSSC GGNNGSAFAGFNANTVFLNVSLGLVMLFARFLPIIGTLAIAGSLAGKKKIATSAGTLSTTNGM FVFLLILIVLIIGALSFFPALALGPLAEFFSNVI

1E-231	779.1	31.8	1E-231	778.9	22.1	1	1	KDPA_RHIME	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RA1255 SMa2333	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Rhizobium meliloti (Ensifer meliloti) (Sinorhizobium meliloti), Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	266834	[illegible] OS=Rhizobium meliloti (strain 1021) GN=kdpA PE=3 SV=1 MSVIGWLQISLLFLAVLVVVKPLGLYMAGVLSGEPNVLSPILGPVERGLYGAAGIDPTREQG WLAYTLSMLAFSIAGFLLLFAILRLQAWMPLNPQGFGNVPPDLAFNTAVSFVTNTNWQNYG GETTLSHFSQMMGLTVQNFVSAATGISIALAVTRSFARSAAPTIGNFWVDLTRSTLYVLLPLA VLVAVAFVAMGLPQTFRASVEATTLEGVKQTIALGPVASQEAIKQLGTNGGGFFNVNAAHP FENPTALSNYLNIFAMLSVSAALLYTFGQLVGNRRQGWAFIAVTYAFLIVGVGIVYWAEAQG NPILSQLGLDPALGNMEGKEVRFGQAMTALYATVTTGLSDGGVNGMHGSFTGLGGLVPMF LIQLGEVLPGGIGSGLYGMIVFAILAVFVAGLMVGRTPELLGKKIEAREMKYAMLAVLILPLSIL GFTAISAVMPSAVASVGTAGPHGLSEILYAYTSAGGNNGSAFGGLSGNTLWYNTTLGFAML LGRFAYAVPVLAIAGSIAAKTRASTSKGTFPTDTPLFAGLLIGIILILGGLQFLPALALGPIVEHF AMLSGQTF
1E-231	779	39.2	2E-231	778.7	27.2	1	1	A0A099W4Y6_9LIST	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA EP56_12780	Listeriaceae bacterium FSL A5-0209	557	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, unclassified Listeriaceae, Listeriaceae bacterium FSL A5-0209	1497679	>tr|A0A099W4Y6|A0A099W4Y6_9LIST Potassium-transporting ATPase potassium-binding subunit OS=Listeriaceae bacterium FSL A5-0209 GN=kdpA PE=3 SV=1 MEILQIVVVILILFCLIKPLGSYMYKIFAGAPTKGNRFFEKIEAGIFRLAGLSERPAMTWKRYAF SLVLVNGILMIVGFVIVFMQGLWANPDGLKGLDPTLAFNTVISFMTNTNLQHYSGETALTNM TQMIFITMMMFTSAATGISVAIAFIRGITSKGETLGNFYEDFTKAITRLLLPLAFILTLVLVGLAV PQTLASSHVMTTLEGVKQTIALGPVASLEAIKHLGTNGGGFFGANSAHPFENPTPLTNVLEM LAMWCIPASLTYTYGRFAKNQKQGWVIFSAMFVLFIVFLGLIFMSEKAGNPVLTELGVSNAQ GSMEGKEMRFGLGGSTLFSTITTAATTGSVNNMHDTLTPLGGMGTLALMMLNVVFGGDGV GLINMLMYAMLGVFLCGLLIGRTPEFLGRKIEPREMKLITLTLLIHPIIILIPTAVALLTSAGTDAI SNPGFHGMTQVLYEFTSSAANNGSGFEGLGDNTAFWNMTTGIVMFLGRYLSIVLLLAVAGS MTRKQFIPETIGTFRTDNGLFTGILVMVVLIIGALTFLPVLVLGPIAESLTL
2E-231	778.7	21	2E-231	778.3	14.5	1.1	1	I0HQX6_RUBGI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RGE_20720	Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	596	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Rubrivivax, Rubrivivax gelatinosus (Rhodocyclus gelatinosus) (Rhodopseudomonas gelatinosa), Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	983917	>tr|I0HQX6|I0HQX6_RUBGI Potassium-transporting ATPase potassium-binding subunit OS=Rubrivivax gelatinosus (strain NBRC 100245 / IL144) GN=kdpA PE=3 SV=1 MSGAWLQLAVFLLVLFAAAWPLGRAIEAVMDGRFALGRRVEAPLFRLAGVDPAEDQPWTR YALGLLVFNGLGLLAVYALQRLQPMLPLNPQDWPAVAPDSALNTAVSFVTNTNWQGYGGE TTMSRLTQMLGLAVQNFLSAATGIAVAVALARGFARRTASGIGNVWADLTRATLWVLLPLAF VAALFFVSQGVVQTLAPDRTVATVETLNWQQPRLDAAGQPLLDAQGAPQTETVTTTTQTL ALGPVASQQAIKLLGTNGGGYFNANSAHPFENPTPLANAVQMLAILLIPAALCFSFGRIVGDA RQGWALLGAMTLLFVVAVVAVTQAEYAGNPLLPPLGVDTLPSALQAGGSMEGKEVRFGLD ASALFAAVTTAASCGAVNAMHDSLTPLGGAVPLVLMQLGEVVFGGVGSGLYGMLVFALLAV FIAGLMIGRTPEYLGKKIEAHEMKLVSIAILVTPLLVLGGSALAVSVDAGRAGILNPGAHGFAE VLYALTSAANNNGSAFAGLSANTPFYNLLLAVAMWLGRFGVLVPVLALAGALAAKPRLAVTR GTLPTHGPLFVALLVGIVLLVGLLNYVPALALGPVAEHLALWAR
2E-231	778.6	24.8	2E-231	778.4	17.2	1	1	D4IJY6_9BACT	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AL1_06390	Alistipes shahii WAL 8301	563	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, Alistipes shahii, Alistipes shahii WAL 8301	717959	[illegible] OS=Alistipes shahii WAL 8301 GN=kdpA PE=3 SV=1 MNTEISGVILQWTLLVTLCYPLGRYIAKVYRGERTWLDFMAPVERAIYRFCGIDPAVEMNWK QFLKALLTVNLFWFFWGMLLLVFQGWLPLNPDGNPGQSPDLAFNTCISFMVNCNLQHYSG ETGLSYFTQLFVIMLFQFVTAACGMAAMAGMMKALAGKTKKTIGNFWVFLTRSVTRILLPLS LAVGILLVINGTPMSFDGKQTLTTLEGTEQVISQGPTAAIVPIKQLGTNGGGYFGTNSAHPLE NPNAFTNILECWSILILPMAMVFAFGFYTRRRSLATWIFGVMLLAYTAGVVLSVWQETGGSR QIDGMGISQELGSMEGKEIRIGSAASAMWGMTTTVTSNGSVNSMHDSQTPLSGMLQMLN MQINCWFGGVGVGWMNYFAFLIIAVFISGLMVGRTPEFLGRKVEAREMKIATLVVLLHPFLIL VGTGISAAVAAANPEIGWLNNPSFHGLSEMLYEYTSSAANNGSGFEGLADNTPFWNISTGI ALIMGRYFPIVGQVAIAGLLASKKCIPESAGTLRTDTGTFSLMTFAVIIIVAALSFFPALALGPIA DYLTF
2E-231	778.5	29.5	2E-231	778.3	20.5	1	1	A0A0D5V607_9BURK	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OI25_470	Burkholderia fungorum	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia fungorum	134537	>tr|A0A0D5V607|A0A0D5V607_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia fungorum GN=kdpA PE=3 SV=1 MNSNNVLQTGLFIVVLLAAAVPMSRYLSNVMDGSSRVVRLGGPLERLLYRIAGVDPSAEMG WKHYAIATIAFNALGALFLYVLLRVQGWLPGNPQQFGPMTVDGAFNTAVSFVTNTNWQDY TPEQTVGYLTQMLGFTVQNFFSAATGIVVVIALIRGFARHTAQTIGNFWVDLTRVTLYVLLPM SAIIAAVLMSQGVIQNFKAYQDVPTLQTTTYAAPKLDAQGNPVKDAKGNPVTVDTPVKTQTI AMGPVASQEAIKMLGTNGGGFFNGNSAHPYENPTPFSNFLQIFSILIIPAALALVFGRMIADR KQGVAVLAAMTIAFTACVVGEISAEQSGNPAFAALNVDQSANALQSGGNTEGKETRFGIAQ SGIFTVATTAASCGAVANTHDSLTPIGGLYPMLLMQLGEVIFGGVGSGMYGMLVFALLAVFV AGLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPLLVLVGTSIAVLTEAGKAGIANPGAHGFSEIL YAFSSAANNGSAFAGLTVSTPFYNWLTAIAMWFGRFGTIIPVLAIAGSLAAKKRIGVTGGTL PTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLMMMGAH

2E-231	778.5	38.1	2E-231	778.3	26.4	1	1	KDPA_CALS4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TTE2012	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	561	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	273068	>sp|Q8R8I5|KDPA_CALS4 Potassium-transporting ATPase potassium-binding subunit OS=Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) GN=kdpA PE=3 SV=1 MYSNIELFTMIAIIVLLTKPLGTYMYNIFEYKPMRSDKIFLPVENFIYKITGINPEEEMDWKKYA LTFLLVNMVMMIITYFILRVQQFLPLNPTGAKNMESSLAFNTVISFMTNTNLQHYAGEDGITFL SQMIVIVFLMFTSAASGLVTAAAIMRGLSKKTTNLGNFYADFVRITVRLLLPISMLATLILVWQ GVPQTFAGKVVVDTLEGGKQTIITGPVAVLESIKHLGTNGGGFFGANSSHPFENPTWLTNMI EMLLMMLLPTSLIYTYGLMINNKKHALVLYISLFVIFILLAVGAVYAENHPGVAYSKLHIYGKPY GNYEGKEVRFGVSQSPLFATVTTAFTTGSVDSMHDSYTPLGGAVPLILMMLNTIFGGDGAG LQNIIMYTILTVFLTGLMVGRTPEYLGRKIETKEIKLIALAILVHPFLILFSSALTVMLKVGASSVT NPLYHGLTQVLYEFSSAAANNGSEFAGFIGNTVFMNIMTGLVMFFGRYITIILMLAVAGSMAE KIPAPPSPGTFRTDNAIFGAIFIAVVLIVGALTFFPAVILGPISEFLSMT
2E-231	778.3	21.4	3E-231	778	14.9	1	1	A0A0F2R1D5_9PSED	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VR76_04370	Pseudomonas sp. BRH_c35	566	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. BRH_c35	1629711	>tr|A0A0F2R1D5|A0A0F2R1D5_9PSED Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas sp. BRH_c35 GN=kdpA PE=3 SV=1 MHANDYWLIAAFFILVLAPAPWLGRYLYRAMEGERTWLTPVFQPVERLCYRIAGIDQEGEQ NWMSYCLALLGLTAFSLLGLLAMLMLQGQLPLNPQELPGLEWHLALNTAVSFVTNTNWQA YSGEAQLSYFSQMLGLGVQNFVSPAVGLAVLVVFCRALSRRNAGAVGNFWVDMTRAVLY GLLPFSLILALLLVWQGVPQSLAEYVPVVTLQGGEQSIPLGPAASQIAIKQLGTNGGGFFGV NSAHPFENPTAWSNLLEVASILLLPAALVFMFGHYVRDLRQSRAILACMLVLFSLGLGTTLLA EHQPNPAFVGIAVEQTGPLEGKESRLGIAASALWATVTSAASNGSVNAMHDSFSPLGGMV PMFNMMLGEIVFGGVGAGLYGMLLFVLVTVFLAGLMIGRTPEYLGKKLEAREVRLLVASLLV MPVGVLVLAALGVSLPGPAASITNPGPHGLSQILYAYTSGTGNNGSAFAGFGAGTTYHNLMI ALAMLLGRFGFILPVLAIAGSLAAKNRAPLDANSFPTHGPLFVTLLTLVILLVGGLTFLPALALG PLAEHFVLLQGF
2E-231	778.3	35	3E-231	778.1	24.2	1	1	E3EDK0_PAEPS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PPSC2_06405	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus polymyxa (Bacillus polymyxa), Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	886882	>tr|E3EDK0|E3EDK0_PAEPS Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus polymyxa (strain SC2) GN=kdpA PE=3 SV=1 MELLQIGVVIVILLLLVKPVGTYMYHVFSNEPNRTDRIFGETEKPIYKVVGLKKQDSMRWTTY AMSFIATNVVLVGISYLLLRLQAILPGNPVGNSNMEASLAFNTVISFMTNTNLQHYSGESGLT YLTQMAFVTMMMFTSAASGFSVAAAFMRGLTRRGEGLGNFFQDFIKANIRIFLPLAFVLTLV LVGLKVPQTLQSTADITTLSGTQQQIAMGPIASLESIKHLGTNGGGFAGANSAHPFENPSPW TNVLEILAMWVMPASLPYTFGLFARNRKQGWIIFSSMMVLFLIFLSITYVSEKTGNPLIQALG MDASQGSMEGKEVRFGIGQSALFTAVTTAATTGSVNNMHDTLTPLGGMAALGEMMLNVIF GGKGVGLMNMLMYAILGVFICGLMVGRTPEFMGRKIEGKEMKLIAIAILVHPFLILAPTALAFM SHWGYDAVSNPGYHGLTQVLYEYASSAANNGSGFEGIADNNVFWNVTTGAVMFFGRYVS MIALLAVAASLNAKAPTPVTTGTLRTDNKLFGAILIGVVLLIGALTFLPVIVLGPVAEFLTM
2E-231	778.1	33.5	3E-231	777.9	23.2	1	1	H6NGX7_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PM3016_1494	Paenibacillus mucilaginosus 3016	556	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus mucilaginosus, Paenibacillus mucilaginosus 3016	1116391	>tr|H6NGX7|H6NGX7_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus mucilaginosus 3016 GN=kdpA PE=3 SV=1 MYATLSIVVTLLLVLVLARPVGLYMAQVFDYEKSKWDKWFGWIEKPIYTISGICRDNQTWKQ YALAVVFSNLVMIILVYLIFRFQKFLPLNPSGIANMEPTLAFNTAISFMTNTNLQHYSGESGLS YLSQMIAIVFMMFTAPATGLAAAIAIIRALAGKPIGNFFVDLIRSITRILLPVAFVAALIFIALGVP QTLEPTVTAHTIGGEVQEIARGPVGSFLSIKELGNNGGGFFGANSAHPFENPDAISNLLQIVL MLLFGTAIPFTYGKMVGNAKQGRVLFVSMAMLFIMMLGISLVAETAGNPVLNASGIQHDQG SMEGKETRFGVIQSSFYSVVTTASETGAVNTMHDTMTPIGGLVTLANMMLNTVFGGAGVG FINVLMYTIIGVFLSGLMVGRTPEFLGKKIEGREMKLIAVTLLIQPFIILAPTALALFIYPETISNP GFHGLTQALYEFTSSAANNGSGFEGLGDNTPFWNISTGIVMYLGRFFSIVTMLAVAGSLAA KKPVPETSGTFRTDNGLFAGVFLGTVLIVGALTFFPALVLGPIAEQLTLKP
3E-231	778	32	3E-231	777.7	22.2	1	1	B8ESF4_METSB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Msil_0874	Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	572	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Methylocella, Methylocella silvestris, Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	395965	>tr|B8ESF4|B8ESF4_METSB Potassium-transporting ATPase potassium-binding subunit OS=Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906) GN=kdpA PE=3 SV=1 MTVYGVLLIVILLVVLVLTIRPLGGYMAWVFAGRHTSIHPLKFIEDSLFRLTGVDPESEQNWL NYAAALIIFNLAGILLLFAFLLLQDALPLNPRGFGPMAPDLAFNTAVSFVTNTSWQAYGGETT LSYFNQMGGVAVQSFLSAATGMAVAIAMARGFARHGAETVGNAWVDITRATLYVLLPLSVI GALFLASQGAPQTFEGTVAAATLDGAVQTIARGPVASQEAIKLLGGDGGGFFNVNSAHPFE NPTALTNFFEMLLIFLIGAALTNTFGRMVGDERQGWSLFGAMLILFAVGLFVVYFSEASGNP HFAALGVDQTAGPLQAGGNMEGKDVRFGIAGSALFANVTTTSADGAVNAMHDSFTPLGGG MVLANMMMDEVIVGAPGSGLFGMLLYVLVAVFVAGLMVGRTPEYLGKKIESAEVKMAVLAL LVVPATILIPTALAAVLPTALAALSNAGPHGFSELLYAYTSAAATNGSAFAGLGANTPFFNLTL AAAMLSGRFLVILPVLAIAGSLAAKAKVPVSAGTLPTDGTQFIFLIVGAVVIFGMLTFFPALAL GPLAEHFAGPQLY

3E-231	777.9	25.6	3E-231	777.6	17.7	1	1	W8EUK3_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Hsw_0618	Hymenobacter swuensis DY53	566	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Hymenobacter, Hymenobacter swuensis, Hymenobacter swuensis DY53	1227739	>tr|W8EUK3|W8EUK3_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Hymenobacter swuensis DY53 GN=kdpA PE=3 SV=1 MNNELLSIGGIYLITLVLALPLGAYLARVFRGEKNLLDFMRPVENGIYRLSGIDARREMTWQQ HMVALLTINLVWFLLAMLVLCTQGSLPLNPDGNPSMSPDLAFNTAISFLVNCNLQHYSGESG LSYLSQIVVITFLQFVSAATGIAAAVVVFNALQTRTTEKLGNFYDYFVKSLTRLLLPGSLLIALIL AFNGTPMTLQGKQELISLQGDSVAVSRGPVAAMVAIKELGTNGGGFYGANSAHPLENPNFI TNAVENIALVIIPIAMVFALGFYLKRRKLAYMIFGVMTVGFVALLAPTVYYEMHGNPAISKLGV DQALGAMEGKEIRLGAAASAYWSITNTIISCGSVNSMHDSFMPISGMSQMLGMMTNAFYG GCGVGLLNFFAYLIAVFIAGLMVGRTPELLGKKIEAREMKIAVIVTLLHPLLILAGTALTAHLYA GNPTEYAGWLANPGYHGFSEILYEFTSASANNGSGFEGLGDNTPWWNISTGVVLLLARFL PIVGPVAIAGLLARKKYVPESAGTLPADTATFGVMVLAVIVIIAALAFFPALALGPLAEHFSLY
3E-231	777.8	31.4	4E-231	777.6	21.7	1	1	D4KH82_9FIRM	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MHY_05020	Megamonas hypermegale ART12/1	607	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	657316	>tr|D4KH82|D4KH82_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Megamonas hypermegale ART12/1 GN=kdpA PE=3 SV=1 MSADIIMQYIVFLVVLVVLSIPLGTYMAKVMNGEHVFLSKILLPIENLIYKIIGVKKDEEMTWKT YLSSVIWFFFIGLGFLYIFQCFQDKLPFNPQNIDPMSWHLSFNTAASFATNTNWQSYSGEA QLSYFSQFMGLTTQNFVSAATGIAVLFALIRAFVRAKSHTIGNFWVDLTRSTIYILLPLSVVVT MALASQGVVQNLSPGQAVQLVEPIAVDSEGNIIENATIDKDNNIVFVDGEKVEGATIVTKQFV PMGPGASQIAIKQLGTNGGGFFGVNSAHPLENPNSLTNMIECTALLLIPAGLCFTFGRNIRDK KQGIAIFAAMYIMLIAFLSIIAINEQNGTPQLAQNAAVDIVSTDYQAGGNMEGKEARFGIVQSS TWAAYTTAASNGSVNSMHDSYTPLGGLVTMLQMQLGEVIFGGVGCGLYGMLAFAILTVFIA GLMVGRTPEYLCKKIEPFEMKWAVLVCLATPIGILVASGIAAIVPSVADSLNNVGAHGFSEVL YAYSSAGGNNGSAFAGFNANTPFLNTSIGLTMIFARLLPIVGILAIAGSLVQKKKVAVTAGTLS TSNAMFVFLLIFIVILVGALNFFPALSLGPIAEYFSMIS
3E-231	777.8	30.6	4E-231	777.6	21.2	1	1	K8GCZ3_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OsccyDRAFT_4623	Oscillatoriales cyanobacterium JSC-12	562	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, unclassified Oscillatoriales, Oscillatoriales cyanobacterium JSC-12	864702	>tr|K8GCZ3|K8GCZ3_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Oscillatoriales cyanobacterium JSC-12 GN=kdpA PE=3 SV=1 MLQGWIQIAITLLIVVVITPFLGRYMARVFMGQQTLLDPVLNPLEQVIFSLSGIRSNEEMTGW QYARAVVYSNTVMLVFIFSIFMFQGVLPFNPTGLTAPSWDLALHTAISFVTNTNQQHYSGET TYSYFSQFAALGFMMFTSAATGIAVAIAFIRGLTGSPLGNFYSDLIRGITRILLPISIVGAIVFIAA GVPETLAGPAILPTLENSAMSQAIARGPVAHFEIIKELGENGGGFFGVNSAHPFENPNGFTN LVELVALLSIPSSLIITYGIFAHNQKQAWMVYSIPLAILVVFIIITAIGEYNGNPAINALLGTEAPN LEGKEVRFGWAQSALFAVFTTATMCGAINSMHDSFMPNGGFVTLSNMFLQIVFGGQGTGT AYLFAYLILAVFVTGLMVGRTPEFLGRKIEKREVVLASCLILLVHPIAILIPTAVTLAFPEQLAGI SNPGFHGLSQVIYEYTSAAANNGSGFEGLGDNTLWWNLSASFSLLAGRYIPIVALLLLADSM SRKQPVPATVGTLRTDTGLFTGVTAGVILILGALTFFPVLALGPIAEAFQIFG
4E-231	777.4	25.7	5E-231	777.2	17.8	1	1	K9TR50_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Oscil6304_4990	Oscillatoria acuminata PCC 6304	560	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria acuminata, Oscillatoria acuminata PCC 6304	56110	>tr|K9TR50|K9TR50_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Oscillatoria acuminata PCC 6304 GN=kdpA PE=3 SV=1 MLQGFIQITLTLGILVAIVPFFGRYMAAVYLEERTFLDGGCRPIERWIYQIGGISSWESMTGW QYARAVLISNLMMGILVFLIFMFQGILPLNSTGLEAPSWDLALHTAISFTTNTNQQHYSGETT FTYASQMFALGFLMFTSAGTGLAVAIAFIRGLTGRPLGNFYVDLTRSITRILLPISVIGAIVLLLA GVPETLAGPATVTTLEGATQTLARGPVAHFEIIKELGENGGGFFGINSAHPYENPNGFTNLV ETVIMVSIPASLIYTYGIIAGNKKQGWLLFWMIFILYVALIAITAVGEYYGNPLVNNLLGSSTPN LEGKEVRFGWAQTALWAVTTTGTMCGAVNGMHDSLMPTGGFSTLFNLFLQIIWGGQGTG TAYLFVFLILTVFLTGLMVGRTPDFLGRKIEKREIVLASVILLVHPIAILIPSAIAIAYPELLGNISN PGFHGISQVVYEYASAAANNGSGFEGLGDDTLWWNLSTSMSLLAGRYVPIIALLLLADSMA NKQPVPETPGTLRTDTPLFTSVTAGVMLILGLLTFFPVIALGPLAEAFQLGRY
4E-231	777.3	27.8	5E-231	777	19.3	1	1	KDPA_CYAP8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PCC8801_1929	Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	559	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	41431	>sp|B7JY03|KDPA_CYAP8 Potassium-transporting ATPase potassium-binding subunit OS=Cyanothece sp. (strain PCC 8801) GN=kdpA PE=3 SV=1 MVQGLIQIAITLLLLLIIVPNLGNYMAKVYLKQKTVLDPILLPLENLIYAISGLRSQREMTGWQY ARSVIFSNILMGIFVFSLFSFQAILPFNPTQLAAPSWHLALHTTISFVTNTNQQHYSGETTFSY GSQLFALGFLMFTSAGTGLAVAMAFIRGLIGEPLGNFYVDLTRSITRILLPIALISGLILLSQGV PETLSPPASVTTLQGATQTLARGPVAHFESIKQLGENGGGFFGINSAHPFENPNGFSNLIET LLMLCIPTSLIYTYGVMIGNKKQAWLLFSMIFIIYVFLIAITALGEYQGNPLVNNLLTTQQPNLE GKEIRFGWAQTVLWAISTTGTMCGAVNGMHDSLMPLGGLSTLFNLFLQIIWGGQGTGTAY LFVFLIITVFLTGLMVGRSPEFLGRKIEKREIVFASVILLVHPFAILVPGAITLVFPEILSGISNPG FHGVSQVVYEYASAAANNGSGFEGLGDNTLWWNLSTSVVLLLGRYVPIIALLLLAESMRQK QPVPETTGTLRTDTGLFTAVTAGVILILGALTFLPVLALGPIAEGFKLGW

6E-231	776.9	33.7	7E-231	776.7	23.4	1	1	R6UL B1_9 FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN746_00 930	Erysipelotrichaceae bacterium CAG:64	572	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, environmental samples, Erysipelotrichaceae bacterium CAG:64	1262981	>tr|R6ULB1|R6ULB1_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Erysipelotrichaceae bacterium CAG:64 GN=kdpA PE=3 SV=1 MNSALILQDVVYVVALLAIGYPLGCYIYKIYNGERVALMRIFAPLEQLLYRVMGVDEEQQMHA KKYASSVLWFSLFGFLIVMGLHLVQAWLPLNPEQLENTSVHLAYNTAASFVSNTNWQAYSG ETTLSYLTQMAGLTVQNFVSAATGIAVLFVLCRGFVRRETKNLGNFWSDLVKITLYILLPLSV VVCLILVSQGVVQTLDPYASYTTLEGTQGVLPLGPAASQIAIKQLGTNGGGFFGVNSAFPYE NATPLSNIIEALCLLLIPAALCFTFGKAVKDTRQGKTILVVMTVIFVAALVGLSCAEIFGAPSWD SVASLGGSMEGKETRFGVGGSSLWAAATTAASNGSVNAMHDSLTPLGGMITMFLMQLGE VVFGGVGCGLYGMLAFALLTVFMAGLMVGRTPEYIGKKINAFDMKMVCIIILVPPLCLLLATAI TTLFPAAQQLQADGGWLSNTGSHGFSEILYAYTSMAGNNGSAFAGFQANTVLTNVMGGTV MLLVRFLPMVAVIYLAQSLASKKYVPAGSGTLATTSPLFVGFLIVIVLIVGALTFLPVLALGPLA EFFTQLHVLG
6E-231	776.9	28.6	7E-231	776.6	19.8	1	1	B2JE 27_B URP8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bphy_205 7	Burkholderia phymatum (strain DSM 17167 / STM815)	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia phymatum, Burkholderia phymatum (strain DSM 17167 / STM815)	391038	>tr|B2JE27|B2JE27_BURP8 Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia phymatum (strain DSM 17167 / STM815) GN=kdpA PE=3 SV=1 MSLNNVLQPAFFIVVLLAAAVPVSGYLSRVMDGSSRVVKLGGPIEGLLYRLAGVDPSQEMG WKRYAIATLAFNLLGVVFLYALLRVQGSLPGNPQQFGAMSADGAFNTAISFVTNTNWQDYT PEQTVGYLTQMLGFTVQNFLSAATGIVVVIALVRGFARHTAQTIGNFWVDITRVTLYVLLPM AAIIAALLMSQGVIQNFKSYEDVPTLQTTTYAAPKVDAQGNPVKDAKGNPVTVDTPVKSQTI AMGPVASQEAIKMLGTNGGGFFNGNSAHPYENPTPFSDFVQMFSILIIPAALCLVFGRMIGD RRQGIAVLAVMTIAFAVAVAGEIGAEQGGNPLFTSLHVDQSASALQAGGNMEGKETRFGIA QSGIFTVATTAASCGAVTNTHDSLTPLGGLVPMLLMQLGEVIFGGVGSGLYGMLVFALLAVF VAGLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPLLVLVATSIAVLTDAGKAGILNPGAHGFSEI LYGFSSAANNNGSAFAGLTVGTPFYNWLTAVAMWFGRFGTIVPVLAIAGSLAAKKRIAVTG GTLPTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLMMIAGH
6E-231	776.8	30.6	7E-231	776.6	21.2	1	1	R5UV N1_9 PORP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN709_01 650	Odoribacter laneus CAG:561	565	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter laneus CAG:561	1263089	>tr|R5UVN1|R5UVN1_9PORP Potassium-transporting ATPase potassium-binding subunit OS=Odoribacter laneus CAG:561 GN=kdpA PE=3 SV=1 MNTEILGSVLQVVAMVVLAYPLGRYMAKVYKGERTWSDFMAPIEKWIYKLCGINPQEEMN WKKFLVALLTINVFWFFWGMILLVCQGWLPLNPDGNAGQTPDLAFNTCISFMVNCNLQHYS GESGLTYFTQLFVIMLFQFITAATGMAALAGIFKAMATRSGKQIGNFWNLLVKSCTRILLPLS LIVGFILILNGTPMGFDGKMELTTLEGARQSVSQGPTAAIVPIKQLGTNGGGYFGVNSAHPL ENPTFLTNMVECWSILILPMAMVFALGFYLKRKKLAYTIFGVMLFAYLLGVVGAHYYEMNGN PRIDEMGIAQNRGAMEGKEIRLGSAATALWSQTTTVTSNGSVNGMHDSVMPLTGMMTMLN MMINSWFGGVGVGFMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIAMIVALAHPFIILV GTGIASYLAAHQPELAGAWLNNPSFHGLSEMLYEYTSAAANNGSGFEGLGDNTYFWNFTT GLVLILGRYLPIVGQVAIAGLLASKKFIPESAGTLKTDTGTFAVMTFAVILIVAALSFFPALTLGP IAEYLSL
7E-231	776.6	26.2	8E-231	776.4	18.2	1	1	F2IFU 1_FL UTR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Fluta_054 4	Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	575	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Cryomorphaceae, Fluviicola, Fluviicola taffensis, Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	755732	>tr|F2IFU1|F2IFU1_FLUTR Potassium-transporting ATPase potassium-binding subunit OS=Fluviicola taffensis (strain DSM 16823 / RW262 / RW262) GN=kdpA PE=3 SV=1 MNTELFGVIAMFILTVAIAIPLGRYIGKVYLGEKTLLDPIFNPIERFFFRISGLDGTREMNWEQH IYALLGINLVWFFICFLLLLNQGWLPLNPDHNPSMSPDLAFNTTISFLVNCNLQHYSGETGLS YLSQIGGIMFLQFVTAGTGMAACAMVFNAMRNRQSDQLGNFYNYFIKSCTRVLLPVSFVAAI ILVVSGTPMTWEGKETFTTLQGDEQVVSRGPAAAMVAIKQAGTNGGGFFGVNSAHPLENP TYLTNMVENILIVLIPIAMVFALGYYLKRKRMAWMIMGVMTVGFLALFLPSITNEVKGNRAITE MGIDQSSGSMEGKEVRFGAEASAYWGITTTVTSNGSVNAMHDSFTPITGGMAMLGMMAN SFYGGVGVGFLNFYIFIILAVFLSGLMVGRTPEFLGKKVEAREVKIAAFIAILHPLLILAGTALSA YFVSHNTQMGYWYDGKASGWLNNPGHHGFSEMLYEYTSSAANNGSGFEGLADNNPFWN MTTGIVMLLSRYLPIIGPLAIAGLLAGKKHIPESAGTLQTDTPIFGVMIFAVIFIIAALSFFPALAL GPFAEYFSQIH
7E-231	776.6	38.5	8E-231	776.4	26.7	1	1	K8W7 S0_9 ENTR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OO7_129 19	Providencia sneebia DSM 19967	566	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia sneebia, Providencia sneebia DSM 19967	1141660	>tr|K8W7S0|K8W7S0_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Providencia sneebia DSM 19967 GN=kdpA PE=3 SV=1 MAMNAFLLIGSFLLILFLLAKPLGNIIACLIEGDLPRYILKTESLLWRLAGAKQTGREMAEMNYL QYAFAILLFNLLGFVLLFTILIFQGSLPLNPQKLAGMNWDLAFNTAISFITNTNWQAYSGENTL SYFSQMVGLTVQNFLSAATGIAVVFALIRAFSRHNSKTLGNAWVDIARITLYLLLPLSVIFALF FVGQGVIQNFSAYILSNNLDSTSQLLPMGPVASQEAIKLLGTNGGGFFGANSSHPFENPSAL SNFVQMLAIFLIPTSLCFAFGRTVGNNKQGHALLWVMAIIFVIAAIVVIQAEYVGNPFLLDITNS SINMEGKESRFGILGSALFAVVTTAASCGAVNAMLDSFTAFGGMLPMWLMQIGEVVFGGV GSGLYGMLLFVLLAVFLAGLMIGRTPEYLGKKIEVREMKMVAIAILVTPTLVLIGTTIALMTDA GRAGIFNPGTHGFSEVLYAFSSAANNGSAFAGLSANTPFYNVLLAIAMFLGRFGVIFPVLAI AGSMAMKKPQAISAATLPTHGPLFIGLLILTILLIGALTFVPALALGPIAEHLQTWLVA

8E-231	776.4	25.4	9E-231	776.2	17.6	1	1	A0A089YP99_9PSED	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LT40_01775	Pseudomonas rhizosphaerae	564	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas rhizosphaerae	216142	[illegible] subunit OS=Pseudomonas rhizosphaerae GN=kdpA PE=3 SV=1 MHSHDFALIAAFFALILLPAPWLGRFYYKVMEGQRTWLSVPLQPVEKLCYRFAGIDAQQQQ TWQRYALALLAFNLAGFGVLFAILMLQGYLPLNPQHLPGQEWTLAFNTAVSFMANTNWQA YSGETSLSYLSQMAGLGVQNFLSAATGLAVLVALCRGISRRSASTLGNFWVDVTRATLYGL LPLALLLAVFLVWQGVPQTFAPYVDALTLQGNAQTIPLGPAASQIAIKQLGTNGGGFFGVNS AHPFENPTAWSNLFELAGILIIPVALVFTFGHYVKDLRQSRAILACMLTLLLLGLGLSLYAEQQ PNPSLASAMVDQAAPLEGKESRFGTTASVLWSVATTAASNGSVNAMHDSLSPLSGMVALV NMMLGEVIFGGVGAGLYGMLLNVLLTVFLAGLMIGRTPEYLGKKLQAREVRWLVASLLVMP VGVLVLGAIAVSLPGPAGAVSNPGPHGFTQLLYAYTSASANNGSAFAGLSANTAFHNLMLA LGMLLGRFGYILPVLALAGALASKNASAPSADSFATHGLLFITLLTVTLLIVGGLTFLPVLALGP IAEHLNMHF
9E-231	776.3	24.4	1E-230	776.1	16.9	1	1	KDPA_BEII9	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bind_1096	Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	568	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Beijerinckia, Beijerinckia indica, Beijerinckia indica subsp. indica, Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	395963	[illegible] OS=Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712) GN=kdpA PE=3 SV=1 MNWQGWAEIAFILGLTVALGWPLGLFLARLWEGEQTWLDPVLKPVERLVYRACGIDPRQS QTWSSYALALLAFSAASFILLYAILRLQGWLPLNPQGFAGLPPHLAFNTAISFVSNTNWQSY VPEATVSAFSQMAGLTSHNFLSAAAGIAVAAAVTRAFAANREEGLGNFWVDLTRVSLYLLLP LSIVIALVFVALGEPQTLSAHVTATTLEGVQQTIALFPTASQEAIKQLGTNGGGIFNANSAHPF ENPNPLTNLIEIVEMNVLGFACVVAFGRLVSARRDARALITVMAIFVAVAASVIYWTETRPAP ALVGAQAEASVNMEGKEVRFGAPATAIWTAATTGASDGGVNAMFDSFMPLGGGMAMFMI QLGEILPGGVGSGLYGMIVLALIAVFVAGLMVGRTPEYLGKKVEAREVKYAMLAVLILPLAIL GFSAAAAVLPVALEGLANTGAHGLSEILYAYSSATGNNGSAFAGFSANTPWWNTTLGIAML LGRFGYVIPVLAIAGSLAAKPKLTVTAGTFPTDGPLFIGLLIGVILILGGLQFFPALALGPIVEHF QVLQALAR
1E-230	776	34.4	1E-230	775.8	23.8	1	1	R6H804_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN490_00083	Firmicutes bacterium CAG:137	604	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:137	1263004	>tr|R6H804|R6H804_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Firmicutes bacterium CAG:137 GN=kdpA PE=3 SV=1 MTAVIQYILYLVILVALAVPLGAYIKKVMNGEKTFLSRVLTPCENLVYKVMRVNRDEQMNWK QYTASVLIFSGIGLVFLFLLQILQGVLPGNPQGLPGVKWDLSFNTASSFVTNTNWQAYSGES TLSYLSQSLGLTVQNFVSAATGIAVLFALIRGFIQVKTSGLGSFWVDMTRIIIHILIPLNLVISLLL VGGGVIQNLKGAETVSLVEPVAVSADGEILDGAVIDEDAGTVTVDGILVPDAEIVTEQFVPM GPAASQVAIKQSGTNGGGFNGVNSAHPLENPNAFTNLIEMISILLIPAALCFTFGSAVKNKKQ GVAIFAAMFICLCVALGCIAVSEQAGTAQLAQDGAVNMTMIDQAGGNMEGKETRFGIAASS TWAAFTTAASNGSVNSMHDSYTPLGGMITMLLMQLGEVIFGGTGCGLYGMLAFAILTVFIA GLMVGRTPEFLGKKIEPFEMKWAVLVCLATPIGILVGSGIAALVPSVMDSLNNGGTHGFSEM LYAYSSAGGNNGSAFAGFNANTVFLNVSIGLVMLFVRFLPVVGTLAIAGSLAQKKKIAATAGT LSTTNAMFVFLLIFVVLLIGALSFFPALALGPLAEFFGSLA
1E-230	776	25.3	1E-230	775.8	17.6	1	1	KDPA_DESDA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Ddes_1677	Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	583	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio desulfuricans, Desulfovibrio desulfuricans subsp. desulfuricans, Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	525146	>sp|B8J1E9|KDPA_DESDA Potassium-transporting ATPase potassium-binding subunit OS=Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949) GN=kdpA PE=3 SV=1 MENIIWQCLLYLSLLTALAWPLGKYIGKVMDGEPFWLQRALAPCERALYRLMGVDPAEQMG WKCYMACVIAFSAVSLVALTALLMAQHLLPLNPRNVSGASWHLALNTAISFVTNTNWQSYA GESTMSYLSQMAGLTVQNFVSAAVGIAVLFALIRGVRASGGIGLGNFWADATRAVLYILLPL SLVMSLLLIEQGVPQNFTDYRAAALLEPLAAEDGAPITHQLVPMGPQASQVSPKQLGTNGG GFNGVNSAHPHENPTPASNMLEMLALLLIPAALCFTFGAKIGDMRQGVAIFAAMFILLTSAVS FTVQAELNATPQIAQGGQVLVAPQSGLQGQAGGNMEGKETRFGIAGSALWASATTAVSN GSVNAMHDSFTPLGGMIPMVLMQLGEVIFGGVGSGLYGMLAFVLLTVFLAGLMVGRTPEYL GKKIEPFEMKMAVVVCLTTPVVILAGGGLMCLAPQIVDSLNNPLPHGFSEILYAATSAGANN GSAFAGLNANTPFLNVLLGVLMLAGRFAPIAAILAMADGLAGKKICPPGAGTLSTCNGLFIFLL IFVILLVGALSFFPALALGPLAEHLQMTR
1E-230	775.9	29.8	1E-230	775.6	20.6	1	1	A0A088EVH3_9SPHI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KO02_06975	Sphingobacterium sp. ML3W	562	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. ML3W	1538644	>tr|A0A088EVH3|A0A088EVH3_9SPHI Potassium-transporting ATPase potassium-binding subunit OS=Sphingobacterium sp. ML3W GN=kdpA PE=3 SV=1 MNTEIIAIIVLFLGTIALAIPLGRYIAKVFAGDKTFLDPIFYPIEGFFYKITGIDSKVEMNWKQQM VALLTINMLWFLLGMSVLMTQGMLPLNPDHNPSMSPDLAFNTVISFVVNCNLQHYSGETGV SYLGQYWLMFLQFVSAGTGMAAVVTLFRAFRDKTAIDLGNFYEYFIKSCTRILLPLSFVVAIL LVFQGTPMTFDGKDTMVSLQGDTVQVSRGPAAAFVAIKHIGTNGGGFFGANSAHPFENPT YFSNMVEMAAQMIVPFAMIFAFGYFIKRRKLSWMMFAVMTVGFLLLAIPNIRMEMNGNPAIE KLGIDQSLGAMEGKEIRIGAATSGFWSIVTTVISTGSVNSMHDSSMPLSGMNELLAMMINSF YGGAGVGILNFFIFIILAVFISGLMVGRTPEFLGKKIEAREMKIAMIIALIHPFLILVGVGLATAFP GQGAATLNNPGFHGFSEILYEYTSSSANNGSGFEGLGDNTPWWNISTGIVLIFSRFLPIIGPV AIAGLLAQKKFIPQGEGTLQTDTATFGILIFTVIAIVAALSFFPALALGPIAEYFSMH

2E-230	774.9	31.3	3E-230	774.7	21.7	1	1	D3VAM5_XENNA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA XNC1_1398	Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	565	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus nematophila (Achromobacter nematophilus), Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	406817	>tr|D3VAM5|D3VAM5_XENNA Potassium-transporting ATPase potassium-binding subunit OS=Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6) GN=kdpA PE=3 SV=1 MVASAFLLIASFLLILFLLSKPLGNLIACLVEGELPRWLIKAETSLWRSCGLQKPGNNINEMN WRQYFFSVLIFNIAGLLLLFILLISQGHLPLNPQHFSGMRWDLALNTAISFITNTNWQAYSGE NTLSYLSQMAGLTVQNFLSAATGIAVAFAFIRAFSRQGIKTLGNAWVDIVRITLYLLLPLAIIIAL FFVSQGVIQNFSPYVLIHSLENQQQLLPMGPVASQEAIKLLGTNGGGFFGANSAHPFENPT SLSNFVQMLVIFLIPSALCFAFGLVVRDEHQGYTLLWAMSIVFVIAASIVMYAEIAGNPYLISP DISHHFNMEGKETRFGVLVSAFYSVVTTAASCGAVNAMLDSFTALGGMVPLWLMQIGEVIF GGAGSGLYNLLLFVLLAVFIAGLMIGRAPEYLGKKIDVYEMKMVALAILVTPSLVLLGTALAIST DAGRDAITNPGAHGFTEILYAFSSAANNNGSAFAGLNTNNIFYNLLLGIVMFLGRFGIILPILAI AGSMINKKRQPISSGTLPTYGFLFTGLLILVVLLIGALTFIPALALGPIAEQLQLWR
2E-230	774.9	29.8	3E-230	774.7	20.7	1	1	E1T3S5_BURSG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BC1003_2356	Burkholderia sp. (strain CCGE1003)	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. (strain CCGE1003)	640512	>tr|E1T3S5|E1T3S5_BURSG Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia sp. (strain CCGE1003) GN=kdpA PE=3 SV=1 MNSNNVLQAGLFIVVLLAAAVPVARYLGGVMDGTSRVLRIGAPLERLLYRMAGVDPSSEMS WKQYALATIAFNVLGALFLYLLLRVQGWLPGNPQQLGAMTVDGAFNTAVSFVTNTNWQDY TPEQTVGYLTQMLGLTVQNFLSAATGIVVAIALLRGFARHSAQTIGNFWVDLTRVALYVLLP MSIILATLLMSQGVIQNFKAYENVPTLQTTSYAAPKLDAQGNPLKDAKGNALTVDTPVSTQTL AMGPVASQEAIKMLGTNGGGFFNGNSAHPFENPTPFANFLQMFAILIPAALALVFGRVIADR RQGIAVLAAMTIAFGVCVFAEIGAEQSGNPAFAALHVDQSANAMQSGGNAEGKETRFGIAQ SGIFTIATTAASCGAVANMHDSLTPLGGLYPLLLMQLGEVIFGGVGSGLYGMLVFALLAVFV AGLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPLLVLVGTSIAVLSDAGKAGIANPGAHGFSEIL YAFSSAANNGSAFAGLTVGTPFYNWLTAIAMWFGRFGTIVPVLAIAGSLAAKKRIGVTGGT LPTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLTMMGAH
3E-230	774.8	35.7	3E-230	774.6	24.7	1	1	Q11TL6_CYTH3	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CHU_1982	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	578	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Cytophaga, Cytophaga hutchinsonii, Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	269798	>tr|Q11TL6|Q11TL6_CYTH3 Potassium-transporting ATPase potassium-binding subunit OS=Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469) GN=kdpA PE=3 SV=1 MVICATYCLNLKNSNPMNTEISGILLMYALVIALAIPLGRYIGKIFNYEHTWLDIIFDPLDKLFFK LSAIDPTKEMNWKQHLIALLTINLVWFIMAMLVLTNMSWLPLNPDGNPSMSGDLAFNTAVSF VTNTNLQHYSGESGLSYLGQLILMLWQFISAGTGIAICAVVFVAMKERTTNTLGNFYSFFVR SCTRILLPIAFVVAIVLAFNGMPMTFEGKDTMVTLQGDTIQVSRGPVAGFVAIKHLGTNGGG FFGVNSAHPFENPNYFTNITEMVTQMLIPIAMIFALGFVLKRKKLSWMIFGVMSIGFILLTIPTI LFEMHGNQNITTMGIAQEMGSMEGKEVRFGSAASAYWSIATTVISTGSVNSMHDSFTPLSG MNQMLAMMINSFYGGCGVGMLNFYIFIILAVFISGLMVGRTPEFLGKKIEAKEMKIAMIIALLH PLLILVGTAIACSAPAVTAGTLSNPGFHGFSQMLYEFTSSSANNGSGFEGLGDNTPFWNIAC GLVMLLGRYLPIIGPVAIAGILASKKYIPESNGTLNTDTATFGLMVFAVIALVAALAFFPALTLG PIAEYFSII
3E-230	774.8	36.1	3E-230	774.5	25.1	1	1	A0A089MGJ0_9BACL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PGRAT_25550	Paenibacillus graminis	555	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus graminis	189425	>tr|A0A089MGJ0|A0A089MGJ0_9BACL Potassium-transporting ATPase potassium-binding subunit OS=Paenibacillus graminis GN=kdpA PE=3 SV=1 MSYIAIAVTLLLSLLLARPAGLYMAQVFNYERTGLDRWVGWLEKPVFAIGGIRKENYSWKQY ALAAVLSNAVMMLLVYLIFRFQGVLPLNPSGIASMEPTLAFNTAISFMANTNLQHYSGESGLS YLSQMLAIVFMMFTSPATGLAVGIAIIRGLTGKPLGNFFVDMVRGITRILLPISFVLALVFVALG VPQTLEPTALGHTLEGMTQEIARGPVASFLSIKELGNNGGGFFGVNSAHPFENPDAVSNLL QILLMLLLGTGLPFTYGKMVGNKKQGRVLFVSMAMMFIVFLGISLASENAGNPAVNALGIQH QQGSMEGKEVRFGVAQSALYSVVTTASETGAVNTMHDTLTPIGGLITIGNMMLNTVFGGVG VGFVNVLMYTMIAVFLSGLMVGRTPEFLGKKIEGKEMKLIAVTLIINPMLILLPTALALLTQSDT LSNPGFHGLTQALYEFTSAAANNGSGFEGLGDATPFWNISTGIVMFLGRYFSMIAMLAVAG SLAAKKTVPETSGTFRTDKALFGTVFLGTVLIVGALTFFPALALGPIAEFLTLKP
3E-230	774.6	32.1	3E-230	774.4	22.3	1	1	H1ZCI8_MYROD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Myrod_0226	Myroides odoratus DSM 2801	564	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteria, Flavobacteriales, Flavobacteriaceae, Myroides, Myroides odoratus (Flavobacterium odoratum), Myroides odoratus DSM 2801	929704	>tr|H1ZCI8|H1ZCI8_MYROD Potassium-transporting ATPase potassium-binding subunit OS=Myroides odoratus DSM 2801 GN=kdpA PE=3 SV=1 MNTEIIGILVTFLVAIGISIPLGKYIAKVYAGQPTFLDTIMSPLEQFCYKSSRIKPEEGMNWKQH LVALLTLNAVWFVVAFILLLTQGSLPLNPDHNPSMSPDLAFNTAISFLVNCNLQHYAGETGAT YLAQLALMFLQFVSAATGMAAAVALFEAFRNKTTTLLGNFYVYFVKSITRILLPLSVIVAAILIF QGTPMTFEGKDTITTLEGQQVEVSRGPAAAFIAIKHLGTNGGGFFGTNSAHPFENPTYLTN MVEMIAQLIIPLAMIFAFGYYINRKRFSWMMFGVMTLGFLCLAIPNVVMEANGNPNITAMGID NSLGAMEGKEVRIGAAASGFWSIVTTVISTGSVNSMHDSTMPLSGMNQLLAMMINAFYGGV GVGILNFFVFIVLAVFISGLMVGRTPELFGKKIEAKEMKIAMVIALIHPFLILSSTALGAAFPEFT KDTLNNPSFHGFSEILYEYTSSAANNGSGFEGLGDNTPWWNFSTGIILLLGRFLPIIGPVALA GCLAQKRYVPESAGTLATDTTTFGMIVFTVILIVAALAFFPVLTLGPIADYFTILSL

3E-230	774.5	37.6	3E-230	774.3	26.1	1	1	M1E4S0_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Thena_0835	Thermodesulfobium narugense DSM 14796	564	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermodesulfobiaceae, Thermodesulfobium, Thermodesulfobium narugense, Thermodesulfobium narugense DSM 14796	747365	>tr|M1E4S0|M1E4S0_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Thermodesulfobium narugense DSM 14796 GN=kdpA PE=3 SV=1 MNLFLDLLQFALFIILLTLCVKPFGLYIAKVFQGEKIFISKIISPIEQFVYKLSFVNPENQMDWKE YAVSMLLFNMIGFIFLFLLLLTQQLLPLNPEHFQGFSLDLALNSAISFITNTNWQAYSGESSTS YLTQMLGFTVQNFLSAATGIAILIALIRGFASRQTKVIGNFWVDITRTTLYILLPLSIIFAVFLISQ GVIQNFNNYQIVHFVSSQIIPMGPVASQEAIKLIGTNGGGFFNANSSHPYENPTPLTNFLEAF MIIIIPASLTYTFGTMIKNKKQGWAIYFVMLFLFAIFLSIQYSANTGKDPIISNLGVSGPYIEGQE VRFGVGGTTLFSTTTTAVACGAVNAMHDSLLPLGGMIPMILMLLGEVVFGGVGSGLYTMLA FVIIAVFVAGLMIGRTPEFLGKKIEVKEMWMSIIIVLTSGILVLIFTSIALVTKGGLSSILNPGPHG LSEILYAYASTANNNGSAFAGLNANTPFYNISTALAMLIGRYVPAVAAIYMASSLAEKKYTPP SIGTLPTDCVPFMIWLVLIIITVGALTFFSALALGPFLENLIMQRGF
4E-230	774.1	28.8	5E-230	773.9	20	1	1	F8EK12_RUNSL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Runsl_3034	Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	584	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Runella, Runella slithyformis, Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	761193	>tr|F8EK12|F8EK12_RUNSL Potassium-transporting ATPase potassium-binding subunit OS=Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4) GN=kdpA PE=3 SV=1 MLQEILGIVLLFVLTVLLALPLGRYIAKVYLGQPTWLDFMSPLEHFIYKVCRINPKKEMTWQE HLTALLTINFLWFFWMMFILMNQGWLPLNPDGNPSMSPDLAFNTAVSFLVNCNLQHYSGET GVTYFSQLAGLMFMQFVTAGTGMAAAAIVFKAMKPHPSPPLKGGSFYISLSLTGERFGVGL GNFYHYFLKSCTRILLPISLISAIILVFNGTPMNWEGKANIVTVQGDSVQVSRGPAAALIAIKQ AGTNGGGYYGVNSAHPLENPNYLTNIVENILIILIPIAFVFALGFYLNRKKLAWMIFGVMTIGFL LLLSVSVYFEMQGNPALHKMGIRQTLGSMEGKEIRFGSAASAFWGITTTTTSNGSVNAMHD SMTPLSGAMQMIDMMINALYGGVGVGFLNFYVFIISVFISGLMVGRTPEFLGKKIEAKEMKIA TIIALLHTFLILAFTALSSYVFTQDPSIGWLNNPGFHGFSEMLYEYTSSSANNGSGFEGLGDN NPFWNITCGIVLILSRYLPIIGPVAIAGILANKKYIPESAGTLQTDTATFGFMVFAVIFIIAALSFF PALALGPLAEFFTLR
5E-230	773.8	28.3	6E-230	773.5	19.6	1	1	C7PUT0_CHIPD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cpin_3616	Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)	570	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Chitinophaga, Chitinophaga pinensis, Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)	485918	>tr|C7PUT0|C7PUT0_CHIPD Potassium-transporting ATPase potassium-binding subunit OS=Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034) GN=kdpA PE=3 SV=1 MNSEITGVILTFILTLVIAFPLGKYIARVFQGERTFTDFLNPVERFIYRICGIDPHKEMNWKQH MAALLSINLVWLIYAFFILLFQSHLPLNPDGNPDMTPDLAFNTAISFLVNCNLQHYSGETGVT YLSQLIVITFLQFVSAATGVAAVAVLFRAFADKTTEKLGNFFVFFTKTITRILLPLSIIMAITLAFN GTPASFDGKDSIVTLQGDSVQVSRGPAAGMIAIKHLGTNGGGWFGANSAHPLENPNYFTN VVEIVAQVILPMALIFAFGFFIRRRKLGYVIFGVMTAGMLTLMIPNMISEISGNPLLHHLGLKDI TAMEGKEVRLGVPASAYWQVMTTIISTGSINSMHDSSMPLSGAMQMLGMMTNCFYGGKG VGLLNYFIFLIIAVFISGLMVGRTPEFMGRKVEAREMKIAAIIALFHPFLILVGTALSAYFAAHHP QMVWSVQPANWFNNPSNHGFSEMLYEYTSSSANNGSGFEGLADNNIFWNITTGIVMILGR FIPIIGPVAIAGILAKKKYIPESAGTLQTDTSTFGIMTYAVIMIVAALAFFPALTLGPIAEYFQSY
6E-230	773.7	41.5	7E-230	773.4	28.8	1	1	X2GUB6_9BACI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA T479_15015	Lysinibacillus varians	564	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus varians	1145276	>tr|X2GUB6|X2GUB6_9BACI Potassium-transporting ATPase potassium-binding subunit OS=Lysinibacillus varians GN=kdpA PE=3 SV=1 MWQIAIVCIIYLPLVILTGHYLFRVTMHKKTWLDPLMDKVDHVIYKVCGIKQVDMTGKQYVLS LIISNAFMVFIGYILLRIQSFLLLNPNDIENMEASLSFNTIISFMTNTNLQHYSGESGLSYLSQML VIIFMMFTSAATGYAACMAFCRRLVAKSDTLGNFFVDFVRVITRVLMPISIVVAIILVSQGAPQ TFSANQTVQTIEGKMQDIALGPVASLESIKHVGTNGGGFNGANSTTPFENPTVISNIVEMLS MMLLPGACVVAFSLMVAYRKKKTIFGKQGLAIFAAMGMLFLIGLVTVYIAERAGNPLISNLGIT QELGSMEGKEMRFGVAQSALFTTVTTAFTTGSVNNMHDTLTPIGGMVPMFNMMMLNVVFG GKGVGLMNMMMYVLLTIFIACLMIGRTPQFLGKKIEEKEMKLIALCILIHPAIILLFSALAVATTS GVAGITNPGAHGLSQVLYEFASASANNGSGFEGLADNSTFWNVTTGLAMFFGRYLTIILQLA IASLLAKKMWHSDSVGTLKTDTSMFTFLLVAIVLMIGALTFLPALALGPITEHLQIHS
6E-230	773.6	34.2	7E-230	773.4	23.7	1	1	R7GCL6_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN631_00318	Eubacterium dolichum CAG:375	578	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium dolichum CAG:375	1263076	>tr|R7GCL6|R7GCL6_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Eubacterium dolichum CAG:375 GN=kdpA PE=3 SV=1 MLQIIGTLLIFLILIFPIGNYVYHIATGKKSFVDPLFDRIDNTLYKVLRIHTASMGWKTYALSLLLV NACLIFVGYLILRLQATSLLNPNGVGGMEEALSFNTIISFMTNTNLQHYAGESCLSYLSQMLVI IMMMFTSAASGYAACMAMIRGLLGKPMGNFYVDFIRIITRFLLPMSFFVGLFLVWQGVPQNL ASNITVTTLEGKLQDIASGPIAALESIKHLGTNGGGFLGANSATPLENPTILTNLAELYSMMLL PASCVFVFGRMAYDKHQERKIKEGVLSISEAPVQKRVWLGKEGRTIFIAMSVLFVIGLGLCF YSESQGNSAVEAVGISQTAGNMEGKEVRFGVAQSSLFTTVTTSFTTGTVNNMHDTLTPLG GFVPMLHMMLNVVFGGVGVGLMNMLIYAILAVFICGLMIGRTPEYLGKKIEGKEMKLAALSIII HPLLILAFSALAVSTQAGLEGISNPGYHGLSQILYEFASSAANNGSGFEGLADNTLFWNLAC GVVMFLGRYMSIIIQLGIAGSLMQKTEVNETIGTLKTDTASFAIILVVVVYIFAALTFLPSLALGP IAEFLTI

6E-230	773.5	32.1	7E-230	773.3	22.3	1	1	A0A0F0CBK3_9CLOT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CLFS41_27470	Clostridium sp. FS41	570	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. FS41	1609975	>tr|A0A0F0CBK3|A0A0F0CBK3_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium sp. FS41 GN=kdpA PE=3 SV=1 MFQILMTLLIYMVLVVPVGIYLYHVATKQKTFADPVFDRIDNRIYKVCRIERGNMSWKTYALN LLMTNAVMILIGYLVLRLQGLLFLNPNKIGAMEPTLSYNTIISFMTNTNLQHYSGESGLTYLSQ VVVIIFMMFTSAATGYAACMAFCRGMSGRPMGNFYEDMVRNTTRILIPIAFIVGLILIWQGTP QNFQSNFTVHTMEGKLQDIATGPIAALESIKHVGTNGGGFLGANSSTPLENPTIISNIAELYS MMILPGACVIAFGRMIADKRRELGKKTIFGKQGRTVFAAMAIIFMAGLAVCYVSEKAGNPILA GVGLNQDMGSYEGKEVRFGIAQSALFTTTTTSFTTGTVNNMHDTLTPLGGLVPLLHMMLNC VFGGKGVGLMNNMVMYVILAVFISGLMIGRTPEYLGKKIEGREMKLVAVCLIIHPLLILGFSALA VSTAGGLEGITNPGFHGLSQVLYEYSSSAANNGSGFEGLADNSVFWNMTAGLAMYFGRFP AIILQLAIAGSILAKRKVNETIGTLRTDNVIFTLILVFVVYIFAALTFFPALALGPIAEHLTVWFPV MG
8E-230	773.2	28.9	9E-230	773	20.1	1	1	D0IYN9_COMT2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CtCNB1_0529	Comamonas testosteroni (strain CNB-2)	568	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Comamonas, Comamonas testosteroni (Pseudomonas testosteroni), Comamonas testosteroni CNB-1, Comamonas testosteroni (strain CNB-2)	688245	>tr|D0IYN9|D0IYN9_COMT2 Potassium-transporting ATPase potassium-binding subunit OS=Comamonas testosteroni (strain CNB-2) GN=kdpA PE=3 SV=1 MWLPWMEFAAVLTAATLLTIPMGQWLARCFTSERHGWLERLSYRVMGVNPQERMGWQR YGTALVLSNALMMLLGYLLLRLQGALPLNPLEIAAQAPDLAFNTAASFITNTNWQAYSGENS LSNATQMVVITFLMFAGATTGVAAGAGFVRGLARSSSKDVGNFWVDFVRVFWRVLLPLSFI MALVYVWQGIPQTLHTDAVATTLEGGRQQLLMGPVASLESIKHLGTNGGGFFGMNAAHPF ENPTPLTNLLHILSMLLIPAGMTYAFGSMLLRRKQGWVLFAACMVMFVGFLSLVFVAEQNG SQLLARAGADQQYSLIQSGGNMEGKELRFGIADTALFVATTTAATTGSVNAMHDSLTPLGSI TPLAQMMLNCVFGGDGVGLINLIQYAILTVFLAGMMIGRTPEFLGKKIEVREIKLVMLAVLVPP ACVLGFTALAVLWPDAAASLNNRGPHGFSEILYAYASATANNGSAFAGLNANTPFFNTTTG LAMLAGRFLTLVPMLAVAGSLAAKATVPPGPGTFPTATPLFMGLLVFVVLVVGGLTFLPALA LGPVIEHLQMLVAQLYA
8E-230	773.2	30.8	9E-230	773	21.3	1	1	K9UV66_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cal6303_0702	Calothrix sp. PCC 6303	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix parietina, Calothrix sp. PCC 6303	1170562	>tr|K9UV66|K9UV66_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Calothrix sp. PCC 6303 GN=kdpA PE=3 SV=1 MLQGWIQIALTLLIVIATTPLLGGYIARVYMGERTLIDPIITPIERVIYALSGVRTQQDMTGKQY ATAVLYSNLMMGILVFSILMLQGFLPLNPTGLGTPTWDTALHTTISFLTNTDQQHYSGETTFS YASQMFALGFLMFTSAGTGLAVGIAFIRGLTGKALGNFYVDLTKSITRILLPISIIGGLLLILAGV PETLAGVATATTLEGSTQAIARGPVAHFEIIKQLGENGGGFFAINSAHPFENPNGFSNLLETL AMISIPTALIYTGVFANNRKQAWLAFWMVFAIFIVLVGIAAVGEYQGNPQVNALLGSQQPN LEGKEVRFGWAQTALWAVITTGTMCGAVNGMHDSLMPLGGFVTLFNLFLQIIWGGQGTGT AYLFIYFILAVFLTGLMVGRTPEFLGRKIEKKEIVLASVVLLVHPFAILIPWAIVFAFPDTLGGIS NPGFHGVSQVVYEYASAAANNGSGFEGLGDATLWWNLSTSVTILAGRYIPIIALLLLADSMS RKQPVAMTSGTLRTDTGLFTGVTGGVILILGALTFFPVLVLGPIAEGFLMGRGG
9E-230	773	31.2	1E-229	772.8	21.6	1	1	F4C4K6_SPHS2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Sph21_4254	Sphingobacterium sp. (strain 21)	562	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. (strain 21)	743722	>tr|F4C4K6|F4C4K6_SPHS2 Potassium-transporting ATPase potassium-binding subunit OS=Sphingobacterium sp. (strain 21) GN=kdpA PE=3 SV=1 MNTEIFGVVFMFLLTCVLAIPLGKYIAKVYSGERTWLDFLFGNIENTIYRLGKIDSKHEMSWK QHLVALLTINSIWFLVGMFILMNQDWLPLNPDTNPAMSAHLAFNTVISFVVNCNLQHYSGES GLSYLGQLWLMFLQFVSAGTGMAAAAVLFNALKERTTDKLGNFYVYFLKSCTRILLPISLLVA ILLVFNGTPMTFEGKDTMISLQGDTVQVARGPAASFIAIKHVGTNGGGFFGANSAHPFENPN YLTNMVEMVAQMIIPLAMIFGLGYYLNRKKLSYMIFATMTAGFLALAIPNVLMEMRGNPAIGS MGIDNALGAMEGKEIRFGAAASGFWSIATTVISTGSVNAMHDSTMPLSGMNELLAMITNSFY GGVGAGILNFYIFIILAVFISGLMVGRTPEFLGKKVEAREVKIAIIIALVHPFLILAGTALSVALPQ LTLSTLNNPGFHGFSEMLYEFTSSSANNGSGFEGLGDNTPWWNISTGIVLILSRFIPIIGPVAI AGLLANKKYTPESAGTLKTDTATFGLMVFAVIVIIAALTFFPALALGPIAEYFTMR
1E-229	772.7	35.8	1E-229	772.5	24.8	1	1	W0PFX0_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MIM_c38480	Advenella mimigardefordensis DPN7	567	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella mimigardefordensis, Advenella mimigardefordensis DPN7	1247726	>tr|W0PFX0|W0PFX0_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Advenella mimigardefordensis DPN7 GN=kdpA PE=3 SV=1 MSMDIIQFAGILVLTTCLAVVLGKWIARVFTGEKDTILESGTYALLGVDPHQKMNWTTYGLAL LLSNAAMMLLGYFLLRIQQTIPGDTLQRAAQTPDLAFNTAASFITNTNWQAYSGESSLSNFS QMAVITFLMAVSAATGVAAAGGFIRGLSRRSAADIGNYWVDFTRVLYRVLLPLCFVMALVYV WQGMPQTLSADAVVTTLEGAKQQIIMGPVASLESIKHIGTNGGGFFGMNAAHPFENPTPLT NTLHMLSMLLIPAALTYAFGTMIANRKQGWSFFAAFLVMFLGFLALVYSAEHNGNPLFSSLG VDQSHSTIQSGGNMEGKELRFGIAQTSMFAAVTTAATTGSVNSMHDSYTPLGGLVPIAQM MLNNVFGGDGVGLINLVTYVILTVFLVGMMIGRTPEFLGKKIEAREMKFIMLAVLAHPMTILG FTAIASLFPASMESLANMGPHGFSEVLYAYTSGTANNGSAFAGLNANTPFFNLTIGLAMLLG RYFTLLPMLAVAGVMASKKPVPASAGTLSTASPLFTGLLVFVILVVGGLTFLPSLALGPIVEHL LMLAGKTF

1E-229	772.7	30.3	1E-229	772.4	21	1	1	D5W5H2_BURSC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BC1002_0919	Burkholderia sp. (strain CCGE1002)	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. (strain CCGE1002)	640511	>tr|D5W5H2|D5W5H2_BURSC Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia sp. (strain CCGE1002) GN=kdpA PE=3 SV=1 MTTNDVLQASLFIVVLLAAAVPVASYLGAVMDGSSRVVRFGAPLERLLYRIAGVDPAAEMG WKHYAIATVAFNVLGVVFLYVLLRVQGWLPGNPQQFGAMSVDGAFNTAVSFVANTNWQD YTPEQTVSYLTQMLGLTVQNFLSAATGIVVVMALIRGFARHTAQTIGNFWVDITRVTMYVLL PMAAIVAALLMSQGVIQNFKAYQEVPTLQTTTYAAPKLDAQGNPVKDAKGNPVTVDTPVKS QTIAMGPVASQESIKMLGTNGGGFFNGNSAHPYENPTPVSNFLQIFSMLIIPAALALVFGRVI GDRRQGVAVLAAMTIAFGVCVFGEISAEQSGNPAFAALNVDQSANALQAGGNAEGKETRF GIAQSGIFTVATTAASCGAVANTHDSLTPIGGLYPMLLMQLGEVIFGGVGSGLYGMLVFALL AVFVAGLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPLLVLVGTSIAVLTDAGKAGILNPGPHG FSEILYAFSSAANNNGSAFAGLTVSTPFYNWLTAIAMWFGRFGTIVPVLAIAGSLAAKKRIGV TGGTLPTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEQLMMIGVK
1E-229	772.6	32.9	1E-229	772.4	22.8	1	1	W0I187_9ENTR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Sant_3537	Sodalis praecaptivus	560	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Sodalis (tsetse S-endosymbionts), Sodalis praecaptivus	1239307	>tr|W0I187|W0I187_9ENTR Potassium-transporting ATPase potassium-binding subunit OS=Sodalis praecaptivus GN=kdpA PE=3 SV=1 MAAEAFLLLASFLAVLLLLAQPLGRLMTGLVLDRPLPLTAGFERTLWRLCGIGGAMHWRHYL CAILLFNLLGGALLLAILLLQGLLPLNAQHLPGLSWHLALNTAISFVTNTNWQSYAGETTISYF STLAGLAVQNFLSAATGIAVLFALIRGFARHSTQDLGNAWRDLVRVTLFVLLPLSLLLALFLVN QGVIQNISPYLTVTTLEGAQQTLPMGPVASQEAIKMLGTNGGGLFNANSAHPFENPTALSN FVQMLAIFLIPAALCFTFGEAVGDRRQGKTVLWAMVLMFVAAAVLVMLAEVHGNEHLTALG ADSAMNWEGKESRFGILTSSLFAVITTAASCGAVNAMHDSFTALGGLIPLWLIQLGEVVFGG VGSGLYGMLINVLLAVFIAGLMIGRTPEYLGKKIGVPEMKMAAIYILITPALVLLGTALAMMTD AGRAGMLNPGAHGFSEVLYAVSSAANNGSAFAGLSANTPFWNVLLAVAMLLGRFAPFVP LMVIAGSLAARRTQPASSGTLPTHGALFVALIIGTVLLIGALTFIPSLALGPIVEHLQLTGH
1E-229	772.5	29.8	2E-229	772.2	20.7	1	1	F4KRB0_HALH1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Halhy_6481	Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	572	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Saprospiraceae, Haliscomenobacter, Haliscomenobacter hydrossis, Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	760192	>tr|F4KRB0|F4KRB0_HALH1 Potassium-transporting ATPase potassium-binding subunit OS=Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O) GN=kdpA PE=3 SV=1 MNTNLTGVVATLILTIVLAIPLGRYLAKVYQGERVWTDFLRPFERLLYRLGGINPAEEMSWQ RFLRALLTINMLWLVYGFIMLFYQGVLPLNPDGNPSMTPDLTFNTVISFVVNCNLQHYSGES GLSYLSQVGVIMYFQFVSAATGMAALAGVYRAMQEKQSSTLGNFYVYFIQSITRVLLPLSIVL AVALLACGTPMTFDGKIVLNTLQGVEQSISQGPAAAMIAIKQLGTNGGGFFGVNSAHPLENP NFLSNMLQTISILLVPIALVFALGYYLKRRRLAWIIFGVMTMGFLSFVMGTIMAETAGNPAIAQ MGINQDLGSMEGKETRIGAEASALWGIATTATSNGSVNAMHDSMTPISGFLQMLDMMINAL YGGVGVGLLNYYIFIIIAVFISGLMVGRTPELLGKKVEIREMKIATLITLLHPFLILMGTALSSYLI VHHADIGWAVKPANWLNNPGNHGFSEMLYEYTSASANNGSGFEGLGDNNFFWNVSTGIV LLMGRFLPIIGPVAIAGLLAQKQYIPESSGTLRVDTPTFGLMTFAVIFIVAALAFFPALALGPLA EYFSMHP
2E-229	771.7	34.1	2E-229	771.5	23.6	1	1	A0A099GAM6_9RHOB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA IX56_15180	Paracoccus sp. 5503	561	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 5503	1525717	>tr|A0A099GAM6|A0A099GAM6_9RHOB Potassium-transporting ATPase potassium-binding subunit OS=Paracoccus sp. 5503 GN=kdpA PE=3 SV=1 MSADLSYFALFLAGLTVLGLALAPWMARVFDGRVILLAPVERALYRAAGVSGAGQRWTGY AAAVLAFNAAGFVLLYLILRLQGWLPLNPQGFGAMEASQAFNTAVSFMTNTNWQSYGGET ALSHFSQMAGLTVQNFVSAATGIAVAVAVIRGLAARSAADLGNFWVDLTRATLYLLLPGAILV ALLLLWQGVPQNLAASVTATTLEGAQRVIAQGPVASQEAIKLLGTNGGGFFNVNSAHPYEN PTALSNLIECLSILAIPAAFPLLFGRMVGDRRQGWAVYAAMAALFAGVLLWAYFAEAAGNPL HAGITEAGVSMEGKETRFGLAGTVLFEVVTTVASCGAVNAMHDSLMALGGLIPLFNMLLGEI IFGGVGAGFYGMVLYVVLTVFLAGLMVGRTPEWLGKKIEAREMKLAALTLLVMPLGVLVLSA ASILTGNAQGAVQDAGPHGLTELIYAYTSGTANNGSAFAGFGANTVWHNTLIGLAMLLGRW GYIIPVLAIAGSLAGKTRAEATAGTFPTHGVAFTVLLVVTILIVGALTFLPVLALGPIAEHVSIAA GQSF
2E-229	771.6	30.8	4E-229	771	21.4	1.2	1	D5X2Y2_THIK1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Tint_0065	Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	597	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Thiomonas, Thiomonas intermedia (Thiobacillus intermedius), Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	75379	>tr|D5X2Y2|D5X2Y2_THIK1 Potassium-transporting ATPase potassium-binding subunit OS=Thiomonas intermedia (strain K12) GN=kdpA PE=3 SV=1 MTPEFFALLAVLLLVVLGAARPLGRYFAWIMDGGPAWRPLARLEAGLLRLCGVDAAGMRW SRYAVALLVFSLLGTLLVYALQRLQGVLPLNPQQFGAVSPDSSFNTAISFVTNTNWQGYAG ESTLSNLTQMMGLAVQNFVSAASGIAVAFALIRGFARHRATEIGNFWVDLYRITIYALLPLSM LLAMALVSQGVIQTFSADTPVTTLQPTTYVAPKLDTAGQPMSDAAGQSVQQTVTVTQQILP MGPVASQEAIKELGTNGGGFFSANSAHPYENPNALSNLLEMIAVLLIPAALVYTFGLAVGDT RQGWALLAAMTLVFAVAVTGLAAAEQQGNPTIAALGIDQAHGALQSGGNMEGKETRFGIA ASALFNAVTTTTSCGAVNAMIDSFTPLGGLVPMALMQLGEVVFGGVGTGLAGMLVFALVAV FVGGLMIGRTPEYVGKKVEAFDMKMVSIAVLLMPALVLLGTALAVVVPAGLAGLANPGAHG FSEIFYAFTSAANNNGSAFAGLSVNTPFYNGWLGAAMLFGRFAVMVPTLALAGSLAAKKRIP AGGGTLPTHGPLFVSLLIGVLLLVGALNFFPAWGLGPIVEQLQLWK

3E-229	771.4	24.1	3E-229	771.2	16.7	1	1	K9WZA3_9NOST	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cylst_2649	Cylindrospermum stagnale PCC 7417	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Cylindrospermum, Cylindrospermum stagnale, Cylindrospermum stagnale PCC 7417	56107	>tr|K9WZA3|K9WZA3_9NOST Potassium-transporting ATPase potassium-binding subunit OS=Cylindrospermum stagnale PCC 7417 GN=kdpA PE=3 SV=1 MGQGFLQIGLTLCIVIAITPVLGRYMARVFLGERTLLDPIINPIERSIYVLAGISRKEDMTGWQY IRAVLYSNLIMGILVYSLIYFQRILPWNPNGFGAPTWDILLHTTISFLTNTDQQHYSGETTLSY FSQVAALGFLMFTSAATGLAVGIAFIRGLTGRKLGNFYVDLTRAIMRILLPISIIGAIALLASGVP QTLSGTMAVETLEGGTQYIARGPVASFEMIKMLGENGGGFFGVNSAHPFENPNPASNLIETI AMISIPAALIYTYGLFANNIKQSWLLFWMVFVIFVVLVWVTAVGELQGNPLINNNLGLEQPNL EGKEVRFGWAQTALWAVTTTATMCGAVNGMHDSLMPQGTFSTLFNLFIQIIWGGQGTGTA YLFIYLILTVFLTGLMVGRTPEFFGRKIEKREIVLASVVLLIHPIVVLIPSAIALAYPISLSGISNPG FHGISQVVYEYASAAANNGSGLEGLKDDSLWWNLSTLISLLAGRYIPIIAILLLADSMSGKPTV PETPGTLRTDSLMFTSVTAGVTLVLGVLTFFPVLALGPIAEGFRLASGN
3E-229	771.2	20.9	4E-229	770.9	14.5	1	1	A0A089WUY6_9PSED	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LK03_14235	Pseudomonas cremoricolorata	569	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas cremoricolorata	157783	>tr|A0A089WUY6|A0A089WUY6_9PSED Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas cremoricolorata GN=kdpA PE=3 SV=1 MHSYDYALLIAFFVLLLAPAALLGRFFYQVMEGQRTWLSPLLAPLERGCYRLAGVDPAQEQ SWQRYALALLSFNLAGFMLLLAILLLQGHLPLNPRQLPGQDWSLALNTAVSFVTNTNWQAY SGESSLSALSQMLGLTVQNFLSAATGLAVLVALCRGIARRSASTVGNFWVDLTRATLYGLLP LSLLLALLLVWQGVPQTFTDSVQALTLSGDRQTLPLGPVASQIAIKQLGTNGGGFFGVNAAH PFENPTAWSNLFELVAIVLIPAALVFTFGHYVKDLRQSRAILGCMLALFVLGGATALWAEYQ PNPALLDPQVEHTAPLEGKEVRFGTTGSVLWAVTTTAASNGSVNAMHDSLNPLTGLVTLGN MMVGEVIFGGVGAGLYGMLLFVLIAVFLAGLMIGRTPHYLGKSLQAREVKLLVATLLVMPLG ALVLGAIAASLPGAQTALSNPGPHGFSQLLYAYTSATANNGSAFAGFAGNSVLHNLLLSLAM LIGRFGYILPVLALAGSLAAKRCVACGADSFPTHGVLFASLLLVTVLLVGGLSFLPTLALGPLA DHLSQGFQGVAP
3E-229	771.1	38.9	4E-229	770.9	27	1	1	D9R2J7_CLOSW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Closa_4114	Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	561	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	610130	>tr|D9R2J7|D9R2J7_CLOSW Potassium-transporting ATPase potassium-binding subunit OS=Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1) GN=kdpA PE=3 SV=1 MSVMVMQDLIYMAVLVGLSIPLGIYIYKVMTGQRVFLTPVLAPVERVIYKLMGTAAGEEMNA GKYAVSVLLFSGVGFVFLFLLLMLQGALPFNPERMKGTSWHLAFNTAASFTTNTNWQAYS GESDLSYFTQFTGLAVQNFVSAATGIAVLFALIRGLVLRQKKTIGNFWADLVRTTLYLLIPLSF VVALLLVSQGVVQTFGPYKDVTMLESGALQTIPLGPAASQIAIKQLGTNGGGFFGVNSAFPL ENPTAFSNMVQSLSILLIPAALCVSFGGAVKDSRQGRSIYLTMLIFFGAALAATTASEQFAGP VFEQVAASGSMEGKEVIHGVGASSLWAVVTTAASNGSVNAMHDSLTPLGGMVPMFLMQL GEIVFGGVGSGLYGMLAFVLLTVFIAGLMVGRTPEYLGKKVEPFDMKMVCLIVLVPPLLTLLG TSAAVAVPEARSWLTNSGAHGFSEILYAFSSMANNNGSSFAGFQANTVFTNVLGGIIMLLVR FIPMTAVIFLAGNMAQKKAVAVSEGTLSTSNTVFVGLLIGVILIIGALSFLPALALGPIADFLTTQ
4E-229	771	38.7	4E-229	770.8	26.9	1	1	F0TA34_METLA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Metbo_1761	Methanobacterium lacus (strain AL-21)	567	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium lacus (strain AL-21)	877455	>tr|F0TA34|F0TA34_METLA Potassium-transporting ATPase potassium-binding subunit OS=Methanobacterium lacus (strain AL-21) GN=kdpA PE=3 SV=1 MSLDEIILIILFFIIVSLAAVPVGKYISRVLTGEKTFITPVIRPVEKFIYRICSIDENSEMSWKTYAI ALLIFNILGIIFLFTLQLIQNYLPLNPAGMPAVRWDTALNTAISFTTNTNWQSYVGESTMSYLT QMLGMTLQNFLSASVGVATLLALIRGFTRKNSDTIGNFWVDITRTALYILLPLAVIFALVFASQ GVVQTVGPYVTAHTLEGINQTIALGPVASQEAIKMIGSNGGGYFNANSAHPFENPNGFTNIL ETFAILLIPMSLVFAFGYIIRNFRQGLAIFAAMMILLLGGMGVAYWAETQPNPTIEKLGVSGGN LEGKELSFGVTESILWGVPTTAVSNGGVNSMHDSTMPLTGLVYMFNLGVGEVIFGGLGVGL IGMLFYVILTMFIAGLMIGRTPEFLGKKLGPYEMVMAVIALLTPAIMILILSAVAISLPQGLTGLN NPSAHGISEILYAYASALANNGSAFAGLSANTVFYNLTLGLGMLIGRFVVIIPALAIAGALAKK GRVPVDASSFPSTNVLFVIMLVSVVLVVGALTFFPVFSLGPILEQLFLQGGMTF
4E-229	770.9	32.7	5E-229	770.6	22.7	1	1	U5VVR4_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AFR_13810	Actinoplanes friuliensis DSM 7358	548	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	1246995	>tr|U5VVR4|U5VVR4_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Actinoplanes friuliensis DSM 7358 GN=kdpA PE=3 SV=1 MAGWLFVITLFVALVAVHRPFGDYMYRVVTGTKNNVVERGVYRLVGVNPSAEQTWGVYAR SVLAFSAVSILFLYLFLRVQDKLWLSLGMPAVTDHVAWNTAVSFVTNTNWQAYSGESTLGH LVQMAGLAVQNFVSAAVGIAVAVALIRGFAARKNGTLGNFWVDLTRIALRILLPACLLITIVFMI AGMVQNLSGGTDVTTLTGATQHLTGGPVASQEAIKELGTNGGGFYNVNSAHPFENPTTWT NWLEIFLLLVIPFSLPRVFGRMVGQNRQGYAIVAVMAILAVGSIALTVGFETHGGGTVPQAV GAAMEGKDVRFGVANSATFAAATTLTSTGAVNSFHDSYTPFGGMMPIVNMMLGEVAPGGT GSGLYGLLVLAIITVFVAGLMVGRTPEYLGKKIGAREMKFASLYFLVTPTIVLAGTAAAFATG NNSTALNVGPHGLSEVLYAFTSAGNNNGSAFGGITVNTPWWDTALGLAMLLGRFLPIVLVL ALAGSLARQKATPESEGTLPTHQPLFVGMVVGVTVVLVALTFLPALALGPIAEGLS

4E-229	770.7	40.5	5E-229	770.4	28.1	1	1	W0JFF5_DESAE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DESACE_07665	Desulfurella acetivorans A63	573	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfurellales, Desulfurellaceae, Desulfurella, Desulfurella acetivorans, Desulfurella acetivorans A63	694431	>tr|W0JFF5|W0JFF5_DESAE Potassium-transporting ATPase potassium-binding subunit OS=Desulfurella acetivorans A63 GN=kdpA PE=3 SV=1 MPISDIIQFLVFIVLVSLLVKPLGSYMANVFNGEKTVLSLVFRPIEIFIYKIANIDETYEMNWKEF AISMLIFNAIGFVVLFLILVLQQFLPLNPQHFKGFNLDLAFNTAVSFITNTNWQAYSGENTASY FTQMLGLAVQNFLSAVTGIVVLLALIRGFTRKQTTNLGNFWVDSVRTTLYILLPLSVLAAVILM SQGVIQNFSSYKTVQLLEPYINAGKVVSHQILPMGPVASQEAIKLLGTNGGGFFGANSAHPF ENPNGFTNFFEAFLIILIPAALTYTFGSMIKNKKQGWAIYLVMLTMFVVFLGIEYTSSLGNDPLI SRLGVTGHYIEGQEVRFGIGGTSLFATTTTAVACGAVDAMHDSLLPISGMVPTVLMLLSEVV FGGVGSGLYTMIAFIIIAVFVAGLMIGRTPEFLGKKIEVKEMWMAIIVALTSGILVLIFTTIAFITK AGVSSILNPGPHGLSEILYAFASTANNNGSAFAGLNADTVFYNITTAIAMLIGRYIPAVAIIYMS GALAQKKYTPPSVGTLPTDKVPFMVWLILVILIVGALTFFSALALGPFLENILMLRGA
5E-229	770.5	29.3	6E-229	770.3	20.3	1	1	A0A077EBJ5_9FLAO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BD94_1141	Elizabethkingia anophelis NUHP1	564	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Elizabethkingia, Elizabethkingia anophelis, Elizabethkingia anophelis NUHP1	1338011	>tr|A0A077EBJ5|A0A077EBJ5_9FLAO Potassium-transporting ATPase potassium-binding subunit OS=Elizabethkingia anophelis NUHP1 GN=kdpA PE=3 SV=1 MNTEILGIIAMFVLTLIIGLFLGKYIARVYGYEKTFLDPVFNPVEKLFFKISGINPNRQMNWKQN MYAMLTINLVWFVIGFILLQTQQWLPLNPDNNPNMSPDLAFNTTISFLVNCNLQHYSGETGV SYLSQLFLMFLQFVTAATGMAAMAVLFKAFKEKTTTELGNFYDYFMKSMTRILIPISIIVAFILS ANGSPMTFEGKDHITTLEGQKSDISRGPVAAFVAIKHLGTNGGGFFGTNSAHPLENPNYVT NITEMATQMIIPFALVFALGFYLKRKKLSRIIFTVMTVGFLALAIPNIINEASGNPLITQMGANSN LGAMEGKEIRFGSASSGYWSIATTVISTGSVNSMHDSTMPLSGMNELLAMMINCFYGGCG VGILNYFIFIILAVFISGLMVGRTPEFLGKKIEAKEMKIAMIVALFHPFLILAGTALTAYLPEFGTK TLNNPGFHGFSEMLYEFTSSSANNGSGFEGLGDNTPWWNISTGIVLLLSRFIPIIGPIAIAGCL AEKKFIPEGSGTLKTDTLTFGFMTLAVIILIAALSFFPSLTLGPIAEQLQYFSK
5E-229	770.5	31.9	6E-229	770.3	22.1	1	1	A0A088F3W5_9SPHI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KO02_22135	Sphingobacterium sp. ML3W	562	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. ML3W	1538644	>tr|A0A088F3W5|A0A088F3W5_9SPHI Potassium-transporting ATPase potassium-binding subunit OS=Sphingobacterium sp. ML3W GN=kdpA PE=3 SV=1 MNTEILGIIVMFTLSILLAIPFGKYIAKVYAGEKMLLDNIFSPLERFFYRISGINPQIEMTWKQQ MAALLTINMVWFLLGVLILMTQGSLPLNPDNNPSMSADLAFNTTISFVVNCNLQHYSGESGL SYLGQFWLMFLQFVSAGTGMAAAVVVFRAFRDKSATYLGNFYNYFVKSCTRILLPVSFIVAII LTFQGTPMTFEGKDTIITLQGDTVEVSRGPAAAFVSIKHVGTNGGGFFGVNSAHPFENPTYL SNMVEMIAQLIVPLAMIFAFGYFIKRRKLSWMIFGVMTAGFLMLALPNINMEMSGNPAIEAM GIDISLGAMEGKEIRIGAPASGFWSIVTTVISTGSVNSMHDSTMPLSGMNELLAMMINSFYG GVGVGILNFFVFIILAVFISGLMVGRTPEFLGKKVEAREMKIAMIIALLHPFLILVGTALATSLPQ YTTESLNNPGFHGLSEMLYEYTSSSANNGSGFEGLGDNTLWWNISTGFVLILSRFLPIIGPV AIAGLLARKKYIPEGDGTLKTDTVTFGLIIFVVIAIIAALAFFPVLALGPIAEYFSLY
6E-229	770.3	43.5	6E-229	770.1	30.1	1	1	KDPA_LISMO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA lmo2682	Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	561	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, Listeria, Listeria monocytogenes, Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	169963	>sp|Q8Y5Z6|KDPA_LISMO Potassium-transporting ATPase potassium-binding subunit OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) GN=kdpA PE=3 SV=1 MKYIVMQDVFFVVLLLVLAVPLGIYMYKVMIGEKVFLSRVLEPVERFGYRLMGVSEVGMSAK RYAVSVLAFSAVGFVFVMAVLMLQGFLPLNPEGMKGLSFSLAFNTAASFVSNTNWQAYSG ETALSYFSQSIGLTVQNFVSAATGIAVLFAVIRGFIWKKQKTVGNFWQDLFRVTLYILLPLSLI LALLLVSQGVVQSFADYSVVETLENGAKQLIPLGPAASQIAIKQLGTNGGGFFGANSAFPFE NPSSFTNLIEMLAILLIPVALVVMFGRAVKDSKQGRAIMTAMMIVFVIGVVAITISEQFAGPSY QGVATSGSMEGKEVRFGVGGSSLFAASTTAASNGAVNAMHDSLTPLGGLVPMFFMQLGE VIFGGVGSGLYGMIGFIILTVFIAGLLVGRTPEYLGKKIEPYDMKMVCLLILVPPLLTLFGTAVA VMMPSVQASVSASGAHGFSEVLYAFTSMGNNNGSAFAGFAADTTFTNMVGAVMMLLARFI PLVAALYLAQNMAGKSSVAASSGTLSTKNGMFIGLLIGVVVLVGALSFLPALALGPIADFFTT FK
6E-229	770.2	28.3	7E-229	770	19.6	1	1	W0EX99_9SPHI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NIASO_10415	Niabella soli DSM 19437	566	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Niabella, Niabella soli, Niabella soli DSM 19437	929713	>tr|W0EX99|W0EX99_9SPHI Potassium-transporting ATPase potassium-binding subunit OS=Niabella soli DSM 19437 GN=kdpA PE=3 SV=1 MNAEIPGIILMYGLAVLLAIPLGRYIGKVYSNDKTWSDRIFKPVDTIFYRLGGIDPSKEMNWK QHLIALLTINLFWFLGCMFVLMNMSWLPLNPDKNPSMSADLAFNTAISFICNTNLQHYSGET GISYFGQLTLMLFQFVSAGCGMAIAATVFFALRERTSVKLGNFYFLFVRSCTRILFPIALIVALL LLFNGTPMTFAGKDTITTLQGDTVQVSRGPAAVFVAIKHLGTNGGGFFGPNSAHPFENPNY FTNIIEMVTQMLIPIAMIFALGYILRRRKLALVILGVMTIGFMLLLVPTVVGELKGNPALAKMGIG QAIGNMEGKEVRFGSAASAYWSIATTVISTGSVNAMHDSFLPLSGMNQMLGMMVNCFYGG VGVGFLNFFVFIILAVFISGLMVGRTPEFLGKKIEAREMKIAMIIALLHPLLILTGTAISSYLYAHH PGTYAGWLNNPGYHGFSEMLYEFTSSGANNGSGFEGLGDNTPFWNIACGTVMLLARYLPII GPVAIAGSLAAKKYVPESAGTLKTDTATFGLMVFAVIAIVAALSFFPALTLGPIAEYFSLY

6E-229	770.2	25.9	7E-229	770.1	18	1	1	R5QXP0_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN521_01699	Coprobacillus sp. CAG:183	549	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:183	1262853	>tr|R5QXP0|R5QXP0_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Coprobacillus sp. CAG:183 GN=kdpA PE=3 SV=1 MNGKKVFLSRILEPCENFIYRVLHVKKDEEMSWKKYLVSVLIFSGFGLVFVFLLQMLQGVLP GNPAKVEGTTWDLALNTAISFVTNTNWQAYSGESGLSYLTQSLGLTVQNFVSAGTGLAVLY ALIRGFTRIKAKGLGNFWVDLTRSVIYVLMPLSVVLSIILVSQGVTQSIDEYQTVKLAEPIVLED GTEITEQTVPLGPAASQIAIKQLGTNGGGFYGVNSAHPLENPTGLSNLVEVVSILLIPAALCFS FGKGIKDSRQGIAIFVAMGIMLVAALGSIAVSEQMATPQLEQNGIVDISNHDQAGGNMEGKE SRFGIVGSSTWAAFTTAASNGSVNSMHDSYTPLGGMVTMLLMQLGEVIFGGVGCGLYGML GFVILAVFMAGLMVGRTPEYLGKKIEPYEMKWAVVVCLATPVAILVGSGIASLVPQVADSLN NSGAHGFSELLYAYSSAGGNNGSAFAGFAANTPFINVTLGLVMLFVRFIPILGILAIAGSMVQ KKKVAVTAGTLSTCSPLFVFLLVFVVLLVGALSFFPALALGPIAEFFGMF
7E-229	770.1	34.8	8E-229	769.9	24.1	1	1	J7U1A2_MORMO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MU9_3395	Morganella morganii subsp. morganii KT	560	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Morganella, Morganella morganii (Proteus morganii), Morganella morganii subsp. morganii, Morganella morganii subsp. morganii KT	1124991	>tr|J7U1A2|J7U1A2_MORMO Potassium-transporting ATPase potassium-binding subunit OS=Morganella morganii subsp. morganii KT GN=kdpA PE=3 SV=1 MAANAFLIAGFLIVLLIAAKLLSNLLVCFIDGTPLPVLRRVEGVLWRFAGIGRDEMRWQGYL TALLLFNALGLIFLTAILMLQADLPLNPRHFPGMSWDLALNTAVSFVTNTNWQSYSGESAVS YFSQMAGLTVQNFLSAATGIAVAFALIRALCRRSVQTLGNAWADLTRITLWLLLPLSVIIALFFI SQGVIQNFHDYQTIITPEGVQQVLPMGPVASQEAIKLLGTNGGGFFGANSAHPFENPTALTN FVQMLAIFLIPAALCFAFGRCAGNPGQGSALLAAMTIVFVAAAVAVMWSETHGNPAFAGMG IDSTFNMEGKESRFGILATGLFVAVTTAASCGAVNSMHDSLTPLGGLVPLWLMQIGEVIFGG VGAGFYGMMLFVFLAVFIAGLMIGRTPEYLSKKIEVREMKLTALAILVTPALVLGGTALAMMT EAGRGAMLNPGAHGFSEVLYALSSASNNNGSAFAGLSTNTPFWNLLLAFCMLAGRFVVIAL VMMLAGSLVSKTIRTAGAGTLPTTGPLFTGLLIAAILLIGALTFVPALALGPVAEFLDLLK
8E-229	769.8	29.6	9E-229	769.6	20.5	1	1	Q142K9_BURXL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bxe_A3252	Burkholderia xenovorans (strain LB400)	601	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia xenovorans, Burkholderia xenovorans (strain LB400)	266265	>tr|Q142K9|Q142K9_BURXL Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia xenovorans (strain LB400) GN=kdpA PE=3 SV=1 MNSNNVLQAGLFIVVLLAAAVPMSRYLGAVMDGSSRVVRFGGPVERLLYRIAGVDPATEMS WKHYAIATIAFNTLGVAFLYVLLRVQGWLPGNPQQFGPMTVDGAFNTAVSFVTNTNWQDY TPEQTVGYLTQMLGFTVQNFFSAATGIVVVIALIRGFARHTAQTIGNFWVDLTRVTLYVLLPM SAILAALLMSQGVIQNFKAYEDVPTLQTTTYAAPKLDAQGNPVKDAKGNAVTVDTPVKTQTL AMGPVASQEAIKMLGTNGGGFFNGNSAHPYENPTPFSNFLQIFSILIIPAGLALVFGRMIADR KQGVAVLATMTIAFAVCVFGEISAEQTGNPAITALHVDQSANALQSGGNAEGKETRFGIAQS GIFTVATTAASCGAVANTHDSLTPIGGLYPMLLMQLGEVIFGGVGSGMYGMLVFALLAVFVA GLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPLLVLVGTSIAVLSDAGKAGILNPGAHGFSEILY AFSSAANNNGSAFAGLTVGTPFYNWLTAIAMWFGRFGTIVPVLAIAGSLAAKKRIGVTGGTL PTHGPLFVVLLLGTVLLVGALTYVPALALGPGVEHLMMMGAH
1E-228	769.2	32.4	1E-228	769	22.5	1	1	KDPA_PHOLL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA plu1420	Photorhabdus luminescens subsp. laumondii (strain TT01)	568	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Photorhabdus, Photorhabdus luminescens (Xenorhabdus luminescens), Photorhabdus luminescens subsp. laumondii, Photorhabdus luminescens subsp. laumondii (strain TT01)	243265	>sp|Q7N6W5|KDPA_PHOLL Potassium-transporting ATPase potassium-binding subunit OS=Photorhabdus luminescens subsp. laumondii (strain TT01) GN=kdpA PE=3 SV=1 MAASAFLLITSFLLILMLLAKPLGNIIANLIDGDIPRWLTKIESGLWRCCGLQKPGGTVKEMNW WQYALAITIFNLTGLLLLFTLLVTQHALPLNPEHFPGLKWDLALNTAISFITNTDWQAYSGEN TLSYFSQMTGLTVQNFLSAATGIAVAFALIRTFSRHGVNTAGNAWVDITRITLYLLLPLSMVIA LVFVSQGVIQNFEPYQLAHTIEGQPQLIPMGPVASQEAIKLLGTNGGGFFGANSSHPFENPT AISNFIQILSIFLIPCALCFAFGQVVGDNRQGHTLLWAMSIIFVIATVGVMYAELKGNLHFSLLG ANSNINMEGKENRFGILATSIYAVVTTAASCGAVNAMHDSFTALGGMIPMWLIQIGEVVFGG VGSGLYGMLLFVLLTVFIAGLMIGRAPEYLGKKIEVFEMKMVALAILVTPTLALLGTALTISTAS GRAGILNPGAHGFSEVLYALSSTANNNGSAFAGLNTNNMFYNLLLAIILFLGRFGMILPVLAIA GSLAVKKRQPASNGTLPTYGPLFISLLILTIMLIGALTFIPALILGPVIEHLQIWLMAR
1E-228	769.1	22.4	2E-228	768.8	15.5	1	1	A0A0F0HMT4_9PSEU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UK12_27130	Saccharothrix sp. ST-888	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix sp. ST-888	1427391	>tr|A0A0F0HMT4|A0A0F0HMT4_9PSEU Potassium-transporting ATPase potassium-binding subunit OS=Saccharothrix sp. ST-888 GN=kdpA PE=3 SV=1 MSSTLAGWLQAIALVGALALCYRPLGDYIAKLLTTAKHLRVERGLYKVIGVDGDADQRWPVY LRSVLAFSAASVLFLYLLQRIQSVLPLSLGNKGVEPHTAWNTATSFVSNTNWQSYAGESTL GHLVQMAGLAVQNFVSAAVGIAIVAALIRGFTRNRTDRVGNFWVDLTRISLRLLLPVSIVFAL VLVANGVVQNFHGFHDIATLGGDTQSIPGGPVASQEVIKELGTNGGGFFNANSAHPFENPT GFTNLLEIFLLLVISFALPRTFGKMVGDNRQGYAIVAVMGIFWVASAALMTLAEQHHGGAAL QAAGSAMEGKEQRFGVAASSLFAVSTTLTSTGAVDAAHDSLTPFGGGITIFNMMLGEIAPG GTGSGLYGMLILAIVAVFVAGLMVGRTPEYLGKKLGGREMKFASLYILTTPTLVLVGTGVAM ALPGERAAMLNSGAHGFSEVLYAFTSASNNNGSAFGGLTVNTEWYDTALGLAMLFGRFLP MVFVLALAGSLAQQQPVPATPGTLPTHKPLFVGLLSGVVLIVVGLTYFPALALGPIAEGLH

1E-228	769	28.2	2E-228	768.8	19.5	1	1	K9RWG4_SYNP3	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Syn6312_2727	Synechococcus sp. (strain ATCC 27167 / PCC 6312)	563	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27167 / PCC 6312)	195253	>tr|K9RWG4|K9RWG4_SYNP3 Potassium-transporting ATPase potassium-binding subunit OS=Synechococcus sp. (strain ATCC 27167 / PCC 6312) GN=kdpA PE=3 SV=1 MLFGFLQISLILIILVLVAPPLGYYMAGVFSGEQAKLGRIFQPVERLLFQASGINPHISMTAWQ YIRALLMSNLVMGLFVFVLQLAQGFLPLNPTGLGEPTWDLALHTAVSFITNTNQQHYSGETT YSYLTQAGGLGYLMFTSAATGIAVAIAFIRGLTGQPIGNFYQDLVLAITRILLPISMIGAILLVIA GVPETLAGPAQATTLEGATQFIARGPVAHFEIIKQLGENGGGFFGINSAHPFENPNNFSNLL ETVIMLVIPAGLVITYGKMANNPKQGWLLFWLVFLIFTFLIVITAIGEFEGNPIVNQLLGESAPN LEGKEVRFGWALTALWAVATTGTMCGAVNGMHDSLMPPGGFSALSDMFLQIIWGGQGTG TAYLFVFLILTVFLTGLMVGRTPEFLGRKIEKKEIVLASVILLIHPIAILIPAAITLAFPEQLAGISN PGFHGISQVVYEYASAAANNGSGFEGLGDNTVWWNLSATFSLLAGRYIPIMALIFLAEGLAQ KQPVPETIGTLRTDTVLFTAVTGGSILILGALTFLPVLALGPITEAFELIHLSGN
2E-228	768.6	34.5	2E-228	768.3	23.9	1	1	I0H1S8_ACTM4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AMIS_17450	Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	548	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes missouriensis, Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	512565	>tr|I0H1S8|I0H1S8_ACTM4 Potassium-transporting ATPase potassium-binding subunit OS=Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431) GN=kdpA PE=3 SV=1 MAGWMFVLSLVAAIVVVHRPFGDYMYRVVSGTRHTVVERAVYRTVGVDAAAGQTWGVYA RSVLAFSAVSLLFLYLFLRVQDALWLSLGLPAVTDHIAWNTAVSFVTNTNWQAYSGESTMG HLAQMAGLAVQNFVSAAVGIAVAVALIRGIAARKKTTLGNFWVDLTRITLRILLPVCVLATVVF MIAGMVQNLSGGTEISTLTGGTQHITGGPVASQEAIKELGTNGGGFYNANSAHPFENPTTW TNWLEIFLILLIPFSLPRVFGRMVGQNRQGYAIAAVMAVLALGSIALTVGFETHGAGTVPQAV GAAMEGKETRYGVTNSAVFAAATTLTSTGAVNSFHDSYTSLGGMMPMVNMMLGEVAPGG VGSGLYGMLILAVITVFVAGLMVGRTPEYLGKKIGAREMKLASLYFLVTPIVVLAGTAAAFAT GNNATALNSGPHGLSEVLYAFTSAANNNGSAFAGITVNTGWWDTALGLAMLLGRFLPLILV LALAGSLAKQQPAPESEGTLPTHQPLFVGMVAGVTVVLVALTFLPALALGPLAEGLS
2E-228	768.3	29.8	3E-228	768.1	20.7	1	1	K9VVM6_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cri9333_1263	Crinalium epipsammum PCC 9333	561	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Crinalium, Crinalium epipsammum, Crinalium epipsammum PCC 9333	1173022	>tr|K9VVM6|K9VVM6_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Crinalium epipsammum PCC 9333 GN=kdpA PE=3 SV=1 MLQGLLQIVLTLLILIAIVRPFGSYIAHIFLGEKTFLDSVINPVDSMIYKLGGLRTESMTGWQYA RAVLYSNLVMGIFVYLILMLQGILPLNPTGLSSPTWDTALHTTLSFLTNTDQQHYSSETTLSY ASQILALGFLMFTSAATGLAVGIAFIRGLSGRSLGNFYVDLTKSITRILLPISVVGAVVLVILGVP ETLAGTAIATTLEGSTQAIARGTVAHFEIIKQLGENGGGFFAINSAHPFENPNSISNLIETLAM VAIPASLIYTYGIIAGNKKQGWLLFWMVFTIFVTLIGITAIGEYQGNPLVNQLLGEQQPNLEGK EVRFGWAQTALWAVTTTATMCGAVNGMHDSLMPVGGFSTLFNMFLQIIWGGQGTGTAYL FIYLILTVFLTGLMVGRTPEFLGRKVEKREIVLASVILLVHPILVLIPSAIALAFPDTLAGISNPGF HGISQVVYEYTSAAANNGSGLEGLADSQPASTALWWNLSTCISLLGGRYIPIIALLLLADSMA NKQPVPETTGTLRTDTTLFTSVTAGVILILGALTFFPVLALGAIAEAFQF
3E-228	768.2	21.2	3E-228	767.9	14.7	1	1	KDPA_GLOVI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA glr0573	Gloeobacter violaceus (strain PCC 7421)	575	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter violaceus, Gloeobacter violaceus (strain PCC 7421)	251221	>sp|Q7NW41|KDPA_GLOVI Potassium-transporting ATPase potassium-binding subunit OS=Gloeobacter violaceus (strain PCC 7421) GN=kdpA PE=3 SV=1 MAFEGVLQIVATLVLMVAIVPFFGTYMARVFQGESTWLDRVLGPIENLVYRLGGVRPELTM DWWSYARAVLASNAAMFVPVFAVLLLQGSLPLNPNGISGMSWDLALHTAISFLTNTNQQHY SGETGASHLAQMVCFQFLMFTSAATGLAVGIAFIRGLLGKPLGNFYVDLTRSVSRILMPISIA FAVVLLSQGVPQSLGGTTEAQLVDPYRTEQDGKREQVTAQKLVSGPFASMESIKELGENG GGSYGINSAHPYENPNPFTNLLEILLLLAVPTSLIYTFGVLANNKKQGWVLFGTIFVLFVGLV GVAALGEYWGNPTVNALLGSANPNFEGQEVRFGWAQSALFATATTGTMTGAVNAMHDSL TPLAGLVTLFNLCLQVIWGGQGTGIAYILVFLIIAVFLTGLMVGRTPEIFGRKLEKREVALASIIF LVHPVIILVPTAIALAIPGLAGNSNPGFHGLTQVVYEYASAAANNGSGFEGLGDATPWWNLS TSVVLLLGRYAPIVALLALAGGLQRKQPVPETPGTLRTDTVLFGSVTAGTILILGALTFFPVFA LGPIAEWIANLAGKTL
3E-228	768.1	22.2	3E-228	767.9	15.4	1	1	A0A0F0KRH8_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RL72_02370	Microbacterium azadirachtae	561	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium azadirachtae	582680	>tr|A0A0F0KRH8|A0A0F0KRH8_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Microbacterium azadirachtae GN=kdpA PE=3 SV=1 MGAADIWLGVLQAATLIAVLVLLYRPLGDYMARVYTGARDLRVERGLYRLIGVDPSSEQTW RAYARSVLAFSVVGLLLLYLLQRVQQVLPLSLGLPAVPEGLAFNTAASFVANTNWQSYSPE QTMGHLVQLAGLAVQNFTSAAVGIAIAIALVRGFARRGSATIGNFWVDLIRGLIRLLLPLAVLS ALALIAGGAVQSLSGFTEVHTLAGTAQSIPGGPVASQEAIKLLGTNGGGFYNANSAHPFENP TPWTNLLEIVLILAIPFALPRTFGRMVGDHRQGYAIAAVMGTIFLVSLVALSALELGGGGTAT QLAGSAMEGKEQRFGILGSTLFGTASTLTSTGAVNAMHDSFTPLGGMMPMINMMLGEVAP GGVGSGLYGMLILAVIAVFVGGLLVGRTPEYLGKRLGPREIKLASLYILVTPTLVLAGTALSFA IPGIRSDVEKTSILNPGPHGLSEVLYAFTSAANNNGSAFAGLTANTPWLNTALGAAMLLGRF VPIVFVLALAGSLAQQQHVPETAGTLPTHRPQFVGLLIAVSVVVTALTYFPVLTLGPLAEGLV R

3E-228	768	33.8	3E-228	768	23.4	1.3	1	A7I6Q1_METB6	Potassium-transporting ATPase, A subunit (EC 3.6.3.12)	Mboo_0894	Methanoregula boonei (strain 6A8)	811	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula boonei, Methanoregula boonei (strain 6A8)	456442	>tr|A7I6Q1|A7I6Q1_METB6 Potassium-transporting ATPase, A subunit OS=Methanoregula boonei (strain 6A8) GN=Mboo_0894 PE=3 SV=1 MTTTGSIGSLIKKQAKPAVLIFLLLTLIVGLLYPLVVTGIAQLAFPVQANGDLLVHNGQVAGSS QIGQPFSSPQYFWGRLSATSPVPYNAGSSTGSNLGPNNPALVQQVQARIDALHAVDPSNT QEIPVDLVTASGSGLDPDISVAAAYYQVPRVARERNLTQAAVSSLVASQVEPRQFGIFGEPR VNVLSLNLALDDLSENKISVSETGSSLPLLNHPPDLVFGMLIADWIQVLLFIVIVALISIPLGAW MAKIFTGKPNFLSPLISWVETKVLTACGIAPGEEMDWKEFAVAVMVFTVPCIAAVFILQEIQQ FLPLNPSGLGAVPWDLSLNTAVSFATNTNWQAYVPEVTLSYFTQMVGLVVQNFVSAAVGL AVLIALIYAFSRKSATTLGNFWVLLVRSVMILLPIAVIIALVLVSQGTPQTFGGPVTVPLLDKLN DTTGALVATQTIPLGPVASQVAIKMLGTNGGGYYNANSAHPLENPTPFSNFVEMFAMIIIPAA LCITFGTMIGSRRKGVALILAMTLIFLPLLGLTIWSEQGGNPVLTPLGVDQAPSAFQSGGNME GKEVRFGAVTSALFAVSTTSTSCGAVNSMHDSFMPVAGGVLLFDMHLGEVVFGGVGSGLY GMLIFVIIAMFIAGLMVGRTPELYGKKIEQHEMKIATIVILIPIIMILAFTSLAVLTPAGQAGVANP GPHGFSEILYAYTSASQNNGSAFAGLNANSLFYNLTTAIAMFIGRYAIIILTLALAGSLVTKKIV PPSEGTLRDHRPLFILWLVFVILIVGALSFLPALSLGPVAEYMGMVAGGLVHVI
3E-228	767.8	28.2	4E-228	767.6	19.6	1	1	K9ZHJ9_ANACC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Anacy_3304	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	272123	>tr|K9ZHJ9|K9ZHJ9_ANACC Potassium-transporting ATPase potassium-binding subunit OS=Anabaena cylindrica (strain ATCC 27899 / PCC 7122) GN=kdpA PE=3 SV=1 MLQGWIQIALTLLIVIATTPLLGKYIARVFLGEKTLLDKVLNPLEKVIYTFSGVRPDDEMTGWQ YIQAVLYSNLVMGILVYLILMLQGWLPLNPTGLSAPNWHLALHTTLSFLTNTDQQHYAGETT YSYASQTFALGFLMFTSAATGIAVGIAFIRGLTGRTLGNFYIDLTKSITRILLPMSVVGGLLLM MAGVPETLAGVATATTLEGTTQAIARGPIAHFEIIKQIGENGGGFFGINSAHPYENPNGFTNL LETWAMISIPSAFIYTYGVFANNIKQAWLVFWMVFIIFVILVGVAAIGEYQGNPLVNNLLGEQ QPNLEGKEVRFGWAQTALWAVMTTATMCGAVNGMHDSLMPPGGFATLFNLFLQIIWGGQ GTGTAYLFLYLILAVFLTGLMVGRTPEFLGRKIEKKEIVLASVVLLIHPFAILIPWSIVFAFPDAL GGITNPGFHGVSQVVYEYASAAANNGSGFEGLGDGTLWWNLSTSISILAGRYISIIALLLLAD SMSRKQLVPISAGTLRTDTKLFTGITGGVILILGALTFFPVLVLGPIAEAFLINRGG
4E-228	767.5	24.4	5E-228	767.3	16.9	1	1	A0A0F2TK51_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VM95_06635	Streptomyces rubellomurinus	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rubellomurinus	359131	>tr|A0A0F2TK51|A0A0F2TK51_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces rubellomurinus GN=kdpA PE=3 SV=1 MGSTLAGWMQALALVGALALCYRPLGDYIAKLLTTSKHLRVERGIYKVIGVDGDADQRWSV YLRSVLAFSAVSVLFLYGLIRLQGYLLLNLGVPQMEGHQAWNTAISFVANTNWQSYAGESA MGHLAQMAGLAVQNFVSAAVGIAVVAALIRGFTRNRTDRVGNFWVDLVRINIRLLLPLSIVFA LVLAASGVIQNFHGFTEVTTLSGEVQKIPGGPVASQEVIKLLGTNGGGFFNANSAHPFENPT GFSNLVEIFLILVIPFALPRAFGRMVGDNRQGYAILAVMGLFWVASTALLTWAEASHQGSAL QAAGAAMEGKEQRFGIAASTLFASSTTLTSTGAVNSFHDSYTPFGGGLTVFNMMLGEIAPG GVGSGLYGMLVLAIVAVFVAGLMVGRTPEYLGKKLGGREMKFASLYILTTPTLVLVGTGVAM ALPGERAGMLNSGAHGFSEVLYAFTSAANNNGSAFGGITVNTDWYDTALGLAMIFGRLLPI VFVLALAGSLAQQQPVPATPGTLPTHKPLFVGLLSGVILIVVGLTYFPALALGPLAEGLS
4E-228	767.5	27.1	5E-228	767.3	18.8	1	1	A0A0C3MBV9_9PORP	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BA92_10890	Sanguibacteroides justesenii	565	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Sanguibacteroides, Sanguibacteroides justesenii	1547597	>tr|A0A0C3MBV9|A0A0C3MBV9_9PORP Potassium-transporting ATPase potassium-binding subunit OS=Sanguibacteroides justesenii GN=kdpA PE=3 SV=1 MNTEILGSILQVVMMVVLSYPLGRYIARIYKGERTWSDFMAPVEKWMYRMSGINPAEEMN WKKFLVALLTVNVFWFFWGMVLLVSQGYLPLNPDGNAGQSPDLAFNTCISFMVNCNLQHY SGESGLTYFTQLFVIMLFQFITAATGMAALAGIFKAMATKTTRNFGNFWVLLIKSCTRILLPLS LVVGCILIIEGTPMGFEGKERITTLEGVEQAVSQGPTAAIVPIKQLGTNGGGYFGPNSSHPLE NPTFLSNMIECWSILIIPMSMVFALGFYLRRKKLAYTIYGVMLFAFLVGVVGAHYFELKGSPQI DAMGIAQERGSMEGKEIRLGTAATALWSQVTTVTSNGSVNGMHDSLTPLTGMLSMLNMQI NCWFGGVGVGLMNYYVFIIAVFISGLMVGRTPEFLGKKIEAREMKIAVIVALAHPFFILVFTAI SSFLATRNPELAEAWLNNPSFHGLSEMLYEYTSSAANNGSGFEGLRDNTYFWNFTCGIVLI MGRYLPIVGQVAIAGLLAKKKFIPESAGTLKTDTGTFAVMTFTVIFIIAALSFFPVLTLGPIAEYL SF
4E-228	767.4	27.2	5E-228	767.2	18.8	1	1	K9PIF2_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cal7507_2479	Calothrix sp. PCC 7507	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix sp. PCC 7507	99598	>tr|K9PIF2|K9PIF2_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Calothrix sp. PCC 7507 GN=kdpA PE=3 SV=1 MGQGFLQIGLTLLIVVVITPILGKYLARVFLGEKTLLDPLMKPIERSIYLLAGVRRTDDMKAGQ YARAVLLSNLIMGIVVYFLLYFQRFLPWNPNGLSVPTWHIVLHTVVSFVTNTDQQHYSGETT LSYFSQVAALGFLMFTSAATGLAVGIAFIRGLTGRTLGNFYVDLTRGITRVLLPISVMGAIALIL LGVPQTLAGTLVVKTLEGGTQYIARGPVASFEMIKMLGENGGGFFGANSAHPFENPNGAS NLIEAIAMIAIPAALIYTYGIFANNIKQAWLLFWMVFIIFVVLVGVTAVGELQGNPLINTTLGLEQ PNLEGKELRFGWAQTALWAVMTTATMCGAVNGMHDSLMPPGIFSTLFNLFLQMIWGGQG TGTAYLFVYLILTVFLTGLMVGRTPEFLGRKIEKREIVLASVVLLIHPITVLIPSAIALAYPISLSGI TNPGFHGISQVVYEYASAGANNGSGLEGLKDNTLWWNLSTCFSILAGRYIPIIALLLLAESMS HKPPVPETPGTLKTDSLLFTSVTSIVILILGVLTFFPILALGPLAEGFKLTSGS

6E-228	766.8	33.2	7E-228	766.6	23	1	1	F0S640_PSESL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Pedsa_1584	Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	562	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Pseudopedobacter, Pseudopedobacter saltans, Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	762903	>tr|F0S640|F0S640_PSESL Potassium-transporting ATPase potassium-binding subunit OS=Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) GN=kdpA PE=3 SV=1 MNTEILGIIAMFGVTLLLAIPLGKYIAKVYAGERTFLDPVFNPIERLFYKVSGINPDNEMNWKQ HLVALLTINLLWFLMSMGILMNMESLPLNPDGNPNQSADLAFNTTISFLVNCNLQHYSGETGI SYLGQIWLMFLQFVTAGVGMAAAVVLFKAFREKSTTQLGNFYNYFLKSCTRILLPISLILAAIF VFEGMPMTFEGKDTLTNLQGDTIEVSRGPVAAFVPIKHVGTNGGGFFGANGAHPLENPTYL TNMVEMFGQFIIPMAMVFAFGFFIRRKKFAWMMFGVMTVGFLLLAIPNINMEMNGNPAITQ MGIDNSLGAMEGKEIRLGAAASGFWSIVTTVISTGSINSMHDSSMPLSGMNELLAMMINAFY GGVGAGILNFLIFIILAVFISGLMVGRTPEFMGKKIEAREMKIAMIIALAHPFLILVGTALAAALP QYTSATLANPGFHGFSEMLYEYTSSAANNGSGFEGLGDNTVFWNISTGIVLLLGRFLPIIGP VAIAGLLAEKKFIPESSGTLKTDTSTFGLMVFAVIAIIAALAFFPALALGPIAEYFSLY
7E-228	766.8	28.7	8E-228	766.6	19.9	1	1	D2B153_STRRD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Sros_0433	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	479432	>tr|D2B153|D2B153_STRRD Potassium-transporting ATPase potassium-binding subunit OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=kdpA PE=3 SV=1 MSPTLAGILFIGSLVLALVLTHRPLGDYMYRVYTGTKHTAVERVVYRAIGVRPDTEQRWSVY ARGVLAFSLISVLFLYGLQRLQDKLFLSLGVPPVTDHVAWNTAISFVTNTNWQAYSGESTM GHLVQMAGLAVQNFVSASVGMAVAVALVRGFARSRTENLGNFWVDLVRGTVRILLPIAFVG AIVLVAGGLIQNFAEPHTVTTLTGGRQAITGGPVASQEVIKVLGTNGGGFYNANSAHPFENA APWTDWVEIFLILLLIPFAMPRTFGRMVGQVRQGYAIVAVMATLALASVALTNVFELSGGATV PQAVGAAMEGKEMRFGVSNSATFAAATTLTSTGAVNSFHDSYTPLGGMMTMFNMMLGEV APGGVGAGLYGMLVLAVITVFVAGLMVGRTPEYLGKKISAREIKLASMYFLVTPVLVLIGTAL AMGSAEQRASMLNGGPHGLSEVLYAFTSASNNNGSAFGGITVNTPWYDTALGLCMASGR FLPIIFVLALAGSLARQAPVPESAGTLPTHRPQFVGMVVGVTIVLVALTFLPALALGPLAEGIH
8E-228	766.5	27.2	1E-227	766.3	18.9	1	1	KDPA_NOSS1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA all4246	Nostoc sp. (strain PCC 7120 / UTEX 2576)	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	103690	>sp|Q8YPE8|KDPA_NOSS1 Potassium-transporting ATPase potassium-binding subunit OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=kdpA PE=3 SV=1 MGQGLLQIGLTLCIVIAITPVLGRYIARVFLGERTILDRVMNPIERSVYVISGVRPKDEMTGWQ YIRAILYTNLFMGILVYSLIYFQRLLPWNPNGLGVPSWDIVLHTVISFVTNTDQQHYAGETTLS YFSQVAALGFLMFTSAATGLAVGIAFIRGLTGRKLGNFYVDLTRGITRILLPISVIGAIALVLLG VPQTIGETLTITTLEGGTQYIARGPVASFEMIKMLGENGGGFFAANSAHPFENPNGLTNLIET IAMIAIPAAMIYTYGVFAKNIKQAWLLFWMVFIVFVILVWVAAGGELQGNPLVNGTLGIEQPN LEGKEVRFGWAETALWAVMTTATMCGAVNGMHDSLMPQGLFATLFNLFLQIIWGGQGTG TAYLFIYLILTVFLTGLMVGRTPEIFGRKIEKREIVLASLILLIHPIVVLIPSAIALAYPFSLSGISNP SFHGISQVVYEYASASANNGSGLEGLTDNSLWWNLSTSLSILTGRYVPIIAMLLLADSMSRK QTVPQTPGTLKTDSLIFTTVTAGIVLILGVLTFFPVLALGPIAEGFKLASGS
1E-227	766.1	43.2	1E-227	765.9	29.9	1	1	C2W4B7_BACCE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA bcere0022_6190	Bacillus cereus Rock3-44	554	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock3-44	526986	>tr|C2W4B7|C2W4B7_BACCE Potassium-transporting ATPase potassium-binding subunit OS=Bacillus cereus Rock3-44 GN=kdpA PE=3 SV=1 MVWVAAIVTILLFVLLAKPMGAYLEKAFQGSKTLDKVFGPIERLIFKMGGIKQNNQSWIQYAL AMLLTNGCMILFVYLVFRLQGILPLNPSKIEGMEPTLAFNTAISFMTNTNLQHYSGESGLSYL SQMIGITFMMFTAPATTLALAIAFIRGLAGKELGNFFVDFVRAIIRVLMPIAFVMALIFVAQGMP QTFSGTAVAHTLEGTKQMIPRGPLASLESIKMLGNNGGGFFGVNSAHPFENPTAITNVLQM MLMMLITTSLPFTYGRMIGSKKQGRILFVSMLMMFIIGFGTVVTAELQGNPVLNHLGMDRTE GNMEGKEVRIGTVMTSLFATVTTASETGGVNAMHDTFTPIGGMLPLVNMLLNTVFGGVGA GFINVIMYAMIAVFISGLMVGRTPEFLGKKLEGKEMKLIAVTLLFQPLLILGASAIAFSTNLGTD AITNSGFHGITQVIYEFTSSAANNGSGFEGLADNTPFWNISTGLVMYLARFFGLVTMLAVAA SLKEKTLVPKTVGTFRTDNGLFGGIFVGTIFIVGALTFFPVLVLGPIAEFLTL
1E-227	766.1	38.2	1E-227	765.8	26.5	1	1	KDPA_MAGSA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA amb1909	Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	556	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum magneticum, Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	342108	>sp|Q2W612|KDPA_MAGSA Potassium-transporting ATPase potassium-binding subunit OS=Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) GN=kdpA PE=3 SV=1 MDAHGVLQFLLFLALVLALTPILGRFMTWLFQAPVGRVEDGFYRLLGIDPTREQGWAAYAV SLLIFHLLAVFGLYALQRFQGMLPLNPAGQGAVPPDLAFNTAISFATNTNWQNYGGESTMS HLTQMAGLTVHNFLSAAAGIAVAVALMRGFARHSTRTVGNFYVDITRVTLGLLLPLCLVGAL VLVGQGVPQNFDAPVTVTTLEGVSQVIAQGPVASQMMIKHLGTNGGGFFNANAAHPYENP NALVNLIHMLAIFAIGAALTNTFGRMAGDRRQGWALLGAMAALFLAGLGAAWWAEAQGNP VLGGIANMEGKEVRLGVAASMLFAVVTTVTSCGAVNAMHDSLLPLAGMIPMVNMLLGEVVV GGVGSGLYGMVVFALLTVFIAGLMVGRTPEYLGKKIEAREIKLAVIAILATPVAVLGIGGLAITL PMGQAGIAAAGPHGLSEVLYAFASAGNNNGSAFGGLSGNTIFYNATMAAAMMIGRFVVMIP VLAIAGALAAKMAVPASAGTFPTHGWLFVVLLVGIVLVVGGLTYFPVLVLGPVVEHLALSAGI LF

1E-227	765.9	37.2	1E-227	765.7	25.8	1	1	A0A0C2Y686_BACBA	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpASD77_1462	Bacillus badius	564	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus badius	1455	>tr|A0A0C2Y686|A0A0C2Y686_BACBA Potassium-transporting ATPase A chain OS=Bacillus badius GN=kdpA PE=3 SV=1 MWQIAIILAIYLPLVILAGHYLFRVTMHQKTFLDPVLDKADRLIYKISGIKQENMTGKQYVLALIL SNACMIFVGYVLLRIQSVLFLNPNGIGNMEATLSFNTIISFMTNTNLQHYSGESGLSYLSQML VITFMMFTSAATGYAACMAFCRRLVAKTDTIGNFFVDFVRVITRVLMPLSVGVALLLVSQGS PQTLSGNQTVETIEGKMQDIALGPVASLESIKHVGTNGGGFNGANSTTPFENPTAISNIIEILS MMLLPGACVVAFSLMAARRKKNTLFGKQGLAIFSAMAALFLIGLTVIYAAEQAGNPIIDSLGIN QELGSMEGKEMRFGIPQSVLFTAVTTAFTTGSVNNMHDTLTPVGGLVAMFNMMLNVVFGG KGVGLMNMMMYVLLTIFIACLMIGRTPQFLGKKIEEKEMKLIALCILIHPAIILLFSALAVATAAG SGGITNPGAHGLSQVLYEYASASANNGSGFEGLSDNSYFWNITTGLAMFFGRYLPIIIQLAV ASLLAKKMWHSDSTGTLKTDNAMFSFLLAAIVLLIGALTFLPALALGPITEHLQIHR
1E-227	765.9	32.8	2E-227	765.6	22.8	1	1	A0A0D5LRR6_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpATM49_16160	Martelella endophytica	558	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	1486262	>tr|A0A0D5LRR6|A0A0D5LRR6_9RHIZ Potassium-transporting ATPase potassium-binding subunit OS=Martelella endophytica GN=kdpA PE=3 SV=1 MSDLSGFLLYGVVLVAAASALAVHMAAVYDGRRHVMSPVLGFAERRIYRFAGVNTSRPQG VRSYALSVLALNFAGFLLLYAVLRLQPLLPFNPDGIGPVSPAIAFNTAISFVTNTNWQAYSGE AQLSYFSQMVGLTVENFLSAATGMAVAVAVIRGFSGKGLGNFWVDATRSVLYILLPLSLLLG LFLAFQGVPQTLSGAAHVTTLEGVEQVIARGPAASQIAIKQLGTNGGGFFGVNSAHPFENPT VLSDLAQTLAILLIPVAFCFLFGRMVSDRRQGRAIFAAMAVMFVAGLLVIHFSELAGNPLIGAG ANMEGKEMRFGAALSALWAEATTAASNGSVNAMHDSFMPLSGLVMLINMQIGEVIFGGVG AGLYGMLLYVVLTVFLAGLMVGRTPEYLGRKIEAKEVTLAVIAFLSMPIGILAGGALTAVVPAA LASVQDGGPHGLSEILYAYSSAVGNNGSAFAGFGAATTWQTTALGVLMLFGRYAIIVPMLAI AGSLSAKRASPASTGSFPTHGPLFVALLVITVVVLGALTFFPVLALGPIAEQTALHAGQTF
1E-227	765.9	31.1	2E-227	765.6	21.6	1	1	C6VYG5_DYAFD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpADfer_0375	Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	562	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Dyadobacter, Dyadobacter fermentans, Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	471854	>tr|C6VYG5|C6VYG5_DYAFD Potassium-transporting ATPase potassium-binding subunit OS=Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114) GN=kdpA PE=3 SV=1 MNTELFGIIALFVGTVALAVPFGKYIAKVYGGEKTLLDPVLGPLEKGFYRLSGIRPNVEMSWK EHLFALLTINMVWFFLGMLVLMNQGWLPLNPDGNPSQSADLAFNTAISFVVNCNLQHYSGE TGMSYLGQLFLMFLQFVTAGTGMAAAAVVIMAIKERTTDKLGNFYDLFVKSCTRILLPVSFVI ALILLSNGTPMTFNGKDTMVTLQGDTVQVSTGPVAAFVPIKHVGTNGGGFFGANSAHPLEN PNYATNMTEMFGQMIIPLAMIFALGYYVKRKRLSWMIFSVMTLGFLLLTIPTIVTELHGNPKIA QMGIDMSCGAMEGKETRFGTTASAFWSIATTVISTGSINSMHDSFMPVSGLTQMLSMMTN AFYGGAGAGILNFYIFIILAVFISGLMVGRTPEFMGKKIEAREMKIAMIVALLHPLLILAATGLGV SLPGLTAGTLNNPGFHGFSEMLYEYTSSAANNGSGFEGLGDNTPWWNISCGIVLILSRFIPII GPVAIAGILAGKKHVPQSAGTLQTDTGTFGIMVFAVIVIITALSFFPALTLGPIAEYFSMQ
1E-227	765.8	28.1	2E-227	765.6	19.5	1	1	A0A0F0LS09_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpARR49_02069	Microbacterium ginsengisoli	560	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium ginsengisoli	400772	>tr|A0A0F0LS09|A0A0F0LS09_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Microbacterium ginsengisoli GN=kdpA PE=3 SV=1 MDAATIWAGIAQAATLILVLVVLYRPLGDYMAWIFTARKNLVVERGIYRVIGVDAASEQTWQ AYLRGVLLFSFVGVIFVYALERLQQWLPYSLGLPAVPEGLAFNTAISFVTNTNWQSYSPEQT MGYTVQFAGLAVQNFVSAAVGIAIAVALVRGFARRRATTIGNFWVDIVRVIWRLLLPVSIIAA VALIVAGVVQNVSSWTDVTTVTGQTQSIPGGTVASQEAIKELGTNGGGFFNANSAHPFENP TPWTNLLEMVLMLAIPFALPRTFGRMVGDNRQGYAIVSVMGTLFLASIVAVSWLEASGLGA AAQAAGGAMEGKEQRFGILGSALFSSTTTLTSTGAVNSMHDSFTPLGGMIPMVNMMLGEV APGGTGSGLYGMLILAIIAVFVGGLLIGRTPEYLGKKIGPREIKLASLYLLATPTLVLLGVGASF AIPPIRDEIENVSMLNPGVHGFSEVLYAFTSAANNNGSAFAGLTANTGWLDAALAVAMLLGR FVPIVLVLALAGSLAAQGTLPTTAGTLPTHRPQFVGLLIGVSIIFTALTYFPVALGPLAEGLS
2E-227	765.2	24.9	2E-227	765	17.3	1	1	R6DLS0_9BACE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpABN772_03515	Bacteroides sp. CAG:754	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:754	1262750	[illegible] OS=Bacteroides sp. CAG:754 GN=kdpA PE=3 SV=1 MNTEILGVVAQIALMVILAYPLGKYIARVYKGEKTWSDFMAPVERVIYKVCGIDPKEEMNWK QFLKALLILNAFWFFWGMVLLVSQGWLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSG ESGLTYFTQLFVIMLFQFITAATGMAAMAGIMKSIAAKTTKTIGNFWQFLVVSCTRILLPLSLIV GFILIVQGTPMGFDGKMKVTTLEGQEQMVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLEN PTYLTNMAECWSILIIPMAMVFALGFYTRRKKLGYSIFGVMLFAYLVGVCINVDQEMGGNPRI DELGIAQDNGAMEGKEVRLGSAATALWSITTTVTSNGSVNGMHDSTMPLSGMMEMLNMQI NTWFGGVGVGWMNYYTFIIITVFISGLMVGRTPEFLGKKVEAREMKIATIVALLHPFVILVFTA ISSYIYAHYPEFVESEGGWLNNPGFHGLSEQLYEYTSCAANNGSGFEGLGDNTYFWNWTC GIVLILSRFIPIVGQVAIAGLLAQKKFIPESAGTLKTDTLTFGVMTFAVIFIIAALSFFPVHALSTIA EHLSL

3E-227	764.9	26.5	3E-227	764.6	18.4	1	1	R5UU16_9BACE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN535_00854	Bacteroides caccae CAG:21	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides caccae CAG:21	1263037	>tr|R5UU16|R5UU16_9BACE Potassium-transporting ATPase potassium-binding subunit OS=Bacteroides caccae CAG:21 GN=kdpA PE=3 SV=1 MNTEILGVVVQIALMVILAYPLGKYIAKVYKGEKTWSDFMAPVERVIYKVCGINPDEEMNWK QFLKALLILNAFWFFWGMVLLVSQGWLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSG ESGLTYFTQLFVIMLFQFITAATGMAAMAGIMKSIAAKTTKTIGNFWQFLVVSCTRILLPLSLV VGFILILQGTPMGFDGKMKVTTLEGQEQMVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLE NPTYLTNMAECWSILIIPMAMVFALGFYTRRKKLGYSIFGVMLFAYLVGVCINVSQEMGGNP RIDELGIAQDNGAMEGKEVRLGAGATALWSITTTVTSNGSVNGMHDSTMPLSGMMEMLNM QINTWFGGVGVGWMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVALLHPFVILVF TAISSYIYAHYPEFVESEGGWLNNPGFHGLSEQLYEYTSSAANNGSGFEGLGDNTYFWNW TCGIVLILSRFIPIVGQVAIAGLLAQKKFIPESAGTLKTDTLTFGVMTFAVIFIVAALSFFPVHAL STIAEHLSL
3E-227	764.7	32.6	3E-227	764.5	22.6	1	1	A0A0D5EF23_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BW23_4439	Burkholderia ubonensis MSMB22	567	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	1249668	>tr|A0A0D5EF23|A0A0D5EF23_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia ubonensis MSMB22 GN=kdpA PE=3 SV=1 MFNNLIQFVIVLAITLALAPVVGKWLAHAFTSPRHAWAEQRTYALLGVDPAETMSWKRYGM VLLLSNAGMMLLGYLLLRVQDMLPFDSLQRASQSPDLAFNTAASFITNTNWQAYAGESSLS NFSQMAVITFLMTVSAATGVAAAGGFIRGLSRRNAADIGNYWVDFTRVIYRVLLPLCFVMAL VYVWQGMPQTLASDAWATTLEGARQQIVTGPVASLESIKHIGTNGGGFFSMNAAHPFENP TPLTNTLHMLSMLLIPSALTYALGSMIGRRRQGWVILGAFVVMFVGFLAVIYQAEQHGNPLL AGLGVDQAMSAEQPGGNMEGKEMRFGIAQTSLFATVTTAATTGSVDAMHDSLTPLGALVP LAQMMLNNVFGGDGVGLINLFTFAILTVFLVGMMIGRTPEFLGKKIEAREMKLVMLAVLAHP FSILGFTAVAAMMHSTMASLANLGPHGFSEVLYAYTSGTANNGSAFAGLNANTPFFNTTIGF AMLIGRYLTLLPMLAVAGCLAAKKSIPESVGTLSTSTGLFAGLLIFVILVVGGLTFLPALALGPI VEHLLMTSGQLF
3E-227	764.7	28.5	3E-227	764.5	19.8	1	1	R5JMJ2_9BACE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN523_02392	Bacteroides sp. CAG:189	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:189	1262737	>tr|R5JMJ2|R5JMJ2_9BACE Potassium-transporting ATPase potassium-binding subunit OS=Bacteroides sp. CAG:189 GN=kdpA PE=3 SV=1 MNTEILGVALQIVLMVVFAYPLGKYIARVYKGEKTWSDFMAPVEKLIYKVCGIDPKEEMNWK QFLKALLILNAFWFFWGMVLLVSQGWLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSG ESGLTYFTQLFVIMLFQFITAATGMAAMAGMMKAMAAKTTKTIGNFWQFLVVSCTRILLPLS LIVGFILILQGTPMGFDGKMKVTTLEGQEQMVSQGPAAAIIPIKQLGTNGGGYFGVNSSHPL ENPTFLTNAVECWSILIIPMAMVFAFGFYVKRKKLAYSIFGVMLVAYLIGVFINVSQEMGGNP RIDEMGISQAGGAMEGKEVRIGAASGALWSVTTTVTSNGSVNSMHDSTMPLSGMIEMLNM QINTWFGGVGVGWMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVALLHPFVILVG TALSSYLYAHHPEFVTSEGGWLNNPSFHGLSEQLYEYTSSAANNGSGFEGLGDNTYFWNY SCGIVLILSRFIPIVGQVAIAGLLAQKKFIPESAGTLKTDTATFGVMTFAVIFIVAALSFFPVHAL STIAEHFSL
4E-227	764.3	27.3	5E-227	764	18.9	1	1	L0J1B4_MYCSM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mycsm_05132	Mycobacterium smegmatis JS623	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis JS623	710686	>tr|L0J1B4|L0J1B4_MYCSM Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium smegmatis JS623 GN=kdpA PE=3 SV=1 MTTTTAGILFLALLIVALAVVHVPFGDYMYRVYSSDKHSRVERVIYRLMGADPKSEQSWGAY ARSVLAFSAISVLFLFIFQLIQGKLPWHLNDPATPMTPALAWNTAISFVTNTNWQAYSGEST QGHLVQMAGLAVQNFVSASVGIAVAIALVRGFARKHTGDLGNFWVDLVRGTIRILLPISVVA AIILIAGGAIQNFHLHDQVVNTLAGGQQTITGGPVASQEAIKELGTNGGGFYNANSAHPFEN PTSWTNWLEIFLLLVISFSLPRTFGRMVGSKKQGYAITSVMASLFLISVSFMMWFQLQHHGT VPTSVNAAMEGVEQRFGIANSAVFADATTLTSTGAVDSFHDSYTSLGGMITLFNMQLGEVA PGGTGSGLYGMLILAVITVFVAGLMVGRTPEYLGKKINPREIKLAASYFLVTPLIVLTGTAIAM AMPGQRAGMLNTGPHGLSEVLYAFTSAANNGSAFAGISVNTEWYNTALGLAMVFGRFLP MVLVLALAGSLAKQGTTPESIGTLPTHRPQFVGMVAGVTLILVALTFLPMLALGPLAEGIH
5E-227	763.8	25.2	6E-227	763.6	17.4	1	1	V5XHA6_MYCNE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA D174_21880	Mycobacterium neoaurum VKM Ac-1815D	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	700508	>tr|V5XHA6|V5XHA6_MYCNE Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium neoaurum VKM Ac-1815D GN=kdpA PE=3 SV=1 MSTTTAGIVFLAALVLVLALTHVPLGDYMYRVYTRAEDSRLERGIYRLIGADPKAEQTWGAY ARSVLAFSAVSIVFLFVFQLVQGKLPLHLNDPATEMTPALAWNTAVSFVTNTNWQAYSGET TQGHLVQMAGLTVQNFVSAAVGMAVAIAFVRGLVRRSTGDLGNFWVDLVRGSLRILLPLSV IGAIVLIAGGVIQNFALHDQVVDTIAGGQQTLPGGPVASQEVIKELGTNGGGFYNANSSHPY ENPTPWTNWVQILLICLIPFALPRTFGRMVDNKKQGLAIVAVMATIATLSVSVLMLVQLQAHG TVPTAVGAATEGVEQRFGVADSAVYAAATTLTSTGAVNSFHDSYTSLGGLITMFNMQLGEV APGGVGSGLYGMLILAIITVFVAGLMVGRTPEYLGKKITPREIKFAATYFLITPLLVLTGTALAM AMPGQRDGMLNTGPHGLSEVLYAFTSASNNGSAFAGISVNTEWYNTALGLAMVFGRFLP IILVLALAGSFAAQARTPESAGTLPTHRPQFVGMVTGVTLILVALTFLPMLALGPLAEGIH

6E-227	763.7	29.4	7E-227	763.5	20.4	1	1	KDPA_DELAS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Daci_5925	Delftia acidovorans (strain DSM 14801 / SPH-1)	568	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Delftia, Delftia acidovorans (Pseudomonas acidovorans) (Comamonas acidovorans), Delftia acidovorans (strain DSM 14801 / SPH-1)	398578	>sp|[illegible]|KDPA_DELAS Potassium-transporting ATPase potassium-binding subunit OS=Delftia acidovorans (strain DSM 14801 / SPH-1) GN=kdpA PE=3 SV=1 MWLTWMEYALVLLLMTALAVPMGQWLARCFTSEHHAWIERLSFRALGVNPAERMGWQR YGLALLLSNGAMLLLGYALLRAQGWLPLNALGNAAQTPDLAFNTAASFVTNTNWQAYSGES SLSNATQMVAITFMMFAGAITGVVAAAGFIRGLARSSASDLGNYWVDYVRVLWRVMLPLSF VVALVYVWQGVPQALDGQVWATTLEGARQQILLGPVASLESIKHIGTNGGGFFGMNAAHP FENPTPLTNAIHILGMLLIPSAMTYAFGSMLLRRRQGWVLFGACLVMFVGFLALVFTAEQAG NPLLTAAGADQQISATQPGGNMEGKELRFGIADTALFVATTTAATTGTSVNAMHDSLTPLGG LVPLAQMMINCVFGGDGVGLINLLQYAILTVFLAGMMIGRTPEFLGKKIEAREIKLVMLAVMA HPISVLGFTALAAVWPDTLASLANRGPHGFSEVLYAYASGTANNGSAFAGLNANTPFFNTTI GLAMLAGRYLTLLPMLALAGSLAAKPTVPAGPGTFPTATPLFMGLLVFVVVVVGGLTFLPSL ALGPVVEQLQMLSGQVYP	
9E-227	763.1	26.6	1E-226	762.8	18.4	1	1	KDPA_BACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BT_2425	Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides thetaiotaomicron, Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	226186	>sp|Q8A1S6|KDPA_BACTN Potassium-transporting ATPase potassium-binding subunit OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) GN=kdpA PE=3 SV=1 MNTEILGVVAQVALMVILAYPLGRYIAKVYKGEKTWSDFMAPIERVIYKVCGIDPKEEMNWK QFLKALLILNAFWFVWGMVLLVSQGWLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSG ESGLTYFTQLFVIMLFQFITAATGMAAMAGIMKSMAAKTTKTIGNFWHFLVVSCTRILLPLSLI VGFILILQGTPMGFDGKMKVTTLEGQEQMVSQGPAAAIVPIKQLGTNGGGYFGVNSSHPLE NPTYLTNMVECWSILIIPMAMVLALGFYTRRKKLAYSIFGVMLFAFLVGVCINVSQEMGGNP RIDELGIAQDNGAMEGKEVRLGAGATALWSIVTTVTSNGSVNGMHDSTMPLSGMMEMLNM QINTWFGGVGVGWMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVALLHPFVILVF TAISSYIYVYHPDFVESEGGWLNNLGFHGLSEQLYEYTSCAANNGSGFEGLGDNTYFWNW TCGIVLILSRFLPIIGQVAIAGLLAQKKFIPESAGTLKTDTLTFGIMTFVVIFIVAALSFFPVHALS TIAEHLSL	
1E-226	762.7	27.5	1E-226	762.4	19	1	1	G8X3F4_STREN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SCATT_46340	Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cattleya, Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	1003195	>tr|G8X3F4|G8X3F4_STREN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057) GN=kdpA PE=3 SV=1 MSPTAADVLQVLALVVALALVHRPLGDYMAAVYTSRRHLRAERWIYRCIGADPDAEMRWP AYLRGVLAFSVVSVLFLYLLQRVQNHLPGSLGFAAVTPQQAFNTAASFVANTNWQSYSGES TMGHVVQTGGLAVQNFVSAAVGIAVAIALVRGFARSRTGELGNFWSDLVRTTVRILLPIAFV AAVVLVACGAIENFAGWHEVTTVTGAHQAMPAGAVASQEAIKELGTNGGGYFNANSAHPF ENPTAFTNLFEIFLILVIPFSLTRTFGKLVGSLKQGYAILAAMGVIWLVFTVLMTWSESAHPGA ALQAAHGAMEGKEQRFGVGASSLFATSTTLTSTGAVDAFHSSFSAFGGGIAMLGMMLGEIA PGGTGSGLYGMLIMAVIAVFIAGLMVGRTPEYLGKKIGSRQIKYAACYILITPALVLVFTALSM ALPTPIRSAANPGAHGFSEVLYAFTSAANNNGSAFAGLNANTDWFNTTTGLAMLLGRFLPM VFVLALAGSLAEQRPVPETAGTLRTEKPLFAGLLVGTVIIVTGLTYFPALALGPIAEGLS	
1E-226	762.5	29	2E-226	762.3	20.1	1	1	KDPA_SYNY3	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA slr1728	Synechocystis sp. (strain PCC 6803 / Kazusa)	558	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechocystis, Synechocystis sp. PCC 6803, Synechocystis sp. (strain PCC 6803 / Kazusa)	1111708	>sp|P73866|KDPA_SYNY3 Potassium-transporting ATPase potassium-binding subunit OS=Synechocystis sp. (strain PCC 6803 / Kazusa) GN=kdpA PE=3 SV=1 MLQGFVQIALILAILVATAPLLGRYMARVFLGQSTWLDKIARPLESLIFAGSGITKHPSMGATQ YVSAALISNLVMGVFVFLILMFQGSLPLNPTGLAAPSWDLALHTAISFVTNTNQQHYSGETT YTYFSQAGALGFLMFTSAATGIAVAIAFIRGLTGQAIGNFYQDLVLSITRILLPISLVGAILLLVA GVPETLAGPAQVTTLEGATQWIARGPVAHFEIIKELGENGGGFFGINSAHPFENPNNFANLL ETVIMMVIPAGLIITYGIMAGNPEQGWLIFWMVFILYGILIAIAAVGEFQGNPLINQILGETQPN LEGKEVRFGWVLTALWAVSTTGTMCGAVNGMHDSLMPPGGFVTLSDLFLQIIWGGQGTG TAYLFVFLILTVFLTGLMVGRTPEFLGRKIEKREIVLASLILLLIHPIAILIPTAITLAFPDTLAGISNP GFHGISQVAYEYASAAANNGSGFEGLADNTLWWNLSASFSLIAGRYVPIVALIFLADGMARK QPVPETSGTLHTDTTLFTGITAGAIIILGALTFLPILVLGPVAEAFNLV	
3E-226	761.4	24.3	3E-226	761.2	16.8	1	1	R5INU0_9PORP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN472_02769	Tannerella sp. CAG:118	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:118	1262978	>tr|R5INU0|R5INU0_9PORP Potassium-transporting ATPase potassium-binding subunit OS=Tannerella sp. CAG:118 GN=kdpA PE=3 SV=1 MNTEILGIAIQIILLVVLSYPLGKYIAKVYKGEKCWSDFMTPIENFIYKICGIDPKEEMGWKKFL KTLLILNAFWFLWGMVLLVIQHLLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSGESGL TYFTQLFVIMLFQFITAATGMAAMAGIMKSISLKTTRTIGNFWYFLVRSCTRILLPLSLIVGFILI VQGTPMGFDGKMTIPTLEGGEQTVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLENPTYLT NMVECWSILIIPMAMVLAFGFYLKRKKLAYSIYGVMLFAFLVGVGINTYQEMNGNPRIDDMGI AQENGAMEGKEIRIGSGGTALWSIVTTVTSNGSVNGMHDSTMPLSGMMEMLNMQINTWF GGVGVGWMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVALLHPFVILVGTALSSY LYAHNPEFVESEGGWLNNPGFHGLSEMLYEYTSCAANNGSGFEGLGDNTWFWNYTCGLV LILSRFIPIVGQVAIAGLLAEKKFIPESAGTLKTDTVTFGVMTFAVIFIIAALSFFPVHALSTIAEH FSL	

4E-226	761	25.3	4E-226	760.8	17.5	1	1	A0A0F0KH56_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RN50_02061	Microbacterium foliorum	565	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium foliorum	104336	>tr|A0A0F0KH56|A0A0F0KH56_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Microbacterium foliorum GN=kdpA PE=3 SV=1 MGAGISTGAELWFGILQAAVLIVALVLLYRPVGDYMARVFSTPRDLKLERGVYRLIGVNPES EQTWRAYARGVLAFSAVGLLLVYGLQRLQAFLPQSLGLPAVPEGLAFNTAASFVANTNWQ SYSPEQTMGYTVQLAGLTVQNFVSAAVGLAVAVALIRGFARRGSTTIGNFWVDLIRGLGRIL LPIALLAAIALIAGGVVQNFAGFTDVTTVSGGTQTIPGGPVASQEAIKLLGTNGGGFFNANSA HPFENPTGWTNLLQILLILVIPFSLPRTFGRMIGDHRQGYAIAAVMGTIFLVSTFALSALELAG RGSAPELAGAAMEGKEVRFGILGSTLFGSASTLTSTGAVNSMHDSYTALGGMMPMLNMML GEVAPGGVGSGLYGMLVLAIIAVFVGGLLVGRTPEYLGKRIGPKEIKLASLYILVTPTLVLAGT ALSFAIPGIRADVEATSILNPGVHGMSEVLYAFTSAANNNGSAFAGLTANTPWFNTALGVAM LLGRFLPIVLVLALAGSFAAQQRVPENTGTLPTHRPQFVGLLTAVAVIITALTYFPVLALGPLA EGLV
6E-226	760.4	25.1	7E-226	760.2	17.4	1	1	A0A0F4JTN7_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VR45_11660	Streptomyces sp. NRRL S-495	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-495	1609133	>tr|A0A0F4JTN7_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. NRRL S-495 GN=kdpA PE=3 SV=1 MSSTLAGWLQVLALVGALALCYRPLGDYIAHTLTTSRHLRAEKALYKVIGVDADADQRWPV YLRSVLAFSAVSVLFLYTLIRVQQWLPLGLGVDQMPGHQAWNTAISFVANTNWQSYSGEA AMGHLAQMAGLAVQNFVSAAVGIAVVATLIRGFTRNRTDRLGNFWVDLTRISVRLLLPISIVF ALALVATGVVQNFHGFHEVATLAGDPQSVPGGAVASQEVIKLLGTNGGGFYNANSAHPFE NPTGLSNFLEIFLILVIPFALPRAFGRMVGDNRQGYAIVSVMGLFWVASVALMTLAESHHAG TALQSAGGAMEGKEQRFGIAASSLFAASTTLTSTGAVNSFHDSYTAFGGGLTMFNMMLGEI APGGVGSGLYGMLVLAIVAVFVAGLMVGRTPEYLGKKLGGREMKFASLYILTTPTLVLVGTG VAMALPGQRAGMLNSGAHGFSEVLYAFTSGANNNGSAFAGITVNTDWYDTAIGLAMVFGR FLPMVFVLALAGALAQQQPVPATPGTLPTHKPLFVGLLSGVVLIVVGLTYFPALALGPIAEGL S
6E-226	760.4	25.4	7E-226	760.2	17.6	1	1	KDPA_PARD8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BDI_3930	Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	569	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides distasonis, Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	435591	>sp|Q8EQG6|KDPA_PARD8 Potassium-transporting ATPase potassium-binding subunit OS=Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152) GN=kdpA PE=3 SV=1 MNTEILGVALQILLLLVISYPLGKHIAKVYKEGNDCMRFMAPIERFIYKLAGINPNEEMDWKAF LKSLLIINVFWFFWGMILLVSQGYLPLNPDGNSGQSPDLAFNTCISFMVNCNLQHYSGESGL TYFTQLFVIMLFQFITAATGMAAMAGIMKSMAAKTTKTIGNFWHYLVISCTRILFPMSLIVGFIL IIQGTPMGFDSKMTIPTLEGAEQTVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLENPTYLT NIVECWSILIIPMALVFALGFYLKRKKLGYVIYGVMLFAYLLGVFCNVHYEMAGNPKIDEMGID QSCGAMEGKETRLGPGATALWSVTTTVTSNGSVNGMHDSTMPLSGMVEMLNMQINTWF GGVGVGFMNYYAFLIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVSLAHPFVILIFTAISSYV WVYAPEFVESEGGWLNNPGFHGFSEMLYEYTSSSANNGSGFEGLGDNTYFWNYTCGLAL IISRYLPIVGQVAIAGLLANKKYTPESAGTLKTDTVTFGVMTFFVIVIVAALSFFPAQTLGPIAE YFSIY
8E-226	759.9	30.2	1E-225	759.6	20.9	1	1	A0A0A1FWC5_9MYCO	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA G155_23780	Mycobacterium sp. VKM Ac-1817D	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. VKM Ac-1817D	1273687	>tr|A0A0A1FWC5|A0A0A1FWC5_9MYCO Potassium-transporting ATPase A chain OS=Mycobacterium sp. VKM Ac-1817D GN=kdpA PE=3 SV=1 MTTTTAGIVFLVVLVVAVAAVHVPLGDYMYRVYTSERHSRAERVIYRLIGADPKAEQTWGAY ARSVLAFSAISILFLFTLQLVQGKLPLRLNDPGTPMTPALAWNTAVSFVTNTNWQAYSGEST QGHLVQMAGLAVQNFVSAAVGMAVAMTLVRGLVRRNTGDLGNFWVDLVRGNLRILLPISIV GALILVSGGVIQNFALHTEVINTLVGGTQTIPGGPVASQEVIKLLGTNGGGFFNANSAHPFEN PTTWTNWVEIFLILMIPFSLPRTFGRMVGSPRQGLAIASAMGVIATISVSLMMLFQLQAHGTV PTAAGAAMEGVEQRFGVANSAVFADATTLTSTGAVDSFHDSYTSLGGMITMFNMQLGEVA PGGVGSGLYGMLILAIITVFVAGLMVGRTPEYLGKKITPREIKLAATYFLVTPLIVLTGTAVAM AMPGQRAGMLNTGPHGLSEVLYAFTSAANNNGSAFAGISVNTEWYNTALGLAMVFGRFLP IIFVLALAGSLARQGKTPESVGTLPTHRPQFVGMVSGVTLILVALTFLPMLALGPLAEGIH
1E-225	759.6	27.1	1E-225	759.4	18.8	1	1	R6K3Q1_9BACE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN506_01198	Bacteroides cellulosilyticus CAG:158	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides cellulosilyticus CAG:158	1263038	>tr|R6K3Q1|R6K3Q1_9BACE Potassium-transporting ATPase potassium-binding subunit OS=Bacteroides cellulosilyticus CAG:158 GN=kdpA PE=3 SV=1 MNTEILGVALQVILMVVLAYPLGKYIAKVYKGQKTWSDFMKPVERLIFKVSGINPQEEMNWK QFLKALLILNAFWFVWGMVLLVTQHWLPLNPDGNGPQSPDQAFNTCISFMVNCNLQHYSG ESGLTYFTQLFVIMLFQFITAATGMAAMAGIMKSISAKTTKTIGNFWNFLVLSSTRILLPLSLIV GFILILQGTPMGFDGKMEVTTLEGQEQLVSQGPAAAIVPIKQLGTNGGGYFGVNSSHPLEN PTYLSNMVECWSILIIPMAMVFALGFYSNRKKLAYSIFGVMLFAYLAGVGINVYQEMNGNPRI DELGIAQDGGAMEGKEVRLGSAATALWSITTTVTSNGSVNGMHDSTMPLSGMMEMLNMQI NTWFGGVGVGWMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIATVVALLHPFVILVGT ALSTYLFAHHPDFVASEGGWLNNPGFHGLSEQLYEFTSCAANNGSGFEGLGDNTYFWNY SCGWVLILSRFIPIVGQVAIAGLLAQKKFIPESAGTLKTDTVTFAVMTFAVIFIVAALSFFPVHA LSTIAEHFSL

1E-225	759.4	25.6	1E-225	759.2	17.7	1	1	A0A0F2CAC8_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RS85_01847	Microbacterium sp. SA39	559	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium sp. SA39	1263625	>tr|A0A0F2CAC8|A0A0F2CAC8_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Microbacterium sp. SA39 GN=kdpA PE=3 SV=1 MDASIWFGILQVAAVVVVLVMLYRPLGDYIAHVYSAPRDLRVERGLYRLIGVDSRSEQTWR AYARSVLAFSVVGVVLVYGMQRLQAFLPQSLGLPAVPEGLAFNTAASFVTNTNWQSYSPE QTMGYVVQLAGLTVQNFVSAAVGLTIAIALIRGLARRGSSTIGNFWVDLTRGLGRLLLPLALI GAVVLLAGGVIQNFAGFTDVTTVSGGTQTIPGGPVASQEAIKLLGTNGGGFFNANSAHPFE NPTAFTNLVQILLILVIPFSLPRTFGRMIGDHRQGYAIAAVMSTIFLVSTFALSALELAGRGSAP ELAGAAMEGKEVRFGILSSTLFGSASTLTSTGAVNSMHDSYTALGGMMPMLNMMLGEVAP GGVGSGLYGMLVLAIIAVFVGGLLVGRTPEYLGKRIGPREIKLASLYILVVPALVLGGTALSFA IPGIRADVEATSILNPGVHGMGEVLYAFTSAANNNGSAFAGLTANTPWFNTALGVAMLLGR FLPIVLVLALAGSFAAQERIPATSGTLPTHRPQFVGLLLAVTVIVTALTYFPVLALGPLAEGLV
1E-225	759.4	27.4	1E-225	759.1	19	1	1	E8N7S4_MICTS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MTES_1366	Microbacterium testaceum (strain StLB037)	555	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium testaceum (Aureobacterium testaceum) (Brevibacterium testaceum), Microbacterium testaceum (strain StLB037)	979556	>tr|E8N7S4|E8N7S4_MICTS Potassium-transporting ATPase potassium-binding subunit OS=Microbacterium testaceum (strain StLB037) GN=kdpA PE=3 SV=1 MSIVLTSLTLLVALGLAYRPLGDYIARIYTGRRDLAVERGTYRLIGVDPRSAQTWAAYLRSVL LFSFVGVVLVYALMRLQAVLPFSLGLGAPSEALSFNTAVSFVTNTNWQSYGGESTLGYTVQ FAALTVQNFVSAAVGIAVAVALVRGFAYRRSGVIGNFWVDLVRGTFRLLLPFSVVAAVVLLA GGVIQNLNGFTDATTLTGAAQSIPGGPVASQEAIKLLGTNGGGIFNANSAHPFENPTPWTNL FEIFLMLVIPFSLPRAFGRIVGDDRQGYTILGVMGAIFVASTALLTWAEMAGAGTAPMLAGG AMEGKEVRFGIFGSTLFGTTSTLTSTGAVNSMHDSYTALGGMMPMVNMMLGEIAPGGVGS GLYGMLILAVIAVFVGGLLIGRTPEYLGKKIGPREIKLASLYILVTPTLVLAGTALSFGIPGIRSD VESTSILNPGVHGLSEVLYAFTSAANNNGSAFAGLTANTPWFNTALAVAMLLGRFLPIVFVL ALAGSLAAQDAVPATAGTLPTHRPQFAGLLAGVSVIVTALTYFPVLTLGPLAEGLVR
1E-225	759.3	29.2	2E-225	759	20.2	1	1	KDPA_FLAPJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA FP1692	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	573	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium psychrophilum, Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	402612	>sp|A6H086|KDPA_FLAPJ Potassium-transporting ATPase potassium-binding subunit OS=Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511) GN=kdpA PE=3 SV=1 MNTELFGVISIFIVSIVLAIPLGRYIAKIYSNDKTLLDPIFNPIEKFIFKISGINATEVMNWKQHLK ALLSINMVWFFLCFFILLFQGSLFLNPDNNPSMPPDLAFNTAISFLVNCNLQHYSGESGVSYL SQLFLMFLQFVSAGVGMAAAAMVFTAMKERTTDKLGNFYNFFIKSCTRILLPLSVIVAVALLF SGTPMTFEGKDTITTLQGDTVEISRGPAAAFIAIKHIGTNGGGFFGANSAHPLENPTYFTNAV ELWAQLIIPFAMIFALGFYLKKRKFSYVIFGVMTVGFLLLVIPTVISELNGNPAIERMGITQATG AMEGKEVRFGPAVTGFWSIATTVISTGSVNSMHDSSMPVSGSMELLAMMINAFYGGCGVG ILNFYIFIILAVFISGLMVGRTPEFLGKKIEAREVKIAAFIAILHPLLILSGTALASYFAANDTAMG YWFSGNATGWLNNPGHHGFSEMLYEYTSSAANNGSGFEGLADNNPFWNITTGIVLLLSRF LPIIGPLAIAGLLANKKYIPESAGTLKTDTTIFGVMVFAVIAIIAALSFFPALALGPLAEYFTLK
2E-225	758.9	29.1	2E-225	758.7	20.2	1	1	W5TN82_9NOCA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NONO_c56330	Nocardia nova SH22a	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia nova, Nocardia nova SH22a	1415166	>tr|W5TN82|W5TN82_9NOCA Potassium-transporting ATPase potassium-binding subunit OS=Nocardia nova SH22a GN=kdpA PE=3 SV=1 MSTTTAGVVFAATLIIALAAVHVPLGDYMYRVYAGTRHSRAERILYRAIGVHPGVEQTWGVY ARSVLAFSAVSVLFLFFLQLIQGHLPLHLHEPGTEMTPALAWNTAISFVTNTNWQNYAGEST QGHLVQMAGLAVQNFVSAAVGMAVAVALVRGFARRHTGDLGNFWVDLVRGTIRILLPIAFV FAIVLVAGGVIQNFHLHDQIAQTVTGTTQTIPGGPVASQEVIKELGTNGGGFFNVNSAHPFE NPTTWTNWIEIFLILLIAFSLPRTFGRMVGSRKQGYAIASVMGVLALISVVLTNFLQLRHHGTV PTAVGSALEGVETRFGVSDSATFAASTTLTSTGAVDSAHDSYTSLGGMMTMVNMQLGEVA PGGVGSGLYGMLILAVITVFVAGLMVGRTPEYLGKKITPREIKFAASYFLVSPLIVLVGTAIAM ALPGERAAMANSGPHGLSEVLYAFTSAANNNGSAFAGLSGNTVWWNTALGLAMVFGRFV PIVLVLALAGSLARQGHTPESAGTLPTHRPQFVGMVAGVTLILVALTFLPMLALGPLAEGIH
2E-225	758.9	28	2E-225	758.7	19.4	1	1	K9ZBC6_ANACC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Anacy_0434	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	272123	>tr|K9ZBC6|K9ZBC6_ANACC Potassium-transporting ATPase potassium-binding subunit OS=Anabaena cylindrica (strain ATCC 27899 / PCC 7122) GN=kdpA PE=3 SV=1 MGQGFLQIALTLSIVIFITPKLGRYIAKVFLGESTILDVIMNPIEKILYILVGVRKNDEMTGWQYI RAVLCSNLVMGIFVYAVLHYQRLLPWNPNGFGVMRWDTLLHTTISFLTNTDQQHYIGETTLS YFSQIAALGFLMFTSAATGLAVGIAFIRGLTGRKLGNFYVDLTRAITRILLPLSIIGAIALIALGVP QTLDQTLVIQTLEGGTQYIARGPVASFESIKMLGENGGGFFAANSAHPFENPNGASNLLEIIA MLSIPTSLIYTYGVFANNLKQTWLLFWMVFVIFVILIWMTAVGEMQGNPLINKIVSAEIPNLEG KELRFGWAETALWAVTTTATMCGAVNGMHDSLMPQGVFSTLFNLFLQIIWGGQGTGTAYL FIYLILTVFLTGLMVGRTPEFFGRKIEKREIVLASVVLLIHPILVLIPSAIALAYPISLSGISNPSFH GISQVVYEYASAAANNGSGLEGLKDNTLWWNLSSSFSILAGRYIPIIAILLLADSMSGKPKVT ETRATLKTDSLMFTSITAGVTIILGILTFFPVLALGPIAEAFKLASGN

2E-225	758.8	33.3	2E-225	758.6	23.1	1	1	KDPA_DESVH	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DVU_3339	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	569	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	882	>sp|Q72EY6|KDPA_DESVH Potassium-transporting ATPase potassium-binding subunit OS=Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303) GN=kdpA PE=3 SV=1 MQLMEYTQLALFLGLLALMSPVLGRFIGRAVLRGEQTWMHSVLGPVERLIYRASGIRPEAR QSWRQYAASLCAFSAAGFLMTFGVLMLQDKLPLNPQGFPGLSWHLAFNTAVSFLTNTNW QSYAGESTVSHFSQMVGLAYHNFVSAAAGLAVAVAVMRGLASQESKTIGNFWADLVRSVL YVLLPISLVLAVVLVGQGVVQTMSAGTEVATLEGGRQFIAMGPTASQVAIKMLGTNGGGFF NANAAHPLENPTALSNLLQMLAIFIIPSSLVFTLGGAVSNRRHAWTVWFVMACLFMVGACSL YRAETLGTPLLTEVAQAPVTNMEGKEVRFGIFGSAMFATVTTDASCGAVNAMHDSLTPLGG LVTLVNMQMGEVIFGGVGSGLYGMVLFILLTVFLAGLMVGRTPDYLGKRIEGREVTLAMLALI IAATPPLLFSAVAAVSGWGQAALNNAGAHGFSEILYAYTSGVQNNGSAFAGLNANSPAWN VTIALAMLIGRFGIMLPMLGVAGSMASRKARPIGEFSFPVSGFTFGLLLTLVIVIVGALTYLPAL ALGPVVEHFQMLDGLLH
2E-225	758.7	29.6	2E-225	758.5	20.5	1	1	S0GEU5_9PORP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA C803_05524	Parabacteroides goldsteinii dnLKV18	569	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides goldsteinii, Parabacteroides goldsteinii dnLKV18	1235789	>tr|S0GEU5|S0GEU5_9PORP Potassium-transporting ATPase potassium-binding subunit OS=Parabacteroides goldsteinii dnLKV18 GN=kdpA PE=3 SV=1 MNTELLGSIAQIVLMVVLAYPLGKYIAKVYKGEKTCLDFIAPVERWIFKLCGIDPNVEMSWKS FLKALLTINLFWFFWGMFLLYFQQYLPLNPDGNASQSSHLSFNTCISFMVNCNLQHYSGES GLTYFTQLFVIMLFQFITAATGMAALGGVFKAMASKSTHTIGNFWNLLMKSSTRILLPLALVV GFILIIEGTPMGFDGKMKLTTLEGQEQLVSQGPAAAIIPIKQLGTNGGGYYGVNSSHPLENPT YLTNMVECWSILILPMAMVFALGFYLKRKKLAYSIFGVMLFAYLVSVGINTYYETKGNPMISA MGIDQQAGAMEGKETRLGPAATALWSCTTTVTSNGSVNGMHDSTMPLSGMMEMLNMQIN TWFGGVGVGFMNYYAFLIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVALAHPFVILIGTAV ACYYWVYNPAFVEAEGGWLNNPGFHGFSEMLYEYTSASANNGSGFEGLGDNTYFWNFTT GLALIISRYLPIVGQVAIAGLLAQKKYIPESAGTLKTDTATFAVMTFSVIFIVAALSFFPALTLGPI AEYFSIY
2E-225	758.6	38.3	2E-225	758.4	26.5	1	1	KDPA_BACCR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BC_0753	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	555	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	226900	>sp|Q81HQ1|KDPA_BACCR Potassium-transporting ATPase potassium-binding subunit OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) GN=kdpA PE=3 SV=1 MIWVAVIITMLLFILVAKPTGIYLEKAFQGSKTLDKVFGPFEKLIFKITGVKAYNQTWKQYALS LVLLNGFMIVVVYFIFRLQGVLPLNPAHIEGMEPTLAFNTAISFMADTNLQHYSGENGLSYLS QLIGITFLMFAAPATTLALVMAFIRGLAGKELGNFFVDFTRALTRVFLPIAFIAALVFVALGVPQ TLDGAVTAQTIEGAKQSILRGPVASFVSIKELGNNGGGFFGANSTHPFENPGQMSNILQMM LMMLLPTALPFTYGRMVGNKKQGRILFVSLFMVFLLGFITITTSELNGNPALNGMGIEHVQG STEGKEVRFGTVFSSLYATVTTAAETGAVNTMHDTLTPIGGLVPLVNMMLNTVYGGVGAGF VNIIMYAIIAVFISGLMVGRTPEFLGKKIEGKEMKLIAVTILFHPLLILGFSALALSTNLGTDAISH SGFHGLTQVVYEYTSSAANNGSGFEGLGDNTPFWNITTGLVMFLGRYFSLITMLAVAASLK EKTVVPETVGTFRTDNSLFGGIFIGTIVIVGALTFFPMLVLGPIAEFLTLK
2E-225	758.5	31.8	2E-225	758.3	22.1	1	1	R4LHV8_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA L083_3146	Actinoplanes sp. N902-109	548	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	649831	>tr|R4LHV8|R4LHV8_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Actinoplanes sp. N902-109 GN=kdpA PE=3 SV=1 MAGWLFVITLAVALVAVYRPFGDYLYRVVAGTRHNAAERGILKLVGVNPAAGQSWGVYAR SVLAFSAVSILFLYLFLRVQDKLWLSLGLPAVTDHIAWNTAVSFVTNTNWQAYAGESTLGHL VQMAGLAVQNFVSAAVGIAVAVALIRGFAARRSPELGNFWVDLTRVTLRILLPLSVLAAIVFM VGGMVQNLSGGTDVTTLTGATQHLTGGPVASQEAIKELGTNGGGFYNVNAAHPYENPTA WTNWLQIFLIFLIPFSLPRVFGRMVGQNRQGYAVVAVMAVLAVASIALTVGFEVHGAGTVP QAVGAAMEGKEVRFGVPDSAAYAAATTLTSTGAVNSFHDSYTAFGGMMPMVNMMLGEVA PGGTGSGLYGLLILAVVTVFVAGLMVGRTPEYLGKKIGAREMKLASSYFLVTPALVLTGTAL AFATGNSATALNVGPHGLSEVLYAFTSAANNNGSAFGGITVNTPWWDTALGLAMLLGRFLP IVLVLALAGALARQKVTPESAGTLPTHRPLFVGMVVGVTVVLVALTFLPALALGPIAEGLS
2E-225	758.5	29.4	2E-225	758.3	20.4	1	1	R7DMT8_9PORP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN686_00686	Tannerella sp. CAG:51	570	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:51	1262979	>tr|R7DMT8|R7DMT8_9PORP Potassium-transporting ATPase potassium-binding subunit OS=Tannerella sp. CAG:51 GN=kdpA PE=3 SV=1 MNTEILGSVLQIVILLVFSYPLGRHIAKVYKGEKSRWDFFTPIENFIYKLVGVDPKEEMNWKQ FLKALLVLNLVWFFWGMVLLCTQQWLPLNPDGNANQTADQAFNTCISFMVNCNLQHYSGE SGLTYFTQLFVIMLFQFITAATGMAAMAGIMKAMAAKTTKTIGNFWYFLVRSCTRILLPLSLLV GFVLILEGTPMGFDGKMEVNTLEGGTQMVSQGPAAAIVPIKQLGTNGGGYFGVNSSHPLE NPTFLTNIFECCSILIIPMAMIWALGFYLKRKKFGASIFAVMFFAYIVGVGINTYYEINGNPAID NMGIAQENGAMEGKEVRLGAAGTAFWSVTTTVTSNGSVNGMHDSTMPLSGLIEMLNMQIN TWFGGVGVGFMNYYVFIIIAVFISGLMVGRTPEFLGKKVEAKEMKIATIVALLHPFVILVGTAL ASYLYVHNPAFVESEGGWLNNPSFHGLSEMLYEYTSCAANNGSGFEGLGDNTMFWNYTC GIVLILSRFIPIVGQVAIAGLLAEKKYIPESAGTLKTDTATFGAMTFAVIFIVAALSFFPVHALSTI AEHLSLYI

2E-225	758.4	25.4	3E-225	758.1	17.6	1	1	KDPA_MYCPA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MAP_1000c	Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium avium complex (MAC), Mycobacterium avium, Mycobacterium paratuberculosis, Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	262316	>sp|Q741T7|KDPA_MYCPA Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10) GN=kdpA PE=3 SV=1 MSSTTAGLIFLAVLVAALVAVHVPLGDYMFRVYTTDRDLATERTIYRLIGVDARSEQTWGAY ARGVLAFSSVSIIFLFVLQLVQGKLPLHLHDPATKMTPSLAWNTAVSFVTNTNWQAYSGETT QGHLVQMAGLAVQNFVSAAVGMAVAVALVRGFARRRTGELGNFWVDLVRGTLRILLPISIV GAVLLVAGGAIQNFHLHDQVVTTLGGTAQTIPGGPVASQEVIKELATNGGGFYNANSAHPF ENPTAWTNWLEVFLILVIGFSLPRTFGRMVGNPKQGYAIASVMASLYLLSTGFMLWFQLQH HGTVPSAVGAAMEGVEQRFGVPDSGVFAAATTLTSTGAVDSAHDSLTSLGGMITMFNMQL GEVAPGGTGSGLYGMLVLAVITVFVAGLMVGRTPEYLGKKINPREIKLAASYFLVTPLIVLTG TAIAMALPGERAGMANSGPHGLSEVLYAFTSAANNNGSAFAGLSANTEWYNTALGLAMAF GRFLPIVLVLALAGSLARQGSTPDSAGTLPTHRPQFVGMVAGVTLIVVALTFLPMLALGPLAE GIH
3E-225	758.3	29.7	3E-225	758	20.6	1	1	H6R5W3_NOCCG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NOCYR_3890	Nocardia cyriacigeorgica (strain GUH-2)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia cyriacigeorgica, Nocardia cyriacigeorgica (strain GUH-2)	1127134	>tr|H6R5W3|H6R5W3_NOCCG Potassium-transporting ATPase potassium-binding subunit OS=Nocardia cyriacigeorgica (strain GUH-2) GN=kdpA PE=3 SV=1 MSTTTAGVVFVVSLIVALAVVHVPLGDYMYRVYTGTRHSRIERVIYRVIGVQPEVEQTWPVY ARSVLAFSAVGVLLLFGFQLVQGGLPWHLNDPATEMTPALAWNTAVSFVTNTNWQNYSGE STQGHLVQMAGLAVQNFVSAAGGMAVAVALVRGFARRHTGDLGNFWVDLVRGTLRILLPI AFVAAIALIAGGAIQNFQLHDQAAQTLNGSEQTITGGPVASQEVIKELGTNGGGFYNANSAH PFENPATWTNWLEILLILVISCSLPRTFGRMVGSRKQGYAIVAVMGTIALASVALTNLFQLQH HGTVPTAIGASMEGVEQRFGVANSATFAASTTLTSTGAVNSFHDSYTSLGGLMTMFNMQL GEVAPGGVGAGLYSMLILAVITVFVAGLMVGRTPEYLGKKITPREIKLAAAYFLVSPLIVLVGT AIAMAMPGQRASMLNTGPHGFSEVLYAFTSAANNNGSAFAGLTGNTEWYNTALGLAMLFG RFLPIILVLALAGSLARQGVTPASIGTLPTHRPQFVGMVAGVTVILVALTFLPALALGPLAEGIH
3E-225	758.2	29.3	3E-225	758	20.3	1	1	K9V7P3_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cal6303_4967	Calothrix sp. PCC 6303	562	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix parietina, Calothrix sp. PCC 6303	1170562	>tr|K9V7P3|K9V7P3_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Calothrix sp. PCC 6303 GN=kdpA PE=3 SV=1 MPQGLFQIGLTLLIVIAIAPFFGKYLAKVFLGENTPFDFIFSPIEKILFALGGIRRRENMTGGQY ARAVLYTNTIMGILVYFLLVTQKYLPFNPMRLVAPRWDLALHTTISFLTNTDQQHYAGETTLS YFSQTSAIAFLMFTSAATGLAVGIAFIRGLTGRQLGNFYVDLTRGIIRVLLPLSIIGAIALLTQGV PQTFLPTQVVQTLDGGSQYIARGPVASFEMIKQLGENGGGFFGANSAHPLENPNPVSNLLE TLAMVAIPSALIFTYGIFANNLKQAWLLFWMVFVIFLALVFITATGEYGGNTLINGTIGAEFANL EGKELRFGWAQTALWAVLTTATMCGAVNGMHDSLMPGGGFATLLNMFLQIVWGGQGTG TAFLYVFLILTVFVTGLMVGRTPEFLGRKIEKPQIVLASIILLIHPIAVLIPSAIALSFPKTLAGISN PGFHGISQVVYEYASAAANNGSGFEGLNDGSLWWNLSTCFSLLLGRYVPIIALLLLADSMSR KQVVAETSGTLRTDNSLFVTITAGIILILGVLTFFPVLALGPIAEGFKLASGIK
3E-225	758.2	23.1	3E-225	757.9	16	1	1	KDPA_MYCSK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mkms_4292	Mycobacterium sp. (strain KMS)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. (strain KMS)	189918	[illegible] OS=Mycobacterium sp. (strain KMS) GN=kdpA PE=3 SV=1 MSTTTAGILFALSLALALAAVHVPLGDYMYRVYASEKHWRAERVAYRIIGADPAAEQGWGS YARSVLAFSAVSILFLFGLQLLQGRLPLHLNDPATEMTPALAWNTAVSFVTNTNWQAYSGE STQGHLVQMAGLSVQNFVSAAVGMAVAMAFVRGLARRDTGELGNFWVDLIRGSLRILLPLS IIGAIILVSGGVIQNFALHDTVVSTLSGAQQTIPGGPVASQEAIKELGTNGGGFFNANSAHPF ENPTTWTNWVEIFLLSCIAFSLPRTFGRMVGSRKQGAAILAVMAVIATLSLSLMMLFQSQTH GTVPTAVGSATEGVEQRFGVADSAVFADLTTLTSTGAVDSFHDSYTSLGGLMTLFNMQLG EVAPGGVGSGLYSMLVLAVITVFVAGLMVGRTPEYLGKKITPREIKLAATYFLVTPLIVLIGTA VAMALPGQRDGMLNTGPHGLSEVLYAFTSAGNNNGSAFAGLSVNTEWYNTALGLAMVFG RFLPIILVLALAGSFARQGRTPESVGTLPTHRPQFVGMVTGVTLILVALTFLPVLALGPLAEGL H
3E-225	758	29.2	4E-225	757.8	20.3	1	1	KDPA_HYDS0	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HY04AAS1_0717	Hydrogenobaculum sp. (strain Y04AAS1)	576	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Aquificaceae, Hydrogenobaculum, Hydrogenobaculum sp. (strain Y04AAS1)	380749	>sp|B4U8E3|KDPA_HYDS0 Potassium-transporting ATPase potassium-binding subunit OS=Hydrogenobaculum sp. (strain Y04AAS1) GN=kdpA PE=3 SV=1 MNIFLDIFSFILFFGILTIISPILGKYMADIYEGRVHPSLKPIRYVEKTIYKILGIDESKEMNWKEY LYALLSFNFLGFLVLFLTLLFQKYLPLNQYHIPNMSWDLAFNTAVSFVTNTNWQAYAGETQA TYFSQITGLALQNFLSAASGIVVALVLIRAFARKNTIYLGNFYVDFTRTILYVLLPVAFFSALFLV SQGVIQNFSHYKTIELLEPYKDSKNIITTQTLPMGPVASQEAIKLLGTNGGGFFNANSAHPFE NPTPLSNVFEAFLIILIPASLVFTFGYMIKDKRQGWFLYSVMLFVLMLFMGIQYYFEWFGNPI VKKLGIEGPYLIGKELRFGIGGTVLFSSITTATSCGAVNSMLDSFTPLGGLVPMSLISLGEIIFG GVGSGLYGMIAMVIIAVFVAGLMIGRTPEYLNKKIESREMWSSVVITLVSGITALLLTTLALYT KWGLSSMSNPGPHGLSEVLYAYISTSNNSGSAFAGLNANTVFYNITTGLAMLIGRFIPIIAVF YMASSLSLKKHVPPSPGTLPTHTLVFGVWLVFIIIVVGALTFLPAFSLGPILEHMLMLEGVTL

3E-225	757.9	46.4	4E-225	757.7	32.2	1	1	A7GLG3_BACCN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bcer98_0624	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	555	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cytotoxicus, Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	315749	>tr|A7GLG3|A7GLG3_BACCN Potassium-transporting ATPase potassium-binding subunit OS=Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98) GN=kdpA PE=3 SV=1 MVTWVAAIVTIVLFILLAKPMGTYVEKAFQGSRTLEKVFGPIESIIFKVGGIQKKNQTWIQYVF AMLFTNACMILFVYLVFRLQGVLPLNPSKVEGMEPTLAFHTAISFMTNTNLQHYSGESGLSY LAQMIGITFMMFTAPATTLAFAIAFIRGLAGKEVGNFFVDFVRAIIRVLMPIAFIMALIFVAQGM PQTLSGSAVAQTLEGAKQVIPRGPIASLESIKMLGNNGGGFFGVNSAHPFENPTAITNVLQM MLMMFITTSLPFTYGRMIGSKKQGRILFVSMLIMFVIGFGMAVTTELQGNPVLNQFGMDHAQ GNMEGKEVRFGTIMTALFATVTTASETGGVNAMHDTFTPLGGMLTLVNMLLNTVFGGVGA GFINVIMYAMIAVFISGLMVGRTPEFLGKKLEGKEMKLIAVTLLFQPLLILGASAVAFSTNFGT EAITNSGFHGITQVIYEFTSSAANNGSGFEGLADNTPFWNISTGLVMYGARFFSLVTMLAVS VSLKEKAVVPETVGTFRTDNGLFGGIFVGTIFIVGALTFFPVLVLGPIAEFLTL
4E-225	757.8	27.4	4E-225	757.6	19	1	1	R5M252_9BACE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN711_01958	Bacteroides intestinalis CAG:564	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides intestinalis CAG:564	1263049	>tr|R5M252|R5M252_9BACE Potassium-transporting ATPase potassium-binding subunit OS=Bacteroides intestinalis CAG:564 GN=kdpA PE=3 SV=1 MNTEILGVILQIVLMVALAYPLGKYIAKVYKGQKTWSDFMKPIERLIFKVCGINPTEEMNWKQ FLKALLILNAFWFVWGMVLLVTQHWLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSGE SGLTYFTQLFVIMLFQFITAATGMAAMAGIMKSISAKTTKTIGNFWNFLVLSSTRILLPLSLIVG FILILQGTPMGFDGKMEVTTLEGQEQLVSQGPAAAIVPIKQLGTNGGGYFGVNSSHPLENPT YLSNMVECWSILIIPMAMVFALGFYSNRKKLAYSIFGVMLFAYLTGVGINVYQEMNGNPRIDE LGIAQDGGAMEGKEVRLGAAATALWSITTTVTSNGSVNGMHDSTMPLSGLMEMLNMQINT WFGGVGVGWMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIATVVALLHPFVILVGTAL STYLFAHHPDFVASEGGWLNNPGFHGLSEQLYEFTSCAANNGSGFEGLGDNTYFWNYAC GWVLILSRFIPIVGQVAIAGLLAQKKFIPESAGTLKTDTVTFAVMTFAVIFIVAALSFFPVHALS TIAEHFSL
4E-225	757.8	32.9	5E-225	757.4	22.8	1	1	G5KAR3_9STRE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA STRPS_2026	Streptococcus pseudoporcinus LQ 940-04	578	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pseudoporcinus, Streptococcus pseudoporcinus LQ 940-04	875093	>tr|G5KAR3|G5KAR3_9STRE Potassium-transporting ATPase potassium-binding subunit OS=Streptococcus pseudoporcinus LQ 940-04 GN=kdpA PE=3 SV=1 MLQIIFVLTIACLLILPTGKYLYHIASQQKTFADPIMDPIDRGIYRLLDVDKKGMTWKQYAVALV LTNAVMALVAYVILRTQAFLFLNPNRVGPLESSLSFNTVISFITNSNLQDYVGERDLSFLSQM VVITFMMFTSAASGYAAAMAFIRGVSGKYQDMGNFYVDFVRVITRVLLPFSIVGALVLISQGV PQTLAKELDVTTLEGKLQGIAMGPVASLEIIKHLGTNGGGFFAANSAAPFENPNVITNIIEMLS MMLLPGAMLVAFGYMVAAQRKGSHPLPPLQKASSNPMPMQLGRQARPLLLVMTFLFLAGL ALIVWSESKGNPFLHQLGLNQSMGNMEGKEVRFGIPMSGLFTEITTAFTTGSVNNMHDTLT PLSGGVAMVNMMLNVIFGGKGVGLMNMMLYVLLTVFICGLMIGRTPVYLGKKIEGKEMTLIA LGIVVHPVIILGFSALAVLLPAGLSSVSNPGFHGLSQVIYQFTSASANNGSGFEGLKDNTPFW NVSTGLAMFLGRYVTLILQLAVAGSLMTKSPVNASLGSLKTETGTFTLSLGMVVLIISALTFLP TLVLGPLAEFLTQ
4E-225	757.7	31.7	4E-225	757.5	22	1	1	E3GLH2_EUBLK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ELI_1559	Eubacterium limosum (strain KIST612)	561	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium limosum, Eubacterium limosum (strain KIST612)	903814	>tr|E3GLH2|E3GLH2_EUBLK Potassium-transporting ATPase potassium-binding subunit OS=Eubacterium limosum (strain KIST612) GN=kdpA PE=3 SV=1 MSSAFIQDIIFLVAVIGLGFPIGKLTYKIMEGGKIKFLGFLRPVELCVYKAMGVDENRGMSGR QYAIATLLFSLFGLLFLTALLMCQGFLPFNPEGLPGLSWDLAYNTAASFVSNTNWQAYSGET TLSYLSQFLGLTVQNFVSAATGIAVLFALIRGFILKKSKTVGNFWCDLVRTVLYLLLPLSLIVAII LMSQGVVQTLAPYAQAAFLQGGGSQIVPLGPAASQIAIKQLGTNGGGFFGVNSAFPLENPT AISNFVECWAIIVIPAALCFTFGKAVKDSKQGRSILIAMTLVFIVALTLTTMSEYNLGPQFNNVE SSASIEGKEVRFGAGGSALWGVTTTAASNGSVNSMHDSFTPLGGMFLMFMMQLGEIIFGG VGSGLYAMLAFAILAIFIAGLMVGRTPEYLGKKIEPYDMKMTCVILLVPPLLILGGTAIATMMP QASDWLTNSGAHGFSEILYAYTSGGANNGSAFAGYAANNVFNNVMIGSEMLIVRFIPMAAVI CLGANLASKKAVPKSDGTLSTTGPMFVGLLIGVFLILGALSFLPALALGPIADYFTML
4E-225	757.6	26	5E-225	757.4	18.1	1	1	D6D7V5_9BACE	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BXY_09350	Bacteroides xylanisolvens XB1A	554	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides xylanisolvens, Bacteroides xylanisolvens XB1A	657309	>tr|D6D7V5|D6D7V5_9BACE Potassium-transporting ATPase potassium-binding subunit OS=Bacteroides xylanisolvens XB1A GN=kdpA PE=3 SV=1 MVILAYPLGKYIAKVYRGEKTWSDFMAPIERVIYKVCGIDPNEEMNWKQFLKALLILNAFWFF WGMVLLVSQGWLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSGESGLTYFTQLFVIML FQFITAATGMAAMAGIMKSIAAKTTKTIGNFWQFLVISCTRILLPLSLIVGFILILQGTPMGFDG KMKVTTMEGQEQMVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLENPTYLTNMVECWSILI IPMAMVLALGFYTRRKKLAYSIFGVMLFAFLVGVCINVSQEMGGNPRIDELGIAQDNGAMEG KEVRLGAGATALWSIVTTVTSNGSVNGMHDSTMPLSGMMEMLNMQINTWFGGVGVGWM NYYTFIIITVFISGLMVGRTPEFLGKKVEAREMKIATIVALLHPFVILVFTALSSYIYVHHPDFVE SEGGWLNNLGFHGLSEQLYEYTSCAANNGSGFEGLGDNTYFWNYTCGIVLILSRFIPIIGQV AIAGLLAQKKFIPESAGTLKTDTLTFGVMTFVVIFIIAALSFFPVHALSTIAEHLSL

4E-225	757.5	30.2	5E-225	757.3	20.9	1	1	KDPA_FLAJ1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Fjoh_1975	Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) (Cytophaga johnsonae)	573	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium johnsoniae (Cytophaga johnsonae), Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) (Cytophaga johnsonae)	376686	>sp|A5FIF9|KDPA_FLAJ1 Potassium-transporting ATPase potassium-binding subunit OS=Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) GN=kdpA PE=3 SV=1 MNTELLGVIGIFILTIVLAIPLGKYIAKVYLGDKTLLDPIFNPIEKFIFKISGINSAEEMNWKQHLK ALLSINIVWFFLCFFVLLFQGSLPLNPDNNPSMTADLAFNTAISFLVNCNLQHYSGESGVSYL SQIVLMFLQFVSAGIGMAAAAMIFTAMKERTTEKLGNFYNYFIKSCTRILLPLSAIAAVALVFS GTPMTFEGKDAITTLQGDHVEVSRGPAAAFIAIKHIGTNGGGFFGANSAHPLENPTYFTNGV ELWAQMIIPFAMIFALGFYLNKRKLANIIFGVMTVGFLLLVVPTVMSEINGNPAITKMGIAQTT GAMEGKEVRFGPAISGFWSIATTVISTGSVNSMHDSSMPVSGAMQLLSMMVNAFYGGCG VGILNYYIFIILAVFISGLMVGRTPEFLGKKIEAREVKIAAFIAILHPLLILAGTALASYFTAHDTA MGYWFNGNATGWLNNPGNHGFSEMLYEYTSSAANNGSGFEGLGDNNPFWNITTGIVLLL SRFIPIIGPLAIAGLLAGKKYIPESAGTLKTDTSIFGIMTFAVIAIIAALSFFPALALGPLAEYFTLK
5E-225	757.3	29	6E-225	757.1	20.1	1	1	B2UR91_AKKM8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Amuc_1151	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	569	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales, Akkermansiaceae, Akkermansia, Akkermansia muciniphila, Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	349741	>tr|B2UR91|B2UR91_AKKM8 Potassium-transporting ATPase potassium-binding subunit OS=Akkermansia muciniphila (strain ATCC BAA-835 / Muc) GN=kdpA PE=3 SV=1 MMKTEILGVIAQIVLMVALSYPLGKYIAKVYKKEKTWLDFMKPVERLMFRLSGINPEEEMNW KQFLRALLTVNLFWFVWGMVLLVSQGYLPLNPDGNVGQTCHQAFNTCISFMVNCNLQHYS GESGLTYFTQLFVIMLFQFITAATGMAAMAGIMNALSKKTTKTIGNFWDYLVLSSTRILLPLSL VVGFILITQGTPMGFDGKMEVTTLEGVEQTISQGPAAAVVPIKQLGTNGGGYFGVNSSHPL ENPTYLSNMVECWSILIIPMAMVLAFGFYLKRKKLGYSIYGVMLLAFLIGVCINVYQEMNGNP RIEEMGIVQESGAMEGKEIRLGSAATALWSVVTTVTSNGSVNGMHDSTMPLSGMIQMLNM QINTWFGGVGVGWMNYFAFMIIAVFISGLMVGRTPEFLCKKVEAREMKIASIVALLHPFVILV GTALACYLFVYAPSFVEGEGGWVNNPGFHGLSEFLYEYTSSAANNGSGFEGLADNTWFW NYSCGIVLILSRFIPIIGQVAIAGLLAGKKYIPETSGTLKTDSVTFSAMTFAVIFIVAALSFFPVHA LSTIAEHLSL
5E-225	757.3	37.4	6E-225	757	26	1	1	KDPA_BACAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BA_0739 GBAA_0739 BAS0703	Bacillus anthracis	555	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus anthracis	1392	>sp|Q81UW7|KDPA_BACAN Potassium-transporting ATPase potassium-binding subunit OS=Bacillus anthracis GN=kdpA PE=3 SV=1 MIWVAVVITMLLFILVAKPTGIYLEKAFQGSKKLDKVFGPFEKLIFKITGVKEYNQTWKQYALS LVLLNGFMIVVVYFIFRLQGVLPLNPAHIEGMEPTLAFNTAISFMADTNLQHYSGENGLSYLS QLIGITFLMFAAPATTLALVMAFIRGLAGKELGNFFIDFTRALTRVFLPIAFMAALVFVALGVP QTLDGAVTAQTIDGAKQSILRGPVASFVAIKELGNNGGGFFGANSTHPFENPGQMSNILQM MLMMLLPTALPFTYGRMVGNKKQGRILFVSLFMVFLLGFITITTSELNGNPALNAMGIEHVQ GSTEGKEVRFGTVFSSLYATVTTAAETGAVNTMHDTLTPIGGLVPLVNMMLNTVYGGVGAG FVNIIMYAIIAVFISGLMVGRTPEFLGKKIEGKEMKLIAVTILFHPLLILGFSALALSTSLGTDAIS HSGFHGLTQVVYEYTSSAANNGSGFEGLGDNTPFWNITTGLVMFLGRYFSLITMLAVAASL KEKTVVPETVGTFRTDNGLFGGIFIGTIVIVGALTFFPMLVLGPIAEFLTLK
5E-225	757.2	29.6	6E-225	757	20.5	1	1	KDPA_BACFN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BF0528	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides fragilis, Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	272559	[illegible] OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) GN=kdpA PE=3 SV=1 MNTEILGVAVQIVLMVVLAYPLGRYIARVYKGEKTWSDFMAPIERVIYKICGINPQEEMNWK QFLKALLILNAFWFVWGMVLLVSQGWLPLNPDGNGAQTPDQAFNTCISFMVNCNLQHYSG ESGLTYFTQLFVIMLFQFITAATGMAAMAGVMKSMAAKSTQTIGNFWHFLVISCTRILLPLSL VVGFILILQGTPMGFDGRMQLTTLEGQEQMVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPL ENPTYLTNMVECWSILIIPMAMVLALGFYTNRRKLGYSIFGVMLFAYLAGVFINVGQEMGGN PRISEMGIAQDHGAMEGKEVRLGAGATALWSVTTTVTSNGSVNGMHDSTMPLSGMVEML NMQINTWFGGVGVGWLNYYTFIIMAVFISGLMVGRTPEFLGKKVEAREMKIATFVALLHPFV ILVFTAISSYVYTHHPDFVESEGGWLNNLGFHGLSEQLYEYTSSAANNGSGFEGLGDNTYF WNWTCGIVLILSRFIPIVGQVAIAGLLAQKKFIPESAGTLKTDTVTFAVMTFAVIFIVAALSFFP VHALSTIAEHLSL
6E-225	757.1	17	6E-225	756.9	11.8	1	1	KDPA_ANADE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Adeh_0895	Anaeromyxobacter dehalogenans (strain 2CP-C)	578	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Anaeromyxobacteraceae, Anaeromyxobacter, Anaeromyxobacter dehalogenans, Anaeromyxobacter dehalogenans (strain 2CP-C)	290397	>sp|Q2IPD5|KDPA_ANADE Potassium-transporting ATPase potassium-binding subunit OS=Anaeromyxobacter dehalogenans (strain 2CP-C) GN=kdpA PE=3 SV=1 MTAAALAEIAAFFGLLTAAAVPLGAYAARVLSTAPPHGRGPVARLERGLYRLAGVDPAEQM GWRRYAAAALTFNAAGLLAVFALERLQAALPGNPAGLPAVSPLVAWNTAVSFATNTNWQA YGGESTMSHLTQMGALTVQNFLSAATGISVLAALVRALAGPAGSGLGSFWVDLTRVTLRLL LPLAAALALLLAWQGVPQTSSAAARWPTLSATAASPGAEQVVALGPVASQVAVKQLGTNG GGYFNANSAHPYENPTPLSNLLEALSILLVPAALCFAFGALVKDRRQGWTVYSAMLAILVPL TVATVSAEQRGNPALAALGVDASPSALQPGGNMEGKEARLGPVDSAIWAAATTAASNGSV NAAHDSFTALGGLWPLWLMQLGEVVFGGVGSGLYGMLLFAILAVFLAGLMVGRTPEYLGK KVEAYEVKMASLAILAPSATVLLGTAAACLLPAGYGAVGNPGPHGFTELLYALSSTANNNGS AFGGLAASTPFWTLLTGVAMLVGRYWVMLPVLAIAGAFARKRPVPAGPGTLPTHGPLFAGL LVATVLLVGALTFLPALALGPVIEHLQAVPR

6E-225	757.1	38.2	7E-225	756.8	26.5	1	1	C2WYJ7_BACCE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA bcere0024_6380	Bacillus cereus Rock4-18	555	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock4-18	526988	>tr|C2WYJ7|C2WYJ7_BACCE Potassium-transporting ATPase potassium-binding subunit OS=Bacillus cereus Rock4-18 GN=kdpA PE=3 SV=1 MIWVAVIITMLLFILVAKPTGIYLEKAFQGSKMLDKVFGPFEKLIFKITGVKGYNQTWKQYALS LVLLNGFMIVVVYFIFRLQGVLPLNPAHIEGMEPTLAFNTAISFMADTNLQHYSGENGLSYLS QLIGITFLMFAAPATTLAIVMAFIRGLAGKELGNFFVDFTRALTRVFLPIAFIAALVFVALGVPQ TLDGAVTAQTIDGAKQSILRGPVASFVSIKELGNNGGGFFGANSTHPFENPGQMSNILQMM LMMLLPTALPFTYGRMVGNKKQGRILFVSLFMVFLLGFITITTSELNGNPALNGMGIEHVQG STEGKEVRFGTVFSSLYATVTTAAETGAVNTMHDTLTPIGGLVPLVNMMLNTVYGGVGAGF INIIMYAIIAVFISGLMVGRTPEFLGKKIEGKEMKLIAVTILFHPLLILGFSALALSTSLGTDAISHS GFHGLTQVVYEYTSSAANNGSGFEGLADNTPFWNITTGLVMFLGRYFSLITMLAVAASLKE KTVVPETVGTFRTDNGLFGGIFIGTIVIVGALTFFPMLVLGPIAEFLTLK
7E-225	756.9	26.6	8E-225	756.6	18.5	1	1	F4F4Y7_VERMA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VAB18032_21880	Verrucosispora maris (strain AB-18-032)	551	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Verrucosispora, Verrucosispora maris, Verrucosispora maris (strain AB-18-032)	263358	>tr|F4F4Y7|F4F4Y7_VERMA Potassium-transporting ATPase potassium-binding subunit OS=Verrucosispora maris (strain AB-18-032) GN=kdpA PE=3 SV=1 MTGTSTGVLFVLSLVVALAVVHRPLGDYLYRVVCAERHSRVERGIYRLIGVNPAAEQSWGV YARAVLAFSAVSVLFLYAFLRLQNHLWLSLGFDPVVAHGAWNTAVSFVTNTNWQWYSGES TMGHLVQMAGLAVQNFVSAAVGIAVAVALVRGFARSRAGQLGNFWVDLTRITLRVLLPLSV LAALVLMIGGAVQNLSAGTEITTLTGGGQRITGGPVASQEAIKNLGTNGGGFYNVNSAHPFE NPTAWTNWWEIFLLLVIPFSLPRVFGRMVGQVRQGYAIVAVMATLALASVALTTAFEVSGH GTVPQAIGAALEGKEVRFDVSNSATFAAATTLTSTGSVNSFHDSYTALGGGVLLVNMMLGE VAPGGVGAGLYGLLILAVITVFVAGLMVGRTPEYVGKKIGPREIKLASLYFLIPPALVLIGTAAA FATGNHLTALNAGPHGLSEVLYAFTSASNNNGSAFAGLTVNTPWWNTALGLCMLVGRFAPI ILVLALAGALARQQPTPASPGTLPTHRPLFVGMVVGVTVVLVALTFLPALALGPLAEGL
7E-225	756.8	27.9	8E-225	756.6	19.3	1	1	A0A0C1FL99_9FLAO	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OA93_21620	Flavobacterium sp. KMS	573	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium sp. KMS	1566023	>tr|A0A0C1FL99|A0A0C1FL99_9FLAO Potassium-transporting ATPase potassium-binding subunit OS=Flavobacterium sp. KMS GN=kdpA PE=3 SV=1 MNTELFGVISIFIITIVLAIPLGKYIAKVYLGDKTLLDPIFNPIEKLIFKISGINSTEEMNWKQHLKA LLSINMVWFLCFFILLFQGSLFLNPDNNPSMSPDLAFNTAISFIVNCNLQHYSGESGVSYLS QIFLMFLQFVSAGVGMAAAAMVFTAMKERSTDKLGNFYNYFIKSCTRVLLPLAAIVATALVFS GSPMTFEGKDAITTLQGDNVEVSRGPAAAFIAIKHIGTNGGGFFGANSAHPLENPTYFTNAV ELWAQLIIPFGMIFALGFYLKKRKLSYVIFGVMTVGFLLLVIPTVISEINGNPAIERMGITQATG AMEGKEVRLGPAISGFWSIATTVISTGSVNSMHDSSMPVSGAMELLAMMVNAFYGGCGVG ILNFYVFIILAVFISGLMVGRTPEFLGKKIEAREVKIAAFVAILHPLLILSGTALASYFAAHDTAM GWWFNGNATGWLNNPGNHGFSEMLYEYTSSAANNGSGFEGLGDNNPFWNITTGIVLLLS RFIPIIGPLAIAGLLANKKYIPESAGTLKTDTSIFGVMVFAVIAIIAALSFFPALALGPLAEYFTLK
9E-225	756.5	31.1	1E-224	756.2	21.5	1	1	D9T8N5_MICAI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Micau_0595	Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	551	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Micromonospora, Micromonospora aurantiaca, Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	644283	>tr|D9T8N5|D9T8N5_MICAI Potassium-transporting ATPase potassium-binding subunit OS=Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442) GN=kdpA PE=3 SV=1 MSMTTAGVLFVLSLVAALVAVHRLFGDYMHRVVAGTRSSRVERGIYRLVGVNPVAEQTWG VYARSVLAFSAVSLLFLYAFQRLQNHLWLSLGLDPVVPHGAWNTAVSFVTNTNWQWYSGE STMGHLVQMAGLAVQNFVSAAVGIAVAVALVRGFARSRTGELGNFWVDLTRVTLRILLPIAV LGALALMLGGVVQNLSGGTEVTTLTGGTQTVTGGPVASQEVIKELGTNGGGFYNVNSAHP FENPTAWTNWLEIFLILVIPFSLPRVFGRMVGQKRQGYAIVAVMAILALAGITLTNVFELTGD GTVPQAVGAALEGKEVRFDVSNSATFAAATTLTSTGAVNSFHDSYTALGGMMTLGNMMLG EVAPGGVGAGLYGLLILAVITVFVAGLMVGRTPEYLGKKIGSREIKFASMYFLITPALVLTGTA AAFATGNASTALNVGPHGLSEVLYAFTSASNNNGSAFAGITVNTQWWNTALGLCMLLGRFL PIIFVLALAGSLARQQPTPASEGTLPTHRPLFVGMVVGVTVVLVALTFLPALALGPLAEGL
9E-225	756.4	24.7	1E-224	756.2	17.1	1	1	R6L4A4_9BACE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN507_02376	Bacteroides clarus CAG:160	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides clarus CAG:160	1263039	[illegible] OS=Bacteroides clarus CAG:160 GN=kdpA PE=3 SV=1 MNTEILGVVLQIFLLVVISYPLGKYIAKVYKGEKTWSDFMKPVERLIFKAVGVNPDEEMNWK QFLKALLILNAFWFVWGMVLLVSQGWLPLNPDGNGPQTPDQAFNTCISFMVNCNLQHYSG ESGLTYFTQLFVIMLFQFITAATGMAAMAGIMKSISRKTTSTIGNFWNFLVLSCTRILLPLSLIV GFILITQGTPMGFDGKMEVTTLEGQEQTVSQGPVAAIVPIKQLGTNGGGYFGVNSSHPLEN PTYLSNIAECWSILIIPMAMVFALGFYTKRMKLAYSIYGVMLCAYLAGVGINVYQEMNGNPRI DDMGIAQDNGAMEGKEIRLGAGATALWSITTTVTSNGSVNGMHDSTMPLSGMMEMLNMQI NTWFGGVGVGWMNYYTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVALLHPFVILVGT ALSCYLFAHHPGFVESEGGWLNNPGFHGLSEQFYEFTSCAANNGSGFEGLGDNTYFWNY ACGWVLILSRFLPIVGQVAIAGLLAQKRFVPESAGTLKTDTFTFAVMTFAVIFIVAALSFFPAH ALSTIAEHFSL

1E-224	756.3	24.5	1E-224	756.1	17	1	1	K9Q855_9NOSO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Nos7107_1177	Nostoc sp. PCC 7107	581	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	317936	>tr|K9Q855|K9Q855_9NOSO Potassium-transporting ATPase potassium-binding subunit OS=Nostoc sp. PCC 7107 GN=kdpA PE=3 SV=1 MLQGWIQIGLTLLILVAITPFFGRYMARVYQEQRTFFDPILNPIERILYSLVGVQTKAEMTGW QYARAILYSNLVMGLLIFLIIMNQGWLPFNPTKIPAPTWDTALHTTISFITNTNQQHYSGETYL SYASQMWGLGYHMFTSAATGLAVGIAFIRGLTGRPLGNFYVDLIRSITRVLLPICIVGGIALMA AGVPETLAGPVVFPTLEDSNISQAIARGPVAHFEIIKQLGENGGGFFAINSAHPFENPNGFSN LIQIVAMLSIPTSLIYTYGLFANNTKQAWLVYGMVGVIYITFIIITAIGEYNGNPAVNALLGSTQP NLEGKEVRFGWAQSALFAVSTTGTMCGAVNSLHDSFMPNGGFVTLSNMFLQIIWGGQGT GTAYLFAYLILAVFVTGLMVGRTPEFLGRKIEKREVVLASFLILLVHPISIMIPAGIALAFPDQLA GISNPGFHGFAQVLYEYASAAANNGSGFEGLGDSQPSPIAIAAGAKTTATALWWNLSTCFS LLAGRYIPIIGLLLLADSMSRKPQVPFTVGTLRTDTGLFTGVTAGVILILGALTFFPVLAFGPIG EAFWIAKGIG
1E-224	756.3	29.1	1E-224	756	20.2	1	1	E3JBQ1_FRASU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA FraEul1c_3046	Frankia sp. (strain Eul1c)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain Eul1c)	298654	>tr|E3JBQ1|E3JBQ1_FRASU Potassium-transporting ATPase potassium-binding subunit OS=Frankia sp. (strain Eul1c) GN=kdpA PE=3 SV=1 MGANGAGILFIAILVVALVLTYRPFGDYMARVFTSDKHLRVERGIYRLVGVDPDSEQRWPVY ARSVLAFSAVSVLFLYLFQRLQNHLWLALGFPAVKPALAWNTSVSFVTNTNWQAYSGEST MGHTVQMAGLAVQNFASAAVGIAVAIALVRGLARKKSDTLGNFWVDLVRTVVRILLPISIVAA VVLIAGGAIQNLHGTRTVGTLAGGQQSITGGPVASQEVIKELGTNGGGFYNVNSAHPFENP TAWTNWFEIYLILMIGISLPRTFGKLVGSTRQGLAIVAVMAVLALGSVTLNLAFQGVHHGTVP MAVGAASEGTETRFGVPDSATFATATTLTSTGAVDSFHDSYTSLGGATLLFNMMLGEVAP GGTGSGLYGMLVLAVITVFVAGLMIGRTPEYLGKKIGSREIKLASLYILTTPLVVLTGTAVAMA LPGERAGMLNTGAHGLSEVLYAFTSAGNNNGSAFAGITVNTDWYNTALGLAMAFGRFLPMI FVLALAGSFAAQQQVPATAGTLPTHRPQFVGMLVAVTVIVVALTYFPALALGPLAEGLH
1E-224	756.2	27.4	1E-224	756	19	1	1	F7UZ80_EEGSY	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA EGYY_06120	Eggerthella sp. (strain YY7918)	593	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, Eggerthella sp. (strain YY7918)	502558	>tr|F7UZ80|F7UZ80_EEGSY Potassium-transporting ATPase potassium-binding subunit OS=Eggerthella sp. (strain YY7918) GN=kdpA PE=3 SV=1 MMGEVLEYGIYLALLVALAIPLSGYINRVMAGERVAVLSRVLVPVENFIYRSIRVDKYENMGW KTYLVSALAFSAVSLAGLFAILMLQGVLPGNPEGLPGLSWDLALNTAISFVTNTNWQAYSGE AALSYFSQALGLTVQNFVTPAVGMAVLFALFRGIVAENTPGLGNFWKDATRAVLFVLLPLSL VVAIVDVAQGSPQNLAPYETVQLLEPVGVTADGAIVDAEDPAAVQTITQEIIPLGPQASQVAI KQLGTNGGGYNGVNSASPLENPTPLTNLIQCLSLLLIPVALVFSFGRFVNDRRHGRTLFAAL FVLLLVGLVAIAYFEQTGTPQLAQDGAVYLGLTGQSGGNMEGKETRFGVTDSALWAAFTTA ASNGSVNAMHDSLTPLGGMVPMILMALGEVVFGGVGCGLYSLIGFVLLTVFIAGLMVGRTP EYLGKKIGPREMRMAVILCITTPLVILVGTAVLCLDPATANALTNTGAHGFSEVLYAAISAGGN NGSAFAGLDANTPLINVVLGLEMLVNRFMPMAAALVLAGSLAKRTKVATSAGTLSTSNAMF AFLLLVIVLLVGALTMFPALALGPVAEHLQMVLG
1E-224	756	24.5	1E-224	755.8	17	1	1	A0A0F0LHT5_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RS83_00572	Microbacterium oxydans	559	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium oxydans	82380	>tr|A0A0F0LHT5|A0A0F0LHT5_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Microbacterium oxydans GN=kdpA PE=3 SV=1 MTPEIWFGILQLTAVVVVLVLLYRPLGDYIAHVYTSGRDLRLERGIYRLIGVDPRSEQTWRAY ARSVLVFSVTGLILVYALQRLQAFLPESLGLPAVPEGLAFNTAASFVANTNWQSYSPEQTM GYVVQLAGLTVQNFVSAAVGLTIAIALIRGLARRGSTTIGNFWVDLFRGLGRLLLPIALISAVA LLAGGVIQNFAGFTDVTTISGGTQTIPGGPVASQEAIKLLGTNGGGFFNANSAHPFENPTG WTNLLQVLLILVIPFALPRTFGRMIGDHRQGYAIAAVMGTIFLISTFALSALELAGRGTAPQLA GAAMEGKEQRFGILGSTLFGSASTLTSTGAVNSMHDSYTALGGMMPMLNMMLGEVAPGG VGSGLYGMLVLAIIAVFVGGLLVGRTPEYLGKRIGPREIKLASLYILVVPALVLGGTALSFAIPG IRADVEATSILNPGVHGMSEVLYAFTSAANNNGSAFAGLTANTPWFNTALGIAMLLGRFIPIV LVLALAGSFAAQERIPATSGTLPTHRPQFVGLLLAVTVIVTALTYFPVLTLGPLAEGLV
1E-224	756	29.3	1E-224	755.8	20.3	1	1	K0F4T1_9NOCA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA O3I_031405	Nocardia brasiliensis ATCC 700358	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia brasiliensis, Nocardia brasiliensis ATCC 700358	1133849	>tr|K0F4T1|K0F4T1_9NOCA Potassium-transporting ATPase potassium-binding subunit OS=Nocardia brasiliensis ATCC 700358 GN=kdpA PE=3 SV=1 MNTTTAGIAFVASLIIALALVHVPLGDYMFRVYNGRKHSRAERVIYKAIGVQPEVEQTWGVY ARSVLAFSAVGILFLFFFQLVQGKLPLHLNDPATEMTPALAWNTAVSFVTNTNWQNYSGES TQGHLVQMAGLAVQNFVSAAVGMAVAVALVRGFARRHTGDLGNFWVDLVRGTLRILLPIAF VFAIVLVAGGAIQNFHLHDQVAQNLNGTAQTIPGGPVASQEVIKELGTNGGGFYNANSSHP FENPTTWTNWVEIFLILMISFSLPRTFGRMVGSKKQGYAIVAVMGTIALVSTVLQNVFQLAH HGTVPTAIGASLEGVETRFGVADSATFASATTLTSTGAVDSFHDSYTSLGGMMTMFNMQL GEVAPGGTGSGLYGMLILAVITVFVAGLMVGRTPEYLGKKITPREIKLAASYFLVSPLIVLVGT ALAMAMPGQRASMLNTGPHGLSEVLYAFTSAANNNGSAFAGLSGNTEWYNTALGLAMVF GRFLPIIFVLALAGSLAQQGSTPESIGTLPTHRPQFVGMVVGVTVILVALTFLPALALGPLAEG IH

1E-224	755.9	24.8	2E-224	755.6	17.2	1	1	D3PV93_STANL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Snas_1440	Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Glycomycetales, Glycomycetaceae, Stackebrandtia, Stackebrandtia nassauensis, Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	446470	>tr|D3PV93|D3PV93_STANL Potassium-transporting ATPase potassium-binding subunit OS=Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21) GN=kdpA PE=3 SV=1 MSDSTAGILFVVAMVVALAIVHRPLGDYVYRVVTRKRDRKVERGVYRLVGVKSDVEQTWG GYARSVLAFSAVGVFFLYGFQRLQPLLPWSNDMAAVEPATAFNTAVSFVTNTNWQSYSGE STMGHLVQMAGLAVQNFVSAAVGIAVAIVLVRGFARKLTDKLGNFWVDLTRITIWVLLPISIIA AIVLIAGGAVQNLHASIEAHGLNGTVQLLTGGPVASQEAIKELGTNGGGFYNVNSAHPFENP TSWTNFIEIFLILCIPFSLPRTFGRLVGDKRQGYAITAIMGIMALASTFLVFGFEAVGNGTVTS AIGAAMEGREVRFGTGNSSVFAAATTLTSTGAVDSFHDSYSGLGGGVLTLNMLLGEVAPG GVGAGLYGMLVLAVITVFVAGLMVGRTPEYLGKKIGAREIKLASLYFLVTPALVLIGLAASIAV PSNLESMQDAGPHGMSEMLYAFASASNNNGSAFAGFGAATDWFNTALGLCMLFGRFLPIIL VLALAGSLAKQKPVPESAGTLPTHKPLFVGMVIGVTVILVALTFLPVLALGPLAEGLM
1E-224	755.8	30	2E-224	755.5	20.8	1	1	F8L2P0_PARAV	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PUV_26220	Parachlamydia acanthamoebae (strain UV7)	563	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Parachlamydiaceae, Parachlamydia, Parachlamydia acanthamoebae, Parachlamydia acanthamoebae (strain UV7)	765952	>tr|F8L2P0|F8L2P0_PARAV Potassium-transporting ATPase A chain OS=Parachlamydia acanthamoebae (strain UV7) GN=kdpA PE=3 SV=1 MSIPNGIQILVFLALLLIVTPLLGQYIAAIFSEKDPLMKRVLGRLEDGCYQMGGVDPHLEMTW QEYAKVLGIFNLLGFIFLFFLLLLQGILPLNPQHFPGVSWHLAYNTAISFVTNTNWQSYAGET TLSYLTQMVGLTVQNFLSAATGMATLLVLVRGMTRKMVNTVGNFWCDLVRTIVYLLLPLSII MAICLVAEGVVQTFSPYVEAIGLEGHEQTIPLGPVASQVAIKQLGTNGGGFFNTNSAHPFEN PSAFSNFWEAFAILVIPAATVYAYGIMIGSKKHAWILYVVMLLLWMGGLGLSLYSENLANPIL DAFPHLEGKETRFGVANSLLWTVSTTGTSNGSVNAMISSLSPMAGGIAMFNIMLGELIFGGV GVGLCAMLMYTILTVFLSGLMVGRTPEYLGKKIEKQEVKWVMLSVLMPSALILLGSGVSSILP KALSSLSNQGPHGLSEILYAFSSAAGNNGSAFAGLNANTPYYNLVLGTIMLICRISTILPSLAI GGLLAEKKFIPPSIGTFSAESLLFAILLGGIILIVGGLVFFPAFALGPIVEHFLMLKKVSF
2E-224	755.7	37	2E-224	755.5	25.7	1	1	S5Z0Q6_PARAH	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA JCM7686_pAMI4p340	Paracoccus aminophilus JCM 7686	561	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus aminophilus, Paracoccus aminophilus JCM 7686	1367847	>tr|S5Z0Q6|S5Z0Q6_PARAH Potassium-transporting ATPase potassium-binding subunit OS=Paracoccus aminophilus JCM 7686 GN=kdpA PE=3 SV=1 MTGDLIFFALFLAGLTVVGLGLGAYMERVFTGRFMLFNPVERRLLQLAGVSGRGQRWTSFA MSLLAFNAAGFALLYLVLRLQGWLPFNPQGVGAMEASQAFNTAVSFMTNTNWQSYSGET ALSNFSQMFGLTVQNFVSAASGIAVAVAVVRGLVGRSVQDLGNFWVDLTRATLYLLLPGAV LITLVLIWQGQPQNLLGHVTATTLEGARQIISQGPVASQDAIKMLGTNGGGFFGVNAAHPYE NATALTNLVQIYAILCIPAAFPFFFGRMAGDRRQGIAIYLAMSLLFVAVLLAAYFFEAHGNPLY AGITEPGVSMEGKETRFGLAQTVLFTVATTVASCGAVNAMHDSLMALGGMIPLFNMLLGEII YGGVGAGFYGMVLYIVLTVFIAGLMVGRTPEWLGKKIEAREMKLAALSLLVMPTGVLILSALS ILTGNAQTAVQDAGPHALTELVYAYTSGTANNGSAFAGFGANTVWHNTMIGLAMLIGRWG YIVPVLAIAGGMAAKTRAPETAGTFPTHGRVFILLLIATILIVGALTFLPVLALGPIAEQVAISAG QTF
2E-224	755.7	22.3	2E-224	755.4	15.5	1	1	D7C421_STRBB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SBI_09269	Streptomyces bingchenggensis (strain BCW-1)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7C421|D7C421_STRBB Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces bingchenggensis (strain BCW-1) GN=kdpA PE=3 SV=1 MTGALAGWLQILALVAALALSYRPLGDHLAHTLTTARHLRAERLVYRLGGVDGDADQGWP AYLRGVLAFSAVSVLFLYGFLRLQNHLLLSLGRQPMPADQAFNTAASFATNTNWQSYSGES TLGHLVQMAGLAVQNFVSAAVGIAVVAALIRGFTRERTDQVGNFWVDLTRIVVRVLLPIAFV FAIVLVAGGVIQNFHGVESIRTVVGGHQNLIGGPVASQEAIKELGTNGGGFYNANSAHPFEN PNPFTNWLEIYLLLVISFSLPRTFGRMVGDHRQGYAIVTVMAVIWAASVAVVTVNELHSVSS RAGHAAGGMLEGKEQRFGIWASALFAAPTTLTSTGAVNSAHDSYTPFGGGMTIFNMMLGE IAPGGTGSGLYGILILAIIAVFVAGLMVGRTPEYLGKKLGAREMKFASLYILTTPAIVLVGAGLA MALPGQRAAMLNHGPHGFSEVLYAFTSAANNNGSAFAGLGANTAWYNTALGLVMLLGRYL PMVFVLALAGSLARQQPVPVTAGTLPTHRPQFVGLLTGVVLIVVGLTYFPALSLGPLAEGLQ
2E-224	755.7	27	2E-224	755.5	18.7	1	1	C8WN70_EGGLE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Elen_2846	Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (Eubacterium lentum)	591	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, Eggerthella lenta, Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (Eubacterium lentum)	479437	>tr|C8WN70|C8WN70_EGGLE Potassium-transporting ATPase potassium-binding subunit OS=Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) GN=kdpA PE=3 SV=1 MIDELFEYGVYLALLVALAIPLSAYLNKVMAGQKTVLSRVLVPVENAVYRCIRVDKSEDMGW KRYLVSAFAFSAICLVGLFAILMLQGLLPLNPEGIPGMSWDLAFNTAVSFVTNTNWQAYSGE SALSYFSQAIGLTVQNFVTPAVGLGVLFALFRGIVSEGNPGLGNFWVDVTRAVLFVLIPLSLV VTMIDVQQGSPQNFNEYETVQLLEPVGVTADGSIVDADDPAAVETIDQATVPMGPQASQVA IKQLGTNGGGYNGVNSASALENPTPLTNLVQCLSLLLIPVACVFSFGRFVMDRRQGRAVFA AMFILLVGALVAIAVFEQMGTPQLAADGQVYMGASGQSGGNMEGKETRFGVTDSSLWAAF TTAASNGSVNAMHDSFTPIGGMVPIVLMALGEVVFGGVGCGLYGMLGFVILTVFIAGLMVG RTPEYLGKKIGPKEMRMAVILCITTPLLILVGAGIMSLDPATANSLNNPGVHGFSEVLYAATSA GGNNGSAFAGFNGNTPLINLVLGFEMLANRFIPIAAVCVLAGSLAVRPKVATSAGTLSTSNAL FVFLLVLMVLLIGALTMFPALALGPVAEQLMMVL

2E-224	755.6	32.6	2E-224	755.4	22.6	1	1	KDPA_BACV8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BVU_3267	Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides vulgatus, Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	435590	[illegible] OS=Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154) GN=kdpA PE=3 SV=1 MNTEVLGVIAQIVLMVVLSYPLGKYIAKVYKGEKTWSDFMKPVERVMFKLSGINPNEEMNW KQFLRALLVVNLFWFLWGMVLLVTQGVLPLNPDGNVGQTAHQAFNTCISFMVNCNLQHYS GESGLTYFTQLFVIMLFQFITAATGMAAMAGIMKALAAKTTQTIGNFWNYLVLSCTRVLLPLS LVVGFILIVQGTPMGFDGKMKVTTMEGATQYVSQGPTAAIVPIKQLGTNGGGYFGVNSSHP LENPTYFANMVECWSILIIPMAMAFAFGFYLKRKKLGYSIYGVMLFAYLVGVCINVSQEMGG NPRIDEMGIAQDNGAMEGKEIRLGSAATALWSITTTVTSNGSVNGMHDSTMPLSGMMEML NMQINTWFGGVGVGWMNYFTFIIIAVFISGLMVGRTPEFLGHKVEAREMKIASIVALLHPFIIL VGTALAAYLFVHAPAFVESEGGWLNNPGYHGLSEMLYEYTSCAANNGSGFEGLGDNTWF WNYSCGIVLILGRFVPIVGQVAIAGILAKKKFIPESAGTLQTDTVTFGVMTFAVIFIVAALSFFP VHALSTIAEHLSL
2E-224	755.5	26.5	2E-224	755.2	18.4	1	1	H1YB12_9SPHI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mucpa_5986	Mucilaginibacter paludis DSM 18603	571	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Mucilaginibacter, Mucilaginibacter paludis, Mucilaginibacter paludis DSM 18603	714943	[illegible] OS=Mucilaginibacter paludis DSM 18603 GN=kdpA PE=3 SV=1 MNTELSGVILTYLLTLIIAVPLGLYMAKVFKGEKTWLDFMAPVERLIFRLSGIDAQREMNWKQ HLYAMLTVNAVWLFYAFFCLLYQSHLPLNPDANPSQTPDLAFNTAISFLVNCNLQDYSGESG ATYFTQHFVFMFLHFASAATGIAALVALFRGLKDKVTDKLGNFWDNFVKTITRILLPFSILIAIIL AFNGMPTSYQGKDTLIGMQGDTIHVSRGPVAAMVAIKHLGTNGGGWFGANSAHPLENPNY LTNTVELVAQLIIPIGLVFALGFYLNKKKFAYVMFGVMTIGMLCLMIPTLNAEVNGNPAIAHMG ISQPTGAMEGKEVRFGPLNSAYWSVMTTITSTGSVNSMHDSAMPVSGFSMMMGMMVNCF YGGVGVGFLNFYIFIIIAIFISGLMVGRTPEFFGRKIEAREMKIASLIALLHPFIILVGTAISSYVLV HFPNADWAVKPSAWLNNPGSHGFSEMLYQYSSCAANNGSGFEGLGDNNIFWNVSAGFV MILGRFLPIIGPVAIAGILANKKFVPESAGTLKSDTSTFGVMVFAVIVIIAALSFFPALALGPIAE HFSLK
2E-224	755.5	28.4	2E-224	755.2	19.7	1	1	U5WQV5_MYCKA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MKAN_08390	Mycobacterium kansasii ATCC 12478	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium kansasii, Mycobacterium kansasii ATCC 12478	557599	[illegible] OS=Mycobacterium kansasii ATCC 12478 GN=kdpA PE=3 SV=1 MSDTTAAVLFLGLLVAALAAVHVPLGDYMFRVYSSETHWRTERFIYRLIGADPDAEQTWAA YARSVLAFSAVSVIFLFALQLVQDKLPLHLAHPATPMTPALAWNTAVSFVTNTNWQAYSGE STQGHLVQMAGLAVQNFVSAAVGMAVAVALVRGFARNRTGELGNFWVDLVRGTLRILLPIA VLGAVVLVMGGVVQNFHLNDQVVTTLAGTPQTIPGGPVASQEVIKELGTNGGGFYNANSA HPFENPTAWTNWVEIFLLLVISSALPRTFGRLVGSKRQGYAIAAIVAVIAVFSVTTMMSFQLQ HHGTVPTAVGASTEGVEQRFGVADSAVFADATTLTSTGAVDSTHDSYTSLGGMMTLFNMQ LGEVAPGGTGSGLYGILILAVITVFVAGLMVGRTPEYLGKKITPREMKLAAGYFLVTPLIVLVG TAVAMALPGARAAMANTGPHGLSEVLYAFTSAANNNGSAFAGLAVNTVWYNTALGLAMLF GRFLPMILVLALAGSLARQGATPESAGTLPTHRPQFVGLVVGVTVILVALTFLPALALGPLAE GIH
2E-224	755.4	24.6	2E-224	755.2	17.1	1	1	R6Y855_9PORP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN675_02907	Parabacteroides merdae CAG:48	569	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides merdae CAG:48	1263094	[illegible] OS=Parabacteroides merdae CAG:48 GN=kdpA PE=3 SV=1 MNTEILGVALQILLLIVISYPLGKHIAKVYKEGNDCMRFMAPIERFIYKLAGINPNEEMDWKVF LKSLLIINVFWFFWGMILLVSQGYLPLNPDGNSGQSPDLAFNTCISFMVNCNLQHYSGESGL TYFTQLFVIMLFQFITAATGMAAMAGIMKSMAAKTTKTIGNFWHYLVISCTRILFPMSLIVGFIL ILEGTPMGFESKMTIPTLEGSEQIVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLENPTYLTN IIECWSILIIPMALVFALGFYLKRKKLGYVIYGVMLFAYLLGVFCNVHYEMAGNPKIDEMGIDQ SCGAMEGKETRLGPGATALWSVTTTVTSNGSVNGMHDSTMPLSGMVEMLNMQINTWFG GVGVGFMNYYAFLIIAVFISGLMVGRTPEFLGKKVEAREMKIATIVSLAHPFVILIFTAISSYVW VYCPGFVESEGGWLNNPGFHGFSEMLYEYTSSSANNGSGFEGLGDNTYFWNYTCGLALII SRYLPIVGQVAIAGLLANKKYTPESAGTLKTDTVTFGVMTFCVIVIVAALSFFPAQTLGPIAEY FSIY
2E-224	755.2	24.9	3E-224	755	17.3	1	1	K9QT59_NOSS7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Nos7524_2432	Nostoc sp. (strain ATCC 29411 / PCC 7524)	560	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain ATCC 29411 / PCC 7524)	28072	>tr|K9QT59|K9QT59_NOSS7 Potassium-transporting ATPase potassium-binding subunit OS=Nostoc sp. (strain ATCC 29411 / PCC 7524) GN=kdpA PE=3 SV=1 MGQGLLQIALTLCIVILITPVLGRYIARVFLGERTLLDRFMNPIERSFYVLAGIRPKDEMTGWQ YIRAILYTNLCMGILVYSLLYFQKLLPWNPNGFGAPRWDTILHTVISFVTNTDQQHYIPETTLS YFSQVAALGFLMFTSAATGIAVGIAFIRGLTGKKLGNFYIDFIRAITRILLPISVVGAIALVFLGV PQTIKPPLDVTTLEGGTQYIARGPVASFEMIKMLGDNGGGFFATNSAHPLENPNGATNFIELI AMIAIPAAMIYTYGVFANNMKQAWLMFWMVFVFVFLLVWVAAGGELEGNPLVFNALGLEQ PNLEGKEVRFGWAETALWAVMTTATMCGAVNGMHDSLMPPGLFSTLFNLFLQIIWGGQGT GTAYLFVYLIITVFLTGLMVGRTPEFFGRKIEKREIILASVVLIIHPVLVLIPSAIALAYPFSLSGIT NTGFHGISQVVYEYASASANNGSGLEGLADDSLWWNLSASFSILAGRYIPMVAILLLADSMS RKQTVPQTSGTLKTDSLIFTTVTAGIVLILGVLTFFPVLALGPIAEGLKIGGS

3E-224	755	31	3E-224	754.7	21.5	1	1	F8I8V0_SULAT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TPY_3245	Sulfobacillus acidophilus (strain TPY)	568	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiales incertae sedis, Clostridiales Family XVII. Incertae Sedis, Sulfobacillus, Sulfobacillus acidophilus, Sulfobacillus acidophilus (strain TPY)	1051632	[illegible] OS=Sulfobacillus acidophilus (strain TPY) GN=kdpA PE=3 SV=1 MSVNGWMGIAVLLVLMMGIGLGVGTYLERVLPVQGEVRPRSLFGRLETAIYRAAAINPRVE MDWKTYMKSVLAANLMMALVGYLLLRLQGRLPLNPAKVSAPSWDLAWNTVVSFVTNTNW QNYAGESALSYWSQMTVITYLQFASAATGIAVALAVVRGLVRQKARTLGNFWVDWVSVQT RVLLPFALILGFVFIALGVPQTLGGPVHVVGLSGVGQTIARGPVASLEAIKQLGTNGGGFFNA NSAHPFEDPTPLTAVLEILAMTAIPLGLVFYFGRQIKNHRQAWVIVTYLMALLILGIFLIYQSQS HGNPWLSQQLGIHGPNYEGQEWRFGPALSSVFTAVTTAFGTGAVNGMHDSLMPLAGMVA LVFMMLNVVFGGSGVGLINILMFLLITVFLSGLMVGRTPEMFGKKIEAREIKLATVAMLVHPFL ILVPTAVALLTPAGLKSLGNPGLHGFTEILYAFTSTAANNGSAFAGLNGNTLFYNLLLGWVML LGRYVSLIAMLAIAGSLAEKATIPETLGTLKTDSYAFGGVFVGVVLIVGALTFFPALAVGPIGE HLQLWAQSGH
4E-224	754.5	27.7	4E-224	754.3	19.2	1	1	R5YYG3_9BACE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN496_01541	Bacteroides sp. CAG:144	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:144	1262736	[illegible] OS=Bacteroides sp. CAG:144 GN=kdpA PE=3 SV=1 MNTEILGVVAQIVILLLLSYPLGKYIAKVYKGEKTVLDFMKPVERLMYRLSGINPEEEMDWKQ FLRALLMVNLFWFVWGMVLLVSQGYLPLNPDGNIGQTCHQAFNTCISFMVNCNLQHYSGE SGLTYFTQLFVIMLFQFITAATGMAAMAGIMKALAAKTTKTIGNFWKFLVLSCTRILVPLSLIV GIVLITEGTPMGFDGKMEITTLEGETQMVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLENP TYLTNIFECCSILIIPMAMAFAFGFYIRRKKLGYAIYGVMFAAFLIGVIINVSQEMGGNPRIDDM GIAQEHGSMEGKEIRLGAGGTALWSVVTTVTSNGSVNGMHDSTMPLSGMIEMLNMQINTW FGGVGVGWMNYFTFIIIAVFISGLMVGRTPEFLCHKVEAREMKVASIVALLHPFVILVGTALA CYLYAHAPAFVASEGGWLNNPGFHGLSEMLYEYTSCAANNGSGFEGLSDNTWFWNYSC GIVLILSRFIPIVGQVAIAGLLAQKRYIPEGAGTLKTDTVTFSIMTFAVIFIVAALSFFPAHALSTI AEHFSL
5E-224	754.1	30.7	5E-224	753.9	21.3	1	1	B1XRB5_SYNP2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SYNPCC7002_G0060	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	568	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	32049	>tr|B1XRB5|B1XRB5_SYNP2 Potassium-transporting ATPase potassium-binding subunit OS=Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) GN=kdpA PE=3 SV=1 MTQGFFQLAIALAILLSVAPFLGRYMARVFMGQKTLLDPIAIPLERLLFTIGGFANQSSMTGR KYVSAVLVSNLVMGILVFFIFLLQRALPLNPTNLTAPSWHLALHTAISFVTNTNQQHYSGETT YSYFSQVGALGFLMFTSAATGIAVAIAFIRGLTGNALGNFYVDLTLSITRILLPISIVGAIVLVIA GVPETFAGPAVAQTLEGATQYIARGPVAHFEIIKELGENGGGFFGINSAHPYENPNNFVNLF TNIIMLIIPAGLILTYGIMARKPRQGWLIFGMVFIFYVLMVGITAYGEYVGNPLVNNILGEQVPN LEGKEVRFGWALTALWAVSTTGTMCGAVNGMHDSLMPPGGFATLSDIFLQIIWGGQGTGT AYLFVFLILTVFLTGLMVGRTPEFLSRKIEKREIVLSSIILLAHPIAILIPGAVTLALPEALAGISNP GFHGVSQVIYEYASAAANNGSGFEGLGDNTLWWNLSTSFSLIVGRYVPIIALIYLADSMAQK QSVPETAGTLYTDSFLFTGVTAGTILILGALTFLPVLALGPIAEGFAIAKAAAEVTAGL
8E-224	753.3	30.6	1E-223	753	21.2	1	1	B8GER2_METPE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mpal_2488	Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	564	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanosphaerula, Methanosphaerula palustris, Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	521011	>tr|B8GER2|B8GER2_METPE Potassium-transporting ATPase potassium-binding subunit OS=Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c) GN=kdpA PE=3 SV=1 MTYPDPLLDAVGIIVFVLLLTAVAFPLGKYMSRLFFQDRPPAIIRTLEAPVYRLLGVDPTAEET WRGYARDLLIFNGIGVAFLFVLLLLQGFLPLNPAGVSGFSPDLALNTAISFVTNTNWQAYSG EVAASYLSQMVGFAVQNFLSAATGLAVTVVLIRGLTRRETDRVGCFWVDLTRGVLGVLLPL AIIGALVLASQGVIQNLDPYVQTSDGLQTIAMGPVASQEAIKEVGTNGGGFFNANSAHPFEN PNPFTNLAEIFLILLIPAALPFMFGEAVGDRRQGYILYAVMLALFLGAFAVLYTAELSGNPLISG TSGFPMEGKEVRFGLGGTALFSTATTATSTGAVNTMFDSLTPLGGLVPLALILLSEVIFGGV GSGFYTMIAFVVIAVFVAGLMIGRTPEYLGKKIGAFEMKMAVATVLTAGILTLILSGIALSLPAG TSSILNPGAHGLSEIVYAFASMANNNGSAFAGLNATTLFYTLTGSLAMALGRFVPIIAILALAG ALAAKKTVPPSFGTLPTHTVPFAIWLVLVVLIVGALTFFPIFAMGPIAEHLQMVGGMVL
1E-223	753	27.4	1E-223	752.8	19	1	1	KDPA_CLAMS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CMS0462	Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	558	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Clavibacter, Clavibacter michiganensis, Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	31964	>sp|B0RCI3|KDPA_CLAMS Potassium-transporting ATPase potassium-binding subunit OS=Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) GN=kdpA PE=3 SV=1 MDTLAGILQVASVVLVLVLVHRPLGDLMARMYESRHDTRVERGIYRLIGVDPRSEQTWPAY LRAVLAFSLVGVLVVYGMQRLQAFLPYALGLPAVPEGISFNTAVSFVTNTNWQSYSPEATM GYTVQLAGLAVQNFVSAAVGIAVAIALVRGFARTRSGTIGNMWVDLIRGSLRLLLPLSLVTAV VLIAGGVIQNFAGFQDVQTLAGGTQTIPGGPVASQEAIKMLGTNGGGFFNANSAHPFEDPT AWTSAFQVLLMLVIPFSLPRTFGKMVGDTRQGTAIAAVMATIAVASLTALTLFELQGAGSAP MAAGAAMEGKEQRVGIIGSALFGTVSTLTSTGAVNSMHDSYTALGGMMPMLNMMLGEVAP GGVGSGLYGMLVLAVIAVFVAGLLVGRTPEYLGKKIGPREIKLASLYILVTPILVLVGTALSFAI PAVRDDVEGTSILNSGLHGLSEVVYAFTSAANNNGSAFAGLTASTPWFTTALGVAMLLGRF VPIVLVLALAGSLAAQDRIPTTSGTLPTHRPQFVGLLIGVTVIVTALTYFPVLALGPLAEGLAS

															>tr|I4Z9Z1_9BACT|I4Z9Z1_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Prevotella bivia DSM 20514 GN=kdpA PE=3 SV=1 MNTELVGVAAQIVLMVGLSYPLGKYIARVYKGEKTWLDFLRPVERMIFRLSGINPGEEMNW KQFLRALLTVNLFWFVWGMVLLVLQGSLPLNPDGNLGQTAHQAFNTCISFMVNCNLQHYS GESGLTYFTQLFVIMLFQFITAACGMAAMAGIMKALAAKTTQTIGNFWNYLVLSVTRILLPLS LIVGFILIVEGVPMGFDGKMEVTTLEGTVQQISQGPAAAIIPIKQLGTNGGGYFGVNSSHPLE NPTYLTNMVECISILLIPMAMAFAFGFYLKRKRLGSVIYGVMLVGFLMGVGINVSQEMGGNS RIDAMGIAQNGGSMEGKEVRFGSAATGLWSVVTTVTSNGSVNGMHDSTMPLSGMMEMLN MQINTWFGGVGVGWMNYFTFIIMAVFISGLMVGRTPEFLGHKVEAREMKIASIVALLHPFIIL VGTALAAYLFVYAPDFVASEGGWLNNPGYHGLGEILYEYTSSAANNGSGFEGLGDNTWF WNFSCGLVLILGRFVPIIGQVAIAGLLAEKRYVPESAGTLRTDTATFGVMTFAVILIIAALSFFP AQALSTIAEHFSL	
1E-223	752.8	31.6	1E-223	752.6	21.9	1	1	I4Z9Z1_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PrebiDRAFT_1322	Prevotella bivia DSM 20514	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella bivia, Prevotella bivia DSM 20514	868129	
															>sp|A1TED2|KDPA_MYCVP Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1) GN=kdpA PE=3 SV=1 MSTGLAGILFLASLVIALVAVHVPLGDYMYRVYNTAKDSRAENVVYRLIGADPKAEQTWGAY ARSVLAFSAVSLLFLFILQLVQGRLPSALTDPGTPMTPALAWNTAVSFVTNTNWQAYSGES THGHLVQMAGLAVQNFVSAAVGMAVAIALVRGFARKRTGELGNFWVDLVRGTIRILLPISVI AAILLITGGAIQNFHNYDQVVNTLAGAQQTIPGGPVASQEAIKDLGTNGGGFYNVNSAHPFE NPTTWTNWIEIFLLLVIAFSLPRTFGRMVGNKKQGYAIVGVQAVLAVISWSATLFFQLQAHG TVPTAVGAAMEGVEQRFGVANSAVFAASTTLTSTGSVDSFHDSYTSLGGLVLLFNMQLGEV APGGVGAGLYGILILAVITVFVAGLMVGRTPEYLGKKITPREIKLAATYFLVTPLIVLTGTAVAM AMPGQRAGMLNTGPHGLSEVLYAFTSAANNNGSAFAGITVNTEWYNTALGLAMVFGRFLPI ILALALAGSLAQQGKTPPSIGTLPTHRPQFVGMVAGVTLILVALTFLPMLALGPLAEGIH	
1E-223	752.6	28.2	2E-223	752.3	19.6	1	1	KDPA_MYCVP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mvan_4759	Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium vanbaalenii, Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	350058	
															>tr|B5H3H5|B5H3H5_STRC2 Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602) GN=atkA PE=3 SV=1 MSPVLAGALQLLALMAALALVYRPLGDYMARVYSSDKHLRVEKWIYKGIGANPNTEMRWP AYLRGVLALSAIGVLFLYLLQRVQGSLPGSLGFQSIDPDQAFNTAASFVANTNWQSYYGEQ AMGHVVQTGGLAVQNFVSAAVGIAVAVALVRGFARSRTGELGNFWADLVRGVVRILLPISVI AALLLVACGAIQNFSGIHEVGQFQGGVQQWNGGAVASQEAIKELGTNGGGYFNANSAHPF ENPNGLSNLLEIFLILVIPFALTRTFGRMVGNVRQGYAILGTMALIWVGFSALMMWTEFAHP GAAFQEAGGAMEGKETRFGIGGSAIFAVATTLTSTGAVNSFHSSYTGFGGGITMLGMQLG EIAPGGVGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGTREIKLAACYILVTPALVLGFTAV ALALPTPANSMTNAGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNTTIGLAMLLGRFL PIVLVLALAGSLAEQKPVPATTGTLRTEKPLFTGLLVGTILIITGLTYFPALALGPLAEGLAS	
2E-223	752.2	26.9	2E-223	752	18.6	1	1	B5H3H5_STRC2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	atkA kdpA SCLAV_5144 SSCG_06161	Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces clavuligerus, Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	443255	
															>tr|A8KYG3_FRASN|A8KYG3_FRASN Potassium-transporting ATPase potassium-binding subunit OS=Frankia sp. (strain EAN1pec) GN=kdpA PE=3 SV=1 MSMTVAGILVALLLVGALATTYRPFGDYMFRVYTSEKHLPVERAIYRLTGVNPNAGQRWTV YARSVLAFSAVSVLFLYLLQRVQDHLPWDLGFSGVSPALAWNTAVSFTTNTDWQAYSGES TMSHFTQMAGLAVQNFASAAVGIAVAIAVVRGFARRRAPVAAGPGSMDGVVGTGDEIGNF WVDLTRTIVRILLPICVLGAIVLIAGGAIQNLHGNHVVTTVAGGRQAITGGPVASQEVIKELGT NGGGFYNVNSAHPFENPATWTNLFEIYLLLMIGFSLPRTFGRLVGDRRQGLAIVAVMALIAL GSLTVNMAFQVAHHGTVPEAVGAAAEGTDARFGVANSAIFATATTLTSTGAVNSFHDSYTS LGGASLLFNMMLGEVAPGGVGSGLYGMLVLAVVTVFVAGLMIGRTPEYVGKKIGAREMKFA SLYFLTTPIIVLLGTGVAMALPGQRAGMLNSGAHGLSEVLYSFTSAGNNNGSAFAGITVNTT WYNTALGLAMMFGRFLPIIFVLGLAGSLARQTPVPVTAGTLPTHRPQFVGMLAGVTLIIVALT FFPALALGPFAEGIH	
2E-223	751.7	28.5	3E-223	751.4	19.7	1	1	A8KYG3_FRASN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Franean1_0600	Frankia sp. (strain EAN1pec)	569	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain EAN1pec)	298653	
															>tr|K9VF82_9CYAN|K9VF82_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Oscillatoria nigro-viridis PCC 7112 GN=kdpA PE=3 SV=1 MLEGLIQIALTLIIVVAIAPIFGNYMARVYMGEPTILDPAIKPVEQLIYKASNIRSVDSMTGWQY TRSLLYSNAAMGIFVYLIFMLQGVLPLNATSLSAPTWDTALHTTISFLTNTDQQHYSGETTFT YLSQLTLGFLMFTSAATGLAVGIAFIRGLTGRPLGNFYIDLIQSITRILLPISLIIALLLLMSGVPE TLAGPAVARTLEGDTQIIARGPVAHFESIKQLGENGGGFFAINSAHPFENPNPFTNLLETLGM VSIPAAMIHTYGRFANNKKQGWLIFWMVFGIYVILIGIAAFGEYGGNPQINNLLGSQQPNLEG KEVRFGWAETALWAVTTTGTMCGAVNGMHDSLMPPGGFATLFNLFLQIVWGGQGTGTAY LFIYSILSVFLTGLMVGRTPEFLGRKIEKREIVLASVVLLIHPIAVLIPGAISLAFTDSLSGISNQG FHGISQVMYEYASAAANNGSGFEGLADSQPAPTGLWWNLSTCFSLLLGRYVPIIALLLLADS MTKKQLVPETTGTLRTDSVLFTSVTAGVIIILGALTFFPVLALGPIAEGYEISSGKFEPTPITAP PLATPSPLATPSPEATTPTPNSGQ	
3E-223	751.6	22.8	3E-223	751.4	15.8	1	1	K9VF82_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Osc7112_2126	Oscillatoria nigro-viridis PCC 7112	598	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria nigro-viridis, Oscillatoria nigro-viridis PCC 7112	179408	

3E-223	751.5	21.4	3E-223	751.2	14.8	1	1	D7B3X9_NOCDD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Ndas_1510	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	446468	>tr|D7B3X9|D7B3X9_NOCDD Potassium-transporting ATPase potassium-binding subunit OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=kdpA PE=3 SV=1 MTVLLAALPVAALALILALLYRPVGDYTARVFTSPKDLRIERGFYRLVGVDPRSEQSWPAYL RAVLAFSAVGLVLLYLLQRLQHVLPHALGLPPVPEGLAFNTAASFVTNTNWQSYSPELTLGY TVQFAGLAVQNFVSASTGIAVAVALVRGFARRRSGTIGNFWVDLTRGTLRLLLPVSLLAALV LVAGGVVQNLNGFTEATTLTGATQTVPGGPVASQEAIKILGTNGGGFFNANSAHPFENPAP WTSLFQVLLMVIIPFTLPRAFGRMVDSHRQGYAILAAMAVLFTASLTALTLLEAHGAGTAPEA AGGAWEGKEQRFGVYASTLFGSASTLTSTGAVNSMFDSYTALGGMMPMVNMMLGEVAP GGVGSGLYGMLVLAVLAVFVGGLLVGRTPEYLGKKLGPREIKLASLYILVTPTLVLAGTALSF AVPAVRADVVATSLLNTGPHGLSEVLYAFTSASNNNGSAFAGLTADTPWFNTALGVAMLLG RFVPVVFVLALAGSLAAQDRVSATPGTLPTHRPQFVGLLVGVTVLVTALTYFPVLALGPLAE GL
3E-223	751.3	26.4	4E-223	751	18.3	1	1	A0A0E9MU61_9SPHI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA FPE01S_01_00250	Flavihumibacter petaseus NBRC 106054	571	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Flavihumibacter, Flavihumibacter petaseus, Flavihumibacter petaseus NBRC 106054	1220578	>tr|A0A0E9MU61|A0A0E9MU61_9SPHI Potassium-transporting ATPase potassium-binding subunit OS=Flavihumibacter petaseus NBRC 106054 GN=kdpA PE=3 SV=1 MSGEIIAIISIFLVTLILAWPLGKYISKVFRGERTLTDFMSPLERFIFRFSGINPNEPMSWKQFL KAMLTVNALWLFYAMGLLIYQDRFPLNPDGNAAQTPDLAFNTAISFLVNCNLQHYSGESGLT YFTQLFVITFLQFVSAATGIACLIGLFNGFRERTTNNLGNFWNYLVLSVTRILLPLSIVVAVILV FNGTPSSFAGKDTITTLQGDTVQVSRGPAAGMIAIKQLGTNGGGWFGVNSAHPLENPNYLT NAVETISILLIPIALIFSLGFYLQRRKLAVMIFGVMSVLFILFTAINTWYETKGNPAIDRLGIAQLQ GSMEGKEVRIGAAATALWSVATTSTSNGSVNGMHDSLTPISGGVVILDMMINALYGGVGVG LLNFFIFIVIAVFLSGLMVGRTPEFMGHKVEAREVKIAALITLLSAFLIKGFTALAAYMVAHHPEI AWSVKPGAWLNNPSFHGFSEMLYEFTSSNANNGSGFEGLADNNIFWNVTTGIVLILGRYLP IIGPIAIVGLLANKKFIPESPGTLRTDSITFGVMTLAVIIIVTALSYLPALALGPLAEYFSLY
4E-223	751	27	5E-223	750.8	18.7	1	1	D7E5A4_NOSA0	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Aazo_3973	Nostoc azollae (strain 0708) (Anabaena azollae (strain 0708))	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Trichormus, Trichormus azollae (Anabaena azollae), Nostoc azollae (strain 0708) (Anabaena azollae (strain 0708))	551115	>tr|D7E5A4|D7E5A4_NOSA0 Potassium-transporting ATPase potassium-binding subunit OS=Nostoc azollae (strain 0708) GN=kdpA PE=3 SV=1 MGQGFLQIALTLSIVVLITPQLGRYIARVFLGENTILDLILNPIEKILYILAGVRKKEEMTVWQYI RAVIYSNLVMGISVYALISFQRLLPWNPNRFGTPTWDILLHTTISFLTNTDQQHYTGETTLSY FSQTAALGFLMFTSAATGLSVGIAFIRGLTGRKLGNFYFDITRAITRILLPLSIIGAITLIALGVPQ TFNETLVVQTLEGGTQYIARGPVASFEMIKMLGENGGGFFGANSAHPFENPNGAANLIEIIA MLAIPTSLIYTYGVFANNLKQTWLLFWTVFIIFVVLIWITAAGELQGNPLINNALGVQLPNLEG KELRLGWAETALWAVATTATMCGAVNGMQDSLMPSGIFSTLFNMFLQIIWGGQGTGTAYL FIYLILTVFITGLMVGRTPEFFGRKIEQPEIVLASIVFLIHPIVVLIPSAIALAYPISLSGISNPGFH GISQVVYEYASASANNGSGLEGLKDNTLWWNLSTSFSILAGRYIPIMAMLLLADSMSHKPKP PETRGTFRTDSLLFTTVTAGVTIILGLLTFFPVLALGPIAEGFKLAGGS
4E-223	751	37.8	5E-223	750.8	26.2	1	1	B1HTG1_LYSSC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bsph_3681	Lysinibacillus sphaericus (strain C3-41)	538	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus sphaericus (Bacillus sphaericus), Lysinibacillus sphaericus (strain C3-41)	444177	>tr|B1HTG1|B1HTG1_LYSSC Potassium-transporting ATPase potassium-binding subunit OS=Lysinibacillus sphaericus (strain C3-41) GN=kdpA PE=3 SV=1 MQQKTWLDPLLDKVDAAIYKVCGIKRVNMTGKEYVLSLIISNAMMVFVGYIILRIQALLVLNPN NINNMEATLSFNTIISFITNTNLQHYSGESGLSYLSQMLVITFMMFTSAATGYAACMAFCRRL VAKTDTIGNFFVDFVRVITRILMPFSIVVALILVSQGSPQTIEGNQTVQTIEGKLQDIALGPIASL ESIKHIGTNGGGFNGANSTTPFENPTVLSNIVEILSMMLLPGACVVAFSLMVAYRKKKTIFGK QGLAIFTAMSILFLVGLVTVYIAEKAGNPFISELGITQELGSMEGKEMRFGVAQSALFTTVTT AFTTGSINNMHDTLTPLGGLVPMFNMMLNVVFGGKGVGLMNMMMYVLLTIFIACLMIGRSP QFLGKKIEEKEMKLIALCILIHPAIILLFSALAVATPSGIVGITNPGAHGLSQVLYEFASASANNG SGFEGLADNSTFWNVTTGLAMFFGRYLTIIIQLAIASLLANKVRHSDSVGTLKTDTTTFTFLLV AIVLMIGALTFLPALALGPITEHLQLYS
5E-223	750.8	30.4	6E-223	750.5	21.1	1	1	R5P3F7_9PORP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN783_01717	Odoribacter sp. CAG:788	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter sp. CAG:788	1262909	>tr|R5P3F7|R5P3F7_9PORP Potassium-transporting ATPase potassium-binding subunit OS=Odoribacter sp. CAG:788 GN=kdpA PE=3 SV=1 MNTEILGVIVQIVLMVAISYPLGKYIAKVFKGEKTWLDFMKPIERWIFKLSGIHPEKEMNWKQ FLKALLTVNLCWFLWGMLLLVMQGVLPLNPDGNPGQTAHQAFNTCISFMVNCNLQHYSGE SGLTYFTQLFVIMLFQFITAACGMAAMAGIMKALAAKTTKTIGNFWNYLVLSCTRILLPLSLIV GFILILQGTPMGFDGKMEVTTLEGATQLVSQGPTAAIVPIKQLGTNGGGYFGVNSSHPLENP TYLTNMVECIAILIIPMAMALAFGFYLRRRKLGYCIYGVMLVAYLIGVGINVSQEMGGNPRIDE MGIAQGNGAMEGKEVRLGAGATALWSVTTTVTSNGSVNGMHDSTMPLSGMIQMLNMQIN TWFGGVGVGWMNYFTFIIIAVFISGLMVGRTPEFLGKKVEAREMKIASVVALLHPFIILVGTG LAAWLFVHAPGFVTGEGGWLNNPGYRGLGEMLYEYTSSAANNGSGFEGLGDNTWFWNF SCGLVLILGRFLPIVGQVAIAGLLAQKKFIPESAGTLKTDTVTFSVMTFAVIFIVAALSFFPVQV LSTIAEHLSL

6E-223	750.5	29.9	7E-223	750.3	20.7	1	1	K9UDW3_9CHRO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cha6605_2204	Chamaesiphon minutus PCC 6605	569	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Chamaesiphon, Chamaesiphon minutus, Chamaesiphon minutus PCC 6605	1173020	>tr|K9UDW3|K9UDW3_9CHRO Potassium-transporting ATPase potassium-binding subunit OS=Chamaesiphon minutus PCC 6605 GN=kdpA PE=3 SV=1 MLQGWLQIGLTLVLIVAITPIFGGYIARVYLGQRTLLDRVLHPVERLIFGLSGVKPEVQMTGW QYARAILYSNLAMAILLFAILMLQGVLPLNPTGLGAPTWDTALHTTISFITNTNQQHYSGETTI SYLTQTVGLGFMFFTSAATGIAVAIAFIRGLTGRSLGNFYVDLTLAITRILLPISVVGAILLVAAG VPETLSGPIVVPTLEDPNLRQAIALGPVAHFEIIKQLGENGGGFFAINSAHPFENPNGFSNLIQ ILTMISIPTAMIYAYGVIANNRKQAWLVFGMVFIIYVAFIIVTAIGEYQGNPLVNSILGSTQPNLE GKEVRFGWAQSALFAVTTTGTMTGAVNSMHDSFMPAGGFVLLSNLFLQIIWGGQGTGTAY LFSYLILAVFVTGLMVGRTPEFLGRKIEKNEVVLTSFLLLLVHPIFVLLPGAIALALPEQLAGISN PGFHGLAQVLYEYASATANNGSGFEGLADSQPAPTALWWNLSTSLSLLGGRYIPIVALLILA DGMSRKQPVPFTTGTLRTDTVLFTSVTAGVILIMGALTFFPVLALGPIAEAFQLAKGA
7E-223	750.3	29.7	8E-223	750	20.6	1	1	K9Z7H8_CYAAP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cyan10605_2258	Cyanobacterium aponinum (strain PCC 10605)	561	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobacterium, Cyanobacterium aponinum, Cyanobacterium aponinum (strain PCC 10605)	755178	>tr|K9Z7H8|K9Z7H8_CYAAP Potassium-transporting ATPase potassium-binding subunit OS=Cyanobacterium aponinum (strain PCC 10605) GN=kdpA PE=3 SV=1 MWQGFLQIILTLVLVVIITPILGNYMACVFLGKPTFLDRFLKPIESRLYSLFGLRILEATNSNGY QYVKDVIASNLVMGILVYLILMTQGFLPLNPTDLSAPTWHLGLHTAISFLTNTNQQHYSGETT FSYASQVLALGFLMFTSAGTGLAVAIAFIRGLTGQRLGSFYVDLTLSITRILLPISIVGAIVLIISG VPETLSPPVTATTLEGANQVIAIGPVAHFEIIKELGENGGGFFGINSAHPYENPNPFSNLFTIL AMMSIPTSLIYTYGVFANNKRQAWLIYGMVFSIFVVLIAISAVGEYYGNPLVNNLLGDTQPNL EGKEVRFGWSQTALWAVMTTATMCGAVNGMHDSLMPTGGFSTIFNLFLQIIWGGQGTGT AYLFIYLILTVFLTGLMVGRTPEFLGRKIEKPEIVLASVILLVHPIAILIPSAITLAFPEALAGISNP GFHGISQVVFEYASAAANNGSGFEGLGDNTLWWNLSATFSLILGRYVPIIALLLLADNMSRK QLVPLTSGTLRTDTVLFTSITAGVILILGALTFFPVLALGAIAEGFQLAG
8E-223	750.1	33.6	9E-223	749.9	23.3	1	1	V6KD56_STRRC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA M878_19660	Streptomyces roseochromogenus subsp. oscitans DS 12.976	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	1352936	>tr|V6KD56|V6KD56_STRRC Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=kdpA PE=3 SV=1 MGPELAGVLQLLALIGALALAYVPLGNYMAKVYSSRGHLRVEKWIYKAIGANADTEMTWPA YLRGVLAFSAASVLFLYLLQRLQGVLPGSMNFSSVDPAQSFNTAVSFVTNTNWQSYSGEQ AMGHVVQTAGLTVQNFVSAAVGMAVAVALVRGFARSRTGELGNFWSDLVRGTLRILLPGA AIAAVILVACGVIQNFSGIHEVGQFMGGSQQWNGGAVASQEAIKEFGTNGGGYFNANSAH PFENPTPFTNLLEIFLILVIPFSLTRTFGVMVGNVKQGYAILATMFTIWLSFVALMMWSEFAH HGAALQAAGGAMEGKEVRFGIGSSSIFATSTTLTSTGAVDSFHSSFTGLGGGIAMLGMMLG EIAPGGTGSGLYGMLIMAVIAVFIAGLMVGRTPEYLGKKIGGREMKLAACYILITPALVLVFTA ASMALPTPPHSMLNSGAHGFSEVLYAFTSASNNNGSAFAGLNANTDWFNTMTGLAMLLGR FLPMVFVLALAGSLAEQKPVPVTAGTLRTEKPLFTGLLVGAILIITGLTYFPALALGPLAEGLA
9E-223	749.9	22	1E-222	749.6	15.2	1	1	A0A059VZ54_STRA9	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DC74_374	Streptomyces albulus	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	68570	>tr|A0A059VZ54|A0A059VZ54_STRA9 Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces albulus GN=kdpA PE=3 SV=1 MGDTAAGWLQVTALVVALGLSYRPLGDGLAHVLTTERHWRVERLVYRAGGVNGDVDQR WPVYLRGLLAFGLVSVLFLYAFLRLQDHLMLSLGHEPVPADLAFNTAASFVTNTNWQAYSG ESTMGHLVQMAGLAVQNFVSAAMGIAVVAALLRGFTRQRTQQVGNFWADLTRLVLRVLLP LAFVFALVLVAAGVIQNLHGTHDLVTVAGGHQSLPGGPVASQESIKELGTNGGGFFNANSA HPFENPSGLTNLIEIYLMLVIPFALPRTFGAMVGDHRQGYAVVAVMVVLWVASVALVTVNEL HRISSPAGHAAGAMLEGKETRFGIWASALFAVSTTLTSCGAANSAHDSYTPGGGGMTLFN MMLGEIAPGGTGSGLYGILILAVVAVFVAGLMVGRTPEYLGKKLRGREMRYASLYLLTTPAL VLVGAGLAMAFPGERAAMLNPGPHGFSEVLYALTSAANNNGSAFAGLSADTVWYNTVLGV VMLLGRFLPMVFVLALAGSLAGQQRVPVTAGTLPTHRPQFVGLLTGVILIVVGLTYFPALALG PLAEGLR
9E-223	749.9	23.8	1E-222	749.6	16.5	1	1	Q2J7U8_FRASC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Francci3_3287	Frankia sp. (strain CcI3)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain CcI3)	106370	>tr|Q2J7U8|Q2J7U8_FRASC Potassium-transporting ATPase potassium-binding subunit OS=Frankia sp. (strain CcI3) GN=kdpA PE=3 SV=1 MGTNAAGVIFIVSMVLALALTYRPFGDYMARVYMSGKHLRVERGIYRLVGVDPDAEQRWSV YARSVLAFSLVSVLFLYLFQRVQNHLWLALGLPAVKPDLAWNTAVSFTTNTNWQAYSGEST MGHLVQMSGLAVQNFVSAAVGIAVAIAVVRGFARKKTDQLGNFWVDLVRTVVRILLPVCAL AAIVLIVGGAIQNFHGNTTVPTLAGGEQAVTGGPVASQEAIKDFGTNGGGFYNANSSHPFE NPTSWTNWFEIYLLLSIGFALPRTFGKMVGSTRQGLAIVAVMAVLALGSLGANEVFQAIHHG TVPTAVGAAREATETRFGVPDSALFATGTTLTSTGSVDSFHDSYTSLGGATLLFNMMLGEV APGGTGSGLYGILVLAVITVFVAGLMIGRTPEYLGKKIGSREIKFASLYFLTMPVIVLVGTGLA MALPGERAGMLNSGPHGLSEVLYAFTSAANNNGSAFAGITVNTDWYNTALGLAMAFGRFL PMVFVLGLAGSLAKQQPVPETAGTLPTHRPQFVGMLTGVTVIIVALTFFPALALGPLAEGLH

9E-223	749.9	28	1E-222	749.7	19.4	1	1	K9QI75_9NOSO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Nos7107_3967	Nostoc sp. PCC 7107	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	317936	>tr|K9QI75|K9QI75_9NOSO Potassium-transporting ATPase potassium-binding subunit OS=Nostoc sp. PCC 7107 GN=kdpA PE=3 SV=1 MGQGFLQIGLTLCFVIAIAPILGRYIARVFMGARTLLDPLMNPIEHSIYLVAGVNRKDDMTGW QYIRAILASNLVMGILVFGLIHYQRFLPWNPNGFFAPRWHTLLHTVISFVTNTDQQHYTPETT LSYFSQVAALGFLMFTSAGTGLAVGIAFIRGLTSKRLGNFYVDLIRGITRILLPISVVGAIALVLL GVPQTLDNPLIVETLEGSTQYLARGPVASFEMIKMLGENGGGFFAANSAHPFENPNGASNLI ELIAMISIPAALIFTYGMFAKNLKQAWLLFWMVFTAFVILVWVTVSGELQGNPLVNGTLGVEL PNLEGKEVRFGVIQTALWAVTTTATMTGAVNGMLDSLMPQGLFVTLFNLFVQIIWGGQGTG IAYLLIYILTVFLTGLMVGRTPEFLGRKIEKREIILASVVLLIHPMMILIPSAIALAYPFSLSGITN PGFHGISQVVYEYASAAANNGSGLEKLNDNTLWWNLSTGLSMLAGRYIPIIAILLLADNMSR KPVTPETAGTLKTDSLLFTTVTAGIVLILGVLTFFPVLALGPIAEGFKLASGS
9E-223	749.9	28.2	1E-222	749.6	19.6	1	1	K4RDN4_9ACTN	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN159_7223	Streptomyces davawensis JCM 4913	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces davawensis, Streptomyces davawensis JCM 4913	1214101	>tr|K4RDN4|K4RDN4_9ACTN Potassium-transporting ATPase A chain OS=Streptomyces davawensis JCM 4913 GN=kdpA PE=3 SV=1 MGPVLAGVLQLVALIAALALAYVPLGNYMAKVYSSDKHWRVEKWIYKGIGANPDTEMRWP AYLRGVLAFSVIGILFLYGLQRLQGALPGSLGFSAIDPDQAFNTAVSFVTNTNWQSYYGEQA MGHVVQTAGLAVQNFVSAAVGIAVAVALVRGFARSRTGELGNFWADLVRGTVRILVPLAAV AAVVLVACGAIQNFSGIHEVGQFMGGRQEWNGGAVASQEAIKELGTNGGGYFNANSAHPF ENPTPFSNLFEIFLILVIPFALTRTFGVMVGSVKQGYAILATMGTIWLGFVSLMMWTEFSHHG PAFELANGAMEGKEVRFGVGASAIFATSTTLTSTGAVDSFHSSFTGLGGGITMLGMMLGEI APGGVGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGTREIKLAACYILITPALVLVFTAFAM ALPTPANSMTNSGAHGFSEILYAYTSASNNNGSAFAGLNADTQWFNSTLGLCMLFGRFLP MVFVLALAGSLAEQKPVPATAGTLRTEKPLFTGLLVGAILIITGLTYFPALALGPLAEGLA
1E-222	749.8	24.9	1E-222	749.5	17.2	1	1	C8XB13_NAKMY	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Namu_5034	Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	551	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Nakamurellales, Nakamurellaceae, Nakamurella, Nakamurella multipartita, Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	479431	>tr|C8XB13|C8XB13_NAKMY Potassium-transporting ATPase potassium-binding subunit OS=Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) GN=kdpA PE=3 SV=1 MSPTVAGVVMVGSLVLALALAHRPVGDYLYRVLEPGRPARVERGIYRLVGVDAGSEQSWG VYARSVLAFSAVSVLALYALQRVQQHLWLSLGFDAVAPDQAWNTAVNFVTNTNWQSYSG ETTMGYLVQAAGLAVQNFVSAAVGIAVAAALIRGFARAATDRLGNFWVDLVRIVIRVLLPVAV IGAVVLVAGGVVQNLSAGTDVATLAGGTQHLTGGPVASQEAIKQLGTNGGGFYNANSAHP FENPTSWTNWLEIFLLLVIPFSLPRTFGRMVGNRRQGYAILAVMATLALLSVIAVNALQLAHQ GTVPEAVGAATEGTESRFGVSQSATFAAATTLTSTGAVNSFHDSYTALGGGVPILNMLIGEV APGGVGSGLYGMLVLAVITVFVAGLMVGRTPEYLGKKISAREITFASLYFLVTPLIVLVGTAA AFATGNNDTALNTGPHGLSEVLYAFASAGNNNGSAFAGLGVNTGWWNTALGLAMLLGRFL PIVLVLGLAGSLARQRPTPASVGTLRTDQPLFVGMLTGVTVVLVALTYLPALALGPLAEGL
1E-222	749.7	35.1	1E-222	749.5	24.3	1	1	Q4K7X6_PSEF5	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA_2 kdpA PFL_4573	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	568	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	220664	>tr|Q4K7X6|Q4K7X6_PSEF5 Potassium-transporting ATPase potassium-binding subunit OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=kdpA_2 PE=3 SV=1 MLSTVLEYAVILGLMTGLAALMGQWLARVFSGRGHALPERATYRLLGIDPAETMGWARYG SALLLSNAAMMLLGYLLLRLQGSTPLNPLGLAAQTPDLAFNTAASFITNTNWQAYSGESSLS NFSQMAVITFLMFVGATAGVVAAAGFIRGLSRSSSADLGNYWVDFTRTLYRVMLPLCLIMAL VYVWQGMPQTLNSQALATTLEGAQQQLIVGAVASFESIKHIGTNGGGFFSMNAAHPFENPT PLTNVLHILSMLLIPSALTYAFGSMLLRRRQGWVFFGTFLVMFVGFLAIVFTAEQGGNPLLTQ AGADQQMSETQSGGNMEGKELRFGIADTALFVTTTTGATTGSVNAMHDSLTPMGGFVPLA QMMLNCVFGGDGVGFINLIQYALLTVFLVGMMIGRSPEFLGKKIEAREIKLVMLSVLAHPICIL GFTALAALWPGTLNSLNNLGPHGFSEVLYAYASGTANNGSAFAGLNANTPFFNTTIGLAML MGRFFTMLPMLAVAGSLAAKKNIPAGAGTIPTATPLFMLLVVFVVLVVGGLTFLPALALGPLV EQLQLLAGQTYK
1E-222	749.7	27.8	1E-222	749.5	19.2	1	1	B5HZB2_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SSEG_09552	Streptomyces sviceus ATCC 29083	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sviceus, Streptomyces sviceus ATCC 29083	463191	>tr|B5HZB2|B5HZB2_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sviceus ATCC 29083 GN=kdpA PE=3 SV=1 MGPVLAGVLQLLALIAALALAYVPLGDYMAKVYSSERHWRIEKWIYKAIGANPDTEMRWPA YLRGVLAFSAVSVLLLYLLQRLQGHLPGSLGFSAIDPDQAFNTAASFVTNTNWQSYYGEQA MGHVVQTAGLAVQNFVSAAVGIAVAVALVRGFARSRTGELGNFWSDMVRGVTRILLPGAF VAAIVLVACGALQNFSGIHEVGQFLGGAQQWNGGAVASQEAIKELGTNGGGYFNANSAHP FENPTPFTNLFEIFLLLVIPFALTRTFGVMVGSVKQGYAILATMATIWVGFVALMMWTEFAHH GPALQLAGGAMEGKEVRFGVGSSSIFAVSTTLTSTGAVDSFHSSFTGLGGGITMIGMMLGE IAPGGTGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGRKIGTREIKLAACYILVTPALVLLFTAAA MALPTPGHSMTNSGAHGFSEVLYAYTSASNNNGSAFAGLNADTQWFNSTLALCMILGRFL PMVFVLALAGSLAEQKPVPTTAGTLRTEKPLFTGLLVGAILIITGLTYFPALALGPLAEGLAS

1E-222	749.7	31.4	1E-222	749.4	21.7	1	1	U1YHB2_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAN879_04875	Alcaligenes sp. EGD-AK7	567	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Alcaligenes, Alcaligenes sp. EGD-AK7	1386079	>tr|U1YHB2|U1YHB2_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Alcaligenes sp. EGD-AK7 GN=kdpA PE=3 SV=1 MLDDLMQFLVILAVSTVLLVVVGKWIAHFFSSPNHSLIERGTYRLLGVNPEEKMSWKRYGLA LLLSNAAMLLLGYILLRVQGWIPGDSLQRAAQTPDLAFNTAVSFTTNTNWQAYSGESSLSNF SQMAAITFLMMISATTGLAAAGGFIRGLSRKSSADIGNYWVDFTRSLYRLLLPCSFLLALLYI WQGMPQTLSSDVVVNTLEGLKQQIILGPVASLESIKHVGTNGGGFFGMNAAHPFENPTPLT NTVHMLSMLLVPSALTYAFGSMLARRRQGWAFFAAFLVMFIGFLSLIYSAEQAGNPLLTSLG VDQTQSSTMGGGNLEGKELRFGVAQSSLFATVTTAATTGSVDAMHSSLTPLGGLVPIAQM MLNNVFGGIGVGFISLVSYAILTVFLVGMMIGRSPEFLGKKIEAREMKYVMLAMLAHAFSILG FTALASVLPSTMDSLSNMGPHGFSEVLYAYTSGTANNGSAFAGFNANTPFFNTTIGLAMLV GRYLTLLPLLALAGALAAKKAVPAGPGTLSTATPLFTGLLIFVVLVVGGLTFLPALALGPIVEH LLMLDGITF
1E-222	749.4	35.5	1E-222	749.2	24.6	1	1	E3GWW4_METFV	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAMfer_0049	Methanothermus fervidus (strain ATCC 43054 / DSM 2088 / JCM 10308 / V24 S)	567	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanothermaceae, Methanothermus, Methanothermus fervidus, Methanothermus fervidus (strain ATCC 43054 / DSM 2088 / JCM 10308 / V24 S)	523846	>tr|E3GWW4|E3GWW4_METFV Potassium-transporting ATPase potassium-binding subunit OS=Methanothermus fervidus (strain ATCC 43054 / DSM 2088 / JCM 10308 / V24 S) GN=kdpA PE=3 SV=1 MNADNITYIIAFYILLTFLAWPLGKYMARVFTGKKTFITPIVRPIENFIYKICNIDEKREMNWKE YAIAFTIFNTVMLTALFLLQEIQAFLPLNPQGFPPVRWDTALNTAISFMTNTNWQAYAGENT MSYLTQMIGLTVHNFLSAAAGMAPLLAFIRGFIRSNTDKIGNFWVDVTRMTLYVLLPLCIIFAL FLISQGVIQTFSPYITAKTFEGGKQIIALGPVASQEAIKILGTNGGGFFGTNSAHPFENPNIYT NFAETLLFSLIPAAQIFMFGYLIRNSRQGIAIYVAVMVIISMALALALWSEYKLNPLLEKIGVTG ENLEGKEVRFGVTPSVLFGIQTTGIECGAVNHMHDSDMPLTGMMYMFLMGVSNIFGGCGV GLVLMLYYIILTMFIVGLMIGRTPEFLRKKLGIFEMKMAVIGVIGINVSMLTLAAIAATTPYGLSS LGNPSAHGLSEILYAYFSAHANNGSAFAGLNVNTLFYNITTGIGMLVARYLSLIPGIAIGSALA KKGKIPATAVSFPTTNPVFVIMLISVIIIVGALTFFPILTLGPGLEHLFLQEGKVFM
1E-222	749.4	27	1E-222	749.2	18.7	1	1	KDPA_MYCS2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAMSMEG_5392MSMEI_5244	Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	246196	>sp|A0R395|KDPA_MYCS2 Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=kdpA PE=3 SV=1 MSPTTAGIAFLASLVAAVVLVHVPLGDYMYRVYTSEKDSRAERLIYRVIGADPRAEQSWGSY ARSVLAFSAVSIVFLFGLQLVQGRLPLHLHDPATPMTPALAWNTAVSFVTNTNWQAYAGES TQGHLVQMAGLAVQNFVSAAVGMAVAIALVRGFARRHTGELGNFWVDLVRGNLRILLPLAI VGALLLVAGGAIQNFALHEQVVTTLSGAAQTIPGGPVAGQEAIKELGTNGGGFFNVNSAHP FENPTPWTNWLENFLILLIPFSLPRTFGRMVGSARQGVAIAAIMGAIALASVSLTMLLQLHH GTVPTAVGAAMEGVEQRFGVADSAVFAGSTTLTSTGAVNSFHDSYTSLGGLMTMFNMQL GEIGPGGVGSGLYGMLILAIITVFVAGLMVGRTPEYLGKKITPREIKLAASYFLATPLIVLTGSA IAMAMPGQRAGMLNTGPHGLSEVLYAFTSTANNNGSAFAGISVNTEWYNTALGLAMVFGR LLPIILVLALAGSLASQGVTPSSVGTLPTHRPQFVGMTVGVTLILVALTFLPILALGPLAEGIH
1E-222	749.2	38.2	2E-222	749	26.5	1	1	U5LJM5_9BACI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAN288_25420	Bacillus infantis NRRL B-14911	557	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus infantis, Bacillus infantis NRRL B-14911	1367477	>tr|U5LJM5|U5LJM5_9BACI Potassium-transporting ATPase potassium-binding subunit OS=Bacillus infantis NRRL B-14911 GN=kdpA PE=3 SV=1 MITTILSIIVTMAAVILIAKPAGIYLAKAFDYSQTGLDKVFGPIENILFKISGIKKINQTWKQYAMT LVLANGFMILLVYMVFRLQGILPLNPSGNPGMDPTLAFNTAISFMTNTNLQHYSGESGLSYL GQMIGILFMMFAAPGTALAAAIAFVRALSGKEIGNFLVDLFRAITRVLMPIAIVSGLILVALGVP QTLEPTVTVNTIEGTAQEIARGPVGTFLSIKELGNNGGGFFGVNSAHPFENPNAISNIIQILLM FLLPTALPFAYGKMLGNAKQGRVLFVSMLMVFTVFLGTALFYEYQGNPALNALGINTDQGS MEGKEVRFGTGQSIFYALVTTASETGAVNTMHDTLTPIGGMLALSNMLLNTVFGGVGAGFI NVIMYAMIAVFLSGLMVGRTPEFLGKKIEGREMKLIALTMLMHPLLILGASAIALYTPLGAGAI SNSGFHGISQVVYEYTSSAANNGSGFEGLGDATPFWNISTGIVMYAGRFFGLVTMLAVAGS LSSKKIVPETIGTFRTDTPLFGVILVGTFFIVGALTFFPALVLGPVAEYLTL
2E-222	749.1	23.4	2E-222	748.9	16.2	1	1	A0A0F4JYE9_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAVR44_02695	Streptomyces katrae	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces katrae	68223	>tr|A0A0F4JYE9|A0A0F4JYE9_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces katrae GN=kdpA PE=3 SV=1 MSPQIAGVLQLLALIAALALAYRPLGDHMAKVYSSEKHYKPEKWIYKAIGADPTTEMRWPAY LRGVLAFSVVGVLFLYALQRLQGVLPGSLGFRSIDPDQAFNTAASFVANTNWQSYAGEQA MGHVVQTGGLAVQNFVSAAVGMAVAVALVRGFARSRSGELGNFWADLVRGTVRILLPIAVL GAIVLVACGAIQNFAGIHEVGQFTGGTQQWNGGAVASQEVIKELGTNGGGYFNANSAHPF ENPTPFSNLFEVFLILVIPFALTRTFGRMVGNLRQGYAILATMAVIWLGFTALMMWTEFAHH GPALQAAGGAMEGKETRFGIGGSAIFSVATTLTSTGAVNSFHSSYTGLGGGIQLLGMQLGE IAPGGVGSGLYGMLVMAVIAVFIAGLMVGRTPEYLGKKISTREIKFAACYILVTPALVLCFTAA AMALPTPPHSMLNSGAHGFSEVLYAYTSGANNNGSAFAGLNADTQWYNSTIGIAMLLGRFL PMVFVLALAGSLAEQKPVPETVGTLRTDKPLYAGLLVGTIIIITGLTYFPALALGPLAEGLAS

2E-222	749.1	24.2	4E-222	747.6	16.8	1.6	1	B8DR38_DESVM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DvMF_2577	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	612	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	883	>tr|B8DR38|B8DR38_DESVM Potassium-transporting ATPase potassium-binding subunit OS=Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637) GN=kdpA PE=3 SV=1 MTPRDYLQLALFLGILAAASPPLGRYIHRVLEGGRTWLHPLLGPVERLIYTAAGIDPASDQP WQRYAASLLGFTLAGFCLTFGVLLFQDVLPLNPQHFPAPSWDLALNTAVSFVTNTNWQAY GGETAMSHLSQVVALTYQNFVSAAVGMAACMAVVRGIARTEAQGIGNFWADLVRSTLYVL LPLCVPGALLLVGQGMVQTLAASFTATTPEGAVQTIAVGPVASQVIIKMLGTNGGGFFNANA AHPFENPTAVANFIQMLAIFLLPSSLVFTLGAAVRRPRHAWTVWGVMAAVFVAGTLLTAHFE YRGTPAMAQAVAPGSPAASGSSTSAASAGASIAASGVTPHPASAPASAPVPVSVAVSASVP NMEGKEVRFGIFSSSLFATVTTDASCGAVNAMHDSLTPLGGLVTLLNMQLGEIIFGGVGSGL YGMVLFIILTVFLAGLMVGRTPDYLGKRIEGREVTLAVAALLLPALPLLGFTALAAVGWGPQA LANAGAHGFSELLYAYTSSAQNNGSAFAGLAANSPVFNLTTAASMLIGRFGVMLPMLAVAG SLAARRPRPVTDASFPVEGATFALLLASVILIVGALTYLPALSLGPIVEHLQMIENQLY
2E-222	749	24.8	2E-222	748.8	17.2	1	1	A0A0F7N9B1_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AA958_15120	Streptomyces sp. CNQ-509	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. CNQ-509	444103	>tr|A0A0F7N9B1|A0A0F7N9B1_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. CNQ-509 GN=kdpA PE=3 SV=1 MSPILADVLQVSALVVALALVHRPLGDYMAGVYGGKKHSRVERWIYRTIGADPDAGMRWP AYLRAVLAFSLAGVLFLYLLQRVQDKLPLSLGFAAISPDQAFNTAASFVANTNWQSYSGESA MGHLTQTGGLAVQNFVSAAVGMAVAVALIRGFARSRTGELGNFWADLVRGTLRILLPMAAV AAVLLVACGAIQNFSGTESVTTVTGQTQHLTGGAVASQEAIKDLGTNGGGFYNANSSHPFE NPTGISNLLEIFLLLVIPFALPRTFGRMVGSVRQGYAVVAAMAGIWLAGVITVTALEAAHPGA AAQVAGGAMEGKEQRFGEGASSLFAVSTTMTSTGSVNSFHDSFGGLSGGVLLFGMMIGEI APGGVGSGLYGMLVMAIVAVFIAGLMVGRTPEYLGKKIGPREMKLAACYILVTPALVLTGTA LAMGTGNGESSMTNTGPHGFSEVLYAYTSASHNNGSAFAGFSANTGFHNTALGLCMLLGR FLPMVFVLALAGSLAGQRPVPATAGTLRTDKPLFTGVLVACIAIVAGLTFFPSLALGPLAEGL AA
2E-222	748.4	26.7	3E-222	748.2	18.5	1	1	B2J5S1_NOSP7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Npun_R0302	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	63737	>tr|B2J5S1|B2J5S1_NOSP7 Potassium-transporting ATPase potassium-binding subunit OS=Nostoc punctiforme (strain ATCC 29133 / PCC 73102) GN=kdpA PE=3 SV=1 MGQGFLQIGLTLCIVIAITPLLGRYIAHVFLGERTLLDFLMNPIERSMFVLAGVRRKDDMTVSQ YIRAVLYSNLIMGISVYLLLYFQRLLPWNPNGFGAPSWDVLLHTTISFVTNTDQQHYAGETTL SYFSQVAALGFLMFTSAATGLSVGIAFIRGLTGRRLGNFYVDVVRAITRILLPISIIGAIALLLTG VPQTLAKTMDVRTLEGGTQYLARGPVASFEMIKLLGENGGGFFGVNSAHPFENPNGASNLI EMIAMISIPAALIYTYGIFANNIKQAWLLFWMVFVIFVVLVGVTAVGELQGNPLVNNAFALEQP NLEGKEVRFGWLQTAFWAVMTTATMSGAVNGMHDSLMPQGIFSTLFNLFIQVIWGGQGT GTAYLFIYLILTVFLTGLMAGRTPEFLGRKIEKREIVLASVVLLIHPILVLIPSAIALAYPISLSGIS NSGHHGISQVVYEYASATANNGSGLEGLKDNTLWWNLSTLVSLIGGRYIPIIAILLLADGMSR KQQVQETPGTLRTDSLVFTGITAGVTLVLGVLTFFPVLALGPIAEGLKLASGN
3E-222	748.2	22.1	3E-222	748	15.3	1	1	E4NDZ7_KITSK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KSE_36240	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Kitasatospora, Kitasatospora setae, Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	452652	>tr|E4NDZ7|E4NDZ7_KITSK Potassium-transporting ATPase potassium-binding subunit OS=Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) GN=kdpA PE=3 SV=1 MGPTLAGWLQAIALVGALALCYRPLGDHIAKLLTSARHLRAEKALYKVVGVDADADQRWPV YLRSVLAFSALSVLFLYGLIRLQTHLLLSLGVPEMAAHQAWNTAISFTTNTNWQSYSGESAM GHLVQMAGLAVQNFVSAAVGIAVVAALIRGFTRNRTDRVGNFWVDLTRISLRLLLPLAVLFAL VLAANGVVQNFHGFEQVTTLTGGQQSLPGGPVASQEVIKLLGTNGGGFYNANSAHPFENP TGFTNLLEVFLLLVIPFALPRTFGRMVGDHRQGYAIAAVMGLFWTASAVLITFFEHQHAGSA LQAAGAALEGKEQRFGVAASGLFAASTTLTSTGAVNSFHDSFTPFGGGLTVFDMMLGEIAP GGTGSGLYGMLILAVVAVFVAGLMVGRTPEYLGKKLGGREMKFASLYILTTPAIVLIGAGTAI ALPGERAGMLNDGAHGFSEVLYAFTSAANNNGSAFAGITVNTDWYDTALGLAMVFGRFLP MVFVLALAGSLARQRPVPAGAGTLPTHRPLFVGLLSSVILIVVGLTYFPALALGPIAEGLH
4E-222	747.8	27.3	4E-222	747.6	18.9	1	1	A0A0F5VMN1_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TN53_39180	Streptomyces sp. WM6386	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	1415558	>tr|A0A0F5VMN1|A0A0F5VMN1_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. WM6386 GN=kdpA PE=3 SV=1 MGPVLAGVLQLLALIGALALVHIPLGNYMAKVYTSDRHWRVEKWIYKGIGADPNSEMRWPA YLRGVLAFSAVSVLFLYLLQRLQGVLPGSLGFASIDPDQAFNTAVSFVTNTNWQSYYGEQA MGHVVQTAGLAVQNFVSAAVGIAVAVALVRGFARSRTGELGNFWSDMVRGVTRILLPGAF VAAIVLVACGAIQNFSGIHEVGQFMGGSQQWNGGAVASQEAIKEIGTNGGGYFNANSSHP FENPTPFTNLFEIFLILVIPFALTRTFGLMVGSLKQGYAILATMATIWIGFSALMMWTEFAHHG PVFDIAGGAYEGKEVRFGVGGSSIFATATTLTSTGAVDSFHSSFTGLGGGITMLGMMLGEIA PGGTGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGTREIKLAACYILITPALVLVFTAAAMA LPTPGNSMTNSGAHGFSEILYAYTSASNNNGSAFAGLNADTQWFNSTLGLCMLFGRFLPM VFVLALAGSLAEQKPVPATAGTLRTEKPLFTGLLVGAILIITGLTYFPALALGPLAEGLAS

7E-222	746.9	30.1	8E-222	746.6	20.8	1	1	R5NZ60_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN471_01394	Paraprevotella clara CAG:116	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Paraprevotella, environmental samples, Paraprevotella clara CAG:116	1263095	>tr|R5NZ60|R5NZ60_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Paraprevotella clara CAG:116 GN=kdpA PE=3 SV=1 MNTEILGVVAQIVLLVVLSYPLGKYIANVYKGKKTCLDFMKPIETAIYRFSGINPEEEMNWKQ FLRALLIVNLFWFIWGMLLLVLQGYLPLNPDGNAGQTAHQAFNTCISFMVNCNEQHYSGET GLTYLTQLFVIMLFQFVTAGTGMAAMAGIMKALGEKTTKTIGNFWKYLVLSCTRILFPLSLIV GFILITQGTPMGFDGKMEITTMEGATQNVSQGPTAAIVPIKQLGTNGGGYFGCNSSHPLEN PTYLSNMTECWSILILPMAMAFAFGFYIKRKKLGYSIYGVMLFAFLVGVCINVYQEMNGNPRI DAMGIAQDNGAMEGKEVRLGAGATALWSIVTTVTSNGSVNGMHDSTMPISGLMEMLNMQI NTWFGGVGVGWMNYFTFIIIAVFISGLMVGRTPEFLCHKVEAREMKVASIVALLHPFVILVGT ALAAYLYVHAPAFVENEGGWLNNPGFHGLSEMLYEFTSVAANNGSGFEGLGDNTWFWNY ACGIVLILSRFIPIVGQVAIAGLLASKKYIPESAGTLKTDTVTFSVMTFAVIFIVAALSFFPVHAL STIAEHFSL
8E-222	746.8	30.9	9E-222	746.6	21.4	1	1	R7JDD1_9PORP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN646_01834	Parabacteroides sp. CAG:409	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides sp. CAG:409	1262913	>tr|R7JDD1|R7JDD1_9PORP Potassium-transporting ATPase potassium-binding subunit OS=Parabacteroides sp. CAG:409 GN=kdpA PE=3 SV=1 MNTELLGVIAQIVLMMVLSYPLGKYIAKVYKGKKVWSDFMKPVENLIFRLSGINPEEEMNWK QFLRALLVVNAFWFVWGMILLVMQGYLPLNPDGNIGQTVHQAFNTCISFMVNCNEQHYSG ETGLTYFTQLFVIMLFQFITAATGMAAMAGIMKALGEKTTQTIGNFWKYLVLSCTRILLPLSLV VGFILITQGIPMGFDGKMEITTLEGNPQSISQGPAAAVVPIKQLGTNGGGYYGVNSSHPLEN PTYLSNMIECCSILMIPMAMVFAFGFYVNRKKLGYSIYGVMLAAFLIGVCINVSQEMGGNPRI DAMGIAQDGGAMEGKEVRLGAGATGLWSVVTTVTSNGSVNGMHDSTMPLSGMIEMLNM QINTWFGGVGVGWMNYFTFIIITVFISGLMVGRTPEFMCHKVEAREMKIASIVALLHPFVILV GTALATYLYVHVPAFVESEGGWLNNPGFHGLGEMLYEFTSCAANNGSGFEGLGDNTWFW NVSCGIVLILSRFIPIIGQVAIAGLLAQKKYIPESAGTLQTDTVTFGVMTFAVIFIVAALSFFPAQ ALSTLAEHFSL
1E-221	746.4	25	1E-221	746.1	17.3	1	1	C6XZL6_PEDHD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Phep_2508	Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290)	572	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Pedobacter, Pedobacter heparinus (Flavobacterium heparinum), Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290)	485917	>tr|C6XZL6|C6XZL6_PEDHD Potassium-transporting ATPase potassium-binding subunit OS=Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290) GN=kdpA PE=3 SV=1 MNTELLGIVATYLLTLVIAIPLGKYLAKVFAGEKVWTDFLKPLENGIFKLSGINPKEEMNWKQ HMKALLTINLVWLVYGFFVLIYQDKLPLNPDGNPGMTADLSFNTIISFVVNCNLQHYSGESG VSYLTQHYVLMFLQFVSCATGIAAAVVFFKAFRDKTSVKLGNFWDFFVKSITRLLLPLSLIMA LILAFNGTPTSYEGKDQFISLQGDTVNVSRGPAAGFIAIKHLGTNGGGWFGANSSHPLENPN YLTAMVELIAQVIIPIAMVIAFGYFIRRKKLAWMIFGVMTIGMLLLLVPTLSSELGGNPAIAKMG ISQATGAMEGKEVRFGPAISAYWSTVTTIISTGSVNSMHDSTMPLTGTWQLLGMMINSFYG GCGVGMLNYFIYLIIAVFISGLMVGRTPEFLGHKVEAREIKIAALITLLSPFLILAGTAIASYVFT NHGDAAWAVQPKNWLNNPGFHGFSEMLYEMTSSNANNGSGFEGLGDNNVFWNVATGFV LILGRFLPIIGPVAIAGLLGAKKYIPESAGTLKTDTLTFSLMTFAVILVLNALSYFPALALGPLAE YFTMLK
1E-221	746.3	26	1E-221	746.1	18	1	1	A0A0D5EDF0_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BW23_4024	Burkholderia ubonensis MSMB22	579	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	1249668	>tr|A0A0D5EDF0|A0A0D5EDF0_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Burkholderia ubonensis MSMB22 GN=kdpA PE=3 SV=1 MIGNAWTQVGVFLFVLTFLVKPLGTAIARVALGDLPGPLRRVAVVERAIYRLAGIAPDEEMD WKRYAVALVAFNALGAVALYLLQRIQVWLPLNPQHLPNVEPGLAFNTAVSFATNTSWQAYA GETTLSHLTQMLGIGVQAFLSAASGMVVMLALIRGLVRRGSKTIGNVWIDLTRMTLYVLVPL AALFAAAFIGQGVVQNFAPNREVAIVQPHASTPAAALTLPMGPVASQESIKLMSGDGGGFF NANSAHPYENPTPFANFLQMLAMLIIPAALCHTFGTMIQDRRQGWAIYAAMLTMFAAAAAM VIRAEQAAGPALSAPGIDTVASASQPGGNMEGKETRFGIVSSALYATVSTSSGDGAVDAMH DSLTPLGGLVPMALMQTGEVVFGGPGSGLYSMLMVVLLAVFVAGLMIGRAPEYVGKKIEAY EMKMVSIAILATPAIVLVGTAIAAVTPAGVAGLGNPGAHGFSEMLYAFSSAANNNGSAFAGL SANTTFYDTSLAAAMWFGRFTVIVPVLAIAGSLAAKQRRAAGDGTLPTHGPLFVCMLLSTVV LVTLLTFLPALALGPIAEHLAMTAGR
1E-221	746.1	17.4	1E-221	745.9	12.1	1	1	I4ETN2_MODMB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MODMU_1295	Modestobacter marinus (strain BC501)	567	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Geodermatophilales, Geodermatophilaceae, Modestobacter, Modestobacter multiseptatus, Modestobacter marinus (strain BC501)	1144889	>tr|I4ETN2|I4ETN2_MODMB Potassium-transporting ATPase potassium-binding subunit OS=Modestobacter marinus (strain BC501) GN=kdpA PE=3 SV=1 MSAAAAGWLQVGLLVLALALVHRPLGDAMARAFSTDPPLPPKARSRRNSGGHWRVERLVY RAVGVDADAEQRWPTYLRSVLAFSLVSVLFLYLLQRVQQWLPLGNGMPAVEQGSSWNTA VSFVTNTNWQGYAGESTMGHLVQMAGLAVQNFLSAAVGLAVAVALVRGFARTRTDRLGN AWVDITRAVTRILLPLSVLAAVVLVLGGVVQNLGSGTEATTLSGATQFLPGGPVASQEAIKQ LGTNGGGFFNANSAHPFEGPSAWISLFEVFLMLAVPFSLPRTFGRLVGDRRQGYAILGVMA TLASASLALTSWAQARAGGAALQLAGAATEGQEVRFGGPLSALFGTATTLTSTGAVNSLHD SYTPAGGLLTMFDMMLGEVAPGGVGSGLYGMLVLAVIAVFVAGLMVGRTPEYLGKKLGRR EMTLASLYVLATPAIVLVGTAVAMSVDAGRSSMLNDGPHGLSEVLYAFTSAANNNGSAFAG LSADTPFYNVALGLAMAFGRFLPIVFVVLALAGRLAAQGRTPVTAGTLPTHRPLFVGLLAAVVL VVVGLTYFPVLSLGPLAEGLS

2E-221	745.8	24.8	2E-221	745.6	17.2	1	1	I0K505_9BACT	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA FAES_1198	Fibrella aestuarina BUZ 2	571	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Fibrella, Fibrella aestuarina, Fibrella aestuarina BUZ 2	1166018	>tr|I0K505|I0K505_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Fibrella aestuarina BUZ 2 GN=kdpA PE=3 SV=1 MTTELLGIVATYLITMLLAIPLGKLYAKVFANKPNALDFMAPLERLLYRVGGVDPNRDMTWKE NLVALLTINLVWLVYAFVLLLTQGSLPLNPDGNPSMTPDLAFNTAISFLVNCNLQHYSGESGL TYLTQLGVITFLQFVSAATGIAALVLIFRSFLPATTDRSGNFYTFFIKSITRILLPLCLLVAIVLAF NGTPASFDGKDQFISMQGDTVNVSRGPAAGMIAIKHLGTNGGGWFGANSAHPLENPNYLT NMVEMVSQVLIPVAMLFALGFFIQRRKFAWVVYGVMTAGLLVLLVPTILTEIHGNPAIAQLGV GQPTGAMEGKEVRFGPTASAYWSIVTTIISTGSVNSMHDSSMALSGAMELLGMMTNAFYG GCGVGFLNYYIFLIIAVFISGLMVGRTPEFFGRKVEAREMKIASLIAILHPFLILVGTALSSYLVK NGIGSDWAVQPANWLNNPGFHGFSEMLYEYTSSAANNGSGFEGLGDNNIFWNVSTGFLLL LGRFLPIVGPLAIAGLLTQKKFVPESAGTLPTDTGTFGLMTFAVIWIIAALSFFPALALGPLAEY FSLK
2E-221	745.8	33.5	2E-221	745.6	23.2	1	1	KDPA_TOLAT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Tola_1192	Tolumonas auensis (strain DSM 9187 / TA4)	566	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Tolumonas, Tolumonas auensis, Tolumonas auensis (strain DSM 9187 / TA4)	595494	>sp|C4LED2|KDPA_TOLAT Potassium-transporting ATPase potassium-binding subunit OS=Tolumonas auensis (strain DSM 9187 / TA4) GN=kdpA PE=3 SV=1 MFSSGVALLTSYMLVLLLLAWPLGIALTRLVDDRLPLWLIRVESHIKFLENSQMKWQTYAAAI LVFNLLGAALLFLLMLFQGSLPLNPLHLPDVSPLLAMNTAISFITNTNWQAYAGETTLSPLSQ MLGLTVHNFLSAANGIAVAFVLMRALTRTGSQQLGNAWVDIWRITVYLLLPLSVIYALFLAQQ GVVQSLMAQISVPGLSGVEQHIPLGPVASQEAIKMLGTNGGGYFNANSAHPFENPTALTNF VQMVSILLIPAALCICFGRVAGDNRVGSALLWTMGIMLSVAALLIMWAESQGHPVLANLAVD QQMSAIQSGGNMEGKETRFGLWASSLFATITTAASCGAVNAMHDSLTPLGGLIPMVLMQL GEVVFGGVGSGWYGMMLFVFLTVFLAGLMIGRTPEYLGKKIEIYEMKMVTIGLLIPPALVLLG TALAVILPQGLVSLQESGAHGFSEMLYAFSSAANNNGSAFAGLNSNTPFMNITLAVLMFVGR FGVMLPVLAIAGALIEKRHQPASAGSLACHGPLFVGMLIGVVLLIGALTFIPALALGPIVEHLTL WQTH
2E-221	745.7	27.2	2E-221	745.5	18.9	1	1	B2J9H1_NOSP7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Npun_F0718	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	581	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	63737	>tr|B2J9H1|B2J9H1_NOSP7 Potassium-transporting ATPase potassium-binding subunit OS=Nostoc punctiforme (strain ATCC 29133 / PCC 73102) GN=kdpA PE=3 SV=1 MLEGWIQIALTLLIIVAITPFFGSYMARVYLEQSTFLDPVLNLVERVLYALVGVKAKENMTGW QYGRAIVYSNVVMGLLLFFIIMSQGWLPLNPTGINAPTWDTALHTTISFITNTNQQHYSGETY MSYASQMWGLGYHMFTSAGTGLAVGIAFIRGLTGRSLGNFYVDLIRSITRILLPICIVGGIVLI AAGVPETLAGVAVFPTLEDPNISQAIARGPVAHFEIIKQLGENGGGFFAINSAHPFENPSGFT NLIQIVAMLSIPTSLIYTYGLFANNTKQALLLYGMIGVIFLGFLIVTAIGEYNGNPAVNALLGSQ QPNLEGKEVRFGWAQSALFAVSTTGTMCGAVNSLHDSFMPAGGFIFLSNMFLQIMWGGQ GTGTAYLFAYSILAVFVTGLMVGRTPEFLGRKIEKREVVLASFLILLVHPIAILIPGGIALAFPDQ LAGISNPGFHGFSQVIYEYASAAANNGSGFEGLGDSQPSPLAIANGTQPTATALWWNLSTC FSLLAGRYIPILGLLLLADSMSRKQAVPYTTGTLRTDTGLFTGVTAGVLILGALTFFPVLALGP IAEAFFIAKGIG
2E-221	745.6	41.4	2E-221	745.3	28.7	1	1	A0A0D6DXK3_9LACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LACPI_1314	Lactococcus piscium MKFS47	589	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Lactococcus (lactic streptococci), Lactococcus piscium, Lactococcus piscium MKFS47	297352	>tr|A0A0D6DXK3|A0A0D6DXK3_9LACT Potassium-transporting ATPase potassium-binding subunit OS=Lactococcus piscium MKFS47 GN=kdpA PE=3 SV=1 MLQITVVLIISILLMLPMGKYLYHIATRAHTFGDPVFDRVDNLIYKVIGVKNRGLTGMNWQKYI MTLLLTNAVMVVIGYFILRLQAMPFLNPNQIPGMEQGLALNTVVSFITNTNLQDYSGESSLSY LSQMIVIIFMMFTSAASGFAAAMAFIRGLSGKVTDMGNFYADFIRIITRVLLPLSILGAMILMSQ GVPQTLMHNLTVHTVEGKLQDIALGPVAALEIIKHLGTNGGGFFGANSAMPFENPTILTNIIE MLSMTLLPGGVLVAFGLMVSDRHKEKNRTIVANTSPLSALYPKKRHKVWLGSQAKPLFIVM SVLFLLGLGAILWSEFQGNPILKHLGLSQAMGSMEGKETRFGVVMSGLFTEITTAFTTGSVN NMHDSLTPLSGGVAMMNMMLNVVFGGKGVGLMNMVIFVILTVFICGLMIGHTPVYLGKKIE GKEMKLTAMAIIVHPLIVLVFSAIAVSVAAGVAGISNPGNHGLSQIVYQYTSSSSNNGSGFEG LKDNTLFWNVTAGIAMFVGRYVTLILQLAIVASLMAKQKVNDSIGSLKTDTMTFTTVLFVIVIVI SALTFLPVLVLGPIAEFLKMRG
2E-221	745.2	25.7	3E-221	745	17.8	1	1	K7WU80_9NOST	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ANA_C11291	Anabaena sp. 90	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena sp. 90	46234	>tr|K7WU80|K7WU80_9NOST Potassium-transporting ATPase potassium-binding subunit OS=Anabaena sp. 90 GN=kdpA PE=3 SV=1 MSQGFLQIALTLCIVVFITPILGKYIARVFLGERTILDPVMKPIEAIIYILGGVGKKNDMTGWQYI RALLCSNLVMGVIVYALLYYQKFLPWNPNELGRMRWDLLLHTTISFLTNTDQQHYATENTFS YFSQTSALGFLMFTSAASGLVVGIAFIRGLTGRKLGNFYVDFTQAITRILLPLSIVGAIALIICGV PQTLAKTLVVETLEGRIQYIARGPVASWEMIKMLGENGGGFFAANSAHPFENPNGASNLIEII AMLAIPTSLIYTYGIFANNLKQAWLLYWMVFIIFVVLIGVTATGELQGNPLINNALRLELPNLEG KEVRFDWAQTALWAITTTATMCGAVNGMHDSLMPNGTFSTLFNLFLQIIWGGQGIGTAYLF IYLILTVFITGLMVGRTPEIFGRKIEKREIVLASVVLLIHPMMVLIPSAVALAYPISLSGISNPGFH GISQVVYEYASAAANNGSGLEGLNDGTLWWNLSTTVSIFAGRYLPIIALLLADSMSEKQVV CESRGTLKTDSLLFTGITAGVTLILGILTFFPVLALGPIAEGFKLAAGS

4E-221	744.5	32.8	3E-173	586.5	14.9	2	2	A0A068NL36_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OP10G_0754	Fimbriimonas ginsengisoli Gsoil 348	631	cellular organisms, Bacteria, Armatimonadetes, Fimbriimonadia, Fimbriimonadales, Fimbriimonadaceae, Fimbriimonas, Fimbriimonas ginsengisoli, Fimbriimonas ginsengisoli Gsoil 348	661478	>tr|A0A068NL36|A0A068NL36_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Fimbriimonas ginsengisoli Gsoil 348 GN=kdpA PE=3 SV=1 MTILGTLQVLVFFAMIVLVTKPLGIYMQKVFDGERTFLSSIFGPLERHWYRLLGVRPEDDMK WTTYAVAMLLFSAVSILFTYAALRLQGFAPAILNPQKFDGAQMPPHLAFNTANSFGTNTNW QSYSPEVTVNYWSNMVALAIHNWASAAVGMAIAIALVRGFARKSANGIGNFWADTVRATLY VLLPICVVAGVVMIGLGTPQNFAAPMAIKTVEGTAQTIAMGPVASQEVIKMLGTNGGGFFNA NSAHPFENPSNASNLLQILLIFCIPAALTYTFGRMVGNVKQGWAVFGAMSVLFLAGAFACIS AEQGGTDHLRAAHIQTGATATQPGGNMEGKEVRYGISASALFATVTTDASCGAVNSMHDS YTPLGGMVPIFNMMSGEVIFGGVGAGLYGMLMFAVIAVFIAGLMVGRTPEYLGKKIGKFEV QMAMLATLVLAGNLLLWTAISANSNYATTTDPAAKDRYVSVSVDPKKPADLAKLPAVANWN AWPATAYGNATDTYYGSTRNNLNNSGSHGFSEILYTYASATGNNGSAFAGITANTPHYNTT IGIALLVGRFLMIVPLLAIAGSMARKKTVPMSAGTFPTDGGTFVALLVGVVVIVNVLSYFPALS LGPIVEHFQMKEMKTQ
5E-221	744.2	22.6	6E-221	743.9	15.7	1	1	A0A0A8F4C9_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GZL_08793	Streptomyces sp. 769	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	1262452	>tr|A0A0A8F4C9|A0A0A8F4C9_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. 769 GN=kdpA PE=3 SV=1 MGDTAAGWLQAAVLVAALALSHRPLGGALAHVLTTDRHWRSERLVYRAGGVNGDVDQR WPVYLRSLLAFSFVSTLFLYAFLRLQDHLLLSLGRRPVPADLAFNTAASFVTNTNWQAYAGE TTMGHLVQMAGLAVQNFVSAAVGIAVVATLIRGFTRKRTDRVGNFWVDLTRLVLRVLLPISF VFAVVLVAAGVIQNFHGAHAVATLAGGRQSLPGGPVASQETIKLLGTNGGGFFNANSAHPF ENPSGLTNLIEIYLLLVIPFSLPRTFGAMVGDVRQGYAVVTVMALLWAASVVLVTANELYRVS SPAGHAAGAMTEGKETRFGIWSSALFAVSTTLTSCGAVNSAHDSYTPGGGGMTIFNMMLG EIAPGGTGSGLYGILILAVVAVFVAGLMVGRTPEYLGKKLRGREMRYASLYILTTPALVLVGA GLAMAFPGERAAMLNPGAHGFSEVLYALASAANNGSAFAGLSADTVWYNTVLGVVMLLG RFLPMVFVLALAGSLAGQQPVPVTAGTLPTHRPQFIGLLTGVILIVVGLTYFPALALGPLAEG LR
5E-221	744.1	29.3	6E-221	743.9	20.3	1	1	K7WVS0_9NOST	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ANA_C11906	Anabaena sp. 90	564	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena sp. 90	46234	>tr|K7WVS0|K7WVS0_9NOST Potassium-transporting ATPase potassium-binding subunit OS=Anabaena sp. 90 GN=kdpA PE=3 SV=1 MLQGWIQIALTLIIVIATTPLLGRYIACVFLGESTLLDSVLNPIERIIFVLIGVRPQDEMTGWQYA KAVLYSNIVMGILVFTILITQAWLPFNPTGLGTPTWDTALHTTFSFLTNTDQQHYSGETTLSY ASQTFALSFLMFVSSATGLSVGIAFIRGLTGRTLGNFYIDITKSITRILLPMSIIMGLLLIMAGVP ETLAGVATATTLEGATQAIARGPVAHMEAIKQIGENGGGFFAINSAHPFENPSGFSNLLQTW GMISIPTALIYTGVVFANNLKQAWLAFWMVFTIFTILWIVTTIGEYQGNPLVNSLLGSQQPNL EGKEVRFGWAQSSLFATITTGTMCGAVNALLDSFMPPGGFVFLFNLFLQIVWGGQGTGTA YLFIYYILAVFLTGLMVGRTPEFLGRKIEKKEIVLSSVVLLVHPFAILIPWAIVFAFPDALSGISN PGFHGVSQVVYEYASAAANNGSGFEGLADSQPAATGLWWNLSASFSILAGRYIPIIALLLLA DSMSNKQPVPMTAGTLRTDTGLFTGVTGGVILILGALTFFPVLVLGPIAEWFLISK
5E-221	744.1	28.8	6E-221	743.8	20	1	1	F9ZPN8_ACICS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Atc_0137	Acidithiobacillus caldus (strain SM-1)	586	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus caldus, Acidithiobacillus caldus (strain SM-1)	990288	>tr|F9ZPN8|F9ZPN8_ACICS Potassium-transporting ATPase potassium-binding subunit OS=Acidithiobacillus caldus (strain SM-1) GN=kdpA PE=3 SV=1 MMPSILLTLTLLVVTIILAIPLGRYMYRVYQGENFWASKLLAPVERALYRVSGISPDQEMDWK RYAITLLVFSLFGGLFLYALLLAQRSLPLDPLHFRGVPAGSAFNTAVSFLTNTNWQDYSGGS TMSYLSQMLGLTVQNFLSAAVGITFLLPLIRAFSRHSTRDVGNFWVDLTRTVLYVLLPLASIL AIALMEQGVVQTLVADVSVHLVAPFLSHGKEIVSQTLHVGPVASQEAIMMLGNNGGGFFNM NDAHPFENPTGLTNLLETGAMILIPIALVFLFGHMVQSKRNAWIILVAMLVIFVPLTFISQHFEL AGNPLLTQMGVNQSNTVNLAGGGNLEGVEDRIGAAASALFATVATATSTGAANCAYDSLM PLSGGINLFLMQMGEVVFGGVGSGLASFLTFMIFAVFIGGLMVGRTPEFLGKKIESYEIKMA SLSILIMPLLVLIGTAIAVSTHAGRAGVFNPGPHGFSEILYAVTSPANNNGSAFGGLSNDARF YNILTGMCMLFGRYWVYLPLLAMVGSLVEKKRVPASVGTLATDTPIFMGLTVGVILLVGALN FFPALALGPIAEQLTPVTSVLTHRG
6E-221	743.8	33.8	7E-221	743.6	23.4	1	1	B7J712_ACIF2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA-2 kdpA AFE_2475	Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	583	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus ferrooxidans (Thiobacillus ferrooxidans), Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	243159	>tr|B7J712|B7J712_ACIF2 Potassium-transporting ATPase potassium-binding subunit OS=Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) GN=kdpA-2 PE=3 SV=1 MIFTIMLTAAVLLLTILLALPLGRYMHRVYAGERFWATRLMSPVERGLYRVIGVSASEEMDW KRYAIALLIFNLIGGVFLYALLLAQGALPLNPLHFGGVPSASAFNTAVSFITNTNWQDYSGGS TMSYLSQMLGLTVQNFLSAATGITIVLPIIRALARHKTKNLGNFWVDMTRTVLYVLLPLSALFA LILMEQGVVQTLTGVVRADLIAPFVSGGKTILHQMIHVGPVASQEAIMMLGNNGGGFFDMN DAHPFENPTGFTNFLEMVAMILIPSALVFMFGHMVKAKRTAWAIMIATLVLFVPLTVVSEHFE LLGNPLLTHLGATQANMASLAGGGNLEGIEDRIGAGASALFGSIATATSTGAANSTYDSFMP LSGGINLFFMQMGETVFGGVGTGLATVLAFMIFAVFLGGLMVGRTPEFLGKKIESFEIKMAS LAILIMPLLVLIGTAVAVSTTAGRAGALNPGAHGFSEILYAITSPANNNGSAFDGLSSDTTFYN LITGMAILFGRYWPYLPLLALAGALAGKKKIPAGAGTLTTHTPIFIGLLVGVILLVGALNFFPAL ALGPIADQLAPISTLTH

6E-221	743.8	26.4	7E-221	743.5	18.3	1	1	D2Q289_KRIFD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Kfla_6794	Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Kribbella, Kribbella flavida, Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	479435	>tr|D2Q289|D2Q289_KRIFD Potassium-transporting ATPase potassium-binding subunit OS=Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399) GN=kdpA PE=3 SV=1 MSDTAAGLLQAALLLLLAAAYRPLGGYLARVYTAGRDTRVERGAYKMLGVDAKADQTWA VYARSVLAFSVVGLVLLYLLQRLQAYLPLSLGLPGVGSGSAFNTAASFVSNTNWQSYSPEA TMGHLIQFAGLAVQNFLSAAVGIAVAIALIRGFSRSRTERLGNFWVDLTRTVLRVLLPLAVVG GLVLVATGVVQNFSGAHEVTTLTGQPQSVPGGPVAGQEVIKQLGTNGGGFYNANSGHPFE NPNPVSNLFEIFLLLLLIPVCLTRTFGLLVKDTRQGSAVLGVMATLWAVFTIAATAFETRGGGS ATQAAGAAMEGKETRFGEWASALFAASTTGTSTGAVNAAHDSFTPLGGGTALFHMMLGE VSPGGAGSGLYGMLVLAVLAVFVAGLMVGRTPEYLGKKVTAREMKLVSLYILTTPALVLTGS AIAMGLATARASIFNTGSPHGFTEVLYAFTSAGNNNGSAFGGLSANVPFYNTALGVVMLLG RFLPILLVLALAGSFARQQPVPVTDGTLPTHRALFVTLLVGVVLIVTGLTYFPALTLGPLAEGL
1E-220	743	32.9	1E-220	742.8	22.8	1	1	A0A0F5L065_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VW35_18805	Devosia soli	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia soli	361041	>tr|A0A0F5L065|A0A0F5L065_9RHIZ Potassium-transporting ATPase potassium-binding subunit OS=Devosia soli GN=kdpA PE=3 SV=1 MNWQGWAEIALTLGLALALGWPLGVFMSRVWNGEKTWLDPVLRPVERVFYAATGVDPNK SQSWIGYGASLIAFNLFGFVLLYAMLRLQGVLPLNPQGFAGVTPDLAFNTAVSFVTNTNWQ NYGGETTMSHFTQMAGLTVQNFVSAATGAAIAAALARAFAGNKLSGVGNFWADLVRTTLY VLLPLSIVFGVALIGTGVVQNFAASVTATTLDGANQTISVAPAASQLAIKQLGINGGGIFNVNS AHPFENPSPLSNLLTAVAINTLGWAAFFAFGRTAIARKDIRALATAAILILAAGASVIYVTESQP APALVAAGVENPVYMEGKETRFGIASTAAWAAQTTGASNGSVNGMHDSFSPLGGGMAML LMMLGEILPGGIGSGIAIMVVMAVLSVFVAGLMVGRTPEYLGKKIEAREIQFAMVALLIVPLST LGFAALTVAWPGALASLFNPGAHGLSELLYAYTSATANNGSAFGGISANVPWWNTTLGFA MLLGRFVPIVAVLAIAGSLAAKPKLAPSAGTLPTQGTLFVGLLIGIIILGALQYFPALALGPIVE HFQVLEALGAN
1E-220	742.9	27.1	1E-220	742.6	18.8	1	1	KDPA_STRCO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SCO3718 SCH35.06	Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albidoflavus group, Streptomyces coelicolor, Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	100226	>sp|Q9X900|KDPA_STRCO Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) GN=kdpA PE=3 SV=1 MSPVLAGVLQLLALTAALALAHVPLGNYLARVYSSPKHLRIEKWIYKSIGADPDTEMRWPAY LRGVLAFSLAGVLFLYLLQRLQGVLPGSLGFASIDPDQAFNTAASFVANTNWQSYYGEQAM GHVVQTAGLAVQNFVSAAVGIAVAVALVRGFARSRTGELGNFWADLVRGVVRVLVPIAAVG AVILVACGVIQNFSGIHEVGQFMGGTQEWNGGAVASQEVIKELGTNGGGYFNANSAHPFE NPTPFTNLFEIFLILLIPVALTRTFGIMTGSVRQGYAILGTMAAIWAGFVALMMWTEFAHHGP ALQAAGGAMEGKELRFGIGGSSLFAVTTTLTSTGAVDSFHSSYTGLGGGITMLGMMLGEIA PGGVGSGLYGMLVMAVVAVFIAGLMVGRTPEYLGKKIGTREIKFAACYILITPALVLVFTAAA MALPTPGDSMTNSGAHGFSEILYAYTSASNNNGSAFAGLNADTQWFNSTLGLAMLLGRFV PMVFVLALAGSLARQQPVPATAGTLRTEKPLFAGLLAGAVLIITGLTYFPALALGPLAEGLAA
1E-220	742.8	29.1	1E-220	742.6	20.2	1	1	R7LGH6_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN805_00530	Prevotella sp. CAG:891	568	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:891	1262937	>tr|R7LGH6|R7LGH6_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Prevotella sp. CAG:891 GN=kdpA PE=3 SV=1 MNTEIIGIVAQVVLMVVLSYPLGKYIARVYQGKKVWTDFMKPIEGWIFRLSGIHPDEEMNWK QFLRALLTVNLFWFIWGMVLLTLQGWLPLNPDGNLAQSAHQAFNTCISFMVNCNEQHYSG ESNLTYFTQLFVIMLFQFLTAATGMAAMAGVMKALGEKTTQTIGNFWKFLVLSCTRILLPLSL VVGFILITQGIPMGFDGKMEVTTLEGETQYVSQGPAAAIIPIKQLGTNGGGYFGVNSSHPLE NPTYLSNMIECWSILIIPMAMAFAFGFYVNRKKLGYSIYGVMLVAFLIGVCVNVSQEMGGNP RIDAMGIAQENGSMEGKEIRLGSGATGLWSVVTTVTSNGSVNGMHDSTLPLSGMIEMLNM QINTWFGGVGVGWMNYFTFLIIAVFISGLMVGRTPEFMGHKVEAREMKIASIVALLHPFVILV GTALAAYLYVHAPAFVASEGGWLNNPGSHGLGEMLYEFTSCAANNGSGFEGLGDNTWFW NFSCGIVLILSRFIPIIGQVALAGLLAQKRYIPESAGTLKTDTVTFAVMTFAVIFIVAALSFFPAQ ALTTLTEHFSL
2E-220	742.5	22.5	2E-220	742.3	15.6	1	1	C5C4A0_BEUC1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bcav_3782	Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	558	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Beutenbergiaceae, Beutenbergia, Beutenbergia cavernae, Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	471853	>tr|C5C4A0|C5C4A0_BEUC1 Potassium-transporting ATPase potassium-binding subunit OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432) GN=kdpA PE=3 SV=1 MTTESVVVWAALAQIALVLAVLAAVHVPFGAYMARVVSSPKHLRVERAGYRLARVDPDADQ TWSTYLLSLLGFSLVSVLFLFGLGRLQEYLPWNLGFVGLDPAGAWNTAVSFVTNTNWQWY SGEAAAGHLYQMAGLAVQNFVSAAVGMAVAIALVRGFARSRADGRIGNFWSDLTRSVTRIL LPIAFVAAIILMANGVIQNLLPHTPLDTLMGDSQSALGGPVASQEAIKELGTNGGGFFNANSA HPFENPNPFTNLLEILLILVIPFTLPRTFGILVGDRRQGAAIAGVMATLFAAGLALTTWAEMAG PGAAPQAAGAAMEGKEARFGLAASALFGASTTGTSTGAVNSMHDSFTAPGGGVVMFNML LGEIAPGGVGAGLYGMLIVAVVSVFIAGLMVGRTPEYLGKKIGQREITLVALYVLTMPAIVLLG TAASVVLPAGLAGIQESGPHGLSEVLYAFTSAGNNNGSAFGGLTTGTPYYNTLLGLAMLAG RFVPIALVLALAGRLASQKAVPAGSGTLPTHRPLFVGLTSGVALVVVGLTFIPVLSLGPIVESL S

2E-220	742.5	26	2E-220	742.3	18	1	1	KDPA_STRGG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SGR_2679	Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces griseus group, Streptomyces griseus subgroup, Streptomyces griseus, Streptomyces griseus subsp. griseus, Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	455632	>sp|B1W3K2|KDPA_STRGG Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350) GN=kdpA PE=3 SV=1 MSSQVAGLLQLTALIAALALAYRPLGDYMARVYSSEKHYRPEKWMYKAIGANPAAEMRWP AYLRGVLAFSAMSVLFLYLMQRVQGSLPGSLGFSSIDPDQAFNTAASFVANTNWQSYYGE QAMGHVVQTGGLAVQNFLSAAVGMAVAVALVRGFARSRTGELGNFWADLVRGTVRILVPI SVIGAIVLVAAGAIQNFSGIHQVGQFAGGTQEWNGGAVASQEAIKELGTNGGGYFNANSAH PFENPNPLSNLFEVFLILLIPFALTRTFGRMAGSLKQGYAILGAMAVIWIGFTALMMWTEFAH RGPAFEIAGGAMEGKEARFGIAGSSIFAVATTLTSTGAVNSFHSSYTGFGGGITLLGMQLGE IAPGGVGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGTRQIKFAACYILITPALVLGFTAVA MALPTPADSMTNSGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNTTIGIAMLLGRFLP MVFVLALAGSLAEQQPVPETAGTLRTDKPLYSGLLVGTILIITGLTYFPALALGPLAEGLAS
2E-220	742.4	29.5	2E-220	742.1	20.4	1	1	H2JYA2_STRHJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SHJG_2398	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	1133850	>tr|H2JYA2|H2JYA2_STRHJ Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces hygroscopicus subsp. jinggangensis (strain 5008) GN=kdpA PE=3 SV=1 MGPVLAGVLQLLALIGALALAYVPLGTYMARVYSSDRHLRVEKWIYRGIGANPDTQMRWPA YLRGVLAFSVAGVLFLYLLQRLQGVLPGSLGFSSVDPAQSFNTAVSFVTNTNWQSYYGEQT MGHVVQTAGLAVQNFVSAAVGMAVAVALVRGFARSRTGELGNFWADLVRGTLRVLVPIAA VAAVVLVACGAIQNFSGIHEVGQFMGGSQQWNGGAVASQEAIKELGTNGGGYFNANSAH PFENPTPLTNLLEIFLILVIPFSLTRTFGVLVGNVKQGYAILATMGVIWLGFTALMMWTEFAHR GPALQIAGGALEGKEVRFGVGGSSIFAVATTLTSTGAVDSFHSSFTGLGGGITMLGMMLGEI APGGVGSGLYGILILAVIAVFIAGLMVGRTPEYLGKKIGAREMKLAAAYILVTPALVLVFTAAS MALPTPPHSMLNPGAHGFSEVLYAFASAANNNGSAFAGLNANTDWFNTMTGLAMLFGRFL PMVFVLALAGSLAEQKPIPVTAGTLRTEKPLFTGLLVGAILIITGLTYFPALALGPLAEGLA
2E-220	742.1	26.7	2E-220	741.9	18.5	1	1	B2HPR5_MYCMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MMAR_0631	Mycobacterium marinum (strain ATCC BAA-535 / M)	552	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium marinum, Mycobacterium marinum (strain ATCC BAA-535 / M)	216594	>tr|B2HPR5|B2HPR5_MYCMM Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium marinum (strain ATCC BAA-535 / M) GN=kdpA PE=3 SV=1 MAGILFLASLMVALVAVHVPFGDYMYRVYTSDKHSRVERWIYRAIGADPHAEQGWGAYAR SVLAFSASGILVLFTFQLMQGKLPLHLNDPATPMNPVLAWNTAVSFVTNTNWQAYSGESTQ GHLVQMAGLAVQNFVSAAVGMAVAMAVVRGFARRHTGDLGNFWVDLVRGTIRILLPVSVV AAIVLVAGGAIQNFHLRDQIVSTLSGAEQTITGGPVASQETIKDLGTNGGGFFNVNSAHPFE NPTAWTNWVEIFLLLVISFSLPRTFGRMVGSPKQGIAIASVMAVLALISWSTTMSMQLQRHG TVPTAVGAAMEGVEQRFGVANSAVFAASTTLTSTGSVDSFHDSYTSLGGLVLLLNMQLGEV APGGVGSGLFGMLILAVITVFIAGLMVGRTPEYLGKKITPREIKLAATYLLISPLIALTGSAVAM AMPGQRAAMLNTGPHGLSEVLYAFTSAANNNGSAFAGISVNTDWYNTALGLAMVFGRFLPI VLVLALAGSLVRQGTTPESIGTLPTHRPQFVGLVAGVTLILVALTFLPMLALGPLAEGIH
2E-220	742	25.7	2E-220	741.8	17.8	1	1	K9PF24_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cal7507_1560	Calothrix sp. PCC 7507	581	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix sp. PCC 7507	99598	[illegible] OS=Calothrix sp. PCC 7507 GN=kdpA PE=3 SV=1 MLQGWIQIALTLLIVVAITPFFGKYIARVFLEQSTVLDLILNPVERVLYSLVGVKTKENMTGWQ YARAILYSNIAMGLLIFLIIMSQGWLPLNPTKIGAPTWDTALHTTISFITNTNQQHYSGETYMS YASQMWGLGYHMFTSAATGIAVGIAFIRGLTGRPLGNFYVDLIRSITRILLPICIVGAIALIASG VPETLAGPAVFPTLEDPNISQAIARGPVAHFEIIKQLGENGGGFFAINSAHPFENPSGFSNLI QIVAMLSIPTALIYTGVFANDTKQAWLVYGMVGVIYLGFLIVTAIGEYNGNPAVNTLLGSQQ PNLEGKEVRFGWAQSILFAVSTTGTMCGAVNSLHDSFMPNGGFVTLSNMFLQIIWGGQGT GTAYLFAYLILAVFATGLMVGRTPEFLGRKIEKREVVLASFLILMVHPIAILIPAGITLAFPEQLA GISNPGFHGFSQVIYEYASAAANNGSGFEGLGDSQPSPLAIATGAKTTVTALWWNLSTCFS LLAGRYIPIFGLLLLCDSMSRKQLVPLTSGTLRTNTGLFTGVTAGVILILGALTFLPVLALGPIG EAFWIAKGIG
4E-220	741.2	23.9	5E-220	740.9	16.5	1	1	A0A0F4K4N1_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VR46_25140	Streptomyces sp. NRRL S-444	559	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-444	1609134	>tr|A0A0F4K4N1|A0A0F4K4N1_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. NRRL S-444 GN=kdpA PE=3 SV=1 MSPVTAGVLQLLALVAALALAYCPLGDHMARVYSSKKHYRPEKWIYKVIGANPWAEMRWP AYLRGVLAFSAVSVLFLYLLQRVQGVLPGSLGFVSIDPDQAFNTAASFVANTNWQSYSGEQ AMGHVVQTGGLAVQNFVSAAVGMAVAVALVRGFARSRTGELGNFWADLVRGTVRILLPISL IGAIVLVACGAIQNFAGIHEVGQFVNGHSTAAGQQWNGGAVASQEVIKELGTNGGGYFNAN SAHPFENPTPFSNLFEIFLILLIPFALTRTFGRMVGSLRQGYAILATMATIWLGFTALMMWTE FAHHGPAFDIAGGAMEGKETRFGIGASAIFSVATTLTSTGAVNSFHSSYTGLGGGIQLLGMQ LGEIAPGGVGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGTREIKLAACYILITPALVLCFTA AAMALPTPGNSMANPGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNSTIGIAMLLGRF LPIVFVLALAGSLAEQQPVPETAGTLRTDKPLYAGLLVGTITIITGLTYFPALALGPLAEGLAS

4E-220	741	26.9	5E-220	740.7	18.7	1	1	L8EUC3_STRRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SRIM_19087	Streptomyces rimosus subsp. rimosus ATCC 10970	558	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rimosus, Streptomyces rimosus subsp. rimosus, Streptomyces rimosus subsp. rimosus ATCC 10970	1265868	>tr|L8EUC3|L8EUC3_STRRM Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces rimosus subsp. rimosus ATCC 10970 GN=kdpA PE=3 SV=1 MSPILAGVLQLIALVAALALAYRPLGDYMAATYSSRKHLRVEKIIYRCIGANPDTEMRWPAYL RGVLAFSLAGVLFLYLLQRLQGSLPLSFGFASISPDQAFNTAASFVANTNWQSYSGEQAMG HVVQTAGLAVQNFVSAATGMAVAIALVRGFSRARTGDLGNFWADLVRGTVRVLIPIAVIGAL VLVACGAIQNFSGIHEVGQFMGGTQQTNGGAVASQEVIKELGTNGGGYFNANSAHPFENP NGFTNLFEVFLILVIPFSLTRTFGKLVGNVRQGYAVLATMGVIWLGFTALMMWTEFAHGGP ALQAAGGALEGKETRFGIGGSSIFSVATTLTSTGAVDSFHDSFTAFGGGIQLLGMMLGEIAP GGVGSGLYGMLVMAVIAVFIAGLMVGRTPEYLGKKIGTREIKLAACYILITPTLVLGFTAASMV LPDALGSILNTKALGAGPHGFSEVLYAFTSGANNNGSAFGGLNANTPWYNTTIGLAMLLGR FLPMVFVLALAGSLAGQKPVPETAGTLRTEKPLFAGLLVGTILIITGLTYFPALALGPIAEGLS
5E-220	740.9	28.1	5E-220	740.7	19.5	1	1	G8TDF8_NIAKG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Niako_4132	Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10)	571	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Niastella, Niastella koreensis, Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10)	700598	>tr|G8TDF8|G8TDF8_NIAKG Potassium-transporting ATPase potassium-binding subunit OS=Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10) GN=kdpA PE=3 SV=1 MNTELFGVIITFLLTVLLAWPLGKYIARVFKGERTITDFMNPVERFIFRVSGINPNASMDWKQ FLKAMLSINLLWFVYAFFALLFQDKLPLNPDGNPAQTPDLAFNTAISFLVNCNLQHYSGETGL TYFTQLAVITFLQFVSAATGIAALLGLLNGLKEKTTNNLGNFWNLLVKSITRILLPLCIIGGIIMA FNGTPASFDGKDSIVTLQGDSVQVSRGPAAGMIAIKHLGTNGGGWFGANSAHPLENPSYF TAMLQLVMQVVIPIAMIFAMGFYIQRKKFAYVIFGVMTIGMLCLLIPTIVTEIHGNPAIARLGVT QATGAMEGKEVRFGPALSGYWSIVTTIISTGSVNSMHDSSMAISGLMQLLAMMINAFYGGC GVGILNYYIYIIIAVFISGLMVGRTPEFMGHKVEAREIKIASMVWLLSAILVKGGAAFAAYMVA HHPDVAWAVKPSAWLNNPSYHGFSEMLYEFTSANANNGSGFEGLGDNNIFWNVSTGIVLI LARFIPIIGPLAIAGLLANKKFIPESPGTLRTDSLTFGAMTFAVIVIVNALSFFPALALGPIAEYFS LQ
7E-220	740.4	28.8	8E-220	740.1	19.9	1	1	H8KMI0_SOLCM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Solca_3775	Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) (Flexibacter canadensis)	571	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Solitalea, Solitalea canadensis (Flexibacter canadensis), Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) (Flexibacter canadensis)	929556	>tr|H8KMI0|H8KMI0_SOLCM Potassium-transporting ATPase potassium-binding subunit OS=Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) GN=kdpA PE=3 SV=1 MNTEIIGVIFTYAITVLLAIPLGKYIAKVFGGEKTWSDFMAPMESLFFKLSGINPKQEMNWKQ FLKALLTINMVWFVFGFLLLLFQGALPLNPDGNPSQTPDLAFNTIISFMVNCDLQHYSGESG VTYLTQLFVMNFLMFVSAATGIAALVALLNALKAKTTNNLGNFWEIFVKTNTRILLPLCVVVAT ILIFNGTPASYAGKDAIVTLQGDSVQVSRGPAAGMIAIKHIGTNGGGWFGANSAHPLENPNY ITAVTELVAQVLIPIAMIFALGFYLKRKKLSYVIYGVMTIGMLCLVVPTVVSEINGSPAIEKLGIA QPSGAMEGKEVRFGPALSGYWSTVTTIISTGSVNSMHDSSMPASGMFQLLGMMINSFYGG CGVGILNYFIYIIIAVFISGLMVGRTPEFMGHKVEAREVKIAALITLLSPFLILAGTALSSFMVTH HAEIGWATKPAAWLNNPDFHGFSEMLYEYTSANANNGSGFEGLGDNNIFWNVTTGFVLIL GRFLPIIGPVAIGGLLAGKKYIPESAGTLKTDSLTFGVMTLTVIIIINALSYFPALALGPIAEYFTM K
9E-220	739.9	28.9	1E-219	739.7	20	1	1	I3THP9_TISMK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TMO_0448	Tistrella mobilis (strain KA081020-065)	566	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Tistrella, Tistrella mobilis, Tistrella mobilis (strain KA081020-065)	1110502	>tr|I3THP9|I3THP9_TISMK Potassium-transporting ATPase potassium-binding subunit OS=Tistrella mobilis (strain KA081020-065) GN=kdpA PE=3 SV=1 MISTDFGRIALYLAILALIAVPLGRWTVAAASSSGRLGRVFAPVEAGILGLSGVRAGRESSWL GYALGLITFNYAGFLLLYGVLRLQGVLPWNPAGIPPLDPAVAFNIAISFVTNTNWQAYSGEA QLSSFSQAFGLGVQNFLSAATGIAVMVALARGFARAETPTIGCLTTDVTRITLRLLLPLAVAV TILLVLQGVPQVMTGTLASVGLDGHAQAIPLGPVASQVAIKQLGTNGGGFYGVNSAHPLEN PTAWSNLIEVVAILALPAAMPFAFGRLAGDPRQGRALFLAMLIPFAVFVGLTVWAETTGNPI HHALGLAGPNMEGKEVRFGAADSAIWAAATTAASNGSVNAMHDSFTPLGGMVAMIGMML GEVIFGGVGSGLYGLIIFAVIAVFAAGLMVGRTPEYMGKKIEAREMTLAMLALIGLAVAMLVP AALSAVLPAGRAAVQDAGPHGLSEILYAYASAAGNNGSAFAGFGAAQTFHAIAVGIAMMIGR YLPVVVVLAIAGSLAAKKKIPATAGTLPTHGPLFIGLLIGTVAIIGGLTYFPALALGPVAEHLSM LLGRTF
1E-219	739.6	24.8	1E-219	739.4	17.2	1	1	A0A022LX23_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA H489_014350	Curtobacterium flaccumfaciens UCD-AKU	560	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Curtobacterium, Curtobacterium flaccumfaciens, Curtobacterium flaccumfaciens UCD-AKU	1292022	>tr|A0A022LX23|A0A022LX23_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Curtobacterium flaccumfaciens UCD-AKU GN=kdpA PE=3 SV=1 MGAADLWAGIAQVATLVLLLVVAYRPLGDWMAKVFTPVRHNRVERGVYRLIGVDPDAEQS WPVYLRGVLLFSVAGLLLVYLLQRIQVVLPGDLGLPAVGPSLAFNTAASFVSNTNWQSYSP EVTLGYSVQMAGLAVQNFLSAAVGLSVAVALVRGFARRKSGTLGNVWVDVVRGLGRLLLP GAFVFAIILVAGGVVQSWGSGTDVTTLIGGTQHIPDGFVASQEAIKELGTNGGGYFNANSAH PFENPQAWTNLVEIFLMLVIPFSLPRTFGRLVGDDRQGYAILAVMGAIFLVSLSVMSIAELGG GGVATHAAGAAMEGKESRFGILGSTLFSTATTSTSTGAVNAMHDSYTPIGGMMALVNMML GEVTPGGVGSGLYGMLVLAVITVFIGGLLVGRTPEYLGKKIRAKEMTFAALYILVTPTLVLLAT GLSLVIPGVREQVLGTSIFNPGNHGLTELLYAFTSGANNNGSAFGGLTANTTWMNSSLGVV MLLGRFVPMVFVLALAGSLAAQDRVPETAGTLPTHRPLFIVLLGGVAVIVTALTYFPVLALGP LAEGLS

1E-219	739.5	23.4	1E-219	739.3	16.2	1	1	A0ZL39_NODSP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NSP_19410	Nodularia spumigena CCY9414	561	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nodularia, Nodularia spumigena, Nodularia spumigena CCY9414	313624	>tr|A0ZL39|A0ZL39_NODSP Potassium-transporting ATPase potassium-binding subunit OS=Nodularia spumigena CCY9414 GN=kdpA PE=3 SV=1 MGQGFWQIGLTLCIVIAIVPVLGRYMARVFLGERTLLDPLMNPIERSFFLLAGVGRKDDLTG GEYIRAVLYSNLVMGILVYSLISFQKLLPWNPNGFDAPSWDILLHTVVSFVTNTDQQHYTGE TTLSYFSQVAALGFLMFTSAATGLAVGIAFIRGLTGKKLGNFYVDLTRAITRILLPISVIGAIALV FCGVPQTLDQTLVVQTLEGRTQYIARGPVASFEMIKMLGDNGGGFFGVNSAHPFENPNGA ANLIEIIAMIAIPASLIYTYGVFAKNIKQAWLLFWMVFVVLIILISVALGGEQEGNPLVNGTLGLE QPNLEGKEIRLGWTQTALWAVITTATMCGAVNGMHDSLMPSGLFSTLFNLFLRMIWGGQG TGTAYLFIYLILAVFLAGLIVGRTPEFLGRKIERREIILASVVLVIYPIVVLIPSAITLAYPFSLSGIT NPGFHGISQVVYEYASAAANNGSGLQGLNNNTLWWNLSTCLSMFAGRYIPIIALLLLADGM SRKPTIPETPNTLKTDSLLFTTATAGLVVILGMLAFFPVLVLGPVAESFKLASGS
2E-219	739.2	27.1	2E-219	739	18.8	1	1	Q8YSD4_NOSS1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA all3154	Nostoc sp. (strain PCC 7120 / UTEX 2576)	579	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	103690	>tr|Q8YSD4|Q8YSD4_NOSS1 Potassium-transporting ATPase potassium-binding subunit OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=kdpA PE=3 SV=1 MLQGWTQIALTLLIVVAITPVFGRYMARIYQEQRTVFDPLLNPVERLIYVLIGVQTRENMTGW QYARAILYSNLVMGLFVFLLMMNQGWLPLNPTNIGAPTWDTALHTAISFITNTNQQHYSGET SLSYGSQMFGLGYHMFTSAATGLAVAITFIRGLTGRPLGNFYVDLTRTITRILLPICIVGGIAL MAAGVPETLAGPIVLPTIENPNISQAIARGPVAHYEIIKELGENGGGFFAINSAHPFENPNGFS NLIEIMAMLSIPTALIYTYGLFANNIKQAWLVYGMVGVIYLAFIIITAIGEYNGNPDVNALLGSIQ PNLEGKEVRFGWAQSALFTVSTTATMCGAINSLHDSFMPNGGFVTLSNMFLQIVWGGQGT GTAYLFAYLILAVFVTGLMVGRTPEFLGRKIEKREVVLASFLILLVHPIAIMIPSAITLAFSEQLA GISNPGFHGFAQVIYEYASAAANNGSGFEGLGDSQASPLAIASGAQPTITGLWWNLSTSFS LLAGRYIPIIGLLFLADSICRKQQVSFTSGTLRTDTGLFTGVTAGVILILGALTFFPLLAFGPIGE AFWIGNG
2E-219	739	32.2	2E-219	738.8	22.3	1	1	C7LZF2_ACIFD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Afer_1178	Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)	564	cellular organisms, Bacteria, Actinobacteria, Acidimicrobiia, Acidimicrobiales, Acidimicrobiaceae, Acidimicrobium, Acidimicrobium ferrooxidans, Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)	525909	>tr|C7LZF2|C7LZF2_ACIFD Potassium-transporting ATPase potassium-binding subunit OS=Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP) GN=kdpA PE=3 SV=1 MTFATELIVLAVALAVTWRVLGAYMAGVYEGRYSLLVRLERPVLALVGVSASEEQSWQRYA RSLLVFSGVSIVVTYLIIVSQAHLPLDPQHLVGVPPALAFNTAVSFVTNTNWQNYAGETTMS YFSQMAALAVQNFVSAAVGIAVAIALVRGIARRGRATIGNFWVDTVRGVLWILLPISLVMAVV FVWQGALETLGGPVHVVDALNGVHQVIPRGPVASQEVIKQLGTNGGGYFNANGADPFENP TGLTNVLSIYLILAIPVALTYTFGRMVASVRDGVAVLAAMGIIFGVTLAVALVAEHQPNPAIQH AAGALASRGNLVGKESRFGIDNSTLYNIVSTQTSTGSVNSSMDSYTPIGGLAMMAGMAFGD ITPGGVGSGLYTMLIFAIVTVFIAGLMVGRTPEYLGKKIQRTEIIWASVGVLVMPITVLVATGV AIALPSARAAILNAGPHGFSEVFYAMLSQGNNNGSAFAGLSSNTDFYNIVGGIVMLLGRFGV MVPVLALAGSLAAKEPVPATAGTFDTATPMFAGLLIGVIILVGALNFFPALSLGPIAEAVAHGR FFA
2E-219	738.8	27.4	2E-219	738.5	19	1	1	A0A088QD84_9CORY	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DR71_939	Corynebacterium sp. ATCC 6931	545	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium sp. ATCC 6931	1487956	>tr|A0A088QD84|A0A088QD84_9CORY Potassium-transporting ATPase potassium-binding subunit OS=Corynebacterium sp. ATCC 6931 GN=kdpA PE=3 SV=1 MGFVPVIIVMAALAILYIPLGNYMGRVFTTDKHLGVERGFYRAIGVRPEANQHWTKYTASVL SFSAVSVIFVYLLQRVQQWLPLNHGKGPVSPDQAWNTAVSFTTNTNWQSYSGEEAMTVLT QMAGLAVQNFVSAAVGIAVAVALVRGLANRHGDGNIGNFWVDLTRTVLRVLLPIAAIGAILLI SQGAIQNFSAPQTIQTVTGGSQTIPSGAVASQEVIKELGTNGGGYFNANSAHPFENPNAWT NMLEIFLILLLIPVSLTRAFGVIIGDKRQGWAILSTMAVLYFISLAVVMSSETALQTFQGGGMEG KEMRFGVLPSSFFAVTTTMTSTGAVDSFHSSYSPLAGGMLMLNMLLGEISPGGVGSGLYG MLIIAILTVFIAGLMVGRTPEYLGKRIGVSEITKVCLYVLVMPVLVLAGVGISTMLPSTLDSVSA DGPHGFSDLIYAFTSASNNNGSAFAGFGADTPWFNMSLGFAMLFGRFLPIAMVLGLAGDFA KQRPAAETAGTLPTHRPQFVGLTVAIAIIVSALTFLPTLVLGPLTEALS
2E-219	738.7	31	3E-219	738.5	21.5	1	1	A0A0A8EN80_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GZL_02859	Streptomyces sp. 769	551	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	1262452	>tr|A0A0A8EN80|A0A0A8EN80_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. 769 GN=kdpA PE=3 SV=1 MLQLTALIAALALAYRPLGDYMAAVYSSPRHLRVEKVIYRCIGANADTQMRWPAYLRGVLAF SLAGVLFLYLIQRLQGHLPLSLGFAAISPDQAFNTAASFVANTNWQSYSGEQAMGHVVQTG GLAVQNFVSAATGMAVAVALVRGFARSRTGELGNFWADLVRGTIRVLIPISIIGALVLVACGA IQNFSGIHEVGQFMGGAQQTNGGAVASQEVIKELGTNGGGYFNANSAHPFENPTAFTNLF EIFLILVIPFALTRTFGKLVGNVKQGYAILATMGIIWLGFTALMMWTEFAHGGAALQAAGAAM EGKENRFGVGSSAIFSVATTLTSTGAVDSFHSSFTAFGGGLQLLGMMLGEIAPGGVGSGLY GMLVMAVIAVFIAGLMVGRTPEYLGKKIGTREIKLAACYILITPTLVLGFTAASMVLPDALGSM LNTKAVGAGPHGFSEVLYAFTSGANNNGSAFAGLNANTPWYNTTIGLAMLLGRFLPMVFVL ALAGSLAEQQPIPETAGTLRTEKPLFAGLLVGTILIITGLTYFPALALGPLAEGLS

3E-219	738.2	28.7	4E-219	737.9	19.9	1	1	Q4JUS0_CORJK	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA jk1269	Corynebacterium jeikeium (strain K411)	550	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium jeikeium, Corynebacterium jeikeium (strain K411)	306537	>tr|Q4JUS0|Q4JUS0_CORJK Potassium-transporting ATPase potassium-binding subunit OS=Corynebacterium jeikeium (strain K411) GN=kdpA PE=3 SV=1 MSGAITGWIPVIMVIIALAACYVPLGNYMAATFTSKKHNAFERGFYRLIGVNPDGQQKWTRY CASLLAFSAISVVFVYLLQRVQQALPLNHGKEPVHWDQAWNTAVSFTTNTNWQSYSGETA MTILTQMAGLAVQNFVSAAVGITVAIALIRGLANRMGNGQIGNFWVDLTRAVFRVLLPMAIIG AILLISQGAIQNFHAPTTVDTITGGQQTIPGGAVASQEVIKELGTNGGGYFNANSAHPFENPN AWTNMLEIFILVIPVSLTRTFGKMVNDTRQGWAVLAAMAVLYFSSLAIVMSNETSLAAFQG GGMEGKEYRLGVLPSSFFAVTTTMTSTGAVDSFHSSYHPLAGGMLILDMMLGEISPGGVG TGLYGMLMIALLSVFVAGLMVGRTPEYLGKRIGVSEITKVSLYILVMPTLVLAGVGISTMLSST RDSVSADGPHGFSDIVYAYTSASNNNGSAFAGFGADTPWFNITLGLCMLLGRFLPIIFALALA GSFAKQKPAAETAGTLPTHRPQFVGVMVGIAIIVGALTFLPTLVLGPLTEALS
3E-219	738.2	30.7	4E-219	738	21.3	1	1	G2P881_STRVO	Potassium-transporting ATPase A chain (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Strvi_6695	Streptomyces violaceusniger Tu 4113	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces violaceusniger, Streptomyces violaceusniger Tu 4113	653045	>tr|G2P881|G2P881_STRVO Potassium-transporting ATPase A chain OS=Streptomyces violaceusniger Tu 4113 GN=kdpA PE=3 SV=1 MGPVVAGVLQLLALIGALALAYVPLGNYMAKVYSSEKHWRVEKWIYKGIGANPDTEMRWA SYLRGVLAFSAAGVLFLYLLQRLQGSLPGSLGFSSIEPAQAFDTAASFVTNTNWQSYYGEQ AMGHVVQTAGLAVQNFVSAAVGIAVAVALVRGFARSRTGELGNFWADLVRGTVRVLVPGA AIAAVVLVACGALQNFSGIHEVGQFMGGSQQWNGGAVASQEAIKELGTNGGGYFNANSAH PFENPTPFTNLFEIFLILVIPLALTRTFGIMVGSVKQGYAILATMVTIWVGFVALMMWTEFAHH GPALEAAGGAMEGKEARFGVGASALFGVSTTLTSTGAVDSFHSSFTGLGGGITMLGMMLG EIAPGGVGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGAREMKLAACYILVTPALVLTFTA ASMALRTPPNSMLNSGAHGFSEVLYAFTSASNNNGSAFAGLNANTDWFNTMTGLAMLLGR FVPMVFVLALAGSLAEQKPVPATAGTLRTEKPLFTGLLVGAILITTGLTYFPALALGPLAEGLA
3E-219	738	34.3	4E-219	737.8	23.8	1	1	KDPA_CAUSK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Caul_4242	Caulobacter sp. (strain K31)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter sp. (strain K31)	366602	>sp|Q3SYU7|KDPA_CAUSK Potassium-transporting ATPase potassium-binding subunit OS=Caulobacter sp. (strain K31) GN=kdpA PE=3 SV=1 MNWQGWAEIALTLGLAVAIGWPLGVYMSRVWNGERTWLDPVLRPVEAVFYKAGGIDAQK SQSWWGYAGALLAFNFVGFLLVYAVLRLQGVLPMNPQGFSGLSGHLSFNTAISFVTNTNW QSYAGETTMSTLSQMLVLTVQNFLSAATGATVAAALARAFVANRGEGVGNFWADLVRTTL YVLLPLSFVVAIVLVALGLPQTLAAGVTAHTLEGADQKISLYAVASQEAIKMLGINGGGVFNA NSAHPFENPTPLTNLITAVSINVLGWAAFFAFGRSVLAKKDIRALVIAASILLSAGAATVYWTE TQVAPAQVAAQVDTSVNMEGKETRFGAPATAAWVAMTTGASNGSVNGMHSSLMPLGGG MAMFLMHLGEILPGGIGSGIAVMIVMAVLAVFVAGLMVGRTPEYLGKKIEAREVQLALLTVLA IPVATLGFSAIAAVLPEALKGLMHSGPHGMSEILYAYTSATANNGSAFAGLTANAPWWDTT MGVAMAMGRFMPIVAVLAMAGSLVGKPKLAPSAGTLPTHGGLFVGLLIGVILILGGLQFFPA LALGPIVEHFQVLAAVAGH
4E-219	737.9	27.2	4E-219	737.7	18.9	1	1	U5QJ68_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GKIL_2710	Gloeobacter kilaueensis JS1	575	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter kilaueensis, Gloeobacter kilaueensis JS1	1183438	>tr|U5QJ68|U5QJ68_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Gloeobacter kilaueensis JS1 GN=kdpA PE=3 SV=1 MATEGFLQIAVTIALMVAIVPLFGTYMARVFQFERTWLDPLFDPIEGLVYRLGGVDSAADMD WWTYARAVLVSNLAMFVPVFTILLFQGSLPFNPNAIAGMSPDTALHTAISFLTNTDQQHYSG ETGTSHFAQMAGLQFLMFTSAATGLAVGVAFIRGLLGRPMGNFYVDLTRSISRILMPISIVFA VVFLSQGVPQNLSALTEVKLTDPYQTTVDNKTGTVATQKLFTGPFASMESIKQLGENGGGS YGVNSAHPYENPNPFTNLVQILLMLSIPTAFIYTFGVMAGNKKQGWVIFWTIFVLFVALVGVA ATSEFFGNPTLNAVLGSANPNFEGQEVRFGWAQTALFATSTTGTMTGAVNGMHDSLTPLA LLATIFNMFMQVIWGGQGTGLAYILVFLIIAVFVTGLMVGRTPEVFGRKIEKREVALASVIFLIQ PIITKVPTAIAVAIPGLISLGNPSYHGLMEPFYEYTSAAANNGSGLGGLTSAVPWWNLTCALV LLLGRYAPIIALLALAGGLQKKQPVPETPGTLRTDTPLFGAVTAGTILILGGLTLFPIAALGPIAE FFANLAGKTF
4E-219	737.9	24.7	5E-219	737.6	17.1	1	1	KDPA_STRAW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SAV_919	Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces avermitilis, Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	227882	>sp|Q82PI3|KDPA_STRAW Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680) GN=kdpA PE=3 SV=1 MSPVLAGVLQLVALIAALALAYRPLGDYMAKVYSSDKHLRVEKWIYKGIGADPDTQMRWPA YLRGVLAFSAVSVLFLYVLQRVQGSLPGSLGFRSIDPDQAFNTAASFVTNTNWQSYYGEQA MGHVVQTGGLAVQNFVSASVGIAVAVALVRGFSRSRTGELGNFWSDLVRGTVRVLLPVSVI AAIVLVACGAIQNFSGIHSVGQFMGGSQQWNGGAVASQEAIKEAGTNGGGYFNANSAHPF ENPGPFSNLFEIFLILLIPFALTRTFGRMVGSLRQGYAILATMVTIWIGFTALMMWTEFAHHG PAFQIAGGAMEGKETRFGVGGSSIFAVATTLTSTGAVDSFHSSFTGLGGGITLLSMQLGEIA PGGTGSGLYGILIMAVIAVFIAGLMVGRTPEYLGKKIGTREIKFAACYILITPALALVFTAAAMA LPTPGHSMTNSGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNTTIGIVMLLGRFVPMV FVLALAGSLAEQKPIPATVGTLRTEKPLFTGLLVGAILIITGLTYFPALALGPLAEGLAS

4E-219	737.8	33.3	5E-219	737.5	23.1	1	1	KDPA_METB6	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mboo_0443	Methanoregula boonei (strain 6A8)	584	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula boonei, Methanoregula boonei (strain 6A8)	456442	[illegible] OS=Methanoregula boonei (strain 6A8) GN=kdpA PE=3 SV=1 MSVNDWAFLVLIGVILALLLIPTGEFMFRVYTGKKTFLSPLFVPVEAWILKACGAGSDEEMD WKSFAVAMMIFSVIGIVFVFILQEVQQFLPLNPLGATAVPWDLSLNTAVSFATNTNWQFYVP ETTVSYLTQMIGLTVQNFMSAAVGMVVLVAFIYGFSRRSSHTIGNFWVLLLRSIWILLPLSFVI ALVLVSQGAPQTLSGPVTVPLLNATNDSGGNIITTQLISLGPAASQIAVKMLGTNGGGFFNA NSAHPFENPTWFTDLVEIVAILLIPVSLCFMFGKMIGSVKKGIAILIAMMILFVPLLGLGIWSEIG GNPAFTPLGISQAPSHLQSGGNMEGKEVRFGPVQSAAFSVITTVTSCGAVNSMHDSFMPL GGLVQIFDIQLGEIVFGGVGSGLYCMLVFVIIAMFIAGLMVGRTPELYGKKIEPYEMKLSTIHIL IPIFLILIGTAIAVSITAGTSMTANPGPHGFSEILYAFSSVSQNNGSAFAGLSSDTFYNLTTAFC MFVGRYAIAIITLALAGAFVAKKIVPPGEGTLQDHRPLFIIWVVFTILIIGALSFLPALSLGPVVE FLIQMGRGVIHV
5E-219	737.5	27	6E-219	737.2	18.7	1	1	G8RR42_MYCRN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MycrhN_3446	Mycobacterium rhodesiae (strain NBB3)	564	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium rhodesiae, Mycobacterium rhodesiae (strain NBB3)	710685	[illegible] OS=Mycobacterium rhodesiae (strain NBB3) GN=kdpA PE=3 SV=1 MSTAAAGILFLISLIIGLALVHVPLGDYMYRVYSADRHLRGERVVYRLIGADPKAEQTWGSYV RCVLAFSAISLLFLFVFQLVQGKLPLHLNDPGTEMTPALAWNTAVSFVTNTNWQAYSGEST QGHLVQMAGLAVQNFVSAAVGMAVAMAFVRALARRDTTYLGNFWVDLVRGSIRILLPLSIIG ALILVVGGTIQNWDLHTQIANTLVGGQQTITGGPVASQEAIKLLGTNGGGFFNANSAHPFEN PTAWTNWVEIFLLSCIAFSLPRTFGRMVGSGKQGYAIVAVMSVIALFSMTLMMTFQVQGHG TVPTAVGSAMEGVEQRFGVPDSAVFADLTTLTSTGAVDSFHDSYTSLGGMMTLFNMQLGE IAPGGVGSGLYGMLVLAIITVFVAGLMVGRTPEYLGKKITPREIKLAATYFLITPLIVLTGTAVA MAMPGLGPHVSRGRASMLNTGPHGLSEVLYAFTSAANNNGSAFAGISVNTDWYNTALGLA MLFGRFLPIIFVLALAGSLAKQGKTPESVGTLPTYRPQFVGMVAGVTVILVALTFLPMLALGP LAEGIHS
6E-219	737.3	23.3	7E-219	737	16.2	1	1	A0A0B5EPV8_9ACTN	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SLNWT_3273	Streptomyces albus	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albus	1888	>tr|A0A0B5EPV8|A0A0B5EPV8_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces albus GN=kdpA PE=3 SV=1 MSPQIAGVLQLLALVAALALAYRPLGDYMATVYSSEKHYRPEKWIYRAIGAHPAAEMRWPA YLRGLLAFSAVSVLFLYLLQRLQGSLPGSLGFSSIDPDQAFNTAASFVANTNWQSYYGEQA MGHVVQTGGLAVQNFLSAAVGMAVAVALVRGFARSRTGELGNFWADLVRGTVRILIPLSVV GALVLVACGALQNFAGIHEVGQFTGGTQEWNGGAVASQEAIKELGTNGGGYFNANSAHPF ENPSPLSNLFQIFLILVIPFALTRTFGRMVGSLRQGYAILGTTAVIWLGFTALMMWTEFAHRG PAFEIAGGAMEGKETRFGIAGSSLFAVATTLTSTGAVNSFHSSYTGFGGGITMLGMQLGEIA PGGVGSGLYGMLIMAVIAVFLAGLMVGRTPEYLGKKIGTRQIKLAACYLLVTPALVLGFTAAA LALPTPGNSMTNSGAHGFSEILYAYTSGANNNGSAFAGLDADTQWFNTTLGIAMLLGRFLPI VFVLALAGSLAEQKPVPTTAGTLRTDKPLYAGLLVGTILLITGLTYFPALALGPLAEGLAS
7E-219	737.1	36.2	8E-219	736.9	25.1	1	1	B7J5L9_ACIF2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA-3 kdpA AFE_2232	Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	583	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus ferrooxidans (Thiobacillus ferrooxidans), Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	243159	[illegible] OS=Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) GN=kdpA-3 PE=3 SV=1 MISTIILTAVVLFLTILLALPLGRYMHRVYAGDRFWATRLMGPVERGIYRVTGVSASEEMGW KRYAIALLIFNLIGGVFLYALLLAQGALPLNPLHFGGVQGGSAFNTAVSFLTNTNWQDYAGG STMSYLSQMLGLTVQNFLSAATGITIVLPIIRAIARHKTKDLGNFWVDMTRTVLYVLLPLSALF ALILMEQGVVQTLTGEVRADLIAPFVSGGKTILHQIMHVGPVASQEAIMMLGNNGGGFFNM NDAHPFENPTALTNFLETLAMILIPSALVFLFGHMANAKRTAWAILISMLMLFIPLTLVSQHYQ LAGNPVFTQLGISQANTASLAGGGNMEGVEDRIGAGATALFATVATATSTGAANGAYDSLM PLSGGVNLFLMQLGEVVFGGVGSGLATFLAFMIFAVFLGGLMVGRTPEFLGKKIESFEIKMT SLSILVMPLLVLIGTALAVTTVAGRAGVFNPGAHGFSEVLYAVTSPANNNGSAFGGLSSNTR FYNLLTGMCMLLGRYWTYLPLLALAGALVEKKKIPAGSGTLTTYTPIFIGLTIGVILLVGALNFF PALALGPVAEQLAPLATLTH
9E-219	736.7	29.2	1E-218	736.5	20.2	1	1	A0A0B5DHE8_9ACTN	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SNOD_04830	Streptomyces nodosus	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces nodosus	40318	>tr|A0A0B5DHE8|A0A0B5DHE8_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces nodosus GN=kdpA PE=3 SV=1 MSPVLAGALQALALIAALALVHAPFGTYMARVYSSGRHGRVEKWIYKGIGVNPDTQMRWP SYLRGVLAFSAAGVLFLYLLQRIQGVLPGSLGFSSIDPAQSFNTAVSFVTNTNWQSYAGEQ AMGHVVQTAGLAVQNFVSAAVGMCVALALVRGFARSRTGELGNFWSDLVRGVVRILLPAA AIAAVVLVACGAIQNFSGVHEVGQFMGGTQQWRGGAVASQEAVKELGTNGGGYFNANSA HPFENPTPFSNLFEIFLLLVIPVSLTRTFGVLVGSVKQGYAILATMATIWVGFVALMMWTEFA HHEGALRLAGGALEGKELRFGVGASSLFAVSTTLTSTGAVDSFHSSFTGLGGGITLLGMML GEIAPGGTGSGLYGILIMAVIAVFIAGLMVGRTPEYLGKKIGSREIKLAAVYILITPALVLVFSAF SMALPTPRHSMLNTGAHGFSEILYAFTSAANNNGSAFAGLNANTDWFNTMTGLAMLLGRFL PMVFVLALAGSLAEQKPVPVTAGTLRTERPLFTGLLVGVILIITGLTYFPALALGPLAEGLAS

9E-219	736.6	24.7	1E-218	736.4	17.2	1	1	F3ZA18_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA STTU_0878	Streptomyces sp. Tu6071	563	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. Tu6071	355249	>tr|F3ZA18|F3ZA18_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. Tu6071 GN=kdpA PE=3 SV=1 MSPVLAGILQLLALVVALGLSYRPLGDYMARVYSSPRHLRVEKWIYRVIGANPDTAMRWPA YLRGVLAFSLVSLLFLYALQRLQGILPGSLGFSSIDPDQAFNTAASFVANTNWQSYYGEQAM GHVVQTGGLAVQNFVSAAVGMAVAIALVRGFAHPRLLGRKLGAGTGELGNFWSDLVRGTV RVLLPIAAVAAVLLVACGAIQNFAGIHEVGQFSGGTQQFNGGAVASQEAIKELGTNGGGYF NANSAHPFENPNPLSNLLEIFLILVIPFSLTRTFGRMVGSVRQGYAILATMGFIWLGFTALMM WTEFAHHGPAFQLAGGAMEGKETRFGVGGSSLFAVATTLTSTGAVNSFHSSFTGLGGGIT MLGMQLGEIAPGGVGSGLYGMLVIAVIAVFLAGLMVGRTPEYLGKKIGPREIKLAALYILVTP ALVLCFTAAAMALPTPGNSMTNSGPHGFSEILYAYTSAANNNGSAFAGLNADTQWFNTTTG LAMLLGRFLPMVFVLALAGSFAARRPVPETAGTLRTAKPLFTGVLTGTLLIVTGLTYFPALAL GPLAEGLAS
1E-218	736.4	27.2	1E-218	736.2	18.8	1	1	Q3IYE0_RHOS4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RSP_1265	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	551	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides), Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	272943	>tr|Q3IYE0|Q3IYE0_RHOS4 Potassium-transporting ATPase potassium-binding subunit OS=Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158) GN=kdpA PE=3 SV=1 MSEIWGLLLFLAALAGGGWLLGAGMARLYAGDGLPAGRRLLGRSARPQGWTDYAMAVLA FNAAGFLALYALLRLQGLLPLNPDGVAGMAPDLAFNTALSFVTNTNWQAYSGEAQLSYLAQ MLGLTVQNFVSAGTGMAVGVAVIRGFTAPKGESLGNFWTDLSRSVLWVLLPLSAGLALILIL QGVPQTLLGAVRATTLEGAEQIIARGPAASQIAIKQLGTNGGGFFGVNSAHPFENPTILSDLV QCYAILVIPVAFCFLFGRMAGDGRQGRAIFAAMSVLFLAGLAVILWQESAGNPLMALSGGN MEGKEVRFGPILSGLWAAATTAASNGSVNAMHDSFLPLSGLVMLVNMQVGEVIFGGVGSG LYGMLLYVVLAVFLAGLMVGRTPEYLGRRVEAREVVLAVLAFLSMPVGILAGGALSASIPAM AASVQEAGPHGLSEILYAYSSATGNNGSAFAGWNAATPWQTTALGLLMLFGRFAMIVPML AIAGSLVRKTPAPATAGTFPTHGPLFVTLLVLTVAVFGALTFFPVLALGPLAEQAALAAGQSF
1E-218	736.1	26.4	2E-218	735.9	18.3	1	1	E6STC1_BACT6	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bache_0222	Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	570	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides helcogenes, Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	693979	>tr|E6STC1|E6STC1_BACT6 Potassium-transporting ATPase potassium-binding subunit OS=Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108) GN=kdpA PE=3 SV=1 MNTEISGVVLQILLMVALSYPLGKYIAKIYKGEKTWSDFMKPMEKLIFKAGGIDPEEEMDWKL FLKTFLMLNAFWFVWGMLLLVTQHWLPLNPDGNSSQTPGQAFNTCISFLVNCNLQHYSGE NGVTYFTQLFVVMLFQFLSASAGMAAMAGVMQSMAAKTTKTIGNFWKFMVLSCTRILFPLS LVVGFLLITQGVPMGFDGKMEVTTLEGQRQMVSQGPVAAIVSIKQLGTNGGGYFGANSSH PLENPTYLSDVIECCSIMLIPMAMVLAVGFYTKRKKLAYCIYGVMLFACLSGICINICQEMQGN PCLDGLGIAQDNGAMEGKEIRFGTASTALWSIVTTATSNGSVNGMHSSMMPLSGMMEMLN MQVNTWFGGVGVGWMNYYTFIILAVFISGLMVGRTPEFLGKKVEAREMKIATVVALLHPFVI LTGTALSCYLLVHHPEFVVGEGGWLNSQGFHGLSEQLYEFTSSAANNGSGFEGLGDNTLF WNYACGWALILCRFIPIVGQVAIAGLLAEKRFIPESSGTLKTDTLTFGVMTFVVIFIVAALAFFP VHALSTIAEHFSINR
1E-218	736	28.2	2E-218	735.8	19.6	1	1	F8AWS9_FRADG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA FsymDg_2987	Frankia symbiont subsp. Datisca glomerata	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia symbiont subsp. Datisca glomerata	656024	>tr|F8AWS9|F8AWS9_FRADG Potassium-transporting ATPase potassium-binding subunit OS=Frankia symbiont subsp. Datisca glomerata GN=kdpA PE=3 SV=1 MNTTTAGVVFAASLAVALGLTYRPFGDYLARVYTSERHLRAEKMTYRLVGVDPDADQRWS VHLRAVLAFSCVSALFLYVFLRLQGRLPFNLGFDGMAPGQAFNTAASFVTNTNWQSYAGE STLGYLAQMAGLAVQNFASAAVGISVAIALVRGFSRSHTDRLGNFWVDLVRTVVVRVLLPISVI GAVVLVAGGVVQNFHGVRTVSTIAGGGQAITGGPVASQEIIKELGTNGGGFYNVNSAHPFE NPTVWTNWLQIYLLLAIPFALPRAFGKMVGDTRQGLAIVSVMAVLAITGVFLVNGFQLAHHG TVPTAVGAATEGVETRFGVSGSATFAAATTLTSTGAVNSAHDSYTGLGGAVLLLNMMLGEI APGGAGSGLYGMLVVAVLAVFVGGLMIGRTPEYLGKKIAAREVKFAALYILTTPALALGVTAV AMALPGERANMLNSGAHGLSEVLYAATSVANNNGSAFAGLTVNTAWWNTVLGISMLLARF LPVVFVLGLAGSLARQKTAPVSSGTLPTHRPLFVGLVTGVAFVVVALTYFPAIALGPFAEGLH
1E-218	736	30.5	2E-218	735.8	21.2	1	1	D5VJB7_CAUST	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cseg_1853	Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (Mycoplana segnis)	570	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter segnis, Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (Mycoplana segnis)	509190	>tr|D5VJB7|D5VJB7_CAUST Potassium-transporting ATPase potassium-binding subunit OS=Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) GN=kdpA PE=3 SV=1 MTWQGWAEIALTLGLAVAIGWPLGVFLSRVWNGERTFLDPVMRPVEGLFYKACGVDPGK SQSWHAYALALLAFNLVGFIFVYTVLRLQGVLPLNPQGFPGLSGHLSFNTAISFVTNTNWQS YAGESTMSTLSQMLVLTVQNFVSAATGATVAAALARAFVANRGEGVGNFWADLIRTTLYLL LPLAFVVAVVLVALGLPQTLAAGVTAHTLEGADQKISLYAVASQEAIKMLGINGGGIFNANSA HPFENPTPLTNLITAVSINTLGWSAFFAFGRMVLAKKDVRALVIAAFVLLFAGAAGVYATETQ PPPAQVAAKVDASVNMEGKEVRFGAPATAAWVAMTTGASNGSVNGMHSSLMPLGGGIAM FLMQLGEILPGGIGSGLAIMVVMALLSVFVAGLMVGRTPEYLGKKVEAREIQFSILAVVIIPLS MLGFSGLAAVLPEALKGLMHSGPHGLSEILYAYVSGTANNGSAFAGLTANAPWWNVTLGIA MALGRFLPIVAVLAIAGSLVAKPKLAPTAGTLPTDGGLFIGLLIGVILILGGLQFFPAMALGPIV EHFQALGAVAALR

2E-218	735.6	27	2E-218	735.3	18.7	1	1	A5FWE7_ACICJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Acry_0708	Acidiphilium cryptum (strain JF-5)	565	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acidiphilium, Acidiphilium cryptum, Acidiphilium cryptum (strain JF-5)	349163	[illegible] OS=Acidiphilium cryptum (strain JF-5) GN=kdpA PE=3 SV=1 MTLHGIGFIALALALVFGAAFPLGAYLARLYRGELRFLAAIEAPIYRLCGIDPQRQMAWGAYA VGLLLLSLIHFLLLYAILRLQYFLPFNPEHIRGMSPKLAFNTAVSFTTNTNWQAYAPESQISYG AQMFGLAVHNFLSAAAGLAAAAALMRAFAGGGIRTLGNFYVDLVRITLYLLLPIAVVAALFLIG SGVPMTLAPYAHVHALAGGMQTIARGPVALQEAIKELGTNGGGFFNANSAHPFENPTAWT NLLEIWLILVIGFALPIAFGHVAGRRRDGRALFAVMAVILACGMVGAYAAEAANNPILVHAGL AAHPGNMVGKEVRFGVAQSTTFNIAATGTSTGAVNSFTDSYLPLGGLTALFMMQLGEIAPG GVGSGLYGIVLFALLAVFVAGLMVGRTPEYLGKKIEAREMKLAMLAILVQTLFILAGAGFSLLT KSGLASLANAGPHGLSEMLYGWTSATENNGSAFAGLSANTMLLDYGLGLAMLFGRFAVMI PVLAIAGSLGAKPRLPHSEGTFPTDGPLFIGLLIGVIVILVGLQFMPADLLGPIVEHYLLLAGKT F
2E-218	735.6	27.7	2E-218	735.3	19.2	1	1	C9YYK7_STRSW	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SCAB_7211	Streptomyces scabiei (strain 87.22)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces scabiei, Streptomyces scabiei (strain 87.22)	680198	[illegible] OS=Streptomyces scabiei (strain 87.22) GN=kdpA PE=3 SV=1 MGPVLAGVLQLLALMTALALAHAPLGTYMAGVYSSDRHWRVEKWAYRCIGADPDTEMRW PAYLRGVLALSTVGVLFLYLLQRLQGVLPGSLGFDAVGPAQSFNTAVSFVTNTDWQSYYGE QTMGHVVQTAGLAVQNFVSAAVGIAVAVALVRGFARSRTGDLGNFWADLIRGTFRILVPGA AIAAVVLVACGAIQNFSGIHEVGQFMGGSQQWNGGAVASQEAIKELGTNGGGYFNANSAH PFENPTPFTNLFEIFLLLVIPFSLTRTFGVMVGSVKQGYAILAAMAIIWVGFVALMMWTEFAH HGPALQIAGGAMEGKELRFGVGSSSIFAVSTTLTSTGAVDSFHSSFTGLGGGVTMLGMML GEIAPGGTGSGLYGMLIMAVVAVFIAGLMVGRTPEYLGRKIGTREIKLAACYILITPALVLVLT AVSLALPTPPHSMLNSGAHGFSEVLYAFTSAANNNGSAFAGLNANTDWFNTMTAIAMLLGR FLPMVFVLALAGSLAGQQPVPETAGTLRTEKPLFTGLLVGAILIVTGLTYFPALALGPLAEGL AS
3E-218	735.1	25.6	3E-218	734.9	17.7	1	1	R4TDT9_AMYOR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AORI_5980	Amycolatopsis orientalis HCCB10007	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis orientalis (Nocardia orientalis), Amycolatopsis orientalis HCCB10007	1156913	>tr|R4TDT9|R4TDT9_AMYOR Potassium-transporting ATPase potassium-binding subunit OS=Amycolatopsis orientalis HCCB10007 GN=kdpA PE=3 SV=1 MSDTAAGLLQAGLLLVALAVVYRPLGDYMARVFSTEKHTKAERGLYRLFRVNPGSEQHWK TYASAVIGFSFVSVVLLYLLQRLQAILPWSLGKEPVSPAVAFNTAVSFVTNTNWQSYSPEAT MGHFVQMAGLTVQNFLSAAVGLAVAIAVVRGFVRSKTDRLGNFWVDLTRGTIRILLPIAFVA AIALIALGVVQSLKSGVDVLNPDGSTSKIALAPAASQEAIKELGTNGGGIFNANSSHPFENPN AWTNLIEIFLILVIPVSLTRTFGKLVGNTKQGYVLLSVMAGLWTAMLAVTWLAEANASGPASL AAGANLEGKEQRFGIGLSSLFANSTTGTSTGAVNSMHDSYSGLGGGGTLLNMLLGEISPGG VGTGLYGILVMAVIAMFLAGLMVGRTPEYLGKKLGKREVTCAAVSMLAMPTVVLLGAGIALM NPGNLAALNNPGAHGLSEVLYAYASAGNNNGSAFAGITVTNDWFQSSLGVAMLLGRFIPILA VLCLAGSLASQRKVPETAGTLPTTGPLFGTMLAGTIVLVAALTFIPALALGPIAEALA
4E-218	734.5	22.6	5E-218	734.2	15.6	1	1	V4IZX0_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA B590_07900	Streptomyces sp. PVA 94-07	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. PVA 94-07	1223307	>tr|V4IZX0|V4IZX0_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces sp. PVA 94-07 GN=kdpA PE=3 SV=1 MSSPIAGILQLLALLAALALAHRPLGDHLARVYSSGKHYRPERWMYRAIGADPSAVMRPPAY LRAVLAFSAAGVLLLYLLQRAQGALPASLGFAPTDPDQAFNTAVSFVTNTNWQSYNGEQA MGHLVQTGGLAVQNFVSAAVGMAVAVALVRGFTGARTGEIGNFWADLVRGITRVLLPLSVA GALVLVACGVIQNFSGIHAVGQFSGDAQQWNGGAVASQEAIKELGTNGGGYFNANAAHPF ENPTPFSNLFEIFLILLIPFSMTRTFGRMAGSLRQGYAVLGAMAVIWLAFTALMMWTEFAGR GPAFEAAGGAMEGKETRFGIAGSSLFAVATTLTSTGAVNSFHSSYTGFGGGITLLGMQLGE IAPGGVGSGLYGMLIMAVVAVFVAGLLVGRTPEYLGKKIGTRQITYAACYLLVTPALVLGFTG LALALPGPAESMTNSGPHGFSEILYAYTSAANNNGSAFAGLNADTPWFNTTTGIAMLLGRFL PMVFVLALAGSLAEQRQVPATAGTLRTDKPLYSGLLVGTILIVTGLTYFPALALGPLAEGLAS
5E-218	734.3	31.3	5E-218	734.1	21.7	1	1	D9QG06_BRESC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Bresu_3242	Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (Caulobacter subvibrioides)	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas, Brevundimonas subvibrioides, Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (Caulobacter subvibrioides)	633149	[illegible] OS=Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) GN=kdpA PE=3 SV=1 MTLQGWAEIALTLGLSVALGWPLGLYLSRVWNGERTWLDPVLRPVEKVFYGLAGVNPDRS QGWVGYAGALVVFNAMGFGLLYAILRLQGGLPLNPQGFEGVSPHLAFNTAISFVTNTNWQ SYGGETTLSTFTQMVGLTVQNFLSAATGAAIAAALARAFVASRGEGVGNFWADMTRTTLYL LLPASIVLAVLLAGLGVAQSLAASATATTLEGADQTIALFPVASQLAIKMLGINGGGVFNVNSA HPLENPSALTNLITAVSINVLGWAAFFAFGRSVMAKKEVRALVLAGLILLGGLTAAMYVAESQ PAPALQAAGISQPVNMEGKETRFGIASSVAWAAQTTGASNGSVNAMHASFMPLSGGIQMF LMQLGEILPGGIGSGIALMVVMAILSVFVAGLMVGRTPEYLGKKIEAREIQYAMIGLLAMPAAI LGFGAVAAVYPEALTGLLNAGPHGLSEILYAYTSAAANNGSAFAGLTANAPWWNTTLGIGM LLGRFVPAVAVLAIAGSLVAKPKLAPSAGTLPTDGGLFIGLLIGVILILGGLQFFPALALGPIVE HFQMLAAAARS

5E-218	734.2	29	6E-218	734	20.1	1	1	F9ZTB8_ACICS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Atc_0285	Acidithiobacillus caldus (strain SM-1)	588	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus caldus, Acidithiobacillus caldus (strain SM-1)	990288	>tr|F9ZTB8|F9ZTB8_ACICS Potassium-transporting ATPase potassium-binding subunit OS=Acidithiobacillus caldus (strain SM-1) GN=kdpA PE=3 SV=1 MNDALLLTFTTIALSIVLAWPLGIYMRRIYSDEHCLAKRLLGPVERAIYVVAGIDAKADMGWK QYALLWILFNVVGGVFLYVLLYFQNYLPLDPMHFGSPGVQISFNTAASFVSNTNWQDYGGE TTMSYLSQMLGMAVQNFLSAASGIVLAIAMIRGFTRAEKPGIGNLWVDLVRTTLYVLIPLSIVL ALFFVEQGAIQNFAAYVHADLLQPFVHQGKLMTQQVIAMGPAASQEAIKLLGTNGGGFFNA NSGHPFENPTGLTNLFQMVAIFLIPFALVFYFGHRVKNLRLGVGILAVMLLLFTPLALLSQQQ ELAGNPLLTAVGVDQNNTPALAGGGNMEGVEERIGAAGSALFGAVATGTSTGAANSAYDS FMPLSGMVNLLLMQLGEVTPGGVGTGIASMLAFVLIAVFLAGLMIGRTPEFLGKKIEAYEIKM ASLAILVMPLLVLIGTAVAVSLPGGRDAVLNPGAHGFSEILYAVTSPSNNNGSAFGGLNANTT FYNLLTGLCVLVNRYLAYLPLLAIAGSLAAKKRIPASPGTLNPATPLFVVFTTIVVLLVGALNFI PALGLGPIAEQLSLPSAVHTASTGH
5E-218	734.2	33.9	6E-218	734	23.5	1	1	A0A0A7FTU1_9CLOT	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA U729_177	Clostridium baratii str. Sullivan	551	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium baratii, Clostridium baratii str. Sullivan	1415775	>tr|A0A0A7FTU1|A0A0A7FTU1_9CLOT Potassium-transporting ATPase potassium-binding subunit OS=Clostridium baratii str. Sullivan GN=kdpA PE=3 SV=1 MEIIASLLLIVLFIISTIYIGKYMYSILFNTKSFVDPVMDKIDNAIYKICGVKGKDMNWKQYIIALL VTNAIMLIVGFILLMTQNYIVGSSSELLDMNWHTAFNTAISFITNTNLQDYVGELNLTNISQMIV ITMYMFTSAATGFAICGAFIKGLTGHEFGNFYRDLIRIITRLLLPISIIAAIILISQGVPQTLESHRV VQTLEGETQTLSYGPVASLESIKHLGTNGGGFFGANSSHPFENPTPLTNFIEMLLMMLTPGA YCYVFGKACKNKKQGRAIFIAALFLFLVVIPVIYFAELKGNPVMNELGITNTIGNMEGKEVRN GIFDSSLFSVITTSFTTGSVNNMHDSLTPIGGAVPMWNMMLNCVFGGKGVGFINLLLYAML GVFICGLMVGRTPEFLRKKIEGKEMKLIAIVILIHPILILIPSAIATMFGQGSLSGYHGLSEIIYQF TTSAANNGSGFEGLNDTTVFWNVSTGIVMLIGRYLSMILLLKLASLMKEKSLVPKSSVAFRT DTPLFIGVLIVTIIIIGALTFMPVLVLGPGAEFLSL
5E-218	734.2	24.6	6E-218	734	17	1	1	D6E871_9ACTN	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GPA_12580	Gordonibacter pamelaeae 7-10-1-b	591	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Gordonibacter, Gordonibacter pamelaeae, Gordonibacter pamelaeae 7-10-1-b	657308	>tr|D6E871|D6E871_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Gordonibacter pamelaeae 7-10-1-b GN=kdpA PE=3 SV=1 MDELLEYGIYLALLVALAIPLSGYINKVMAGERVAVLSRVLVPVENVVYRCIRVDRADVMGW KRYLISALVFSALSLAGLFAILMLQGVLPGNPEGLPGLTWDLAFNTAASFVTNTNWQAYSGE SALSYFSQAIGLTVQNFVTPAVGMAVLFALFRGLVSEGGPGLGNFFVDATRAVLFVLIPLALV VTVVDVWQGSPQNVSEYQEVQLLEPVGIDSEGEVVEADDPAAVQVIDEGVVPMGPQASQ VAIKQLGTNGGGYNGVNSASALENPTPLTNLVQCISLLLIPFALVFSFGRFVADRRQGRAIFA AMFIVLVASLAVIAFFEQVGTPQLAADGSVYMGTYDQSGGNMEGKEARFGVTDSSLWAAF TTAASNGSVNSMHDSYTPIGGMVPIILMGLGEIIGGGIGCGLYGMIGFVILTVFIAGLMVGRTP EYLGKKIGPREMRMATILCITTPMVLLIGAAVMCLDPATVDSLNNSGAHGFSEVLYAATSAG GNNGSAFAGFNGNTPMINVVLGFEMLANRFIPLAATLVLAGSLCTRPKVAVSAGTLSTSNAM FVFLLILIVLLVGALSMFPALALGPIAEQLHMVL
6E-218	734	23.9	9E-218	733.4	16.6	1.2	1	KDPA_FRAAA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA FRAAL5302	Frankia alni (strain ACN14a)	587	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia alni, Frankia alni (strain ACN14a)	326424	>sp|Q0RF16|KDPA_FRAAA Potassium-transporting ATPase potassium-binding subunit OS=Frankia alni (strain ACN14a) GN=kdpA PE=3 SV=1 MSTSVAGVLAVALLVAALWVTYRPFGDYMYRVFAAKRHLRVERAIYRLTGVNPDTGQRWP VYARSVLAFSLVSVLLLYLLQRVQEHLPLNLGFGAVGPALAWNTAVSFMTNTNWQAYSGES TMGHTVQMTGLAVQNFVSAAVGIAVAIAVVRGFARRRAPVAVGGPGGPNGPGGPGGPNG PGAGSRDDVIGTGDELGNFWVDLTRTVIRILLPVCVIAAIVLVAGGAIQNLHGNRVVSTLAGG HQTITGGPVASQEAIKEFGTNGGGFYNVNSAHPFENPTSWTNLVEIFLLLAIAFSLPRTFGR MVGDRRQGLAIVAVMAVLALGSFAVNAAFQTAHHGTVPVAVGAATEGTDTRFGVPNSALF ASATTLTSTGAVNSFHDSYTSLGGATLLFNMMLGEVAPGGTGSGLYGMLVLAVVTVFVAGL MIGRTPEYLGKKIGSREIKFASLYFLATPAIALLGTGVAMGLPGERASMLNSGAHGLSEVLYA FTSAANNNGSAFGGISVNTTWYNTALGLAMLFGRLLPMLLVLGMAGSFARQHPVPATAGTL PTHRPQFAGMLGAIALIIVALTFFPALALGPLAEGIH
6E-218	733.9	26.8	7E-218	733.7	18.6	1	1	B2UQC8_AKKM8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Amuc_0830	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	566	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales, Akkermansiaceae, Akkermansia, Akkermansia muciniphila, Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	349741	>tr|B2UQC8|B2UQC8_AKKM8 Potassium-transporting ATPase potassium-binding subunit OS=Akkermansia muciniphila (strain ATCC BAA-835 / Muc) GN=kdpA PE=3 SV=1 MSSHDLLIIVLFIGILVSFTPFLGKWLASVLMGRQTWLPPVLGPVERCVYRMAGVDPTREMD WKKYLTAVLLFNAAGFLVLFLSLLCQKWLPLNPAGTENMRWDIALNTAISFVTNTNWQFYS GEGPEGVSYFVQMTGLGVQNFVSAGTGIAVMSALIRGLERRCASTLGNFWTDLTRSMLYF LVPVSTVIALLLVSQGVVQSFDGPIAVPGMDGVEQMIPSGPAASQIAIKQLGANGGGFFGNN STHPFENPTPFSNMVEMLSLLLAGCACPYAYGVMIGKKRQGWIIFGAMMILLVAAIVLSQWA EHAGNPLFPGMEMLEGKEVRLGVTNSSLWSVATTASSNGSVNCMHSSMSPLGGGIALFN MLLGGVIFGGLGCGLYSMLMFAMITVFLCGLMVGRTPEFLGKKMGAREVCCSMVGILLPGM AVLVMSGLAAATETGRASICNAGPHGLTEILYCFGSQAGNNGSAFAGLAAGDTPFYSLLGG LAMLLARFGTIISVMMIAGSMASRKTAPPAQGTMGTDNLMFMVLLVAVVLVVGALTFFPALA LGPILEHLLLYSGAML

6E-218	733.9	24.7	8E-218	733.6	17.1	1	1	KDPA_PROAC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA PPA0115	Propionibacterium acnes (strain KPA171202 / DSM 16379)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Propionibacterium, Propionibacterium acnes, Propionibacterium acnes (strain KPA171202 / DSM 16379)	267747	>sp|Q6ABJ2|KDPA_PROAC Potassium-transporting ATPase potassium-binding subunit OS=Propionibacterium acnes (strain KPA171202 / DSM 16379) GN=kdpA PE=3 SV=1 MTWICFLAGLALLAIALGIAQHHLGTYMARVFTSDKDTRVETWCYRVMGVNPRAGQTWKS YARAVLAFSFCGVVFLYALQRLQPWLPWSLGKGSVNPAVSFNTAISFVTNTNWQAYSPEA TLGHFVQLAGLCVQNFVSAATGIAIAVALIRGFVGHGEHTIGNFWVDLTRCTLRILMPIAAVA AFLLIAGGAVQNFTGFLHVTGVAGGNQVIPGGPVASQEAIKELGTNGGGFFNGNSSHPFEN PQPWTNMLEIFLILLIPFSLPRTFGKMVEDVRQGRAILAAMVVLFTVNLCAMAAAEFSGHGT AARLAGAPMEGKEQRFGLAQSVLFANSTTMTSTGAVDSMHDSFTAIGGMFTLLNMMLGEIS PGGVGSGLYGMLVIAVIAVFIAGLLVGRTPEYLGKKIGPREMKLSDLYILVMPTLVLCGVALSL AVPGLRSSVNTSIANPGEHGLSELVYAFTSAANNNGSAFAGLDASTNWLCAALGAAMLLGR FVPIILILALSGALVEREPVPVTAGTLPTHNALFTTLIVFTAILVTALVFFPVLTLGPLAEGLI
6E-218	733.9	29.5	7E-218	733.7	20.4	1	1	A0A059W4G1_STRA9	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DC74_5942	Streptomyces albulus	558	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	68570	>tr|A0A059W4G1|A0A059W4G1_STRA9 Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces albulus GN=kdpA PE=3 SV=1 MSPALAGVLQLTALIAALALVYRPLGDYMAAVYSSPRHLRVEKVIYHCIGANADTQMRWPAY LRGVLAFSLAGMLFLYLLQRLQGHLPLSLGFASISPDQAFNTAASFVANTNWQSYSGEQAM GHVVQTAGLAVQNFVSAATGMAVAVALVRGFARSRTGELGNFWADLVRGTIRVLIPLAIVG ALILVACGAIQNFAGIHEVGQFMGGAQQTNGGAVASQEVIKELGTNGGGYFNANSAHPFEN PTAFTNLFEIFLILVIPFSLTRTFGKLVGNVKQGYAILATMGIIWLGFTALMLWTEFAHGGPAL QAAGAAMEGKEDRFGIGGSAIFSVATTLTSTGAVDSFHASYTAFGGGLQLLGMMLGEIAPG GVGSGLYGMLVMAVISVFIAGLMVGRTPEYLGKKIGTRQIKLAACYILITPTLVLGFTAAAMVL PDALGSMLNTKALGAGPHGFSEVLYAYTSGANNNGSAFAGLNANTPWYNTTIGLAMLLGR FLPMVFVLALAGSLAEQQPVPETAGTLRTEKPLFAGLLVGTILIITGLTYFPALALGPLAEGLS
7E-218	733.8	28.9	8E-218	733.6	20	1	1	KDPA_KINRD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Krad_1016	Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	557	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Kineosporiales, Kineosporiaceae, Kineococcus, Kineococcus radiotolerans, Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	266940	>sp|A0A0R3|KDPA_KINRD Potassium-transporting ATPase potassium-binding subunit OS=Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216) GN=kdpA PE=3 SV=1 MGDLGAGLLQAGLLLLLLAAVHVPLGDFLARTFAGTRHLRLERGIYRVLRVDADADTRWPTY ALSVLGFSTVSILFLYAFLRLQGFLPLSLGRPGMEPTQAWNTAVSFVGNTNWQSYAGESTL GHLVQMAGLTVQNFLSAAVGLAVAVALVRGLVARGTGTIGNFWVDLTRGTLRVLLPLAFAG AVLLLLTGVVQNFTGATTYPTLAGGSQTILGGPIASQEAVKELGTNGGGFFNANSAHPFENP NAVSNLLEVFLILVIPFSLPRAFGTLVGDHRQGLAVLSVMGTIFGASLALTTWAETHAGGSVP QAAGAAMEGKETRFGEWASALFATATTATSTGAVNSAHDSYTAAGGGVVLLNLVMGEVTP GGVGSGLYGMLVLAVITVFVAGLMVGRTPEYLGKRIGQREITCAALYVLVTPAVLLTGTAVA LSDAATRSALLNTGSHGLTEMLYAFASAANNNGSAFAGLSANTPFYNTALGLAIWLGRFLP MVLVLALAGAFAAQRTAAETAGTLPTRSPTFAGMHLAVVVVVSALTFFPALALGPIAEALTG AQS
8E-218	733.5	26.7	1E-217	733.2	18.5	1	1	V6KFX4_STRNV	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA M877_08445	Streptomyces niveus NCIMB 11891	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces niveus (Streptomyces spheroides), Streptomyces niveus NCIMB 11891	1352941	>tr|V6KFX4|V6KFX4_STRNV Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces niveus NCIMB 11891 GN=kdpA PE=3 SV=1 MSSVLAGVLQFLALMVALALAYRPLGDYMAGVYSSPKHLRVEKWIYRAVGADPATEMRWP AYLRGVLGFSLVSVLFLYLLQRVQGILPGSLGFASIDPDQAFNTAASFVSNTNWQSYYGEQ AMGHVVQTGGLAVQNFLSAAVGMAVAVALVRGFARTRTGELGNFWADLVRGTVRILLPIAL VGAVLLVACGAIQNFAGIHEVGQFTGGSQQWNGGAVASQEAIKELGTNGGGYFNANSAHP FENPNGLSNLLEIFLILLIPLSLTRTFGRMVGSVKQGYAILATMTVIWVVFTGLMMWTEFHHG APAFDIAGGALEGKETRFGIGASSIFSVATTLTSTGAVNSFLSSYTGFGGGIAMLGMQLGEIA PGGVGSGLYGILVMAVIAVFLAGLMVGRTPEYLGKKIGTRQIKFAACYILITPALVLCFTGVAM ALPTPVNSLTNSGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNTSIGVAMLLGRFLPM VFVLALAGSLAEQKPVPATAGTLRTDKPLFSGLLVGTIMIVAGLTYFPALALGPLAEGLAS
1E-217	733.1	32.2	1E-217	732.9	22.3	1	1	D7BWR0_STRBB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SBI_00295	Streptomyces bingchenggensis (strain BCW-1)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	749414	>tr|D7BWR0|D7BWR0_STRBB Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces bingchenggensis (strain BCW-1) GN=kdpA PE=3 SV=1 MSPVLAGVLQLLALIAALALVYVPLGNYMAGVYSSDKHWRVEKWIYKGIGANPDTEMRWPA YLRGVLAFSAVGVLFLYLLQRVQGALPGSLGFASIDPDQAFNTAASFVTNTNWQSYYGEQA MGHVVQTAGLAVQNFVSAAVGIAVAVALVRGFARARTGELGNFWADLVRGTVRILVPVAAI AAVVLVACGAIQNFSGIHEVGQFMGGSQQWNGGAVASTEAIKEVGTNGGGIFNANSAHPF ENPIPFTNLFEIFLILVIPLSLTRTFGVLVGSVKQGYAILATMATIWIGFTALMMWTEFSHHGP AFEIAGGAMEGKEVRFGVGGSSIFAVATTLTSTGAVDSFHSSFTGLGGGITMLGMMLGEIA PGGVGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGTREIKLAAMYILVTPALVLIFTAAAMA LPTPQNSMTNSGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNTTIGLAMLLGRFVPMV FVLALAGSLAEQKPVPATAGTLRTEKPLFTGLLVGAILIITGLTYFPALALGPLAEGMAS

1E-217	733.1	26.9	1E-217	732.8	18.7	1	1	A5FU08_ACICJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Acry_3488	Acidiphilium cryptum (strain JF-5)	565	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acidiphilium, Acidiphilium cryptum, Acidiphilium cryptum (strain JF-5)	349163	OS=Acidiphilium cryptum (strain JF-5) GN=kdpA PE=3 SV=1 MTLHGIGFIALALALVFGAAFPLGAYLARLYRGDLRFLAAIEAPIYRLCGIDPQRQMAWGAYA VGLLLLSLIHFLLLYAILRLQYFLPFNPEHIRGMSPKLAFNTAVSFTTNTNWQAYAPESQISYG AQMFGLVVHMFISAAAGLAAAGALMRAFASGGIRTLGNFYVDLVRITLYLLVPIAIVAALFLIG SGVPMTLAPYAHVHALAGGMQTIARGPVALQEAIKELGTNGGGFFNANSAHPFENPTAWT NLLEIFLLLVIGFALPIAFGHVAGRRRDGRALFAVMAVILACGMVGAYAAEAANNPILVHAGLA AHPGNMVGKEVRFGVAQSTTFNVAATGTSTGAVNSFTDSYLPLGGLVPLFMMQLGEIAPG GVGSGLYGIVLFALLAVFVAGLMVGRTPEYLGKKIEAREMKLAMLAILVQTLFILAGAGFSLLT KSGLASLANAGPHGLSEMLYGWTSATENNGSAFAGLSANTMLLDYGLGLAMLFGRFAVMI PVLAIAGSLGAKPRLPHSEGTFPTDGPLFIGLLIGVIVILVGLQFMPADLLGPIVEHYLLLAGKT F
2E-217	732.6	25.1	2E-217	732.3	17.4	1	1	F2R3F4_STRVP	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SVEN_2510	Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces venezuelae, Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	953739	>tr|F2R3F4|F2R3F4_STRVP Potassium-transporting ATPase A chain OS=Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745) GN=kdpA PE=3 SV=1 MSPVLAGVLQLLALVVALGLSYRPLGDHMARVYSSDKHLRVEKWIYKGIGANPSVEMRWP AYLRGVLAFSAVSVLFLYLLQRVQGSLPGSLGFVSIDPDQAFNTAASFVANTNWQSYYGEQ AMGHVVQTGGLAVQNFVSAAVGIAVAVALVRGFTRSRTGELGNFWADLVRGVVRVLLPISV VGALVLVACGAIQNFAGIHEVGQFMGGTQQWNGGAVASQEVIKELGTNGGGYFNANSAH PFENPNGLSNLFEIYLILVIPFALTRTFGRMAGSLKQGYAILGTMAAIWLGFTALMMWTEFAH HGPAFDLAGGATEGKETRFGIGGSSIFAVATTLTSTGAVNSFHSSYTGFGGGITMLGMQLG EIAPGGVGSGLYGMLIMAIIAVFIAGLMVGRTPEYLGKKIGTREIKFAALYILITPALVLCFTAAS FVLDTPSHSLTNSGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNSTIGIAMLLGRFLPM VFVLALAGSLAEQTPVPETAGTLRTEKPLFTGLLVGTILIVAGLTYFPALALGPLAEGLAA
2E-217	732.2	31.5	2E-217	732	21.9	1	1	D3F9I8_CONWI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cwoe_0722	Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	576	cellular organisms, Bacteria, Actinobacteria, Thermoleophilia, Solirubrobacterales, Conexibacteraceae, Conexibacter, Conexibacter woesei, Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	469383	OS=Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577) GN=kdpA PE=3 SV=1 MTAEGWIQILVFFAVLTALTPLIGAYMHKVFRGDAILAPVLGPVERGFYKLLRVDPRQEQDW KAYARAVLFFSLGSWLLLYAILRLQGSLPFNPAGFGAAPADVNFNTASSFVANTNWQYYAG ETTLSNFSQMGGLAVQNFLSAAVGIAVVIAVIRGFSARSLRTLGNFWSDLTRTLLYILLPISFV GALFLVSQGVVQSLSPAEAFTSLEGVRQAITLGPVASQEVIKLLGTNGGGFFNVNSAMPFE NSSGLVNFFEMLLILIIPAGLTATFGRMVGNRRQGWAIYGAMFAMFAVAVAIVYAAEGHGSP AQHLAGIEGGNFEGKETRFGIPSSALFAAVTTVASCGAVNAAMESLTGIGGAVPMANMMTG EVIFGGVGSGLYGMLMFVILAVFIAGLMVGRTPEFLGKKIGAREIKLTMIGTLAVPLFVLVLTA AAISSKYGLRSIYNGGPQGFSETLYAYVSQTNNNGSAFAGYTGFVQPNGPGNSGAFGITFA DLLGGGAMLAGRFLPLLAVLAIAGALAGRKVAPAGPGTMRTDTGTFTVLTVGTVLLVALLTF VPALLLGPVVQGLTDRMF
2E-217	732.1	20.8	3E-217	731.9	14.4	1	1	A0KED5_AERHH	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AHA_0017	Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	560	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Aeromonas, Aeromonas hydrophila, Aeromonas hydrophila subsp. hydrophila, Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	380703	OS=Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240) GN=kdpA PE=3 SV=1 MWQEIIYPVAFVLLVLLPAPLLGNYLYRVFEGKSRWLAPLERATLACCGTDGREQDWKSYA LSLLAFNGAGFGLLFLILLAQGLLPLNPQQLPGLNWQLAFNTAVSFMTNTNWQAYSGEASL SYFSQMVGLTTQNFVSAATGAAVAIALFRGIARQQTTHLGNFWQDLVRFCLYVLLPMALILA LLLVWQGVPQSLSAYLPFHALEGQEQLLPLGPAASQIAIKQLGSNGGGFFGINSAHPFENPT ALSNWLEMVALLTLAAAMVCTLGRYVKDLAHSRAILIAMTIMLVLGLCLAIGQELQPDPALAH LTSEAGNWEGKESRFGPVLSSIWEVATTAASNGSVNAMHDSFAPLAGMVAMINMLLGEVV FGGVGAGIYGMMLFVLLTVFLCGLMVGRTPTYLGKRLGITEMKWVVASMLVMPVGVLVIGG ITLLMPDSATVIGHDGPHGLSRLIYAYASAAGNNGSAFAGFAAADSWQCIAIGLAMLLGRFG YIIPVLAIAGQLARAPRQERSEGDFPVSGPLFITLLIVTVLLMGGLSFLPVLALGPVAEHLSLLG GAF
4E-217	731.3	15.2	5E-217	731	10.5	1	1	E2Q1F7_STRC2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SCLAV_5516	Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces clavuligerus, Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	443255	OS=Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602) GN=kdpA PE=3 SV=1 MNATLAGWLQILALVAALALSHRPLGDHIARCLTDGRHLRAERVVHRAAGVPPDADQTWPA YLRSVLAFSLVSLALLYVLLRAQHLLPLSLGRPGVPPDLSFNTAVSFVTNTDWQAYAGERTL GHLVQMAGLTVQNFLSAAVGIAVAAALVRGFTRERSERVGHFWTDLTRLVVRVLLPIAFLFA LVLAAGGVVQNLHGDQSLSTVAGGLQTLPGGPVASQESIKLLGTNGGGFYNANSAHPFEN PTALTHLIEVYLLLVVPVALPRTFGTLVGDRRQGRAVLAVMALIWAVSVAVVTANEVLGVSS TAGREAGAMLEGKEQRLGVWASALFAAATTLTSCGATSSAHDSFTPGGGGILLFNMMLGEI APGGAGSGLYGMLVLAVVTVFVAGLMVGRTPEYLGKKLGSREIKFASLYVLTTPVLALAGA GIAMGLPGERAAMGNPGPHGFSEVLYAFVSAANNNGSAFAGLQADTVWYNTALGLVMLV GRLLPMVFVLALAGSLAAQRRVPVTAGTLPTHRPQFVGLLTAVVLVVVGLTYFPALALGPLA EGLR

6E-217	730.5	32.7	7E-217	730.3	22.7	1	1	KDPA_CAUCR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CC_1591	Caulobacter crescentus (strain ATCC 19089 / CB15)	570	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter vibrioides (Caulobacter crescentus), Caulobacter crescentus (strain ATCC 19089 / CB15)	190650	[illegible] OS=Caulobacter crescentus (strain ATCC 19089 / CB15) GN=kdpA PE=3 SV=1 MTWQGWAEIALTLSLAVAIGWPLGVFLSRVWNGEKTFLDPVMRPVEGLFYKACGVDPSKS QSWHAYALALLAFNLIGFVFVYAVLRLQGVLPLNPQGFPGLSGHLAFNTAISFITNTNWQSY AGETTMSTLSQMLVLTVQNFVSAATGATVAAALARAFVANRGEGVGNFWADLVRTTLYLLL PLAFVVAVVLAALGLPQTLAAGVTAHTLEGAEQKISLYAVASQEAIKMLGINGGGIFNANSAH PFENPTPLTNLITAISINTLGWAAFFAFGRTVLAKKDVRALVIAAFVLLFAGAVGVYATETQAP PAQVAAQVDTSANMEGKEVRFGAPATAAWVAMTTGASNGSVNGKHSSLMPLGGGIAMFL MQLGEILPGGIGSGVAIMVVMALLSVFVAGLMVGRTPEYLGKKVEAREIQFSILAVVIIPLSML GFSGIAAVLPEALKGLMHSGPHGLSEILYAYVSGTANNGSAFAGLTANAPWWNVTLGIAMA MGRFMPIVAVLAIAGSLVTKPKLAPTAGTLPTDGGLFIGLLIGVILILGGLQFFPAMALGPIVEH FQALDAVAALR
7E-217	730.4	29.3	8E-217	730.1	20.3	1	1	A0A0D4DJI7_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA T261_2157	Streptomyces lydicus A02	551	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	1403539	>tr|A0A0D4DJI7|A0A0D4DJI7_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces lydicus A02 GN=kdpA PE=3 SV=1 MLQLIALIAALALAYRPLGDYMAAVYSSPKHLRIEKIIYRCIGANADAQMRWPAYLRGILAFSV VGVLFLYLLQRVQGGLPLSFGFASISPDQAFNTAASFVANTNWQSYSGEQAMGHVVQTAG LAVQNFVSAATGMAVAVALVRGFARSRTGELGNFWADLVRGTVRVLIPLSVVGALVLVACG AIQNFSGIHEVGQFMGGSQQTGGGAYASQEVIKELGTNGGGIANANSAHPFENPDAFTNLF EIFLILVIPFALTRTFGKLVGNVKQGYAILATMGVIWLGFTALMMWTEFAHGGPALQAAGAA MEGKETRFGVGASSIFSVATTLTSTGAVDSFHSSFTAFGGGIQLLGMMLGEIAPGGVGSGL YGMLVMAIIAVFIAGLMVGRTPEYLGKKIGTREIKLAACYILITPTLVLGFTAASMVLPDALSSM LNTKAVGAGSHGFSEVLYAFTSGANNNGSAFGGLNANTPWYNTTIGLCMLLGRFLPMVFVL ALAGSLAEQKPIPETAGTLRTEKPLFAGLLVGTILIITGLTYFPALALGPLAEGLS
1E-216	729.4	25.9	2E-216	729.2	18	1	1	G2NR14_STREK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SACTE_5029	Streptomyces sp. (strain SirexAA-E / ActE)	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. (strain SirexAA-E / ActE)	862751	[illegible] OS=Streptomyces sp. (strain SirexAA-E / ActE) GN=kdpA PE=3 SV=1 MSPVLAGVLQMLALVAALALAYRPLGDHMARVYSSTKHLRIERWIYRAIGADPATGMRWPA YLRGVLAFSAVGVLFLYALQRLQGTLPGSLGFASIDPDQAFNTAASFVANTNWQSYYGEQA MGHVVQTGGLAVQNFVSAAVGMAVAVALVRGFARSRTGELGNFWADLVRGTVRILLPLSV VGALVLVATGVIQNFSGIHEVGQFGGGTQQWNGGAVASQEVIKELGTNGGGYFNANSSHP FENPDGLSNLFEIFLILLIPSAMTRTFGRMVGSPEQGYAILATMATVWLGFTALMMWTEFSH HGPAFDLAGGAMEGKETRFGIAGSSVFAVATTLTSTGAVNSFHSSYTGLGGGITMLGMQL GEIAPGGVGSGLYGMLITAIVAVFLAGLMVGRTPEYLGKRIGTREIKFTACYILITPALVLCFTA AAVALPTPADSMTNTGAHGFSEILYAYTSGANNNGSAFAGLNADTQWFNTTLGIVMLLGRF LPMVFVLALAGSLARQSPVPVTAGTLGTQKPIFSGLLLATVVVVTGLTYFPALALGPLAEGLA S
1E-216	729.4	25.9	2E-216	729.2	17.9	1	1	A0A0C5FLG2_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TU94_02400	Streptomyces cyaneogriseus subsp. noncyanogenus	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cyaneogriseus, Streptomyces cyaneogriseus subsp. noncyanogenus	477245	>tr|A0A0C5FLG2|A0A0C5FLG2_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces cyaneogriseus subsp. noncyanogenus GN=kdpA PE=3 SV=1 MGPVLAGVLQLLALTSALALVHKPLGNHMAKVYSSDEHWRVERWIYRGIGVDPGAQMRW PAYLRGVLAFSVAGVLFLYLVQRAQGVLPLSLGFRAVDPDQAFNTAVSFVTNTNWQSYSGE QAMGHLVQTAGLAVQNFTSAAVGMAVAVALVRGFARSRTGELGNLWADLVRGTVRVLVPL ATLGAVVLAACGVIQNFSGIHEVGRFTGGSQQWNGGAVASQEAIKLLGTNGGGYFNANSA HPFENPTPFTNLFEIFLILVIPFSITRTFGVMVGSVRQGYAILATMATFWIAFVALMMWTEFSH RGPALEIAGGAMEGKEVRFGVGASSIFAVSTTLTSTGAVDSFHSSFTGLGGGIAMLGMMLG EIAPGGVGSGLYGMLVMAVTAVFIAGLMVGRTPEYLGKKIGTREIKLAACHLLVTPALVLILTA CAMALPTPVNSTTGSGAHGFSEILYAYTSGANNNGSAFAGLDADTQWFNTTIGLAMLLGRF LPMVFVLALAGSLAGQRPVPVTTGTLRTDKPLFSGLMVGAILILAGLTYFPALALGPLAEGLA A
2E-216	728.9	18.1	2E-216	728.7	12.5	1	1	D7BJD8_MEISD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mesil_3490	Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	569	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Meiothermus, Meiothermus silvanus, Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	526227	>tr|D7BJD8|D7BJD8_MEISD Potassium-transporting ATPase potassium-binding subunit OS=Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) GN=kdpA PE=3 SV=1 MTDVILILLLVLLLAWPLGGYLARVFSGERTLLDFLAPLERGIYRLLGVNPERGMDWRGYAK ALLGSNLLLALAAYGVLVLQGKLPLNPDGVPSMSWHLALHTVASFITNTNQQHYSGQAQLS YLAQMLAITALQLITPAAGLATLVAILRALRPPAGRKAGDLGNYFVDVTRALTRVLIPLSVAWA LLLTWQGVPSTFSGAKVAELLEPQTLTVEGKPQTVREQVIPVGPVAAMVAIKQLGTNGGG WYGPNSAFPLENPTPFSNLLETVAILLLPVAQVFMIGHLLRNLAFARLVFGVMAAFSVLFIALI LPMEQAPNPAFAQLAAPGPNWEGKELRLGPLPSALWATLTTQTSNGSVNAMHDSLQPLSI LIALVDMFINATWGGVGVGAINFLLYVVLAVFIAGLMVGRTPELFGKKLEAREIKLASIAILLQP LLVLVPTALALGSGLANTSNPGFHGLSQVLYEYTSAYANNGSGLAGLGNTTVWWNLSCAV VLILARYIPMIAPLAIAAFLAAKRTAPQTVGTLRTETPTFGLTVFSIIVIVQGLNFFPYLILGPIAE QLVGVR

2E-216	728.9	25.8	2E-216	728.7	17.9	1	1	D1BAQ9_SANKS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Sked_27060	Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Sanguibacteraceae, Sanguibacter, Sanguibacter keddieii, Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	446469	>tr|D1BAQ9|D1BAQ9_SANKS Potassium-transporting ATPase potassium-binding subunit OS=Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74) GN=kdpA PE=3 SV=1 MTMSETWTAVGQISLLVAALAAVHLPLGAYLAHVYTSPRHLRVERLGYRVMRVDADAEQR WTSYLFSLLGFSLVSLLALYAMGRLQEHLPMNLGVSAFDPAGAWNTAVSFVANTNWQWY SGEAAAGHVFQMVGLAVQNFVSAAVGISVAIALVRGFARSGTDGRVGNFWSDLTRTCVRV LLPMSLLAAVALLATGVIQSFDPHTAVQTVSGGSQHLLGGPVASQEAIKELGTNGGGFFNA NSAHPLENPSPVSNLLEIFLILVIPFTLPRAFGLMVRDTRQGFAIVSVMGSLFLAGTALLTWAE MSGPGLAAQAAGGALEGKELRFGTAGSALFAAATTGTSTGAVNAMHDSLTAPGGGIATFN MLLGEIAPGGVGSGLYGMLVLAIVAVFIAGLMVGRTPEYLGKKIGRQEITLVALYILTVPLLVL VGTALAISLPAGQAGIQEAGPHGLSEVLYAMTSAANNNGSAFAGLTTATPFYNTLLGVLMLV GRFVPIALVLALAGRFASQKTVPATAGTLPTHQPLFAGLLGSVALVVVGLTFIPVLSLGPIVES LS
3E-216	728.4	29.7	4E-216	728.1	20.6	1	1	F8DYL1_CORRG	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CRES_1320	Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	550	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium resistens, Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	662755	>tr|F8DYL1|F8DYL1_CORRG Potassium-transporting ATPase potassium-binding subunit OS=Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026) GN=kdpA PE=3 SV=1 MSGTFTGWIPVIIVIIALAGLYVPLGNYMAATFTSEKHNGFEKVFYRLIGVNPDGHQKWTRYT ASLLAFSTISVVFLYLLQRVQQWLPLNHGKAPVNWDQAWNTAVSFTTNTNWQSYSGEEAM TILTQMAGLAVQNFVSAAVGITVAIALIRGLANRIGNGVIGNFWVDLTRAVFRVLLPMAVIGAI LLISQGAIQNFHAPTTIQTITGGQQTIPGGAVASQEVIKELGTNGGGYFNANSAHPFENPNA WTNMLEIFLILVIPVALTRTFGKMIGDTRQGWAVLAAMAVLYFTSLAVVMSSESSLAAFQGG GLEGKEYRLNVLPSSFFAVTTTMTSTGAVDSFHSSYHPLAGGMLILDMMLGEISPGGVGTG LYGMLMIALLSVFVAGLMVGRTPEYLGKRIGVSEITKVSLYILVMPTLVLAGVGISAMLPSTRE SVSASGPHGFSDIVYAYTSASNNNGSAFAGFGADTPWFNITLGLCMLLGRFLPIVMALALAG DFAKQKPAAETAGTLPTHRPQFVGVMVGIAVIVGALTFLPTLVLGPLTEALS
4E-216	728.1	30.7	4E-216	727.9	21.3	1	1	K9SX66_9SYNE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Syn7502_02572	Synechococcus sp. PCC 7502	567	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. PCC 7502	1173263	>tr|K9SX66|K9SX66_9SYNE Potassium-transporting ATPase potassium-binding subunit OS=Synechococcus sp. PCC 7502 GN=kdpA PE=3 SV=1 MLQGWLQIGLTLILIVAIAPIFGSYIAKVYLGQKTLLDPVLRPIEALIFRLSGINPENPKNGWQY AGGVLYSNLIMSVFLFLMLMLQGLLPLNPTGLPAPTWDTALHTTISFMTNTNQQHYSGETTL SYFTQTLGLGFMFFTSAGTGIAVAIAFIRGLTGRPLGNFYSDLTLAITRILLPISIVGAIVFMAAG VPETLSVPIIVPTLENPNLSQAIAIGPVAHFEIIKQLGENGGGFFAINSAHPFENPNNFTNLIQIL AMISIPTALIFTYGEITNNRKQSWLLFGLVFIIYVAFIIVTGVGEYQGNPLVNTLLGGQSPNLEG KEVRFGWAQSALFAVTTSGTMTGAVNSMLDSFMSNGGFVFLSNLFLQILWGGQGTGTAYL YAYSILAVFVTGLMVGRTPEFLGRKIEKQEVVLTSFLILLVHPIFILIPGAIALAFPDQLAGISNP GFHGLSQVIYEYASAAANNGSGFEGLVDSQPAATGLWWNLSTSVSLLGGRYIPIVALLLLAD GMSRKQTVAMTAGTLRTDTILFTSVTAGVILIMAALTFFPVLALGPIAEAFQLSY
4E-216	727.9	37.3	5E-216	727.7	25.8	1	1	K8E2F1_CARML	Potassium-transporting ATPase potassium-binding subunit (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN424_661	Carnobacterium maltaromaticum LMA28	560	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium maltaromaticum (Carnobacterium piscicola), Carnobacterium maltaromaticum LMA28	1234679	>tr|K8E2F1|K8E2F1_CARML Potassium-transporting ATPase potassium-binding subunit OS=Carnobacterium maltaromaticum LMA28 GN=kdpA PE=3 SV=2 MSAIVVNQILFLVILIGLGIPLGIYSYRVMSGKKVFLSRVIEPIENQVYKFIGKPAKLEMTAKKYA LAIVSFSLFSFLAVFLLMLGQGFLPANPNGFSGTSIGLAFNTAMSFVTNTNWQAYSGEVTLS PFTQMVALTVQNFVSAGVGIAVLFALLRGFIARNKETLGNFWQDLTKAVLYILVPVSFVIALLL VSQGVVQSFSADVPVFSLETGQKILIPLGAAASQIAIKQLGTNGGGYFGANSAFPFENPTVF SNFIENLAILLIPVALIVAFGLFVKNAKQGRTIFIVSLVLLGLALVGVTMSESYTGPSYPGVVES GSLEGKETRFGVGWTSLWAVSTTAASNGSVNGMHDSLTPLGGMIPMFLMQLGEIVFGGA GSGLYGMIAFVILTVFIAGLLVGRTPEYLGKKIDPFDMKMVCLLILTPPLLVLLGTMSFVMLPN GMEWLTNSGPHGFSEVLYAFSSLANNNGSAFAGLTSDTPFLNVVGGVIMLVVRFVPMFAAL FLGGNLAKKKMVAVSDGTLSTTNGTFVGMLIGVILLIGALSFLPAMALGPIAEYFMH
8E-216	726.9	29.3	9E-216	726.7	20.3	1	1	W5WRG8_9CORY	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA CFAL_06855	Corynebacterium falsenii DSM 44353	550	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium falsenii, Corynebacterium falsenii DSM 44353	1451189	>tr|W5WRG8|W5WRG8_9CORY Potassium-transporting ATPase potassium-binding subunit OS=Corynebacterium falsenii DSM 44353 GN=kdpA PE=3 SV=1 MSGAWTGWIPVAVVIIALAALYLPMGKYMAWALNNPKDTRIESGFYRLIGVKADGKQHWVK YSASVMAFSAVSVVFLYLLQRTQQFLPLNHGMSAVDPDQAWNTAVSFTTNTNWQSYSGE EAMTQLTQMAGLGVQNFVSAAVGISVAIALVRGLANRAGDGAIGNFWVDLTRTVLRILLPVA TLGAIILLANGVIQNFNAPETFTTITGGQQTIPGGAVASQEVIKELGTNGGGYFNANSAHPYE NPNMWTNMLEIFLILLIPVSLTRTFGIMVKDKRQGWAILAAMAILFVASFAVIASSEHALTFVQ GGGMEGKEVRFGVLPSNFFANSTTMTSTGAVDSFHSSYAPLAGGMLILNMMLSEISPGGV GSGLYGMLMIAILSVFIAGLMVGRTPEYLGKRIGVKEITKVCLYILVMPTLVLFGVGISTMLPS TLDSVSVSGPHGFSDIVYAFTSASNNNGSAFAGFGADTWWFNMSLGFAMLLGRFVPIVMV LALAGDFAKQKPAPETAGTLPTYRPQFVGVIVGVAIIIGALTFLPTLVLGPFTEALS

8E-216	726.9	33.1	9E-216	726.7	22.9	1	1	A0A0F3L9X1_9CAUL	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VH88_12705	Brevundimonas sp. KM4	569	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas, Brevundimonas sp. KM4	1628191	>tr|A0A0F3L9X1|A0A0F3L9X1_9CAUL Potassium-transporting ATPase potassium-binding subunit OS=Brevundimonas sp. KM4 GN=kdpA PE=3 SV=1 MNMQGWGEIALTLGLAVMLGWPIGVYMSRVWNGERTWLDPVLKPVEAVFYGAAGVDPKR SQGWLGYAGALLAFNLAGFVLLYAILRLQGVLPLNPQGFAGVSPHLAFNTAVSFVTNTNWQ SYGGEATLSTFTQMVGLTVQNFVSAATGATIAAALARAFVANRGEGVGNFWADLTRTTLYV LLPAALILAVALSGLGIVQSLAAHVTATGVEGGSQTLPLFPAASQVAIKQLGINGGGVFNVNG AHPFENPNAITNLLTAVAINVMGWAAFFAFGRTAMAGRDIRALAAAALILLSAASAAMYVIET QPAPALVAAQVDASINMEGKEVRFGAPASTVWSVVTTGASNGSVNAMHASFMPLGGGLQ MFLMQLGEILPGGIGSGIAIMVVMALLSVFVAGLMVGRTPEYLGKKIEAREIQFAMIAVLILPL AILGFTAVSAVFPTALAGLLNKGPHGLSEILYAYTSAAANNGSAFAGLTANAPWWNTTLGLG MLFGRFIPAVAVLAIAGSLVTKPKLAPSPGTLPTDNGLFIGLLIGVILILGGLQFLPALALGPIVE HFQVLAAVAGA
1E-215	726.6	18.8	1E-215	726.4	13	1	1	L0DLW9_SINAD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Sinac_5536	Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	580	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Singulisphaera, Singulisphaera acidiphila, Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	886293	>tr|L0DLW9|L0DLW9_SINAD Potassium-transporting ATPase potassium-binding subunit OS=Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10) GN=kdpA PE=3 SV=1 MLWIHPFWAFLLPIAASLPIGWSMFRTLDVPTDRAGRGLDALPMFLCRLIGRREPARMDWK KYAVAFIVFNLALFILTFGLLYAQPRMPLNPDGKGSLGALGYKDTAGVDHPGADTAVVFNTV CSFVTNTNLQHYAGEQNLSYFSQLACIVWLMFVTPAAGLAVMLATLRGLRGDSHLGDFYAD LMRSLVYVFMPYCFLVAILLVGSGVPMTFQPAAQATTLDGLATKMETQTIARGPVAALVAIK QSGTNGGGFFGPNSTHPFENPTPWSNMLGVVSIIVLPMASLIMAGLMLKNMRHAVVIFSVM LLLLFSGLVVAVWAESYPSAATQGLPVVRGPNMEGKEVRLGPVAAATWAAITTATSNGSVN SMHDSLNPIAGMVPMALMMLNVVFSGIGAGFENMLMYVIVAVFLAGLMVGRTPEYLGKKVE AKEVKLAMIAILFHPLLICAGAGLFAATDWGAKTVANPGSHGFSEILYEFDSAAANNGSGFE GLGDNNPPWNIATGVVLLLGRFPALILPLALAGSLAVKKRVPETIGTLRVDNLTFAGMLLGTV LLVGALSFMPAVVLGPVADQLAAVPK
2E-215	725.9	30.8	2E-215	725.7	21.4	1	1	KDPA_LEPIN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LA_3112	Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	557	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira interrogans, Leptospira interrogans serovar Lai, Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	189518	>sp|Q8F1M1|KDPA_LEPIN Potassium-transporting ATPase potassium-binding subunit OS=Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) GN=kdpA PE=3 SV=1 MVTEWIQLLIFLFALLIFSPLFGLGLYKVYLYKTSGFEKFLYKICGIDPNRNMDWKEYALSLLV FNFFGFLLLFLILFFQNYLPLNPENFPGLVWDLAFNTAVSFATNTNWQAYSGESTLSFFSQM AGLTTQNFLSATTGLCVLLALSRGISVNYNVFALGNFWKDMIRGTLYVLLPLSFIFALFLVGF GVVQTFSESVSAITLEGNTQIIPLGPVASQVAIKQLGTNGGGYFGVNASHPFENPSPISNFLQ MFSILILPGACVFLYGRITGSIRHAWAIFSVMFTILCVGILIVWTFESSWNPISGTLGFWEGKEI RFGILNSSIWEVATTVASNGSVNSMHDSFSPIGGLVGILNIQLREIVFGGVGAGMYGMILFVL LTVFLSGIMVGRSPEYLGKKIEKREIQMSILGILLPSTIILLFTAISVSVSDALSSLTNRGPHGLS EILYAFSSGAGNNGSAFAGLNANTTYYNVMIAIAMILGRFGVILPVLVIAGSLAQKKRSEIVSE GSFSTEGGTFYILLLSVIIIVGALTFFPVLTIGPILEHFIMFQNLTF
2E-215	725.8	23.7	2E-215	725.6	16.4	1	1	W5WRB9_9PSEU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KALB_7347	Kutzneria albida DSM 43870	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Kutzneria, Kutzneria albida, Kutzneria albida DSM 43870	1449976	>tr|W5WRB9|W5WRB9_9PSEU Potassium-transporting ATPase potassium-binding subunit OS=Kutzneria albida DSM 43870 GN=kdpA PE=3 SV=1 MNDTWAGLLQLALLLAALAVVYRPLGDYMARAFTSKGHWKLERALYKVVRVNPDSEQRWS TYAYGVLGFSFVSVLFLYLLQRLQTVLPLGLGRPEISPSVAFNTAVSFVTNTNWQSYVPEQA FGHLVQMAGLTVQNFVSGAVGIAVAVALIRGFTRANTDRLGNVWVDITRAVVRVLLPIAVLF AVVLMGLGVVQSLSGGVDVTGIDGAQHTVALAPVASQEVIKELGTNGGGVLNANSAHPFEN PNGWTNLIEIFILLVIPVSLTRTFGTMIGDRKQGYTLLSVMTFLWGGMLAVIWWAEAHPNGP AALLAGSAMEGKETRFGIPSSALFADSTTGTSTGAVNAAHDSLTGLGGGGALLNMLFSEISP GGVGTGIYSILVFAIIAVFLAGLMVGRTPEYLGKKLGRKEITMASIAILAMPTLVLVFAGIAVVL PATGDALTNSGAHGLSEVLYAYASASNNGSAFGGLTVTNDWFQSTLGVCMAFGRFIPILA VLCLAGGLAAQRKVPPSAGTLPTSGPLFASMVAGSVLLVAALTFVPALALGPIAEALS
2E-215	725.7	19.5	2E-215	725.5	13.5	1	1	A0A0F7CNE5_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SXIM_13870	Streptomyces xiamenensis	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces xiamenensis	408015	>tr|A0A0F7CNE5|A0A0F7CNE5_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Streptomyces xiamenensis GN=kdpA PE=3 SV=1 MNDAAAGLLTIAALVALLALVHVPLGDYLARVYTGERHLGVERLLYRIARVDPRADQRWTAY ALSLLAFSAVSALFLYAFLRLQGVLPLAQGHAGVHPSGAFNTALSFVSNTDWQWYAGETTL GPPAQMAGLAVQNFLSAAVGLAVAVALIRGFARSRTDRLGNFWVDLVRGTVRVLLPLAVLA AIVMAAAGVVQNFHGVREIVTLGGDRQALTGGPVASQEAIKLLGGNGGGYYNANAAHPYE NPNPFTNFFQVFLLLLIPSALPRTFGRMTGSPRHGWAVLAAMTALWAIGLAAVTTAEATHH GDVPQAVGAATEGKEWRFGVWNSALYANATTTTSTGSVDAAHESFTPLGGGMLLLNMLL GEVAPGGVGVGLYGMLVLAMLAVFLAGLMVGRTPEYLGKKLRQREITLLALYVLAMPFAVL TGTALALAFPEPRARILAGPPHGLSEVLYAYASAGNGNGSAFAGLGADTTFYTTTLGLVMLM GRFVPMVLVLALAGALAAQHRTPTGAGTLPTHTPLFTGLLVTVAVVVAGLTFFPMLALGPLA EGLR

2E-215	725.6	25.4	2E-215	725.4	17.6	1	1	D2QBF3_SPILD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Slin_0062	Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896)	573	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Spirosoma, Spirosoma linguale, Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896)	504472	>tr|D2QBF3|D2QBF3_SPILD Potassium-transporting ATPase potassium-binding subunit OS=Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896) GN=kdpA PE=3 SV=1 MSTELIGVIVMYGLTVLLAIPLGKYIANVFRPESANGPLERFIYRVGGIDPTREMSWKENLTAL LTINAVWLAFSFTLLLLQGMLPLNPDGNPSMTPDLAFNTAISFMVNCDLQHYSGESGLTYLT QLFVINFLMFVSAATGIASLLLIVRSFLPKVVDTVGNFYVFFVKAITRILLPLSFVVSLILAFNGT PASFDGKDSIVTMQGDTVGVSRGPAAGMIAIKHIGTNGGGWFGVNSAHPLENPNYLTNMV EMVAQVLIPIAMLFALGFLINRRRFTWVVYGVMTLGMLCLLIPTLVTEVHGNPAIAQLGVSQP TGAMEGKEVRFGPLASAYWSIVTTIISTGSVNSMHDSSMALSGTMELLGMMTNAFYGGCG VGFLNYYYYLIIAVFISGLMVGRTPELFGRKVEAREIKIASIVALLSTLLVKGGTALAVWFFVKY PDAAAGVASDWAVKPSAWLNNPGNHGFSELLYEFTSANANNGSGFEGLGDNNFFWNYAT GIVLILGRFIPIIGPVAIAGLLAQKKYVPESAGTLPTDTGTFGLMTFAVILIITALSFFPALALGPL AEYFSLK
3E-215	725.2	29.2	3E-215	725	20.2	1	1	KDPA_MYCA9	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MAB_3254c	Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	572	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium chelonae group, Mycobacterium abscessus subgroup, Mycobacterium abscessus, Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	561007	>sp|B1MBE1|KDPA_MYCA9 Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543) GN=kdpA PE=3 SV=1 MNSALAAGLQIGFVILALAIAYVPLGDYMARVFTGPHSLRASGLSTIKHSRVERLIYRVGRVD PETEQTWVGYTLSLLGFSFASVIFLYVLQRIQGVLPLSGGLGAVSPAVAFNTAVSFVTNTNW QSYTPETTMSNLTQMVGLAVQNFVSAAVGLTVAVALIRGVVRTTSGGELGNFWVDLVRGS LRILLPLSFAVALILLSQGTIQSVYTHFEATALDGTAQHIALAPVASQEAIKEIGTNGGGILGAN SAHPFENPTPLSNVIEILAILIIPVCLTRTYSTMVGDKRQGLTVLSVMGTLFGGMLALVTWAE SSPRGIAAQAAGAMMEGKEVRFGIPGSALFAVSTTGTSTGAVDAAHDSFTAAGGGALILNM LLGEIAPGGVGTGLYGILVLAIIAVFVGGLLVGRTPEFLGKKIGRRQITMAALSVLVMPALVLV GTGISVALSTTTGYQGNSGDPGTPSSIHGFSEVLYAYASAANNNGSAFGGLTVTSHWFQA SLGMAMLLGRFLPIIFTLALAGSLATQRKTPASAGTLHTHGPMFAGLHTGTVLLVAALTFFPA LALGPIAEAVL
4E-215	724.8	30.1	4E-215	724.6	20.9	1	1	V5XQW1_ENTMU	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA EMQU_1744	Enterococcus mundtii QU 25	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus mundtii, Enterococcus mundtii QU 25	1300150	>tr|V5XQW1|V5XQW1_ENTMU Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus mundtii QU 25 GN=kdpA PE=3 SV=1 MMSAVFQGLFFFFILLVLAAPLGWYIKLIMTGETPKYVRFIQPIERFFYQLIGPESQKKMTAKR YLAHVLGIGICSLLFLTGLLMVQGWLPGNNGVENLSFDLAVNTAVSFVTNTNWQAYAGEVT LSNTTQMLGLTVQNFLSAAVGLAVLCALIRGIIQRKSSQLGNFWQDLVRSLLYIFLPLSLITAV LLISQGVVQTFSHGMSYTGLSGESLWLYLGPVASQVAIKQLGTNGGGFFGANSAHPFENPT IFSNFIENLAILLIPTALIFAFGYWVKEWKQGRTILIVSFVFLFAAFVGVAISEYHGPAFTDVLG SLNMEGKEVRFGVGWSSLWAVSTTAASNGSVNAMLDSFTPLGGGIPLFLMQLGEIIFGGV GSGLYGMLAFLLLTVFIAGLLVGRTPEYLGKKIEAFDIKMASLVILTPVLLTLFGTMAVSLHPD VLTWLTNKGPHGFSELLYNVTSLANNNGSAFGGLTADKPFLNLLGSVLMLCSRYIPIVAILFL AENMGRKKTIAINDGTLSTTNGTFISMLMIVILVVGALSFLPALALGPIADHFTLS
7E-215	723.8	31.4	8E-215	723.6	21.8	1	1	F5XJD1_MICPN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MLP_28170	Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Microlunatus, Microlunatus phosphovorus, Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	1032480	>tr|F5XJD1|F5XJD1_MICPN Potassium-transporting ATPase potassium-binding subunit OS=Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1) GN=kdpA PE=3 SV=1 MSDTASGLLTIAALIVLLALAYVPLGDYLAAVLTPTRHTRLERGLYRLFGVNPDGEQNARSYA TAVLAFSLVSILLLVAILSWQPLLPFSRGMAGMSLPMAINTAVSFVTNTNWQSYAGESTLGY TAQAAGLTVQNFVSAAVGIAVAAALLRGLAARQTTALGNFWVDLTRIVLRLLLPLSVVVAILLL VCGVIQNLDPDRVISTIAGGRQALPGGPVASQESIKLLGTNGGGFFNANSAHPYENPTPVSN LIEIAALMVIPVSLTRTAGTMLGDRRQGTALLAAMAVLWGSALALATWAELTGSGSVPAAAG AAMEGKETQFGIWSSALFATATTGTSTGAVNAMHDSMTAAGGGIVLLNMVLGEVSPGGVG SGLYGILIAAIVAVFIAGLMVGRTPELLGKKIGAREMTWVAGYVLSSPALVLLGLGIAMAVPST LGAMANSGPHGFSEVFYAYASAANNNGSAFAGLTVTSTFFQLTLAAVMALGRFVPMIAVIAL AGRLAGPPSVARSEGTLPTHTPLFVSLLVGVIVLVSGLTFFPALALGPIAEALS
8E-215	723.7	24.4	9E-215	723.4	16.9	1	1	A0A0F2GLW5_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UG56_03110	Nocardioides luteus	554	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Nocardioides, Nocardioides luteus	1844	>tr|A0A0F2GLW5|A0A0F2GLW5_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Nocardioides luteus GN=kdpA PE=3 SV=1 MNTVVAAVLQVAVLIAALALAVPFLGRYLAHIYTTEKHLRVEKVVYRVLRVDPDADQRWRSY ALAVLGFSLVGILFLYLLARVQQWLPLSLGFDPFPSDGAWNTAVSFVTNTNWQWYSGEAA AGNLLQMAGLTVQNFVSAAVGMSVAAAFARGLARGRGNGRVGNFWADLVRTTLRVLLPIS FVGALVLVGFGAIQNLRADLAMTTLDGGQQILTSGAIASQEVIKELGTNGGGPYNVNSAHPF ENPTPFTNLLEIFLLLVIPFAMAWAFGLIVKDRRQGGAVLATMATLWLGAVGLLTWAEIAGP GTAPQLAGGAMEGKEARFGEAASALFASSTTGTSTGAVNAMHDSLTAPGGGIAMFNMML GEVAPGGVGSGLYGMLMLAIVTVFLCGLMVGRTPEYLGKKIGQREIVLVALYILATPILVLVG AAVAVSFPAGPAGMLNSGAHGFSEALYAVTSAANNNGSAFGGLTAGTPFWNTLLGVLMLF GRFLPIVFVLGLAGRFATTQHLPAGAGTLPTHRPLFVVLLTGVALVVVGLTYVPALALGPIVE SLS

1E-214	723.3	27.7	1E-214	723	19.2	1	1	A0A0F5MVM2_9MYCO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA WR43_16150	Mycobacterium arupense	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium terrae complex, Mycobacterium arupense	342002	>tr|A0A0F5MVM2|A0A0F5MVM2_9MYCO Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium arupense GN=kdpA PE=3 SV=1 MSTAVAGAVFLASLVLALAAAHIPLGDYMYRVYERQTHSRSERLIYSAIGVDPESKQTWAAY ARSVLAFSAVCVVFLFGLQLIQGRLPLHLHQPATPMTPGLAWNTAVSFVTNTNWQAYAGES TQGHLVQMAGLGVQNFVSAAVGMAVAVAFVRGFVGRRTAVLGSFWVDLVRGALRILAPLA VAGAVVLIAGGVVENFHLHDQAVTTVAGMSQTIPGGPVAGQEAIKLLGTNGGGFYNANSAH PFENPTSWTNWVEIFLLLVIAFSLPRTFGRMVGATKQGHAIVAVMAVLAFIGVGLLSWAQLV HHGTVPTAVGAATEGIEQRFGVADSAVFAAATTLTSTGAVDSAHDSYTSLGGLMTMVDMQ LGEVAPGGVGSGLYGILILAVITVFVAGLMVGRTPEYLGKKIGAREIKLAASYFLVMPVIVLCG TAISIALPGPRSAMANSGPHGLSEVLYAFTSAANNNGSAFAGLAANGTWFETTLGIAMLLGR FVPIIVVLALAGALAAQGSAPESLGTLPTHKPQFVGLVVGVTVILVALTFLPSLALAPLAEGLH
1E-214	722.9	43.8	2E-214	722.6	30.3	1	1	A0A0F2IZS9_9BACT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MCHI_002513	Candidatus Magnetoovum chiemensis	560	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Candidatus Magnetoovum, Candidatus Magnetoovum chiemensis	1609970	>tr|A0A0F2IZS9|A0A0F2IZS9_9BACT Potassium-transporting ATPase potassium-binding subunit OS=Candidatus Magnetoovum chiemensis GN=kdpA PE=3 SV=1 MNNYDYLTIVIYLGALALSVPLLGTYMELALNNYLPFNSRIISKMEIGLYKICGINHLKQMSHRE YLYSVLVFNLFGFALLMAIMLFQKYLPFNPQGLEGVPFFLALNTAVSFVTNTNWQAYSGEAV MSYFTQAMGLCVQNFVSAATGIAVFMALARGIVKQEAKQLGNFWVDLTRTALFILIPMSFILA VLLMNEGVVQSLSGYVEATTLEGAEQVIPMGAAASQIAIKQLGTNGGGFFGVNSAHPFENP TPLSNFLQTLAILIIPAALTYTYGRVVGKKKEGLTLFYVMSFIFLVSLGLALYFEYCGYPKLFNG LTMMEGKETRFSTTSSVLWGMATTVASNGSVNAMHSSFSPITGGLAILNMMFGEIVFGGV GSGMYGMLMFVILTVFITGLMVGRTPEYLGKKIEQKEIIMAAVAIIQPGAFILIGSLIAVLTNAG LSSLSQGGPHGLMEILYAFTSASQNNGSAFAGLSVNTNFYNIMLAICMIAGRYGVIVPVLIAG SLSSKKHIPASSGTFTTDNALFAALLVAIIIIVGALTFFPALSVGSIVEHLIMTQ
2E-214	722.4	20.3	2E-214	722.2	14.1	1	1	KDPA_MICAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MAE_59800	Microcystis aeruginosa (strain NIES-843)	581	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Microcystis, Microcystis aeruginosa, Microcystis aeruginosa (strain NIES-843)	449447	>sp|B0JJS4|KDPA_MICAN Potassium-transporting ATPase potassium-binding subunit OS=Microcystis aeruginosa (strain NIES-843) GN=kdpA PE=3 SV=1 MLQGWIQIALTILIIVAITPFFGRYMARVFMERRTLLDPLCDRVESLLYTFVGVKGKENMTGW QYTRAVLYSNAVIAILVFSLIAGQGVLPLNPTGIPAPSWDTTLHTTISFITNSDQQHYSGETTL SYGSQIWGLGYQMFTSAGTGLAVGIAFIRGLTGRPLGNFYVDLIRAITRILLPISIVGAIALIIAG VPETLAGPAILPTLENPNLSQAIARGPVAHFEIIKELGENGGGFFASNSAHPFENPNGFVNLV QLVAILSIPTSLIYTYGVFADNLKQARLIYLIPLGIFIGFTIITAIGEYNGNQAVNSLLGVERAVNF EGKEVRFGWAQSALYAVTTTATMCGAVIAMHDSLMPNGGFATLSNLFLQIVFGGQGTGTA YLFAYLILAVFVTGLMVGRTPEFLGRKIEKREVVLASFLILLVHPIAILIPGAIALAFPDFQGISNP GFHGLSQVIYEYASAAANNGSGFEGLGDSQPAPLAIAAGAKPTITALWWNLSACFSLLAGR YIPIAALLLLADGMSRKQPVPATTGTLRTDTGLFTSVTAGVILILGALTFLPILALGPIAEAFQIT RMIG
5E-214	721.1	28.2	5E-214	720.9	19.6	1	1	A4FMI7_SACEN	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SACE_6089	Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharopolyspora, Saccharopolyspora erythraea (Streptomyces erythraeus), Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	405948	>tr|A4FMI7|A4FMI7_SACEN Potassium-transporting ATPase A chain OS=Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338) GN=kdpA PE=3 SV=1 MSSPLVGLVQAGLLVLAVVAVYRPFGDYMARVYTGAEHWRVERALYRAVRIDGDAPQRWT TYAAGVLGFSFVSIVLLYLLQRLQHLLPLSFGRGPVEPATAFNTAVSFVTNTNWQSYVPETT LGHTVQMAGLTVQNFLSAAVGMAVAVALVRGFTGTATNRVGNVWVDITRGVTRILLPISLAA AVVLVALGGAMSLASGIEVTGVDGHTYTIATAPIASQEAIKELGTNGGGILNANSAHPFENPS GWSNFLELFLILVIPLCLTRTFGTMVGDRRQGHVLLSVMVSILLLMTGAAWWAETHPNGPA TLAAGGAMEGKEARFGLFLSTLWAVVTTGTSTGAVNSMHDSFTGLGGGVPLLNMLLGEVA PGGVGSGLYGMLVLAVIAVFLAGLMVGRTPEYLGKKLGRREITAAAVSILAMPTVVLLGAGA ALALPGTLEALNNSGAHGLSEVLYAYASAGNNNGSAFAGLTATGDFFQSTLGVAMLVGRFV PVLAVLALAGALAQQQRVPATAGTLPTTGPLFAGLLGGTVVLVAALTFLPALALGPIAEALA
5E-214	721	28.2	6E-214	720.8	19.5	1	1	K9RK69_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Riv7116_5537	Rivularia sp. PCC 7116	560	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Rivularia, Rivularia sp. PCC 7116	373994	>tr|K9RK69|K9RK69_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Rivularia sp. PCC 7116 GN=kdpA PE=3 SV=1 MGQGFLQIGLTLLLVLIVTPTFGKYIAKVFMGRTTLLDRVMNPLELLIYKLADVNPQENMRGK EYAYCVLQSNLFIGLLVYLFISFQKFLPWNPSNLGAPRWDLTLHTTISFLTNTGQQHYLGEKT LSHFSTMAGLTFLMFVSAGTGLAIGIAFIRGLTGKPLGNYYADLIKAITRILLPISIVGAILLLAQ GVPQTLAASVAVETLEGRTQYIATGPVASFEIIKLLGTNGGGFFGANSAHPFENPNSFTNLV EIIAMISIPAAMIFVYGEFSHNIKQAWRLFWMIFLIFLALLWITAVGEFQGNPLVNSNLGFDQP NLEGKEVRFGWAQTALWAVVTTATMNGAVNGMHDSLMPAAGFSTLLSMFLHVIWGGIGT GIIYLLIYQYLTAFWAGLMIGRTPEFFGRKITRTSIVLASLVILIHPIAVLIPSAIALAYPISLSGISN PGFHGVSQVVYEYISASANNGSGFEGLIDGTFWWNLSTSASMLVGRYVFLFAVLLLADIMV HTKPVPEIPATLKTDTLLFTSLSAGVIFILSFLIFFPILVNGPLAEGLRLAAQ

6E-214	720.7	27	7E-214	720.5	18.7	1	1	R5X9J0_9FIRM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN568_00208	Blautia sp. CAG:257	541	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	1262756	>tr|R5X9J0|R5X9J0_9FIRM Potassium-transporting ATPase potassium-binding subunit OS=Blautia sp. CAG:257 GN=kdpA PE=3 SV=1 MSWKKYLVSVLAFSGFGLLVLFLLQVFQKFLPFNPQHIEGMSWDLSLNTAISFVTNTNWQA YSGESQLSYLSQALGLTVQNFVTPATGIAVLYALIRGFTRVKGKGVGNFWTDLTRSTLYVLM PLSLAGALMIASQGVPQTWKAAETVELMEPVAFDADGNYLEDARINGDTVTVDGEVVEDAE VVTEEIVPLGFAASQIAIKQLGTNGGGYYGVNSAHPLENPNWFSNLLEMLFLLLIPASLCFSF GRDVKDKKQGIAVFMAMFLMLIAAMSVVAVNEQSASTVLTENEYVDTSTDGQAGGNMEGK EARFGIGSSVTWATWTTAASNGSVNSMHDSYTPLGGMITMLLMQLGEVVFGGVGCGLYG MLGFAILTVFIAGLMVGRTPEYLGKKIEPYEMKWAVLVCLATPIAILVFSGIAAAVPSVAESLN NSGAHGFSEMLYAYSSAGGNNGSAFAGFGADTPFLNLTLGGAMLLARFLPITGILAIAGSMV QKKKLAVTAGTLSTSNGMFVFLLIVIVLLIGALSFFPALALGPIAEFVG
3E-213	718.4	32.9	4E-213	718.2	22.8	1	1	A0A0A1DUG7_NOCSI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KR76_23690	Nocardioides simplex (Arthrobacter simplex)	552	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Pimelobacter, Nocardioides simplex (Arthrobacter simplex)	2045	>tr|A0A0A1DUG7|A0A0A1DUG7_NOCSI Potassium-transporting ATPase potassium-binding subunit OS=Nocardioides simplex GN=kdpA PE=3 SV=1 MSDTAAGLLSIAVLVLLLAAVYVPLGDHMARVYTSSRHLRVERLVYRLSGVRPDVEQSPRSY ALSVVGFSLVGVVVLMAILIGQSHLPMSRDLPGMPFWMSFNTAASFVANTNWQSYAGEST LGFTAQMAGLAVQNFLSAAVGMAVAIALVRGFVRVKDGTLGNFWVDLTRGTVRILLPIAFVG AVLLIAGGVIQSFSDSTMHTLSGADQVLTGGPVASQEAIKELGTNGGGFFNANSAHPFENP SGYTNLLEIFLILVIPIALTRTLGTLLGRRRQGLAVLGAMVFLMAVSLTVVTVAEVGGHSATAQ AAGAAMEGKETRFGEWASALFGMATTGTSTGAVNSAHDSFTPAGGGGVLVNMMLGEITP GGVGSGIYGILVMAILTVFVAGLMVGRTPELLGKKIGSRQMTYVALYTLTTPALVLLGTGVAM ALGATPDTMGNPGGHGFSEVLYAYTSGANNNGSAFGGITVTSTFFQVTIGLAMLLGRLIPIV LVLLLAGSLAQQGKVPETAGTLPTHKPLFVGMLVGVILIMTGLTYFPALALGPIAEALA
4E-213	718.1	39.6	4E-213	717.9	27.4	1	1	KDPA_STAHJ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SH0033	Staphylococcus haemolyticus (strain JCSC1435)	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus haemolyticus, Staphylococcus haemolyticus (strain JCSC1435)	279808	>sp|Q4LAI3|KDPA_STAHJ Potassium-transporting ATPase potassium-binding subunit OS=Staphylococcus haemolyticus (strain JCSC1435) GN=kdpA PE=3 SV=1 MSIVLFLIVFILLSLIVSRYLYSVALNVPSKIDVVFNPIEKLIYRLIGTNLEHMSGKTYIKHFLLFN GLMGGLSFVLLLIQQWLFLNPNHNLNQSVSLAFNTMASFLTNTNLQHYAGETGLSYLTQMC VITFLMFTSAASGYAVCIAMLRRLTGMTDVIGNFYQDITRFIVRVLIPFALIISLFLISQGTPQTL KGNLVIETLSGVKQTIAYGPMASLESIKHLGTNGGGFLGANSSTPFENPTYWSNYAEALSM MLIPGSLVFLFGRMLKTKQQIHPHAIMIFVAMFVMFIGFLVTCLYFEFAGNPELHHLGIAGGN MEGKETRFGIGLSALFTTITTAFTTGTVNNMHDSLTPLGGMVPMVLMMLNAVFGGEGVGLM NMLIYVMLTVFICSLMIGKTPSYLGMKIEGKEMKLIALSFLVHPLLILVFSALAFIVPGASDALTN PQFHGVSQVLYEFTSSSANNGSGFEGLGDNTVFWNISTGIVMLLARYIPIVLQILIVSSLVNK KTYQQHTQDVPINNLFFSSVLIIFIILLSGLTFLPDLMLGPIGEQLLLHV
5E-213	717.8	38.2	6E-213	717.5	26.5	1	1	A0A075LMM1_9BACI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GZ22_12605	Terribacillus aidingensis	548	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Terribacillus, Terribacillus aidingensis	586416	>tr|A0A075LMM1|A0A075LMM1_9BACI Potassium-transporting ATPase potassium-binding subunit OS=Terribacillus aidingensis GN=kdpA PE=3 SV=1 MIVSLIALILVLVLIGVSLKPMGLYMAAVFSDSRLDRFFLPVENILYSISGIKKQKQTWKQYVFS MLLLNMVLLVFIYAVFRLQGILPLNPLDIAGMDPALAFNTAVSFITNTNLQHYSGESGLSLFSQ LTAILFMMFAAPSTALAVAIGFIRLLGGKPIGNFFEDFLRALVRVLLPISFIAAIIFVALGVPQTF SGAVHATTITGAEQSILRGPIGAFLSIKELGNNGGGFFGVNSAHPFENPNAYTNLLQCWLML LLPASLPFTYGKMTGKPKQGVMLFGAMAAVFLVMLAAGIAAEMQGNPLLQGAMMEGKETR FGVIGSVFYSIVTTAAETGAVNTMHDTLSPLTGMLALGNMLLNTVFGGGGTGFMNVILYVMI AVFIAGLMVGRTPAFLGKKLEGAEMKLLAITLLVQPILILLGTAIAMYFPAGNEAISNPGYHGL TQVLYEITSSAANNGSGFEGLGDATTFWNVLTGIIMFLGRYISIITLIAVAASLARKTAVQESK GSLRIDSPLFASLLVGTFFLVGALTFLPVLVLGPIAEYVTL
1E-212	716.4	27.5	1E-212	716.2	19.1	1	1	E9T4H3_RHOHA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HMPREF0724_13393	Rhodococcus equi ATCC 33707	566	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus hoagii (Corynebacterium equii), Rhodococcus equi ATCC 33707	525370	[illegible] OS=Rhodococcus equi ATCC 33707 GN=kdpA PE=3 SV=1 MNPALAAGLQIALVVAVLAILYVPVGDYMAKVYTTDTDFRSGDLRIETVVYRLCRINPRTEQT WYGYAGSLLGFSAASVLLLYFLQRIQGVLPLGGGLEGVSPAVAFNTAASFVANTNWQSYVP ETTMSHLTQAAGLAVQNFVSAAVGMAVAAALIRGFVRVSRGGEIGNFWVDLTRGALRILLP FAFVIALILLSQGVIQSFRTGFSSTGLDGTTVTNALAPVASQEAIKELGTNGGGILAANSAHPF ENPTPITNIVEILAILLIPVSLTRTFGTLVGDRRQGLTLLAVMSTLFFGLLAVTLAAESGARGAA ATAAGSMMEGKEVRFGIPGSALFAVATTGTSTGAVNSAHDSMSPLGGGAVLLNMLLGEIAP GGVGTGLYGILVLALIAVFVGGLLVGRTPEYLGKKLGQREITLAALSVLVMPALVLIGTGITVIL GSTVGYLGNSGDPGTPQSIHGFTEVLYAFASASNNNGSAFGGLTVTSDWFQSALGVCMLL GRFLPILFVLALAGSLSAQRRTPAGAGTLPTSGPMFTGLLTGTVVLVAALTFFPALALGPISE ALQ

1E-212	716.2	34.7	2E-212	716	24.1	1	1	A0A0D5AF39_9NOCA	Potassium-transporting ATPase A chain (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NY08_3525	Rhodococcus sp. B7740	550	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. B7740	1564114	>tr|A0A0D5AF39|A0A0D5AF39_9NOCA Potassium-transporting ATPase A chain OS=Rhodococcus sp. B7740 GN=kdpA PE=3 SV=1 MVGFFQICAVIVVLAVAYVPLGDYMARVFDSSHDTRVERLLYRVARVNSSSEQTWVGYSTS LLGFSFAGVVFLFVLQRIQGVLPLNGGLSGVSPAMAFNTAASFVTNTNWQSYVPETTLSNL TQPLGLAVQNFVSAAVGLAVAIAVIRGFVRVSTGGELGNFWVDLTRGTLRILLPLSLLVAVILL TQGTIMSFSTGFTSTGLDGQTVTNALAPVASQEAIKEIGTNGGGILAANSAHPFENPTPLTNI VQIISLLLIPVALTRTFGTMIGNRKQGLTLLAVMATLWGVLLAVTLYAESGTRGVAATAAGAM MEGKEVRFGIPASALFAVSTTGTSTGAVNSAHDSMSALGGGAVLLNMLFGEIAPGGVGTGL YGLLVLAVIAVFVGGLLVGRTPEFLGKKLGRRAITMAALSVLVMPILVLVGTSITVILESTTSYQ GNPGIHGFTEVLYAYASASNNNGSAFGGLTVTSDWFQISLGIAMLLGRFLPIVFVLALAGSLA TTKRSAPNAGTLPTDGPLFGSLLIGTAILVAALTFFPALALGPIAEAMQ
2E-212	715.7	22.1	2E-212	715.5	15.3	1	1	KDPA_METI4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Minf_0035	Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	574	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, unclassified Verrucomicrobia, Methylacidiphilales, Methylacidiphilaceae, Methylacidiphilum, Methylacidiphilum infernorum, Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	481448	>sp|B3DWR8|KDPA_METI4 Potassium-transporting ATPase potassium-binding subunit OS=Methylacidiphilum infernorum (isolate V4) GN=kdpA PE=3 SV=1 MNTSPGIELGLFIALLAVLNIPLGTHLYKVLDKEGKTVFDPILKPLENLTYKLCSIDRSKEQSWI EYAVGLLCFNFVGILVSYLILRLQSILPLNPEKIGPMAPHIAFNTAISFATNTNWQSYVPEKQV SYFAQMFGLAVPNFTSAATGIAAAAALVRGIVRTEMKTVGNCWVDLIRIHYYLLLPLSLFIAIIL LSQGVPQNFNAYVSYIPLELKSSLANLPVKLPQGPIASQEAIKLLGTNGGGFLNANSAHPYE NPTPLSNFVEMLSIFLIPSALTYYFGLSCKKLGHGWSIWLTMTFCFLILTLSCFIFEQAGNPLF SSLGIKNQLNMEGKEMRFGIFDSSFFASVTTLASCGAVNSLHDSFQPLAGMIPLFNMGLGEL IFGGVGSGLYGILLFVILSVFLFGLMIGRTPGYLGKRIGSYEIKMAVLALMIQYVLILGLSALALN SSWGTAALGNKGPHGLTEVLYAFTSTTENNGSAFGGLNATSKPFALLLLGVAMFLGRYFVLI PILAIAGSLANQKRYASQTVFPTGGWLFIFVLGATIFLLAALNFFPALTVGPILEHFMIGMGKS F
2E-212	715.7	20.4	2E-212	715.5	14.2	1	1	G0FV49_AMYMS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RAM_09605	Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis mediterranei (Nocardia mediterranei), Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	713604	>tr|G0FV49|G0FV49_AMYMS Potassium-transporting ATPase potassium-binding subunit OS=Amycolatopsis mediterranei (strain S699) GN=kdpA PE=3 SV=1 MTDTAAGLIQLGLLLAALAAVYRPLGDYLARVFSSEKHLKLEKGLYRLFRVDPGSEQRWPTY AAGVLGFSFVSVVLLYLLQRLQPLLPWSLGRGSVSPGVAFNTAISFVTNTNWQSYVPETTIG HFVQMAGLTVQNFLSAAVGLAVAIAVTRGFVRAKTDRLGNFWVDLTRGTVRVLLPMAFLVA LVLVALGVVQSLKAGVAVTNPDGSGSTIALAPAASQEAIKELGTNGGGIFNANSAHPFENPN AWSNLVQLFLILVIPVSLTRAFGSLVGSRRQGYVLLSVMGLLWTASLALIWFSEAYANNPAA RAAGASVEGKEQRFGIGLTSLFADTTTGTSTGAVNGAHDSLSGLGGGGPLLNMLYGEISPG GVGTGLYGILVLAIIAMFLAGLMVGRTPEYLGKKLGKREVTCAAIAMLAMPTVVLLGSGIALLL PGTAGALGNPGAHGLSEVLYGYASTGNNNGSAFGGLTATSDWFQSSFGVAMAVGRFVPV LAVLCLAGSLAAQRKVPETAGTLPTTGPLFATLLTGTVVLVAALTFIPALALGPIAEALA
2E-212	715.6	39.8	3E-212	715.3	27.6	1	1	KDPA_STAEQ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SERP2487	Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus epidermidis, Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	176279	>sp|Q5HK63|KDPA_STAEQ Potassium-transporting ATPase potassium-binding subunit OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) GN=kdpA PE=3 SV=1 MSIVLFLIVFILLSLIVSRYLYSVALNVPSKIDVVFNPIEKLIYQLIGTKLEHMSGKTYIKHFLLFN GLMGGLSFVLLLIQQWLFLNPNHNLNQSVSLAFNTMASFLTNTNLQHYAGETDLSYLTQMC VITFLMFTSAASGYAVCIAMLRRLTGMTDVIGNFYQDITRFIVRVLIPFALIISLFLISQGTPQTL KGNLVIETLSGVKQTIAYGPMASLESIKHLGTNGGGFLGANSSTPFENPTYWSNYAEALSM MLIPGSLVFLFGRMLKTKLQIHPHAIMIFVAMFVMFIGFLVTCLYFEFAGNPVLHHLGIAGGN MEGKETRFGIGLSALFTTITTAFTTGTVNNMHDSLTPLGGMVPMVLMMLNAVFGGEGVGLM NMLIYVMLTVFICSLMIGKTPSYLGMKIEGKEMKLIALSFLVHPLLILVFSALAFIVPGASDALTN PQFHGVSQVLYEFTSSSANNGSGFEGLGDNTVFWNISTGIVMLLARYIPIVLQILIVSSLVNK KTYQQHTQDVPINNLFFSSVLIIFIILLSGLTFLPDLMLGPIGEQLLLHA
3E-212	715	26.6	4E-212	714.7	18.4	1	1	KDPA_RHOE4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RER_37260	Rhodococcus erythropolis (strain PR4 / NBRC 100887)	561	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus erythropolis (Arthrobacter picolinophilus), Rhodococcus erythropolis (strain PR4 / NBRC 100887)	234621	>sp|C1A1E9|KDPA_RHOE4 Potassium-transporting ATPase potassium-binding subunit OS=Rhodococcus erythropolis (strain PR4 / NBRC 100887) GN=kdpA PE=3 SV=1 MSPALAAGLQIAFVLAVLAIAYVPVGDYMARVYSSTRDLRVESVIYRVGRIDSRAEQTWYGY AASVLGFSLASALFLYFLQRIQGVLPLSDGLSGVSPAVAFNTAISFVANTNWQSYTPETTMS NFVQPVGLAVQNFVSAAVGMAVAIALVRGFIRVARGGEIGNFWVDLTRGSLRILLPFSFVIAL ILLSQGVIQSFHSGFASTGLDGNAVTNALAPVASQEAIKELGTNGGGILAANSAHPFENPTPL SNIVEILAILLIPVCLTRTFGTLVGDRRQGLTLLAVMGILWSGLLAVTLAAESGARGVAATAAG SMMEGKEVRFGIPGSALFAVATTGTSTGAVNSAHDSMSPLGGAVLLNMLLGEIAPGGVG TGLYGILVLALIAVFVGGLLVGRTPEYLGKKLGRREITLAALSILVMPALVLIGTAITVILGSTTG YQGNGGDPGTPGSIHGFSEVLYAFASASNNNGSAFGGLTVTSDWFQSSLGICMLLGRFLPI IFVLALAGALASQKKVAPTAGTLPTSGPMFTGLLTGTVVLVAALTFFPALALGPLAEALQ

4E-212	714.7	30.2	5E-212	714.5	20.9	1	1	V9XPZ2_9NOCA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Y013_25405	Rhodococcus pyridinivorans SB3094	566	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus pyridinivorans, Rhodococcus pyridinivorans SB3094	1435356	>tr|V9XPZ2|V9XPZ2_9NOCA Potassium-transporting ATPase potassium-binding subunit OS=Rhodococcus pyridinivorans SB3094 GN=kdpA PE=3 SV=1 MNPAVAAGLQIAMVVAVLAVTYVPLGDYMARVYTTDLALRWKEFRVESLMYRLCRIDPRAE QTWYGYAASVLGFSLASALFLYALQRLQGVLPLDHGLGAVSPAVAFNTAVSFVTNTNWQS YVPETTMSPLTQSVGLAVQNFVSAAVGMAVAVALIRGLVRVGGGGGEIGNFWVDLTRGTVRI LLPLAFVIALILLSQGVIQSYRSGFTATGLDGNTVTTALAPVASQEAIKELGTNGGGILAANSA HPFENPTPISNIVEILAILLIPVALTRTFGTMIGNRRQGLTVLAVMALLYTTVLAVTMAAESGTR GVAANAAGAMMEGKEVRFGIPGSVLFAVTTTGTSTGAVNSAHDSMSPLGGGAVLLNMLLG EIAPGGVGTGLYGILVLSVIAVFVGGLLVGRTPEFLGKKLRRREITLAALAVLVMPALVLTGTG ITVILSSTTGYLGNSGDPGTPGAIHGFTEVLYAYASASNNNGSAFGGLTATSDWLQSSLGM CMLFGRFLPILFVLALAGSFATQRRVPSGSGTLPTAGVAFAGLLTGTTVLVAALTFFPALALG PIAEALQ
4E-212	714.6	42.3	5E-212	714.5	29.4	1	1	R2SZ45_9ENTE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UAW_02557	Enterococcus haemoperoxidus ATCC BAA-382	560	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus haemoperoxidus, Enterococcus haemoperoxidus ATCC BAA-382	1158608	>tr|R2SZ45|R2SZ45_9ENTE Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus haemoperoxidus ATCC BAA-382 GN=kdpA PE=3 SV=1 MSAIFIQQAIFFIVLIGLAVPLGFYIHKVMTGQKTLLTRIINPIENTIYRFLGTPAQKEMNAKQYS FSVLFFSLFSLLLLMAMMLGQQFLPLNPEKLPGTSFSLAFNTAASFVTNTNWQAYAGEDTLS IFTQAFGLTVQNFVSAAVGIAVLFVLLRGFTNRTTKYIGNFWQDLTRITLYVLLPSLFIVSLILIS QGVVQTFAGSVETTSLELGQKIFLPLGTVASQVAIKQLGTNGGGFYGGNSTYPFENPNLISN FVENISILLIPAALIVAFGLYVKEWKQGRTIMIVSLGFLIAAMIGVTLSEYYGPQFSHVLGQMNL EGKEMRFGVGWSSLWAVSTTAASNGSINAMLDSFMPLGGLIPMFLMQLGEIIFGGTGSGLY GMIAFILLAIFIAGLLVGRTPEYLGKKIEPFDMKMVCLVILTPLLLTLLGTMLFILNPQAMSWLT NSGPHAFSEVLYGFSSLANNNGSAFAGLTADTTFLNILGGMIMIFSRFIPMLAIIYLAANLGKK KIVATGSGTLSTTNATFVTMLIIVILVIGALSFLPAMALGPIAEHFITK
5E-212	714.5	24.5	5E-212	714.3	17	1	1	E8U851_DEIML	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Deima_1591	Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	582	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus maricopensis, Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	709986	>tr|E8U851|E8U851_DEIML Potassium-transporting ATPase potassium-binding subunit OS=Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34) GN=kdpA PE=3 SV=1 MTILFTYLLVFALAWPLGGYIARVFRGERTLTDALAPLERALVRLIGANPDRGMTWQAYGRA LLLSNIPLALLAFLVYAFQAPLPLNPDRIGNMPWFVALNTAASFITNTNWQNYSGQAQLGYL AQMLGVTALQFITPAAGIAVLFAILRGLNGGVNADAPAGAPRDFGNYYVDVVRALTRVLLPA SVVLALLLTWQGVPSTFSGAKTAALLEPQTVTVNGAAQPVTTQTIPVGPVAAMVAIKQLGTN GGGWYGPNSAVPLENPTALSNVLEGAAILVLPVALVFATGAFLRRPKFGVMILGVMTLLSAA LVALSVVAERAPNPAFAGLASGANLEGKELRLGVDASAFWAAITTQTSNGSVNAMHDSLNP LTGAVPLAGLFLNDVYGGLGVGVINFLLFVLLTVFIAGLMVGRTPELFGRKIEAREIKLVSLAL LLQPLLILGFTAVTLAMPAVTANSNPGFHGLSQVLYAYTSQFANNGSAFAGLGTANSVWHN VTGAAVLILARYIPMLAPLAIAGSLARKRVAPHTLGTLRVDTPVFAGTLLSVMLILTLLNFLPAL MLGPVGEHVTARAGTFQGAPR
5E-212	714.4	20.6	6E-212	714.2	14.3	1	1	K0CGH7_ALCDB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA B5T_02494	Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	555	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Alcanivorax, Alcanivorax dieselolei, Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	930169	>tr|K0CGH7|K0CGH7_ALCDB Potassium-transporting ATPase potassium-binding subunit OS=Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5) GN=kdpA PE=3 SV=1 MKEVALIYLVTLGLAWPLGRYLSWLFGERSVSGGIATVENGLLRLAGINPNADMSWSDYAR VLLKLHLLLAIVIFLVLTLQQWLPLNPDHIPNMSWDLALHTVISFLTNTNQQHYSGQAQLSYF AHTLGIVTLQVVTPAAGLATLVAILRTLFSKAPSGETVSVGNFHRDLLRSVLWVMLPLSLIASL LLASQGVPSTYQGAAEVSTLQDGATQTVPLGPVAAMVAIKQLGTNGGGWFGPNSSVPLEN PTFFSNLVETTALMLIPMALVFMLGFMARRRRLGWCVAAVMFALSLVSTSLNVFSERQPNA AVAAAGIQGPNMEGKEVRFGTDLTALWGSWTTQTSNGSVNGMHDSFNPLGGMSELMNM FLNVTFGGIGVGLIGYLLFMFVAAFIGSLMIGRAPSFLGRPLETREMKLASLALLLQPILILGLT AVTLAVPGWAGTSNPGPHGLSQVLYEYTSAFANNGSGFEGLGDDSVWWNLSCALALVGG RFIPMLAPLAIAASLASKRPSAQSRGTLNVDTPTFAVLTLGVIVLFALLSFLPALVLGPIAEAL
6E-212	714.2	30	7E-212	713.9	20.8	1	1	A7HRV4_PARL1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Plav_1014	Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966)	560	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhodobiaceae, Parvibaculum, Parvibaculum lavamentivorans, Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966)	402881	>tr|A7HRV4|A7HRV4_PARL1 Potassium-transporting ATPase potassium-binding subunit OS=Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966) GN=kdpA PE=3 SV=1 MLSSAIIFVVFIVGGTALLSWPLGRYMKWAMDPAASASRSADRFTHMFQTIGGGVARQSQD WKRYLTAMLVFNAIMFVVSFAILALQQYLPLNPDGKEAIEGSLIFNTAASFTSNTNLQHYSGE VSLSLYSLQALMWLQFVSAATGIAALAALARGLAGREMGNFFVDLQRASFLVLLPLAFVFA CVLVIGGLPMTFDGAVVATTLEGIQQTIARGPVAAFVAIKQLGTNGGGFFGPNSTHPLENPT FWTNAIEMIAIILPMACVWMFGRIVGRTRHAAIVFTVMLTLLLVKITGAVWFEAAPTQAFAGL PIEQEVGNLEGKELRFGATGGPLWSVLTTSTSNGSVGAMHDSLNPMTGLMPMIGMWLNAT FGGVGVGMINMFLYIIVGVFIAGMMVGRTPEYLGWRVEAREVKFAILALVAHGLFILGGTAIF AATPWGFETLNNTGPHGFSEILYEFSSASANNGSGFEGLGDNTAPWNIATGIIMLLARFIPIIL PLAIVGSLMAKRRNAESVGTLGVEDGTFGGMLLATILVVGALTFFPAATLGPIAEHLMYMN

6E-212	714.1	28.9	7E-212	713.8	20	1	1	C7Q1T1_CATAD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Caci_6791	Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897)	561	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Catenulisporales, Catenulisporaceae, Catenulispora, Catenulispora acidiphila, Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897)	479433	>tr|C7Q1T1|C7Q1T1_CATAD Potassium-transporting ATPase potassium-binding subunit OS=Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897) GN=kdpA PE=3 SV=1 MSDTWAGVLQVAALVLMLAVSYRPLGDYMAHILTSRKHLRAELALYKTMGVDAEADQTWG TYLRSVFAISAVGILLLYLLLRVQHHLMTALGMPKMNADLAYNTAASFVTNTNWQNYGGENT LGYVAQVTGLAVQNFVSASVGIAVVATLIRGFTRNRTDRLGNFWVDLTRVLIRLMLPFSIVFA VILVAGGAVESLGNHLTVVHTINGDQNLYTGGTASQEVIKLLGTNGGGIFNANSAHPFENPT GFTNLVEIYLLLVIGFALPRTFGKMVGSHRQGYTILSVMAIIWIGSLAFSTFFEVHHHGIDLAN GHAALEGKESRFGIPASTLFMTSTTLTSTGAVNSWHDSYTPFGGGAAMFNMMLGEIAPGG TGSGLYGMLILAIITVFIAGLMVGRTPEYLGKKIRPTEMKYAALYILTTPAVVLIFTGLAMALKG ETASINSGNLGPGGAPAPHGFSEVLYAFTSMGNNNGSAFGGLSGNTHWWNTAGALAMMF GRFLPMIWVLALAGSLAKQKPVPETEGTLKTASPLFAGMLLGTVLLVVGLTYFPALSLGPLA EGLH
9E-212	713.5	26.7	1E-211	713.3	18.5	1	1	A0A059MJV5_9NOCA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA N505_0124945	Rhodococcus sp. BCP1	566	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. BCP1	931223	>tr|A0A059MJV5|A0A059MJV5_9NOCA Potassium-transporting ATPase potassium-binding subunit OS=Rhodococcus sp. BCP1 GN=kdpA PE=3 SV=1 MTPAVAAGLQIGLVVAVLALAYVPLGDYMARVYTTDTDLRWKDLRIESLMYRLCRIDPRAEQ TWYGYAASVLGFSLASVLLLYTVQRLQGVLPLGRDLGGVSPAVAFNTAVSFVTNTNWQSY VPETTMSPLTQSAGLAVQNFVSAAVGMAVAIALIRGLVRVGRGGEIGNFWVDLTRGTLRILL PLAFVIALILLSQGVIQSYRSGFSATGLDGNAVTTALAPVASQEAIKELGTNGGGILAANSAHP FENPTPVTNIVEILAILLIPVTLTRTFGTMIGNRRQGLTVLGVMALLYGTVLAVALAAESGTRG VAANAAGAMMEGKEVRFGIPGSVLFAVSTTGTSTGAVNSAHDSMSPLGGGAVLLNILLGEI APGGVGTGLYSMLVLAVIAVFVGGLLVGRTPEFLGKKLRRREITLAALAVLVMPALVLTGTAI TVILSTTTGYLGNSGDPGTPGAIHGFTEVLYAYASASNNNGSAFGGLTVTSDWFQSSLGMC MLLGRFLPIVFVLALAGSLAAQRRTPAGAGTLPTTGAAFAGLLTGTAVLVAALTFFPALALGP VAEALH
1E-211	713	19.1	2E-211	712.8	13.2	1	1	C6W8P0_ACTMD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Amir_3231	Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	540	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Actinosynnema, Actinosynnema mirum, Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	446462	>tr|C6W8P0|C6W8P0_ACTMD Potassium-transporting ATPase potassium-binding subunit OS=Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971) GN=kdpA PE=3 SV=1 MSSTTAGLLQVALLIAALAAAYRPFGDYMARVYTDAKHTRVERLLYRAARVDPDSQQRWGT YAQGVLGFSLVGVALLYLMQRVQPWLPFDHDRGAVSPGMAFNTAASFVANTNWQSYVPE TVLGHTVQMAGLTVQNFVSGAVGMAVAVALVRGFTREGSDRLGNFWVDLTRGTLRVLLPV SFVFAIVLVATGVVMSLKAGVDVDGQQVAIAPAASQEAIKELGTNGGGIFNANSAHPFENPN GWSNLVEIFLILLIPVSLTRTFGTLVGNRKQGYVLLSVMGVLWTAMLAVIWAAEAHGLRPLE GKELRFGVPGSALFANTTTATSTGAVNAMHDSLTGLGGGATLLNMLFGEMTPGGVGTGLY SILVMAIIAMFLAGLMVGRTPEYLGKKLGRREVTCAALSILAMPALVLVGAGISAVLPSTAGYL NNPGEHGLSEILYAYASASNNNGSAFAGITVTSDWFQSSLGVCMLLGRFVPIIAVLCLAGSL ARQKRAPRTAGTLPTDSPLFASLLVGAIVLVAALTFVPALALGPIAEALL
2E-211	712.2	24.7	3E-211	712	17.1	1	1	D5UVP7_TSUPD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Tpau_3244	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	552	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Tsukamurellaceae, Tsukamurella, Tsukamurella paurometabola (Corynebacterium paurometabolum), Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	521096	>tr|D5UVP7|D5UVP7_TSUPD Potassium-transporting ATPase potassium-binding subunit OS=Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) GN=kdpA PE=3 SV=1 MGNTSSGILTIVTLVAALAICYRPLGDYLAHVVTTTRHWRVERAVYKIVGADPEAEQGYRTY AVAALAFSAVSIIALTILLLAQGLLPGFHPRQWRFDEALNTAISFVTNTNWQWYGGESMANL VAQAVGLAVQNFVSAAVGIAVAVALIRGFVRSRTDRLGNFWVDLTRITVRVLLPISVIGAVILL AQGVVQTLWQRTEIATIDGGKQVLTGGLVASQEVIKLLGTNGGGYFNANSAHPFENPTATT NLFQIFLILLIPVALPRMLGNLVGSHRQGYAILGAMGVIFSISLAISTWSQLAGQGTAPRAAGA PLEGQELQFGQWGTALFATATTSTSTGAVNASHDSLTPGAGGAALVNMLLGEVSPGGVGS GLYGMLVIAVLTVFLCGLMVGRTPEYLGKKIGRQEITLAALYILVMPALVLVGTASTVIQDQGT AAMANDGPHGLSEVLYAFASAANNGSAFPGLSVDTPWFNYTLGAAMLLGRFAPMVAILAL AGALAKQHPVPTTAGTIPTHRPLFVGLTVGVVVLVAGLTFVPALALAPISEVTR
2E-211	712.1	26.6	3E-211	711.9	18.5	1	1	KDPA_NOCFA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA NFA_15660	Nocardia farcinica (strain IFM 10152)	561	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia farcinica, Nocardia farcinica (strain IFM 10152)	247156	>sp|Q5YZH5|KDPA_NOCFA Potassium-transporting ATPase potassium-binding subunit OS=Nocardia farcinica (strain IFM 10152) GN=kdpA PE=3 SV=1 MSPALAAGLQIASVVAVLALVYVPLGDYMARVYTSSSDLRAESWLYRLARVDPRAEQTWC GYAGSVLGFSLAGVLVLYVLQRIQGVLPLSHGLAGVSPAVAFNTAVSFVTNTNWQSYVPET TMSPLTQSAGLAVQNFVSAAVGMAVAVALIRGLVRVGRGGEVGNFWVDLTRGTLRILLPLA FVIALILLSQGVIQSYRSGFTGVGLDGRPVTTALAPVASQEAIKELGTNGGGVLAANSAHPFE NPTPLSNVVQILAILLIPVALTRTFGTMIGNRRQGLTVLAVMAGIYAVILGVTTAAESGARGAA ATAAGAMLEGKEVRFGIPGSVLFAVSTTGTSTGAVNSAHDSMSPLGGGAVLVNMLLGEIAP GGVGSGLYGILVLAVIAVFVGGLLVGRTPEFLGKKLRRREITLAALAVLVMPALVLIGTAITVV LPETAAALGNSGDPGTPGAVHGFSEVLYAYASASNNNGSAFGGLTVTSDWFQSSLGLCML FGRFLPILFVLALAGSLAAQPRTPATAGTLPTAGAGFAGLLLTGTVVLVAALTFFPVLALGPIAE ALQ

5E-211	711	28.9	6E-211	710.7	20.1	1	1	A0A075JIA9_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HX89_12880	Dermacoccus nishinomiyaensis	545	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Dermacoccaceae, Dermacoccus, Dermacoccus nishinomiyaensis	1274	>tr|A0A075JIA9|A0A075JIA9_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Dermacoccus nishinomiyaensis GN=kdpA PE=3 SV=1 MNVTLQAICMIATIALLLAFIHVPLGTWMYRCFTDERDWAPERLIYRAVGVDPRIEQGWRTY AVASVMFGVASVVLLFALIMAQGVLPWGLGRSQDWHTAFNTAVSFTTNTNWQTYGGESG AGYTVQMAGLTVQNFVSAATGIAVAVALCRAIARSNAATIGNFWVDLVRACTRILLPIAFVGA LVLVAGGVIQNLSSPHDVTTLVGGSQTIQGGPVASQEVIKLLGTNGGGFFNANSAHPLENP NGWTNLFEILLVLAIPFSLPWMYGLMVGDRRQGAVFTTAMGALFTLSAGLGIWAETSGALG SMEGKEQRFGIVGSVLFGTATTGTSTGGVNMMHDSMSPLGGGLMMLNMMLGEVSPGGV GTGLYNIIIFALLTVFIAGLMVGRTPELLGKAIGRREITYAALAVVVMPALVLVFTAAGVVLPVA KDALLNHGPHGLSEMMYAYTSASNNNGSAFAGLSADQPYLNLTLAACMFLGRFLPIVLVLA VAGALVSQQRRPATAGTMPTHGPVFTSLLVGIIVIVAGLTFFPSLALGPIAEALS
7E-211	710.7	23.8	8E-211	710.4	16.5	1	1	KDPA_RHOJR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA RHA1_ro01232	Rhodococcus jostii (strain RHA1)	571	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus jostii, Rhodococcus jostii (strain RHA1)	101510	>sp|Q0S7A5|KDPA_RHOJR Potassium-transporting ATPase potassium-binding subunit OS=Rhodococcus jostii (strain RHA1) GN=kdpA PE=3 SV=1 MTPALAAGLQVAFVLAVLAVAYVPVGDYMARVYESRRHLRFESVLYRLCRINPHTEQTWYG YAGSVLGFSTASVLFLYALQRIQGVLPLSGDLSGVSPAVAFNTAVSFVTNTNWQSYAPETT MSNLTQPVGLAVQNFVSAAVGMAVAVALIRGFVRVSRGGEIGNFWVDLTRGSLRILLPFSF VIALILLSQGVIQSFHPGFASTGLDGNSVTNALAPVASQEAIKELGTNGGGILAANSAHPFEN PTPVSNIVEILAILLIPVSLTRTFGTMVGDPHDRASEVSGHRQGLTLLAVMGILWGSLLAVTLA AESGRRGVAATAAGAMMEGKEVRFGIPGTALFAVSTTGTSTGAVNSAHDSLSPLGGGAVL LNMLLGEIAPGGVGTGLYGILVLALIAVFVGGLLVGRTPEYLGKKLRQREITLAALSVLVMPAL VLIGTGITVILSSTTGYQGNSGDPGSPGSIIHGFSEVLYAFASASNNNGSAFGGLTVTSDWFQ TALGLCMLFGRFLPIIFVLALAGSLASQKKTAAGAGTLPTAGPMFTGLLTGTVVLVAALTFFP ALALGPIAEALQ
1E-210	710.1	26.1	1E-210	709.9	18.1	1	1	F4CT92_PSEUX	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Psed_4147	Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	553	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Pseudonocardia, Pseudonocardia dioxanivorans, Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	675635	>tr|F4CT92|F4CT92_PSEUX Potassium-transporting ATPase potassium-binding subunit OS=Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190) GN=kdpA PE=3 SV=1 MSDTLAGLFQVAALLVLLGVCYVPLGDYMARVFTAERHWRIESMLYRLVRVDASSGQRWP TYAAGVLGFSFVSCALLYLLQRLQPVLPASFGRGPVPPATAFNTAVSFVTNTNWQSYVPEQ TLGDTVQMAGLTVQNVLSAAVGLAVAVALIRGFVRSGTDRLGNVWVDLTRGTVRILLPLAFV AAVLLLVMGVTMSLHAGVDTTGVDGAAHTLPLAPTASQEAIKQLGTNGGGIFNANSAHPFE NPNAVSNLFQIFLMLLIPVCLTRTFGTMVRNPRQGTVLVSVMGVLWAGLLAVAWYAEMHPN GPAALAAGGALEGKEVRFGIPSSVLFGISTTGTSTGAVNSMHDSFTGGAGGATLLNMLLGE VAPGGVGTGLYGILVLAVIAVFLAGLMVGRTPEYLGKKLGRREVTAAAVSILVMPTIVLIGAGL AIALPGTAGALNNGGAHGFSEVLYAYASTANNNGSAFAGITVTGNFFQSTLGVAMLLGRFV PILAVLALAGSLAAQRRVEPGAGTLPTDKPQFAVLVGGTVVLVAALTFFPALALGPIAEALA
1E-210	709.6	23.9	2E-210	709.3	16.5	1	1	D3RSD8_ALLVD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Alvin_1158	Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	569	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Allochromatium, Allochromatium vinosum (Chromatium vinosum), Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	572477	>tr|D3RSD8|D3RSD8_ALLVD Potassium-transporting ATPase potassium-binding subunit OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) GN=kdpA PE=3 SV=1 MNEVLLIYAAALLLAWPLGRYLAAIYSATPTALDQVFGPVEWVIYRAIGVDPLAPMSWKAYG KALLKLHLIIALALVILVQQGWLPANPDGVEGMSWDLALHTTASFITNTNQQHYSGQAQLSY FAHLVAIVSMQVITPAAGIAALVAILRTAFTQRDTTASTPEGAVSVGNFHADLVRAIVRVMLPV AFITALLLAWQGVPNTFMGARTVTPLDSSAGLVEQRIPVGPVAPMVAIKQLGTNGGGWYG PNSSVPLENPTPVSNFVETIAIVLIPMALVFMAGYLTGRRRLAILVMGVMLSLSALLTGINIWS ENQPNAAFAGLAADGPNLEGKEVRFGATATALWGSFTTQTSNGSVNGMHDSFNPLGGAA TLMDMFINATFGGVGVGLINFLLFLLLAVFLGSLMVGRSPEVYGRALEAREIKLICIALLIQPLLI LGLTATAVAIPGLAQNSNPGFHGLSQVLYEYTSAFANNGSGFEGLGDDTVWWNLSCAVALI LGRFIPILAPLALAAHLAGKRVAPMTLGSLAVETPTFAVLTLGVILMFALLSFFPVLALGPVAEF LSLAN
2E-210	709.5	31.3	2E-210	709.3	21.7	1	1	R2QEW8_9ENTE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UAU_02479	Enterococcus pallens ATCC BAA-351	557	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus pallens, Enterococcus pallens ATCC BAA-351	1158607	>tr|R2QEW8|R2QEW8_9ENTE Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus pallens ATCC BAA-351 GN=kdpA PE=3 SV=1 MSSLIYQGIFFFVLLAAALPLGWYIKEVMQGRIPRYARFLQPLERLFYKVIGPVSKKEMRGK TYFVHVLLLSFSSLVVLLLLMTQQWLPGGEKVVNLPFDLALNTAVSFVTNTNWQAYAGETT LSHFSQIFGLTVQNFVSAGIGLSVACALIRGISQKQKRMIGNFWQDLTRSLVYILLPLAFILAIV LISQGSVQTFSNGTAYQGLEGKSLWLYLGPVASQVAIKQLGTNGGGFFGANAAHPFENPTI LANFFENLAILLIPAALIFAFGFWVKDWKQGRTILIASLFFVSLAFVGVVVNEYYGPQLANVVG AMNMEGKEVRFGIGWSSLWAISTTAASNGSVNAMLDSFTPLGGAIPLFLMQLGEIIFGGVG SGLYGMMAFLLLAVFIAGLLVGRTPEYLGKKIEAFDIKMASVVILTPLLLTLFGAMALVLHPDV MSWLTNSGPHAFSELLYGATSLANNNGSAFAGLAADTPFINLLGSLLMTLSRYLPMLVILLLA ENMGSKKKSALSEGTLSTSSPTFVTMLIIVIFVVGALSFLPAMALGPIAEYFRI

2E-210	709.2	40.6	2E-210	708.9	28.2	1	1	E8SI98_STAPH	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SPSINT_0107	Staphylococcus pseudintermedius (strain HKU10-03)	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus pseudintermedius, Staphylococcus pseudintermedius (strain HKU10-03)	937773	>tr|E8SI98|E8SI98_STAPH Potassium-transporting ATPase potassium-binding subunit OS=Staphylococcus pseudintermedius (strain HKU10-03) GN=kdpA PE=3 SV=1 MEIVIFLITFFLCAFLLSRYLYSVALLTPTPADKVFSGVEKGIYKVLGTQLEHMSGKTYLKHFLL FNGLMGALTFVLLLIQQWLFLNPNHNLNQSVSLAFNTAVSFLTNTNLQHYAGESGLTYLTQM MVITYLMFTSSASGYAVCIAMLRRLTGMTDIIGNFYQDMVRFLVRVSIPLSFIVSLLLISQGTP QTLKGNLTLHTITGKVQHIAYGPMASLESIKHIGTNGGGFLGANSATPFENPTVWSNYIEML SMMLIPGALVFLFGRMLTKNGKHIHAHAYVIFGTMLLFFLVCFVIALIAEYKGNVVLAHLGVIG PNMEGKEVRFGPGLSALFTAITTAFTTGTVNNMHDTLTPIGGLVPIVLMMLNAIFGGEGVGL MNMLIYVLLTVFICSLMVGKTPHYLGMKIEGREMKLIALTFLIHPVLILIATALAFIVPGASAAIT NPSFHGISQVLYEMSSSAANNGSGFEGLSDNTAFWNISTGIVMLLARYTPIILQVMIASSLVN KKAYQKSDQTIAIDKPFFGVSLTIFIILLSGLTFLPVLLLGPIGEFLSLK
3E-210	708.5	36	4E-210	708.3	25	1	1	C9A6Y5_ENTCA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ECBG_00515	Enterococcus casseliflavus EC20	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus casseliflavus (Enterococcus flavescens), Enterococcus casseliflavus EC20	565655	>tr|C9A6Y5|C9A6Y5_ENTCA Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus casseliflavus EC20 GN=kdpA PE=3 SV=1 MSSYFMQGFLFLLILLAAAVPLGWYIKEIMQGKTPRFVRFIQPIERLTYRVIGSVSKKEMTAK TYLFSVLAVSVFSIIGLTGLLMVQHWLPQGAAVENMSFDLALNTAVSFVTNTNWQAYAGEE ALTNLSQALGLTVQNFLSAAVGLAVLCALIRGLQQKQKRTVGNFWQDITRSLLYILLPLSLML AILLLSQGVVQTLSSGVEVNGFEGESFWMALGPVASQIAIKQLGTNGGGFFGANAAHPFEN PTMFSNFLENLAILLLPAALIFAFGFWIKEWKQGRTILITATVFLILAFIGVVISEAYGPQFSQVL GNANLEGKEVRFGVGWSSLWAVSTTAASSGSVNAMLDSFTPLGGAIPMFLMQLGEIIFGG VGSGLYGMIAFLLLTVFIAGLLVGRTPEYIGKKIEAFDIKMTSIVILTPLLLTLFGAMLMTLHPDI MSWLTNQGAHGFSELLYAATSFSNNNGSAFGGLTADTVFLNSLGSILMFVSRFVPIAAILYL AENMGAKKKTVRNEGTLSTTSPVFVTMLIIVIIVIGALSFLPAMALGPIADFFTTK
4E-210	708	23.6	5E-210	707.8	16.3	1	1	B0VM37_ACIBS	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ABSDF1597	Acinetobacter baumannii (strain SDF)	569	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter calcoaceticus/baumannii complex, Acinetobacter baumannii, Acinetobacter baumannii (strain SDF)	509170	>tr|B0VM37|B0VM37_ACIBS Potassium-transporting ATPase A chain OS=Acinetobacter baumannii (strain SDF) GN=kdpA PE=3 SV=1 MLELILVLFIAIFLAWCLSKYLSKVMANQPMWGDGLFRWIENPVYRLLGVSPQQQMNWKQY SLAFVVSCIFLAVAILAIFMTQAWLPLNPNHAPNMSWDLALHTVISFLTNTNQQHYSGQAQL SYLSQMTGIVGLQIITPMMGLALVVATLRAFFYQRPSHIAADVAEQPDQILIGNYWADVIRPT VRFLLPLCFVWSLLLNSQGVPATFQGGPEVQFIDKAHTVQTQKIPLGPVAPMVAIKQLGSNG GGWYGPNSSVPLENPTPLSNLLEMIAILLIPITVIFMVGHFTQRKKFAYFVFGSMLFMSIISGA AAVWSESMSSTASQLAVMEGKEQRFGPAASAVWAALTTQVNNGSVNMMHDSSAPLTGLV ELINMLINAIWGGVGCGLQQFMIYLLLAVFIASLMTGRTPELFGRKIEAAEIKLLAIIILQPLVILA FTALSLSVPGISGISNPGPHGISQVFYEYVSAFANNGSGFEGLGDNTVWWNVTCSIALLLGR FPTSILPLMIATRLAAKRKAPETAGSLQVETPTFALTLITIVVLLTLLQFMPVLVLGPIADQLLLV KG
7E-210	707.2	20	9E-210	707	13.9	1	1	A0A0F5VG03_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KY46_04855	Photobacterium halotolerans	574	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	265726	>tr|A0A0F5VG03|A0A0F5VG03_9GAMM Potassium-transporting ATPase potassium-binding subunit OS=Photobacterium halotolerans GN=kdpA PE=3 SV=1 MLDIFIICSLALILAMPLGMYMTGVFSGKPHLSDKIFGPIENGLYRLMGVNQQQGMSWKVYG SAFLLSNLILGILAFLILKFQHLLPFNPDQIGPLSWDLALHTAVSFLTNTNQQHYSGQAQLSYL SQGFLIVTLQFVTPAMALAVCVAILRGMRGGRNHESAKEGETRDLGNYYVDLVRGVVRVLL PVAAVVALLLTWQGVPSSFSGAQHVNTVDSASQVATQEVPIGPVAPMVAIKQLGTNGGGW YGPNSSNPLENPTPVSNAIETIALVLIPMAVVFMAGGLLRYKRFSTMSLVAMGVMSVGFIAA TVYSELQPNAAFAHLSAAGPNMEGKEVRFGPELSALWGTLTTQTSNGSVNAMHDSFNPIG GLMTRSGMLISAIWGGIGCGFVNFIVYVWLAVFLSGLMIGRTPEIFGRKIETKEITLLASLIVLP TFCILVLTAVTVAFPALTGNSNPGFHGISQVFYEYTSAFANNGSGFEGLGDDTPWWNISCVL ALLAGRYLPLVLPLAVAGSMARKRVSPDSAGSLKLASPTFCVTLIAVILIINFLSFLPAAVMGPI GEALQLAETGMGY
1E-209	706.6	20.1	1E-209	706.4	13.9	1	1	F4GEN4_ALIDK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Alide2_1436	Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	566	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Alicycliphilus, Alicycliphilus denitrificans, Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	596154	>tr|F4GEN4|F4GEN4_ALIDK Potassium-transporting ATPase potassium-binding subunit OS=Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601) GN=kdpA PE=3 SV=1 MVEPLLLLALLVVLGWPLGHYLAAVMRGDPMRSDVLFRWIERPLYALLGTRPEVGMGWCG YAKAFLLSNLVLALVVWAIFMTQAWLPLNPDGVPNMGWDLALHTVVSFLTNTNQQHYAGQ AQLSYLSQMTGIVGLQVVTPVMGLAVAAATLRGLFGGRQPQAQGQPVDVGNYWADVVRA TLRFVLPLCLILSALLTWQGVPATLAGGPVAAPVEAGAQFNVQKIPLGPVAPMVAIKQLGSN GGGWYGPNSAVPLENPTPLSNFLQTLAICLIPVSIVFMVGPFTGRRRFGAMVFGTMLAMSV LSTGLAVWSEGHSAIAADIALMEGKEVRLGSDASALWAAVTTQVNNGSVNSMLDSAAPLTG MVAMADMLINAVWGGVGCGLQQFIVYLLLSVFLAGLMTGRTPELFGRKIEGPEVRLLAVLVL LQPLVVLGFTAVALAVPGLAGNSNPGFHGISQVFYEYVSAFANNGSGFEGLGDATVWWNL SCAIVLAAGRFPALVIPLAIAAMLAAKRRAPEGAGTLQVETPTFALVLIGIVIILTLLQFMPVLVL GPVADHLALASLLAR

1E-209	706.5	18.1	1E-209	706.3	12.6	1	1	A0A0A8E1C4_9XANT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SB85_09150	Xanthomonas sacchari	572	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas sacchari	56458	>tr|A0A0A8E1C4|A0A0A8E1C4_9XANT Potassium-transporting ATPase potassium-binding subunit OS=Xanthomonas sacchari GN=kdpA PE=3 SV=1 MIDTLLVYALALLLGWPLGLYLAKVMRGAPMRGDALFGWIERPLYRLLGTDPARGMHWRA YAGAFLASNLVLGVLVFVLFVTQAWLPFNPDAVPNMRWDVALHTMVSFLTNTNQQHYSGQ AQLSYLSQAVGVVGLQFITPMMGLALVAATLRGLFGGRGQDAARKAAAIGGETAQEVDLGN YWADVIRPTLRFLLPLCLLWTLLLTQQGVPSTLAAGPVATPLDASAGQQTQKIPLGPVAAMV AIKQLGTNGGGWYGPNSAMALENPTPFSNLLEMLGIVLIPVAVAFMVGPFTGRRKFTALVF GSMLVMSLASTAVSLWAEGHAPGSAALMEGKEVRFGVDASAAWSSLTTQTSNGSVNAMH DSLAPLTGGVAMINMLINAIWGGIGCGLQQFLVYLLLSVFLAGLMTGRTPELFGRKIEAPEVR LLALLILLQPLVLLGFTAVTLALPASISATSNPGFHGISQVFYEYTSAFANNGSGFEGLGDGIP WWNLSCTVVLLLGRYPALIVPLIVAAQLARKRVAPETGGSLQVETPTFALTLIAVIAILTVLQF TPALVLGPIADHLTLAAH
1E-209	706.5	32.5	1E-209	706.3	22.5	1	1	S0LI83_ENTAV	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA OMU_00616	Enterococcus avium ATCC 14025	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus avium (Streptococcus avium), Enterococcus avium ATCC 14025	1140002	>tr|S0LI83|S0LI83_ENTAV Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus avium ATCC 14025 GN=kdpA PE=3 SV=1 MSSVIYQGLFFLFILLALALPLGWYIKEIMQGKIPKGVRFLQPLERLFYKVIGPISKKEMSAKR YGASVLLLSISSIILLIVILMTQHFMPGGSSVKNLSLPLALNTAVSFVTNTNWQAYAGETTLSN TSQMFGLTVQNFISAGVGLSVLVALLRGLSQVKKKALGNFWQDLTRSLVYILLPLSIIFAILLIS QGTVQTFKSGISYEGLEGKNLWLHLGPVASQVAIKQLGTNGGGFFGANSAYPFENPTIFSN FLENLAILLIPAALIFAFGFWVKDWKQGRTIMIVSLFFLLLAFIGVAFSEFYGPEFAHVLGTTNL EGKEVRFGVGWSSLWSVGTTAASNGSVNAMLDSFMPLGGVIPMFLMQLGEIIFGGVGSGL YGMLAFLLLAVFIAGLLVGRTPEYLGKKIEAFDIKMASIVILTPLMLTLFGTMVFVLHPEVLTWL TNQGPHAFSELLYGATSLANNNGSAFGGLLADTPFINLLGSLLMLVSRYLPIIAILLLAESMGS KKKAALSSGTLSTVSPTFVSMLIIVILVIGALSFLPALALGPIAEYFTMK
3E-209	705.5	38.8	3E-209	705.3	26.9	1	1	KDPA_STAA8	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SAOUHSC_02312	Staphylococcus aureus (strain NCTC 8325)	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus aureus, Staphylococcus aureus subsp. aureus, Staphylococcus aureus (strain NCTC 8325)	93061	>sp|Q2FWH9|KDPA_STAA8 Potassium-transporting ATPase potassium-binding subunit OS=Staphylococcus aureus (strain NCTC 8325) GN=kdpA PE=3 SV=1 MEIILFLTMMVMITYVFSGYLYRVALVQSSRVDLIFTRFENMCFKIIGTDLEHMSAKTYVKHFL AFNGFMGFITFVLLIVQQWLFLNPNHNLNQSIDLAFNTAISFLTNSNLQHYNGESDVTYLTQM IVMTYLMFTSSASGYAVCIAMLRRLTGLTNIIGNFYQDIVRFIVRVLLPLSCLISILLMTQGVPQ TLHANLMIRTLSGHIQHIAFGPIASLESIKHLGTNGGGFLAGNSATPFENPNIWSNFIEMGSM MLLPMSMLFLFGRMLSRHGKRVHRHALILFVAMFFIFIAILTLTMWSEYRGNPILANLGIYGP NMEGKEVRFGAGLSALFTVITTAFTTGSVNNMHDSLTPIGGLGPMVLMMLNVVFGGEGVGL MNLLIFVLLTVFICSLMVGKTPEYLNMPIGAREMKCIVLVFLIHPILILVFSALAFMIPGASESITN PSFHGISQVMYEMTSAAANNGSGFEGLKDDTTFWNISTGIIMLLSRYIPIILQLMIASSLVNKK SYHQDKYTIAIDKPYFGVSLIVFIVLLSGLTFIPVLLLGPIGEFLTLK
5E-209	704.6	24	5E-209	704.4	16.6	1	1	Q6F8C8_ACIAD	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ACIAD2978	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	569	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	62977	>tr|Q6F8C8|Q6F8C8_ACIAD Potassium-transporting ATPase A chain OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) GN=kdpA PE=3 SV=1 MAFAMWEFITVFVLALILAYPLGHYLADVMQAKPMKSDRLFRWIEQPLYRVLGVRQTGMN WRQYLGAFVISNVVLFVVSVVILMTQAWLPLNPDHVPNIKWDLALHTTISFLTNTNQQHYSG QAQLSYLSQMTVIVGMQFLSPIIGLALLTAMLRTLFLQSGKTQSKDKQHWQEINLGNYWLDL IRPLLRFFLPLAFIFSLLLTWQGVPATLSGGPVAQNLDQSVEVKTQHIPLGPVAPMVAIKQLG SNGGGWYGPNSSVPLENPTPFSNVIEMLAILLIPLSVVFMIGRFVQRRKLMWMIFGTMLLMS LASTMLSMWTEKFSLLPNVAQMEGKEVRFGVEASALWSSLTTQVNNGSVNMMHDSSSPL NGLVQLCNMLINAIWGGIGCGVLQFFIYLLLAVFIAGLMTGRTPEIFGRKIEVTEIKLLAFVILLQ PVVILGLTALAIAFPSLTANSNPAFHGISQVFYEYVSAFANNGSGFEGLGDNTVWWNLSASV ALLAGRYSVLIVPVLIAVSLATKPKATEGKGSLHIESPTFALTLIGIVLILTVLQFMPVLVLGPIA DYLSVHI
1E-208	703	28.5	2E-208	702.7	19.7	1	1	G1UPS2_9DELT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HMPREF1022_00595	Desulfovibrio sp. 6_1_46AFAA	554	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio sp. 6_1_46AFAA	665942	>tr|G1UPS2|G1UPS2_9DELT Potassium-transporting ATPase potassium-binding subunit OS=Desulfovibrio sp. 6_1_46AFAA GN=kdpA PE=3 SV=1 MLYVFLLVALCVVVSWPIGKMATWAMSDPVSDRGFRRAVENLFVKCGGNVVRGQQNWK QYALSMLLFNALIFTFIYLVLGTQQWLPLNPDGKGALEGSLIFNTTASFTSNTNLQHYSGEQA LSYIGQFALMFLQYLTPATGLACLAALARGLSGKVLMGNFYADVMRATFLVLLPLCLVTASM LVLGGVIMTFDGSVVAQTLEGAKQIIARGPVAAFVTIKQLGTNGGGFFGPNSTHPFENASFF TNFIETMSIIVIPMACVWMFGRLTGRMKHAAVIFAVMLSLLCVKLGCAVYFESAPSAAFHGLD IENSSNLEGKELRYGTSGGPAWSIITTATSNGSVNAMHDSLNPLAGLMPMIGMWLNVVFGG VGVGFINMFLYIIVGVFISGMMVGRTPEYLGRKVETREMKLALLAILAHPFFILGGTALFAATS WGADTVANAGFHGFSEILYEFTSSAANNGSGFEGLGDNTVPWNIATGLVMLLARYIPIILPLA MVGSLAAKTPAPETAGTLRTDTLLFGGVLLGCVLIVGALLFMPVAVLGPIADHLSVMR

4E-208	701.6	29.1	5E-208	701.3	20.2	1	1	R7C503_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN641_00702	Sutterella sp. CAG:397	561	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Sutterellaceae, Sutterella, environmental samples, Sutterella sp. CAG:397	1262976	OS=Sutterella sp. CAG:397 GN=kdpA PE=3 SV=1 MQPALIALTVFSIVLFLITKPLGLWLTPLAKGRAPAVVEPADRAVLHFLGLTNTPQTWAAYAA SAVVFNMAGAVFLYLILRFQGWLPFNPQGVDGMGALQAFNVAVSFVTGTNWQSYSGEVS VSYFSQAVGLAVQNFCCSCTGTAVSFALMRGFSRKLTDDLGNFWADVVRCALWVYLPLCV IYALFLVSQGVIENWSDYAVIQTLAGGEQTIAMGPVASQEAIKMIGTNGGGFFAVNSAHPFE NPTQITNFIASLAILAVPAGLTYTFGVMVRDTRQGWTIWAAMWLIFALCTVVFAWFELDTPH VLTDLGVPEGVMSPEGKEARFDIAATALFSMATTAASCGAVNAMHDSFTALGGMFPLWLM QMDEVVFGGVGAGFYGMIVFAVVGVFAAGLMVGRTPEYIGKKITPVQMKLAGVAMLTPPMI VLFGTAVTCVYPPALESLTNPGAQGFSEILYAWSSAANNNGSAFAGLNADTDFFNAGLALA MWFGRFVCLISVTALAGSLARQKMTAAGDGTLKTYGLLFTVFLSVTVLVVGALTYMPALALG PVAAYSGTVLP
4E-208	701.4	19.5	5E-208	701.2	13.5	1	1	J9Z8M5_LEPFM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LFML04_0552	Leptospirillum ferriphilum (strain ML-04)	567	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Leptospirillum, Leptospirillum sp. Group III, Leptospirillum ferriphilum, Leptospirillum ferriphilum (strain ML-04)	1048260	OS=Leptospirillum ferriphilum (strain ML-04) GN=kdpA PE=3 SV=1 MTANDWIQILVSLGLIVLLSPLVGRYLAWIFQSPHLSIEKGLYRLLGLDADREMGWKEYASTL LVSNGFFFVAGYLVLWAQGGLPLNPRNLPPLTPEVVFNTAASFVTNTNWQAYAGEAQLSN FSQMVAITFLMFVGANTGLASLVAIIRGFVREGSATIGNFWSDFFRFFLRAFLPACFLLAIVHV EQGTPQTMTTSITAKTLEGATQTLVVGPVASLESVKNLGTNGGGFYNANGAHPYENPTPLT NMLEFLEMGIFTFSLPFFFGRMIGRPRQGHVFFAVIFALYVAGLGLVEYSEKMPNPLFRTAAI AQKTTPLQDGGNMEGKETRLGITQTSLFSNTTIAATTGAVDASMDSMNPVAVLVYLVHMFL NEEPGGKGVGFAGLLKEAILAIFLAGLMVGRTPEFLGKKIESREIKLAALSLLVTPILVLWLTGI SLVLPAGKSSIDNPGPHGFMEVLYAFASGNANNGSAMAGLNVSTPYYAITIGLEMLLSRFLP LLPLLALAGALARKKTLPENAGTFRTDTPLFVVLLLGFMVLFAALTFFPPLILGPLLEHLSMIHQ IAF
5E-208	701.2	35.3	6E-208	701	24.5	1	1	S0KV97_9ENTE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA I573_00530	Enterococcus sulfureus ATCC 49903	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sulfureus, Enterococcus sulfureus ATCC 49903	1140003	>tr|S0KV97|S0KV97_9ENTE Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus sulfureus ATCC 49903 GN=kdpA PE=3 SV=1 MTSIGYQAFFFLGILLVLSVPLGWYIKQIMQGDIPKWMRWMQPVERLIYRILGPTAHSEMSA KKYVLNVVLLSSCSLIFLVGLLMIQHLLPGGSTFEPISFSLALNTATSFVTNTNWQAYSGETTL SNLSQAFGLTVQNFLSAGVGLAVVTALFRGFVQVKKPTLGNFWQDLTRGLLYLLLPLSFLM AIVLLSQGVVQTFSSGVAYQSLEGKDSWLYLGPAASQIAIKQLGTNGGGFFGANSAYPFEN PTLISNFIENLAILLIPAALIWTFGFWVKEWKQGRTIMIVSLFFVVLAMIGVGMSEVQGPHFAQ VLGHSNFEGKEVRFGIGWSSLWAVATTAASNGSVNAMLDSFTALGGAVPMFLMQLGEIIFG GVGSGLYGMLAFLLLAVFIAGLLVGRTPEYLGKKIEAFDIKMASIVILTPLLLTLFGTMALTIHP DVMKWLTNTGPHGFSEVLYGATSLANNNGSAFAGLTANITFINLLGSVLMGLSRFLPILAILY LAGNMANKKRVALNQGTLSTVSPTFVTMLMIIILVIGALSFLPALALGPIAEFFTIK
1E-207	700.1	22.4	2E-207	699.5	15.5	1.2	1	Q5GW21_XANOR	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA XOO3846	Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85)	597	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas oryzae, Xanthomonas oryzae pv. oryzae, Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85)	291331	>tr|Q5GW21|Q5GW21_XANOR Potassium-transporting ATPase potassium-binding subunit OS=Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85) GN=kdpA PE=3 SV=1 MTETFLVYALAIVLAWPLGRYMAAVMRGAPMRGDALFGWIERPLYALLGTHPQQGMSWR GYAKAFLLSNLVVGLLVWLVFMTQAWLPFNPDAIPNMRWDTALHTVVSFVTNTNQQHYSG QAQLSYLSQMTGIVGLQVVTPMMGLALAVATLRALFGGRAAKQASVAAPASDTTAVAAISE PELSRQGRQHTGSGLEALPEADVGNYWADVIRSSVRVLLPLCLLLTVLLGWQGVPSTFQG AATAVPLDSSAGIAKQTIPVGPVAAMVAVKQLGTDGGGWYGPNSSVALENPTPLSNFLETL AIVLLPMSVVFMVGYLTGRKRLTALVFGTMLTMSAASTALLLWSEAHSASATSPALMEGKE VRIGADASALWAALTTQTSNGSVNAMHDSLAPLSGLVTLVDMLINAIWGGIGCGLQQFVVYL LLSVFLAGLMTGRTPELFGRKIESREVQLLALLILLQPLVVLGFTAVALAVPAITANSNPGFHG ISQVFYEYTSAFSNNGSGFEGLGDATYWWNLSCSLVLALGRYPALVLPLMVAARMAVKRR APESAGSLQVETPTFALTLMAIVLVLTVLQFMPALVLGPIAEHLALAAS
3E-207	698.8	21.9	4E-207	698.3	15.2	1.2	1	Q8PCM2_XANCP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA XCC0702	Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	599	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas campestris, Xanthomonas campestris pv. campestris, Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	190485	>tr|Q8PCM2|Q8PCM2_XANCP Potassium-transporting ATPase potassium-binding subunit OS=Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25) GN=kdpA PE=3 SV=1 MTETLLVYALAIVLAWPLGRYLAAVMRGAPMRGDAVFGWIERPLYAALGTRPQQGMSWR GYVAAFLLSNLVVGVLTWGVFMTQAWLPFNPDAIPNMRWDTALHTMVSFLTNTNQQHYSG QAQLSYLAQMTGIVGLQVVTPMMGLALAVATLRALFGGRAVANANDVAATASGPHSTALQ DATASLATHETQPSIPAGAPLPDADVGNYWADVIRASVRVLLPLCLLWTLLLGWQGVPSTL QGAATATPLDSSAGMATQTIPVGPVAAMVAVKQLGTNGGGWYGPNSSVALENPTPLSNLL ETLALVLLPMSVVFMVGYLTRRKRLTALVFGTMLLMSAASTGLLLWSEAHSVSAASPALME GKEVRIGADASALWAALTTQTSNGSVNAMHDSLSPLSGLVTLVDMLINAIWGGVGCGLQQF VVYLLLSVFLAGLMTGRTPELFGRKIEAREVQLLALLILLQPLVVLGFTAVALSVPAWTANSN PGFHGISQVFYEYTSAFANNGSGFEGLGDATYWWNLSCAVVLALGRYPALILPLMVAARMA TKRRAPESSGSLQIETPTFALTLMAIVLVLTVLQFMPALVLGPIAEHLALAAS

4E-207	698.4	10.9	4E-207	698.2	7.5	1	1	Q31MM1_SYNE7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Synpcc7942_1668	Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	556	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus elongatus, Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	1140	>tr|Q31MM1|Q31MM1_SYNE7 Potassium-transporting ATPase potassium-binding subunit OS=Synechococcus elongatus (strain PCC 7942) GN=kdpA PE=3 SV=1 MLRLLEVGLTLLPVILMTPLLGNYLWRVFSDQSSLLDRLCTPWEQRLFRWITVDSSQSMPT GQYLRSLLWVNAVTAVLSWGLLSLQAWLPLNPSQRSPLRWDLALHTIISFVTNTDQQHYSG ELSLSNASQIGVIGFLMFTSAATGLAVGIAFVRGLAGQGLGNFYRDWTLSLTRVLIPLSFSFA VILLALGVPETLDGVAIAQTLDGSTQAIARGPIAHLEAIKLLGENGGGFLAANSAHPYENPSAL SNWLEAIAMLAIPAALLDTYGRFLGNRRQAWLLLALATALLLALVSLTASSEAAGNPLLQTWL QGPNLEGKEVRFGWLQSSFWSVITTSTMTGAVNADLDSLMPLSDLALLFALFLQVIFGGQG LGAAYLIIFVLLSIFVTGLMVGRTPEFQGRKIEKPQVVLASLILLIHPLFVLIPGAIALSQPDIVQG LSQAGPHGVSQAIYEYASASANNGSGLEGIADDTLWWNLSTSVSLLGGRFIPIAALLALAAG FGQKPQLPPTAGSLRSDTPLFTGVTAIVVVILGALTFFPVLALGPIAEALQVYR
4E-207	698.2	22.1	5E-207	698	15.3	1	1	A6V7N1_PSEA7	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA1 kdpA PSPA7_3712	Pseudomonas aeruginosa (strain PA7)	575	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	381754	[illegible] OS=Pseudomonas aeruginosa (strain PA7) GN=kdpA1 PE=3 SV=1 MIESILLLVLLVALGWPFGRYLAAVMRGAPMRSDVLFGWIERPIYAALGTRPHTGMSWRGY AGAFLLSNLLLAIVVWIIFMTQAWLPLNPDGVPNMSWDLALHTMVSFLTNTNQQHYSGQAQ LSYLSQMTGIVGLQVVTPVMGLAVVAATLRGLFGGRQAMEHGVEGGATAPAGAIDVGNYW ADVTRATLRFVLPLCLVWSALLTWQGVPATLAAGPVAAPIEATAELKEQKIPLGPVAPMVAIK QLGSNGGGWYGPNSSVPLENPTPLSNFLETLAICLIPVSVIFMIAPFTGRRKFGAMVFGTML AMSVVSVGLSLWSEGHSGTATDIALMEGKEVRLGADASALWASVTTQVNNGSVNSMLDSA APLTGMVSMVNMLMNSIWGGVGCGLQQFIVYLLLSVFLAGLMTGRTPELFGRKIEGPEVKL LAILVLWQPLVILGFTAVTLAVPSLTGTSNPGFHGISQVFYEYVSAFANNGSGFEGLGDATV WWNVSCAFVLAAGRFPALVIPLAIAAMLAAKRRAPEGSGTLHIETPTFALTLIGIVIILTLLQFM PVLVLGPVADHLALTQLLAR
5E-207	697.9	31.8	6E-207	697.5	22	1	1	A0A0D5LVF8_9RHIZ	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TM49_04455	Martelella endophytica	552	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	1486262	>tr|A0A0D5LVF8|A0A0D5LVF8_9RHIZ Potassium-transporting ATPase potassium-binding subunit OS=Martelella endophytica GN=kdpA PE=3 SV=1 MFFVVLVVGGTALISWPLGRYMKWAMDPNRGEAGGFTRLFQSIGGATCMQDQNWKRYM VAMLAFNIVMFVVTFGFLALQQALPLNPDGKGALEGSLIFNTAASFTSNTNLQHYSGEVSLS YLSQLGGLMWLQFVSAATGIAALAALARGLAGKPLGNFFVDLQRATFLVLLPVAFVFAILLVL GGVPMTFDGAAVAITLEGVQQTIARGPVAAFVSIKQLGTNGGGFFGPNSTHPLENPSFWTN IIEMVAIILIPMACVWMFGRIFERKRHAMVIFAVMLGFIAVKIAGAVYFESAPTEAFANLSIEQT VGNLEGKELRFGATGGPLWSVLTTSTSNGSVGAMHDSLNPMTGLMPMIGMWLNSTFGGV GVGMINMFLYIVVGVFIAGMMIGRTPEYLGWRVEAREVKFALFALLAHGLFILGGTAIFAATP WGADTLNNVGPHGFSEMLYEFTSASANNGSGFEGLGDGTVPWNIATGIVMLLARFIPIILPL AIVGSLSAKRRSVESSGTLSVESGVFATMLASTIFVIGALTFFPAATLGPIAEHVMFMN
7E-207	697.4	19.8	8E-207	697.1	13.7	1	1	D2UFZ8_XANAP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	KdpA kdpA XALc_2832	Xanthomonas albilineans (strain GPE PC73 / CFBP 7063)	580	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas albilineans, Xanthomonas albilineans (strain GPE PC73 / CFBP 7063)	380358	>tr|D2UFZ8|D2UFZ8_XANAP Potassium-transporting ATPase potassium-binding subunit OS=Xanthomonas albilineans (strain GPE PC73 / CFBP 7063) GN=KdpA PE=3 SV=1 MIDTLFVYALALLLGWPLGLYLAKVMRGAPMCGDALFGWIERPLYRLLGTDPARGMHWRG YTAAFLLSNLVLGVLVFVLFVTQAWLPFNPDAVPNMRWDVALHTMVSFLTNTDQQHYSGQ AQLSYLSQAMGVVGLQFVTPMMGLALVAATLRGLFGGRAHAAAASVGSSAPASSMAEPPH AEVDVGNYWADVIRPTLRLLLPLCLLWTLLLTQQGVPSTLAAGPAATPLDASAGLQTQKIPL GPVAAMVAIKQLGTNGGGWYGPNSAMALENPTPFSNLLEALGILLIPVAVAFMVGPFTGRR KFTALVFGSMLAMSLASTGASMWAEGHSPSSASAALMEGKEVRLGVDAAAAWSSLTTQT SNGSVNAMHDSLAPLTGGVAMINMLINAIWGGIGCGLQQFLVYLLLSVFLAGLMTGRTPELF GRKIEAAEVRLLALLILLQPLVLLGFTALTLAMPAAIIANSNPGFHGISQVFYEYTSAFANNGS GFEGLGDGIPWWNLTCTVVLLLGRYPALIVPLIVAAQMARKRVAPETGGSLQVETPTFALTLI AVIVVLTVLQFTPALVLGPIADHLTLAAH
1E-206	696.8	26.1	1E-206	696.6	18.1	1	1	K0KBH6_SACES	Potassium-transporting ATPase A chain (EC 3.6.3.12) (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN6_67560	Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	540	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix espanaensis, Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	1179773	>tr|K0KBH6|K0KBH6_SACES Potassium-transporting ATPase A chain OS=Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764) GN=kdpA PE=3 SV=1 MSSTAAGLLQVGLLIVALAVVHRPFGDYMARVYTGTKHSRVERVVVYKIARVDPESEQRWGS YALGVLGFSFVGIVFLYVVQRVQSVLPFNFDRGNVEPGMAFNTAISFVANTNWQSYVPETV MGHSVQLIGLTVQNFVSAAVGLAVAVALVRGFVRHQTDRLGNFWVDLVRGTIRILLPVSFLF AIVLVALGVVMSFQSGVTVDGQSVATAPVASQEVIKELGTNGGGVLNANSAHPFENPNGW TNLIEIFLILVIPVSLTRTFGTLVGDRKQGHVLIGVMGTLWAAMLAVIWVAEANGLRPLEGKE VRFGIPSSALFADTTTATSTGAVNSMHDSYTGLGGGGTLLNMLFGEMTPGGVGTGLYSILV MAVIAMFLAGLMVGRTPEYLGKKLGRREVTAAAVSILAMPTVLLIGAGIAAILPSTQGALNNT GEHGLSEILYAYASASNNNGSAFGGITVTNDWFQSSLGVCMALGRFVPIVAVLCLAGSLAA QKKVPVTAGTLPTTGPLFASLLGGSIVLVAALTFVPALALGPIAEALL

1E-206	696.7	22.6	1E-206	696.5	15.7	1	1	B2FJX0_STRMK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Smlt0408	Stenotrophomonas maltophilia (strain K279a)	569	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Stenotrophomonas, Stenotrophomonas maltophilia group, Stenotrophomonas maltophilia (Pseudomonas maltophilia) (Xanthomonas maltophilia), Stenotrophomonas maltophilia (strain K279a)	522373	>tr|B2FJX0|B2FJX0_STRMK Potassium-transporting ATPase potassium-binding subunit OS=Stenotrophomonas maltophilia (strain K279a) GN=kdpA PE=3 SV=1 MTEMLVIIAASLLLAWPLGLYLARVMRGTPMKVDVLFHWIEKPLYKVLGVDPSRAMSWRGY VLAFVLSNVVVAVLTQAVFMTQAWLPLNPDQIPNMRWDTALHTMISFLTNTNQQHYSGQA QLSYFSQMTGITGLQVVTPMMGLALAVATLRALFSRAPQAAATTGAGDDRQVAVGNYYVD VVRLCVRFLLPLCLVWTLVLTSQGVPSTIAGGPQATPIDASAGMAEQKLPLGPVAAMVAAK QLGANGGGWYGPNSSFPLENPTPLSNALEIVGILLVPMAVIFMIGAFTGRRRFGALVFSCML GMSLLSTGAMMWSEGHSASAATPLLMEGKEVRFGADGTALWAAVTTQVSNGSVNGMHD SLAPLSGGIAMVNMLVSAIWGGIGCGLQQFIVYLLLGVFLAGLMTGRTPELFGRKLETPQVR LLALLVLLQPITLLVFTAITLAVPGLAGTSNPGFHGISQVFYEYVSAYANNGSGFEGLGDATL WWNLSCSLVLLLGRFPLLIIPLVVAAQLAAKRQAPESAGSLQIETPTFALTLVSVIVILTVLQF MPALVLGPIADHLSLGLH
4E-206	695.1	28.9	4E-206	694.9	20	1	1	A0A0F0EVL2_9MICO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UB45_09575	Terrabacter sp. 28	548	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Intrasporangiaceae, Terrabacter, Terrabacter sp. 28	1619947	>tr|A0A0F0EVL2|A0A0F0EVL2_9MICO Potassium-transporting ATPase potassium-binding subunit OS=Terrabacter sp. 28 GN=kdpA PE=3 SV=1 MSDTVSGLLTIGVLVAALAASHLPLGAWLARVFTDEHHWRVERLVYRLCRVDPSSEQRWT TYAVAVLGVSVVGIALLSGLVVAQGALPLARGAAMGWDTALNTAVSFVTNTNWQSYAGES GASPLVQTVGLTVQNFVSPAVGLAVAVALVRGLARSGGATVGNFWVDLVRGCVRVLLPLA LVGAVVLLLGGVVQNLGAPTTVTTVSGGSQVIQGGLVASQEAIKLLGTNGGGYFNANSAHP FENPNAVTNLVQVFLMLVIPFSLPRTYGLLVGDRRQGWAVLGFMATLWGLMVAAVTWAEV SASVGPLGAMEGKEVRFGVWSSALFGASTTGTSTGAVNSLHESYSALGGGGVLFSMLLGE VSPGGVGSGLYGALLLALLTVFVSGLMVGRTPELLGKQVGRREITLTALALLVMPALVLVFT GVGMVAPIVSSQMLATGPHGLTEVMYAYVSAANNNGSAFAGFSADTPYTNLTLALCMLLGR FVPIVLVLALAGALVAQRRRPATSGSLPTHTPTFAGLFVGVAVVVTGLTFFPALALGPLAEAL S
8E-206	694	16.6	9E-206	693.8	11.5	1	1	B8GSR6_THISH	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Tgr7_1889	Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	569	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Thioalkalivibrio, Thioalkalivibrio sulfidiphilus, Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	396588	>tr|B8GSR6|B8GSR6_THISH Potassium-transporting ATPase potassium-binding subunit OS=Thioalkalivibrio sulfidiphilus (strain HL-EbGR7) GN=kdpA PE=3 SV=1 MTEFLLVFALAIGLGWPLGRYLAAVMRGAPMRGDRLFLWLERPLYALIGTNPERGMSWRG YAGAFLLSNLVLAVIVWLILMTQAWLPLNPNGAPNMSWDLALHTMVSFLTNTNQQHYSGQA QLSYLAHMTGIVTLQVITPMMGLALVVATLRGFFGGRNAQERKADGQEQAPVDVGNYWAD VIRPTLRFMLPLCLLWSVLLTSQGVPATLDGGPVVAPVDTTVEMKEQKIPLGPVSPMVAIKQ LGTNGGGWYGPNSSVPLENPTPLSNLLETLALILVPVAVVFMIGGLTGRRKFAGLVCGTMLT MSVVSAGFAIWSEGFSSTSQDIALMEGKEVRFGAEPSALWAALTTQTSNGSVNAMHDSLA PLTGLVTISDMLINAIWGGIGSGLQQFLTYLLLGVFLAGLMTGRTPELFGRKIEAPEVRLLAVL VLLQPLILLGLTAITLAVPSLTGSSNPGFHAISQVFYEYTSSFANNGSGFEGLGDATVWWNV TASFVLAAGRYPALIIPLVIAAMLARKRQAPESTGSLHIETPTFALTLIAVIVILTLLQFMPVLVL GPVADHLSLVAR
1E-205	693.1	32.2	2E-205	692.9	22.3	1	1	R3TUG5_9ENTE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA UC3_01129	Enterococcus phoeniculicola ATCC BAA-412	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus phoeniculicola, Enterococcus phoeniculicola ATCC BAA-412	1158610	>tr|R3TUG5|R3TUG5_9ENTE Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus phoeniculicola ATCC BAA-412 GN=kdpA PE=3 SV=1 MSSVIYQGVFFLFILLLLAFPLGWYMKEIMQGRVPKGVRFLQPAERLFYKVIGPVSRKDMSA KRYILNVLLLGFFSLLLLIILLRIQHFLPGGSSVKNLTWPLAINTAVSFVTNTNWQAYAGETDL SNLVQMFGLTVQNFLSAGVGLSVLVAVLRGFSQVKKKTLGNFWQDLTRSLLYILLPLALIFSV LLVSQGTVQTFTSGISYEGLEGNNLWLYLGPVASQVAIKQLGTNGGGFFGANAAHPFENPT LFTNFIENLAILLIPVALIFAFGFWVKEWKQGRTIMLVSLFFILLAFVGVALSEYYGPEFANVLG STNLEGKEIRFGVGWSSLWAVSTTAASNGSVNAMLDSFMPFGGAIPMFLMQLGEIIFGGVG SGLYGMLAFLLLAVFIAGLLVGRTPEYLGKKVDAFDIKMASLVILTPLMLTLFGAMALVLHPEI QSWLTNEGPHAFSELLYGATSLANNNGSAFGGLLANTPFINSLGSLLMVISRYLPMIAILFLA ENMGSKKKAALSSGTLSTVSPTFVSMLIIVILVVGALSFLPTLALGPIAEFFTMN
3E-205	692.2	34.6	3E-205	692	24	1	1	H7C701_ENTFA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA EF_0567	Enterococcus faecalis (strain ATCC 700802 / V583)	558	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus faecalis (Streptococcus faecalis), Enterococcus faecalis (strain ATCC 700802 / V583)	226185	>tr|H7C701|H7C701_ENTFA Potassium-transporting ATPase potassium-binding subunit OS=Enterococcus faecalis (strain ATCC 700802 / V583) GN=kdpA PE=3 SV=1 MNSLIYQGLFFLFILLLLAVPLGWYIKEIMQGEIPKGVSFLQPVERLFYKAIGPISKKEMSAKR YALNVLLLSFFSIVLLIAILMTQHFLPGGSSVKNLTLPLAINTAVSYVTNTNWQAYVGETTLSN TSQMFGLTAQNFVSAGVGLSVLVALLRGLSQVKKKALGNFWQDLTRSLVYILLPISIILAVLLI SQGTVQSFQSGVAYQGLEGKSLWLHLGPVASQVAIKQLGTNGGGFFGANSAYPFENPTLF SNFLENIAILLLPAALIFAFGFWVKDWRQGRTIMIVSLFFLLLAFVGVAFSEYYGPEFTHVLGS TNLEGKEIRFGIGWSSLWSVGTTAASNGSVNAVLDSFTPLGGAIPMFLMQLGEIIFGGVGSG LYGMLAFLLLAVFIAGLLVGRTPEYLGKKIEAFDIKMASLVILTPLMLTLFGAMALVLHPEVMS WLTNQGPHAFTELLYGATSLANNNGSAFGGLLANTTFLNLLASLMMAVSRYLPIIAILLLAEN MGSKKKAALSSGTLSTVSPTFVSMLIIVILVIGALSFLPSLALGPIAEFFTMK

3E-205	692.1	23.3	3E-205	691.9	16.2	1	1	E1VQU5_9GAMM	Potassium-transporting ATPase A chain (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HDN1F_36040	gamma proteobacterium HdN1	584	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, unclassified Gammaproteobacteria (miscellaneous), gamma proteobacterium HdN1	83406	>tr|E1VQU5|E1VQU5_9GAMM Potassium-transporting ATPase A chain OS=gamma proteobacterium HdN1 GN=kdpA PE=3 SV=1 MIEYLLFLALLVALAWPLGRYLAAVMRGAPMRSDALFQWIERPLYALLGARPEAGMSWRGY AGAFLLSNLVLAVVVWIIFMTQAWLPLNPDGIPNMSWDLALHTMVSFLTNTNQQHYSGQAQ LSYLSQMTGIVGLQVVTPIVALAVACATLRGLFGGRARLEGAPLSASIDVGNYWVDVIRAAV RFVLPLCLVWSSLLVWQGVPATLASGPETVPLETLNLSANPSAANEITTTETLATQKIPLGPV APMVAIKQLGSNGGGWYGPNSTVPLENPTPFSNFLEVLGIALIPVSIIFMIGPFTGRQRFGV MVFGTMLTLSVISTSLAMWSESWSGTSADLALMEGKEVRLGAEASALWGATTTQINNGSV NMMMDSSAPLTGLVAITNMLINAIWGGIGCGIQQFIVYLLLAVFLAGLMTGRTPELFGRKIEA PEVRLLAILVLWQPLVLLFFTAVTLAVPGITGNSNPSFHGISQVFYEYVSAFANNGSGFEGLG DATLWWNVSCAFVLAAGRFPALVIPLAIAAMLAAKRQAPEGSGTLQIETPTFALVLMGIVLIL TLLQFMPVLVLGPIADHLSLTSILAQ
3E-205	692.1	34.1	3E-205	691.8	23.7	1	1	A0A0A1CXV6_9MICC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ART_2199	Arthrobacter sp. PAMC25486	551	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. PAMC25486	1494608	>tr|A0A0A1CXV6|A0A0A1CXV6_9MICC Potassium-transporting ATPase potassium-binding subunit OS=Arthrobacter sp. PAMC25486 GN=kdpA PE=3 SV=1 MDLNFFSLATQLAILLVVLAAVHQPLGKYLAKTFTSHKHLAVERGLYKLSGIDPQADQHWKV YLRSLLAFSIVSIVVLFLGQLLQGILPFNQGLGAVDPWVAMNTAVSFVTNTNWQTYAPEATL GFGVQMMLLAVQNFLSAAVGLAVVVALIRGLTRAQTNNLGNFWVDLTRGALRVLLPMAIVG AVVLIITGVIQNWGGTAIHTLVTGAQQTVPGGPVASQEVIKLLGTNGGGYFNANSAHPFENP TAFSSLFQVFLILVIPFSLPAMYGRMVGDKRQSGYTVLTVMVAFWLISTSLMAWAIAAFTGSG TSVGEGFEQRLGGAPSALFATATTLTSTGAVNVAHDSLPPLAGGLAMLNMMLGEIAPGGVG SGLYGMLILAVVAVFIGGLMVGRTPEYLGKKIGAPQMKLVALYILVTPTLVLLGTAITVATPAL AAAAPAEGPHGFSEILYAFTSAANNNGSAFGGITSSGPGLATLLALAMFLGRFLPIALVLALA GSLAKQRKIPATTGTLATHGPLFAVLLGGISLILTALTYFPALALGPAAEGLLK
4E-205	691.5	30.4	5E-205	691.2	21.1	1	1	B7J714_ACIF2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA-1 kdpA AFE_2477	Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	583	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus ferrooxidans (Thiobacillus ferrooxidans), Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	243159	>tr|B7J714|B7J714_ACIF2 Potassium-transporting ATPase potassium-binding subunit OS=Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) GN=kdpA-1 PE=3 SV=1 MTSAIILLVAVLALSVFLALPLGHYMYRVVEGHRFWATRFLGPLEKRIYRLTGVPVDDEMGW KRYSLSLLLFNILGVLFMYFIFQAQGALPLNPQHLPGTSIGTAFNSAIAAITTTNWQDYGGET TLSYLSQMLPYTDLNFIGGASGIAIVLAIIRGVVRKNTHLLGNFWVDITRIILYVLIPMSIILALIFI QQGVIQTFGPYVQVHLIAPFQSGGKQITQQMIAMGPVASQASIAVLCNNGEGFFDASFAHP FENPTALTNFLYMIGMILIPIAIVFMFGHMAKAKGTAWALLIAMLVIFVPLAFLSEHVDLAGNPL FNTLHVTQAHTAVLAGGGNMEGVEDRFGVAASDLFSSLATTTSSGLADCAYDSLMPLSGG VNLFFMDLGECVIGGVGTGLATMLAFAIFTVFLGGLLVGRTPEFLGKKIESFEIKMASLAILIM PLLVLIGTAIAVSTSAGRAGAFNPGTHGFSEILYAITSPANNNGSAFGGLSSDTTFYNIITGIV MLFGRYWPYLALLALAGSLAGKKTIPVGAGTLTTHTPIFIGLLVGVVILLGALNFFPALALGPIA EQLAPLNTLAH
5E-205	691.4	21.4	6E-205	691.1	14.8	1	1	I0INL9_LEPFC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA LFE_1177	Leptospirillum ferrooxidans (strain C2-3)	568	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Leptospirillum, Leptospirillum sp. Group I, Leptospirillum ferrooxidans, Leptospirillum ferrooxidans (strain C2-3)	1162668	>tr|I0INL9|I0INL9_LEPFC Potassium-transporting ATPase potassium-binding subunit OS=Leptospirillum ferrooxidans (strain C2-3) GN=kdpA PE=3 SV=1 MMIANDWIQILVSLSAVVLISPLVGRYLAWIYQSHTLLPERIIYRLLKIDPAKEMTWKEYSVAII ASNGVFFAAGFLVLWGQAFLPLNPRHLSPLTAEVTFNTAASFVTNTNWQAYAGEAQLSNF SQMVAITFLMFVGANTGMAALVAIFRGFTRSGISTLGNYWSDFFRFFVRAFLPACFLMALVH IWQGTPQTLETTVSAKTLEGANQTLIVGPVASLEAVKNLGTNGGGFYNANGAHPYENPTPL TNTLEFLEMGVFTFSLPFFFGRMIGRPRQGQVFFVIVFSLYLAGLGLIEHSEKAKNPLLSPAHI AQGTTPLQDGGNTEGKEVRLGITQTSLFSNTTIAATTGAVDGAMDSMNPLSVLVYLVHMFL NEEPGGKGVGFAGLLKEAILAVFLAGLMVGRTPEFLGKKIESREIKLSALSLLVTPLLVLGLTA VSVVIPAGKSSMDNPGPHGFMEVLYAFASGNANNGSAMAGLNVSTPYYAILIGVEMILGRFL PLLPLLAMASSLARKKTLPETSGTFKTDTPLFVVLLLGFMILFAALTFLPPLILGPLLEHLSILHG VSF
6E-205	691.1	20.3	7E-205	690.9	14.1	1	1	A0A023Y8K2_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA DX03_18395	Stenotrophomonas rhizophila	572	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Stenotrophomonas, Stenotrophomonas rhizophila	216778	>tr|A0A023Y8K2|A0A023Y8K2_9GAMM Potassium-transporting ATPase potassium-binding subunit OS=Stenotrophomonas rhizophila GN=kdpA PE=3 SV=1 MTEILLILLASIVLAFPLGLYLARVMRGAPMRGDALFGLVEKPLYWLLGVNPARGMSWRGYV GAFLLSNVVIAVLVQAVFMTQAWLPFNPDQIPNMRWDTALHTMVSFLTNTNQQHYSGQAQ LSYFAQMTAITGLQVVTPMMGLALVVATLRALFGARPEDVDAQQAAQLSADRRVDVGNYY ADVVRSCVRFMLPLCLLWAVLLTSQGVPSTLAAGPQATPIDAAAGMDTQKLPLGPVAAMVA AKQLGTNGGGWYGPNSSMPLENPTPLSNALELIGILLIPIAVIFMLGAFTGRKRLAGLVFGCM LAMSSVSVAATVWLEGHSATAASPLLMEGKEVRFGADGTGMWAAITTQVSNGSVNGMHD SLSPLAGAVPMVNMLVNAIWGGIGCGLQQFIVYLLLGVFLAGLMTGRTPELLGRKLETPQVR LLALLVLLQPITILGFTAITLAIPSITGTSNPGFHGVSQVFYEYVSAFANNGSGFEGLGDATPW WNLSCTLVLLLGRYPVLVIPLIVAAQLAAKRRAPESAGTLQIETPTFALTLIALIVVLTVLQFMP ALVLGPVADHLSLTLH

1E-204	690.1	25.8	1E-204	689.9	17.9	1	1	N8TEW6_ACIGI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA F981_02741	Acinetobacter guillouiae CIP 63.46	574	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter guillouiae (Acinetobacter genomosp. 11), Acinetobacter guillouiae CIP 63.46	1217655	>tr|N8TEW6|N8TEW6_ACIGI Potassium-transporting ATPase potassium-binding subunit OS=Acinetobacter guillouiae CIP 63.46 GN=kdpA PE=3 SV=1 MLEFILVLVIVVLLAFPLGKYLACIMQNREMKIDPIFNWIEKPIYRVLGTHPDQGMNAKTYSLS FVASCIVIGLVTWLLFMCQASLPLNPNNAPNMSWDLALHTMISFLTNTNQQHYSGQAQLSY LSQMVGIVGLQIITPMMGLAMVVATVRALFYPQSNALSEADQNLSFQNKVEKINVGNYWAD VIRPTFRFLIPLCMIWSLLLNSQGVPSTFQGGPEVQVIDQSTELKTQKIPLGPIAPMVAIKQLG SNGGGWYGPNSSVPLENPTPFSNFLEMIAILLIPVAVIFMLGFLTKRAKFAGFVFGSMLLMS VVSATAAIWSESLSSSAMQIYAMEGKEVRFGEASSALWAAITTQVNNGSVNMMHDSASPL TGLVALANMLINAIWGGIGCGLQQFMIYLFLAVFIAGLMTGRTPELFGRKIEAGEIKLLAVVILI QPITILGLSSIALFFPELTGNSNPQYHAISQVLYEYVSAFANNGSGFEGLADNTVWWNVSCVI ALLLGRFPTLIIPLMIAARLAAKRQAPESSGSLKVETPTFAFTLIAIVVMLTLLQFMPVLVLGPIA DQLLLVQG
2E-204	689.2	22.4	3E-204	689	15.5	1	1	U5QJB7_9CYAN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA GKIL_2712	Gloeobacter kilaueensis JS1	568	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter kilaueensis, Gloeobacter kilaueensis JS1	1183438	>tr|U5QJB7|U5QJB7_9CYAN Potassium-transporting ATPase potassium-binding subunit OS=Gloeobacter kilaueensis JS1 GN=kdpA PE=3 SV=1 MSGANLLQYGIFLLVVALLVQPVGTYLALVFEGEKTLLDPLLRPVERWLLRLFGVDISEQMD WKRYALCFVLFGLGGSLVLYGLLRLQSVLPGGPASYLTTPLTPDLASNTAISFATTTTWQAY GGETTMSYISQIVGLSAQNFLAGAAGLAVGIAFIRGLARQQSTELGNFWVDIVRASLWVLLP LSLAGGLVLVWQGVPLNFDPYTAVTTLEGRQQVIAQGPVAALEFIKNLGTNGGGFFNVNAA HPYENPTSLSNFLEMLAIVVLPAALTCTFGRLIGRPREGWMLFGVMTVLFLLGLLACGWIEQ ANNPQIAALANILPDGNLEGKEVRFGIGGSVLGAITTSNGATGSYNSMHDSYLPLGGAVPLV NMLLGEIIYGGLGTGLYSLIVVQVVALFVASLMVGIVPEYLGKRIGIVEIKLVALYIVLGPLAVLS LTALAVSTAEGRAGLVTNSGFHGFSEILYAYSSSFANNGQNFAGLNANSPFYNLTTAIAMML GRFGQGVIALALAGQFAKQVRRPATSGSLPSATPQFAGFLIAVILITGGLSYFPVLALGPIAE HVRLNW
5E-204	688	28.1	6E-204	687.8	19.5	1	1	A0JW40_ARTS2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Arth_1875	Arthrobacter sp. (strain FB24)	555	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. (strain FB24)	290399	>tr|A0JW40|A0JW40_ARTS2 Potassium-transporting ATPase potassium-binding subunit OS=Arthrobacter sp. (strain FB24) GN=kdpA PE=3 SV=1 MTFNTSSFLTQVAALILALTAAHKPLGVYLARVFEGKTSTRTERLFYRLAGLDASTEQTWPV YLRSVLAFSAVSILAVFGLQRLQRVLPGAGALPGVDPWVAMNTAISFVTNTNWQTYVPETT VGMFVQMCLLAVQNFLSAAVGIVVAVALIRGIARTRTDRLGNFWVDLARTSFRVLLPLAAVA AVVMVIGGVVQNFWSTDVTNQATGISQSIPGGPVASQEAIKVLGTNGGGYFNANSAHPFEN PNVFISLFQVFLLLLIPSALPYAYGRMVGDRKQGYTVAAVMGALWLASVSLMGRAVETAQG TATAAAGGLGEGLEQRFGAAPSAIFAASTTLTSTGAVNVAHDSLPPLAGGVAMVNMMLGEV APGGTGSGLYGMLILSIISVFIAGLMVGRTPEYLGKKIGPTEMKLAALYILVTPVLVLALAGITV LLPDLTANAPATGPHQFSEVLYAFTSGANNNGSAFGGITTSGPYLSVMMGIAMLLGRFLPIA LVLALAGSLARQAKVPASTGTVPTHGPLFGSLLIGVTVILTALSYFPAIALGPLAEGLLK
2E-203	686.2	22.1	2E-203	686	15.3	1	1	C6RQT6_ACIRA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA ACIRA0001_0655	Acinetobacter radioresistens SK82	570	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter radioresistens, Acinetobacter radioresistens SK82	596318	>tr|C6RQT6|C6RQT6_ACIRA Potassium-transporting ATPase potassium-binding subunit OS=Acinetobacter radioresistens SK82 GN=kdpA PE=3 SV=1 MLEFFLLIALVVILAFPLGKYLSDVMQYHKMRSDILFSWIEKPVYAVLGTQPQQEMSTRTYIL SFVLSCFVVGMLVWILFMVQAWLPLNPNHAPNMSWDLALHTMISFLTNTNQQHYSGQAQL SYLSQMVGIVGLQIITPMMGLAMVVATLRALFNLKQPGPIECDNSSALARLNVGNYWADVIR PTFRFLIPLCLLWSLLLNSQGVPSTFEGGPEVQVVQPNAELSTQKIPLGPVAPMVAIKQLGS NGGGWYGPNSSVPLENPTPLSNFLEMLAILLIPVSIIVMLGFLTRRPKFAGFVFGSMLLMSVI SATGAIWSESLSDTATNISSMEGKEVRFAESSSALWAAVTTQVNNGSVNMMHDSSAPLTG LVALSNMLINAIWGGIGCGLQQFLVYLFLAVFIAGLMTGRTPELFGRKVEAPEIRLLAVVILIQP AIILLFTAISLFFPELTGNSNPGSHAISQVFYEYVSAFANNGSGFEGLADNTVWWNISCSIALL AGRFPALIIPLLIAARLAVKRQVPESAGSLKVETPTFALTLIAIVVMLTLLQFMPVLVLGPIADHL LLVQG
2E-203	686.2	22.9	2E-203	686	15.9	1	1	V2UV88_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA P255_00721	Acinetobacter brisouii CIP 110357	569	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter brisouii, Acinetobacter brisouii CIP 110357	1341683	>tr|V2UV88|V2UV88_9GAMM Potassium-transporting ATPase potassium-binding subunit OS=Acinetobacter brisouii CIP 110357 GN=kdpA PE=3 SV=1 MAFAMWEFISVFVLSLLLAYPLGAYLADVMQAKPMKSDRFFKWIEQPIYTALGVKQVGMN WRQYLGAFVLSNILLLVASVTIFMTQAWLPFNPDNIPNMKWDLAVHTAISFLTNTDQQHYSG QAQLSYFAQMTAIVGLQYLSPIIGLALLAAMLRALFLQSGREEGADKKDWSTINLGNYWMDII RPLFRFFIPLSFIFSLLLTFQGVPATLSAGPTAQVLDPTAEVQTQHIPLGPVAPMVAIKQLGSN GGGWYGPNSTVPLENPTPLSNLIEMIAILLIPLSVVFMVGRFIQRKKLMWMIFGSMLLMSLSS TLLTLWTEKSSLIPNMAWMEGKETRFGAEASALWGSLTTQVNNGSVNMMHDSASPLTGLV ELCNMLINAIWGGIGCGLLQFFIYLFLAVFIAGLMTGRTPELFGRKIEVTEIKLLALVILLQPVVI LGLTAIAIAFPAITGNSNPAFHGISQVFYEYVSAYANNGSGFEGLGDNTLWWNLSASVALLA GRYSVLIIPVLIAVSLATKPQAAESKGSLQIESPTFALTLIGIVLILTLLQFMPVLVIGPIADYLSIK V

6E-203	684.5	25.4	7E-203	684.2	17.6	1	1	N8YBU0_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAF960_01565	Acinetobacter gerneri DSM 14967 = CIP 107464	575	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter gerneri, Acinetobacter gerneri DSM 14967 = CIP 107464	1120926	>tr|N8YBU0|N8YBU0_9GAMM Potassium-transporting ATPase potassium-binding subunit OS=Acinetobacter gerneri DSM 14967 = CIP 107464 GN=kdpA PE=3 SV=1 MLELCLLLVLVTILAYPLGKYLALIMQNRDMKIDPLFNWIEKPIYAVLGTNPQQGMNVKSYIQS FVLSCMILGLLVWILFMNQAFLPLNPNHAPNMSWDLALHSMISFLTNTNQQHYAGQAQLSY LSQMMGIVGLQIITPMMGLAMVVATVRALFFNQSNQLSHDEHARDLSTRMRKINVGNYWAD LIRPTFRFLIPLCMVWSLFLTQQGVPSTFQGGPEVQVIDQQNSELKSQKIPLGPVAPMVAIK QLGSNGGGWYGPNSATPLENPSPLSNFMEMFAILLIPISVIFMLGFFTKRGKFAAFVFASML LMSVISATSAIWSESISQTASQLSVMEGKEMRLGESSSALWTAITTQVNNGSVDMMHDSAA PLTGLIAISNMLINAIWGGIGCGLQQFIIYLFLAVFIAGLMTGRTPEIFGRKIEAGEIKLLAVVILI QPITILALTSIALFFPSLTGNSNPAFHGISQILYEYVSAFANNGSGFEGLADNTVWWNVSCSI ALLLGRFPTLIIPLMIATRLAAKRQAPESSGSLKVETPTFALTMIAIVVMLTLLQFMPVLVLGPI ADHLLLVQG
1E-202	683.7	25.9	1E-202	683.5	18	1	1	A0A0F0GLV2_NOCAE	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAUK23_35195	Lechevalieria aerocolonigenes (Nocardia aerocolonigenes) (Saccharothrix aerocolonigenes)	540	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Lechevalieria, Lechevalieria aerocolonigenes (Nocardia aerocolonigenes) (Saccharothrix aerocolonigenes)	68170	>tr|A0A0F0GLV2|A0A0F0GLV2_NOCAE Potassium-transporting ATPase potassium-binding subunit OS=Lechevalieria aerocolonigenes GN=kdpA PE=3 SV=1 MSPLVAGLLQVGILVAALAVVYRPLGDHMARVFQNKGHSKVELAIYRFARIDPNAEQKWST YAYGVLGFSFVSVVFLYVIQRAQSWLPFDFGRGNVAPGMAFNTAISFVTNTNWQSYVPEA VMGHAVQMIGLTVQNFVSAAVGLAVAVALIRGFVRHQTDRLGNFWVDLTRGTIRILLPIAFVF ALVLIAFGVTMSLKSGVDVDGQTIANAPVAGQEAIKELGTNGGGVLNANSAHPFENPGEWT NLIQIFLILVIPVALTRTFGRLVGQHKQGYVLLSVMGVIWAAMLAVIWGAEAGGLRPLEGKEL RLGIPGSAIFADSTTGTSTGATNSLHDSYSGLGGGGTLLNMLFGEMTPGGVGTGLYSILVM AIIAMFLAGLMVGRTPEYLGKKLGRKEVTAAAVSILAMPTVLLIGAGIAAILPSTQGALNNPGA HGLSEILYAYASASNNNGSAFAGITVTNDWFQSSLGLCMLFGRFIPIIAVLALAGSLAAQKKV PVTSGTLPTTGPLFATLLTGSIVLVAALTFVPALALGPIAEALQ
1E-202	683.4	25.8	7E-192	647.8	12.7	2	2	H6MWK6_GORPV	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAGPOL_c44140	Gordonia polyisoprenivorans (strain DSM 44266 / VH2)	609	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia polyisoprenivorans, Gordonia polyisoprenivorans (strain DSM 44266 / VH2)	1112204	>tr|H6MWK6|H6MWK6_GORPV Potassium-transporting ATPase potassium-binding subunit OS=Gordonia polyisoprenivorans (strain DSM 44266 / VH2) GN=kdpA PE=3 SV=1 MNPALAATLQVALLLVVLGLAYVPLGDYMASVYRSERDLGAERVLYRLARIDPKRQQTWVG YTLAVLAFSVVSVLFLYLLQRLQGVLPWADGKPGVNPATAFNTAVSFVSNTNWQSYSPEQV MSNLTQMIGLAVQNFASAAVGLAVAVALIRGLVNRRGDGQLGNFWVDLVRGTIRILLPLSIIM AVILITQGAVQSFKTGFDFTTLNGGSAHSVVGPFASQEAIKELGTNGGGTLSANSAHPFSNP TPLSNIVEIIALLIIPVCLTRTYGTLVGDRRQGYTLLGVMASLWGIMLAVSWYFESRTNGVAA QVAGAMMEGKEQRFGIPASVLFAVSTTGTSTGAVNSAHDSFSAGGGGALLWNMLLGEVA PGGVGSGLYGILMMAVVTVFVGGLLVGRSPEFLGKKVGQNEITMAALYVLVMPALVLIGAGI TVVLSSTLDAQGNGGSPGTAGSIHGFSEVLYAFASAANNNGSAFGGLTVTSDWFQSSLGF AMLLGRFLPIVFVLALAGLLARQRPRGAKADGLEPAPGQEVSRLGAGAPRTSTIETGAVGD DAEAGGAVALEARTDTASTLPTHGLLFGALLFGTILLVAGLTFFPAMALGPIAEAAL
1E-202	683.3	36.4	2E-202	683	25.2	1	1	A0A0F2S6G5_9RHOB	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAVR71_00135	Roseovarius sp. BRH_c41	553	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseovarius, Roseovarius sp. BRH_c41	1629709	>tr|A0A0F2S6G5|A0A0F2S6G5_9RHOB Potassium-transporting ATPase potassium-binding subunit OS=Roseovarius sp. BRH_c41 GN=kdpA PE=3 SV=1 MDHVLVIGLIIGGTALLSLPLGAWMKLAMDPASGGATRWTTLFARIGGTCEEQGWKRYLVA MLIFNAIMFTVTFAILALQHWLPLNPDGKGSLGPTLVFNTAASFTTNTNLQHYSGEVSMSYL SQLAGMMWLQFVSAATGIAALAALARGIAGRATLGNFLVDVQRASFLVLLPVALVVAVLMVL MGVPMTLQGSAVVTTLEGVTQTIARGPVAAFLTIKQLGTNGGGFFGPNATHPLENPSFWTN GLAMIAIMLIPMACVWMFGGILRRRKHAAVIFAVMTLFILVKITGSVSFETAPTPAFADLPVAA DVGNLEGKELRFGATGGPLWAVLTTSTSNGSVGAMHDSLNPLTGLMPMAGMWLNATFGG VGVGMINMFLYIVVAVFVAGMMVGRTPEYLGHRIEAKEVRLAVLALFAHAVLILGGTALFAAT SLGQSTVQETGAHGFSEILYEFTSAAANNGSGFEGLGDGTWAWNIATGVVMLLGRFLPIILP LAIVGSLMTKRRAAESVGTLGVEDATFGIMLGITIVIFGALTFLPAAALGPIAEHFARP
1E-202	683.2	28	2E-202	683.1	19.4	1	1	H8GX36_DEIGI	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpADGo_CA0649	Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	529	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus gobiensis, Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	745776	>tr|H8GX36|H8GX36_DEIGI Potassium-transporting ATPase potassium-binding subunit OS=Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0) GN=kdpA PE=3 SV=1 MDASRGMTWRQYGAALLGTNVLLGVAAYLVFLFQGGLPLNPDGIAGMRWDTALHTAASFI TNTNQQHYSGQSGLSYLSQMVGITALQIVTPAVGMAALFAVLRGLKGEKNVGNYYLDVTRA VGFLVPTSFILALLLTWQGVPSTFSGAKTATLVQPQTTQGQTVTTQTIPVGPVAAMVAIKQL GTNGGGWYGPNSATPLENPTPLSNLLQLVSIILFPVSLVVATGRFLNRARFGVAIMAVMSVM SAALTLGAVLAERGPNAALQGLSALGPNMEGKEVRFGADATALWGAVTTQTSSGSVNGML DSFTPLGGLVPQLGMFLNDVYGGIGVGMINMLIFVVLTVFIAGLMVGRTPELFGRKIEVREM KIASLIILLQPLLVLGFTAAALAMPSITANSNPGFHGLSQVLYEYNSAFANNGSGFEGLGDNT PWWNVTCAVVLILARFLPILGPLAIAGLLAAKKAAPETSGTLRVDTPVFAGMLLSVMLLLQLL NFAPALVLGPVAEQLTLNRTVSQAAAAQSATAQDQP

2E-202	683	26.2	2E-202	682.8	18.2	1	1	N9GJA0_ACIHA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAF927_02457	Acinetobacter haemolyticus CIP 64.3	565	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter haemolyticus, Acinetobacter haemolyticus CIP 64.3	1217659	>tr|N9GJA0|N9GJA0_ACIHA Potassium-transporting ATPase potassium-binding subunit OS=Acinetobacter haemolyticus CIP 64.3 GN=kdpA PE=3 SV=1 MWEFISVFILAMVFAYPLGRYLADVMQAQPMKSDCIFKWIERPIYVVLGVKQVGMNWRQYL GAFIISNVLLLATSVAILMTQAWLPLNPDHIPNMNWDLALHTSISFLTNTNQQHYSGQAQLSY LSQMTVIVGLQYLSPIMGLALLTAMLRALFLQPSQTENSEKKTWKNINLGNFWMDMIRPLFR FFIPLGLFFSLLLTFQGVPSTLSAGPTVQVLDQAVEVQTQHIPLGPVAPMVAIKQLGSNGGG WYGPNSSVPLENPTPLSNVLEMLAILLIPISVVFMIGRFIQRKKLMWMILGTMLLMSLASTVFT LWAEKSSLVPNIALMEGKEVRFGAEASALWGSLTTQVNNGSVNMMHDSASPLTGLVELSN MLINAIWGGIGCGLLQFFIYLFLAVFIAGLMTGRTPELFGRKIEVTEIKLLALVILLQPVVILGLT AIAIAFPSLTGNSNPASHAISQVFYEYVSAFANNGSGFEGLADNTVWWNLSASVALLAGRYS VLIIPVLIAVSLATKPKADETKGSLQIESPTFALTLIGIVLILTLLQFMPVLVIGPIADYLSVKI
6E-202	681	27.9	2E-191	646.6	14.2	2	2	D0L4N2_GORB4	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAGbro_4092	Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	604	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia bronchialis, Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	526226	>tr|D0L4N2|D0L4N2_GORB4 Potassium-transporting ATPase potassium-binding subunit OS=Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) GN=kdpA PE=3 SV=1 MSTTTAGLIQVGILILVLALAYVPLGDYMARVYGSSRDLRVERVVYRIGRIDSRREQTWVGY VLAVLAFSLISFLFLYALQRLQGVLPWSDGKPGVSPSMSFNTAISFVSNTNWQSYSPEVVM SNLTQMLGLAVQNFVSAAVGLAVAMALVRGIVNRRGSGEVGNFWVDLIRSTVRILLPMAFIV ALILLTQGAVQSLGTGFDFTTLGGEQAHSVLGPFASQEAIKELGTNGGGTLSANSAHPFSNP TPLSNLVEILALLIIPVCLTRTYGTMVGDRRQGLTLMGVMATIWSAMLAIVWIFESRTDGIAG QAAGAMMEGKEQRFGIPGSVLFAVSTTGTSTGAVNSAHDSFSAVGGGALIWNMLLGEVAP GGVGSGLYGILIMAIVTVFVGGLLVGRSPEFLGKKIGQNEITVAALYILVMPALVLTGTAITAIL SSTIGFQGNSGDPGSPGSIHGFSEVLYAFASAANNNGSAFGGLTVTSDWFQTSLGLAMLL GRFLPIVFVLALAGLLARQRPRGSTADAASTDTSPVAVSAVVEGGAGAQPAAGGMAVATH GATGPADDAATLPTHGILFGALLFGTILLVAGLTFFPAMALGPIAEAVL
9E-202	680.6	26	1E-201	680.4	18	1	1	A0A060BF51_9GAMM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpAFF32_12925	Halomonas campaniensis	563	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas campaniensis	213554	[illegible] subunit OS=Halomonas campaniensis GN=kdpA PE=3 SV=1 MNDMIAIYAIVALLGVPLGIYIARALSTQPSRIDTLFRVIETPIYRLAGVNSQSVMTWQVYALAI LKLHVGLILLAWLVFMCQGLLPLNPDGIPGMKWDTALHTAVSFATNTNQQHYSGQAQLSHL SQTFAIVTLQFLTPATGLAVLVAIARTLLVARPAGTVKGVGNYYHDMTRTLVRVMLPLAAVVA LLLTSQGVPSSYQAAHQVEMLDSQVEEVQSIPLGPVASMVAIKQLGTNGGGWYGPNSSVP LENPTPLANVIETASLTIIPFALLIAIALISGRRRLMMGIGAVMLTFSLISTSVVVSSERMPNAAL VELSQLGANLEGKELRFGTDLSALWGSWTTQTSNGSVNAMHDSFNPMGGMMVLMDMFV NVTFGGIGVGLIGFFLYLMLAAFVGSLMVGRAPELFGKPLETREMRWISLAILVQPLVILGLS ALTVAMPNAAGTSNPGFHGLTQVLYEFASAFANNGSGFEGLSDDTPWWNLACVITLMVGR FLPMLVPLAVAGWLAAKRTAPAGRGTLPMDSPAFMGLTAGVIVIVNLLGFLPALVLGPIAEAV TQGF
1E-201	680.4	28.5	1E-201	680.1	19.7	1	1	D6ZE64_SEGRD	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpASrot_0867	Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Segniliparaceae, Segniliparus, Segniliparus rotundus, Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	640132	[illegible] OS=Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578) GN=kdpA PE=3 SV=1 MPTGLAAALQLLFILGVLAAVYVPLGDFMARVYTSTEDLAVERVLYKAARVNAAAEQTWQW YTLSLLGFSFVSVFFLYALQRLQGVLHLGGGLAAVSPAVAFNTAVSFVTNTNWQSYTPETT MGVWTQPLGLAVQNFLSAAVGMAVAIALVRGFVHVREGGEVGNFWVDLVRGAVRVLLPLS LLVAVVLLTQGAVQSLHAGFASSQGQVPLGMAASQEAVKELGTNGGGFFAANSAHPFENP TPFSNAVEIIALLVIPVAFTRTFGTLVGDRRQGLALLAVMAFLWGSVLAATWFCESSPSGMA GKAAGAMLEGKEVRFGVPASVVFAVSTTGTSTGAVNAAHDSFSALGGGALTLNMLFGEIAP GGTGTGLYGLLVLALIAVFVGGLLVGRTPEYLGKKVRQREITLAALAVLVMPALVLAGTGISL VLPGTRAAQGNSGDPRTLGSIHGYSEVLYAYASASNNNGSAFGGLAATSDWFQASLAFCM LLGRFLPIILVLALAGSLVAQRHTPPTAGTLPTHRGLFIGLLVGVVLLVAALTFFPALALGPVAE ALG
2E-199	672.5	24	3E-198	668.8	16.6	1.9	1	I0XR77_9LEPT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpALEP1GSC185_3493	Leptospira licerasiae serovar Varillal str. VAR 010	578	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira licerasiae, Leptospira licerasiae serovar Varillal, Leptospira licerasiae serovar Varillal str. VAR 010	1049972	[illegible] OS=Leptospira licerasiae serovar Varillal str. VAR 010 GN=kdpA PE=3 SV=1 MNGNDSIFFFLYFAVLFLLSPFLGIYIADVLKGEISKRFKFLSKFESFLFKNLSLKVQALEVGGF GTDNKISETKEDKNSNWKFYLLDIGIFTLLSLALVVLGLHFQDILPGNPEGKSGVAWDLAWN TSVSFVTNTNWQAYSGEVSLSYFSQMLLLGVQNFVSAGAGIAVLAAMTRGLVSKPGQSSGI GNFYVDLTRSILYILLPISLVASFILVSQGTVMDLSRYVSAIGMEGQSVKIPLGPAASQIAIKQL GTNGGGFFGVNSAHPLENPTVFSSWLQCILILLLPGALPFAYGRWVGSWKAGLSLFIGMTL LFVLSLSVSLWSESNFIGNWEGKETRFGVAQSVLWGMATTAASNGSVNAMHDSFSPLAG GIAVWNILLGEVVFGGVGVGLIGMLFYVVLTVFIAGLMVGRTPEYLGKKIEAKEVKLALAGVLI PGLCILLFTAFSLLYESALSSRTNLGPHGLTEILYSFASASGNNGSAFAGLNANTPFYNLTLSF CMLVGRFAVIIPALGLGGVLSGKKIAPKGEGTFSTESPLFVLLLLSVIFLVGALTFLPVLVLGP GSEHILLQYGQKF

2E-198	669.7	31.1	2E-198	669.5	21.6	1	1	C4KYL4_EXISA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA EAT1b_1250	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	545	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	360911	>tr|C4KYL4|C4KYL4_EXISA Potassium-transporting ATPase potassium-binding subunit OS=Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b) GN=kdpA PE=3 SV=1 MWVTFIITLSLLIAITMTASALLGGYVGRRFVPIQERPNYVGKALETRITRRLRINEREKQSWF GYAKDFLTLNLLFLLIGYVLLRFQGVLPFNPNGAVNLDWHLAFHTVISFMTNTDQQHYSGEA LSHLSQMFVLSTLMFVAPTMAFTMALAFIRGILGKPIGQFYFDFVRVIVYVLLPISLFFGMWLI AFGVPQTLSPNAVVTTLEGASQTIQRGPIASFEVIKQLGNNGGGYYAVNGAHPFENPSDWT NYIHLFLMLLLPMSLPFIYGAMAKKRKQGFLYFSVMLFLFIIGTVFMYATLYANPSLHGQEMR FGAIGTALYGAVTTAAETGAVNAMHDSLPSLSGIILMGNMMLNVVFGGVGAGFMNLMMYVII TIFVAALLIGQTPTVLGKKIEGREMKLVALTLLVSPLLILGFTALALVVQPGQDAITNAGPHGIS QILYEYTSAVANNGSGFEGLLDATPFWNITAGFAMFFGRYIPLLLMVAMAGSLQMKPRVTD DGALRTDTPLFTSLLFGVIVIVGALTFLPVLLVGPFAEWLMIR
2E-198	669.6	33.1	2E-198	669.3	23	1	1	F8I6Z9_SULAT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA TPY_0466	Sulfobacillus acidophilus (strain TPY)	563	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiales incertae sedis, Clostridiales Family XVII. Incertae Sedis, Sulfobacillus, Sulfobacillus acidophilus, Sulfobacillus acidophilus (strain TPY)	1051632	>tr|F8I6Z9|F8I6Z9_SULAT Potassium-transporting ATPase potassium-binding subunit OS=Sulfobacillus acidophilus (strain TPY) GN=kdpA PE=3 SV=1 MSVSTMATWAVALMCFALTIKPLGTYMARVFTFQPTFLDPVFKPVESRLFQWLRIDPRQSM TARQYLQALIVTNALWIVLSYVFLRIQGILPWNPEHFGAVNPALAYNTATSFGTNTNWQAYA GESTMSTFSQFGNLSFLQFVTPAVGGTIAIAFARSLSGKPLGNFFADLVWMCTRILLPLAMV VTLLLVTQGVPETMAPYLTVHTITGHTQVVPRGPIASWEAIEHLGTNGGGYTNANSANPLEN PTPISNLIETVSMGVVSIAFYYALGIMTGRKKLAWTLIGVSGVLFVGMLVLVYLPMDAGNPIL QALGIHGPNWVGQELRFGTGGTALFETSSMAFTTGSIASAHDSALPFTGLAYLAAMFLNMIF GGFGVGLVNMLMLVIITVFLMGLMVGRTPEFLGKKIEAKEVSLAAIAFLLHPMLILAGTAIAVA TPAGMQGIGNPGPHGFTEILYAFASGAANNGSAMAGLNAALPFYEIVIGLTMLIGRFASMVP MLLLGESLLAKRSVPQTAGTMRTEGLLFGTVLVGSALVLNALTFFPVVSLGPLAEHWLLLAH QVF
2E-198	669.5	24.2	2E-198	669.3	16.7	1	1	A0A0F7JVA1_9DEIO	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA SY84_13290	'Deinococcus soli' Cha et al. 2014	560	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, 'Deinococcus soli' Cha et al. 2014	1309411	>tr|A0A0F7JVA1|A0A0F7JVA1_9DEIO Potassium-transporting ATPase potassium-binding subunit OS='Deinococcus soli' Cha et al. 2014 GN=kdpA PE=3 SV=1 MMDILLTYGLALALALPLGLFMARLMEAPASRVTAGLLRACGVDAARGMSWRAYVGALLGT NVIVGLVALATYLLQGGLPLNPDGIANLRWDTAVHTMASFITNTNQQHYSGQSGLSYLSQM LGITALQIFTPAVGFAALFAVLRGLRGDAHLGNYFLDVTRGAALLTVSAAVLALLLTWQGVPS TFAGARTATLVQPQTVEGQAVTTQTIPVGPVAPMVAIKQLGTNGGGWYGPNSTVPLENPT PLSNLLETVSIILFPLALVVATGRFLRRPRFGLVLMGVMSVLSAALTLGAVLAERMPNAALTG LSALGPNMEGKEVRLGADATALWAALTTQTSNGSVNGMLDSFTPLGGLVPQLGMFLNDVY GGIGVGLINMLVFVILTVFVAGLMVGRTPELFGRKIEAPEIKLASLILLLQPLLVLGFTALALAN PAVTANSNPGFHGLSQVLYEYNSAFANNGSGFEGLGDNTPWWNLSCALVLLARFLPIVGP LAIAGLLAAKRAAPEGSGTLRVDTPVFAGMLLSVMLLLQLLNFAPALVLGPVAEKMTLNTVK DVTK
2E-197	666.6	30.4	2E-197	666.3	21.1	1	1	B1YM42_EXIS2	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Exig_2551	Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	546	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sibiricum, Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	262543	>tr|B1YM42|B1YM42_EXIS2 Potassium-transporting ATPase potassium-binding subunit OS=Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15) GN=kdpA PE=3 SV=1 MWTQFLLQFWILLVIALGAAVLLGRYIGTVFAPVGIRKTDWIGKLERRLLLLLGVDERKQDQS WVGYSKSLLLVNLLFFVGGYLLLRFQGSLPLNPNGAVNLDWSTALHTTISFMTNTDQQHYS GEALSYLSQTFVLGTMLFVAPTMAFTVCIAVIRGLANQPLGNFYADFVRFILRILIPVSFLFGLL LILLGVPQTFGGTVTVTTLEGAKQLIYRGPIAAFEVIKQLGNNGAGFFGANGAHPFENPNQY VNFIQMFLMLLIPMSLPVAYGKMIGSAKQGRLFLGVMTLLFIMMTFGMAGSLLANPTAHGQE LRFGQIGTILYSSITTAAETGAVNAMHDSLHPLAGLIQLGNMMLNVVYGGTGAGFLNVLLYAF VAVFLTGLLIGRTPTFLGKKLETFEVKLMAITLLVPPFLILVGTAVSMYVAPGVGAISNPGYHG LSQVLYEFTSATANNGSGFEGLGDANVYWNVSTSFALFFGRYIPLILMLAIAGSLKAKPAVP QDEFSFKTDTPLFGTVFLGTVVLVGALTFLPVLVLGPIADWLTM
6E-197	664.6	27.5	7E-197	664.5	19.1	1	1	L0J218_MYCSM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Mycsm_05130	Mycobacterium smegmatis JS623	538	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis JS623	710686	>tr|L0J218|L0J218_MYCSM Potassium-transporting ATPase potassium-binding subunit OS=Mycobacterium smegmatis JS623 GN=kdpA PE=3 SV=1 MLVVILHVPLGNYMARVYTDSGHWRVERVMYRLIGAQPDNRQRWSNYGFSLLAFSAVSVL FLYGLLLAQTRLPEPWGHTGMTPALAFNTAISFVTNTSWQNYPGESTLGHVGLAVGLGVQ AFASCAVGMCVAVALIRGLAQYQKEELGNFWEDLVRSVVRVLLPLSVVVTLLLLMLGVVNN FHGAQEISTLAGGNQTILGGPVASWESIKLMSGDGGGAFNVNSAHPFENPTPLTNVVEIVA MLLIPVAFLRTFGIMVGDKKQGWALFSAAAILFVVGTVALALATGVADGTVVHAVGGPFEGT ETRFGLPGSALFGQAATASADGAANSSYDSFVSGGGAVLMLNMMLGEVAPGGAGSGLYG LVMMALLAVFLGGLMIGRTPEYLKQRLGARHMKLISLYILALPAAVLVGTAVAMALPGERAS MLNTGPHGLSEVLYAFTSSAANNGSAFAGFSGNTVWYNTALALAMMVGRFLPIIAVLAIAGT FAAQRPGVVTAGTLRTHSPTFVFLIAGATLLIVGLEYLPALALGPAADALR

9E-197	664	25.8	1E-196	663.7	17.9	1	1	B8H6W7_ARTCA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Achl_1704	Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	546	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter chlorophenolicus, Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	452863	>tr|B8H6W7|B8H6W7_ARTCA Potassium-transporting ATPase potassium-binding subunit OS=Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6) GN=kdpA PE=3 SV=1 MQFNIFSFITQIAVLVVALGAVHRPLGAYLAKVADDGGHFRWERWVYRAAGVGSDSGQTW NAYARSVLAFSIAGVLVVYVAQRIQPLLSGGQAAGVDPWVAMNTAVSFVTNTNWQAYVPE STLGFVVQMAFLAVQNFVSAALGIAVSFALMRGFARRSSGSLGNFWVDLTRLTFRVLLPLS AVAAVVLLSAGVVQNFWPAEVHNAVTGVSQSIPGGPVASQEAIKVLGTNGGGYFNANSAH PFENPSSFTNLFEVFLILLIPSALPYTFGRMVGDRKQGYTVLTVMASLWLISMTAMAWTMAA APDLGEGLEQRFGPAASGIFATSTTLTSTGAVNASHDSLPPLAGGMAMFNMMLGEVAPGG VGSGLYGMLVLAIVAVFLAGLMVGRTPEYLGKKIQARHMTLAALYLLVTPVLVLVLTGAATLV PDAVAQAPAQGPHQFSELLYAFTSGANNNGSAFGGITTSGPLLSTLMAAAMWLGRILPIVLV LALAGCFAAQEPIPPSPGTLATYGPLFAGLLGAVTFLLTALNYFPALALGPIAEGTFQ
5E-196	661.7	29.9	1E-185	627.4	15.2	2	2	J9S9K6_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA KTR9_4022	Gordonia sp. KTR9	610	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia sp. KTR9	337191	>tr|J9S9K6|J9S9K6_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Gordonia sp. KTR9 GN=kdpA PE=3 SV=1 MNTTVAGLLQVVALVTILAVAYVPLGDYMARVYAGGKDLRVERVLYRMARVDPSREQTSTG YALAVLGFSLISFLVVYLLQRLQGVLPWSDGKPGVSPSMAFNTAISFVSNTNWQSFSPEVV MSNLTQMIGFAVQNFVSAAVGMAVAMAVIRGIMSRRGTGEIGNFWVDLVRGSIRILLPLSLV LATLLITQGLVQSWHSGFGWTTLDGADARSVVGPFASQEAIKELGTNGGGTLSVNSAHPFS NPTPLSNLLEIVALLLIPVCLTRTYGTLVGDRRQGLTLLAVMAAIWSLMLTLVWAFETRTAGS ASAAAGAMMEGKEVRFGIPGSALFAVSTTGTSTGAVNSAHDSFSAVGGGAVLWNMLLGEV APGGVGSGLYGILVMAMITVFVGGLLVGRSPAFLGKRIGQHEITMAALYVLVMPALVLTGAG ISMILGSTTDAQGNSGDPGSPGSIHGFSEVLYAYASAANNNGSAFGGLTATGDWFQASLGI AMLLGRFLPIVLVLALAGLLARQTPRGGGTSTGTASPVAVSPVAVSPVAGAVNSDDPTTTAV LPAPAGTAPNAVEPDTRSTLPTSGFLFGFLLAATIVLVAGLTFFPAMALGPIAEALL
4E-195	658.5	29.3	5E-195	658.3	20.3	1	1	KDPA_HALSA	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA VNG_6176G	Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	582	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halobacterium, Halobacterium salinarum (Halobacterium halobium), Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	64091	>sp|P91884|KDPA_HALSA Potassium-transporting ATPase potassium-binding subunit OS=Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) GN=kdpA PE=3 SV=1 MASPPPIVEYAVFFTILAVLVFVAGEYLAWVYREQANSDHRPPGYLSWFERLDEIFTPIENGL YRLSGINPRREMTWKGYLKAVLVFNVCIWVLLFVVLMFQDALPMNFVGVGGESWDLAFHT ASSFTSNTNQQHYSGETLSVFTHTFGIGIAMFLTPATGLALMPAFARAFTNKEDPRLGNFYE NVVRGLVRFLLPISLLIAIILMAEGSVQTILGGQLTANTFTMGIQNIRIGPHAGIEAIKMFGTNG GGINAANAATAFENPTPLSNLVLTLAMPIGTFSAIYAWGAWVGNRSHGVAIVAAFFVIYMALT GVAVVGETGTNAGMVVTGNGLHVDQTVGNMEGKETRFGPTASAIWGLSTTGTTNGGVNS MHNSWTALGAFSLLFAFATNNISNGVGTGLLNILMFVILTAFIGALMIGRRPQYLGKKLEWQE MRYVFVVILVLPILVLIPQAAAVVYQGAIDSMNNPGFRGFSEVLYEFFSASANNGSGFEGLG DGTLFFNLVNGVQVLLARYVPITAQLAIAGYLANKKVSPESKGSLDTDTPAFVGLLIGVIIIVSA LVFLPALVFGPIGELLSGGI
2E-194	656.7	28.3	2E-194	656.5	19.6	1	1	D3DFQ3_HYDTT	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA HTH_0188	Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6)	488	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Aquificaceae, Hydrogenobacter, Hydrogenobacter thermophilus, Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6)	608538	>tr|D3DFQ3|D3DFQ3_HYDTT Potassium-transporting ATPase potassium-binding subunit OS=Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6) GN=kdpA PE=3 SV=1 MFLVLFFQNLLPLNPQGFNGFSWDMALNTAVSFVTNTDWQAYSGESAASYASQMLGLTV QNFLSASTGIVVAVALIRGLKRTETPYIGNFWVDMVRATLYVLLPISIAGALFLVSQGVIQNLD PYLKVELLDPALKGKEQIIPMGPVASQEVIKLLGTNGGGFFGANSAHPFENPTPLSNFFECLL MLLIPTALTYTFGKLTGRQKLGWVIFGVMLFFFTSAYLTEYWAMSQLPPSFEKLGISGPYVE GQETRFGLGGSALFGVVTDSTETGAVNGMFDSYLPLAGMVLLMLMGAGVVFGGVGAGLY GMLAYMIIASFIAGLMVGRVPEFLQKKLYPKDMWASVVTALTPTLLVLVLSSIALLTKAGTSSI LNPGPHGVSEVLYAYTSTANNNGSAFAGLNANTVFYNLTTAFAMFAGRFVVIFAVLVLAGSF AQKKLVPVASGSLREDSLTFAVWLVFTVLLLNVLGFFPALSMGPVLEHFLLYGMR
6E-193	651.4	12.2	7E-193	651.2	8.5	1	1	K9PBZ4_CYAGP	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Cyagr_3182	Cyanobium gracile (strain ATCC 27147 / PCC 6307)	556	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobium, Cyanobium gracile, Cyanobium gracile (strain ATCC 27147 / PCC 6307)	292564	>tr|K9PBZ4|K9PBZ4_CYAGP Potassium-transporting ATPase potassium-binding subunit OS=Cyanobium gracile (strain ATCC 27147 / PCC 6307) GN=kdpA PE=3 SV=1 MLPWFLAALTLTVAVLTAFPLGRHLWQVFDDRPQPGWDPWLLPLETALLRWIGDRGQPAA TAWAYLQPFLVANACFGGLAFLLLAFQPAWLNPLGWPGLRWDLALHTSLSFLTNTDQQHV VPEQTLGTFAQLGVIQFLMFVSAASGLAVGFAVVRGLCGLPLGNFHRQLVRSLTRVLIPGSL LLAVPLLFCGVPMTLADPLRITTLEGGSQLLIRGPVALFEAIKQLGENGGGFYGANSAHPFEN PDGFTNLLSCWAMLAIPAASIDAFGRFLGNRRQSTLLLLLVTALLAIGSALAMAAEQGGNPAL AAWISGANLEGKELRFGAGLTAFWAVLTTGSMTGAVNGAMDSLLPLSNLVALFNLFLQVVF GGQGTGIAYLLVFMVLAVFLTGLMVGRTPEFLGRKVEKAEVVWSSLILLLIHPVFVLLPAALTM AGATELAGISNPGPHGISQVVYEYASAAANNGSGMEGLGDGSVWWNLSTSLSLLGGRYLP IAALVLLADGYARKPALPPGPGTLATDTSLFTVVLAVVLLILGALTFFPVLALGPIADALLLAT

6E-191	644.8	21	7E-191	644.6	14.6	1	1	S6C6G0_9ACTN	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AEQU_1607	Adlercreutzia equolifaciens DSM 19450	595	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Adlercreutzia, Adlercreutzia equolifaciens, Adlercreutzia equolifaciens DSM 19450	1384484	>tr|S6C6G0|S6C6G0_9ACTN Potassium-transporting ATPase potassium-binding subunit OS=Adlercreutzia equolifaciens DSM 19450 GN=kdpA PE=3 SV=1 MSAIAGSEFLQAGVLVALVVACALPLSGYLVDVMEGRPLLIRRALGPLERSACRLVGAREDD GMDWRRFLASALAFTAVSFIGLFILLICQGALPWNPEGFPGLALDTAFNMTASFVTNTNWQ PIAGETNLSYFSQAVGLAVQNFLSPAVGIAVAFALLRGLASSDGGKLGNFFVDVVRAVLYVL LPLSLVLALVGVWQGSPQTFQGYETVQLLEPVSVDAEGTLVDADDPTAVQEVTEAVVPLGP QSSQVAIKQLGTNGGGFNGANSASALENPTPLTNLLQCAAMPLIPFALVFAFGRMVGDRRQ SRALMTVVLALLAAGLFSVIAAETAATPQLSADGAVCLGALDQSAGNMEGKECRIGVGESA AWTALTSATSNGSSNASIEAMTPIGTLVPLALIGLGEVVGGGVGTGLVGLLGFTVLAVFVAS LMIGRSPEYLGKKLGPAEMRMAVVIVVAPALAILLAASVLVMSPASAAAVGTPAPFGFTELLY AATSAGGNNGSGLSGLSSNTPLINVVLGVEMLFARLAPLAAALVLAGNLAQRKVQATGAVG LSTSSALFAVLLLVIIVLIGALSLLPAFALGPLAEQFMGAF
1E-190	643.9	19.5	1E-190	643.7	13.5	1	1	A0LLJ6_SYNFM	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Sfum_2620	Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	609	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophobacteraceae, Syntrophobacter, Syntrophobacter fumaroxidans, Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	335543	>tr|A0LLJ6|A0LLJ6_SYNFM Potassium-transporting ATPase potassium-binding subunit OS=Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB) GN=kdpA PE=3 SV=1 MFLQTWSLPFLLLATATLAAFPLSRYLAWIMDGKYRPAPFFRWFEERLDSGPQNWKQYAG SLLAFNTLLFAFGFLVLALQPWMPLNPDGKGMLAPSTIFHSVASFMTNTDLQHYAGERHLS NFSQIFFGMINLFLSAAIGLCALTAIIRALRGDPSLGNFFVDMWRVVVYLFVPAAFLVGFIFLT QGSPMTFRSSYQVSILETADMGIADRSEAKPQTIVVGPVAAFESIKMLGTNGGGFYGMNSA HPFENPNALTNFLATLSMMLFPFSLVLVYGRMLQRVRHSIVIFSVLLLMMAGTIAWTVVFDTL RPNPGLTASPVPRTYEIPSATAPGGKWTVTVPAIPGLPVDQHLGNLEGKELRFGTAAGATF AAITTDVTCGAVNAEADSLNPLAALSPMIGMWLNCIFGGKGVGMINVLLYIIVAIFIAGMMVG RTPEYLGKKIGAREMKLATLALLVHPLMILLPTGLFAATDWGLLAVSNPGAHGFSQMLYQFS SASANNGSAFDGLGVVYGFHHNPTPAPTAVAWDIATALVIIVGRFLPILAPMAMAASLGAKR SSPFGLGTLRDDGITFGVLLLGTVLIIGALLFLPVAALGPFAEHLGPVPFGG
1E-189	640.8	23.1	1E-189	640.4	16	1.1	1	D1Z017_METPS	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA MCP_1967	Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE)	545	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanocellales, Methanocellaceae, Methanocella, Methanocella paludicola, Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE)	304371	>tr|D1Z017|D1Z017_METPS Potassium-transporting ATPase potassium-binding subunit OS=Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE) GN=kdpA PE=3 SV=1 MGFLFGMVQILPIILLALILAIPLGEYLALVFSGKRAPLEPAFSPIEKALSRLLMGMDRHPMDW KEYALSLLALNALLWAVAFAILYSAGMSPDLAFHTATSFVTNTDQQHYSGDTLSPAAQMLAL TMLMFASAATGISSAFALIRGLLATDGKLGNFFSDFIKCIVRVLLPGAFMVAIVFVACGIPQTL GGSLDVKTITGLMQSIPLGPVASLESIKYLGTNGGGYYGANSAHPFENPSPLTNVIQNILALLI PFSIPYAFGIMAGKRRQGAIILIAMLVIFVTGAALMLAGEGWNPALPLNYPDGYLEGKEQRFT AYETTFFLAVDTFVQSGGTSGSVTSMMPDAILGAMSGMMMQCTPGGVGAGFDVMLVFILL SVFIAGLMVGRTPEFLGKKVEPNEMKLVALVIIIHPILVLLPTALTIIVNPHAALNPGPRGFSEIM YEFLSASANNGSGMAGLANTTPYFNILSGLMIATGRYVPLVAMIAIAGLLSRKKPIEATTGTLP TDNPTFLLFLIGIIVIVGAITFLPVLTFGPLAELLGGT
1E-189	640.4	27.9	2E-189	640.2	19.3	1	1	L0JLL8_NATP1	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Natpe_1875	Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	582	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema pellirubrum, Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	797303	>tr|L0JLL8|L0JLL8_NATP1 Potassium-transporting ATPase potassium-binding subunit OS=Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786) GN=kdpA PE=3 SV=1 MGSPPPIVQYTVFFVILAILIYLLGEYLAWIYRDQANSDYDLPRFLTGLKRLDSVFTPIENGIYR LSGINPRREMTWKGYVKAVFVFNAFIWALLYVVLYFQNGLPMNFVDVAGQSWDLAFHTAS SFTSNTNQQHYSGENLSVFTHTFGIGIAMFLTPATGLALMPAFARAFNNEKDPRLGNFFANL VRGLVRFLLPISFLIAIILMAEGSVQTILSGKFTAETFTMGVQNIRVGPHAGIEAIKMFGTNGG GINAANAATAFENPTPLSTLVLTLAMPMGTFSAIYAWGAWVGNRKHGVAIVAAFIVIYMTLT GVAIVGETGPNAAMQVQENGLTVDQSVGNLESKETRFGPTASAIWGLATTGTTNGGVNSM HNSWTALGAFSLLFAFATNNISNGVGTGLLNILMFVILTAFVGALMIGRRPQYLGKKLEWQE MRYVFVVILTLPIIVLLPLAHAVVYQPAVDAMANPGFRGFSEILYEFFSASANNGSGFEGLAD NTIYYNLVDGMQVLLARYVPITAQLAIAGLLANKKISPESRGSLDTETPAFVGLLIGIIIIVSALVF LPALVFGPIGELLSGGI
5E-184	622.1	34.1	5E-184	621.9	23.7	1	1	I4MR10_9BURK	Potassium-transporting ATPase subunit A (EC 3.6.3.12)	Q5W_1531	Hydrogenophaga sp. PBC	441	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Hydrogenophaga, Hydrogenophaga sp. PBC	795665	>tr|I4MR10|I4MR10_9BURK Potassium-transporting ATPase subunit A OS=Hydrogenophaga sp. PBC GN=Q5W_1531 PE=3 SV=1 MLGLTVQNFLSAATGIVVVMALMRGFARHSARAVGNVWVDLTRITLWVLLPISIVLALAFVGL GVVQNLSPYLTLTPLQAGVGDQTLAMGPTASQLAIKMLGTNGGGFFNANSAHPFENPSEW SNALQMLAIFAIPAGLCFTFGRVVGDRRQGWAVLAAMALIFVAAVVAATSFEQQGNPALAAL GADQAASALQSGGNMEGKEVRFGIAASSLFAVITTAASCGAVNAMHDSFTPLGGMVPTAL MQLGEVVFGGVGSGLYGMLVFALLAVFVAGLMIGRTPAYLGKKIEPFEMQMVSIAILVTPLL VLLGTAIAVMTEAGRAGIQDAGPHGFTEVLYALSSAANNNGSAFAGLSANTPFYNVLLAIAM AVGRFGVILPVLALAGSFAAKPRAEASAGSLATHGPLFIGLLVGTVLLVGLLNYVPALALGPV VEHLMLWAK

6E-179	605.2	31.1	7E-179	605	21.6	1	1	R7I6C6_9BURK	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA BN620_00763	Sutterella sp. CAG:351	570	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Sutterellaceae, Sutterella, environmental samples, Sutterella sp. CAG:351	1262975	>tr|R7I6C6|R7I6C6_9BURK Potassium-transporting ATPase potassium-binding subunit OS=Sutterella sp. CAG:351 GN=kdpA PE=3 SV=1 MNTTSAVLLFVGLFAVIFTLSVSIGIYMSAVFDGTLSQKFPWMYRVESIFLWPLGKSGREPM DWKEYCVSLIALTVVGTVIGYLIFRFQGYLPYNPLNFKGLSPDLAFNTAVSFSTSTTWQGYD CENVMSLFSQAFGLCTLTFLSSATGVVAAFAFARGLIQSRDPSLGNAWEDMVRCILWLFLP LAVICSIIAVWQGCTQTMDAMTVVKTIEGPIQKIAVGPVASQAAIRVLAVTGGGFFSANSAHP FAAPTAVVCMIQIILMLLMAASLVFAYGRMTGNVKSGFSILFGMMVLFIGAFMLIAWSESMAN PLVTELGVSRGLGNMEGKEVRFGTLLTSLFATGSSASAAGSSAGSFDSMMPIGGGVALWLI QVGDVIFGGSRSGLYTMLGLAIVAVFILGMLVGKTPRYLGKRIDAYDMKMVCVSLLMPSICTL IGTAIACLTPQGVDAVSAPGPHGFTQILFAFSSVSNFNGSSFGGLAANDFFYNTALAICMWI CRMITLTALLAIAGNMASKPRQLNSVQAIQTDGPVFSFMFIMVAVLLSMITFFPAQSLGPIVES IQLFWGYHS
9E-179	604.6	39.6	1E-178	604.2	27.4	1.1	1	T0LA52_9EURY	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA AMDU3_IPLC00004G0205	Thermoplasmatales archaeon I-plasma	558	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, environmental samples, Thermoplasmatales archaeon I-plasma	667138	>tr|T0LA52|T0LA52_9EURY Potassium-transporting ATPase potassium-binding subunit OS=Thermoplasmatales archaeon I-plasma GN=kdpA PE=3 SV=1 MLTLEDLFVVAVVWGTVIVLSWFLSSYLLGVFTGRKSRLDRILVPVENFIYLLAGIDSSKNMG WKEYFKTLLYLNAGEAILAFFILMFQQSLPLNPMHYSGMSWSLALNTVLSFSSNTNLQHYN GELTLSYLSQMSAIQFLQFTSAATGLAVGVAVIRGFAGKARTIGNFYYDYVRSLTRVLLPLAFI ATIILIFMGVPQALSGYPTVSTLQKGATEILYKGPVASLVSIMQLGTNGGGYFGANSAYPLQN PSQLSDLFEIGMMMFIPTSLLFLFGRMVGDNREGRTLFLAAYAIYGIDLLIAFLSTTVIGRGLE VRIGGVASTLWTVTTTAFTTGSLNASLSGFNPVVILTAFFGMLIQAAPGGVGVGAMYLIMYVI VTIFLVGLMAGRTPEYLGVKIEGSDVKLAVAAFLTHPIIILVPTVVAFAIGAESTVGLAANATGF TRIFYEFTSAAANNGSDYLGAAGNTVFFNVATGIVMWVGRFLPILFMLAIADGVSTRKRSQK QGLKTGSISFVVILVFSIFILTVLTFFPFLVLGPVLQFLQGMKLSIGGVIFGL
7E-174	588.5	39.5	9E-174	588.2	27.4	1.1	1	A0A060HU92_9ARCH	Potassium translocating ATPase, subunit A (EC 3.6.3.12)	kdpA NVIE_027160	Nitrososphaera viennensis EN76	544	cellular organisms, Archaea, Thaumarchaeota, Nitrososphaeria, Nitrososphaerales, Nitrososphaeraceae, Nitrososphaera, Nitrososphaera viennensis, Nitrososphaera viennensis EN76	926571	>tr|A0A060HU92|A0A060HU92_9ARCH Potassium translocating ATPase, subunit A OS=Nitrososphaera viennensis EN76 GN=kdpA PE=3 SV=1 MADPTVQLAVLLGSTVTMAVLFGTYMARMITYESRPLEKTLARVENGFYKMVGIDKDQQMS WKEYLLALVVTNAIVAGFVFVMLMAQGLLPVSQGLDGFSPDLAFHTAASFITNTNLQHYAGD QQLSVFSQMTVITFIMFVAPASGIAAAFAFIRAFIRKNFGLGNFYVDFIRVIVTLLLPVAFVSAL LLVFLGVPQTLAPSATVGTLEGGQQTMVMGPVASLESIKQLGSNGGGYFSANSAHPFENP SGLSSMFETLLMLVIPLSFPIAFAKLVGKGRGVSILIAMLAGFGVMLGIALVQESGPALLETRF GSFGSVLFNVGSLSTNTGAVASSLAGMSPSAVTGLFLGMFVQAIPGADGTGMMTMIVYVVL TLFIVGLMVGKTPEYLSMKISSHDIKLAVFIFLIHPALILIPTAISLMSGDAQTVLGTQGQQTVT ATGYTQTLYEYTSAAANNGSDYFGTSADTPFWNYSTGIVMLLGRYIPIGLMLAIAGSFTVKD RKEVIEPIKTQGPLFITVLVVMTFLLTALTFFPFLAIGPFSMGS
4E-169	572.7	35.3	6E-169	572.3	24.5	1	1	KDPA_THEAC	Potassium-transporting ATPase potassium-binding subunit (ATP phosphohydrolase [potassium-transporting] A chain) (Potassium-binding and translocating subunit A) (Potassium-translocating ATPase A chain)	kdpA Ta1310	Thermoplasma acidophilum (strain ATCC 25905 / DSM 1728 / JCM 9062 / NBRC 15155 / AMRC-C165)	585	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, Thermoplasmataceae, Thermoplasma, Thermoplasma acidophilum, Thermoplasma acidophilum (strain ATCC 25905 / DSM 1728 / JCM 9062 / NBRC 15155 / AMRC-C165)	273075	>sp|P94865|KDPA_THEAC Potassium-transporting ATPase potassium-binding subunit OS=Thermoplasma acidophilum (strain ATCC 25905 / DSM 1728 / JCM 9062 / NBRC 15155 / AMRC-C165) GN=kdpA PE=3 SV=1 MNLIEYEAYFWAKFFVAERAVSGVIIILIYLIIASVLAYILSFHIAKIYLDEKTVFSKITGRIISFFER MIGESPDHGMTFKEYFINLLLFNFFAGLISFLVIMFQKYLPFSYDTVGMSPSLDFNTVVSFLT NTNLQHYSNPMRLSYFSQTFVITGLMFLSAGTGFAASMAFVRGIRTDTGNIGNFYHDFLVSI FDLILPLTVILTVILILAGIPETMQRYITVNAFLTNKVYNIPLGPVATLEAIKNIGTNGGGFYGAN AAYPFENPDWFTNLVEFVSFVIIPLASLISLGIVFGDRKFGRMLYWVVMFFFIFDALFAFFGE FAGVPFLHLGYYTGNMVGKETAIGISQSTIFAVGATITSTGASNAALVSYTPAGIIGVLIGLLLN DPLGGVGTGVLNIFMYIIFTVFIASLMVGKLPEIMSLRISSKEIKYSTLSLITHPLLVVIPLGITLMI PHLMSSFVNPESSRITELLYEFASAASNNGSEMGGFITNQPFFNYLDGVLMLLGRYLLMAFQ LIIAQSFSVKKAKAQYYRSIDTSNWIFGVLLIAAMILIGLLSYFPIIVLGPLLSWAHDFNLILEAM V
2E-167	566.9	23.3	3E-167	566.7	16.2	1	1	R7EPL7_9BACE	Potassium-transporting ATPase A chain	BN594_00619	Bacteroides uniformis CAG:3	422	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides uniformis CAG:3	1263055	>tr|R7EPL7|R7EPL7_9BACE Potassium-transporting ATPase A chain OS=Bacteroides uniformis CAG:3 GN=BN594_00619 PE=3 SV=1 MAAMAGIMKGMAAKSTKTIGNFWKFLVLSCTRVLLPLSLIVGFILILQGTPMGFDGKLEVQT MEGQTQLVSQGPTAAIVPIKQLGTNGGGYFGCNSSHPLENPTYLTDIAECWSILIIPMSMVIA LGFYIKRKKMAYSIYSVMLFAFLVGVCINVSQEMGGNPRIDEMGIAQDNGAMEGKEVRLGS AATALWSIVTTVTSNGSVNGMHDSTMPLSGMMEMLNMQINTWFGGVGVGFMNYYTFIIIAV FISGLMVGRTPEFLGKKVEAREMKIATIVALLHPLIILGGVALSCFLFAHYPEFVAGEGGWLN NPSFHGLSEQLYEYTSAAANNGSGFEGLGDNTYFWNYTTGWTLILGRFLPIVGQVAIAGLL AGKKYVPESAGTLKTDTVTFGVMTFAVIFIVAALSFFPAHALSTIAEHFSL
7E-167	565.4	33.4	8E-167	565.1	23.1	1	1	E6U9J7_ETHHY	Potassium-transporting ATPase, A subunit (EC 3.6.3.12)	Ethha_1757	Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	418	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ethanoligenens, Ethanoligenens harbinense, Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	663278	>tr|E6U9J7|E6U9J7_ETHHY Potassium-transporting ATPase, A subunit OS=Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3) GN=Ethha_1757 PE=3 SV=1 MRKFHKLAAAAAFLRGVAGTGGLGNFYVDIIRFTTRLLLPISIVVAIVYVACGSPQTLGANSIIT TIEGTKQVIPLGPVASLEAIKNLASNGGGFFNANSAHPFENPTPFSNLITILELGLISTSFVVAF GKMTKNKRQARVLFVTLAVLLVASVGITYAAELAGNHAVAAAGLTGQAGNMEGKETRFGIA GTSLFSGATTAYQVGTVNGSMDSMTPMGGMMAMWNMILQTVFGGKGTGFIYVIMYAILTV FICGLMVGRTPEYLGKKIEGKEMKMVAVGILAHPLFVLVPLGVASVIKAGFSSVANPGYHGF SEMLYAFLSASANNGSAFAGLNANTLFWNILMGVIMLLGRYVPLAAMLCAAGSLSQKRIVPE SVGTFRTDRAMFGLTLLFIIIVIGALSFFPALVLGPIAEQLTL

2E-163	553.9	26.1	2E-163	553.8	18.1	1	1	R6EJW8_9FIRM	Potassium-transporting ATPase A chain	BN538_00629	Lachnospiraceae bacterium CAG:215	391	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	1262985	>tr|R6EJW8|R6EJW8_9FIRM Potassium-transporting ATPase A chain OS=Lachnospiraceae bacterium CAG:215 GN=BN538_00629 PE=3 SV=1 MILVSQGTPQTLIGNLTIETVEGKLQDLAMGPVAALEAIKHLGTNGGGFFGANSATPFENPT VISNIVEMISMMILPGACVVTFGHMLAEKRRELKEARIEKKKIWMGRQGAVIFGAMAILFAVG LLICYNAEMAGNPIVSEMGIDQSAGSMEGKEVRFGVAQSSLFTTVTTSFTTGTVNNMHDTL TPLGGMVPMLHMMLNCVFGGKGVGLMNMVMYVILAVFICGLMVGRTPEYLNKKIEGKEMK LVAIVILIHPLLILGFSGLAVSLQAGLDGITNPSFHGLSQVLYEYASSAANNGSGFEGLADNSV FWNVTTGLAMFFGRYIAIVAQLAIAGSLLAKKKVNETIGTLRTDNVTFMIILVFIVYIFAALTFFP ALALGPIGEHLSLWM
4E-161	546.3	32.9	6E-161	545.9	22.8	1	1	T0N7P9_9EURY	Uncharacterized protein	AMDU5_GPLC00002G0045	Thermoplasmatales archaeon Gpl	589	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, environmental samples, Thermoplasmatales archaeon Gpl	261391	>tr|T0N7P9|T0N7P9_9EURY Uncharacterized protein OS=Thermoplasmatales archaeon Gpl GN=AMDU5_GPLC00002G0045 PE=3 SV=1 MSTGITATGNFWSAFFVNNRIVSGVIIIALYLIIISFFGYMIAPYIKKLYTGENTKLRKYTDPIIGFI EKVAGVDRNKTYSFKGYFISLIIFNFVAGTISFLFLIFQGYFFKAPGQDVMSPSLTFNTIISFLT NTNLQHYSSPTTLTYLDLTVVIIGLMFLSAGTGFAASMAFVRGIMNDDKKLGNFFHDFLVAIF DLILPLSLLATVLLIIVGVPDTTYSSIIIHPFFGKMTVNIPIGPVASLEGIKNIGTNGGGFYGANA GYPFENPDWISNLIEVVSFTIIPIGSIFALGQALNNRKFGRVIYGVIVALFIFSALLTFFGEISGIP AMANLGFNYGGNFIGKETAIGISQSSIFSTGATLTSTGAANSALIDYTPAGILGILFPLLLNDPL GGVGTGILNIFSYVIFTVFIVSLMVGKLPEIMSLKVSAKEMKYSTYSLITHPLIIIVPLGIVLLLSPI LMSSFVNTRPDQITQLLYEFASAASNNGSEVGGFATNTAFFNIIDGIIMLMGRFPIMAFQLVIA QSFASKKPKVLYGRTFDIGSFWFGMMLFFTMLLLGLLSFFPILAVGPLLSWGRTFSLIIRGVL
5E-161	545.9	22.9	6E-161	545.8	15.9	1	1	F9ZPP8_ACICS	Potassium-transporting ATPase (EC 3.6.3.12)	Atc_0146	Acidithiobacillus caldus (strain SM-1)	525	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus caldus, Acidithiobacillus caldus (strain SM-1)	990288	>tr|F9ZPP8|F9ZPP8_ACICS Potassium-transporting ATPase OS=Acidithiobacillus caldus (strain SM-1) GN=Atc_0146 PE=3 SV=1 MDWKRYALSFLGFNGLGAPSLYVLLRWQGALPFNPEHFAGMSPIMAFNTAASFVTTTNLQ DYGGESTLSYLSKAAGLAQQNFLAAASGVVTLLAVARAFMRSEGRGLGNFWVDTTRTVLY LFLPLAAIFTVFYIQQGAIENWVAYVHADLIQPFWHDGHWIRHQVLAMGPAASQEAITILAGD GGAVFNAGVAHPFVNPTPLSNLGQMVSFLLIPTALIFWFGRALRRPRVAWAILACTTLLWLP LAVTSEAADLVSNPQFPPSVSRASGPDAGGGGNLEGVDLRFGSGACALFGSLAATTGAGM SGCAYDSMMPLSSGINMVFMQLGELLFGGARVGLESFLATMIFAVFLAGLMTGRSPVFLAK KIEAFEIKMVALSLLVMPVLVLLTTAFAVSVPDGRAAVFNPGPQGFSEVLYEFTSAVNNNGS DMGGLNVNTTFYNALSAMAMLFGRYFGILPLLAMAGSLIQKKRLPQGAGILRESSVLMILFVT FVIVVLGAITFLPAFALGPLAAQWAILPPPQLQW
5E-158	536.2	23.7	6E-158	535.9	16.5	1	1	T0U8X8_9ENTE	Potassium-transporting ATPase A chain (EC 3.6.3.12)	HSIEG1_1770	Enterococcus sp. HSIEG1	408	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	1316414	>tr|T0U8X8|T0U8X8_9ENTE Potassium-transporting ATPase A chain OS=Enterococcus sp. HSIEG1 GN=HSIEG1_1770 PE=3 SV=1 MCIHSWIGSEKESYLGNFWQDMVRGLLYILLPLSTIIAILLISQGVVQTFSSGMAYNSLEGEN LWLYLGPVASQVAIKQLGTNGGGFFGANSAYPFENPTIFSNFIENLAILLLPAALLFAFGFWV KDWKQGRTILFVSLFFLFAAFLGVLISENYGPIFNDVVGSANMEGKEIRFGIGWSSLWAVST TAASNGSVNAMLDSFTPLGGAVPMFLMQLGEIIFGGVGSGLYGMLAFLLLAVFIAGLLVGRT PEYLGKKIEAFDIKMASLVILTPLLLTLFGAMALAMHPDILEWLTNKGAHGFSELLYGATSLAN NNGSAFNGLLADTPFLNVLGSGLMLFSRYIPIIAVLFLAENMGRKKKVAVNDGTLSTVNPTFV TMLMIVILVIGALSFLPALALGPIADFLTLK
2E-155	527.8	22.1	2E-155	527.5	15.3	1	1	C1ABQ5_GEMAT	Potassium-transporting ATPase A chain	GAU_2890	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	391	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	379066	>tr|C1ABQ5|C1ABQ5_GEMAT Potassium-transporting ATPase A chain OS=Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505) GN=GAU_2890 PE=3 SV=1 MHPRAALRATGCATTLDGAAIAHTLDGATQTIARGPVASQEAIKQLGTNGGGFFNANAAHP FENPTPVSNWWSMLAIFLIPAGTVWMFGRGVGSTRHGWALWTAMFVLFIGGTSVAYWAE SRGNPQHAALGVDVAGVVPGHAAGNMEGKEVRFGIANSALYAVVSTDASCGAVNSMHDS FTALGGLVPLVNMQLGELIFGGVGAGLYGTLIMVVLTVFIAGLMVGRTPEYLGKRIQQREVQ MVMCYVLAFPAIVLPLTAISLVLPEGLAGLNNRGPHGLTEVLYAFTSTAANNGSAFAGLTGG TTFYNTLFGIAMLLGRFALIVPVLALAGFLAEQRIAPATAGTFPVTGPMFVTLLLGVILIVGALT YFPALALGPVVEHLLMTGGRLFS
8E-155	525.7	43	2E-154	524.6	29.8	1.4	1	L0ABX1_CALLD	K+-transporting ATPase, A chain	Calag_0872	Caldisphaera lagunensis (strain DSM 15908 / JCM 11604 / IC-154)	535	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Acidilobales, Caldisphaeraceae, Caldisphaera, Caldisphaera lagunensis, Caldisphaera lagunensis (strain DSM 15908 / JCM 11604 / IC-154)	1056495	>tr|L0ABX1|L0ABX1_CALLD K+-transporting ATPase, A chain OS=Caldisphaera lagunensis (strain DSM 15908 / JCM 11604 / IC-154) GN=Calag_0872 PE=4 SV=1 MFISLIQTVIIVAISLMVSYLLSMPISYFIKYEKDLPNTKLNKIENFIFKTLGINKENSMNYKEYLL SLLSLNIIFIVFDTVFLMFQNHLSFIGPNYKGINFDLAFNTAVSFVTNTNLQHYIGETSLSLTSQ MLVIITTMFIGPSTGLATSFAFIRGFIRRGKHLGNFYVDFMRSLIFLILPLSIISAILLIFMGVPQN LNPFYEINSFSHQIIYSGPVASLESIKFLGNNGGGFFGSNSANILENPSNLSNYFEMFLMLIFP LSIPLAFGRILGKKRGYTLLATILISMIITILIAEIIKPVGIVSYRFGNYSAVLFNTFSMLTNTGAVD TSLAAMSYSAIIAFLFSMFIQSIPGAIGVGFMYLIVYVLLTLFILGLMVGKMPEFIGMKISPRDV KLSVMVFLTHPLIILIPTALALTMGYAYHIFGSINSYTYTEVLYEFTSAAANNGSSYLGNIGNTIF FNISTAIVMLLGRYLPIGLMLAISQSFAMKERKRGPEPLPTEGLLFLAVLIFMIFLLVILTFIPFVII GPLSW

4E-154	523.2	37.5	5E-154	522.9	26	1	1	T0LT74_9EURY	Uncharacterized protein	AMDU2_EPLC00005G0239	Thermoplasmatales archaeon E-plasma	587	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, environmental samples, Thermoplasmatales archaeon E-plasma	667137	>tr|T0LT74|T0LT74_9EURY Uncharacterized protein OS=Thermoplasmatales archaeon E-plasma GN=AMDU2_EPLC00005G0239 PE=3 SV=1 MISGGSSTNFWLNFFVNNRLFSGTVIILIYLIVISIFGFIIADHIKKIYLGQRTILTGFSEKAIYFIEK ISGVDENESHTFKGYFFSLLFFNLMAGVFTLFFLLIQTNYFPLPGQRGFSFSLAINTISSFLTN TNLQNYSSPQRLSYYELTIVIIGLMFLSAGTGFAASMAFIRGIIKDDGKLGNFFHDFLVAIFELIL PLSLLATVIFLFIGIPETTSSFLYIHPFFSKSVIGIPIGPVASLEGIKNIGTNGGGFYGANAGYPF ENPNWISNIVEVVSFTIIPMGSIFALGRVLESRNFGRMVFGVIMSLFMLSAFFTFFGEYAGLP TMSNLGLFYTGNFLGKEIALGISQTSIFASGATMTSTGATNSALNAFTPAGILGVLFPMLLND PLGGVGTGILNIFTYVIFTIFLVALMVGKLPELFSLKISSKEIKYSTYSLITHPLLIVVPLGITLLIP ALMSSFVSPRPDQITELLYEFSSAAANNGSAMGGFQVNQAFFNILEAGIMLTGRFLVMGFQL MIAQSFAFKKPKVTYGRSVNVGSFWFGFMLFFTMILLGLLSFFPVLALGPLLAWGKDFNLLI GVIH
4E-151	513.2	29.4	6E-151	512.8	20.4	1	1	Q6L2R0_PICTO	Potassium-transporting ATPase A chain (EC 3.6.3.12)	PTO0157	Picrophilus torridus (strain ATCC 700027 / DSM 9790 / JCM 10055 / NBRC 100828)	576	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, Picrophilaceae, Picrophilus, Picrophilus torridus, Picrophilus torridus (strain ATCC 700027 / DSM 9790 / JCM 10055 / NBRC 100828)	263820	>tr|Q6L2R0|Q6L2R0_PICTO Potassium-transporting ATPase A chain OS=Picrophilus torridus (strain ATCC 700027 / DSM 9790 / JCM 10055 / NBRC 100828) GN=PTO0157 PE=3 SV=1 MTSESIYQIIDSNRGVSGIIIVFIYIFLALLFGYLISNYISKLYMDEEDKTWLYPISGRVTNFFEKL LGEDKNKKMKFKDYFLNLLIFNAAAGVIAFIAIYFQRFFPFYDDNKMGLSLTFNTVVSFLTNTD LEHFSNPLKLSIFSWTFSIMGLMFLSAATGFAASMAFVRGIRNDDGFIGNFYHDFLVSLFYLIF PLSILGAVIFILAGVPETLRAYIDVYPLFSSGPEKLPLGPIATFIAIKYVGTNGGGIYGANAAYPL GNPNWFTNIVSYILFIIIPTGSIMALGRVFIKRFANMLVYVLFTIFAITSLMTYLSEFIGIPEISALG SYSGNMIGKEVYLGLAPTVMFQVGSVFTSTGAASGSIISYTPVGILGLLINLVLNDPLGGVGT GVINIFTYVIFTVFISSLMVGKLPEIMSIRIGSREMKYSTIALLSHPLIVLIPLGVTLLIPGVMETFL NGHASNITNLLYEFASAASNNGSEAGGFLTDSNYFNYLDGIIMLLGRYLILGIQLLLAQQFAFK KPKSEYTRATIDIGSPAFGFMLFAVIIMIGLLSYLPVFALGPLYSWARAFGI
2E-145	494.5	28.9	2E-145	494.3	20	1	1	I3TDE3_THEC1	Potassium-transporting ATPase subunit A	TCELL_0356	Thermogladius cellulolyticus (strain 1633)	535	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Thermogladius, Thermogladius cellulolyticus, Thermogladius cellulolyticus (strain 1633)	1184251	>tr|I3TDE3|I3TDE3_THEC1 Potassium-transporting ATPase subunit A OS=Thermogladius cellulolyticus (strain 1633) GN=TCELL_0356 PE=4 SV=1 MIQSLIVYWLNIFLVTVMTGYVLSGVIRKMVVEWHKKPPRVLEVVYRCLDRIGLDTTNKSFTD YAKDLLFFNFILIAIDTVLLAKQGLFFGGADLSWDLAFNTAVSFATNTNLQHYIGETTLTNMAQ SVVIGSTMFLAPATGIAVSLAFLRSLIGESAGNFYRDLVMAVGLLLLPLSIVSAVLLSVLGVPQ TFNEWIRVDNPYSGSFMLRLGPVASFEAIKLLGTNGGGFYGSNSAYPLENPSGLTNFIESVL MLLIPTSMLFAFGRVLGKRRGLSLFAVAYVTAFIIVGVSVASGVPPLNSLVEPRLGYPGSLVF NTASLLSDTGATASSLLAMKPSAIVAFLTAMFIQAVPGADGVGLLYLLVYVFIIIFIGSLMVGKT PRFINIPISPRVVKLSTVIFLIHPAIILVPTSIALVLRQYTAFSNRLDPLTYTMVLYEYTSAAANNG SGYLGPLGNTVFWNLSTAIVMLLGRYLPIFLFLLIADDISKAKRSVAEEPVETQGLLFVVFSVV MILILTALTFFPFLAIGPLLMGG
6E-144	489.8	34	7E-144	489.5	23.6	1	1	H9ZZC9_FERFK	Potassium-transporting ATPase subunit A	FFONT_0093	Fervidicoccus fontis (strain DSM 19380 / VKM B-2539 / Kam940)	536	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Fervidicoccales, Fervidicoccaceae, Fervidicoccus, Fervidicoccus fontis, Fervidicoccus fontis (strain DSM 19380 / VKM B-2539 / Kam940)	1163730	>tr|H9ZZC9|H9ZZC9_FERFK Potassium-transporting ATPase subunit A OS=Fervidicoccus fontis (strain DSM 19380 / VKM B-2539 / Kam940) GN=FFONT_0093 PE=4 SV=1 MIQVLISYWLAIFIAVSLLGYELSRLLKKMVLEWNFEPPKLLKKVFDVLDIIGLGSSSEKSFLKY IADAFLLNFILIAIDTIMLMKQSLFFGGPDLPWDLALNTAVSFVTNTNLQHYAGEISLTNMAQC VVIGTTMFIAPATGIAVSLAFMRSLKGLQAGNFYRDLVMVTFFLLLPISIIAAVILASLGVPQTF EDHVAFENPYAGSFIMRLGPIASFEAIKLLGTNGGGFFGANSAHPFENPNGLSNFIESVLMLL IPTSLLFTFGRIFGKKRGLSMFAIAYALAFMIIGVAVMNRVPALSYLAEPRLGYEGALAFNTAS LLSDTGATASSLFAMRPSAIASFLIAMFIQSVPGADGVGLLYLLVYIFIIIFIGSLMIGKTPKFLN MGISPKVVKYSTIVFLIHPTIILVPTAIALLTKQYLSFASSLNPQVYTMVLYEFTSAAANNGSGY LGTMGNTAFWNVSTAIVMFLGRYLPLGLFLLIAQDLHRCKRGVADEPVKTQGGLFIVFSVVM IIILTALTFFPFIVIGPMLMGG
5E-139	473.4	13.8	6E-139	473.2	9.6	1	1	R5R1B9_9FIRM	Uncharacterized protein	BN734_00713	Ruminococcus torques CAG:61	380	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus torques CAG:61	1263108	>tr|R5R1B9|R5R1B9_9FIRM Uncharacterized protein OS=Ruminococcus torques CAG:61 GN=BN734_00713 PE=4 SV=1 MLQIILTLAIFVILVIPMGKYMYHIATKQKTFADKVFNPIDRCIYKVCGIKGEDMGWKKYALTLL LVNAVMVFVGYAILRLQSILFLNPNGISNMEPTLSFNTIISFMTNTNLQHYSGESGLSYVAQM CVIIFMMFTSAATGYAACMAFCRGLAGKKIGNFYEDMVRITTRILIPASFIVGLLLVSQGTPQT LQGNFTIETLEGNFQDIAVGPVAALESIKHLGTNGGGFFGANSTTPFENPTVISNIIEMISMML LPGACVVTFGHMLHDKRKEKKAEKVAMNAQVLPGTAQKKVIFGRQGAVVFGAMAIIFLIGLT ICYQSEMAGNPVIQEMGIDQSQGSMEGKEVRFGVPQSALFTTVTTSFTTGTVNNMHDTLTP L
1E-126	432.4	20.7	2E-126	432.2	14.4	1	1	R6ZWX2_9CLOT	Potassium-transporting ATPase A chain	BN593_00574	Clostridium sp. CAG:299	311	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:299	1262792	>tr|R6ZWX2|R6ZWX2_9CLOT Potassium-transporting ATPase A chain OS=Clostridium sp. CAG:299 GN=BN593_00574 PE=4 SV=1 MMLLPGSCVVTFGLMLHDRKDGKKPLFGRQGAVIFGAMAIIFLIGLAVCFSAERAGNPVVGA MGLSQDMGSMEGKETRFGMEQSALFTTVTTSFTTGTVNNMHDSLTPLGGLVPLLHMMLN CVFGGKGVGLMNMVMYVILAVFICGLMVGRTPEYLNKKIEGKEMKLVAIVILIHPLLILGFSAL AVSVQGGLSGITNPGFHGLTQVLYEYASSAANNGSGFEGLADNSLFWNVTTGLAMFFGRY LAIAAQLAVAGSMLAKRRVNESVGTLRTDNTTFMIVLVFIVYIFAALTFFPALALGPVAEHLSL WM

5E-117	400.8	28.3	5E-114	391.1	19.6	2	1	A1S096_THEPD	Potassium-transporting ATPase (EC 3.6.3.12)	Tpen_1479	Thermofilum pendens (strain Hrk 5)	517	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Thermoproteales, Thermofilaceae, Thermofilum, Thermofilum pendens, Thermofilum pendens (strain Hrk 5)	368408	>tr|A1S096|A1S096_THEPD Potassium-transporting ATPase OS=Thermofilum pendens (strain Hrk 5) GN=Tpen_1479 PE=4 SV=1 MASDTAVYVIHASLLLVSVSLAASLLGRLISKLVVDWHRNPPEALALIEGRVLGALRVDTKPK TSWREYLASLLALNFASIALATLALYLQGVVRAGPPVSLDLAFNTAVSLVTNTGLQHYVGER DLSALLQVLVVIPMSFVASATGLSVAVAFMRSLVVGEPGNFFADFLRSLLVVYAPISVLAALA LVAAGVPAGPVASLVAIKLLGNVGAGYFGANSAHPLENPSALTNFFEAFLMLLVPLSLPFAY ERIAGRGRGYSLYAIDLVLLSLLLAIAPLSGFPLLGRGVEPRLGGSPTLIFNVVSALTNTGATS SSLTPMGPSAVSSILMGMFIQSAPGSALGFVYLTVYVVIVVFIGSLMVGKTPRFLGRAVSPR AIKYAVALFLVHPVIILVPTVVAQLTGACGFLGPPGPATFTKVLLEFSSAASNTGMSYLGDAA NTPFWNVSTAIVMLLGRYVPIALMLLIAEDLAGTPPVSLPDPVETRGLLFVAFSTLMILVLFLL TFFPFIAIGPLASG
2E-116	398.8	10.4	3E-116	398.5	7.2	1	1	A0A070C437_BURCE	ATPase (Fragment)	P350_13080	Burkholderia cepacia JBK9	339	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia cepacia (Pseudomonas cepacia), Burkholderia cepacia JBK9	1395570	>tr|A0A070C437|A0A070C437_BURCE ATPase (Fragment) OS=Burkholderia cepacia JBK9 GN=P350_13080 PE=4 SV=1 MNANNLLQTLLFIVVLLAAAVPVARYLSAVMDGSSRVVRVFGPLERVLYRIAGVDAGSEMN WKQYAIATIAFNALGALFLYGLLRLQGFLPGNPQQFGPMTVDGAFNTAVSFVTNTNWQDYT PEQTVSYLTQMLGLTVQNFLSAATGIVVVIALIRGFARHTAQTIGNFWVDLTRVTMYVLVPM SVVIAALLMSQGVIQNMKAYQDVPVLQASTYAAPKLDAQGNPVKDDKGNAVTVPTPLTKQT LAMGPVASQEAIKMLGTNGGGFFNANSAHPYENPTPFANFIQIFAILIIPAALCLVFGRVIGDR RQGIAVLAAMTVAFVIAIGVEVSAEQGGNP
1E-110	379.6	15.4	2E-110	379.3	10.7	1	1	A0A070CED9_BURCE	Uncharacterized protein (Fragment)	P350_05315	Burkholderia cepacia JBK9	259	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia cepacia (Pseudomonas cepacia), Burkholderia cepacia JBK9	1395570	>tr|A0A070CED9|A0A070CED9_BURCE Uncharacterized protein (Fragment) OS=Burkholderia cepacia JBK9 GN=P350_05315 PE=4 SV=1 ALHVDQSASALQPGGNMEGKETRFGIAQTGIFTVATTAASCGAVDTMHDSLTPLGGLVPML LMQLGEVVYGGVGSGLYGMLVFALLAVFVAGLMIGRTPEYVGKKIEAYEMKMVSIVVLLTPL LVLVGTSIAVLADAGKAGIANPGPHGFSEILYAFSSAANNNGSAFAGLTVGTPFYNWMTAIA MWFGRFGTIVPVLAIAGSLAAKKRIAVTSGTLPTHGPLFVVLLLGTVLLVGALTYVPALALGP GVEHLMMWLGA
1E-109	376.7	10.5	1E-109	376.4	7.3	1	1	I3UFD9_ADVKW	p-type ATPase, high-affinity potassium transporter, a chain	TKWG_19665	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	292	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella kashmirensis, Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	1036672	>tr|I3UFD9|I3UFD9_ADVKW P-type ATPase, high-affinity potassium transporter, a chain OS=Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) GN=TKWG_19665 PE=4 SV=1 MSTQAWLNLVLFMAVLTALAPPVGRLLARIARPAATLRPQLFNRLERGIYQFSGVDPTVQM GWKHYLLSLMLFNIVGLLAVFLLQTVQQWLPLNPQDMGAVSADSAFNTAVSFVTNTNWQG YGGETTMSYLVQMVGLAVQNFLSAATGIAVVFALIRGFTSKSQNHIGNFWVDITRITLYALVP LSIILALVFVSQGVIQNFSPSLVIDTLEGGQQTIAMGPVASQEAIKLLGTNGGGFFNVNSAHP FENPGAFSNFAQMIAILLIPAACVSALGAWSVIADRVGPSTRPCR
3E-101	349	13.9	4E-101	348.5	9.6	1.1	1	T0N9N7_9EURY	Uncharacterized protein	AMDU1_APLC00014G0038	Thermoplasmatales archaeon A-plasma	392	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, environmental samples, Thermoplasmatales archaeon A-plasma	667135	>tr|T0N9N7|T0N9N7_9EURY Uncharacterized protein OS=Thermoplasmatales archaeon A-plasma GN=AMDU1_APLC00014G0038 PE=4 SV=1 MIISSVSSQSGGNFWANFFVTNRYVSGSFIIIIYILLATVLAYLLSGYIAKIYKGEPTAMDRISGP VVRAFERFLGEDAKKQMEFREYFTSILVFSLFLGAIGFAVIYFQHDLPFSFSNNHMTPSLIFN TVSSFLTNTNLQHYSNPFDLSYFSTTFVITGFMFISAGIGFAASMAFIRGILSENGKIGNFYHD FLVSEFYLLFPLSVVLTFILVLSGIPQTMTPYLTITPVLSHTAFRLPLGPVATLESIKTIGTNGG GFYGANAGFPLGNPDWFTNMVELEALLLIPLASILSLGKVFDNKRFATMLYGVIMIIFVFTSFL SFFGEMSGIPSITALGMSFTGNMLGKETALGISQSTLFSVGSTITSTGAVNSALINYTPVGIM GPLLIFS
5.5E-77	268.7	6.2	6E-77	268.4	4.3	1	1	A9WQL1_RENSM	Potassium-transporting ATPase A chain (EC 3.6.3.12)	RSal33209_0910	Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	241	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Renibacterium, Renibacterium salmoninarum, Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	288705	>tr|A9WQL1|A9WQL1_RENSM Potassium-transporting ATPase A chain OS=Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235) GN=RSal33209_0910 PE=4 SV=1 MRAKRTICQNGSFTGSQGSTPVRTRSGQLTYAACSPFPWSASSFVFLLQRLQGWGAGQG DPVDPWVAMNTAISFVTNTNWQTYAPETTVGILVQMLLLAVQNFLSDAVGIVVAIALVRGIK RSKTDEIGNFWVDLSRAAFRILLPIAIIGAIVFIATGIVQNFSGTSVTNAALGVQQQIPGGPVAS QEAIKLLGTNGGGYFNANSAHPFENPNAYSNLFSVFLILVIPFSLPYTYGRMVGQ
1.2E-76	267.5	16.5	2E-76	267.2	11.4	1	1	I3UFD7_ADVKW	Potassium-transporting ATPase subunit A (EC 3.6.3.12)	TKWG_19655	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	191	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella kashmirensis, Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	1036672	>tr|I3UFD7|I3UFD7_ADVKW Potassium-transporting ATPase subunit A OS=Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) GN=TKWG_19655 PE=4 SV=1 MGSSGLYGMLIFVILAVFIAGLMIGRTPEYLGKKIEMQEMKMIALALLVPPFLILGGTGLSVVL DVGVASLGNPGAHGLSEVLYAFTSAANNNGSAFAGLSANNVFYNLMLALAMFAGRFAVIGA VLAVAGYLAAKQRVPVNVGTMPTHGVLFGVLLIGVVLIMGALTYIPSLALGPIAEHMQLFSVQ SAE
5.7E-66	232.3	0.6	7E-66	232	0.4	1	1	C1ABQ4_GEMAT	Potassium-transporting ATPase A chain	GAU_2889	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	365	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	379066	>tr|C1ABQ4|C1ABQ4_GEMAT Potassium-transporting ATPase A chain OS=Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505) GN=GAU_2889 PE=4 SV=1 MNVAPTSTNGWMQIALFAVAVLLVTKPMGWYLAQVYEGRMRWLAPIERRLYRLAGVDAES EQHWTTYATSLLLFSAVSMLLTYVVLRLQGWLPFNPVGLGAVTDRQAFETSASFVSNTNW QSYAGESTMSYFAQATQLTFHNFTSAATGLGVAVALMRGIARRGTGNGAGAGRIGNFWVD LVRGTLYVLLPLSCILALLFVQQGVPQRSTVPPSLTRSMAPRRPLPVGRWPVRRPSNNSAP MVAVSSTPTRHILSRIRRQSATGGRCWRSFSSLPAPCGCSAAEWAARGMGGPCGRPCSC CSSAARVSPIGRNRVATRSMPRWVSTWPAWYRGTRPATWKARRCASASPTPRSTPWFP LTPPAAR

1.2E-59	211.5	2.9	1E-59	211.3	2	1	1	Q6MM83_BDEBA	Potassium-transporting ATPase, A subunit (EC 3.6.3.12)	kdpA Bd1757	Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100)	160	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio, Bdellovibrio bacteriovorus, Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100)	264462	>tr|Q6MM83|Q6MM83_BDEBA Potassium-transporting ATPase, A subunit OS=Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100) GN=kdpA PE=4 SV=1 MFLAFTRGIARKQVTGLGNFWVDLTRSTVHVLLTFSLVLALFLVGEGVVQNFSAYVPAKTIE GAEQLLPQGPAASQVAIKQLGSNGGGFFGVNSAHPYENPTPWSNFLEMISLILLASACTYV FGVMVGSKRQGWGLFAAMMSMLVVMLALSLWSEYELR
4.6E-52	186.4	12.3	6E-52	186.1	8.5	1	1	T0LW50_9EURY	Uncharacterized protein	AMDU1_APLC00014G0039	Thermoplasmatales archaeon A-plasma	200	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, environmental samples, Thermoplasmatales archaeon A-plasma	667135	>tr|T0LW50|T0LW50_9EURY Uncharacterized protein OS=Thermoplasmatales archaeon A-plasma GN=AMDU1_APLC00014G0039 PE=4 SV=1 MNDPLGSVGTEVLNIFMYVIFTVFITSLMVGKLPEIMSLKIGSREIRYSTLSLVTHPLLVIIPFGI TLLLPQFMTSFVNTGPDKITQLLYEFATAASNNGSEVGGFVTNQPFFNYVDGIVMLLGRYLL MGFQLLIAQSFSYKKPKVQVARTVDPGSFLFGFTLFFVMILLGLLSFFPILALGPLLAFAKAFN LFILGVIP
1.5E-46	168.2	0.9	2E-46	168	0.6	1	1	Q6MM84_BDEBA	Potassium-transporting ATPase, A subunit (EC 3.6.3.12)	kdpA Bd1755	Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100)	141	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio, Bdellovibrio bacteriovorus, Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100)	264462	>tr|Q6MM84|Q6MM84_BDEBA Potassium-transporting ATPase, A subunit OS=Bdellovibrio bacteriovorus (strain ATCC 15356 / DSM 50701 / NCIB 9529 / HD100) GN=kdpA PE=4 SV=1 MGFNSADLIQIILTLGVVVVATPILGSYMAKVFQGEKTWLSSLLRPLESGTYRLTGVRENDE MDWKEYFLSLLFFNLIGIVVVMFLQMLQAALPLNPQALPNTSWHLAFNTAASFVTNTNWQA YSGESTLSYLTQMLGLGV
1.6E-46	168.1	2.5	2E-46	167.9	1.7	1	1	R6EAU5_9FIRM	Potassium-transporting ATPase A chain	BN538_00628	Lachnospiraceae bacterium CAG:215	206	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	1262985	>tr|R6EAU5|R6EAU5_9FIRM Potassium-transporting ATPase A chain OS=Lachnospiraceae bacterium CAG:215 GN=BN538_00628 PE=4 SV=1 MLQIILTLAIFLILVIPMGKYMYHIATEQKTFADKVFDSVDRLIYKVCGIKGENMGWKTYALTLL TANAVMVFVGYLILRLQNFLFLNPNGIDGMEASLSFNTVISFMTNTNLQHYSGESGLAYVSQ MCVIIFMMFTSAAXXVHIGCQRICGMHGFLPWAFRKKVRKLLSGYGTDHNAYPDPGFLYHC VDPCKPGNAADIDRKSDD
1.3E-45	165.1	0.6	1E-45	165	0.4	1	1	T0VJD5_9ENTE	Potassium-transporting ATPase A chain (EC 3.6.3.12)	HSIEG1_1771	Enterococcus sp. HSIEG1	164	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	1316414	>tr|T0VJD5|T0VJD5_9ENTE Potassium-transporting ATPase A chain OS=Enterococcus sp. HSIEG1 GN=HSIEG1_1771 PE=4 SV=1 MMSFVFQGLFFFFVLLILAAPLGFYIKMIMTGETPRFVRFIQPIERGFYRLIGSESQRKMSAK RYLISVLGLGISSLLFLTVLLMVQGWLPGGAKVDNLSFDLALNTAVSFITNTNWQAYSGELAL SNSTQVFGLTVQNFLSAAVGLAVLCAFIRGLVQKKNPI
7.3E-38	139.5	7.9	8E-38	139.3	5.5	1	1	A9WQL2_RENSM	Potassium-transporting ATPase A chain (EC 3.6.3.12)	RSal33209_0911	Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	156	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Renibacterium, Renibacterium salmoninarum, Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	288705	>tr|A9WQL2|A9WQL2_RENSM Potassium-transporting ATPase A chain OS=Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235) GN=RSal33209_0911 PE=4 SV=1 MTVMGGLWAISTGLMAWAMAAASALGSLGEGFEQRFGPAASSLFASATTLTSTGAVDVAH DSLPPLAGGMALLNMMLGEIAPGGVGSGLYGMLVLAIISVFIAGLMVGRTPEFMGKKITAKA DETCRDVHSGDANSGAGIHRYHHADSRSAGECAG
6E-35	129.9	5.3	7E-35	129.8	3.7	1	1	A9WQL3_RENSM	Potassium-transporting ATPase A chain (EC 3.6.3.12)	RSal33209_0912	Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	102	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Renibacterium, Renibacterium salmoninarum, Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	288705	>tr|A9WQL3|A9WQL3_RENSM Potassium-transporting ATPase A chain OS=Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235) GN=RSal33209_0912 PE=4 SV=1 MYAFTSAANNNGSAFGGITSSGPYFATLLGLAMFLGRFIPIVLVLALAGSLAKQKVVPASSGT APTHGPLFATLLLGISVVLTALTYFPALALGPLAEGLVK
2.7E-28	108	0	3E-28	107.6	0	1	1	Q2T9E0_BURTA	K+-transporting ATPase, A subunit	BTH_II0007	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	182	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, pseudomallei group, Burkholderia thailandensis, Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	271848	>tr|Q2T9E0|Q2T9E0_BURTA K+-transporting ATPase, A subunit OS=Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301) GN=BTH_II0007 PE=4 SV=1 MKRGRTDGRSGRIDGQARLPQIALFAAVLTRHVKPLGQYIVRIANGDPPWPMRMLQPVER CTYRAAGIDPEQAMSWKTHAIALLSLSLVGTIALYALQRAQHALQLNPQALPTVSADSAFNT AVSFAANTSVQGDAGETTLAICPRWAASPCGASCRLPPAPPCCSRRSARSPRAARAPSSC
4.9E-28	107.1	1.2	5E-28	107	0.8	1	1	I3UFD8_ADVKW	Potassium-transporting ATPase subunit A (EC 3.6.3.12)	TKWG_19660	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	97	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella kashmirensis, Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	1036672	>tr|I3UFD8|I3UFD8_ADVKW Potassium-transporting ATPase subunit A OS=Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) GN=TKWG_19660 PE=4 SV=1 MSVIFVVLTVCVLLAEQQANPALSSLPIDQGAQALLQSGGNMEGKEVRFGIVGSALFAAVTT AASCGAVVAMHDSFMPLGGMVPLLLMQLGEVVFGG
3.7E-25	97.6	1.7	4E-25	97.5	1.2	1	1	A0A0C1PTS5_9ACTN	Uncharacterized protein (Fragment)	LK07_62625	Streptomyces pluripotens	66	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pluripotens	1355015	>tr|A0A0C1PTS5|A0A0C1PTS5_9ACTN Uncharacterized protein (Fragment) OS=Streptomyces pluripotens GN=LK07_62625 PE=4 SV=1 MLYAYTSGTANNGSAFAGLNANTPFFNTTIGFAMLIGRYLTLLPMLAVAGSLAAKKRVPESA GTLS
1.8E-24	95.3	1.2	2E-24	95	0.8	1	1	I0HQF3_RUBGI	Potassium-transporting ATPase A chain (Pseudo)	RGE_18990	Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	181	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Rubrivivax, Rubrivivax gelatinosus (Rhodocyclus gelatinosus) (Rhodopseudomonas gelatinosa), Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	983917	>tr|I0HQF3|I0HQF3_RUBGI Potassium-transporting ATPase A chain (Pseudo) OS=Rubrivivax gelatinosus (strain NBRC 100245 / IL144) GN=RGE_18990 PE=4 SV=1 MAAGPRDRGRRPGPLRAGQPPGGAAVPPGRRRRGARARLGRLRARPDAVLRHRCTRRL RGAAAAGGTALKPPSATRSLADSAFNTAISFVTNTNWQGYGGESTMSYLTQMLALTVQNFL SAAIGIAVVVALVRGFACSSTPRGQTRSRPASMPRNTIVMDGRVEASIAQSHGRACLPAVFA

7.4E-18	73.5	1.5	8E-18	73.4	1	1	1	I3E3C5_BACMT	Putative membrane protein	BMMGA3_02260	Bacillus methanolicus MGA3	75	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus methanolicus, Bacillus methanolicus MGA3	796606	>tr|I3E3C5|I3E3C5_BACMT Putative membrane protein OS=Bacillus methanolicus MGA3 GN=BMMGA3_02260 PE=4 SV=1 MTCASTGLAVAIAIIHALFRREKVIGNFYQDFVKANVRVLFPFAVVVTLLLVALGVPQTLASST TVTTLEVKLRQ
1E-10	49.9	0	1E-10	49.5	0	1.1	1	I0HQF2_RUBGI	Potassium-transporting ATPase A chain (Pseudo)	RGE_18980	Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	174	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Rubrivivax, Rubrivivax gelatinosus (Rhodocyclus gelatinosus) (Rhodopseudomonas gelatinosa), Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	983917	>tr|I0HQF2|I0HQF2_RUBGI Potassium-transporting ATPase A chain (Pseudo) OS=Rubrivivax gelatinosus (strain NBRC 100245 / IL144) GN=RGE_18980 PE=4 SV=1 MARRRRPDAGLNGSGNAGALHERLALRRGPARARPAGLSRRSVAAAGGLLVTAAAWLQL AAFVALLLLLIAWPRGRAIGAVVQGRFALGSRLEAPLYRLAGVDVEREHGWVGYALGLMLF YGIGVLAVYAVQRLQAVLPLNPQALPAVSPTRRSTRPSASSRTRTGRATVANRR
0.00014	29.7	10.7	0.0001	29.7	7.4	1.8	1	R7FQ61_9FIRM	Potassium uptake protein TrkH family	BN651_01413	Dorea longicatena CAG:42	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea longicatena CAG:42	1263074	>tr|R7FQ61|R7FQ61_9FIRM Potassium uptake protein TrkH family OS=Dorea longicatena CAG:42 GN=BN651_01413 PE=4 SV=1 MKKTGKQNIRWNTMKILAVGFLSVIFLGAVLLWLPVSNEKSISFLDALFTSTSSVCVTGLVTIV PKYQFTITGKVILLILIQIGGLGVIACITAFFMLLKRKITVKERVVIQEAYNMNSLGGLVLGVRKI LIGTVVVEGIGAVFYAIQFIRDYGVAKGIWYGIFHSISAFCNAGIDILGDDSLARYATDPLINIIT MLLIILGGIGFTVWYDVIDNGKKIWHREIPGKCWFTRLKLHSKIAIITTGFLLIAGTVLNFALEY HNPATIGHLNTGQKLMVSAFQAVTTRTAGFSTFQQSGMYEETGFLNIILMFIGGSPGGTAG GLKTTTFALLFLAFHTMLRGGHDIECFRRKVDEKNFHVAFVTIMLALAIYITGTTFVAVIEPDTI SFQRIMYETASAMATVGLSQDLTTHLRTGSKIVLMIMMYIGRVGPMTIALLFAGKVNLKEKM RTLPTEKIMIG
0.00044	28	17.7	0.0004	28	12.3	2.1	1	E3H6H8_ILYPC	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Ilyop_0603	Ilyobacter polytropus (strain DSM 2926 / CuHBu1)	445	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Ilyobacter, Ilyobacter polytropus, Ilyobacter polytropus (strain DSM 2926 / CuHBu1)	572544	>tr|E3H6H8|E3H6H8_ILYPC Potassium uptake protein, TrkH family OS=Ilyobacter polytropus (strain DSM 2926 / CuHBu1) GN=Ilyop_0603 PE=4 SV=1 MIGFALKKMPPSRILLLVFVVAIFVGSFLLLLPAAVTPGNKIGYLTSIFTVTSAVCVTGLTVVDV SKVFSPFGQSVILFFIQLGGLGIMTFSSILFMMIGKRITYHEMKILKEDLNAENTGEIVQLVKRL VMIVFTIEIIGTIFLTLEFLKEMPFKKALLFGIFHSISAFCNAGFSLFTTGLEGYSGSVIINLTIALL IILGGIGFAVISSFISYYKTKKKRFNLSSKMVLRISTILTLGGMVLFFALEYRNPLTIGKMNFFHK IMASFFQSVTTRTAGFNTVPIGSLTPGTIFLFCVLMFIGASPGSTGGGIKTTTFGVIMVYVVGI VRGQEDIEISNRRITWQILNRALAILVISVAYVSTIILIMLMTDHLGFSETIFEVISAFGTVGLSM GVTADMNEFSRILIIITMLIGRVGPLTFALALGEQSKKKERKYPKENILIG
0.0015	26.3	6.7	0.0015	26.3	4.6	2.1	2	A5UV17_ROSS1	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	RoseRS_2088	Roseiflexus sp. (strain RS-1)	453	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Chloroflexales, Roseiflexineae, Roseiflexaceae, Roseiflexus, Roseiflexus sp. (strain RS-1)	357808	>tr|A5UV17|A5UV17_ROSS1 H(+)-transporting two-sector ATPase OS=Roseiflexus sp. (strain RS-1) GN=RoseRS_2088 PE=4 SV=1 MRLAPRPSVRSPARPRPMPAALRLVIGLAVLVAAGTSILMLPWMGTERPLTWNEALFTAVS ALSVTGLSIITPVHDLSLAGQIVLLLLIQIGGVGFMVVAVIVFQVLGRRITLTDRLALTDSMGLL VPGAIVQLVRRVLLTVLLLEAIGAALLWIHWRDMLGPERALLYAIFHAVSAFCNAGFDLFTGL PDYPYGIPNDSITLAILGSLIFLGGLGIPVLAELLTFWRIRFSLHTRITLTVVIILVSIGAGGLFLTE QQSGHLLEREPLDRQIALALFQSISTRTAGFSALQPLDELSPAGRLLTIVLMFIGCAPASMGG GITTGTFAVLMLAVGAYARGLASPQIGGRTLAPQTVRKAAAILTVSLLVVLTATWLILATHEAT LDDALFEVVSAFATCGLSLTLTSELNLFGQLVICVMMFWGRLGALTLVVALANQRPQLVAYP EEQVLIG
0.0031	25.2	8.3	0.0031	25.2	5.8	1.7	1	C0QAF8_DESAH	TrkB (EC 3.6.3.14)	trkB HRM2_16340	Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2)	461	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfobacterium, Desulfobacterium autotrophicum, Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2)	177437	>tr|C0QAF8|C0QAF8_DESAH TrkB OS=Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2) GN=trkB PE=4 SV=1 MFRQRFSTMVNRFFSSPGPATVFGFLAMIFAGSGLLLLPQATTGTGRGLTFVDALFTSTSS VCVTGLSVTDTGTSFTLFGQTIILTLIQTGGLGIMTLSTLFLMLSGKRLSFSSHTAIRESFTPF QERHPWAILKDIFLFTLVLEGVGAMALFTQFIRTATPSKAFFLSIFHSISAFCNAGFCLFPDSF TAFRSSIVVNLTIGFLIILGGIGFPVMSELKWRLLRGDRQRSPMSLHSKIALSMTAILLVSGTLV FLTMESRVTLDRLPWGQRVLASFFMSVNARTAGFNSLTLENMANETLFFIILLMFVGASPGS CGGGIKTTCFASLIALGQSRLKGEKKPNLFGRAIPEQTIGKAVSILMVSTVIVCLGTMALLMTE LGDVSHPQSRGMFLELLFEVVSAFGTVGLSTGVTASLTNPGKLLVVTIMFMGRLGPLLIAMA VSRPLRLGYTHAEEDFIIG
0.0067	24.1	11.3	0.0067	24.1	7.8	2.2	2	Q7U4A3_SYNPX	Possible sodium transporter, Trk family	SYNW2168	Synechococcus sp. (strain WH8102)	469	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain WH8102)	84588	>tr|Q7U4A3|Q7U4A3_SYNPX Possible sodium transporter, Trk family OS=Synechococcus sp. (strain WH8102) GN=SYNW2168 PE=4 SV=1 MPLRQAIERSQGWHRRLTVPQFTVVTGLLVILLGTLLLATPLCSSSKVGLWEALFTATSAITV TGLSIIDVGADLTTAGQLVLAMMILAGGLGLMAITTFLQGFVVKGTGLRRRLDRGQTLDEFG VGGVGSTFRGIAATAALVILVGALVLYGFGFSDIPDRGERLWASVFHSISAYNNAGFGLWSD SLERYHDNVLVNAVVMVLIVMGGLGWRVTSDLASQGVRRGRRRLSLHTRLVLRTTLLLVVF GTLGLALTEWLNRGEVFIGMAWRERWMTALFESVTARTAGFTTVPFSLENITDSGTLLLMA LMFIGASPGGTGGGIKTTTVAALMAATRSTMRGRDAVVIRNREIPDKVVLRALGITVASLLFV LAMALLLSIASNLNGAEPFTFLEMLFTCISAFATVGLDLGVTEQLGRFGQAVLMLGMFVGRL GILLLLSAIWEVMTREQIHIHRQNRIGYPREDLYV

Sheet 5

All TrkH proteins retrieved from the RFP															
HMMER search output															
Whole protein prediction			TrkH domain prediction					Uniprot entry name	Protein name	Gene name	Organism (and Synonym)	Protein length	Taxonomic lineage (ALL)	Organism ID	Protein sequence
E-value	score	bias	E-value	score	bias	exp	TrkH domain number per protein								
5E-219	737	0	4E-216	727.9	0	2.2	2	TRK1_YEAST	High-affinity potassium transport protein	TRK1 YJL129C J0693	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	1235	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Saccharomyces, Saccharomyces cerevisiae (Baker's yeast), Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	559292	GN=TRK1 PE=1 SV=1MHFRRTMSRVPTLASLEIRYKKSFGHKFRDFIALCGHYFAPVKKYIFPSFIAVHYFYTISLTLITSILLYPIKNTRYIDTLFLAAGAVT QGGLNTVDINNLSLYQQIVLYIVCCISTPIAVHSCLAFVRLYWFERYFDGIRDSSRRNFKMRRTKTILERELTARTMTKNRTGTQRTSYP RKQAKTDDFQEKLFSGEMVNRDEQDSVHSDQNSHDISRDSSNNNTNHNGSSGSLDDFVKEDETDDNGEYQENNSYSTVGSSSNTV ADESLNQKPKPSSLRFDEPHSKQRPARVPSEKFAKRRGSRDISPADMYRSIMMLQGKHEATAEDEGPPLVIGSPADGTRYKSNVNKL KKATGINGNKIKIRDKGNESNTDQNSVSSEANSTASVSDESSLHTNFGNKVPSLRTNTHRSNSGPIAITDNAETDKKHGPSIQFDITKP PRKISKRVSTFDDLNPKSSVLYRKKASKKYLMKHFPKARRIRQQIKRRLSTGSIEKNSSNNVSDRKPITDMDDDDDDDDDNDGDNNEEY FADNESGDEDERVQQSEPHSDSELKSHQQQQEKHQLQQNLHRMYKTKSFDDNRSRAVPMERSRTIDMAEAKDLNELARTPDFQKM VYQNWKAHHRKKPNFRKRGWNNKIFEHGPYASDSDRNYPDNSNTGNSILHYAESILHHDGSHKNGSEEASSDSNENIYSTNGGSDH NGLNNYPTYNDDEEGYYGLHFDTDYDLDPRHDLSKGSGKTYLSWQPTIGRNSNFLGLTRAQKDELGGVEYRAIKLLCTILVVYYVGW HIVAFVMLVPWIILKKHYSEVVRDDGVSPTWWGFWTAMSAFNDLGLTLTPNSMMSFNKAVYPLIVMIWFIIIGNTGFPILLRCIIWIMFKI SPDLSQMRESLGFLLDHPRRCFTLLFPKAATWWLLLTLAGLNITDWILFIILDFGSTVVKSLSKGYRVLVGLFQSVSTRTAGFSVVDLS QLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYGDMGGEPEDTDTEDDGNDEDDDEENESHEGQSSQRSSSNNNNNNNRK KKKKKKTENPNEISTKSFIGAHLRKQLSFDLWFLFLGLFIICICEGDKIKDVQEPNFNIFAILFEIVSAYGTVGLSLGYPDTNQSFSRQFTT LSKLVIIAMLIRGKNRGLPYSLDRAIILPSDRLEHIDHLEGMKLKRQARTNTEDPMTEHFKRSFTDVKHRWGALKRKTTHSRNPKRSST TL
2E-216	729	0	3E-216	728.3	0	1.2	1	E7QGF0_YEASZ	Trk1p	VL3_2520	Saccharomyces cerevisiae (strain Zymaflore VL3) (Baker's yeast)	1086	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Saccharomyces, Saccharomyces cerevisiae (Baker's yeast), Saccharomyces cerevisiae (strain Zymaflore VL3) (Baker's yeast)	764100	SV=1MRRTKTILERELTARTMTKNRTGTQRTSYPRKQAKTDDFQEKLFSGEMVNRDEQDSVHSDQNSHDVSRDSSNNNTNHNGSS GSLDDFVKEDETDDNGEYQENNSYSTVGSSSNTVADESLNQKPKPSSLRFDEPHSKQRPARVPSEKFAKRRGSRDISPADMYRSIM MLQGKHEATAEDEGPPLVIGSPADGTRYKSNVNKLKKATGINGNKIKIRDKGNESNTDQNSVSSEANSTASVSDESSLHTNFGNKVP SLRTNTHRSNSGPIAITDNAETDKKHGPSIQFDITKPPRKISKRVSTFDDLNPKSSVLYRKKASKKYLMKHFPKARRIRQQIKRRLSTGSI EKNSSNNVSDRKPITDMDDDDDDDDDNDGDNNEEYFADNESGDEDERVQQSEPHSDSELKSHQQQQEKHQLQQNLHRMYKTKSFD DNRSRAVPMERSRTIDMAEAKDLNELARTPDFQKMVYQNWKAHHRKKPNFRKRGWNNKIFEHGPYASDSDRNYPDNSNTGNSILH YAESILHHDGSHKNGSEEASSDSNENIYSTNGGSDHNGLNNYPTYNDDEEGYYGLHFDTDYDLDPRHDLSKGSGKTYLSWQPTIGR NSNFLGLTRAQKDELGGVEYRAIKLLCTILVVYYVGWHIVAFVMLVPWIILKKHYSEVVRDDGVSPTWWGFWTAMSAFNDLGLTLTP NSMMSFNKAVYPLIVMIWFIIIGNTGFPILLRCIIWIMFKISPDLSQMRESLGFLLDHPRRCFTLLFPKAATWWLLLTLAGLNITDWILFIIL DFGSTVVKSLSKGYRVLVGLFQSVSTRTAGFSVVDLSQLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYGDMGGEPEDTDT EDDGNDEDDDEENESHEGQSSQRSSSNNNNNNNRKKKKKKKTENPNEISTKSFIGAHLRKQLSFDLWFLFLGLFIICICEGDKIKDVQ EPNFNIFAILFEIVSAYGTVGLSLGYPDTNQSFSRQFTTLSKLVIIAMLIRGKNRGLPYSLDRAIILPSDRLEHIDHLEGMKLKRQARTNTE DPMTEHFKRSFTDVKHRWGALKRKTTHSRNPKRSSTTL

2E-216	729	0	3E-216	728.3	0	1.2	1	E7NJ91_YEASO	Trk1p	FOSTERSO_2475	Saccharomyces cerevisiae (strain FostersO) (Baker's yeast)	1086	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Saccharomyces, Saccharomyces cerevisiae (Baker's yeast), Saccharomyces cerevisiae (strain FostersO) (Baker's yeast)	764101	SV=1MRRTKTILERELTARTMTKNRTGTQRTSYPRKQAKTDDFQEKLFSGEMVNRDEQDSVHSDQNSHDVSRDSSNNNTNHNGSSGSLDDFVKEDETDDNGEYQENNSYSRVGSSSNTVADESLNQKPKPSSLRFGEPHSKQRPARVPSEKFAKRRGSRDISPADMYRSIMMLQGKHEATAEDEGPPLVIGSPADGTRYKSNVNKLKKATGINGSKIKIRDKGNESNTDQNSVSSEANSTASVSDESSLHTNFGNKVPSLRTNTHRSNSGPIAITDNAETDKKHGPSIQFDITKPPRKISKRVSTFDDLNPKSSVLYRKKASKKYLMKHFPKARRIRQQIKRRLSTGSIEKNSSNNVSDRKPITDMDDDDDDDDDNDGDNNEEYFADNESGDEDERVQQSEPHSDSELKSHQQQQEKHQLQQNLHRMYKTKSFDDNRSRAVPMERSRTIDMAEAKDLNELARTPDFQKMVYQNWKAHHRKKPNFRKRGWNNKIFEHGPYASDSDRNYPDNSNTGNSILHYAESILHHDGSHKNGSEEASSDSNENIYSTNGGSDHNGLNNYPTYNDDEEGYYGLHFDTDYDLDPRHDLSKGSGKTYLSWQPTIGRNSNFLGLTRAQKDELGGVEYRAIKLLCTILVVYYVGWHIVAFVMLVPWIILKKHYSEVVRDDGVSPTWWGFWTAMSAFNDLGLTLTPNSMMSFNKAVYPLIVMIWFIIIGNTGFPILLRCIIWIMFKISPDLSQMRESLGFLLDHPRRCFTLLFPKAATWWLLLTLAGLNITDWILFIILDFGSTVVKSLSKGYRVLVGLFQSVSTRTAGFSVVDLSQLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYGDMGGEPEDTDTEDDGNDEDDDEENESHEGQSSQRSSSNNNNNNRKKKKKKKTENPNEISTKSFIGAHLRKQLSFDLWFLFLGLFIICICEGDKIKDVQEPNFNIFAILFEIVSAYGTVGLSLGYPDTNQSFSRQFTTLSKLVIIAMLIRGKNRGLPYSLDRAIILPSDRLEHIDHLEGMKLKRQARTNTEDPMTEHFKRSFTDVKHRWGALKRKTTHSRNPKRSSTTL	764101
2E-216	729	0	3E-216	728.3	0	1.2	1	E7KQ87_YEASL	Trk1p	QA23_2518	Saccharomyces cerevisiae (strain Lalvin QA23) (Baker's yeast)	1087	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Saccharomyces, Saccharomyces cerevisiae (Baker's yeast), Saccharomyces cerevisiae (strain Lalvin QA23) (Baker's yeast)	764098	SV=1MRRTKTILERELTARTMTKNRTGTQRTSYPRKQAKTDDFQEKLFSGEMVNRDEQDSVHSDQNSHDISRDSSNNNTNHNGSSGSLDDFVKEDETDDNGEYQENNSYSTVGSSSNTVADESLNQKPKPSSLRFDEPHSKQRPARVPSEKFAKRRGSRDISPADMYRSIMMLQGKHEATAEDEGPPLVIGSPADGTRYKSNVNKLKKATGINGNKIKIRDKGNESNTDQNSVSSEANSTASVSDESSLHTNFGNKVPSLRTNTHRSNSGPIAITDNAETDKKHGPSIQFDITKPPRKISKRVSTFDDLNPKSSVLYRKKASKKYLMKHFPKARRIRQQIKRRLSTGSIEKNSSNNVSDRKPITDMDDDDDDDDNDGDNNEEYFADNESGDEDERVQQSEPHSDSELKSHQQQEKHQLQQNLHRMYKTKSFDDNRSRAVPMERSRTIDMAEAKDLNELARTPDFQKMVYQNWKAHHRKKPNFRKRGWNNKIFEHGPYASDSDRNYPDNSNTGNSILHYAESILHHDGSHKNGSEEASSDSNENIYSTNGGSDHNGLNNYPTYNDDEEGYYGLHFDTDYDLDPRHDLSKGSGKTYLSWQPTIGRNSNFLGLTRAQKDELGGVEYRAIKLLCTILVVYYVGWHIVAFVMLVPWIILKKHYSEVVRDDGVSPTWWGFWTAMSAFNDLGLTLTPNSMMSFNKAVYPLIVMIWFIIIGNTGFPILLRCIIWIMFKISPDLSQMRESLGFLLDHPRRCFTLLFPKAATWWLLLTLAGLNITDWILFIILDFGSTVVKSLSKGYRVLVGLFQSVSTRTAGFSVVDLSQLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYGDMGGEPEDTDTEDDGNDEDDDEENESHEGQSSQRSSSNNNNNNRKKKKKKKTENPNEISTKSFIGAHLRKQLSFDLWFLFLGLFIICICEGDKIKDVQEPNFNIFAILFEIVSAYGTVGLSLGYPNTNQSFSRQFTTLSKLVIIAMLIRGKNRGLPYSLDRAIILPSDRLEHIDHLEGMKLKRQARTNTEDPMTEHFKRSFTDVKHRWGALKRKTTHSRNPKRSSTTL	764098
1E-214	723	2.9	4E-214	721	0	2	1	TRK2_YEAST	Low-affinity potassium transport protein	TRK2 RPD2 YKR050W	Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	889	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Saccharomyces, Saccharomyces cerevisiae (Baker's yeast), Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast)	559292	>sp|P39304|TRK2_YEAST Low-affinity potassium transport protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TRK2 PE=1 SV=1MPTAKRTSSRASLALPFQLRLVHKKSWGHRLRDFISGFLKSCRPIAKYVFPNFIVVHYIYLITLSIIGSILLYPCKNTAFIDVLFLAAGASTQGGLATKSTNDFNLYQQIVVYVITLLSTPILIHGFLAFVRLYWFERYFDNIRDISKQNFKLRRTMTLQQRELSGSSGNAARSRSFKDNLFRGKFVSREDPRQSASDVPMDSPDTSALSSISPLNVSSSKEESSDTQSSPPNFSSKRQPSDVDPRDIYKSIMMLQKQQEKSNANSTDSFSSETNGPAFIVQERHERRAPHCSLKRHSVLPSSQELNKLAQTKSFQKLLGLRRDEGDHDYFDGAPHKYMVTKKKKISRTQSCNIPTYTASPSPKTSGQVVENHRNLAKSAPSSFVDEEMSFSPQESLNLQFQAHPPKPKRREGDIGHPFTRTMSTNYLSWQPTFGRNSVFIGLTKQQKEELGGVEYRALRLLCCILMVYYIGFNILAFVTIVPWACTRHHYSEIIRRNGVSPTWWGFFTAMSAFSNLGLSLTADSMVSFDTAPYPLIFMMFFIIIGNTGFPIMLRFIIWIMFKTSRDLSQFKESLGFLLDHPRRCFTLLFPSGPTWWLFTTLVVLNATDWILFIILDFNSAVVRQVAKGYRALMGLFQSVCTRTAGFNVVDLSKLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYDSGQDDENITHEDDIKETDHDGESEERDTVSTKSKPKKQSPKSFVGAHLRRQLSFDLWYLFLGLFIICICEGRKIEDVNKPDFNVFAILFEVVSAYGTVGLSLGYPNTNTSLSAQFTVLSKLVIIAMLIRGRNRGLPYTLDRAIMLPSDKLEQIDRLQDMKAKGKLLAKVGEDPMTTYVKKRSHKLKKIATKFWGKH	559292
7E-214	720	1.4	7E-213	717.1	0	2	1	E7KR77_YEASL	Trk2p	QA23_2993	Saccharomyces cerevisiae (strain Lalvin QA23) (Baker's yeast)	889	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Saccharomyces, Saccharomyces cerevisiae (Baker's yeast), Saccharomyces cerevisiae (strain Lalvin QA23) (Baker's yeast)	764098	>tr|E7KR77|E7KR77_YEASL Trk2p OS=Saccharomyces cerevisiae (strain Lalvin QA23) GN=QA23_2993 PE=4 SV=1MPTAKRTSSRASLALPFQLRLVHKKSWGHRLRDFISGFLKSCRPIAKYVFPNFIVVHYIYLITLSIIGSILLYPCKNTAFIDVLFLAAGASTQGGLATKSTNDFNLYQQIVVYVITLLSTPILIHGFLAFVRLYWFERYFDNIRDISKQNFKLRRTMTLQQRELSGSSGNAARSRSFKDNLFRGKFVSREDPRQSASDVPMDSPDTSALSSISPLNVSSSKEESSDTQSSPPNFSSKRQPSDVDPRDIYKSIMMLQKQQEKXNANSTDSFSSETNGPAFIVQERHERRXPHCSLKRHSVLPXSQELNKLAQTKSFRKLLGLRRDEGDHDYFDGAPHKYMVTKKKKISRTQSCNIPTYTPSPSPKTSGQVVENHRNLAKSAPSSFVDEEMSFSPQESLNLQFQAHPPKPKRREGDIGHPFTRTMSTNYLSWQPTFGRNSVFIGLTKQQKEELGGVEYRALRLLCCILMVYYIGFNILAFVTIVPWACTRHHYSEIIRRNGVSPTWWGFFTAMSAFNNLGLSLTADSMVSFDTAPYPLIFMMFFIIIGNTGFPIMLRFIIWIMFKTSRDLSQFKESLGFLLDHPRRCFTLLFPSGPTWWLFTTLVVLNATDWILFIILDFNSAVVRQVAKGYRALMGLFQSVCTRTAGFNVVDLSKLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYDSGQDDENITHEDDIKETDHDGESEERDTVSTKSKPKKESPKSFVGAHLRRQLSFDLWYLFLGLFIICICEGRKIEDVNKPDFNVFAILFEVVSAYGTVGLSLGYPNTNTSLSAQFTVLSKLVIIAMLIRGRNRGLPYTLDRAIMLPSDKLEQIDRLQDMKAKGKLLAKVGEDPMTTYVKKRSHKLKKIATKFWGKH	764098
1E-185	627	3.7	1E-185	627	2.6	1.6	1	TRK2_SCHPO	Potassium transport protein 2	trk2 SPAC1639.02c SPAC1F5.12	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	880	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae, Schizosaccharomyces, Schizosaccharomyces pombe (Fission yeast), Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	284812	>sp|Q10065|TRK2_SCHPO Potassium transport protein 2 OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) GN=trk2 PE=2 SV=1MQLSGFSTNGSGSLNTIVCEKLLFKPNFVQDSFIIGMTILCSVILYGSGNLRYIDALLLASGSCTQTGLQPVDLTQISIYQQLTILLFGVLSTPITVNLGLTLFKLYFYNKRYDMVITNNKLRMTYTYHTVRRRDTPEPSKVGNRKIRVLLDQGNQMHRPVAPETKAEEAEHQENEKHHRHHFRLRKFANAIDRPSFFRGNTMPALPSYAGVRNSQENEDRTEALSPALGKRRMASIDNGSLSVVQNNARNNPVDFYIPSSFEESSFQTIPEDFEPQVHDHENQTQLNHHLDNNSSISSHNPSLETANDGNQETVSSSNSNYSTTRVDNDPHVASYSPQNSNFDHQAAATTNDAHQNVVRGSAITIAPTPVPRHNRRPIYFADDTNGAEQEKGAHRLDGRGRKRGKSFAVTPTLHRNERSMSVLPFQLAKSFTSALPRRLTFNRTHTKASTMSLPYLSYNATVGRNSAFYALTPVEREELAGIEYESLRILTVILVVYFLFWHILGLVAFLIFIYTAKTSGRVVTDGGINRGWWAAFTSSSLFDNLGYSLNSDSLNSFQKAIFPQVLGTILIFLGNTFFPIMLRFIIWIMIRTTRFSPNFQQALYLFEHPRRSFTLLFPSKTTWVLFLNLTLLNFASFFFFMVLDLGNSYVDKIPVGYRIMNAIFQNAATRSAGFTVVDLSQIAPAVMVTYMFMMYISAYPIAMSIRQTNVYEERSLGIYAADTENDDDNNINNNNNDNNTPKRKNFLMDHIQRQLSHDLWYLFLGYFIITIVEGRRLESEAEPQFTLFAILFEVISGYGTVGLSLGYKNDPSLTAQFRKISKLVMVALQIRGRHRGLPSALDRAVLMPSDKNFDREEEDYMRRHGKKNTNRADPVPSS	284812

4E-185	626	2.9	7E-184	621.3	0	2.1	2	J8LLB7_SACAR	Trk2p	SU7_2070	Saccharomyces arboricola (strain H-6 / AS 2.3317 / CBS 10644) (Yeast)	894	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Saccharomyces, Saccharomyces arboricola, Saccharomyces arboricola (strain H-6 / AS 2.3317 / CBS 10644) (Yeast)	1160507	SV=1MSTARRTQSRASLALPFQLRLVHKKSWGHQLRDSISKFQKSCKPVARYVFPNFIVVHYIYLITLSIVGSILLYPCKNTPYIDVLFLA AGASTQGGLATKSTNDFNLYQQIVVYIITCLSTPIIIHGFLAFVRLYWFERYFDNIRDFSRQNFKLRRTMTLKQRELSDGSDSGVAARNR SFKDNLFRGRFVSREDPQQPTDSPGSFASSSVSPLNVSSSKDNSSDTQSLPSQHFSGKRQNSDVDPTDIYKSIMMLHGQHQRDGSD PTASSHSMDDGPAYMVQERRERPGPYLAPERRSISPNSQELDKLAQTEGSQKLPFLQRDEGDYDYDYDYDHASRKVMATPQKSVP KRQSQYASECTHPQVHEIPSKVPQYDEKPAKSTPSSSVDEEMSFSPQESTNLQFQAHPPKPNRPAGDTQHPFTRTTSTNYLSWQPT FGRNSVFIGLTRQQKEELGGVEYRALRLLCNILVIYYVGFNIVAFVIVVPWICTRQHYAEIVRQNGVSPTWWGFFTAMSSFTNLGLALT SNSMVSFSTAPYPLIFMMLFIIIGNTGFPIVLRFVIWIMFKTSKDLSQFKESLGFLLDHPRRCFTLLFPSAPTWWLFITLVFLNATDWILFII LDFDSAVIKQIAKGYRVLMGLFQSVCTRTAGFNVVDLSKLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYDNDQGYGDITDE DDTTDNYNDDGGEQNEPASPKAKAKHKPKKHSPRSFVGAHLRKQLSFDLWFLFLGLFIICICESRRIQDANEPDFNVFSILFEIVSAYG TVGLSLGYPNTNTSLSAQFTVFSKLVIIAMLIRGRNRGLPYTLDRAIMLPSSNLEKIDRLQDMKAKGKLLAKVDEDPMTTYVKKRSHKLR KVATRFWKRH	
8E-183	618	13.4	2E-180	610.2	4.8	2.1	2	TRK1_SCHPO	Potassium transport protein 1	trk1 trkSPAC3F10.02c	Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	841	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae, Schizosaccharomyces, Schizosaccharomyces pombe (Fission yeast), Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast)	284812	PE=3 SV=2MVLNYIQRWFKWVIPTFGFLAIHYIYIISLTIIASILLFTGGTTTKIKYIDALFLASSATTQTGLNSVDLNSLSIWQQFILYGFTAITVPI WMHGSISFIRLYWFRRKFKDVVRQNRTRKFQRKLRKSLMKKSEDDEEQGVRGRKIRVMLPYLHSLRSPTSLKNFSRFDTHDSTNNP YFPDNPPSPKADISKDEYFGKYLPKKSDTLDMDLESHNMTFHDYEPSIENKNYDFGSSHSASMQMYEMDDLHPRLRRQSSFISSVNP LEADDTRETLSEGALVQESLPMAYSYSDTNLVVSRDSFTLTGDDNLFPEGGLRPANTIDGIVRSSLSSSSLSKDTEPSTVDMHIAFTGL NKPTIERERNLKLRKKSRFYKKSLRSRFSRGLHRPIRWTKSFTSNRRNLTLERVLSSAFAKKREPSISSRHTTMSLPYLSYNPTVDRNS AFVALSKEQRDELGGIEYRALKCVCSMVTLYFIIFNIAAFVTFIVFAYTAVGSREVIDSYDLRRGWWALFSSASSFNDLGFSLIPSSFVP MNRNIFLLLISSLFIIAGNTGFPCFFRTFIWTTYKLYPFSFEKKEAMAFLLDHPRRCFTLLFPSGATWVLFFVLLLLNVIDLVLFMVLDTGS KAVASLPKGIRVVNAIFQSVCTRTAGFTSVSISELHPAVLVSYMVMMYISVYPVAINMRNTNVYEERSLGVYRTEDDEGKSFLKDHLTE QLSYDLWYIFLGLFIICICEGGKISNPLDTDFSIFTVLFEVVSAYGTVGLSTGLSSSNCSLSARFTTISKLVIIALELRGRHRGLPRAVDRAI LLPSEKNNLKEEEDYQRRHGFSIDNARGSIAVSRD	
1E-177	601	0.8	1E-177	600.8	0.6	2.1	1	J7S5U8_KAZNA	Uncharacterized protein	KNAG0C02700 KNAG_0C02700	Kazachstania naganishii (strain ATCC MYA-139 / BCRC 22969 / CBS 8797 / CCRC 22969 / KCTC 17520 / NBRC 10181 / NCYC 3082) (Yeast) (Saccharomyces naganishii)	1257	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Kazachstania, Kazachstania naganishii, Kazachstania naganishii (strain ATCC MYA-139 / BCRC 22969 / CBS 8797 / CCRC 22969 / KCTC 17520 / NBRC 10181 / NCYC 3082) (Yeast) (Saccharomyces naganishii)	1071383	8797 / CCRC 22969 / KCTC 17520 / NBRC 10181 / NCYC 3082) GN=KNAG0C02700 PE=4 SV=1MAFGRTSTSVSTSSWFVENYKKTVGHKFRDFIASCGHYIKPFKKYFLPNFIAVHYFYIISLTILGSILMYPVHNFRYIDILFLACGAT TQGGLNTVNVNDLTLYQQLIIYLLCCISTPIAIHGCLAFVRLYWFERYFDGIKDRSKRNFKMRRTRTILQREMTKRSHQATHTFNARTYS SVQTQRSNAVQGPNAADPDFQEKLFSGRKVNRDEQSFHSEESQDTNLPDRMKIDNSSGSSTGDGTHYTETSSSSTNHAGERFASR RNSTDITPVDMYRSIMMFRGQHQDQNEEGEGPALVIKGRNVASDIQRPKHKPLLQDIQSVDEGDESSTEETSQILRPKSLSSGINSQE DRPTLGETHVGGQDSNSIYTDSDDMNHTVDDEVEPPNASAISSQELELFEPGSDVNFSNRSINNHSVSDSNISSENVRDYRGSDYDD DNTGDDGNDEISDDEAESLDDSLSSGSQTDANTPLETGPLEYPDNTQHISFSNDDETRRQRGVTVNQRNRGKLEDSSVRPKEGQSI QFNITARPKRRYQIQGAKKARNPYYHTKKRPAKRLLLKQLKKGKRLREQLQGRLSRATTDKDDYPDNFSAPSTDPRPRAEILENKGN NDMEEYFADDETDEDIPYDISPEELNRLSQTPDFQKMIYKNWKAKHRKTGKLGKASRTLEKTLTSGSHSNFPRPRRNHHLSNDFHKN KPNNGDAGNLSSDDSYGSVLDSERGTDYYNYIDTEDQAQHGNHFEYNFDQNNLNLPLNRTMSTNYLSWQPTIGRNSTFVGLSKSQR DELGGVEYRAIKLLCKILLCYYFGFHVMAFVMMVPWICVKKYYIHIVRSDGVSPAWWGFFTSMSAFSDLGLTVTPDSMTSFNKAIYPQ IVMMWFIIIGNTGFPILLRCIIWVMFKTAPELSQTKESLGFLLDHPRRCFTLLFPEAATWWLLLTLLFLNITDWILFIILDMGSAVLKPLSR GLRVLNGLFQAVSTRTAGFSIVDLSKLHPAIQVSYMLMMYVSVLPVAISIRRTNVYEERSLGMYGKIEEHDDEDEDVDSSDTETKTKKS KKRKNRNNLEEDDEKKDHVSTKSFIGAHLRKQLSFDLWFLFLGLFVICLCENSKIQDTTRPNFNVFSILFEIVSAYGTIGLSLGYPETNQ SFSAQFTSLSKLVIILMLIRGRCRGLPYSLDRAIILPSDRLEHIDHMEDLKLRKNHGRAETIDPVTEYVKHSTGVFRKKLERFNTHGHIPS HIGPSDEFEMTNQNRRRMEHQTM	
3E-176	597	5.3	3E-175	593	0.7	2.4	2	H2AWP9_KAZAF	Uncharacterized protein	KAFR0F02020 KAFR_0F02020	Kazachstania africana (strain ATCC 22294 / BCRC 22015 / CBS 2517 / CECT 1963 / NBRC 1671 / NRRL Y-8276) (Yeast) (Kluyveromyces africanus)	1106	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Kazachstania, Kazachstania africana, Kazachstania africana (strain ATCC 22294 / BCRC 22015 / CBS 2517 / CECT 1963 / NBRC 1671 / NRRL Y-8276) (Yeast) (Kluyveromyces africanus)	1071382	CECT 1963 / NBRC 1671 / NRRL Y-8276) GN=KAFR0F02020 PE=4 SV=1MTVRGSLSRVSTLNYEYQKTLGHKLRDFISVCGDTLKPIKKYIFPNFIAVHYFYIITLTIITSILLYPVHDARYIDILFISTGATTQGGLN TVNINQLSLYQQIIIYISCCISTPIAIHGMLAFVRLYWFERHFDGIRELSKQNFRMRRTRTILGRELSKRQLTKSNNQTNFGRNVEDFQEK LFSGKMVNREENSILHMSLSSASLNSKPDDNDTEDTSNSRVRTEVFAKRRNSTDITPQDMYRSIMILRNKQEHEITGAENNNHHSTDP NSELSHNDMTEDSHTVGGETSEEGYRNQGYDTGEDSNDNPLTSEHSLSYEDDDDEEEFPENSELNHDGDNSDNSISPHTTIRHSNN ETTRAGPSIMFDIQKPPRRKTSQRIVTHNDLKSTRASFVSASKSKIFKRIHKGRKKIGRNLKRRLSTGSIDRANFDSCLSKDAEDYFADN ETDDEHFNLKKISTIDELTQAPDFQKMIYKNWKAKHRRIHPKNLGKKSLFGDNESSLHLDQLFRVHSISNANANPTTSSYQNETSFMH SDGELNSLRTDNTDNYKESINLNHNISFQNDIDEEQDPYDYYGIHFDPNFNFQPKSSKVGKGKNQNKFTRTMSTNYLSWQPTIARNS NFFGLTKQQKEELGGIEYRALKLLCRILLIYYFGFHVVAFVMMVPWICTKKDFIHILRSDGISPAWWGFFTPMSAFNNMGLTLTPDSMN SFSTAIYPLIVLMWFIIIGNTGFPVLLRFIIWIMFKISPDLSQIKESLGFLLDHPRRCFTLLFPSAATWWLLLTLLFLNFTDWILFIILDFGSSV VKVFSKGHRVLIGLFQAVCTRTVGFSVIDLNKLHPAIQVSYMIMMYVSVLPLAISIRRTNVYEERALGLYSSSQSDTSDAEDTEDSDSEI SDIESGSSTRNESSSTNEPRKKRKKKKHPATELSAKSFIGAHLRRQLSFDLWFLFLGLFIICICEDGKIRDTSKPDFNVFAILFEVVSAYC TVGLSFGYTNTYESLSAQFTTLSKLVIIALLIRGRNRGLPYSLDRAIILPSNRLDHIDHIEDLKLKNRNDTATVGQMDPVTEYVERHTKSF RQKFKRIITLGRSNRSNEERQGLAEEYEL	

2E-175	594	3.8	7E-175	591.6	0	2.2	1	J7REQ5_NAUDC	Uncharacterized protein	NDAI0G06160 NDAI_0G06160	Naumovozyma dairenensis (strain ATCC 10597 / BCRC 20456 / CBS 421 / NBRC 0211 / NRRL Y-12639) (Saccharomyces dairenensis)	1248	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Naumovozyma, Naumovozyma dairenensis, Naumovozyma dairenensis (strain ATCC 10597 / BCRC 20456 / CBS 421 / NBRC 0211 / NRRL Y-12639) (Saccharomyces dairenensis)	1071378	[illegible] 421 / NBRC 0211 / NRRL Y-12639) GN=NDAI0G06160 PE=4 SV=1MQLRRRLSRVSTLTPFTIPYKKTLGHKLRDFIDELGQKFTPIKKYIFPNFIAVHYFYIISLTIIASILMYPIKNARYIDILFLAAGATTQG GLNTVDLNGLTLYQQLIIYLTCMLSTPIIIHGCLAFVRLYWFERYFDGIRDSSKRNFEIRRTKTTYRKRINCKDKNEYVPSSLFKIAFFSVP QRRDDFQEKLFSGKMVNRDEQESINDTITGHSRYAAIRPQANSHNSDSNSSSVPTSSSTKDEASVTKPYINHTLGVSEPQIRHNDGSF DRDYEDETENFARRRMSEDILPEDMYRSIMLLRNQHDDAKEDDGPALIVKAPTGRSLNFYDREISPKDITENSLQPRPADIIDNNSSAV ESLSTFGNIPNSRNDSENASDRSTDFNNVESGADLSDTEGVLSPHSSRQSLGSISPKTRSRSPVSNKHYMLNSEWKPDEANILNRQR PTIQFDITKPPKRRLQRERQIKAHNATMEVDSPRSYFAHTRRSSRNIFKHIPKGRRIRQKIKRSLSTGSTEKRTGKSTRRSRGQYTEHD GDNEEYFADDETDDEQENLSSNNNVNRTHWEETVSRPPLRQNRSSFDNSQGHDIVHPLHKSRTYDQALVKTLDELARKPDFQKVIY EDWKAKHRKSSAFPHFESHFPQNKRASVLFKGDRPLGHPGHGSDQYSSDSHPNPSSMNEDDGYLQSLESTNANKPDIDEEGNYYG LHFDPDINFSRPHGHIERTMSTNYLSWQPTIGRNSNFYGLTQRQKDELGGVEYRAIKLLCRILLAYYIGFNIMAFVMLVPWICVRKHYIS IVRDDGISPAWWGFFTAMSAFSDLGLTLTPDSMSSFNKAIYPLLTMAWFIIIGNTGFPILLRFIIWIMFKLAPDLSQLKESLGFLLDHPRR CFTLLFPSAATWWLLLILLFLNFTDLILFVILDFGSSYLDGIGRGYKVVMGLFQGVCTRTAGFSVMDLSKLHAAIQVSYMLMMYVSVLPL AISIRRTNVYEEQSLGIYGEIRTPEEIEEEEEEEDGEHSDDEQDDNNEEEYDESSNNEEDSTETSGSSRSSNKKKNMRKTKKVSTRSFI GAHLRRQLSFDLWFLFLGLFIICICENGKIKDVARPAFNVFPILFEIVSAYGTVGLSLGYPNTNQSFSGRLTVLSKLVIIAMLIRGRNRGLP YSLDRAIMLPSDRLEHIDHIEDLKLKKRSAISKSDSQSNRDPMNSYVKNGTRWIRRGLKKSFTLPPQQRQSSAATSARSHFLSERSNE Q
5E-175	592	0.1	8E-174	588.2	0	2.2	1	Q6FL73_CANGA	Strain CBS138 chromosome L complete sequence	CAGL0L05654g	Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) (Yeast) (Torulopsis glabrata)	1352	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Nakaseomyces, Nakaseomyces/Candida clade, Candida glabrata (Yeast) (Torulopsis glabrata), Candida glabrata (strain ATCC 2001 / CBS 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) (Yeast) (Torulopsis glabrata)	284593	[illegible] 138 / JCM 3761 / NBRC 0622 / NRRL Y-65) GN=CAGL0L05654g PE=4 SV=1MELRRRLSRVQTLTQFNFSYNKSFGHKFRDFIAKSGHHVKPIQKYIFPNFIAVHYFYIIFMTILASILLYPVKNFSYIDILFLAAGATT QGGLNTVNINELTLYQQMIIYIICCLCTPIAIHGTLAFVRLYWFERYFDNIRDTSKRNYKMRRTKTILEREKTARTLSRLRTNTTIPIHKSN QENSQRSNFQEKLFSGEFVNRDEQNSIESQQDAMDSQSTQNSLPTFKGLGPSKIQKTASPRSLNSTLPSGSVLEDGESRTPYEQPID YTIPNSNPNLTVPVERFKRRRSRDISPQDMYRSIMMLQDKHSNIDDNEEGPALVIGSPQDRQNIKPTVQSQSMGHNALTPVHSISDKE VSPKHVDANEINMGMKVKDKHGNQGPSRRSGSQSPSSENAFPNENDEEENFSPYTNSRKIKLNKHPTGRNYDNSSDDLNSAGNYN SEEGLEGENATQSTEEVSPLDSDDAYSDGDSHEYENTEVNEDSDSIQDIQSGNNRLYRRRTDQERNLNYESEASITQDNIERHNNDSI NSENAASDDSESNGENTNDRNARTPNKGGEPKIQFNITEPPRKRRTQNFHIMEATRPNIPHNAHKRTSSNLFLKQLSKGKRIRHNLKR RLSSGPFEKNESPFNPSIKNVNKQKGSQKETNQDNGEDYFADNESDDDDNNPASSDYNGLSKTVSYNNTEDRKPDPVRLTMERAM TMDNITPEDLNKLAQKPDFQKMVYKNWKRKHRKNKKNRKLGWNKKFDFEDTLPTVFDSHNEGHQRTMSNDEDNEDIRNGNIDRYN TIDYNDGYQIDPDMNEEGYFGVSFNNDYNFSRHPFSRTMSANYLSWEPTVGRNSLFVDLSRAQKEELGGVEYRSIKLLCKILVIYYLG FHIMSFTMLLPWITHKTKYKHIVRDDGVSPGWWGFFTAMSAFNDLGLTLTPDSMSSFNRAAYPLIVMIWFIIGNTGFPVLLRFIIWVMY HLSSDLSQLRESLAFLLDHPRRCFTLLFPSTATWWLFGILVGLNITDWILFIILDFNNVVVKPNPKGYRVLMGLFQAVSTRTAGFSVVDL SQLNSAVQVSYMIMMYVSVLPLAISIRRTNVYEEQSLGLYGNVEDDDSSDSDYEDHLSSEEELLAKNGDNDDDEETLDSQYYSKSIRG RNDSDESSSNEGGSNSSAKKRKRTAKKESSKGKKKKRRVSEKKSKSFIGAHLRRQLSFDLWFLFLGLFVICICENGKIKDVARPAFNV FPILFEIVSAYGTVGLSLGYPNTSQSLSGQFTTLSKLVIIAMLIRGRNRGLPYTLDRAIILPSDRLERIDHIEDLKLKRTAGLHARHQPRPE DERKKSIAKKSFKYIKKGGKGLLYPSKLL
4E-173	586	30.3	5E-173	585.6	21	1	1	Y460_MYCPN	Uncharacterized cation transporter MG322 homolog	MPN_460 H08_orf565 MP381	Mycoplasma pneumoniae (strain ATCC 29342 / M129)	565	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma pneumoniae, Mycoplasma pneumoniae (strain ATCC 29342 / M129)	272634	>sp|P75323|Y460_MYCPN Uncharacterized cation transporter MG322 homolog OS=Mycoplasma pneumoniae (strain ATCC 29342 / M129) GN=MPN_460 PE=3 SV=1MTAAHKQKAKLLAWLKLILWGDSISQRIFHFYIYCILLGAVLLFLPFALKTDYQKVISYEVDLQGHTISKQTASYGFLDALFLAVSAF SDTGLSTTVVSETYSVFGQTVLAILLQLGGIGFVVIAFLVWRLFKLHKKGKYSFYEKLMLQSERGGSKLGTTSEMIVVSVLFLFMVELLY GFLYTILFYFIPAFESASVFQSSGKVSNQLKALIVDSTKRLPVVHNLNLAFQYGFFHSLSAVNNAGIDLLGANSFAPYRTNWGIVIQWLA ISQIIFGGIGYPVLFDAYEAIKKRRLYGKYYKHQFSLFTKLAVLTNLIVTAWCFLMLLMVEFIVITSLTNTIAHLNVEKAYLVEGLKNKSNQ ELQSLIFGPIPAASRVMQLWFGVISSRSAGFSVFPWSAESDIIKGIMVIAMFIGGSPSSTAGGIRTTTLAVIFLTLKAKFRGQKEVKVFKR SIDGQTVINAFLVAVFGLVSVVLIAILLPLSMQQPLSFVDSLFETTSAFGTVGLSSGATKIMALEPTRNLFNYLTLGLLMIMGQVGVSSSV LTFVKKHPQGNSFSYPREDVKVG
2E-172	584	1.1	6E-171	578.8	0	2.1	2	G0V7T6_NAUCC	Uncharacterized protein	NCAS0A09760 NCAS_0A09760	Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) (Yeast) (Saccharomyces castellii)	1210	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Naumovozyma, Naumovozyma castellii (Yeast) (Saccharomyces castellii), Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) (Yeast) (Saccharomyces castellii)	1064592	[illegible] NRRL Y-12630) GN=NCAS0A09760 PE=4 SV=1MFKRTLTQVSTLGPFNREYRKTFGHKLRDLISEIGSKCSPIKKYIFPNFIAVHYFYIILLTIISSILMYPVKNSRYIDILFLATGATTQG GLNTVNVNELTLYQQLVIYLTCIMATPIVIHGCLAFVRLYWFERYFDGIRDSSKKNFEMRRTRTILERELTARTITKNRTNMSQNSRYSR QPNFGNGSQRDDFQEKLFSGKMVNRDENDVLSRRPTNIRDDSSRFKNKLSREDNMTGNNSRHAIKFQDQEQNNDNNSDHFIREQE KFVQRRHSQDISPTDMYRSIMMLRNQHEEHAENEGPALVIKAPSGSDDKKGNDNKNTHSERITGENSSSVKQSRETISNDNTDHDDN DADDADDAGLTSNVSYGGSLSEVATGSESSHDIADETTEEGLTSPFSTEESFNSVSPQSRSKSPLRNLSMNKGFNSTSELNNTDENH VHYTTEPTIQFDISKPPRIDRRKRKLAPKPRPSYFGYTKRSSRNILKHIPKGRRFRKHLKRRLSTNSVAKPNNEELTGKSPVEHPEESD DGDFEEYFADNETDEDEINQPIQTYRPPPPRHRSSSYHNTDISVITNGLKKSKTYDMALSKELDELSQKPDFQKMVYQNWKSKHKKN ARFPHIYHTKTGLTATTDSEDQRNLSSSNGDNSLNSQDYDDSELESRYNTTGMYDGENSERDNGLDEEANYYGLHFDPDVNLTPLH APFSRTMSTNYLSWQPTIGRNSNFYNLTQSQKDELGGVEYRAIKLLCTILLVYYIGFNIMAFVMLVPWICVKKQYIAIVRSDGISPAWW GFFTAMSSFADLGLTVTPDSMSSFDTSIYPQIVMMWFIIIGNTGFPVLLRFIIWVMFKLAPDLSQRKESLGFLLDHPRRCFTLLFPSAAT WWLLIVLLALNITDLILFVILDFSSSYLKGISRGHRVLMGLFQGVCTRTAGFSVMNISDMHASIQVSYMLMMYVSVLPLAISIRRTNVYEE QSLGIYGDVVNPEDVDGEEDENDDEDEEDEEYEDDTHSSENSKDNTSNSSSSTPKKKNSDKKPSATSFIGAHLRRQLSFDLWYLFLG LFVICICENNKIKDINSPNFNVFAILFELVSAYGTVGLSFGYPNTNESFSGRFTTLSKLVIIAMLIRGRNRGLPYSLDRAIILPSERLEHIDHI EDLKLKRRRASTKDSDAMTGYIKKNTRWLRHGIRKGIRRSNTVHSGPSRDAYLMHDIS

5E-172	582	4.8	5E-172	582.2	3.3	2.1	2	G8ZZC1_TORDC	Uncharacterized protein	TDEL0H01060 TDEL_0H01060	Torulaspora delbrueckii (strain ATCC 10662 / CBS 1146 / NBRC 0425 / NCYC 2629 / NRRL Y-866) (Yeast) (Candida colliculosa)	1213	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Torulaspora, Torulaspora delbrueckii (Yeast) (Candida colliculosa), Torulaspora delbrueckii (strain ATCC 10662 / CBS 1146 / NBRC 0425 / NCYC 2629 / NRRL Y-866) (Yeast) (Candida colliculosa)	1076872	>tr|G8ZZC1|G8ZZC1_TORDC Uncharacterized protein OS=Torulaspora delbrueckii (strain ATCC 10662 / CBS 1146 / NBRC 0425 / NCYC 2629 / NRRL Y-866) GN=TDEL0H01060 PE=4 SV=1MLAKKLSHVPTLASLNIRYKKTFGHKFRDVIAACGSYLKPVRKYIFPNFLAVHYCYIIFVTIIASILMYPVRNQKYIDILFLAAGATTQ GGLNTVDTNTLSLYQQIIVYITCVFCTPIVIHGCLAFVRLYWFERYFDGIRDSSKKNYKMRRTKTILGREMTSRTMSKMPQRPTHILSML PTSSRNDENFQDKLFSGKEFFRKEGEDDVDNDKPDTTKPKDKNGFDSNGSSWSSSNTVKENGNPNTHVRGDLVFKEPGIKKPTKP RERFAGRRSSADISPEDMYRSIQMMQGQHQEAREDEGPALVIGAPTDRPVARNEEAKQKQAPEDGTKDDHHSILTENQSKHTSALN SSIDPHHTQTPPVQKVQSSPIASLKTIDEETKMGRKDYDEPEANKPTIQFDVSAQPKRPSSKIVKDSTIRIPRRGNQYRTKSNRGLLKH LPKGKELRQKLKRRLSSNSADGLNSEKRRSYTDDDEPTDKDNMEEYFADNESDEDDEEHPNVYGEGKRLSKVPTTGEVEEPRRSQL AEMPRSLTMDARQAKDLNQLAQTREFQKMIYKDWKKKHRKPNPLRRKSWNAKKFENEYSAGFPWMQEAFNADEDLSSDHDSGEV NSGHGSSFDNVKGNVASDSDDAANQEPSSPRDRDSLDEEQGYYGLTIDPEFTSNARPAIARTMSTNYLSWEPTIGRNSAFTGLSKA QREELGGIEYTSIKLLCRILVIYYAGFLILSFVLIVPWVLHQSHYKAIIRENGVSPTWWGFFTAMSAFTDLGITVTRDSMLSFNKAVYPLV VMMWFIIVGNTGFPVLLRFIIWVLFKLSPELSQFKENLGFLLDHPRRCFTLLFPSAATWWLLATLVALNGIDLVLFIILDFGSAVLRPLAR GFRVLDGLFQAVSTRTAGFTVVDLSKLHPAIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGLYGEMTTEDTSSTDYSTDSEGSSDSG SRRKKKKKKQGKDSNESFIGAHLRRQLSFDIWFLFLGLFIICLCEGGKIQDTSKPEFNVFAVLFEIVSAYGTVGLSLGFPNTNTSFSGQF TTLSKLVIIAMLIRGRHRGLPYALDRAIMLPSDRLEHIDHIEDLKLKRTTRNSTNNVDPVTAYFKKRTGKLHRGFDRLRRSVAEPEEAHL EAYGQHNNSPDYNLPGEDERDYQLETVSQATHSAPSSVHSPGSIDSEQLTDRDSNHDSMHLTHPISYS
2E-171	581	5.4	3E-170	576.4	0.1	2.2	2	A7TQY9_VANPO	Putative uncharacterized protein	Kpol_448p14	Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) (Kluyveromyces polysporus)	1323	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Vanderwaltozyma, Vanderwaltozyma polyspora, Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) (Kluyveromyces polysporus)	436907	>tr|A7TQY9|A7TQY9_VANPO Putative uncharacterized protein OS=Vanderwaltozyma polyspora (strain ATCC 22028 / DSM 70294) GN=Kpol_448p14 PE=4 SV=1MKLRRIVSRVPTFSSINVKYKKSIGHRIRDSIDFVTTYFHPVKKYLFPNFVAVHYFYIISMTILASILLYPVKNHAYIDILFLAAGATTQ GGLNTVDVNSLTLYQQLIIYIICCLSTPIIIHGFLAFVRLYWFERHFDGIRVTSKRDFKMRRTRTIIERQMTARTMSARTTSMGRFNTSDY MHRSSNRNNRNTQKTDFQAQLFSGKMVNRDEQNNIGHFDNLANETPNENSDIQLNRSSASINTAPEDEKYSGAHETSLMFKEPTRE RRNGLKPERFVGRRKSTDITPADMYRSISILQDRHKVERQEDDSGPALVIKAPTYDDSDDQSSDNIESPSDRYSHAKDNNKPANGEIK LNKVNSPEPDGYSNTINHDNNRNRSTGFDSHPISTSSEEVSSLNSDDTIESHDSYDDSSSSGDNHSVNSEVNYDSRVENPDSSLDSE FEEESEGEIRNLSRRNTQGNIENNDHPHNNGPSIQFNLVSPPRKRRTTQSFETRPQPIKRSSSNFLKSFRKKNKFKEKLRQRRASVHD PQFLYDDSFPEHKANVNNSQHSNEDYYSENEDERRSLHDIPNLEKTPVNLKRATTNTSNRGEFNEMNPLERSKTFDVASPSDLDKLT QSPEFQKLVYKNWKENNKKRRGMRNIQWNNNIFENDRPELRHFKSVDTNDGNIYNNIHFGNPNHINEHNSRYISRQDTNLGQNYEA SINNNDEEDIGNYHLHFDHDFNLAYPSHSLSRTMSTNYLSWQPTIGRNSTFVGLNRSQKNELGGVEYRAIKLLCLILLVYYVGFHVMAF IFFLPWVLHKHEYKVIVRGDGVSPTWWGFFTAMSAFNDLGLTLTPDSMSSFKGAVFPLTVMIWFIIIGNTGFPVLLRFIIWVLFKLSPDL SSMKESLGFLLDHPRRCFTLLFPSGATLWLLVTLIALNSTDLVLFVIFDFNSSVVEMLTKGRRVLVGLFQGVCTRTAGFSVIDLSLLHPSI QVSYMLMMYVSVLPLAISIRRTNVYEEQSLGIYGSEGNSPDVDGNDDENSDSDSDSDSDSASDSESESDPDLSPRSKRIRKKKRAKK KKAKKKRAKMKKKARKKPSAKSFIGAHLRRQLSFDLWFLFLGLFIICICEGGKIRDRTKPDFNVFSILFELVSAYGTVGLSLGYPGTNQS FSGQFTTISKLVIIAMLIRGRNRGLPYSVDRAIILPSERLDNMDHIQELENKRNADNDVSSGSDPVTLYLKKRIRRVFKGIRRVKDSIQTV EEPLVHKAAEQFSNSEGHEMQDMGNEQYKYTSKDYDHLSVHKKFGPDNSSVEQEEEELNESTPRNDMEYGEVDPSLLRRRSH
5E-170	576	6.8	9E-170	574.8	1.3	2.1	2	J7S4D8_KAZNA	Uncharacterized protein	KNAG0C01310 KNAG_0C01310	Kazachstania naganishii (strain ATCC MYA-139 / BCRC 22969 / CBS 8797 / CCRC 22969 / KCTC 17520 / NBRC 10181 / NCYC 3082) (Yeast) (Saccharomyces naganishii)	910	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Kazachstania, Kazachstania naganishii, Kazachstania naganishii (strain ATCC MYA-139 / BCRC 22969 / CBS 8797 / CCRC 22969 / KCTC 17520 / NBRC 10181 / NCYC 3082) (Yeast) (Saccharomyces naganishii)	1071383	>tr|J7S4D8|J7S4D8_KAZNA Uncharacterized protein OS=Kazachstania naganishii (strain ATCC MYA-139 / BCRC 22969 / CBS 8797 / CCRC 22969 / KCTC 17520 / NBRC 10181 / NCYC 3082) GN=KNAG0C01310 PE=4 SV=1MAASSWGKAMWCRMWPGRRRPQGKSTWRRVRDTLHAVNTRLRPLERHLFPNFVAVHYCYIIVMSLITSVFLYPIHNYRYIDILF TATNSCTQGGLTVVQTNNLELFQQMVVYTACCLTTPIFIHGSLSFVRLYWFERYFDDIKDSSRRDFLRRRTMTLRRRQNTATRSQQR QHTTNNADDNFQENLFSGKMVSRDANNSADGTTGAARAGRGEVTPGDIYQSMRILQQRQPSVSSSSEHSFSRSSSSQRTAGSPYV VPPRYTDAGSTTDYSSTSSPSTASPSSVSPTERMPHRATLQFDIVKPPRTAQKHKGRGRRRLRHKRAAPAALLHRRGHGKRYVYDS NRIVKSHSEGAAPAPAQLNRDPSNRRTFSLPTRQQTTDTYNSNVTGNSDEELGFDIDDDLATFPDERNRRMSANYLSWQPTLGRNS MFTDLTTQQREELGGVEYRATKLLCLLVVVYYAGWHIVAFVFLLPWICTKKHYAAVVRQNGASPAWWGFFTAMSSFNDLGMTLTAD SMMSFTNAVFPQIVMMWFIIIGNTGFPVLLRFIIWLLFKISPSLSATRESLGFLLDHPRRCFTLLFPRGATWWLFITLLALNITDWILFIILD FNSSFVKSLPKGIKVLIGLFQSVCTRTAGFNIVDLSKLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGVYGSAQSFTEWDNSSK KSKDEGEEDEEEEEDSDARGDHFDESSEVESTASSTGRKRGKHKKPSTRSFIGAHLRRQLSFDMWFLFLGLFIICICESDNIQNTNKPD LNVFSILFEIVSAYGCVGLSLGYPDTNTSLSAEFTVISKLVIIAMLVRGRNRGLPYALDRATILPNKKLQRMDEMQNRRNPNANGEDTTV TEDPVTSYFKDKYSNYMHRWDTIKRAATRASVNKDS
1E-168	571	3.6	6E-168	568.9	0.1	2.1	2	G0VAF0_NAUCC	Uncharacterized protein	NCAS0B07960 NCAS_0B07960	Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) (Yeast) (Saccharomyces castellii)	1051	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Naumovozyma, Naumovozyma castellii (Yeast) (Saccharomyces castellii), Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) (Yeast) (Saccharomyces castellii)	1064592	>tr|G0VAF0|G0VAF0_NAUCC Uncharacterized protein OS=Naumovozyma castellii (strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) GN=NCAS0B07960 PE=4 SV=1MTLNRRLTNVSTLSNFQALYKKTFGHKFRDALDATATKLQPIFKHIFPNFIAVHYCYIIMVTLLSSILMYPVRNAKYIDILFLSAGATT QGGLNTINANDLVLYQQIIIYITCCLSTPIAIHGCLAFVRLYWFERFFDNIKEKSKLDFKRRRTQTLIQRDLTAQMNSRNASSQLSAAEGK FKRVRKPLHFINKGAKRLDPRNYTPNDYEDFQDKLFSGKLLHRRETDFSNIQRMKQNQNQGQNQDQNQDQNQYIDKSTSSSSSSSS SVGQSDESSIVSSEFQQEPASPRERFVGRRKSSDIRPDDIYRSIILMRNQQELEEDRENDEQSATLPPRNEQDNTVGERDSLQATSN NSEENIKPVRGEPTIQFDIVKPPRRNLPSKGISKNLYVNHPKERVSQFPGVSSKRLRRNKEYTPLRLRQHLLSKRRQIKKTSRKNFSLT PRGQTINFQPFGNEGLTTSFILRKQFTEDASRGGTVTDSTTSNTPAPFNPENPNEVNKTLASAPHPLSNTFDEDGDLGTLDTSMTDN EDYSLHFDESAFESPIADRPLSRTMTTNYLSWEPTLGRNSTFYGLTKKQKEELGGVEYRAIKLLCTILVIYYLGFHIMFFVMLVPWICLK NHYGALVRRDGVAPAWWGFFMAMTAFNNFGLSLTPDSMISFNEAIYPLLLMMFFMVIGNTGFPIMLRFIIWVLFHLSRDLSSLKESLG FLLDHPRRCFTLLFPSPATWWLVLTLVVLNGADIILFIILDFGNEILKPLSHGFRFLVGSFQSFSTRTTGLSVVDLSKLHPSIQVSYMLMM YVSVLPLAISIRRTNVYEEQSLGVYSSRDNTDADEAENVDAHDDDDEDREEVGGGSTSSSKDEESSIGEEPKPIKRPTKKKETTRSFIG DHLRKQLSFDLWFLFLGLFIICLCESGKIQDTNEPDINVFSVLFEIVSAYGTVGVSLGYPNTTTSLSAQFTTLSKLVIILMLIRGRHRGLPY SLDRAIILPSQRLEHIDHIEDLKLKRRMHRADTTDPVTGQLRQTVHRLKKNIHLLGETLWKRKSESSSTGDQ

3E-166	563	16.1	3E-165	560	3.8	2.1	2	I6ND35_ERECY	Uncharacterized protein	Ecym_5208	Eremothecium cymbalariae (strain CBS 270.75 / DBVPG 7215 / KCTC 17166 / NRRL Y-17582) (Yeast)	1196	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Eremothecium, Eremothecium cymbalariae, Eremothecium cymbalariae (strain CBS 270.75 / DBVPG 7215 / KCTC 17166 / NRRL Y-17582) (Yeast)	931890	[illegible] 17166 / NRRL Y-17582) GN=Ecym_5208 PE=4 SV=1MGLVRTLSRNPSVQFFQSTYRKTIGHRLRDAISTLTHYLHPIIKYLIPNFIVAHYCYIISLTIICSILIYPVKNWKYIDVLFLSAGATTQG GLNTVDLNSLVLYQQVVVYIICMISTPIWIHGALVFVRLFWFERYFDGIRIWSKKNFEMRRTRTLVAREMSRTMSSGKGRKNPESGRR LSFRTSTGVSDFQSKLFSGKLFTRDGDVNSDVNGNKHRNSGTYQNGEGSNHQSPLSKGKSELPSNFSSGSSSNMTEEHVRGENAD TKDNVTKSKKGFVARRGSRDINPADMYRSISILQKQHQQEVEDDGPALIIKGPIERLNELEEESETEKNRDTSKKYTGGVGKSALDSY NITNSLQEKSHGLVEERYSPTSKISYNSVDLPSTDPKNKQNASLRDSLDGEEGIPDHFSTISRGTRISESGTNANNAPGLSIQFDIRNLP RPSMKKSLQRVDSNNTALNDSLTSKKIRRPSLFRKFSTPGLLRDRLHGSSTTSAADEEDGNDADLEFTDDEEALQSTTDSDYTLKPRV IDSAADQHASFLEQMDSSKKHRPNVVGDSGRKPSGTMHQRKLQASHSFSKMAGNRLPQVPSLKKRRTQSATTMMSHTDTLNSIDS HSNFYDEEVGYSDLEEPALNSVMSSNYLSYAPNVGRNSIFVGLTDTQKIELGGVEYRATKLLCKILTVYYFGFHIIAVVLLLPWINSTKK YKEIVKSNGISPTWWAFFTSLSSFNDLGLTLTADSMASFNAAAYPLIVMIWFIIIGNTGFPILLRFIIWIMFKLTPDLSLMKENLGFLLDHP RRCFTLLFPSAATWWLFLILILMNGLDLILFVIHDLNSTVLNGLHPGYKVLDGLFQAVCTRTAGFSVADLGKLHPSVQVSYMLMMYVSV MPLAISIRRTNVYEEQSLGIYGDMIPVIAENYSKSTSESSSSSTTESEPKTPEKETMSFVSDHLRKQLSHDLWYMFLGLFIICIAEGSKIQ DRSKPDFTIFQVLFEVVSAYGTVGLSLGYPGTNQSFSAQFSALSKLVIIAMLIRGRHRGLPYLVDRAIMLPSDKLKRIDLLEDLKLQRTM TTINSNKDPLLQYWKRRTRSISHGIFNAINRSKSHTCQSNQDVSHYKEAISLDTIPSASSSTTNFHSKATTNLRNDSMAGGGILRRTSS ETYSPGIFCENDNRPHAIDDTRANPEDLVNRHDNTTGASD
3E-166	563	0.5	6E-165	559	0	2.1	1	C5DV25_ZYGRC	ZYRO0D03322p	ZYRO0D03322g	Zygosaccharomyces rouxii (strain ATCC 2623 / CBS 732 / NBRC 1130 / NCYC 568 / NRRL Y-229) (Candida mogii)	1304	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Zygosaccharomyces, Zygosaccharomyces rouxii (Candida mogii), Zygosaccharomyces rouxii (strain ATCC 2623 / CBS 732 / NBRC 1130 / NCYC 568 / NRRL Y-229) (Candida mogii)	559307	>tr|C5DV25|C5DV25_ZYGRC ZYRO0D03322p OS=Zygosaccharomyces rouxii (strain ATCC 2623 / CBS 732 / NBRC 1130 / NCYC 568 / NRRL Y-229) GN=ZYRO0D03322g PE=4 SV=1MISRTISRNPTLATFSVKYKESFGRKFRDAVAKTGHYVKPLRKYLFRNFLMVHYFYIISMTILASIILYPVRNESYIDILFLATGSTTQ GGLNTVNINELELYQQIIIYIFTFLTTPIIIHSALAFVRLYWFERHFDGIRDSSKRNFKMRRTKTLLERELTARTMSKGRQRTGTRQFTSP TRRHDDFQEKLFSGKMVNRDEQDSLADLSHGGNGSSDQSVPNGKSFADPHRLSWSSSNTIEDNAEIHPSGRGLLFREPKPKRHQH YSHGNNNPQQRPLESFARRRRSTDISPEDMYRSISMMKGQRQTNTEDDGPALVIGAPAERSNDKDAAKLDAEKSDLKKKASYDSLR QNKMEKYPIGLPNKSDEEDFENEDEEDDDYNNDQTENSNSTSSSTSTTSNSSSVDNQSDNSPPIPSGSSTGSDSMHSDSVTSNAVT TDDRETMNEADSMSSDHSQPEFPQENRNGPSIHFDIAAPPKRKKLRDQPNLTRKSRRSHYSPGVPIPSAKSISQRLKRRLSLGPMEK PRAKTTRSSGDINTMNNSDDYFSKDGMSDHFPRANTFDQQYDLQDDNFPDVLSKSHSFDLGKTKDWNKLSTSPEFQSMIYEKWKR EKRGRKSILRPKIRRPSINSPNISGLRRFYSNPENNDDGNNTTEELPTDSVRHEHSDNDLTDEENDHGNFVNTRDSLDEEEGYFGNDL SFADDPSRHKLTRTLSANYLSWEPTVGRNSIFVNMTKEQKEELGGVEYRAIKLLCRILVVYYGGFWIMAFIFLVPWIVSRDGYRKIVRN DGVTPVWWGFFTGMSAFADLGLTLTPDSMMSFQTTSYPTIVMMWFIVIGNTGFPVLLRFMIWVMFQLSPDLSLTRESLGFLLDHPRR CFTMLFPSAATWWLVATLVGLNAIDLIIFVILDLGNSVLHNLNRGYRVLVGLFQAISTRTAGFQIVDIGSLHPAVQVSYMLMMYVSVMPL AISIRRTNVYEEQSLGVYGDPDEDASHHGHELDSDDDESLGSSPSPASKKKKKSTTSFIGAHLRRQLSFDLWYIFLGLFIICLAEGGKIQ DERRPEFNIFTILFEIVSAYGTVGLSLGYPNSDTSFSGQFGTISKLIIIALLIRGRHRGLPYTLDRAIMLPSDRLDNIDKFQDMLMRHRASR EGSTDAVTSYFRSKLSAIKKEIHKMRTKSAEGEHLLHDFTDLPHHDNGDSRGDNHQERPSEAASDGYNTNYNNNKSADHVLDIHEEP KEVSKSPNDSSLQPQEPISYFPNTTPSPRKASDELSPSDPLSTIPSQGTPTSRVAPSLESYRMKPLDSARTN
6E-166	562	2.9	6E-166	562.2	2	2	1	C5DKM4_LACTC	KLTH0F05896p	KLTH0F05896g	Lachancea thermotolerans (strain ATCC 56472 / CBS 6340 / NRRL Y-8284) (Yeast) (Kluyveromyces thermotolerans)	1146	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Lachancea, Lachancea thermotolerans (Yeast) (Kluyveromyces thermotolerans), Lachancea thermotolerans (strain ATCC 56472 / CBS 6340 / NRRL Y-8284) (Yeast) (Kluyveromyces thermotolerans)	559295	>tr|C5DKM4|C5DKM4_LACTC KLTH0F05896p OS=Lachancea thermotolerans (strain ATCC 56472 / CBS 6340 / NRRL Y-8284) GN=KLTH0F05896g PE=4 SV=1MQAWKTLSRRPTLASINITYHKTIGHRLRDIIEYVGNVTHPFVKHIFPNFIAVHYFYIITLSIIGSILIYPIKNFAYIDILFMATGAATQG GLNTINVNDMTLYQQIVLYLICCLATPIWIHGVLAFVRLYWFERYFDGIRDWSKKNFKVRRTKTLIQREMTRTATEAQRRHKTAGRANN DFQSKLFSGQMIKREEQGGVKENYEMNSLKDAPTGGSEHKDPHTSSSTGTTKSDQEDSPAIKFGDMPKPHKSPKKPADIEMFSGRR RSEDITPADMFRSIAMLQNRHNEEEEEHDGPALVIRGPAERRQGSDPSWASVPHSGNIEETKDKDSRKPATHSINSPSSAARSPSFH KEADYSPTQWSSQNESRPRTPSSIQFNIGMVPSSKPGNPQYHSSNRKKLNTRIMKKLTPRNRLRKRLRKTASNTDEDGNDADFEQD SLTSGTDHDQDEESLASFGLSSQHSSQAPNMEKVQSTLAVPSGDATGGSKFYKRSLTMEAPGNSDWDVLTKSPSFQKMIYNKWKD ERRRKKGVIHSAYRRPSLAHSTSELDSGFNLGHDARTMTDEALFGNNHDEEYFGTTFEEPTDRPRLKRMSTNYLSWQPKIGRNSTF VGMNEIQRAELGGVEYRAIKLLCKLLLLYYIGFHVMGMVMLLPWITQMKHYAKLVREDGVAPAWWGFFTAMSSFNDLGLTLTPDSMV SFNKAIYPLIVMMWFIIIGNTGFPVFLRFIIWVMFKLSPELSLIKESLGFLLDHPRRCFTLLFPSAPTWWLLFILVTLNAIDLILFIVLDLNSQ VVEGLTSGFKVLNGLFQAVSTRTAGFTILNLSKLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGIYDNGGDDAHHKDSSSDSQS EDERNLEKSAKSFIGAHLRRQLSFDLWLFFLGLFIICISEGGKIQDTNKPDFTVFQVLFEIVSAYGTVGLSLGYPNTDQSFSGQFNTFSK VIIIGMLIRGRHRGLPYSLDRAIILPSQSLERRDQLQDLKQEQHTTEAKDPIVDYLRRQSRSAKGQLRSLLSRRKRPTSDESVPLRSFSN HENLRQPSASNVSNLSPAPRSSPRSQSLSQGDAETYGGEESSSISSDFQDMAASGSSIGPRNEEVPHFSDEPPTALEGPRAFEPNT
9E-166	562	11.2	4E-165	559.5	2	2.3	2	G8BPQ3_TETPH	Uncharacterized protein	TPHA0B03120 TPHA_0B03120	Tetrapisispora phaffii (strain ATCC 24235 / CBS 4417 / NBRC 1672 / NRRL Y-8282 / UCD 70-5) (Yeast) (Fabospora phaffii)	1395	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Tetrapisispora, Tetrapisispora phaffii, Tetrapisispora phaffii (strain ATCC 24235 / CBS 4417 / NBRC 1672 / NRRL Y-8282 / UCD 70-5) (Yeast) (Fabospora phaffii)	1071381	[illegible] NRRL Y-8282 / UCD 70-5) GN=TPHA0B03120 PE=4 SV=1MAIRRTLTRVSTSVSVYYKKTLGHRIRDYISNCGHYFHPIKKYVFPNFIAVHYAYTILITILGSILMYPVRNHKYIDILFLACGAATQG GLNTIDVNSLTLYQQIIIYIMCMISTPIFIHGSLAFVRLYWFERHFDGIRTSSKRDFKMRRTRTILNREITARTMSRGRFDTINSHNITKNTP NDKNPINFQEQLFSGKLQIRDNEKASESDSDANARNSSSKQSAANELREISGNDIEPVGSSGAGKLQFVASNTSNQTQILGRRDSTDI SPADMYRSIAMLQEQHQEREEDDGPALVIGAPNEEKIVEKDNVPKLYPVSSQDELCLENNSNDNIDAQNIKRVLEPGETRDISGNKIKS ENINSTIGSDLNSLKSIRMYNRKLSTDSNPTTQSSNNDSEICDDSRSDASNGSSTINHNKLEYVSRHFLNNKEYQKTKHLHSNNIPLEQ TMTNDDDSVVTSESSNSDYSASSSVAIESNSMVEMQTLDNNSTYDDSPAESSKPSLKNNEESNSEDDLSNHIETSNRNTPRIQFDITE PPRKRRTTSMYQDISPSPKSYKKSYKPHRTKFLRHIPKGDRIKKRIKRTITNNSFDKNKFDFSFSKSHPGNRGLYNAEGAEVEDSFSNK LASEEGSLNSINSAGNNGKNDEHTIHDLTRARTFDVLDNIDLQKLSESPEFQKAVYENWKNKHRKKRSISRNDYNDTGDNNLFHNTLN ESSGEISPNNTKEVIDYFSPSSLHYSRLPKKLDRRSSKENENDFNFMADSNTPYRLHFDPDYALPHQKPKLSRSMSTNYLSWQPVVG RNSTFVGLNSFQKNELGGVEYRATKLLCLLLLIYYIGFHIITFIFLVPWIINRKYYEHIVRADGVSPAWWGFFTAMSGFNDLGLTLTPDS MISFNAAIFPLVVLIWFIIIGNTGFPILFRIVIWFVFKLSPDLSAVRESSGFLLDHPRRCFTLLFPNAATLWLLVTLIALNATDLILFIIFDFGS AVVKDLSKGRRVLVGLFQGVSTRTAGFAVVDLSKLHPAIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGIYSADSGFPEETFEDLSDS SSSSDESDATEGSNLVIDKSERKRLAKIKKEKKRKRKQKRRREKELKKRKNSTKSFVGAHLRRQLSFDLWYLFLGLFIICICEGSKIQDD SIPSFNIFSILFEIVSAYGTVGLSLGYPNSNQSFSGQFTTLSKLVIIALLIRGRARGLPYSVDRAIMLPSGKVEDMDHLQELERIKPRRKSY IAVSPTDDENMANLDTILEEPGDSEPEDPLNTYLKSSIKKASKSYHKVLNKITGSKQKKGHRHHHHRHRHDDNEHNNNNDDNNNETNT KYQNTSDQYGDQQYEYLVNGDIDEENHISPNEIIKGNSKLKSDIYETMAND

4E-164	556	6.6	4E-164	556.3	4.6	2.1	2	C4Y9A0_CLAL4	Putative uncharacterized protein	CLUG_04778	Clavispora lusitaniae (strain ATCC 42720) (Yeast) (Candida lusitaniae)	966	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Metschnikowiaceae, Clavispora, Clavispora lusitaniae (Candida lusitaniae), Clavispora lusitaniae (strain ATCC 42720) (Yeast) (Candida lusitaniae)	306902	>tr|C4Y9A0|C4Y9A0_CLAL4 Putative uncharacterized protein OS=Clavispora lusitaniae (strain ATCC 42720) GN=CLUG_04778 PE=4 SV=1MGLKSIRKFRKEVVGTTFGHTLRNIIGKISGALHPYVRKVVPNFRTAHYVYIISMVFISSVIVYPISNFEYIDILFLMSGACTQAGLNT INLNELKLSQQILVYIITTLTTPIFIHSSLLFLRLYWFERHFDNIKETSKLDHRMRRSATSMARTTSIDPTLVNTVNNSNLGYQEGRFRNED VAQREKTTSPVHVPTTQPEDVSEVEAIDIERTPTPVDHLESSPQKTSASTPEETNGQSTMYSQPSDPASLAEPIPAHIDENKDKIKFGD LPHPSKRRKEFDPSDMYKSIAMLQNNRSDSAAEDDVLVIKSPKEIERDNNTPIYIKKSSTPKKRRKWGVKNLRKKHTWETIRRNSSSGI RRRFSSNSLNENESIDSEDEDNRRRSGFIDDVLDTDNDAETDHNAENYSVFSETSANDDEDDDEVDQKSDSIGPKDTSHLKFAAAPE RHPRPRKTRSRRLSRWRTPTLSRHHTQGTDECSNVDTDDEEPSLSEGEHLRHVMSANYLSWIPTIGRNSTFVHLTEEQKEELGGVE YRAIKLLIKILVVFYIGFHIVAFCLFVGFIKVAKGYAVKMRELGFSPVWWGFFTAQSSFNDLGLTLTPNSMMTYSRSIYILVICSFFVVIGN TGFPIILRFIIWIMFKFARPMSLLKESLGFLLDHPRRCFTLLFPSIPTWWLLFILVVLNATDLILFIVLDFGSEYLSPIPKGLRVLDGLFQAFS TRTAGFSVVDLSQLHPSIQVSYMIMMYISVLPLAISIRRTNVYEEQSLGIYATARDEDATEETPKNFIGSHLRNQLSFDLWYIFLGLFIICI AEGGKLKRNDYRFTVFTILFEIISAYGTVGLSLGYPNIDQSLSHEFTTISKLVIVAMMIRGRHRGLPYSLDRAIMLPDADMQRRDMMQET HAQRTQRVDSISTHSNNDASTIDRLNGLRKTITRKAAAYRKNSLFPAPTKLPEDFYEMNNYPRSSR
3E-163	553	7.2	6E-162	549.1	0.9	2.2	2	S6EYC3_ZYGB2	BN860_05622g1_1	BN860_05622g	Zygosaccharomyces bailii (strain CLIB 213 / ATCC 58445 / CBS 680 / CCRC 21525 / NBRC 1098 / NCYC 1416 / NRRL Y-2227)	1294	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Zygosaccharomyces, Zygosaccharomyces bailii, Zygosaccharomyces bailii (strain CLIB 213 / ATCC 58445 / CBS 680 / CCRC 21525 / NBRC 1098 / NCYC 1416 / NRRL Y-2227)	1333698	>tr|S6EYC3|S6EYC3_ZYGB2 BN860_05622g1_1 OS=Zygosaccharomyces bailii (strain CLIB 213 / ATCC 58445 / CBS 680 / CCRC 21525 / NBRC 1098 / NCYC 1416 / NRRL Y-2227) GN=BN860_05622g PE=4 SV=1MISRTISRNPTLATFSQRYRDSFGKKLRDAIARFGHYVKPMRKYVFRNFLIVHYTYIITMTIVASIILYPIRNEKYIDILFLAAGTTTQG GLNTVNINSLKLYQQIVIYVTTFLTTPIIIHSTLAFVRLYWFERHFDGIRDSSKRNYKMRRTKTILGRDLTARTMSRNWQRSGTRQFTSA SRRNNDDFQEKLFSGKMLHRDEQDSLPDSQNDRGRASKSSQGLGPDDIQRSASTKLQDDQNLHSGRGLSFKEAKPIRDNHHHQPY ERFARRRSREISPEDMYRSIIMMQGHHQPNADDEGPALVIGAPGERSSGKSGVTSTKSEPEENKVDSPENTNERRPTHWANKNVSD GGESLTHDVNNQKGNPINGSFDINSNHSELMSDAEQQSNPFAASSVDSYSTFSGNSGVSSGSLTSDDRRTIGAADTSSSVRPLARFE TPRQGINGPSIHFDISAPPSKRPDRNRVRKNRSNGSRSGFSMPKSKTLGQKLKRRLSFVDKPRMRSRNSFPDRSFEDPGRNNMENM DDYFADDESDKEDDHHSRVERQTHFPRSNTFDQRFSHSQDYLDVLGKSKSYDLGQTQDWNKLSSSPEFQKMIYKDWKRRHKGRK SLLKHRRRMETLNSRTGFKKFYSDPESDYGDSNSQYSPKGHAGSPENNEGEEHFGDTSMESRNSLDEEAGYFGPNDLGFVDSGPG GLSRSYSANYLSWEPTIGRNSTFVGMTKEQKEELGGVEYRAIKLLCRILVAYYGGFWIIAFLFLVPWMVTRHEYKKIIETDGVSPAWW GFFTGMSAFADLGLTLTPDSMQSFQKTSYPTIIMMWFIVIGNTGFPVLLRFVIWLMFQVAPDLSLTRESLGFLLDHPRRCFTMLFPSAA TWWLVLTLVGMNAIDLVLFIILDFGSSTVHYLTHGYRVLVGLFQAISTRTAGFQIVDIGDLHPAVQVSYMLMMYVSVMPLAISIRRTNVY EEQSLGIYADPNEEEEEEAQQMVSSDEGNESESSTSTQAGNKKKKKKKRSNTSFIGAHLMRQLSYDLWFMFLGLFIICIVEGGKIRDN ARPDFTIFAILFEIVSAYGTVGLSLGYPNSETSFSAQFNTLSKLVIIALLIRGRHRGLPYKLDRAIILPSNRLDNIDKQQEVTLRNRLARGTK PGDPVTAYFKSKTAAIKRGLLKIGKTAAEPEEHLLQEFNDHHTSGEDSENQETHEEHRAHGADEAHGANEAHEVHEIQEAQDSKGDS SPQESSSQPQEEAKAYVAQENASSSGTTASKRQSSDPYSTVPDQGGKSAHSVPSLRTYRLRRTNST
2E-162	550	10.6	3E-160	543.5	3.6	2.1	2	S9W3X5_SCHCR	Potassium ion transporter Trk1	SPOG_03771	Schizosaccharomyces cryophilus (strain OY26 / ATCC MYA-4695 / CBS 11777 / NBRC 106824 / NRRL Y48691) (Fission yeast)	831	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Schizosaccharomycetales, Schizosaccharomycetaceae, Schizosaccharomyces, Schizosaccharomyces cryophilus, Schizosaccharomyces cryophilus (strain OY26 / ATCC MYA-4695 / CBS 11777 / NBRC 106824 / NRRL Y48691) (Fission yeast)	653667	>tr|S9W3X5|S9W3X5_SCHCR Potassium ion transporter Trk1 OS=Schizosaccharomyces cryophilus (strain OY26 / ATCC MYA-4695 / CBS 11777 / NBRC 106824 / NRRL Y48691) GN=SPOG_03771 PE=4 SV=1MAFTKVQRWIQWIVPNFGFLAVHYFYIILLIIISSILLFTGGSKISYIDALFLASSSVTQTGLNTLNLIDLTTWQQIVIFLFPIISVPIWM HGAISFVRLYWFRKKFKYVIKQNRTRRCQRKLRQKQLKQEKQNEEQGVRGRKIQVLLPHQADDNLNPAPTFGNLDITSTENPQESIFF NPPSISPKAKPKEQETDVPATLSVQEVSDIDLEDPETNHAVNFSSEFSSKTPYIAEEIEMDDLHPRLRRQNSVLTTLMNTNDDIRETQS YSEKGLPPVPMSCCLSDTNLLNLQDTPVDSSLPASDNKASITIYEPKRKLYPESVSSKSDNPSREDVHIAFTNLHKPTLERKRQEDLIEN KKFFQKKPARFRRMSAPMRWTKSLNVNPRSLTFERVLSSAFGRRREGTISSSRSTVMSLPYLSYNPTVDRNSAFVALSREQRDELG GIEYRALKCVCTMVLIYFILTNIIVFVIFIIFSYTAHGSYLIIDSLKLKRGWWALFTSISSFNDLGYSLSPSSFSPFNKNIFLLLISSLFIIAGNT GFPCFLRLFIWFFYKVLPLSQEKKEAMAFLLDHPRRCFTLLFPSGSTWWLFFILLGLNAIDLILFMSLDIKNESVVGLPRGIRVVNALFQS VCTRTAGFTSVTLSELHPAVLVTYLIMMYISVYPVAINMRNTNVYEERSLGVYTFDEEEHKSFLKDHLTEQMSHDLWCIFLGLLIICIEG GKIANSNDTDFTIFTVLFEIVSAYGTVGLSTGLSDSQCSLSARFTKLSKLVIIALQIRGRHRGLPRAVDRAILLPSEKNNLKEEEDHRRRQ ELSRTISYSRASVSAFRD
3E-162	550	0.5	2E-160	543.9	0	2.2	2	I2GZP6_TETBL	Uncharacterized protein	TBLA0B07820 TBLA_0B07820	Tetrapisispora blattae (strain ATCC 34711 / CBS 6284 / DSM 70876 / NBRC 10599 / NRRL Y-10934 / UCD 77-7) (Yeast) (Kluyveromyces blattae)	1468	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Tetrapisispora, Tetrapisispora blattae, Tetrapisispora blattae (strain ATCC 34711 / CBS 6284 / DSM 70876 / NBRC 10599 / NRRL Y-10934 / UCD 77-7) (Yeast) (Kluyveromyces blattae)	1071380	>tr|I2GZP6|I2GZP6_TETBL Uncharacterized protein OS=Tetrapisispora blattae (strain ATCC 34711 / CBS 6284 / DSM 70876 / NBRC 10599 / NRRL Y-10934 / UCD 77-7) GN=TBLA0B07820 PE=4 SV=1MNLRRTLSRAPTFASISLEYRKTIGHKFRDLIATCDKSISPIKKYIFPNFIAVHYFYILMLTILTSIMIYPVGGHKYIDILFLSTGATTQG GLNTVDVNSLSLYQQMILYISCTFATPIFIHGFLAFVRLYWFERYFDDIKATSKRDFRLRRTKTILERELTARTMSQNRNRTFSKFGTRT LTRGRSGNSRSEDFQEKLFSGEMVNRDEFQTRDKYHENEENEHIHIRSRNPGGIVFEENHPIRRNRRTGEQFEGRRNSTEITPADMY RSIQMMQNQHHDNDEEDGPALVIKSPTENNRFNNSDISLNRVHSVVYEDSGSTADNIREGSEEDEEQEEDNSEDMSSNENEEEMDD ISIVSELSIPRRSFDSNNHLYNDADADADISFSTNTFEASSLVHLADESDNTNQSSRHFLVNNNHDISDDDADEEEEDDDEEEGDGDDN EEEDNIGDELSNEEISKTLNNTSGEEEGALADEDVTIGGYTSGSIQSILSRGLEPLSNYSRNDSLGDAHSNISSINFGSESNSYTNSTNI PSSSITSSEHSKDQASQLDAGPAVTFASNVARPNRRNIEQYTPTAIRNNGPSIQFDVSEPPSTRRRRLSSRNHATDAYISPTRGKHKK KSSKGLFKRIPKGGKIQRRLKKRFTNNSFETPSHIKKSKHTSMSENNGRLHSNTDDMDEYFADNESDENIPHRAEQDYSYSTDAEDE EYDFFSGLQQSQSFDFDNVNSDLSYLAKKRDFQDAVYKNWKAGHKGKNKFSRNWNPSERAQFLHPIRTMTQEFGLNQEQDYDTH GKQNYRRARRPTSVRTQSNTDDDFNFPSRRMSIADTEQGDYTLHFDHDFNLAHPNRALRRRKSYLSYTPTIGRNSTFAGLNKSQRN ELGGVEYRAIKLLCIIIAVYYFGFHVCSFVMLVPWISLKPHYKKIVREDGVSPAWWGFFTAMSAFNDLGLTLTPDSMSSFNSAIYPLLV MAWFIIIGNTGFPILLRFIIWILKIFSPDLSQMQESLQFLLDHPRRCFTLLFPSGATWWLTIILVGMNLTDLILFIILDFESNIIKPYSTGTRTL IGFFQGVSTRTAGFSVTDIRHLHPAIQVGYMLMMYISVMPVAISLRRTNVYEEQSLGIYGQGEPDTSDDEGTEEDSEEESDDNNEEED DDEDDDEEEEEEEEEEEYEEYDNLSRASSQRTKRKKKKALRKAKKRKRAKEKKAASHIGTHIMMQLSFDLWFLFLGLFIICLCEGGK LKDSTKPDFDIFSVLFEIVSAYGTVGLSLGYPNTNQSFSAQFTTLSKLIIIALLIRGRHRGLPNSVDRAIILPSERMEHNDHVAAMKLQRK GRTESTTDPITLSLRKRVTQLSTGFKNVKGIFPAFNAKEKSPVSDVELQDYNNYNQYDEDQLITEQQQDKRSRKRSRPINADEEDSGS NSLWGNNPNYFTTATNSIDFKPQHWTHSHNGLNNIESPYNSYQSESPRHLE

3E-162	550	14.5	1E-161	547.9	5.5	2.1	2	A3LXW3_PICST	Low affinity potassium transporter	TRK1 PICST_61578	Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) (Yeast) (Pichia stipitis)	1024	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Scheffersomyces, Scheffersomyces stipitis (Yeast) (Pichia stipitis), Scheffersomyces stipitis (strain ATCC 58785 / CBS 6054 / NBRC 10063 / NRRL Y-11545) (Yeast) (Pichia stipitis)	322104	[illegible] NBRC 10063 / NRRL Y-11545) GN=TRK1 PE=4 SV=2MLDTIKKYYATYRRKRLESEVGLRVRNQIHRLSSVLGPTVKVLVPNFRAAHYCYIIFWVFFGSVLVYPVRNLRYIDALFFTGGASTQAGLNTVDTNTIALYQQIILYIIATFTTPIFIHGSMLFVRLYFFERHFDNIKEKSKLNFKMRRQATIAARTQSMDATRLNTFTNQNLGFDKSKRNNNRGDNVDKEQKDNGLHTVDVEMANNSSPQSSSTFHGDVEHIDEPSDSDEERGRRAPDDIRLNDLNPDSPHDAVRFGNLPQPSKRARSKELDPSDMYRSIALLQDSHNNSTRNLDDDDEVLVIKSPNEIEKTGGRIYTKRKPKSHRPSGSSGSKPWKKGSKWSNRLRKTFSNSGSSSTPKTKRSYSTASEEIVDDDASIDSENEVVTTDVADDDDENDHDYNHNDNNDDDDDDEEAVDDEDSVNDGDVEDDANPESPRKEGPTTHFAEPANDPRRKRPNLLDVPNGSRKHSFVSSPTYEKFEKFKKNIKKGKLKRIKTPGVSQTSSRLFGYNSSIINVDDDSYVDEDAYDEDDEEASYEENEIGPTITKVMSTNYLSWEPTVGRNSTFIHMTEAQKEELGGVEYRAVKLLIKILVLYYIGFHVLAVVLLLPWILMRESYIEVVRTQGVSPTWWAFFTASSAFNDLGFTLTADSMVSFGRSVYVMIVVSFFIVIGNTGFPVFLFRFIIWILFKTAKPLSLYKESLGFLLDHPRRCFTLLFPSVPTWWLFIILVVLNGVDLVLFIILDLNNNYLKEIPVGYRIVDGLFQAFSTRTAGFAVVDLSQLHPAVQVSYMIMMMYISVLPLAISIRRTNVYEEQSLGVYLKEENHEDDEKTPHTFIGAHLRNQLSFDLWFIFLGLFIMCIAEGGKLNNNDIRFTVFSILFEIISAYGTVGLSLGYTGVNASLSSQFSVISKLVIVAMMVRGRHRGLPYTLDRAIMLPDADMQRRDHLQENHAIRRHTTMERENTLGIGGDNILRRVITREGGILFGRRRSSAFAMPSLSENPSYIITSTSQEEQELEAIRNQV
4E-162	550	4.9	4E-162	549.5	3.4	2.5	1	K0KXT8_WICCF	High-affinity potassium transport protein	BN7_6469	Wickerhamomyces ciferrii (strain F-60-10 / ATCC 14091 / CBS 111 / JCM 3599 / NBRC 0793 / NRRL Y-1031) (Yeast) (Pichia ciferrii)	1152	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Phaffomycetaceae, Wickerhamomyces, Wickerhamomyces ciferrii (Yeast) (Pichia ciferrii), Wickerhamomyces ciferrii (strain F-60-10 / ATCC 14091 / CBS 111 / JCM 3599 / NBRC 0793 / NRRL Y-1031) (Yeast) (Pichia ciferrii)	1206466	[illegible] / CBS 111 / JCM 3599 / NBRC 0793 / NRRL Y-1031) GN=BN7_6469 PE=4 SV=1MAGFNIMKLVRPTKTSNNQDQDQDHGNNINPNRRRSIGSINFITKKTWGWKIRDAVASLEDLFGPYLKKIFPSFIAVHYFYIISIAILGSIFIYPVKNIHYIDALFFASGAATQAGLNTLDANVLTLYQQIIIYIFCCLATPIFIHGSLSFLRLYWFERYFDDIRETSKHNFKMRRTATMMARTQSMERAKTAESQRSRTPGNNRSRNLSKTTTNNNNNNNNIPLTGYSSRTVFENSPDIEQTGEYPEVKDSDTSSSEMVNTNPIPLTQSTPAVNQTQSPPRVSSPSPMPMQQSSYNNSVEHISEPSSDDDHENNHLPPESRSINPHRVDDDLNDEVDISHTKSSPNIKFGDLPNPRNHDVEPRDVFMSIAMLSNNQKRETHDDEHEGPALVIGGPAEREPPIRQNSTSAIQFDLKKPKHERKKHLKKSNNHHHRSSFNAFKFGHHQRSHSNASSHSNERDIDSVLDNDYLSDASNDEEHRLKKAQSNLQLPSSDQTGGSKFNKRSNTLDVTSNKHSLLSKSPTFEKMIKQKLKKPILGRRRFSSSAITDDTMDSSGSDTETDDDFDDNSLIRNMTTNYLSWNPKIGRNSTFVNLSEEQKEELGGVEYRAIKLLAKILLFYYVGFHILGFLFLVPWVVVTKNSYQSHIRESGVTLTWWGFFTSMSSFNDLGFTLTPDSMNSFNTSIYTLLVSAVLIVIGNTGFPILLRFIIWVCFKFARDLSLFKESLGFLLDHPRRCFTLLFPSAPTWWLLFILVVMNAVDLILFVILDLNAAVVKALPVNIRILNGFYQAISTRTAGFACIDLSQLHPGVQVSYVMMMYISVLPLAISIRRTNVYEEQSLGVYAGNNENNDEDQQKATQFIGAHLRKQLSFDLWFVFMGLFIICIAEGGKIQDDSLPDFNVFSVLFEVVSAYGTVGLSLGYPGTTPSFSGQFGVISKLVIIAMMIRGRHRGLPYSLDRAIMLPSEKMEIRDRYQDLHAGNHLQRAETIGSMGDPVVTFFKNATPNILKNRFKRPSFLSGSSSQPFRTNTRGNSYVSGSNQNPPQPVQFSLADNQNDNNINSNNIVNNDNHIGFKDVHFGNKPINNHEYNQESHELNDLDYAHLNRENHNDVDQGNLDDGIDQRDYSVTRSETFGGDEATDLGPRRNSNVTF
2E-161	548	5.7	2E-161	547.7	4	2	2	A5DFD1_PICGU	Putative uncharacterized protein	PGUG_01982	Meyerozyma guilliermondii (strain ATCC 6260 / CBS 566 / DSM 6381 / JCM 1539 / NBRC 10279 / NRRL Y-324) (Yeast) (Candida guilliermondii)	891	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Meyerozyma, Meyerozyma guilliermondii (Yeast) (Candida guilliermondii), Meyerozyma guilliermondii (strain ATCC 6260 / CBS 566 / DSM 6381 / JCM 1539 / NBRC 10279 / NRRL Y-324) (Yeast) (Candida guilliermondii)	294746	[illegible] 6381 / JCM 1539 / NBRC 10279 / NRRL Y-324) GN=PGUG_01982 PE=4 SV=2MAWFPSRLRVHQPETPLGMAVRNFISKVASALYPYVSFVIPNFKAAHYTYIIFWVFLGSVLMYPVHNMRYIDVLFLSGGASTQAGLNTVDINNIKLYQQIIAYLVTMVTTPIFIHGSLLFWRLFFFERYFDGIKERSKLDFKMRRNATLAARTRTNESTRNTGTDSSRNAGTTRVNTPITSVDPTEKSAHEPNHGETSLPSSESTGNAEHYSEPSDDDENHPETSAGIRFGNLPQPRKVAVEPSDMYRSIAMLQNNHHDGGDGGDDDDVLIIKSPGEIENDAANPIYTKRSQIQFNVNKSPIKDWKRKRRRRSQWSMLRKTFSNSGSPRHRRRMSASSIASEENDNDENDDDESISDEDETGHHSDYAVTDDDASERDLGIDERMEAGEAHNDHRRRFRKQLRRLTSSGMVRNFTNASTRPESESESDDEFGLGRTMSTNYLSWVPTVGRNSTFVHLTDEQKDELGGVEYRAVKLLIKIIVVYYVGYHLIALAMMWIYISKRPNYQEILRAQGINPTWWAIFTAQSAFNDLGLTLTANSMASFDRSLFVLIVMSFFIVIGNTGFPVLLRFIIWIMFKFAKPLSLYKESLGFLLDHPRRCFTLLFPSVPTWWLFFILVVLNAVDLILFVVLDLNAAVVKSLHSAVQVSYVMLMMYISVLPLAISIRRTNVYEEQSLGVVLRDENHEEANDDSPQNFVGAHLRNQLSFDLWFIFLGLFIICIAEGGKLDNDDFRFSVFSVLFEVISAYGTVGMSLGYPDVNTSLSGKFTTLSKLVIIAMMIRGRHRGLPYSLDRAIMLPDKQMERRDRVQESHALRREQTLERSATIADNPFTRIFTRRGSNTSGLRRRRSRNSTTGYEMEDMS
4E-161	546	7.8	4E-161	546.2	5.4	2.2	1	Q6CN48_KLULA	KLLA0E15335p	KLLA0_E15335g	Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) (Yeast) (Candida sphaerica)	1069	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Kluyveromyces, Kluyveromyces lactis (Yeast) (Candida sphaerica), Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) (Yeast) (Candida sphaerica)	284590	[illegible] / NRRL Y-1140 / WM37) GN=KLLA0_E15335g PE=4 SV=1MIFRKVVRNPTVQNIQIYRKTLGHQIRDIIEKLTKKIDPFVKFIFPNFIAFHYFYIIAFALLCSILIYPVKNFAYIDILFLATGAATQGGLNTVDLNELSLYQQIVLYITTALTTPIFIHSGLAFVRFYWFERYFDGIRDWSKRDFEMRRTMTLRQRELTKNNTMENASRSTGQGPLNFLTRTFTHGDRDASNFQGRLFRGEVVKRDEDNNDDSSVDTRPPEAHSDHTEKFIGRRKSRDINPADMYRSIAMLQNRHESNDNIKGPALVIKSPAEREKEIEEQRRLQKEREEQQGQSIQFKVEPRPTKSTRSTFEPSGIRKSFTRRKRPSFFKGSQSARIIRDKLRRRSKGSDVNNVDDEEEEQDGHDADMEGSSEDDSVIESSDGQSESISAPNFDHHSSEPTLQSGGTVSAPSSLESNEIEEEEDEELSDLPTGVSYYGLHSGGDPRNRLNRVMSTNYLSYEPKIGRNSTFVGLSESQKVELGGVEYRSTKVLCLLLSIYYLGFSILAMIIFAAWIQPMNNYKEIVRSQGVSPTWWGFWTGMSAFGNLGLTLTPNSMISFHKSIYTLIWMMWFIVIGNTGFPIFLRFVIWILFKLSPDLSLRKDSLGFLLDHPRRCFTMLFPKAATWWLFLILIGMNAIDLILFIILDLNTDVVKDLTAGFKVLNGLFQAVSTRTAGFAVLDLSQLHPSVQVSYMLMMYVSVMPLAISIRRTNVYEEQSLGVYGNGENQEDDGSEKNTKSFIGAHLRRQLSFDLWYMFLGLFIICIAEGGKIQDPSKPSFTVFQCLFEVVSAYGTVGLSLGYPGSNQSFSGQFTTISKLVIIAMLIRGRHRGLPYTLDRAIILPSAKLKENDLLHELTHSRRPTTLGLNGSTSHDNRTTSVADSTSSIGNKHIDRFRDRSRSVWHGLTSAFSMGHQPRPHRTMTSRSLDDTITTDRMMSTQSNQSFNNESQQQTFSDGNNYPMHSMNSNHHYDNRSMTPNQYHVFRDSFDLRSGITEHKGLDGVHANTVEAFDHSNYNSNSNSNSNSNSNSKNTETSSSGPIFNHINSSTSLHSPHSTGSMQSLNSSPR
5E-161	546	4.6	5E-161	545.9	3.2	2.5	2	H2AXK6_KAZAF	Uncharacterized protein	KAFR0G00730 KAFR_0G00730	Kazachstania africana (strain ATCC 22294 / BCRC 22015 / CBS 2517 / CECT 1963 / NBRC 1671 / NRRL Y-8276) (Yeast) (Kluyveromyces africanus)	933	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Kazachstania, Kazachstania africana, Kazachstania africana (strain ATCC 22294 / BCRC 22015 / CBS 2517 / CECT 1963 / NBRC 1671 / NRRL Y-8276) (Yeast) (Kluyveromyces africanus)	1071382	[illegible] CECT 1963 / NBRC 1671 / NRRL Y-8276) GN=KAFR0G00730 PE=4 SV=1MESLARRFSIVPGNVRESISVRYRKTVGHKFRDYVGNFTKKTEFIRKHIFPNFIVVHYFYIITIAILASIFMYPIHNHKYIDILFLASGAATQGGLSTVNLNSLTLYQQIVLYIACNISTPIVIHTALAFVRLYWFERYFDDIKNIAMHGFQKRRAMTLLGRQRTQQSKELQGQESSSSTDTSNSSSSNSSNESNFQQNLFSGKALQRKQSTATTGTQQNQTSQNSSENSTDSSESDYPSIKFAGRRATNEMSLQDIYRSVLMLHEKRNSRKQNNPPEEQHASSSTLPPASSNASTSSLQDSNKNSPGSLSFSNKNESQGLPNNTKLTFDIVKPPTRKRVRKGNIGRKQFYYSTRHGSGTKINLSKGMRPSRRPQSENIAMLRHETSSIDPLCQSNSLPEVPNKKSSGSFKRWNTKIFSHFNTPTNTTSLTSDAESVPSEHPIDFEDNSFNFNILKNRPLSRTMTGNYLSWQPTYGRNSVFIGLNRQQREELGGVEYRSIKLLCLILVLYNVGSHITAFTMLLPWITTKSKYATIVKQAGATPAWWGFFTAMSCYTDLGLTLTPNSMQSFTNAVYPQLVLMWFITIGNTGFPVFLRFIIWVLFKVIDELSPISECLGFLLDHPRRCFTLLFPSAATWWLLVTLLGLNITDWLFILIDLFGTEVLKPFSKGIRVLIGLFQAVSTRTAGFTVIDISQLHPSIQVSYMLMMYVSVLPLAISIRRTNVYEEQSLGVYEGFNELNTDDLKNYINNENSESKDDENDSPDTKKKVSAKSFIGAHLRRQLSFDLWFIFLGLFIICENGKIQDVNKPAINVFSILFEVVSAYGTVGLSLGYPGTNTSLCGQFTTLSKLIIIMMLIRGRHRGLPYSLDRAIILPSDKLRRFDVAEDMKMKRRTVAPDTNDPATGYVKETIGKYKKGVKKLRKFFTVSNQE

5E-160	543	3.4	8E-159	538.7	0.3	2.1	2	Q6BYD8_DEBHA	DEHA2A10340p	DEHA2A10340g	Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) (Yeast) (Torulaspora hansenii)	1050	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Debaryomyces, Debaryomyces hansenii (Yeast) (Torulaspora hansenii), Debaryomyces hansenii var. hansenii, Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) (Yeast) (Torulaspora hansenii)	284592	>tr|Q6BYD8|Q6BYD8_DEBHA DEHA2A10340p OS=Debaryomyces hansenii (strain ATCC 36239 / CBS 767 / JCM 1990 / NBRC 0083 / IGC 2968) GN=DEHA2A10340g PE=4 SV=2MNRVSKLWHSYKRHRVHGDTGLKIRNAIHRTTEKVYPYVKVVIPNFRAAHYTYILFMTFLGSVIFYPIRNIRYIDALFFTGCASTQA GLNTVNLNRLALYQQILIYIITTLTTPIFIHGSLLFIRLYWFERHFDNIKESSKLNNKMRRNATLAARTQSLDPTRLNTEVNRGLGLNNPQS SGPEPVIDEVAFSNSSSTSPASKHSSPPQNPSINSNNVNHISEPSDTDISSGVAPDSRNPINLSRPESPPRSLDGIRFGNLPQPSKIRQ KEIEPSDMYMSIAMLQDNHKSERKDNGDEDDVLIIKSPNEIEKDSQNPIFTKKSQIHFNVNDKPIRKWKKKRRFSRGRQPWSKLKKTF SNSGVSPRKHVRSLSFTSLSNDDDDQSIDSETNNRTTDTDADDDNAIIDDDDDDDEDDGDDDDEDDGDDEDEDDDDEDDEDDDQD DEEDEYNRQNRHDDNLDDIERAQSNLVIPSSDATGGKKFTKRSNTLDVTPGENHELSHSPTFEKMIKSKMKKKKKKPKQTKKQKLKYM KSPTVGLNSSLFSPNYNNGSDYDDSDDSDEDDDDEEEDGKSLSKVMSTNYLSWVPTVGRNSTFVHLSEEQKEELGGVEYRAIKLLIK IIVIYYIGFHILAFTCLLPYILYQPVYKADVINVGITPTWWAFFTAQSAFNDLGHTLTPNSMQSFDKSVYVMVIVAFFIVIGNTGFPVMLRFI IWVLFKLSKPMSLFNESLGFLLDHPRRCFTLLFPSVPTWWLFIILVVLNAVDLILFIVLDLNNKYLESTPIGLRVMDGLFQAFSTRTAGFA VVDLSELHPAVQVSYMLMMYISVLPLAISIRRTNVYEEQSLGVYLKDNNDDNDDAPDDKTPRNFIGAHLRNQLSFDLWFIFLGLFIICIAE GPKLNKNNYRFSIFTILFEIISAYGTVGLSLGYPGVDVSLSGEFTVLSKLVMIAMVIRGRHRGLPYALDRAIMLPDDNMQKRDNLQENHA IRRHQTMETSNSLDDGNAFRRAFTRRASSFGFDNTNILGRRKSSVRSSKPKPETPHYIVTTESHEMDDLA														

1E-157	535	1.4	5E-157	532.9	0	2.2	1	G0W708_NAUDC	Uncharacterized protein	NDAI0B05360 NDAI_0B05360	Naumovozyma dairenensis (strain ATCC 10597 / BCRC 20456 / CBS 421 / NBRC 0211 / NRRL Y-12639) (Saccharomyces dairenensis)	1055	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Naumovozyma, Naumovozyma dairenensis, Naumovozyma dairenensis (strain ATCC 10597 / BCRC 20456 / CBS 421 / NBRC 0211 / NRRL Y-12639) (Saccharomyces dairenensis)	1071378	[illegible] 421 / NBRC 0211 / NRRL Y-12639) GN=NDAI0B05360 PE=4 SV=1MLFGRTLTNISTLTNINNAYKKSIGHRLRDFIDCLGTKFQPIKKYIFPNFIAVHYFYIIFVALFTSILIYPVRNQKYIDILFLSAGAATQG GLNTVNTNELVLYQQIVIYIACWLSTPIVIHGCLAGVRLYWFERHFDNIRESSKKYFKARRTKTILERELSAKLPTRRKSTTSNILSKASQ NFNNRGINNNYDDFRDKLFSGKKLGRENTTDGNSISNPPESINSQLRRDFNPSNTSGSHSTSDSSPESTLLNNEHFVRRRKSSDVKP QDIYRSLLLLQNQRKKENLSDDQYHGPPLIIDSPTKNNSFTRIPDKNIDFTNNGARPPSSERLVQFEIAKPTRSITRRKRNEQMHPKTFR NTDLLYQSSSRFNSHIHLSPRHTLPPTIGKRTRTEDSNYSSLSNITQTDQQGKPDSQQREEMREQSTTLHAIPSKRLRLNNKRKKLINK RKLKSKLHPIKRLRSNDSNISPKSERQPFEEISFHNYDNPNLIPARTDNQFDEEENLNTSDSLNDLRFLDGSNLRNIGRRTSTYLSWEP KLGPNSIIYGLSKAQKEELGGVEYRAIKLLCIILVIYYVGLHLIIAIMFLPWICLKNKYRQIVRNDGIAPAWWAFFTGMSSFCNLGLSLTPD SMNRFSRAIYPLITMIFFIAGNTGFPVFLRAIIWVMFKLSRDLSQIKESLSFLLDHPRRCFTLLFPNDATWWLLMTLVGLNGVDLVLFIIL DRGAEILKEYSGGYRVLLGLFQAVTTRTAGFSALDISLLHPSIQVSYMLMMYVSVLPLAISMRRTNVYEERSLGIYGKMPMSELNQIEA EGKNADGQHSPTLEDDNDEELEEDEDEESKSLASSNSSTSHAIGKERRESNTSKKKKKKNKKEEDDSSNSYIAIHLRRQLSFDMWFM FLGLFIICICESGKIQDPEMPAINVFSILFEIVSAYGTVGLSLGYPGTTTSLSAQFTALSKLVIIVMLVRGRNRGLPYALDRAIMLPSERLER IDDIEDSKLRRQPKNIGKEDPVSGYFKRHLHKLKNGWRRIHSSANENHADNHSMDTPTDGLEGGK
1E-156	532	13	8E-156	528.8	4.2	2.6	2	G8YKM3_PICSO	Piso0_001379 protein	Piso0_001379 GNLVRS01_PISO0F05197g	Pichia sorbitophila (strain ATCC MYA-4447 / BCRC 22081 / CBS 7064 / NBRC 10061 / NRRL Y-12695) (Hybrid yeast)	998	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Millerozyma, Millerozyma farinosa (Yeast) (Pichia farinosa), Pichia sorbitophila (strain ATCC MYA-4447 / BCRC 22081 / CBS 7064 / NBRC 10061 / NRRL Y-12695) (Hybrid yeast)	559304	[illegible] NBRC 10061 / NRRL Y-12695) GN=Piso0_001379 PE=4 SV=1MSRLKDYWVEFRENNEFGLKIRNGIDRLGSKLNPYCKVLFPNFRVVHYCYIIFMCITGSVIIYPKRNIEYIDALFFAVCSSTQAGLN TLDVNNLTLYQQIAIYCVAMLTTPIFIHGSLLFVRLYYFERRFDNIKETSKLNFKMRRTATLAAKSQSFDSTRANTMVNQNLGKTFSRRS FVPQFNQNINYQQHDSKRADDDRHDGSAPRNNQQSNGVYNDSDEISPKESGSSNMTDGNTESMSPTRVESNSSPPNKSSEGIRFG NLPHPTEKRNKEVEPSDMYKSIAMLRDIHRTNTNDDDDVLVIKSPNEIERDSQKPIYTKRSQIQFSLKNEPLKRWKKKRLSRGSPSWS KLKRSFSNTTPHPRKIMRSFSIGSTTNDEDASFDSEEEESEEVSDGGDSTNYDGDPENSEAIVSDEESNSNLSSEASTDEETSKVHRA QSNLQLPSSDQTDGKKFHKRSNTLDAPPGDRSSFTKSPTFERLIRSKLKHKQHKKNKSKKRHSLSKLSTAMFDNDHQLKNSTTDATD NRSLNKVMSTGYLSWTPTIGRNSNFVRMTDEQKAELGGVEYRAVKLLIKILIIYYIGFHVVAVVFLLPYGILKRNYAEMIEKQGISSTWW AFFSAMSSFNDLGYTLTPDSMASFNRSVYVMVIVSFFVVIGNTGFPIMLRFIIWVLFRLSKPLSLFKESLGFLLDHPRRCFTLLFPSMPT LWLFSILVILNGVDLILFVILDIHNKFLEPYPTGIKVMQGLFQAFSTRTAGFTVFSLSNIHSAVQVSYLIMMYISVLPLAISIRRTNVYEEQS LGVYIRGKDDVPNHEDDKTPKNFIGAHLRRQLSFDLWFIFLGLFIICIAEGSKIKKDINFSIFAILFEIISAYGTVGLSLGYPNYNPSLSGKF TKISKLVIIAMMIRGRHRGLPYTLDRAVMLPNETMNRRDMAQENHDLRRHTTQDTAASPGLFKAISRRLSRYGTVDNRNTFSSSHQY PTDNYQRRQGEAVEMDRFDS
2E-155	528	7.3	2E-155	527.6	5	2.2	2	G8YN04_PICSO	Piso0_001379 protein	Piso0_001379 GNLVRS01_PISO0E03788g	Pichia sorbitophila (strain ATCC MYA-4447 / BCRC 22081 / CBS 7064 / NBRC 10061 / NRRL Y-12695) (Hybrid yeast)	998	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Millerozyma, Millerozyma farinosa (Yeast) (Pichia farinosa), Pichia sorbitophila (strain ATCC MYA-4447 / BCRC 22081 / CBS 7064 / NBRC 10061 / NRRL Y-12695) (Hybrid yeast)	559304	[illegible] NBRC 10061 / NRRL Y-12695) GN=Piso0_001379 PE=4 SV=1MSRLKDYWVEFRENIEFGYKIRKGIDRLSKKLNPYFKVLFPNFRVVHYFYIIFMCIIGSIIIYPKRNIEYIDALFFAVCSSTQAGLNTV NANDLTLYQQIVIYCVTMLTTPIFIHGSLLFVRLYYFERRFDNIKETSKLNFKMRRTATLAARTQSFDSTRANTMVNQNLGKTFSRRSFV PRFNQNINYQQHGSSRVDDERRDGPVSGNNQQPNGVYNDSDEISPKESGSSNITEGNTESISPKRVDNNSSPQNKSSEGIRFGNLP LPTEKRNKEVEPSDMYKSIAMLRNIHPTNTNDDDDVLVIKSPNEIERDSQKPIYTKRSQIQFSLQNEPLKRWKKKRLSRGSPSWSKLK RSFSNTTPHPRKSMRSFSIGSTTNDEDASFDSEEEESEEASDAGDSTNYEGDPENSDAIASDEESNSDLSSEALTDEETSKVHRAQS NLQLPSPDQTDGKKFHKRLNTLDAPPGDRSSFTKSPTFEKLIRSTLNHKRHKKNKVKKRRSLSKLSTSIFDNDNQLRNSTTDATDNRS LSKVMSTGYLSWNPTIGRNSNFVRMTDEQKEELGGVEYRAVKLLIKILVIYYIGFHVIAATFLLPYGILMHNYASVIEEQGITPTWWAFF SAMSSFNDLGYTLTPDSMMSFNRSVYVMVIVSFFVVIGNTGFPIMLRLIIWVLFHLSKPLSLFKESLGFLLDHPRRCFTLLFPSMPTLWL FSILVILNGVDLILFVILDIHSKFLDPYPTGIKVMQGLFQAFSTRTAGFSVFSLSNIHSAVQVSYLIMMYISVLPLAISIRRTNVYEEQSLGV YVHGKDEVSKHEDDNTQKNFIGAHLRRQLSFDLWFIFLGLFIICIAEGSKIKKDINFSIFAILFEIISAYGTVGLSLGYPNFDPSFSGKFTKI SKLVIIAMMIRGRHRGLPYTLDRAVMLPNETMNRRDMAQENHDLRRHTTQDSTASPGLFKAISRRLSRYGTNDNRNTFSSVHQHPSD NYHQRQSEAVEMDHLDH
3E-155	527	4.2	4E-152	516.8	0.5	2.1	2	Q6CE78_YARLI	YALI0B17864p	YALI0_B17864g	Yarrowia lipolytica (strain CLIB 122 / E 150) (Yeast) (Candida lipolytica)	970	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Dipodascaceae, Yarrowia, Yarrowia lipolytica (Candida lipolytica), Yarrowia lipolytica (strain CLIB 122 / E 150) (Yeast) (Candida lipolytica)	284591	[illegible] SV=1MFIVDYAKRAYRKLRHFRITFIVVHYFIIIGSAIFGTFLFYPAKTTKYIDALFQCACAATQAGLNTVDLNSLKLWQQMVLYCISMWT NPIVIHSGVVFMRLHWFEKSFKDIKNQSKLQSKLRRTATTLARQDTLENGLFQRPPLRHQNPGVAGLNSNINNDSSDETPHKEGHNN DNPNLNKEITFGNLPQPKRTHSVEPEDMYRSINLLSHEHPEGQSDSDDDGPALVIRGPRDRPDRDDDEEDSPEIERAPRAISFSTQEH PRAQKSALEQFKEEMRESQRQLDAEHAIDEGESSDATQPTSIKREDMYYRQHPDSDSSEGDTVKKVRSNVTVHRPSPEDDDFAGTQ PMNRRAFTLDGDNTEEKNHEGAFAHFKRSLTFDRFLSNRRRGSDAASSSGATSNADLNKTMSSNYLSWSPTVGRNSAFVDLTEEQK EELGGIEYRALKVLSKVLVAYFVGFHLMCAIMLLPWAIYMPKYRDYVYSCGVTPTWWAFFTAQSTFNDVGFTLTPDSMGSYQEAIYV LLTMSFFIVIGNTGFPVLLRFIIWIMFKLSPRDSSLKECTGFLLDHPRRCFTMLFPSTATWWLFATLVILNSVDLVFFIILDFNAPAVTEMR PGYRVVVSGLFQAFSTRTAGFTSVSIAELHPSIQVSYMIMMYIAILPIAISIRRTNVYEEQSLGIYGGGDEESEYDQAPTADEEAENEEND PEHLYKGKKKKHPSYVTAHLRAQLGYDLWYIFLGLFIICICEGTKIKDVTDLGFTGFTVLFEVVSAYGTVGMSMGYDDVNTSLSGKFSTI SKLIIIAMMIRGRHRGLPYSVDRAIILPSDEMHRKDDAVTRSHLRRGRTMSANSNELTETMGLPYPMRSHTMMSSGPGAGGNESYPL RGSSHSRQTSNVSDIGPRDLDPIVPSSPMPSVDEDYLKRMEKREQEQEDNKLRGELSDNKKKLHKDEQGIEMDSYFPELKGPGGLD LADD
3E-153	520	9.6	3E-153	520.4	6.7	1.8	1	C4YMK8_CANAW	Uncharacterized protein	CAWG_02090	Candida albicans (strain WO-1) (Yeast)	1058	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Candida, Candida albicans (Yeast), Candida albicans (strain WO-1) (Yeast)	294748	>tr|C4YMK8|C4YMK8_CANAW Uncharacterized protein OS=Candida albicans (strain WO-1) GN=CAWG_02090 PE=4 SV=1MLYRVSGFYKRHTRNFTNIDYGYYIRNFIHHIASKIYPYAKVVLPNFRAAHYFYILTLVILGSILVYPVKTCAYIDVLFFTAGASTQA GLNTVNVNDLSLYQQIVLYLLATLATPIFIHGSLLFVRLYYFERHFDNIKERSLMDYRMRKSATLARLGSAPTMSSTRLNTFNNQVLGFQ EREAEKGSSSSPQSSSSQTSQPVSTAYNDQGGNDIEHHSEPSDSDDDESGNGPVTFQEKIHFEEPQRPRSQRRHSRTDSGIKFSAL PHPRRRKSIDPEDMYRSINMLQEHKKNQEAKSKGIQFLNIGSPVRRKSRSSNIEAFPEEDTNPSRDDEITPATNSVGTGNNDEDEDDIL IIKPPIEIENSDGANPIFTKKKKLASQIQFKETPGKAKKWITTKKRKHYNPWTSKLKKTLSNSSKKGSLSVVPTDTEDDSEDEEYASIDSE TSDISDNEHAADNAEGSDVDSVGSYEEDEDEDEHNSDDDDDDDGEGERRLGNGASLTKAQSHLVLPSKDETGGKKYTKRSNTLDT PQQNTSDGRKIRKKVPKRKTPRTQRNASFNQHSNVSIGDGSIENVDTNDSYQRLSRTMSGNYLSWTPTVGRNSTFIKLTDEQKEELG GIEYRAVKLLIKIIVVYYVGFNIIPGVMLSIWIYCMPHYKNLMISSSISPAWWAFFTSQSSFNDLGLTLTSNSMMSFNQNAFVQILCSFLIV IGNTGFPILLRFIIWVMFKTARPLSLYKESLGFLLDHPRRCFTLLFPSVPTWWLFFILVVLNGFDLVIFCILDLHDDTFKGVDMGYRVLNG LFQAFCTRTVGFSVMDLSQLHAATQVSYLIMMYISVLPIAISVRRTNVYEEQSGVYAKENAEGVDESAPSNYVGSHLRNQLSYDLWYI CLGLFIICIAEGKRLKEQDLRFSIFAVLFEIVSAYGTVGMSMGYPGVDCSLSGEFNVISKLVIIAMMIRGRHRGLPYTIDRAIMLPNAAMK RHDRLQEEHAINRHNTMERTTTLGRVATFGNGPIDGGNNLLTRAITNIEHRLRKRRDGRSESSTVSEDPRYVVRTVSEV

5E-153	520	5.3	5E-153	519.7	3.6	1.9	1	C5M2R4_CANTT	Putative uncharacterized protein	CTRG_00353	Candida tropicalis (strain ATCC MYA-3404 / T1) (Yeast)	1097	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Candida, Candida tropicalis (Yeast), Candida tropicalis (strain ATCC MYA-3404 / T1) (Yeast)	294747	[illegible] GN=CTRG_00353 PE=4 SV=1MFTRLKELYNRHTRSRFHYGFGYYLREGIHDVASKIHPYAKVLLPNFRAVHYFYIITLVIIGSILIYPVKTTAYIDALFFASGASTQAGLNPVNVSDLSLYQQIIIYLLACLTTPIFIHGSLLFVRLYYFERHFDNIKERSLMDYRMRKSATLARMATKETMSSTRLNTFNNQVLGFKQRRQEHEQDEEKGLSSTPPSSSTQNSDNLTASFIPENNGVEHHSEPSDTENESITQTDENRDSGINGAERIHFQEPVRPAHVRSDSAIKFGTLPNPKRKKSIDPEDMYRSINMLQQNKKNQENESNEVHFSNVESPSKRRPFSPTSISFQLGERPGSRNSNHHYSHNNNNFFHHTHHNNDENQDDDDDDDDDILIIKPPNEIENSDSKNPIFTKKKKNPSHNRDAPSRAKSWIANQRRKSIDPWTNKLRRTLSNNNKRKTLLNAHTDTEDDFDDEDEEEEDASIDSENQVTNEYHGNDHEHAVTDGEDDEDVEDDDNDDDHDEDEDDEEEDGAPVVKSQSHLVLPSRDATGGKKFVKRSNTLDIPDVRNDFSEDITDNRTTRKTPRKRPTKRRTPSFNLPRRSRTQSIDNDSIENVDTNDSYQHLSRTMSGNYLSWAPTVGRNSTFIKMTEEQKDELGGIEYRAVKLLIKIIVVFYIGFLIFPGIALLIWIYCMPHYRRVVRESAISPAWWAMFTGQSSFNDLGFTLTPDSMSSFNSNAFVQILCSFLIVIGNTGFPIILRFIIWVMFKFSRPLSLTKESLGFLLDHPRRCFTLLFPSVPTWWLFFILVVLNGFDLVVFCILDINDDSFDGIDRGYRVLNGLFQAFCTRTAGFSIMDLSQLHAATQVSYLVMMYISVLPIAISVRRTNVYEEQSLGVYAKDEGGSGDSVDENRPSNYVGSHLRNQLSYDLWYICVGLFIICIAEGSKLQKQDLRFSIFAVLFEVISAYGTVGMSLGYTDTDCSFSSKFNVISKLVIIAMMIRGRHRGLPYAIDRAIMLPDADMRRHDRLQEEHAINRQHTMERTTTLGRVATFGGSPMDGGNNLITRVLTNIEGRIKRRRHSTYSEDSSSGRSRDSMAGERSQMVSENPSYLVTTVSHV
4E-152	517	3.7	2E-150	511.4	2.8	2.1	2	G8BFN7_CANPC	Putative uncharacterized protein	CPAR2_203140	Candida parapsilosis (strain CDC 317 / ATCC MYA-4646) (Yeast) (Monilia parapsilosis)	1041	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Candida, Candida parapsilosis (strain CDC 317 / ATCC MYA-4646) (Yeast) (Monilia parapsilosis)	578454	>tr|G8BFN7|G8BFN7_CANPC Putative uncharacterized protein OS=Candida parapsilosis (strain CDC 317 / ATCC MYA-4646) GN=CPAR2_203140 PE=4 SV=1MPSASNVHERYKRARFKHDLGFKVRNFMQRIISAVYPYAKKVLPNFRAVHYFYILSHCFIGSILIYPVKSIPYIDALFFASGASTQAGLNTVDVNKASLYQQIILYIIPCLTNPIFIHGSLLLVRLYYFERHFDNIKENSKLNFQMRKSATLARQNTITSANSTRINTAANKDLGYNHKDDEVESPQSSSSIPGNGSNNQNGKTEHMSEPSDDEDDLGGNVEDKTAPSHAIKFGALPHPRRRKSIDPEDMFRSINMLREKQKSQNNTHNKNDNQEGSRPPQSTSIHFADMASPSRTRRSRLSASASQSPHNEGNGDGDDDDDDDDVLVIKPPNEIEDAASHNAIFTKKKLSKPHQKRRSSWIPLSSRKTHKPWKNRLRRTLSNSSRKRRSQASSELEDEVDDDASIDSEVEESNISGDDATRFDGRSGVETGDDDDDDDDDDYDGEVDESAVTDDEDLAEGDISPTQSAQNSRRHSASNDPESGNTTRTLKFDHALPDKERERRRKRRFKKLKRIRTPIISRLSSGDTAANNDDEDTEESDESDDDDYRDGLARTMSGNYLSFAPTVGRNSTFMKMTDEQKDELGGIEYRAVKLLIKIIVCYYLGFLIVPSFMLLIWVYCMPGYKTMLNDSAITPGWWAFYTAQSSFNDLGLTLTADSMNSFHENAFVQVLCGFLIVIGNTGFPIFLRFIIWIMFKTAPELSLYKESLGFLLDHPRRCFTLLFPSIPTWWLFFILVALNGFDLVIWCIVDLNSSMFDGVPKGYRVLNGLFQALCTRTVGFSIVDLSQLHAATQVGYLVMMYISVLPIAISVRRTNVYEEQSLGVYTKESNEGDENTPSNFVGAHLRNQLSYDLWYIFLGLFIICLAEGSKLQKQEFRFSVFAVLFEVISAYGTVGMSLGYPDVNTSLTGKFNVISKLVIIAMMIRGRHRGLPYAIDRAILLPNAEMSRHDEVEQEHAMNRQNTLDRGTTLARVATFARGGPIDGGDNILSRVLTNVSHLRNKRKRRNRGSTSSNNNGDTRDGEQSLHSSNPNYLVTTVSHV
9E-151	512	14.1	5E-149	506.4	2.9	2.1	2	V5HRM7_BYSSN	Potassium ion transporter (Trk1), putative	PVAR5_0596	Byssochlamys spectabilis (strain No. 5 / NBRC 109023) (Paecilomyces variotii)	824	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Thermoascaceae, Byssochlamys, Byssochlamys spectabilis (Paecilomyces variotii), Byssochlamys spectabilis (strain No. 5 / NBRC 109023) (Paecilomyces variotii)	1356009	[illegible] 109023) GN=PVAR5_0596 PE=4 SV=1MFSSILPTVTSIKEKVPFVRQINLNFITIHYVYIILWAIIGSVVVYAAGDIAYIDALFFASGAATQSGLNTIDFNKLHTSSQVFLYWISMFTTPIFIHSFVVFVRLYWFEKRFQHVVQDARAMRRTKSRSRTVTAGKDLHDNEAAERGVRGRSIVVLRNRSGEAGRSIENEHVVKPEPESPSESSESPRGTRQYYEDAEGAEDEKDGGNEEEGPRSQSGTPSHARNVSGLRVPTQLSPEHHIAFLENQRRDKGALRIPSPREYDRGGVPQALEDDPDALARIDTRRSRQSSRDENREDANGPSHIGPHITINEPDFPRQRSRATTFPRLDTRRTMRDEEGDDMQLEQSRTTRRSRFNTLVRSFTQEREERETMPYLSWNATIGRNSNFVDLTEEQRNELGGIEYRALKTLAVVLISYYFLFHVLGIICLVPWIMHSKTYGAIVTGDGQGRPWWGIFTAASAFNDVGFTLTPDSMNSFYTAIFPLLLMSFLIIIGNTGFPCMLRLIIWVMTKVVSKGSPIWEELVFLLDHPRRCFTLLFPRNATWWLFAILVILNAVDVIFFIVLDLNDPDVTSIPGGIRFLDGLFQAAASTRTAGFGVISLSELHPAIQVSYLIMMYISVFPIAISMRRTNVYEERSLGIYSAADEEDEEDDNSKEPSYIGAHLRRQLSFDLWYVFLGLFVISIVEGSRLQNTNEWAFTLFSVLFEIVSAYGTVGLSLGYPNVNASFSSQFKVLSKLVIIAMQVRGRHRGLPYALDRAILLPSESLQKKDAAEAEKRLRRRSSNVSRMSGPPMRASTALSTARDMDTQSLQQQSLQQRILPEQSTT
1E-150	512	5.1	1E-150	511.7	3.6	2.1	2	B6QF76_PENMQ	Potassium ion transporter (Trk1), putative	PMAA_081220	Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333)	818	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Trichocomaceae, Talaromyces, Penicillium marneffei, Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333)	441960	[illegible] 334.59 / QM 7333) GN=PMAA_081220 PE=4 SV=1MEIRHVKRTAGFGASVLKHLRTIAGVILANVTFLHAKIPYLREIKYNFITFHYVYLTTWAIIGSIVLYAGGTIPYIDSLFFASGAATQSGLNTIDLNLLPTYAQIFLYIIAMWTNPIVIHTFVVFVRLYWFEKRFQHIVKDARALRRTRTRTFTTGRGQQDVDREEQGVRGQSIVVLRNEQGEARDGVQDGLKTETDANSETGTSNSTSNDRRAPEESPQLTPPSPLTDTEGLRLPTQRSPEHHIAFLEHQRTDKGTLRIPSPREYDRGGVPQALDEAVEDSPTSPKSPPAEDERQRQESGNELGNHITINEPDIERFRARTGTGNFPRVSSQRTTFRDEGDNEPTRVRTRRGTFNGIFRSMTQEQDRDTLPYLSWNATVGRNSAFVALTEEQREELGGIEYRALKTLALVLVGYFVGFHVFGVISLVPWILTSKTYGSVVTGDGQGRAWWGVFTSQSAFNDLGFTLTPDSMNSFNEAVWPLLVMSFLIVIGNTGFPCMLRLVIWIVWKFTRAGSALWEELRFLLDHPRRCFTLLFPRNATWWLFAILVVLNGVDLIFFIILDLNDATITAIPPGYRVLDGLFQAFSTRTAGFGVVNISALHPAIQVSYMIMMYISVFPIAISMRRTNVYEERSLGIYGTTEEEDEDVKEPSYIGAHLRRQLSFDLWYIFLGLFIIAIVEADRLESGADNYAFSLFAVLFEIVSAYGTVGLSLGYPNTNASFSAQFRVISKLIIIAMQIRGRHRGLPYALDRAILLPSESLQEKEQDDAERRLRRRESNVSNMTGANGQSSGIYHTSTYDSLGSRTRPRTRRSVDVRD
2E-150	511	13.2	5E-148	503	5.3	2.3	2	I2H3V5_TETBL	Uncharacterized protein	TBLA0D05650 TBLA_0D05650	Tetrapisispora blattae (strain ATCC 34711 / CBS 6284 / DSM 70876 / NBRC 10599 / NRRL Y-10934 / UCD 77-7) (Yeast) (Kluyveromyces blattae)	975	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Saccharomycetaceae, Tetrapisispora, Tetrapisispora blattae, Tetrapisispora blattae (strain ATCC 34711 / CBS 6284 / DSM 70876 / NBRC 10599 / NRRL Y-10934 / UCD 77-7) (Yeast) (Kluyveromyces blattae)	1071380	[illegible] NBRC 10599 / NRRL Y-10934 / UCD 77-7) GN=TBLA0D05650 PE=4 SV=1MSNNNRNHLSRTYSNTSTIATITVKAGKTLGRKTRDIINKTSKKCFILKKYLFKNFIMIHYFYIITNTLIGSILIYPVGNIRYIDALFMAGSSATQGGLNTVDLNMLTTYQQIIIYLICFFCSSIFIHSILASVRLYWFERHFDGIEDYSKQNFKMRRTRSLLEKELSKTQQYQKATNKNQNTFHENLFSGTFINRDSPLMLSATTSLEYQESQSTSNSISYSDSNTENSYLDNILFYKGKNSQRNDIKDIKTYKNIKTLRILQKLNMYNKRKFSSLKKMKLQHFSPNKIKSYNKKCFRNLSFQKNNFYLVKNYLTYIYYRRSIRRDLDLVLNNEQGSVSSQSDTTLSTFQRELAEDETIILPSPNEINPINADISTLKKNPTTIRFEITKPQMKGALKQEKKASNSYKNDENITALQRFKSSFTNEKYLGTKINVVWKDGHTERSFLTLLEKTNKRSKQRRNNEQSYDEPLSGNHSLSFNTDSEASFSASLDNISTVMTYDLPPLSARTMSTGYLSYEPKLDRNSIFIGLTKSQREELGGVEYRALKLLCKIVFCYYFGINLLAFVFLIPWAYSAMTYKNIILEFGSSPGWWAAFTGMSSSNNVGLTLTPNSMASFNTAPYPLIVIMCFVILGNTGFPIFLRFIIWGALKITPESSNRKESLGYLLDHPRRCFTLLFPKAVTWWLLFTLFTLTVFDWLLFIILDLNISTLDPLSKGYRVLAGLFQGIATRTPGFALVDVSVLHPTLQVTYLLMMYISVFPLAISIRRTNVYEEQSLGIYENESTSVIDRSSSFTSTELETQQSLTSCSSGECSNTKKLSTKSFIGSHIRKQLSFDLWFLFVALFIVSICEGSKIRDIERPSFNLFSVLFELVSAYCTVGMSLGYPGTTPSFTGQFSKLSKLVIIILLIRGRHRGLPNSIDRAIILPSEKLERLDIIVEEQSQRQKQLPNLNDPASEYVNTKYKEVLKVLENLKFW

2E-150	511	7.8	2E-150	510.9	5.4	2	1	M3K0D1_CANMX	Potassium transporter, putative	G210_1399	Candida maltosa (strain Xu316) (Yeast)	1038	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Candida, Candida maltosa (Yeast), Candida maltosa (strain Xu316) (Yeast)	1245528	>tr|M3K0D1|M3K0D1_CANMX Potassium transporter, putative OS=Candida maltosa (strain Xu316) GN=G210_1399 PE=4 SV=1MVSQLKQLYNYFTKNRFRFGFGYYMRNLIHDIASKIYPYAKVLLPNFRAVHYFYVISLVILGSILVYPVKTVPYIDVLFFTAGASTQ AGLNTVNVNNLSLYQQIILYILTTLTTPIFIHGSLLFVRLYYFERHFDNIKQRSLMDFRMRKSATLARLGTNNTMSSTRLNTFNNQVLGFN EKNKEDKGSSSSPPSSTSQVTTTATANASVPDIHIRTDTDNNVEHVSEPSDTEDEHDDDRDHGEKIHFQEPERPKHTRADSGIKFGAL PNPKRKKSIDPEDMYRSINMLQEHKKKQEATSSGSTPFHFFSLPSPARRISFSPNTLNFPFNDQNKENKDNDDDDDDILIIKPPNEIEN SDGQNPIFIKKKKDSPQIQFKDSPKKWIANRKRMHYSPWTNKLKRTLSNSGRRKSGIAPTDTDDEYDDDEEENASIDSEIQNQTDEDG SDHAITDDDDDEEDEIDDDDDTPVTKAQSHLVLPSSDATGGKKFAKRSNTFDLSDNTGDGSTETKRTSASKKQRRPRRRSSGLSSR NNSIGNASIEPVDTDDSYRHLSRTMSGNYLSWTPTVGRNSTFMRMTEEQKEELGGIEYRAVKLLIKIIVIYYVGFNVIPSIMLLIWIYCMP HYKNLMLSNAISPAWWAFFTGQSSFNDLGLTLTADSMSSFNQNAFVQILCSFLIVIGNTGFPIFLRFIIWILFKFARPLSLYKESLGFLLD HPRRCFTLLFPSVPTWWLFFILVVLNGFDLVIFCILDLRNAIFDGEPMGYRVLNGLFQAFCTRTVGFSIMDLSQLHAATQVSYLIMMYIS VLPIAISVRRTNVYEEQSLGVYAQDNGDGVEENSPTNYVGSHLRNQLSYDLWYICVGLFIICIAEGKKLQKQDLRFSIFSVLFEIISAYGT VGMSLGYPDVDTSLSGKFNVISKLVIIAMMIRGRHRGLPYAIDRAIMLPDAEMKRHDRLQEEHAIHRQHTMERTTTLGRVATFGNGPM DGGQNILSRVLTNIERRMKTRRGDEDSDASTITGNPNYVVRTVYLLIYIYTWYYYK
3E-150	511	5.8	3E-150	510.5	4	2	2	D5G3V3_TUBMM	Whole genome shotgun sequence assembly, scaffold_1, strain Mel28	GSTUM_00003817001	Tuber melanosporum (strain Mel28) (Perigord black truffle)	809	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, Pezizomycetes, Pezizales, Tuberaceae, Tuber (truffles), Tuber melanosporum (Perigord truffle), Tuber melanosporum (strain Mel28) (Perigord black truffle)	656061	>tr|D5G3V3|D5G3V3_TUBMM Whole genome shotgun sequence assembly, scaffold_1, strain Mel28 OS=Tuber melanosporum (strain Mel28) GN=GSTUM_00003817001 PE=4 SV=1MGLPRRWQFKPHFNFITVHYAYVIGMAIIGSVIIYPYKNMRYIDALFFAAGGATQSGLNTIDANLLKLYQQVVIYFLPMLTTPIFINT LVVFVRLYWFEKRFENIVSLTRQPSRARSALSKGTLDDNVESGREGAGVRGREITVLRAEPGTPLNLSKQSLSPGPGKNTEDRPRSM DSDIAPESVRSQTLQGRSSSDGVHGSDSSGVASSATEGPQTQRQNSEATGIQFVDLPSPSRDGAGCMSAFTSPHIAFTETQRNCVH GKALRIPGPREFEKGCRAQEIDEDDIGTLHRSRTTAEGDRNHDVGSPASRTMSLGNGVNGSNNVRQRKLPPLEQFLPRASTVERVIS SAFSVGQHPKRRNTSPFSRLSRKTAKEPPNMPYLSYTPTLGRNSQFVGLSDEERDELGGIEYRSLKLLAKVLVGYYLFFHVFGVVCFT PWIWASGGYMDYVRSIGVNPTWWAIFSAQTAFNDLGFTLTPDSMVSFQSATFVLIIMTFLIIIGNTAFPCMLRLIIWIMFKLCPKESSHR ESLNFLLDHPRRCFTLLFPSWPTWMLFWIVIVLNCADIILFIVLDLNDGDVTEIPVGHRIMGAIFQAASTRTAGLAVVNLADLHPAVQVSY MLMMYISVFPIAISVRRTNVYEESSLGIYANTDDEDNGRGASFVGAHLRKQLSFDLWYIFLGLFIITISEGSRIQDPKDYAFTTFAILFEVV SAYGTVGLSLGYPNSNASFSAQFGVIGKLVIIAMEIRGRHRGLPYELDRAILLPSESLQQKEAQDAQLRALRRRGSSFTQVGGRPLTG VRSVQSQAIGDD
1E-148	505	15	2E-148	504.1	3.7	2.1	2	B8MAU4_TALSN	Potassium ion transporter (Trk1), putative	TSTA_115780	Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum)	815	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Trichocomaceae, Talaromyces, Talaromyces stipitatus, Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum)	441959	>tr|B8MAU4|B8MAU4_TALSN Potassium ion transporter (Trk1), putative OS=Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) GN=TSTA_115780 PE=4 SV=1MHITHVKRTAGFGASVLKHLRSFAGVIIANLTLMHANIPYIRDIKYNFITLHYVYLVLWAFVGSIVLVAGGNMPYIDALFFASGAAT QSGLNTIDINKIPTYAQIFLYVIGMWTNPIVVNTFVVFVRLYWFEKRFQHIVRDARALRRTRTRTFTTGREQHDVNREEQGVRGQSIVV LRNEQGEARDGTQDSHKTDTDANSDTGTSNATSNDRRDESSKLSPPSPLSDTEGLRLPTQRSPEQHIAFLEHQRTDKGTLRIPSPRE FDRGGVPQALDEAVEDNQDNPTSPQSRPVDEEQQRQESGNELGNHITINEPDIMRFRARTSTFPRINSQRTTMRDEEGDNEPRRLR TRRGTFTGIFRSMTQEQDRDTLPYLSWNATVGRNSAFIALTEEQREELGGIEYRALKTLALVLVGYFVGFHIMGIVCLVPWIVASQKYG AVVTGDGQGRAWWGVFTAQSAFNDVGFTLTPDSMNSFNEAVWPLLIMSFLIVIGNTGFPCMLRLLIWIISKFTITGSALWEELRFLLD HPRRCFTLLFPRNATWWLFAILVVLNGADLLFFIILDLNDPTITSIPAGYRVLDGLFQAFSTRTAGFGVVNLSALHPAIQVSYLIMMYISVF PIAISMRRTNVYEERSLGIYGSAEEEAEDVTEPSYIGAHLRRQLSFDLWYIFLGLFIIAIVEADRLESGADSYAFSLFAVLFEIVSAYGTVG LSLGYPNTNASFSGQFRVISKLVIIAMQIRGRHRGLPYALDRAILLPSESLQQREQDDAERRLRRRTSNLSDMAANGQSSGIFQIGTNY SLGSRTRSRPRRRSEDN
2E-148	504	8.8	3E-147	500.5	4.4	2.1	2	G3BFI4_CANTC	Potassium transport protein TRK1/TRK2	CANTEDRAFT_128188	Candida tenuis (strain ATCC 10573 / BCRC 21748 / CBS 615 / JCM 9827 / NBRC 10315 / NRRL Y-1498 / VKM Y-70) (Yeast)	921	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Yamadazyma, Yamadazyma/Candida clade, Candida tenuis (Yeast), Candida tenuis (strain ATCC 10573 / BCRC 21748 / CBS 615 / JCM 9827 / NBRC 10315 / NRRL Y-1498 / VKM Y-70) (Yeast)	590646	>tr|G3BFI4|G3BFI4_CANTC Potassium transport protein TRK1/TRK2 OS=Candida tenuis (strain ATCC 10573 / BCRC 21748 / CBS 615 / JCM 9827 / NBRC 10315 / NRRL Y-1498 / VKM Y-70) GN=CANTEDRAFT_128188 PE=4 SV=1MKLRYPFVADRPLAWQIREFIDNILSVTLPYLRMFIPNFKAAHYSYIVFWSIIGSIMIFPVKNIKYIDALFFASGASAQAGLNTVDVN LLSLWQQMCLYIIATFTTPIFIHGFVLFFRLWSFERYFDNIKVTSKLNNKMRRTFTMGSRTRTNDSTGINTRANTGYNLQLGNNNNIPM MTFEDPPKDDDQTVMDTTPPSSSTQDASTNLDPQVDHMSEPSDEDEQSSRPPRSPREHQPRSVPSPVPPIKKRNHEIAPSEMYRSI NLLQKNNQQHEDDDEVLIIKSPNQIENEDSSRPIFTKKGPSLSFEPPHRLMSTQKLKTRVRKRFKKIRSMSVNSLEDENDSIDSNDEGE DEDGIDELDESEGGDGEVESEVFSNDDESVDQVRRATSNLALPSTDQSGKKYAKRSNTFDVRTSADETPAAKTHRRNVSRSRFNLT PGVSRSSLDEENSLFTSISRTLTTSLTRSKTTNYLSWEPTIGRNSNFVHLTDEQKEELGGVEYRAMILLIKIVWSYYIGFHVLALVVHLA WISKQPAYKEMIRSYGVTPVWWSFFTAQTTFNDLGFTLTPNSMIGFNKSIYILLWDSFLIIAGNTGFPVFLRFIIWVLYKFARPMSLYEE SLAFLLDHPRRCFTLLFPSGPTWWLFGILIALNGIDWIFFIILDLKNSYLLDIPTGFRVVCGLFNAVNTRTAGLSAVDLGKLHTAVQVSYVI MMYISVLPLAISIRRTNVYEEQSLGIYIKDENHVEEDHEKSPTNFIGNHLRNQLSFDLWFIFLGLFIICIAENSKLDNQDIHFTAFTVLFECV SAYGTVGLSLGYPTANTSLAGQFTVVSKLILIAMMIRGRHRGLPYSLDRAIMTPNANMIKRDQVQAEHAIRRQATLERTQTQATNSAS GNDLFKALSRRGNEILRRRRSTAGGSFSYN
4E-148	503	8.1	1E-146	498.4	1.4	2.1	2	G3Y8I7_ASPNA	Uncharacterized protein	ASPNIDRAFT_205063	Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	826	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	380704	>tr|G3Y8I7|G3Y8I7_ASPNA Uncharacterized protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) GN=ASPNIDRAFT_205063 PE=4 SV=1MFSAVLRRATSVTSRFTSHIPWLKNLRMNFVLIHVYVYIATSLLSSIIIYPGANLDYTDALFLSAGAATQSGLNTVDLNTLHTYQQIV LYVVSMLTTPIFIHTVLVFVRLYWFEKRFQHVVSDARALRHTRSRLRTISEDKDGQSSSREEAGVAGRSIVVLRDTLGHPGSRQQAKE KSGEDSPPASPTARDPPENLGEDASNALNQKLGIGLGNSLGNLRVPAQLSPEHHIAFLENQRRNKGALRIPSPREYDNGGAPQVLEE EEEEDPCDISKEDENDKDEDDEDDDKDEDRPRRLDGPHITINEPDMIRTRTRNSTFPRLDTRPTFRETKNDTDASQLGRLTSRRPTLH NLFRTLTQERERSTQPYLSWNATVGRNSNFVDLTEEQRDELGGIEYRALKTLAVVLISYYAFFHILGILCLVPWIMTTHWGKVVEEIGQ GRPWWAIFMAQSAFNDVGFTLTPDSLSSFQRAIFPLLLMTFLIIIGNTGFPCMLRLIIWVLSKVTRAETPLWEELRFLLDHPRRCFTLLF PRNATWWLFAILVALNGIDLIFFIILDLNDSAVTSLPTGIRIVDGLFQAACTRTAGLAVISVSDLHPAVQVSYLIMMYISVFPIAISLRRTNV YEEKSLGIYASTEDDESDENQTPPSYIGAHLRKQLSFDLWYVFLGLFIITIVEGKRLQQQDEYSFQVWSVLFEVVSAYGTVGLSLGYP GVNASFSSQFQVLSKLVIIAMQIRGRHRGLPYALDRAILLPSESLNQNEIADAERRMRRRTSSLSQMSMDRQQSQGRPEHGASTSLD PKDRASQTWNNGDIIRRQSTIRSQRSQR

5E-148	503	8.1	1E-146	498.3	1.4	2.1	2	A2QGC8_ASPNC	Aspergillus niger contig An03c0080, genomic contig	An03g02700	Aspergillus niger (strain CBS 513.88 / FGSC A1513)	843	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain CBS 513.88 / FGSC A1513)	425011	>tr|A2QGC8|A2QGC8_ASPNC Aspergillus niger contig An03c0080, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=An03g02700 PE=4 SV=1MFSAVLRRATSVTSRFTSHIPWLKNLRMNFVLIHYVYIIATSLLSSIIIYPGANLDYTDALFLSAGAATQSGLNTVDLNTLHTYQQIVLYVVSMLTTPIFIHTVLVFVRLYWFEKRFQHVVSDARALRHTRSRLRTISEDKDGQSSSREEAGVAGRSIVVLRDTLGHPGSRQQAKEKSGEDSPPASPTARDPPENLGEDASNALNQKLGIGLGNSLGNLRVPAQLSPEHHIAFLENQRRNKGALRIPSPREYDNGGAPQVLEEEEEELNRPVRTSSNSSSSERSPCDISKEDENDKDEDDEDDDKDEDRPRRLDGPHITINEPDMIRTRTRNSTFPRLDTRPTFRETKNDTDASQLGRLTSRRPTLHNLFRTLTQERERSTQPYLSWNATVGRNSNFVDLTEEQRDELGGIEYRALKTLAVVLISYYAFFHILGILCLVPWIMTTHWGKVVEEIGQGRPWWAIFMAQSAFNDVGFTLTPDSLSSFQRAIFPLLLMTFLIIIGNTGFPCMLRLIIWVLSKVTRAETPLWEELRFLLDHPRRCFTLLFPRNATWWLFAILVALNGIDLIFFIILDLNDSAVTSLPTGIRIVDGLFQAACTRTAGLAVISVSDLHPAVQVSYLIMMYISVFPIAISLRRTNVYEEKSLGIYASTEDDESDENQTPPSYIGAHLRKQLSFDLWYVFLGLFIITIVEGKRLQQQDEYSFQVWSVLFEVVSAYGTVGLSLGYPGVNASFSSQFQVLSKLVIIAMQIRGRHRGLPYALDRAILLPSESLNQNEIADAERRMRRRTSSLSQMSMDRQQSQGRPXHGASTSLDPKDRASQTWNNGDIIRRQSTIRSQRSQR
5E-148	503	8.6	2E-146	498	1.9	2.1	2	G7XZM3_ASPKW	Potassium ion transporter	AKAW_10496	Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	842	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus kawachii (White koji mold) (Aspergillus awamori var. kawachi), Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	1033177	>tr|G7XZM3|G7XZM3_ASPKW Potassium ion transporter OS=Aspergillus kawachii (strain NBRC 4308) GN=AKAW_10496 PE=4 SV=1MFSAVLRRATSVTSRFTSRIPWLKNLRMNFVLIHYVYIIATALLSSVIIYPGANLDYTDALFLSAGAATQSGLNTVDLNTLHTYQQVVLYVVSMLTTPIFIHTVLVFVRLYWFEKRFQHVVSDARALRHTRSRLRTISEDKDGQSSSREEAGVAGRSIVVLRDTLGQPGSRQQVKEKSGEDSPPASPTARDPPEKLGEDANNALNQKLAIGLGNSLGNLRVPAQLSPEHHIAFLENQRRNKGALRIPSPREYDNGGAPQVLEEEEEETNRPVRTSSNSSSSERSPCDMSKEDENGKDEDDEDDEDDEDRPRRLDGPHITINEPDMIRTRTRNSTFPRLDTRPTFRETKNDSDASQLGRLTSRRPTLHNLFRTLTQERERSTQPYLSWNATVGRNSNFVDLTEEQRDELGGIEYRALKTLAVVLISYYAFFHILGILCLVPWIMTTHWGKVVEEIGQGRPWWAIFMAQSAFNDVGFTLTPDSLSSFQKAIFPLLLMTFLIIIGNTGFPCMLRLIIWALSKVTRAETPLWEELRFLLDHPRRCFTLLFPRNATWWLFAILVALNGIDLIFFIILDLNDSVVTSLPTGIRIVDGLFQAACTRTAGLAVISVSDLHPAVQVSYLIMMYISVFPIAISLRRTNVYEEKSLGIYASTEDDESDENQTPPSYIGAHLRKQLSFDLWYVFLGLFIITIVEGKRLQQQDEYSFQVWSVLFEVVSAYGTVGLSLGYPGVNASFSSQFQVLSKLVIIAMQIRGRHRGLPYALDRAILLPSESLNQNEIADAERRMRRRTSSLSQMSMDRQQSQGRPEHGASTSLDPKDRASQTWNHGDIIRRQSTMRSQRSQR
2E-147	501	12.2	4E-147	500.2	3.5	2.1	2	N1QG74_SPHMS	Uncharacterized protein	SEPMUDRAFT_150009	Sphaerulina musiva (strain SO2202) (Poplar stem canker fungus) (Septoria musiva)	1016	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Mycosphaerellaceae, Sphaerulina, Sphaerulina musiva, Sphaerulina musiva (strain SO2202) (Poplar stem canker fungus) (Septoria musiva)	692275	>tr|N1QG74|N1QG74_SPHMS Uncharacterized protein OS=Sphaerulina musiva (strain SO2202) GN=SEPMUDRAFT_150009 PE=4 SV=1MVNTNDGPLSPLSEVARYFIALIPSKDSFKKPHFNYITLHYMYMVLMSIIGSIMLFPAGPSALMEYIDALFFAAGMATQSGLNTIDVNLLHTYQQVVMMLLTCLCTPIFINTCVVFVRLYWFEKRFEHIVKEARAKAKRGRRFTLSRSKSQMQTEKDPRNSAAGKMEAGGVQGKRIIVNPETARFIDRNGNDEDTEKRREQFREKVGPSIGLEPSNDSPLGSTCTRTNSKDKDANTASSDSTVAVPAVHVDGEHEYPSPKTQSQALAVPIAHVDGDLEHPSPKTQSHALAVPVAHVDEEHDHPSPKTQPETQFMGLNPKLLHREITFADEAPPLGRESPELARVPEQRDVSKHVEFLERQQANAKKGGALYIPGPRDFDRGEKPEAVDDDDLVISRLQKASSFGGPAHRSRSEDGRSVMSHDDRQVHRGITINLPEHPAHRERAATKSKDDEEIDIDEDEEEKSRFARMISGLDRRRHTRVPSISEGRRSFARAWTNLTGPPKDVEPMPYFSWTATTGRNSIFMGLTSEQREELGGIEYRALKTLAKILIAYYVGFHVLGMVVLLPWIRYTQPWNGVVVEDGQNPSWWGVFTPASMFNDLGFTLTPDSMISFQSAVLPLLFGSFLIIIGNTGFPCMLRFIIWTLSKIVSYESEMWKELRFLLDHPRRCFTLLFPSKATWWLFWVLIGLNLLDLVFFIILDINQPVVSDLHPGVRVLNGWFQATSTRTAGFASVNLADLHAAIQVSYMIMMYISVFPIAISVRRTNVYEEKSLGIFGGEEDVSGEGEQSYVSQHLRRQLSFDLWYIFLGLFIIAIVEGDRISNTNEPAFTMFSVLFEIVSAYGTVGLSLGYPGINASFSAEFRTISKLVIIAMMIRGRHRGLPYALDRAILLPSDKLQQREQEEAERQLVRRGSMFAEENQNMFPRNKTWEQGELDQWGLPAQHTRPHSRADHATTVGSGGDHEPEGLRRVVTRRSTALSNKSGTGAVPSSPLRTRGRSLSRVIVGGLSAGPTWSKRD
2E-147	501	3.1	2E-147	501	2.1	2.1	2	M7U67_BOTF1	Putative potassium transporter protein	BcDW1_9374	Botryotinia fuckeliana (strain BcDW1) (Noble rot fungus) (Botrytis cinerea)	907	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Sclerotiniaceae, Botrytis, Botryotinia fuckeliana (Noble rot fungus) (Botrytis cinerea), Botryotinia fuckeliana (strain BcDW1) (Noble rot fungus) (Botrytis cinerea)	1290391	>tr|M7U67|M7U67_BOTF1 Putative potassium transporter protein OS=Botrytinia fuckeliana (strain BcDW1) GN=BcDW1_9374 PE=4 SV=1MFSLLIELWQQIAALKPSFISKSPHFNFITVHYFWIIGMALLGSICLYIRGDIPYIDALFFASGCATQSGLNTININTLNTWQQIVLYLIPIFTNPITINSFVVFLRLYWFEKRFQHIASQNKRNRRSIAKSFSRSRTTGADTVDAEKGVNGRNIVVMHGTTRANVMRDNRDAIDDIQAAIEKEKALNKADAVNGSGSSSNISSTETANDPSPTSHHTQIKFADQVKRSNGLADEELRLPVRRRDEDHIAFLERQRNPEDRTILRIPGPRDADAGVAPQTVEEEEEDPVIRTLSRRGSMYSRRGSIDRGTLNGESQWQDHYPSRKRNVTIEVPTHPKAERAVDDVKAAGATMKGVMRFRNNRNTEGAEATEAQGNGNGAVMSRLKSRAPTFQSIKTALTGEKEDPTPYLSWAPTIGRNSAFVDLTEQQREELGGIEYRSLKSLALILTCYFVGFSIFAVVCLLPWILNSRTYGSIVEQDGQGRVWWSIFTASSAFTDLGFTLTPDSMISFNTAIWPLLLMSFLIIIGNTGFPIMLRFIIWVTTLWVPRNSAVWEELRFLLDHPRRCFTLLFPSKATWWLFWILVILNGVDLLFFIILDLGNSVVTNLPVNIRVLDGWFQAASTRTAGFGVVNLAELHPAIQVSYLIMMYISVLPIAISVRRTNVYEEKSLGIYGSPTEENEDEGEPSYVGAHLRRQLSFDLWYIFLGLFIISIAEGGRLQGTDPSINMFSVLFEIVSAYGTVGLSLGYPGIDASLSAEFNVVSKLVIIAMQIRGRHRGLPYELDRAILLPSEHLAEKEALDAAQRVYRRNSNATAVSNGADLATVNTGVQRANTERQGPPTNFLSSLLHPGPTIPNSHRNQGTTHVRRHSIATPERGRSVSPKASGGIFSKWNSSDKHQNNVDKKISE
4E-147	500	11	1E-146	498.9	4.1	2.1	2	K1WXJ9_MARBU	Potassium transporter	MBM_08456	Marssonina brunnea f. sp. multigermtubi (strain MB_m1) (Marssonina leaf spot fungus)	933	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Dermateaceae, Marssonina, Marssonina brunnea, Marssonina brunnea f. sp. 'multigermtubi', Marssonina brunnea f. sp. multigermtubi (strain MB_m1) (Marssonina leaf spot fungus)	1072389	>tr|K1WXJ9|K1WXJ9_MARBU Potassium transporter OS=Marssonina brunnea f. sp. multigermtubi (strain MB_m1) GN=MBM_08456 PE=4 SV=1MFSILSDIWGQLKSLKPAFISKTPHFNFITVHYFWIIGMALFGSLCLYIRGDLAYIDALFFASGSATQSGLNTVDLNLLNTWQQVVLYLISIVTNPITINSFVVFLRLYWFEKRFQHIARESRKNRLSIAKARTLEPDIGDEERGVRGRRIIVNHASTRPNGMTNKDAIPEDYDDQVKKEKILASDNASGSHSSESTTKGRGSETAVDDDEKYLVGDQSRPQIKFADQVKRSNGLADEPIRLPAQRSHEDHIAFLERQRNQDEGAVLRIPGPRDADAGVAPVTLDHQDQISPIMSRRESRLSGQFSHQDQTSTKQGNEEHPPSARRNITIAEPTQSHITEKIVVDAKAAKDTCGVLRLRRPRIFGGEKTDADEHTQHARRSSTFNTIMTALSRDKDEGMPYLSWEPTVGRNSAFVDLTEEQREELGGIEYRSLKSLVLILIAYYVGFTLFGVVSIVPWIFSDDSYGTIVEAAGASRIWWGIFTSNSAFTDLGFTLTPDSMISFQKAQWLLVVMSFLIIIGNTGFPIMLRIIIWITSKYVPRESGIWEELKFLLDHPRRCFTLLFPSKATWWLFWILVILNGVDLVFFIILDLGNEIVTDLPVHIRVLAGWFQAVSTRTAGFAVVNLAALHPAIQVSYLIMMYISVLPIAISVRRTNVYEEKSLGIYGSYQEDNADMEEPSYVGAHLRRQLSFDLWYIFLGLFIISISEGERIQNGDPAFTMFSVLFEIISAYGTVGLSLGYTNINASFSAEFGIIAKLVIIAMQIRGRHRGLPYELDRAILLPSEHLQKREMDDAVRAMRRRRSSLATMAANGGPVSSGALKTARTRSRSPVNLLGTLLHPGPTIPNSHRDPMPYKSRRASTVSVGMRSRTTRSVSSAHSSCADGPTEKRGRTEGRRSFFQEGVNPAPTVHPETISEATSPATSGNTSMGVSIK

7E-147	499	13.4	2E-145	494.9	3.9	2.1	2	M2ZR93_PSEFD	Uncharacterized protein (Fragment)	MYCFIDRAFT_1070476	Pseudocercospora fijiensis (strain CIRAD86) (Black leaf streak disease fungus) (Mycosphaerella fijiensis)	758	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Mycosphaerellaceae, Pseudocercospora, Pseudocercospora fijiensis, Pseudocercospora fijiensis (strain CIRAD86) (Black leaf streak disease fungus) (Mycosphaerella fijiensis)	383855	>tr|M2ZR93|M2ZR93_PSEFD Uncharacterized protein (Fragment) OS=Pseudocercospora fijiensis (strain CIRAD86) GN=MYCFIDRAFT_107046 PE=4 SV=1HFNFITWHYLYMVGMTILGSIMLYPAGLMDYIDALFFAAGMATQSGLNTIDVNTLYTYQQVVMMLMTCICTPIFINTVVVFIRLYW FEKRFEHIVQEVRAQKRTKTRSIGSRSKSQMREGKDEDADPSKLEQGVRGISLPVNQEDQDAETPQSPFMGLNPRLNREITFADEVP ASGRRSPELARVPSHRDVSKHIEFLQRQQNNAKKGGALYIPGPRDFDRGERPEELEEDLAIQRRKTRPTLGGRRSTDDPRGRGGSD TAKDSPGADHPRRGVTINLPDHPAHRDQMATVEKDDEEDGDGMSRLGRIKSALSLGRSHRNPGEHEHRSFAKTLTNLTHKKEDEDP MPYLSWTATTGRNSMFVGLTSEQREELGGIEYRALKLLAKILIAYYVGFHLLGMLILLPWIASTQPWKGIVRADGQNPVWWGIFTPAS MFNDLGFTLTPDSMISFDNAILPLLFGSFLIIIGNTGFPCMLRFIIWFLSKVVRHGSGTWEELRFLLDHPRRCFTLLFPSKATWWLFWVL VLLNVVDLIFFIILDLDAGVVTDLSPGLRVLNGWFQATSTRTAGFSSVNLAALHAAIQVSYMIMMYISVFPIAISVRRTNVYEEKSLGIFG GEEDPGDDSDQSYVSQHLRRQLSFDLWYIFLGLFVIAVVEGDRIGNTNQYAFTTFSVLFEIVSAYGTVGLSLGYPGINASFSAEFRTTS KLVIIAMMIRGRHRGLPYALDRAILLPSEKLHKKEAEEAAVLTRRLTRRGSIFSE
8E-147	499	13.3	3E-146	497.3	3.8	2.1	2	W1Q8T4_OGAPD	High-affinity potassium transport protein	HPODL_01349	Ogataea parapolymorpha (strain DL-1 / ATCC 26012 / NRRL Y-7560) (Yeast) (Hansenula polymorpha)	1084	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Pichiaceae, Ogataea, Ogataea parapolymorpha, Ogataea parapolymorpha (strain DL-1 / ATCC 26012 / NRRL Y-7560) (Yeast) (Hansenula polymorpha)	871575	>tr|W1Q8T4|W1Q8T4_OGAPD High-affinity potassium transport protein OS=Ogataea parapolymorpha (strain DL-1 / ATCC 26012 / NRRL Y-7560) GN=HPODL_01349 PE=4 SV=1MFGTKTFWFKARKRIYHVQAKLGPIVRKLIPNFLVAHYTYIVFWCIIGSILIYPKKNIKYIDALFFAAGASTQAGLNTVDTNNLSLYQ QIVIYCVTMLTTPIFIHSAIVFLRLFWFEKSFDDIKEKSMQNFKMRRSATLAQFRTQTMDTSRSIHQNRTNTTGFHNKDYNTHNASEDL GTRLNKLNQQQQVEDREHKLDKIFEDEYTVPMSSSSGGSPETKNHEKGQDIELADLYASHDYPTDMGGVVHYSEPSDEEGEQEVQ VPETRSRDIKFVDLPKPPNKRRNKDVEPRDLYMSISMMQQQRDNNIAEDESGPALVIQGPAERTGSKLPGHISRHEKEMKRKQLKKIK KMEKMQDEHPSAFSKPPKEKSIQFQDPARPRKSSTIKWESQTPVPEPEAAEDESALSDEMNSSLEDAGDDPLANDDALSDEENGVG FRHVGRTQSHVMAVPHGKHGTKLDRRAHTFDVPVEKKPESHKKGVNIVKSPTFDKMLRKNMKDKYNRFTRIGRRFTSSRTGHFNAF TDDIETLSDNDLASLYSRSSKHAPPNYLSWTPTIGRNSTFVALTDEQKEELGGVEYRALKLLSTILVSYYIGFHLVGIICFVPFITKRMKY LNIIRSDGVAPAWWGFWYPQTCFNDLGITLTPDSMLSFKENAFTLIIGGFLIVAGNTGFPIFLRFIIWVLHRFSKPLTLYKESLAFLLEHP RRCFTLLFPSGPTWWLLFVLVVLNCIDWLLFIILDFNKSVLESVRPGYRVLDGLFQAISTRTAGLSVVDLSRLSPAVQVSYLVMMYISV MPLAISIRRTNVYEEQSLGVYFDNNDVSSTNNADDNNNNNQNGKSNQTISFIGTHLRKQLSFDLWFLFLGLFIICISEGGRLNQGDIHFT IFSCLFEITSAYGTVGLSLGYPNTTPSFCGQFNTLSKVVLIIMMVRGRHRGLPYAIDRAIMLETDKIKMRDDLQAHHTLRRAQTMLSMPT YASSHHGPLLRVNTTRNEGFDTSNIWPFLKRKASAVAGEFRRNLQTRTYGSEDEEALEFDDESVPSYNGYREAENNERNVMDRNIN ERSSLSPTGPASADPSSKPNRHNSL
1E-146	499	8.4	4E-146	496.9	3.8	2	2	H6BUW9_EXODN	Putative uncharacterized protein	HMPREF1120_03098	Exophiala dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) (Black yeast) (Wangiella dermatitidis)	866	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Chaetothyriomycetidae, Chaetothyriales (black yeasts), Herpotrichiellaceae, Exophiala, Exophiala dermatitidis (Black yeast) (Wangiella dermatitidis), Exophiala dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) (Black yeast) (Wangiella dermatitidis)	858893	>tr|H6BUW9|H6BUW9_EXODN Putative uncharacterized protein OS=Exophiala dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) GN=HMPREF1120_03098 PE=4 SV=1MAPQWTSQFWEFLQQNVIPDALVKKRLNFITIHYIYVIGLSLLLSVILYGIGDIHYIDALFFASGSCTQSGLNTIDINNLYLGQQVVL YMGAMICNPIVVHSAVVFIRLYWFEKRFKDVVRNSNLIRRTRSRQRTETFGKPDPEQGSLGVRGRAIQVLRNTGRTVDPMEKTDGRA IHTNGKAVESSNESKPNHKEAQDPVGDDDYLRLQTTRSEDDVRLPQQVSPEQHIRFLENQRNPSDTTALRIPSPREFERGGRPENVN NSIDDTLMRKITSDPDLSSANEKRSIEQHTRADGVPAHITIDEPRVLRDRNDKVSTFPRLNTRQSTQARQTYDSSEPGSNLRRRRSNT FRTLTRSNTARTMDPAPYLSWQPTIGRNSLFVGLTEEQREELGGIEYRALKTLALILVLYFFLFHICGIICLVPWILHSGKYGKVVTDQS QGRVWWGIFTSGSAFNDLGFTLTNNSMLSFGTAVFPMLLMSFLIIIGNTGFPCMLRLVIWIVSQVVSFGGPLWEELRFLLDHPRRCFT LLFPSNATWWLFAILVMLNGIDLIFFVILDLNDSIVKQMSGGIKFVDGLFQAASTRTAGFAVVNLAELHPAIQVSYLIMMYISVFPIAISMR RTNVYEERSLGIYGKVADEEEDEREPSYIGAHLRRQLSFDLWYVFLGLFIIAIVEGGRLQNTNEYAFTLFSVLFEIVSAYGTVGLSLGYP TINASFSAEFHTLSKLVIIAMQIRGRHRGLPYELDRAILLPSESLQAKEAKEAERVARRRRSSAGQSMMSAVDGHLEGRRFRAETGLSS ATQANDGDEPYQRGRANTNRTHQSTASGSEHPPHHGARHGLGTALYKLTSEIDSIKEESPATRENMG
2E-146	498	6	5E-146	496.5	2	2	2	S3E680_GLAL2	Uncharacterized protein	GLAREA_06881	Glarea lozoyensis (strain ATCC 20868 / MF5171)	944	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Helotiaceae, Glarea, Glarea lozoyensis, Glarea lozoyensis (strain ATCC 20868 / MF5171)	1116229	>tr|S3E680|S3E680_GLAL2 Uncharacterized protein OS=Glarea lozoyensis (strain ATCC 20868 / MF5171) GN=GLAREA_06881 PE=4 SV=1MMNFSSIVMGIWNQIKSLKPAFISKNPHFNFINIHYFWIMGWALTGSICIFANGGIHYIDALFLGSGAATQSGLNTIDINLLTTWQQ VVLYIVPMLTNPITINSLVVVFRLVLFEKRFKKIAAESKKNRRSMAKTFSRSRTTEQNIDSEEMGVRGRSIVVMHNMTASNGMSTDRSR TEEFAHHMEKINAIEEEPARSSNDSDGTKRQPSANGARSKSPGAADRPSTGIKFADQHKPSEKTIAYGELNNGIVDEEERRPSHRSPE EHIAILERQRKQDDGAVLRIPGPRDADAGVAPQAVDDSDVISRTMSRRASTLQSHTADTDAVALNGDDHPTFDNEAAKPRNITIAEPE KEPAGERATKDTSGAKHSNAGLRFRRSRLSRYTTEKDDEASSTTPATRTGTFQAIKSALTSSKDEGAPYLSWEPTVGRNSAFVDLTE DQREELGGIEYRSLKSLAAILLCYFVGFSLLGIVSLLPWILETDTYGSVVSNAGQGKTWWGIFTANSAFTDLGFTLTPDSMISFQTAVW PLLIMTYLIIGNTGFPIMLRIIIWVLAKVVPKNSGIWEELKFLLDHPRRCFTLLFPAGATWVLFLILCGLNGLDLLFFIILDFGNSVVTQLPV HIRFLDGWFQAASTRTAGFAVVNLALLHPAIQVSYLIMMYISVLPIAMSVRRTNVYEEDSLGVYGSSEEENSDAAEPSYIGAHLRRQLS FDLWYIFLGFFIITISEGSRLQSGDPGFSMFSVLFEIVSAYGTVGLSLGYTNINASFSAEFGVIAKLVIIAMQIRGRHRGLPYELDRAILLP SEQLAKREADAAARARRNSDLTQVNTRGTKLDRTASRATSSRGGQNFFSGLLHPGPTIPNNNLGAIRTRPVRERRHSIATTPMRRGL SRSISPTATGIMARENHAMGMALGGDGAESRGRTEGRRSFFKDGVNPAPAPDAQ
2E-146	498	10.8	3E-146	497.2	2.5	2.1	2	Q2UAL1_ASPOR	Na+/K+ transporter	AO090102000343	Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	778	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus oryzae (Yellow koji mold), Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	510516	>tr|Q2UAL1|Q2UAL1_ASPOR Na+/K+ transporter OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=AO090102000343 PE=4 SV=1MFSSFIRGVSSLKSQVPLLKNLHLNYILIHYTYIIAMSIITSIIYPGNDLAYIDALFFAAGAATQSGLNTVDFNLLRTYQQVILYWVSM LTTPIFINTVLVFVRLYWFEKRFQHVVRDARALRQTRSRMRTISEDKDNQTHDREEAGVGGRAIVVLRNNQGDAPGREQQDAIYKTP SDSESGPSSSAARDESGNTSEQETDPNNNLKRGFGSLRVPAQLSPEQHIAFLENQRKPKGALRIPSPREYDRGGVPEALEEGEGEG AEAARQTSNLSDEPPSPRHVEEDDQVGPMEGPHITINEPDMIRTRTRNSTFPRLDTRPTVRETRDFGDPSPLARTTTRRPTFTGVFR SLTQERDRNTLPYLSWNATVGRNSQFVDLTEEQRDELGGIEYRALKTLAVVLISYYVFFHLLGVVCLVPWIMTTRWGAVVTNIGQGR PWWAIFTAASSFNDVGFSITPDSMSSFQEAVFPLLLLAFLIIIGNTGFPCMLRLIIWLLSKFARKESPLWEELRFLLDHPRRCFTLLFPRN ATWWLFAILVALNGIDLIFFIILDLKDSAVTSLSTGIKILDGLYQAACTRTAGFSVVSISELHPAVQVSYMIMMYISVFPIAISLRRRTNVYEE QSLGVYPAEEDDNEDNQTAPSYIGAHLRRQLSFDLWYVFLGLFIITIVEGGRLQRQDDYSFQIWSVLFEVVSAYGTVGLSMGYPGVN ASFASQFQTLSKLVIIAMQVRGRHRGLPYSLDRAILLPSEALNHHEIADAERRMRRRASSLSQISSLALS

3E-146	497	11.1	5E-146	496.6	2.5	2.1	2	B8NQ59_ASPFN	Potassium ion transporter (Trk1), putative	AFLA_004500	Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	917	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus flavus, Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	332952	/ NRRL 3357 / JCM 12722 / SRRC 167) GN=AFLA_004500 PE=4 SV=1METSATAFRLRLRWASGSAKEPIRVSDLPMWRMVEVEPRGGTATGCALPSAAGPQAERLKILPAHHPRENSSTISWLPDGRLF HRLSPSGGTAVVVKMFSSFIRGVSSLKSQVPLLKNLHLNYILIHYTYIIAMSIITSIIIYPGNDLAYIDALFFAAGAATQSGLNTVDFNLLRTY QQVILYWVSMLTTPIFINTVLVFVRLYWFEKRFQHVVRDARALRQTRSRMRTISEDKDNQTHDREEAGVGGRAIVVLRNNQGDAPGR EQQDAIYKTPSDSESGPSSSAARDESGNTSEQETDPNNNLKRGFGSLRVPAQLSPEQHIAFLENQRKPKGALRIPSPREYDRGGVPE ALEEGEGEGAEAARQTSNLSDEPPSPRHVEEDDQVGPMEGPHITINEPDMIRTRTRNSTFPRLDTRPTVRETRDFGDPSPLARTTTR RPTFTGVFRSLTQERDRNTLPYLSWNATVGRNSQFVDLTEEQRDELGGIEYRALKTLAVVLISYYVFFHLLGVVCLVPWIMTTRWGA VVTNIGQGRPWWAIFTAASSFNDVGFSITPDSMSSFQEAVFPLLLLAFLIIIGNTGFPCMLRLIIWLLSKFARKESPLWEELRFLLDHPR RCFTLLFPRNATWWLFAILVALNGIDLIFFIILDLKDSAVTSLSTGIKILDGLYQAACTRTAGFSVVSISELHPAVQVSYMIMMYISVFPIAIS LRRTNVYEEQSLGVYPAEEDDNEDNQTAPSYIGAHLRRQLSFDLWYVFLGLFIITIVEGGRLQRQDDYSFQIWSVLFEVVSAYGTVGL SMGYPGVNASFASQFQTLSKLVIIAMQVRGRHRGLPYSLDRAILLPSEALNHHEIADAERRMRRRASSLSQMSVDHRLSQAQENGTS TGLDPRDKNTSAWFSGSPFMRRQSTMRSQRSQR
4E-146	497	9	1E-143	488.8	2.3	2.1	2	S8BVB5_DACHA	Uncharacterized protein	H072_6953	Dactylellina haptotyla (strain CBS 200.50) (Nematode-trapping fungus) (Monacrosporium haptotylum)	879	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, Orbiliomycetes, Orbiliales, Orbiliaceae, mitosporic Orbiliaceae, Dactylellina, Dactylellina haptotyla, Dactylellina haptotyla (strain CBS 200.50) (Nematode-trapping fungus) (Monacrosporium haptotylum)	1284197	>tr|S8BVB5|S8BVB5_DACHA Uncharacterized protein OS=Dactylellina haptotyla (strain CBS 200.50) GN=H072_6953 PE=4 SV=1MIKIIRPEWIPERFTKFRKLNFITIHYLYIIGWCITASILLYPIKNMQYIDALFFASGASTQSGLNTIDINQLKTYQQVVLMLVACFTNP VVINTGVVFVRLYWFEKRFDTIVEQSKTFVMERKATSRRKSESEGVDGVDSAERGVAGRTINVLFNSGRKTNADSSTNHPERTDEKT TTGNKDLQEFRRNFGVGSTGPHRPISFPGFRGHNRSRSDANHQLALRQSKPGGMFADSNTDNDFAIEDDDDEPQKPPMSPAPFNP ELTGILEKGDPEPSTSTAAPHITFADPKKSQRKESTTYVVPTPFEVETRGSGLATKFMDGEDEEEKGPRDEEPPPETPGPTAVFRRAI TIDEPTMTRDSMYSSGTRQRIKPLNTRAATDQAYLVTPATPGLHRALSDVWKRRRNSSPSRRSSRTVERMPYLSYNPTIGRNSQFNY GELTDEQKEELGGVEYRALRTLAYILVGYFFFQIFGVLCLLPWIHTQLRWAEVVDNAGMNRSWWAIFTASSMFTDLGFTLTPDSMIS FNTATWPLLAGAYLIIIGNTGFPCMLRFIIWALWKMCPQNWVTKESLHFLLDHPRRCFTLLFPSAATWWLFAVLVILNATDVILFIVLDL NNGDVTSLPVNYRILDSFFQAVSTRTAGLAVVNLADLHPGVQVSYLIMMYISVFPIAISVRRTNVYEERSLGVYADHDEDENPNDHSFV GAHLRRQLSFDLWYVFVGLFAICIAEGAKIANRSDYAFTQFSCLFEVISAYGTVGLSLGYPDVNTSFSAQFTTFSKVVIMAMMVRGRH RGLPYELDRAILLPSESLQQKEEEDVALRLQRRADTVERRSLRPMSRGPTNENKINGGMNGTNGGIAPNGIGEMEGGITSGYQIHSP
4E-146	497	1.1	1E-143	488.9	0.4	2	2	C5FHX9_ARTOC	High-affinity potassium transport protein	MCYG_01778	Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) (Microsporum canis)	835	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Arthroderma, Arthroderma otae (Microsporum canis), Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) (Microsporum canis)	554155	>tr|C5FHX9|C5FHX9_ARTOC High-affinity potassium transport protein OS=Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) GN=MCYG_01778 PE=4 SV=1MDTVKAALERCRPSPAVLEKLMAIKQKTPVLRDLHYNFICLHYAWIIGVTLVGSIILYPGGNMTYVDALFFASGSATQSGLNTIDV NRLYTYQQVWLWMGSMIANPIVIHSAVVFVRLYWFEQRFQHVVREAKALRRSRSRSRANTREPDDGNDVHRAEAGVRGRDIVVLRN NEGHAQGRFLDAPKKEPETTSESGSSLQNPAEGQQGESTANGQQAREGPKVDDSLLAPSHFPGDARIQWSVPSDSERHITFLEHQ RRQTGALRIPSPREYDRGGVPEALDETEGSELHRNATVQSDPSADQTGTSLPTSPGPINQHITIDEPNITRTRKATHSRQGERDVDDT STIRRVTSRKSMVASFLRSRTQDQTQEAPYLSWEPTIGRNSAFVDLSETQREELGGIEYRALKTLAVVLLGYFFFHLLGIVCLTPWIL NTRWGEVVRAAGQGRPWWAVFSAGSAFNDQGFTVTPDSMLSFYDAVFPMLLMTFLILIGNTGFPCMLRFIIWFFSKIVPTGSGVWE ELKFLLDHPRRCFTLLFPSSANWWLFWVLVLLNGVDLIFFVVLDLNDPDVTRIPGGIRFVDGLFQAAATRTAGLSVISLTTLHPAIQVSY MIMMYISVFPIAISVRRTNVYEERSLGIYSDPDEYSENEKEPSFVGAHLQKQLSFDIWYIFLGLFVISIIEGTRLDNQTDVGFSLFAVLFEV VSAYGTVGLSLGYPNSNASFSAQFHTLSKLVIIAMEIRGRHRGLPYALDRAVLLPSEALHRKEMDDATKRLRRRNSNVSAISAATGQAS GLFRDDGGLMSRASHSQPAGPSDGPPNTASSGRAKRLSTHQENA
5E-146	497	5.5	5E-146	496.5	3.8	2	1	B6HJ17_PENCW	Pc21g15020 protein	Pc21g15020 PCH_Pc21g15020	Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)	835	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium chrysogenum complex, Penicillium rubens, Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)	500485	>tr|B6HJ17|B6HJ17_PENCW Pc21g15020 protein OS=Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) GN=Pc21g15020 PE=4 SV=1MFSAFFRRVKSYKEKIPVLKDIHLNFILLHYAYIISWAITGSIIVYAGGNIAYIDALFFAAGAATQSGLNTVDLNLLRLYQQIVLYLITC LCTPIFIHSALVFIRLYWFEKRFQHVVRDARAMRRTRSRMETVTDDGDSENINRAELGVSGRPIVVIRDDSGDARDGRMTDPSSKNVN SGINTPEPRASSVVDSSSSEGTDTGSEREPRFGLGSLKVPTHLSPEHHIAFLEKQRKDKGALRIPSPREYDRGGAPEALEEDADQEGEQ AQRPSDQDDQDDQDEQSPVAHPEELDQLGPLEGPHITINEPDISRTRPRGNTFPRLDTRPTVRETKDGNETTTLAPTNTRNTIRGVFR SMTQERDLSTQPYLSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLAVVLITYYIGFHLIGMVSLVGWIMRANKWGDIVRADGIGR PWWGIFTSASAFNDLGFTLTPDSMTSFQRAVFPLLMMSFLIIIGNTAFPCMLRLIIWILSKFTRQGTALWEELKFLLDHPRRCFTLLFPR NATWWLFAILVALNCIDVIFFVILDLNDSAVTSLPPAIRVVDGFFQASATRTAGFGIISLSELHPAVQVSYMIMMYISVFPIAISMRRTNVY EEKSLGIYDTAEEDDDEETNAPTYIGAHLRRQLSFDLWYVFLGLFIITIAEGSKLQQNDNAFQVFNVLFEVVSAYGTVGLSFGYTNANT SFSGQFNVISKLVIIAMQVRGRHRGLPYALDRAVLLPSDALNRHEAAEGERRMRRRASNLSGGGSFAPSQSRTLSQARNDASQSQT RNDAGLSSGMESRDWQPQSAPNGDSLIRRASTLRSNR
5E-146	496	4.1	2E-145	494.3	0.9	2	2	C4JMB4_UNCRE	Putative uncharacterized protein	UREG_03972	Uncinocarpus reesii (strain UAMH 1704)	831	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Onygenaceae, Uncinocarpus, Uncinocarpus reesii, Uncinocarpus reesii (strain UAMH 1704)	336963	>tr|C4JMB4|C4JMB4_UNCRE Putative uncharacterized protein OS=Uncinocarpus reesii (strain UAMH 1704) GN=UREG_03972 PE=4 SV=1MSKLAPKKAWLREAGVSVSRFASRCYTRLCEVKSKIPWVKSIKFNFIFFHYTYILGVTIVGSIYLYPGGHLSYTDALFLAAGSATQ SGLNTVDLNLISTYQQVGLWLGSMIANPIVIHSSVVFIRLRWFEKRFQHVVREAKMLRKTRTRTRSRAVPTDTDAANRAEMGVRGRNI TVLRNSEGQALGRFIEENKRKSEGNSDHGNLTPTDGVSDQILPAEIEHSGAAEAPLDSSTDSTRPYPAQYGAEHHISFVENQRRQTS ALRIPSPREFDRGGVPEAVDYGDTLMRRRTSRSDQGDPLKQLPSPRQHITIDEPNIARSRRATTFPPVNSRFTGDNDAAYNQEPTPE QRLRRRKGTLASFFFFGTHVGARDAPYLSWQPTIGRNSAFVDLSEDQKNELGGIEYRALKTLAYVLAGYFFFFHILGIVSLVPWILHTH WGKFVTRVGVGRPWWAVFISGSAFNDQGFSLTPDSLASFYDAIFPLLLMTFLIIIGNTGFPCMLRFVIWLFWKIFPKHTAIWEELHFLL DHPRRCFTLLFPSSATWWLFWVLVILNGTDLILFIILDLHDRAVSSLPGGIRFVDGLFQAAATRTAGLSVVSLSALHPAVQVSYMIMMYI SIYPIAISLRRTNVYEEKSLGIYYSGEEEEEEYEDPAKEPSYVGSHLRRQLGFDIWYIFLGLFVIAIVEGSRLQDDPQFTMFAILFEVVSA YGTVGLSLGYPNTNTSFSAQFKVISKLVIIAMMIRGRHRGLPYQLDRAVLLPSEALHEKELRDAAMRMKRRGSAFSTAASRRASSRDG FSGTTSGWQHSPSGGAWTLSQGNAVARLPLHRSGSR

6E-146	496	3.8	3E-144	490.5	2	2	2	E5A9B7_LEPMJ	Similar to potassium ion transporter	LEMA_P013880.1	Leptosphaeria maculans (strain JN3 / isolate v23.1.3 / race Av1-4-5-6-7-8) (Blackleg fungus) (Phoma lingam)	796	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Leptosphaeriaceae, Leptosphaeria, Leptosphaeria maculans complex, Leptosphaeria maculans (Blackleg fungus) (Phoma lingam), Leptosphaeria maculans 'brassicae' group, Leptosphaeria maculans (strain JN3 / isolate v23.1.3 / race Av1-4-5-6-7-8) (Blackleg fungus) (Phoma lingam)	985895	[illegible] Av1-4-5-6-7-8) GN=LEMA_P013880.1 PE=4 SV=1MVGSLMLYGDRSSNIPYIDCLFFASGAATQSGLNTIDVNKLSRYQQILLYISACFCTPIFIHGSVVFVRLFWFEKRFMNLAKEARS RSGLRTRTISRRKSEMAADNERDMSQEERGVGNREIRVMRASDGQADGGPIEDEHAFRTGKEGAGIRRSSHSSDGEASPFEVPTTP VQETPSGIVWADHLSTPKDQEEKRLSESVGPKERFPEADKEKSIAFVEAQRNRTEKAKLRIPGPRDFDRGLVPEQIEDQHLDRTMSR VSQDSHARLERGHLMPPAAYADGPGPTTGASVYTRARTQEIGESSGPTPSMHIRNRSRSRTFATFLTRTKEEDEDPMPYLSWTPTIG RNSNFVDLNEEQREELGGIEYRSLKLLAVILLLFYGGFHVLGVTCLAPWINHTPRFTKVVTDVGVNPTWWGFFTAASLFNDLGLTLTP DSMISFQFAVLPLVLGTFLIIIGNTGFPCMLRFVIWTLSKLVPKGSGVWEELRFLLDHPRRCFTLLFPSKANWWLFAVLILLNGIDLIFFIV LDLHDPTVTSIPGGYRFLAGLFQAAATRTAGFAVVNIADLHPAVQVSYLIMMYISIFPIAMSMRQTNVYEERSLGVWAGDEDEDAKSSY LSHHLRRQLSFDLWFVFLGFFLIAIVEGSRLENTNEYAFSLFSVLFEIVSAYGTVGLSLGFPGTNASFSAQFRTLSKLIIIAMQIRGRHRG LPYALDRAILLPSESLHAKENEDATRRARRLSTMDFGAPLDPALSRQGTGLSRRSSVEGEGRSERFAPRRLRRILSGAFTAGPAIREK MS
2E-145	495	6.7	2E-144	491.5	2.4	2.2	2	K9FPA9_PEND2	Potassium ion transporter (Trk1), putative	PDIG_52970	Penicillium digitatum (strain PHI26 / CECT 20796) (Green mold)	824	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium digitatum (Green mold), Penicillium digitatum (strain PHI26 / CECT 20796) (Green mold)	1170229	[illegible] GN=PDIG_52970 PE=4 SV=1MFSALLRRVTTYKEKVPFLNELHLNFIFLHYAYIMAWAIIGSIILYPGGNISYIDALFQSAGAATQSGLNSVDINRLWLYQQIVLYLM TSLCTPIFIHSALVFIRLYWFEKRFQHVVRDARAMRRTRSRMETVTDDGDSDNININRAEHGVSGRPIVVLRDDSGDARDGRLTDPGN KNINSGIHTPEARESSVDSSTEGTDTSIEPRFGLGSLKVPTHLNPEHHIAFLEKQRKDKGALRIPSPREYDRGGAPEALEEDVEDVEDV EQEGEQAQHSSDHYDQDDQQSPGAHPEELDQLGPLEGPHITINEPDISRNRARGNTFPRLETRPTFRETKDGNETTTLAATNTRNTF RGVFRSLTQERDLNTQPYLSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLAVVLITYYVGFHLIGMISMVGWIMTEDKWGDIVRA DGVGRPWWGIFTAASAFNDLGFTLTPDSMYSFQRAVFPLLMLAFLIIIGNTAFPCMLRLMIWALSKFTRQGTALWEELKFLLDHPRRC FTLLFPRNATWWLFAILIALNGIDMIFFVILDLNDSAVTALPPGIRVVDGFFQAAATRTAGFGIISLSELHPAIQVSYLVMMYISVFPIAISM RRTNVYEEKSLGIYDATDEDHDEDSNAPTYIGAHLRRQLSFDLWYVFLGMFIIAIAEGSKLQNQSDHSFQLFTVLFEVVSAYGTVGLSF GYPNVNTSFSAQFNVVSKLVIIAMQVRGRHRGLPYALDRAVLLPSDALNRHEAEEGERRMRRRASNLSGGGSFAQSQSRTLSQARN DAGLSSGMETHDWQTQPSPNADSLVIVS
2E-145	495	5.6	2E-145	494.5	3.9	2	2	S7ZL87_PENO1	Uncharacterized protein	PDE_04395	Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	826	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium oxalicum, Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	933388	[illegible] PE=4 SV=1MFSSLVHRLNHAKQQAPLLNRLHLNFIFVHYFYVFSFVIVGSIILYAGGNLAYIDALFFASGATTQSGLNTVDLNQMYLYQQIVIYFI TMMCTPIFIHSGLVFVRLYWFEKRFQHVVQDARALRSTRSRMRTVTGDKGNQDNDRAERGIRGRSIVVIRNNAGDARGNRLPNPMG QPAEMQPEEDTTDGHPSSEGTSPEESREPTLERRFGLGSLRVPSQLSPEHHIAFLEKQRKNKGALRIPSPREYDRGGQPEALEDEEE NEEDSEAMKQPSSPRSPRQHNPAEASENDQVGPLEGPHITINEPDLPRTRTRGNTFTRLDTRPTIHEEMTKDGEDNALGPSATRNTF RGIFRSLTQERERPTQPYLSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLALVLITYYVGFHLMGIICMIPWIMCESSWGQIVTQD GVGRPWWAIFTSGSAFNDLGFTLTPDSMASFQTAVFPLLLFTFLIIIGNTGFPCMLRLMIWVLSKCVRQGSALWEELKFLLDHPRRCF TLLFPRNASWWLFAILVALNGIDLIFFIILDLNDPTVTALSPGIRVVDGLFQAASTRTAGFSVVSLSALHPAIQVSYLIMMYISVFPIAISMR RTNVYEEKSLGIYGVEEENDEETQTAPSYIGAHLRRQLSFDLWYVFLGLFIITIAEGGRLQANDLSFQVFTVLFEVVSAYGTVGLSFGY PGVNTSFSGQFNTVSKLVIIAMQIRGRHRGLPYSLDRAVMLPSDALNRHEIEESERRMRRRTSNLSGAESLGRPRSRALSQSQGDNG QSSGLDAYDWETHRASNGEQLVHRSSTLRSNR
3E-145	494	5	9E-143	485.8	2.9	2.1	2	S9W2K4_SCHCR	Potassium ion transporter Trk2	SPOG_01990	Schizosaccharomyces cryophilus (strain OY26 / ATCC MYA-4695 / CBS 11777 / NBRC 106824 / NRRL Y48691) (Fission yeast)	931	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae, Schizosaccharomyces, Schizosaccharomyces cryophilus, Schizosaccharomyces cryophilus (strain OY26 / ATCC MYA-4695 / CBS 11777 / NBRC 106824 / NRRL Y48691) (Fission yeast)	653667	[illegible] 4695 / CBS 11777 / NBRC 106824 / NRRL Y48691) GN=SPOG_01990 PE=4 SV=1MSIINGKRPFNLLKACKHYMDRRFQFLEYHYMFIIGMTILNSIILYASGHLQYIDALFLASGAVTQTGIPTVNMTDISIYQQLTLLLFA ALSTPVAVNLGLTIMKLYFYNRRYDKVMKGNRLKMTYTYNTFRRNDGPEPNKVGGRKIQVLLDQGNRLRRPIVPQKDSRELEEPPQP KRKFSRFRRSLSTFPRQNTLPNLPFFRFPRKSVDLEKQDQTAGNSSSPIPSGHGEQDHPPPSEYATRDVDYSSASSSSNHNEEDHS SQNGYSSQDLDYSNPPSPLDRREERDHSTHSEYAPRNVDYLSATRDDSSDEVNVSSKQSNESNDLDSSTRINEHDNSTSSNRTDFS TPKETESGISPLHSANSYPSEYNITRTDNDPRSSTNQPEETSAPPDNLDQISTSGLAEQQEVSNPGEATSPRITIATPPVPDHERKPVH TTGYDEDSSAKKSPMSFGRANRGKTFSMTHRTTENRRSMSLFPRQLTKTFTSNLPEVFRGSNTLRSRNSSTTLPYLSYQPTIGRNSA FYALSAEEREELAGIEYQSLKILTIFVSLYFLLWHILGMIAFLIFIYTAKVSGKVCTDAGINRGWWASFTSASLFNNIGYALHDDSLNQFQ KAIFPQVLGTILILTGNTFFPIGLRLTIWISLYFSKYFTPHYQQSLIFLLEHPRRSFTLLFPSKTTWILTANLVFLNLLSFFFFMVLDLGNQY VKQIPVGYRIMNGIFQNASTRAAGFTVIDIGQIAPAVIVSYMFMMYISAYPVAMSIRQTNVYEERSLGIYSPAADVDNDSDTDNSGEKG DSDMQAKPRRTYLIDHIQRQLSHDLWYMFFGFFIITILEGPRLEKPGEPQYTLFSVLFEVVSGYGTVGLSLGYNNAPSLSAHFRKISKLV MIALEIRGRHRGLPSALDRAVLMPSEKNFDREEEDYIRKHGKKK
3E-145	494	11.9	4E-145	493.4	2.8	2.1	2	Q5AUK1_EMENI	Potassium ion transporter (Eurofung) (Uncharacterized protein)	AN8029.2 ANIA_08029	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	829	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Emericella nidulans (Aspergillus nidulans), Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	227321	[illegible] 112.46 / NRRL 194 / M139) GN=AN8029.2 PE=4 SV=1MFSSFLRQLAQLKARIPWLKDLHLNFILIHYIYIISMALVTSIIIYPGNDLPYIDALFFSAGAATQSGLNTVDFNLLQTYQQVILYFVS MLTTPIFINTALVFIRLYWFEKRFQHVVRDARALRTTRSRLRTISEDKNSQSYGREEAGINGRPIVVLRNQAANPPQEDSPRSAPRSPN ESDSESVSPTSNASSAKMESQSPLATINRDFGDLRVPAQLSPEHHIAFLEKQRKNKGALRIPSPREYDRGGAPEVLEEEENEDNDLSK TRTDQSEPRSPRNLDGDDTNNTPNMDGPHITITEPQLPRTRTRNSTFPRMDTRPTFRETKDDDDPAAFSRANRKSTFNGIFRSLTQE RDRPTLPYLSWDATVGRNSNFIDLTEEQRDELGGIEYRALKTLAVVLISYYVLFHILGVICLTPWIMETHWGNVVTAAGQGRPWWAIF TAASAFNDVGFTLTPDSMMSFQGAVWPLLLMSFLIIIGNTGFPCMLRFIIWTMSKVVSKETPLWEELKFLLDHPRRCFTLLFPRNATW WLFAILVLLNGIDLIFFIILDLNDETVTSLSTGIKILDGLFQATCTRTAGFAVVSIADLHPAVQVSYMIMMYISVFPIAISLRRTNVYEEKSLGI FADDEDDDDDSQTAPSYIGTHLRKQLGFDLWYVCLGLFIITIVEGDRLENKNQYSFQIWSVLFEVVSAYGTVGLSLGYPGVNASFVSQ FRVLSTLVIIAMQIRGRHRGLPYSLDRAILLPSESLQQKEILDAERRMRRRASNLSQIGSLGRQQSQAVSENNAAGVSSALDARERERN TEANTGINAAEPITMRRHPTLRSQQSQR

9E-145	492	8.1	6E-143	486.5	2.1	2	2	G2QDT8_THIHA	Uncharacterized protein	MYCTH_2303819	Thielavia heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) (Myceliophthora thermophila)	899	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Myceliophthora, Thielavia heterothallica (Myceliophthora thermophila), Thielavia heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) (Myceliophthora thermophila)	573729	>tr|G2QDT8|G2QDT8_THIHA Uncharacterized protein OS=Thielavia heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) GN=MYCTH_2303819 PE=4 SV=1MGRFKKALVGQLKALRPAFLSTKPHFHFISVHYFYVVGLALLGSVIVYGAGRGNIAYIDALFLASCSSTQAGLNTVDLNLLNTFQQ VVLYLWPMMANPITINSFVVFLRLYWFEKRFQHIAREARLRRGTVSKAKTAPKANNADLERGVNGRKITVMLNGARSRITNDGMLLEG TQQPSDEQRLDLASPAARQDGAEASDEASEPRRPEIKFARTVTKSDGLGEDPIKLPPVVRPDHEHIAFVERQRKGDDEVLRIPNPRDA ERGMRPKRVEAGDEEEADVPPRSAAAAAAAERYAEPLGNRADSRQQAITIEEPDRNKLQQYDSDDLIETARGPRHVFSFLKLPRPRS LSRMTGRFQSSEPGPSGTARPGAQRRQSIQSIRTAFSRDRVEGTPYLSWEPTVGRNSAFPDLTEEQREELGGIEYRSLKTLALILTGY FWIFAAIGVIGLAPWIAESERYGKIVDQAGVSRAWWAFFTASSAFMDLGFTLTPDSMNSFNTAVWPLLLMAFLIVIGNTGFPIMLRFII WVMSHLVPVGTGVYEELRFLLDHPRRCFTLLFPSGATWWLFWLLVIMNGLDLMFFIVLDLGSGPVVDLPAGLKVLNGLFEAVSTRTA GFSCVNLAALHPAVQFSYMVMMYISVFPIAISVRRTNVYEEKSIGVYSTSDDEEQPGHSDLSYVGSHLRRQLSFDLWYIVLGFFILNISE GDKLMANEFSSFAVLFEVVSAYGTVGLSLGYPGINASLSAKFSVVGKLVIIAMMIRGRHRGLPYALDRAILLPSESLNAREAADADARM NRIHSHASGATGARGSSLARRRSMTVDRGNIIASLLHPGPAVPAEPPLPEMHRAKSTEPPAGSGAPAADDQETYATRVSSRRTEPGA SRRVDSGLPTQRTRTASGDD
2E-144	492	8.7	6E-144	489.6	3	2.1	2	A0A0A2I546_PENEN	Potassium transport protein, high-affinity, fungi	PEX1_056840 PEX2_071460 PEXP_101340	Penicillium expansum (Blue mold rot fungus)	825	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium expansum (Blue mold rot fungus)	27334	>tr|A0A0A2I546|A0A0A2I546_PENEN Potassium transport protein, high-affinity, fungi OS=Penicillium expansum GN=PEX1_056840 PE=4 SV=1MFSAFLRRATTYKEKVPFLNELHLNFIFLHYAYIMAWAIIGSIILYPGGNISYIDALFQSAGAATQSGLNTVDINRLWLYQQIVLYLIT CLCTPIFIHSALVFIRLYWFEKRFQHVVRDARAMRRTRSRMETVTDDGDSGDININRAELGVSGRPIVVIRDDSGDARDGRLTDPGSK TIHSGINTPEARESSVDSSSEGTDTSNEPRFGLGSLKVPTHLNPEHHIAFLEKQRKDKGALRIPSPREYDRGGAPEALEEDVDQEGEQ AQHSSDHDDQDDQQSPGAHPEELDQIGPLEGPHITINEPDISRTRGRGNTFPRLETRPTFRETKDGNETTTLAPTNTRNTFRGVFRSL TQERDLNTQPYLSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLAVVLITYYLGFHLIGMISMIGWIMTENTWGDVVRADGVGRP WWGIFTAASAFNDLGFTLTPDSMYSFQRAVFPLLMLAFLIIIGNTAFPCMLRLMIWVLSKFTRQGTALWEELKFLLDHPRRCFTLLFPR NATWWLFAILVALNGIDMIFFVILDLNDSAVTALPPGIRVVDGFFQAAATRTAGFGIISLSELHPAIQVSYLVMMYISVFPIAISMRRTNVY EEKSLGIYDATDEDHDEDSNAPTYIGAHLRRQLSFDLWYVFLGLFIIAIAEGSKLQNENDNAFQLFTVLFEVVSAYGTVGLSFGYTNVN TSFSAQFNVVSKLVIIAMQVRGRHRGLPYALDRAVLLPSDALNRHEAEEGERRMRRRASNLSGGGSFAQSQSRTLSQARNDAGLSS GMETHDWQTQPSPNADSLVHRSSTVRSNR
2E-144	491	11.3	3E-144	490.6	3.6	2.1	2	K2RVV8_MACPH	Cation transporter	MPH_03812	Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	882	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Macrophomina, Macrophomina phaseolina, Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	1126212	>tr|K2RVV8|K2RVV8_MACPH Cation transporter OS=Macrophomina phaseolina (strain MS6) GN=MPH_03812 PE=4 SV=1MFTPLMEMGAWVRSHLPSRPKGFNWRRPHFNFITLHYLYLILMTILGSILLYPAGGLPYIDALFFASGASTQSGLNTVDVNKLYL YQQVVLMLVACVCNPIFINTFVVFVRLYWFEKRFQGLVAEARTRNHARSRTKSENKEERDLGREEMGVNGRAIHVVRNQDGRAKGA PCNVDGEIEEKEPRSPHASAPGSSSGSDEKEDQFDDMSKAGTMLGAASTAEQSDTIQPFHRDITFAEDVKPPPRRSNLMQEDRLPV RRSAEQHIAFVENQRKPKAKGRLRIPGPREFDRGDKPEQLEEEDGGVHLARELTNESSLRGREEANQPADTVDPGNANGDDHTFKR HVSFDEHVVGVGGKLKSGLNNVKRRFTLGDDHENGNSALKRRASTFRSFVTARSREREQDPTPYLSWTPTIGRNSAFVDLTEEQRE ELGGIEYRALKTLAFVLVFYFVGFHLLGMVCLLPWIVRSKYAGEVLRPDGVSPVWWGFFTPASMFNDLGFTLTPDSMISFQKAVFPM LLGSFLIIIGNTGFPCMLRFVIWLAEKIVPYGSGVWEELRFLLDHPRRCFTLLFPSKATWWLFWVLVLLNGIDLIFFVILDINDDTVLSLSP GYRVLVGLFQAASTRTAGFAAVNIADLHPAVQVSYLIMMYISVFPIAISMRRTNVYEEKSLGIWAETAVPEESGEQSYVATHLRRQLSF DLWYLFLGFFFIAIIEGSRLENTNDYSFTLFSVLFEIVSAYGTVGLSLGYPTINASFSAEFKTLSKLIIIAMQIRGRHRGLPYALDRAILLPS ETLHKKEDEDAARRAAARRNSNLSDMERAEANGFSVGRPPTFRRGSVATARDEEGPTNNQWLSNQRRSASAAGLTKLLSGALSAG PTIQKRD
2E-144	491	6	1E-140	478.6	2	2.1	2	F9XHI7_ZYMTI	K+ transporter (Fragment)	MYCGRDRAFT_61522	Zymoseptoria tritici (strain CBS 115943 / IPO323) (Speckled leaf blotch fungus) (Septoria tritici)	748	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Mycosphaerellaceae, Zymoseptoria, Zymoseptoria tritici (Speckled leaf blotch fungus) (Septoria tritici), Zymoseptoria tritici (strain CBS 115943 / IPO323) (Speckled leaf blotch fungus) (Septoria tritici)	336722	>tr|F9XHI7|F9XHI7_ZYMTI K+ transporter (Fragment) OS=Zymoseptoria tritici (strain CBS 115943 / IPO323) GN=MYCGRDRAFT_61522 PE=4 SV=1MVHYSYIVGMAIFTSILLYPAGLLPYLDALFFAVGCATQSGLNTVDINSLHTYQQVVMMLITCICTPIFINTVVVLIRLYWFEKRFEHI VRETRAQRRTRARSLSSRSRSQMKSETSERTDDPSQSEKGVNGRRIVVLRDSLNPGGMKVPRTPQSPSVSYMGLHPKLNREITFAD EVPKNIEPTQSTSDMARIPEHSDISRHVEFLERQQNDAKKGGAFYIPGPRDFDRGEVPEQIAPDEEDTIERLPTRSDRARSPDHKGIAF ADEEHPKRNITIDVPEHPAHRDRRSTEEPSSSSPVNQKSAFSRMRSNSNRLGERSRSFAQTWTNITQTFTQSRDEEPMPYFAWSAT TGRNSAFLGLTAEQREELGGIEYRSLKTLVKILLSYYVGFHVLGMVVFLPWITNTYWQDTVRSFGQNPAWWGVFTPASMFNDLGFTL TANSMIGFQDSVLALLFGSFLIIIGNTGFPCLLRFIIWTLSKMVPRDSGIWEELRFLLDHPRRCFTLLFPSKATWWLFWVLILLNGIDLMF FIILDLNQAAVTALHPGLQVLNGWFQAVSTRTAGFASVNLADLHSAIQVSYMIMMYISIFPIAISVRRTNVYEEQSLGLFGGEETAAGDG EPSYVSMHLRRQLSFDLWYIFLGLFIITIVEGDRIADPGEPSFTIFAILFEIVSAYGTVGLSLGYPTINASFSAEFKTISKLIIIAMMVRGRHR GLPYALDRAILLPSEKLQQKEAEESERRTNIRRRGS
3E-144	491	0.4	4E-144	490.2	0.3	1.3	1	A0A099NW93_PICKU	Uncharacterized protein	JL09_g4632	Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)	1127	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Pichiaceae, Pichia, Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)	4909	>tr|A0A099NW93|A0A099NW93_PICKU Uncharacterized protein OS=Pichia kudriavzevii GN=JL09_g4632 PE=4 SV=1MTVGERIRRVIYKIEDTVGPLIKKIIPNFIMAHYVYILLWVIVGSIVLYPSKNLDYIDCLMFAAGAATQGGLAPQQLNDVKLYQQITIY MVCMFTTPIFIHGSLTFIRLYWYEKRFDDIKEKSINQYKMRRSKTIANLRSETNARTMSANYTNSHRNFDSHNAQEGLTSRMKRFENM KNFGNSDNIDPLDTENITTKNNNYNSWNVSQRKKRNDNLEISNDHNDDNDCAVTDYDDGDENDKYTANKGSGRYDVDKKLDDSNEV FTSKINTSLNHDHAVESPTTNIKFGELPKPFKKKERDIAPRDLYMSISALQNDSNSDFDDEMGPALHFKSPHELEKDKRKVPLRRRKHR KILREKKLKELKKKALPLLQTEKSIVDTELAEQQGRNFDFTSQTNIDTNADLTKKEKARRAMSSPMLEKPDIGSHQELPLDFDSTAYKP GFKHFQRSHTLHMPEFSKKLFSNFDNSNVSPGPENVDEFPYLKRFKSRRPSIFTKRRTYSNLDQLSDDDFVNNYLTNVPTNYLSWKP TVGRNSKFIALTKQQKIELGGVEYQSMKLLGRILVAYYLGFHILAFVLFVPYVTRRSNYAKNLRSDGVSPAWWGFFSAMSSFNDLGYT LNATSMALFDESAYVQLISGAFILIGNTAFPICLRFIIWLMKHFTKPLTLSHDSLSFLLDHPRRCFTLLFPSGPTWWLFAVLLLLNFLDWIL FIILDFGREGLSYIPRGYQILCGLYQAICTRTAGFNVVNLASLNPAIQVSYMVMMYISVLPLAISIRRTNVYEEQSLGVYEREDEDHTDSK PRLKYIGDHLRKQLSFDLWFLFLAIFIICICEAGRIQSGDVNFTVFQIMFELTSAYGTVGLSLGYPNKNTSFCGEFSKISKLVVVATLIRGR HRGLPNSIDRAIMLSDEKLNLRDDLEAYHAMRRTATTMSNTETMFPSITKVATGQRRQTIDRQPTISENIRQGVIPWGDILTKVGHLLG KTVANILTVSGAPKEEKYARQMTRYSTFDDYPPRSRSTSQYTRRNSNFEDRNMGYDNYHDNDDDISFNSSVGERESVPLRNYPPFS DGRDGKNNHSQTYSQEEKSVRNYYPVRSSNGANGDSESIVTPESYVSDLHSSISSKKRKLN

3E-144	491	7.3	3E-143	487.2	1.4	2.1	2	A0A0A2K9B4_PENIT	Potassium transport protein, high-affinity, fungi	PITC_022490	Penicillium italicum	863	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium italicum	40296	>tr|A0A0A2K9B4|A0A0A2K9B4_PENIT Potassium transport protein, high-affinity, fungi OS=Penicillium italicum GN=PITC_022490 PE=4 SV=1MWPLHEASRYGRKCDSDRKPTPFTTTSTRTVQTLGKDCGSHTMYSAFIHRCSAFYRRANKIKQRTPLLNQLHLNFIFLHYTYIITWALIGSIIVYPGGGIAYTDALFLSVGAATQSGLNTVNLNALQLYQQIVLYIITIICTPIFIHSTLVFIRLYWFEKRFQRVVRDARALRTTRSRMDNVSQDNDSEGTNRAELGDGDRSIVVLRSNTGGARGSKLPDPGGKIIDDAQSETEAPEEHEEHEKSGQSSLEYLQNDRMEHRFGLGSLRVPTQLNPDQHIAFLEDQRKNKGALRIPSPREYDRGGAPETLDGEEDEVNKPVQPSSPQLDHGQSPMHSGKVDQVGPLEGPHIATNEPGMPQINNRGSTFMHLITRSTVQDTMPVNETTGGLGPQGARNIAGGIWRSLTREKDYSSQPYLSWNATVARNSNFIDLTEEQRDELGGIEYRALKTLTVVLVSYYIGFHIIGMVSVVGWIMTQDRWGSVVREDGVGRPWWGIFTSASAFNDLGFTLTPDSMISFQKAVFPLLLMAFLIIIGNTGFPCMLRLVIWSLTKFARPGTALWEELKFLLDHPRRCFTLLFPRNATWWLFAILIALNSIDVIFFIILDLNDPTVTSLPPGIRVLDGFFQAVSTRTAGFGVVNLSDLHPSIQVSYLIMMYISVFPIAISMRRTNVYEEKNLGVCSYGQKDSEKNDQTAPSYIGTHLRRQLGFDLWYVFLGLFVIAIVENGRLQGADDYSFQLFAVLFEVVSAYGTVGLSLGYPGVDTSFCGQFNVISKLVIIALEIRGRHRGLPYTLDRAVLLPSDTLKKHDAVDSERHVRRCASNLSAGGPIDRPQSWPVSRARAGANLPSLSTGREKQGSERNK	
4E-144	490	5.6	3E-142	484.2	2.5	2.1	2	A7EQP2_SCLS1	Putative uncharacterized protein	SS1G_07645	Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum)	796	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Sclerotiniaceae, Sclerotinia, Sclerotinia sclerotiorum (White mold) (Whetzelinia sclerotiorum), Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum)	665079	>tr|A7EQP2|A7EQP2_SCLS1 Putative uncharacterized protein OS=Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) GN=SS1G_07645 PE=4 SV=1MFTLLLELWHQIAALKPSFISKSPHFNFITVHYFWIIGITLLGSLCLYIRGGIDYIDALFFASGGATQSGLNTINLNDLNTWQQTVLYLLPIFTNPITINSFVVFLRLYWFEKRFQHIAAQNKKNRRSIGKSFSKSRTTDVGAVDEEKGVNGRNIVVMHGTTRANVMQDGKDAIVDIQDAIEKERAMNRAEAINGSGSSNLSSTETANDPSPTSHQTQIKFADQVKRSNGMDDEELRLPVRRRDEDHIAFLERQRNPEDRTILRIPGPRDADAGVSPQTVEEEEEGDPVIRTLSRVGSAYSRRGSIDRGTLNGETQWQDHYPSRKRNITIEVPTHPKVDRAVDDMKAAGSTIKGVMRFRNNRTMERNEATETQGNGAVITKLKSRAPTFQSIKTALTGEKEDPTPYLSWAPTIGRNSAFVDLTEQQREELGGIEYRSLKSLALILSCYFIGFSIFAVVCLLPWILNNHTYGSIVEQDGQGRVWWGIFTANSAFTDLGFTLTPDSMISFNTAIWPLLLMSFLIIIGNTGFPIMLRFIIWVTTLWVPRNSGIWEELRFLLDHPRRCFTLLFPSKATWWLFWILVILNGLDLLFFIILDLGNSVVTDLPVNIRVLDGWFQAASTRTAGFGVVNLALLHPAIQVSYLIMMYISVLPIAISVRRTNVYEEKSLGIYGSPTEENEDEGEPSYVGAHLRRQLSFDLWYIFLGFFIISIAEGSRLQGTDPSINMFSVLFEIVSAYGTVGLSLGYPGIDASLSAEFNTVSKLVIIAMQIRGRHRGLPKKLKMQHKEFTVEIQMRQ	
4E-144	490	2.8	4E-144	490.4	2	2.3	2	A0A0A2K6V2_PENIT	Potassium transport protein, high-affinity	PITC_049690	Penicillium italicum	824	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium italicum	40296	>tr|A0A0A2K6V2|A0A0A2K6V2_PENIT Potassium transport protein, high-affinity OS=Penicillium italicum GN=PITC_049690 PE=4 SV=1MFSAFLRWVTNYKEKVPFLNDLHLNFIFLHYAYIMAWTIIGSIILYPGGNISYIDALFQSAGAATQSGLNTVDMNRLWLYQQIVLYLITSLCTPIFIHSALVFIRLYWFEKRFQHVVRDARAMRRTRSRMDTVTDDGDSGDININRAELGVSGRPIVVIRDDSGDARDGRLADPSIKNINSGINTPDARESSVDSSSSEGTDTSNEPRFGLGSLKVPTHLNPEHHIAFLEKQRKDKGALRIPSPREYDRGGAPEALEDDVDQEGEQAQHSSDHDDQDDQQSPGAHPEELDQLGPLEGPHITINEPDMSRTRARGNTFPRLEARPTFRETKDGNETTTLAPTNTKTFRGVFRSLTQERDLNTQPYLSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLAVVLITYYVGFHLIGMISMVGWIMTESTWGDVVRADGVGRPWWGIFTAASAFNDLGYTLTPDSMYSFQRAVFPLLMLAFLIIIGNTAFPCMLRLMIWVLSKIARPGTALWEELKFLLDHPRRCFTLLFPRNATWWLFAILVALNGIDMVFFVILDLNDSAVTALPPGIRVVDGFFQAASTRTAGFGIISLSELHPAIQVSYLVMMYISVFPIAISMRRTNVYEEKSLGIYDTTDEDHDEDSNAPTYIGAHLRRQLSFDLWYVFLGLFVIAIAEGSKLQNENDHAFQLFTVLFEVVSAYGTVGLSFGYTGVNTSFSGQFNVVSKLVIIAMQFRGRHRGLPYALDRAVLLPSDALNRHEAEEGERRMRRRASNLSGGGSFAPSQSRTLSQARNDAGLSSGMETHDWQTQPSPNADSLVHRSSTIRSNR	
5E-144	490	8.5	3E-143	487.2	1.7	2.1	2	Q4WEA2_ASPFU	Potassium ion transporter (Trk1), putative	AFUA_5G02290	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus), Neosartorya fumigata (Aspergillus fumigatus)	821	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Neosartorya fumigata (Aspergillus fumigatus), Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	330879	>tr|Q4WEA2|Q4WEA2_ASPFU Potassium ion transporter (Trk1), putative OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=AFUA_5G02290 PE=4 SV=1MFTPVLRRLASMKSRIPLISGLHLNFISVHYIYIIAMTLITSIILYPGGDLAYIDILFFCSGAATQSGFNTVDFNKLKTYQQVILYFSSMLTTPIFIHSVLVFIRLYWFEKRFQHIVQDTRAMRSTRTRMRTLSRDKDATSLGREEAGIGSRPIVVLRNNTQESNERGREASAGNPEYGSSPGSSSRFDRADSSEVQTGGPNGTLGLGLGSLRVPTQLDPEHYIAFLEKQRKNKGALRIPSPREYDRGGVPEVLEEADDEGEGSKRTRSSESDDENSRNSEESDQVGPLEGPHITINEPDIQQTRTRNSTFPRLDTRPTYRDTKDLNDTSALERSRSRRPTLSNLVRSLTQERERTTLHYLSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLAIVLTSYYLFFHILGMVCLVGWIMTTHWGQVVEQIGQGRPWWGIFTAGSAFNDVGFTLTPDSMTSFQTAVFPLLLMTFLIIIGNTGFPCMLRLIIWVLSKIVPRESAVWEELKFLLDHPRRCFTLLFPRNATWWLFAILVALNGIDLIFFIILDLNDPTVTSLSPGIRVLVGLFQAASTRTAGFGVVSVADLHPAIQVSYMIMMYISVFPIAISMRRTNVYEERSLGIYAGGEDEDEPQTPPSYIGFHLRRQLSFDLWYVFLGLFIIAIVEGNRLQSEDEYAFQMWAVLFEIVSAYGTVGLSFGYPGVNTSFSGQFKVLSKLIIIAMQIRGRHRGLPYALDRAILLPSESLKDKDLQDAERRMRRRVSNLSTMSGMDRTYSQARTENGVATGAEDKDRGATAWTNGDNVIRRHSTMRSQQSQKSQR	
7E-144	489	4.9	9E-144	489	3.4	1.1	1	Q0TYH5_PHANO	Putative uncharacterized protein	SNOG_15513	Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	774	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae, Parastagonospora, Phaeosphaeria nodorum (Glume blotch fungus) (Septoria nodorum), Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	321614	>tr|Q0TYH5|Q0TYH5_PHANO Putative uncharacterized protein OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) GN=SNOG_15513 PE=4 SV=2MCTPIFINTFVVFIRLYWFEKRFQNVVIESRNARHTRTMSRRRSEMKSEEIQRDLGSEERGVGDRHIRVMRSTNGEAEGGKIEDEHAFSGGLGNAGIRKAKPSDDEEVDPLERPMTPVHQVASNVVWADDLTTPRQRERQRLRDSVESPTERLPEKNREQSIAFVEKQREPKQKATLRIPGPRDYELGLQPEEVKEDDEKLDKVTSRQSQESHPKRNRSNSVPPEMMNGDDHPMKYHITIDVPSRQRPTTGASVYNRGRTNTNDDTEGHHTSGLRPRSRSRTFASFLTSTKEEDEDPMPYLSWTPTLGRNSNFVDLTEEQREELGGIEYRALKMLAMILTVYFVGFHLLGMVCLTPWIHSTEYKNILDGNNINHVWWGIFTPASMFNDLGFTLTPDSMVSFQRAILPLTLGTFLIIIGNTGFPCMLRFIIWLCSICVPKFSAKWEELKFLLDHPRRCFTLLFPSKANWWLFWVLIGLNGIDLIFFIILDLNDTTVTSLPPGFRFLAGLFQAAATRTAGFAVVNIAELHPAIQVSYLVMMYISIFPIAMSMRQTNVYEEKSLGVWADTDDSDEQNSYLGHHLRRQLSFDLWFVFLGFFLIAIIEGARLENTNEYAFSLFSVLFEIVSAYGTVGLSLGFPNTNPSFSGQFRTLSKLIIIAMQIRGRHRGLPYALDRAILLPSESLHQKENEDATRRARRSSNALDVGMSTSMSVDRGGAGLTRQGTGLSRISTASGDAGRPSAGDRFKPKQLKRILSGAFSAGPSTRFHSEEKRA	

1E-143	489	17.5	1E-142	485.1	5.8	2.1	2	L8G9X0_PSED2	Uncharacterized protein	GMDG_03510	Pseudogymnoascus destructans (strain ATCC MYA-4855 / 20631-21) (Bat white-nose syndrome fungus) (Geomyces destructans)	960	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Leotiomycetes incertae sedis, Pseudeurotiaceae, Pseudogymnoascus, Pseudogymnoascus destructans, Pseudogymnoascus destructans (strain ATCC MYA-4855 / 20631-21) (Bat white-nose syndrome fungus) (Geomyces destructans)	658429	>tr|L8G9X0|L8G9X0_PSED2 Uncharacterized protein OS=Pseudogymnoascus destructans (strain ATCC MYA-4855 / 20631-21) GN=GMDG_03510 PE=4 SV=1MSTFPSPAVKMVFQPFVDAWHQVKAMKPSFLSRNPHFNFITVHYFWIVGMAFLGSILVFAPGKITYIDALFFSAGSCTQSGLNP LDFNNLNTFQQIVLYLLPMMTNPITNNTFVVFLRLYWFEKRFQHIAKEAKRSRRSMSKTRSQMKGERDTAIMEHGVNGRTIRVIHETT RMGTAGHPATEEHTAENTNANANAPRTPYAPNLDDYAITFDKSESESPKHEAPPLKTAPTIKFADQVKRSDGVDSEYLRVPSTREPET HIEFLERQRRLTGGALRIPGPRDADRGVAPETIDEAQIMSGGMVRSDSDVEPLPRGLNGPNVEPESSQSPSTDSGTSDRSSASENHP ETVDYGREEYASRSQHASESTRAAAHSLGVLRFRKPRLLSGDKVHGEHEKTERSRSRAMTLTRLKSHFTKDKEQSDPMPYISFQPTI GRNSAFVDLSEAEREELGGIEYRSLKTLAIVLVSYFWFGTIFTTISLVPWIVNNARYGPIVDAAGMSRTWWGFFTAMSSFNDLGFSLV PDSMVSFQTAIWPLFVMSFMIIFGNTGFPVLLRFIIYCTSKLVPKTSGIWEELRFLLDHPRRCFTLLFPATATWWLFWVLVLLNGIDLIFF IILDFGNPVVTDLPPNIRVLDGWFQATSTRTAGFAVVSIADLHPAIQISYMVMMYISVFPIAISVRRTNVYEEQSLGIWGGATDDIESKSA EPSYVGSHIRRQLSFDLWFVTLGWFIMAIAEASRIQDTNQPAFNLFSYLFEIISAYGTVGLSLGYPGSNASFSAQFNVVGKLVIIAMQIR GRHRGLPYELDRAILLPSESLHQREMEDATARHRRSSFGTTVGGGEELDTATTNASGRDEGPKGLRRRTRQGSNFLSSMLHPGPS MVPRHRPSMTKRESSMGGRAGSSSSSGNGNGNGNDGGGSGGDGGRDGASIAEPVTRSNTHVPQPTRREHGTSRPIKKRMSI															
2E-143	488	4.9	6E-143	486.3	1.3	2	2	M2UXB8_COCH5	Uncharacterized protein	COCHEDRAFT_1099860	Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis), Cochliobolus heterostrophus (Southern corn leaf blight fungus) (Bipolaris maydis), Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis)	860	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Bipolaris, Cochliobolus heterostrophus (Southern corn leaf blight fungus) (Bipolaris maydis), Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis)	701091	>tr|M2UXB8|M2UXB8_COCH5 Uncharacterized protein OS=Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) GN=COCHEDRAFT_1099860 PE=4 SV=1MFGPWLSFFAWLKQHTPASLKALTPHANFITLHYAYIISWTLIGSVIMYGNGRIPYIDALFFASGSATQSGLNTIDVNNLDLYQQIT LYLMTCLCTPIFIHSSVVVVRLYWFEKRFQNIVLERGSRSGRTRTLSRRKSEAKKTNGADPGREEQAVGSREIRVMRGSNGHAHGGT IENENAFSDGLDSTGNGIRPRRRSSSSEDNMPPFRPQTPQQNAPAGIVWADNLNTPANQKPIRSSVEESPASRLPEINKERSIAFVEA QRNPTTRNKLRIPGPRDFDQGLIPEAVEGEEELDRVTSRMSQDSRAHSAQKNKRSNSLPFALSGDDRQLKNHITIDVPDRQRPNGHS VYDRTRTNDIDSNGPSSSMHLRNRSRSRTFASFLSRNKDEEEDPMPYLSWTPTLGRNSNFVDLTEEQREELGGIEYRALKLLAVILTV FYLGWHIVGVISLAPWISHSPQYRAVVEKVGIHPTWWGFFTSASLFNDLGFTLTPDSMVSFQLTVWPLLIGTFLIIIGNTGFPCMLRFTI WIYSKLVPKGSGVWEELRFLLDHPRRCFTLLFPSQANWWLFWVLIILNGVDLIFFIILDLDDPTVTSLSGGHRFLAGLFQAASTRTAGF AVVNIADLHPAVQVSYLIMMYISIFPIAMSIRQSNVYEEKSLGVWADNELDDAKSSYLSHHLRRQLSFDLWFVFLGFFLIAIIEGTRLENT NEYAFSLFSVLFEIVSAYGTVGLSQGYPGTNASFSAQFKPLSKLIIIAMQIRGRHRGLPYALDRAILLPSETRYQKENEEATRRARRGSN AADMGLTYSTDRITRTGTMLSRRSTTSANGDRVVTETRPEQLKRILSGAFTAGPTGLYREKTN															
3E-143	487	9.8	2E-142	484.8	2.6	2.1	2	M2MBM6_BAUCO	Uncharacterized protein	BAUCODRAFT_36363	Baudoinia compniacensis (strain UAMH 10762) (Angels' share fungus)	936	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Teratosphaeriaceae, Baudoinia, Baudoinia compniacensis, Baudoinia compniacensis (strain UAMH 10762) (Angels' share fungus)	717646	>tr|M2MBM6|M2MBM6_BAUCO Uncharacterized protein OS=Baudoinia compniacensis (strain UAMH 10762) GN=BAUCODRAFT_36363 PE=4 SV=1MVFEPIVEAARRLGQVDPRKWRKLHFNFITCHYMYLVSMTIIGSIILYPKAGLLPYIDALFFAAGASTQSGLNTVDVNNLYLYQQV TLMLIACVCNPIFINSAVVFVRLYWFEKRFHNLVKEVREQRRSRAKTITRTKSEMRNSADLDRLEKGVNGREIKVLHDATKVNGDEDIN AGLTDLQKDVAKKLNDNHALDSESVTPRSSNRHSDQSDEIPPDQLDHVGEREHPNTPAATYLGMPPRLHRDITFADELPAPGSDKTE SMPAPIRDGDDMDKHILFLERQRGAAKETNALRIPGPRDVDLGAVPQELEAGDLRRPQTRGSATQGFADTERSTRSVDGRSDEVTIN QHPRRGITINEPQHPGHHRRDSESVSGSHFDGVRDRVGRVLSGISQRHNRSRGPPVLTGVRRTVTQTLSSLTTARSRERDDDPMPY LSWQATTGRNSAFLGLTPAQREELGGIEYRALKTLAKILIAYFVGFHALGMAVLLPWIMHTQPWKSYVQSVGQDAGWWGVFTPASM FNDLGYTITPDSMISFQTAVLPLLFGSYLIIIGNTGFPCMLRFTIWVASKLTAHGSATWEELRFLLDHPRRCFTLLFPSRATWWLFWILV LLNGIDLVFFIILDLNDTTVTSLAPGFRVLNGWFQAVSTRTAGFGCVNLANLHPAIQVSYLIMMYISVFPIAISVRRTNVYEEKSLGIWGG EEEDGEGGEQSYVGQHLRRQLSFDLWYVFLGFFIICIVEGGRLENTNDYGFTMFSVLFEIVSAYGTVGLSLGYPTINASFSAEFKVISK LVIIAMMLRGRHRGLPYALDRAILLPSDNLHKKDDEIAALSRRRSSIFNTTGSWQEGDLDEMGLPKQHPGGQTTDAAMTAGAGGFDS PDGMSRTRRRPSAVTTASQASDRDVHHQRLRRPQDRRRSVGALLSSGLSAGPTWSRSD															
1E-142	486	4.3	2E-142	484.5	1.8	1.9	1	A1C5B7_ASPCL	Potassium ion transporter (Trk1), putative	ACLA_002960	Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	821	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus clavatus, Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	344612	>tr|A1C5B7|A1C5B7_ASPCL Potassium ion transporter (Trk1), putative OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) GN=ACLA_002960 PE=4 SV=1MYSAILPKVAALKSRIPLLKGLRLNFILIHYIYIIAMSLITSIIIYPGSELDYIDALFFCAGAATQSGLNPVDVNKLRTYQQVILYSSSML TTPIFIHSVLVFIRLYWFEKRFQHIVQDARALRQTRTRNRTISQDKDTGSLSREEAGIGGRPIVVLRNNVQDFAHRDQESAVPTPRDSS PGSPSQADSASSLENQNNRLGLGLGLSLRVPTQLDPEHHIAFLEQQRKNKGALRIPSPREYDRGGVPEVLEEADEGNEDKQAPSID SDDSARSMEDSDQVGPLDGPHITINEPDMQRTKTRNSTFPQLDTRPTFRETKDLEDTSPLGRTGTRRPTFSNIVRSLTQERERTTLPY LSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLAIVLISYYLFFHIFGIISLVGWIMTTHWGTVVEEIGQGRPWWGIFTAGSAFNDV GFTLTPDSMSSFQTAVFPLLLMTFLIIIGNTGFPCMLRLIIWALSKVVRRETAIWEELKFLLDHPRRCFTLLFPRNATWWLFAILIALNGID LIFFIILDLNDPTVTALSPGIRVLDGLFQAASTRTAGFGVVNVANLHPAIQVSYMIMMYISVFPIAISMRRTNVYEERSLGIYAGGDEDDS SDTHSPPSYIGFHLRRQLSFDLWYVFLGLFIIAIVEGPRLQAVNEYAFQMWAVLFEIVSAYGTVGLSLGYPGVNTSFSGQFKVISKLVII AMQVRGRHRGLPYALDRAILLPSESLQDKEIADAEKRMRRRSSNLSTMSDMNRTFSQSRAENGVSTGLENKDKDKDKGRNSHSWM NGDNIIRRHSTLRSSRSQR															
1E-142	486	7.4	2E-142	485.1	1.5	2.1	2	R1EH17_BOTPV	Putative potassium ion transporter protein	UCRNP2_6447	Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	801	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Neofusicoccum, Neofusicoccum parvum, Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	1287680	>tr|R1EH17|R1EH17_BOTPV Putative potassium ion transporter protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_6447 PE=4 SV=1MFTPLMEMAAWVRGHLPSMPTSFRISRPHFNFITLHYLYLILMTILGSILLYPAGGLDYIDALFFASGAATQSGLNTIDVNKLFLYQ QVVLMLVACVCNPIFINTFVVFVRLYWFEKRFQGLVAESRNNRHATRTRSRTRSEDKPERDLGREEMGVNGRSITVVRNEDGHAQG SSTGTEEKDDQLDISKEPTVIGAASTAEQSDSIQPFHRDITFADDVKPPPNRTTTNEERLPVRRDAEQHIAFVENQRRPKAKGRLRIPG PREFDRGDKPQQLEEEDGGVHLARELTNESSLRGREEANQPADTVDPGNMNGDDNTFKRHVSFDEHVAGVQGKLKAGFDNVKRR FTLGEDHDDSNSGLRRRASTFKTFVTARSRERERDPMPYLSWTPTIGRNSAFVDLTEEQREELGGIEYRALKTLAFVLVFYFVGFHLL GMVCLTPWIVRSRYVGDVLRPDGVNAVWWGFFTPASMFNDLGYTLTPDSMISFQKAVFPLLLGSFLIIIGNTGFPCMLRFVIWAAEKV VPYGSGVWEELRFLLDHPRRCFTLLFPSKATWWLFWVLVLLNGIDLIFFVILDINDDTVTSLSPGYRVLDGLFQAASTRTAGFACVNVA DLHPAVQVSYLIMMYISVFPIAISLRRTNVYEEKSLGIYADNPAPDETGEQSYVGTHLRRQLSFDLWYIFLGFFFISIIEGSRLENTNDYS FTLFSVLFEIVSAYGTVGLSLGYPSINASFSAEFKTLSKLIVIAMQIRGRHRGLPYALDRAILLPSETLHKKEDVDAGRRAARRNSNISEM MAADAVVG															

1E-142	485	0.3	3E-142	484.3	0.2	1.4	1	C5GIK0_AJEDR	Potassium ion transporter	BDCG_04532	Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) (Blastomyces dermatitidis)	874	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Blastomyces, Ajellomyces dermatitidis (Blastomyces dermatitidis), Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) (Blastomyces dermatitidis)	559297	>tr|C5GIK0|C5GIK0_AJEDR Potassium ion transporter OS=Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) GN=BDCG_04532 PE=4 SV=1MTFRSGLAKVRRAYWSLLEGFMDAIQVLDSIRSRIPVISSIRINFLSLHYAYIIVCALACSIVIYPNGNMRYIDALLFGTGSATQSGL NPIDLNLLFTYQQVGLWFVSMITNPIVIHSFVVFMRLFWFERRFQHVVREAKTLRRIKTRQRTMTRDAWGREGVETGPNQDREGVGV RGKRIVLVRDSDTGQAQGGSAVPDVMKKSDPESTSDSDKSPKSTTGGRSSSQMEDQTEREERGELANTSESPVADDNDRSVEFRT PQYLSPEHHIAFLEHQRRQTGALRIPSPREYDRGRVPQTVDNTDGGDLTRAQTLQSERPLQSSPFSPFTPPSRGRRITIDEPNAVRM RSRTRTFPRTNSRRGRSQGASEPDTDYAPSERTRKGTLSSLFRSTSAQGADVDSSPYLSWQPTIGRNSAFVDLTEEQRNELGGIEY RALKALAVVLICYFFLFHLLGIICLVPWILKTERFGNVVRAAGVGRPWWAIFTSGSSFNDQGFALTPNSMIPFYDAVFPLLLLTFLIIIGNT GFPCMLRFIIWVLSLLVPTGSPAWEELRFLLDHPRRCFTLLFPRAATWWLFGVLVILNGVDVIFFIILDLSDPDITRIPGGIRFVDGLFQA AATRTAGLAVVNLSEIHPAVQVSYMIMMYISVFPIAISVRRTNVYEEGSLGIYSYPDEDEEDETLGSKKINYVGAHLRRQLSFDLWYIFL GLFIIAIVEGNRLDDTGENGFTLFAVMFEIISAYGTVGLSLGFPNTNTSLCAQFKPLSKLIIIAMEIRGRHRGLPYELDRAIMLPSESLNRK ELLDANKRVRRSGSAASTLSGVIGQQPLPNPLQQESGSSSAYQRDGPASPRSLELTNRPTGAASNRPPLETHHEDV
2E-142	485	1.8	4E-140	477	1.5	2.1	2	F2PRV1_TRIEC	Potassium ion transporter	TEQG_03487	Trichophyton equinum (strain ATCC MYA-4606 / CBS 127.97) (Horse ringworm fungus)	862	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Trichophyton, Trichophyton equinum (Horse ringworm fungus), Trichophyton equinum (strain ATCC MYA-4606 / CBS 127.97) (Horse ringworm fungus)	559882	>tr|F2PRV1|F2PRV1_TRIEC Potassium ion transporter OS=Trichophyton equinum (strain ATCC MYA-4606 / CBS 127.97) GN=TEQG_03487 PE=4 SV=1MDTVKAAIERWKLSPEIREKLWAIKRKTPVLKDLHYNFICLHYAWIIGVTLVGSIILYPGGNMSYVDALFFASGSATQSGLNTIDVN KLYTYQQVWLWMGSMIANPIVINSAVVFVRLYWFEQRFQHVVREVKALRRSRSRSATTREPDDTNDLHRAEAGVRGRDIVVLRNT DGHAQGRFLDAPKKEPETTSESDSSIPPGEGQGETATNENGQSTSNTSLKTSDALLAPSHFPGDARIQWSVPPSDNERHITFLEHQR RQTGALRIPSPREYDRGGMPEALDETDGADLARNATVQSDPPAELTGTSLPTSLGPMNQHITIDEPNITRTRKATHSRGGERDRDRD RDRDRDGEETSTIRRVTSRRSMVPSFMRSRTLEQLQQDAPYLSWEPTIGRNSAFVDLSEMQREELGGIEYRALKTLAIVLIGYFFFH LLGIVCMVPWILNTRWGEVVRAAGQGRPWWAVFSSGSAFNDQGFTITPDSMLSFYDAIFPMLLMTFLILIGNTGFPCMLRFVIWFFS MIVPKGSGVWEELKFLLDHPRRCFTLLFPSSANWWLFWVLVILNGVDLIFFVVLDLNDPDVTRIPGGIRFVDGLFQAAATRTAGLSVIG LTTLHPAIQVSYMIMMYISVFPIAISVRRTNVYEERSLGIYSDPDEYNENEKEPSFVGAHLQRQLSFDIWYIFLGLFVISIIEGSRLDNPKD LGFSLFAVLFEVVSAYGTVGLSLGYPDSNTSFSAQFHTLSKLVIIAMEIRGRHRGLPYALDRAVLLPSEALHRKEADDASKRLRRRSSN VSALSSATGRASGLYRDDGGLMARLSQQQQQQQQQLSSGGGVLGSSSDAPPPTASSARGARRLSTHQEDA
2E-142	485	7.1	2E-142	484.8	4.9	2	1	E3RZK9_PYRTT	Putative uncharacterized protein	PTT_15100	Pyrenophora teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)	858	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Pyrenophora, Pyrenophora teres, Pyrenophora teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)	861557	>tr|E3RZK9|E3RZK9_PYRTT Putative uncharacterized protein OS=Pyrenophora teres f. teres (strain 0-1) GN=PTT_15100 PE=4 SV=1MFTPWITVIAWLKERTPSSLKALAPHANFITLHYAYIIGWTLIGSVILYGGGRMHYIDALFFASGSATQSGLNTIDINTLALYQQITM YLMTSLCTPIFIHSSVVVVRLYWFEKRFQNIVLERGNRSGRTRTLSRRKSEMQNDGDRDVSHEEKAVGAREIRVMRGSNGHAHGGHI ENEFAFSDGMDSTGNGIRARRRSSSSEDEMPPFVRPTTPVRNTPAIVWADNLSTPKARDEDHKNSVEESPGGRLPQSNKEKSIAFV EAQRNPTARNKLRIPGPRDFDQGLIPEAIKGEDEELDKVQSRPSHDSHPRPRYERSNSLPHAANGDDRPFKNHITIDVPDRVNGPTG HSIYDRTGTVDGDAGPTPGMHLRNRSRSRTLASFLSRSKDEDEEPVPYLSWTPTIGRNSNFVDLTEEQREELGGIEYRALKLLAWILTI FYLGWHTIGVICLVPWITHTARYSGVVEAVGINPVWWGFFTSASLFNDLGFTLTPDSMVSFQLAVFPLIIGTFLIIIGNTGFPCMLRFTI WMYSKMVPKTSSMWEELRFLLDHPRRCFTLLFPSKANWWLFWILVVLNGVDLIFFIILDLGDPTVTSLSPGHRFLAGLFQAASTRTAG FAVVNIADLHPAVQVSYMIMMYISIFPIAMSIRQSNVYEEKSLGVWASSGEEEEEENSSYLSHHLRLQLSFDLWFVFLGFFLIAIIEGPRL ENTNEYAFSLFSVLFEIISAYGTVGLSQGFPGVNTSFSGQFKPLSKLIIIAMQIRGRHRGLPYALDRAILLPSETLHQKENEDATRRARRS STAVDMSGGMGDGLSRTTTGISRRSTASGDRMGQSQNRPKQLKRILSGAFTAGPTGQFKRA
3E-142	484	7.4	3E-141	481	3.9	2	2	M2TDM9_COCSN	Uncharacterized protein	COCSADRAFT_288562	Cochliobolus sativus (strain ND90Pr / ATCC 201652) (Common root rot and spot blotch fungus) (Bipolaris sorokiniana)	860	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Bipolaris, Cochliobolus sativus (Common root rot and spot blotch fungus) (Bipolaris sorokiniana), Cochliobolus sativus (strain ND90Pr / ATCC 201652) (Common root rot and spot blotch fungus) (Bipolaris sorokiniana)	665912	>tr|M2TDM9|M2TDM9_COCSN Uncharacterized protein OS=Cochliobolus sativus (strain ND90Pr / ATCC 201652) GN=COCSADRAFT_288562 PE=4 SV=1MFGPWLSFFAWLKQRTPSSLKALTPHANFITLHYGYIISWTLIGSVIMYGNGRIPYIDALFFASGGATQSGLNTIDVNNLDLYQQI TLYLMTCLCTPIFIHSSVVVVRLYWFEKRFQNIVLERGSRSGRTRTLSRRKSEAKKTNGADPGLEEQAVGSREIRVMRGSNGHAHGG TIENENAFSDGLDWTGNGIRPRRRSSSSEDDMPPFRPQTPPQNAPAGIVWADNLNTPANQKPIRSSVEESPGSRLPEMNKERSIAFV EAQRNPTTRNKLRIPGPRDFDQGLIPEAVEGEGELDRVTSRMSQDSRAHSAPKNKRSNSLPFPSNEDDRQLKNHITIDVPDRQRPNG HSVYDRTRTNDVDPNGPSASMHLRNRSRSRTLASFLSRNKDEEEDPMPYLSWTPTLGRNSNFVDLTEEQREELGGIEYRALKLLAVI LTVFYIGWHIVGVISLAPWISHSPQYSAVVKKVGIHPTWWGFFTSASLFNDLGFTLTPDSMVSFQLTVWPLLIGTFLIIIGNTGFPCMLR FTIWIYSKLVPKGSGIWEELRFLLDHPRRCFTLLFPSQANWWLFWILILNGVDLIFFIVLDLDDPTVTSLSGGHRFLAGLFQAASTRTA GFAVVNIADLHPAVQVSYLVMMYISIFPIAMSIRQSNVYEEKSLGVWTDNELDDAQSSYLSHHLRRQLSFDLWFVFLGFFLIAIIEGARL ENTNEYAFSLFSVLFEIVSAYGTVGLSQGYPGTNASFSAQFKPLSKLIIIAMQIRGRHRGLPYALDRAILLPSETRYQKENEEATRRARR GSNAMDMGLSYSTDRITRTGTMLSRRSTASASGERMVTETRPEQLKRIISGAFTAGPTGLYREKTN
3E-142	484	5.1	3E-142	484	3.6	2	2	G2R908_THITE	Uncharacterized protein	THITE_2119891	Thielavia terrestris (strain ATCC 38088 / NRRL 8126) (Acremonium alabamense)	907	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Thielavia, Thielavia terrestris, Thielavia terrestris (strain ATCC 38088 / NRRL 8126) (Acremonium alabamense)	578455	>tr|G2R908|G2R908_THITE Uncharacterized protein OS=Thielavia terrestris (strain ATCC 38088 / NRRL 8126) GN=THITE_2119891 PE=4 SV=1MDNLGAVFVGQLKALRPSFISKEPHFNFITAHYFYIISLAMLGSVIVYGAGKGNIAYIDALFFTTGASTQAGLNTVDVNLLNTFQQV VLYLWPMMTNPITINSFVVFLRLYWFEKRFQHIVRESRLKRGTISKSKAGANFDGADAERGVNGRKITVMLNGARSRITNDGILLGPAP LQSDEQLDPKSTSPNPLGIHGTSESAEPRRPEIKFARTVTKSDGLGEDALKLPPLRSEQEHIAILERQRKGDDEVLRIPNPRDVERGMV PKPVEAGDDEEPDVASPRPTRSATNQDGEPEGPSADGRQQAITIEEPDRRKLQQLGSGDLIEDATAAGRAFSFLKLKRSRFLSRTNS KPRGNEDALGGGPSKAKGRRQSLLLLRTALSRDKVEGTPYLSWEPTIGRNSAFLDLTEEQREELGGIEYRSLKTLALILTAYFWGFSIL GVISLLPWILHTERYGQIVDAAGMARTWWAFFTPNSAFMDLGFTLTPDSMNSFNTAVWPLLLLSFLIIIGNTGFPVMLRFIIWVTSHLVP VGTGLYEELRFLLDHPRRCFTLLFPSGATWWLFWLLVVMNCLDLIFFIVLDLGSGPVVDLPPGLKVLNGLFEAVSTRTAGFSCVNLAAL HPAVQFSYMVMMYISVFPIAISVRRTNVYEERSLGVYSRHDIDEQASQGSDLSYVGAHLRRQLSFDLWYIVIGFFILNIAEGPRIMAGDF SMFAVLFEVVSAYGTVGMSLGYPTVVNASLSSQFTVVGKLVIIAMMIRGRHRGLPYGLDRAILLPSEALHATEAAADADARVVRHLSHTS AATAGGPRLPSSGVRRRKSLSGDHGNILTSLLHPGPLVPLEPPPPPLAPVMTELHSRRASDATAEEPGPYATRVSSRWTEPGGASR RLDPAALAQRPRTSGGDDGAQD

5E-142	483	3.6	5E-142	483.3	2.5	2.1	2	A0A066XPA9_COLSU	Putative trk family potassium uptake protein	CSUB01_05756	Colletotrichum sublineola (Sorghum anthracnose fungus)	921	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum sublineola (Sorghum anthracnose fungus)	1173701	>tr|A0A066XPA9|A0A066XPA9_COLSU Putative trk family potassium uptake protein OS=Colletotrichum sublineola GN=CSUB01_05756 PE=4 SV=1MLKDACGWLLAQLRAAKPSFISKKPHFNFISAHYFWICSLTILGSILIYATAGGQMAYIDALFFASGANTQAGLNTIDLNLLNTFQQICLYVFTMTSNPITIHSSVVFLRLYWFEKRFQGIVREARQRRNTMSKSKSRARDELNQAERGRLNVRNIKVMHTNGQRSRMTNDGILLGMKEDEDGRISPGSNGFVPAHASPAQQSSGDQTPDRASDHDDDDAHGTDVSQGRITFAQHVFRSDGTEPEVKLPPPHSPAHLAILERQRNGPEETLRIPNPRDAERGMKPKRVEDNAAPEPEDERENGIPRIHVAAGEANGLSHGLGNNASRRPTIKIEEPERPRQPERSVKEEIADEAEVIGRTIFPFSLRKPNLHRKGDEKTRSEDGTSDTPLARVRSRTFDTIRTALTREKVEDMPYLSFTPTMGRNSAFPGLTLEQRELGGIEYRSLRTLAVILLCYFWGFSIFAITCFLPWIYTSSNAKYAGIVESSGVSKVWWGIFTANSAFNDLGLTLTPDSMNSFNDATFILMIMAFLIIIGNTGFPIMLRVIIWIMSKIVPKGTGLWEELRFLLDHPRRCFTLLFPAGATWWLFIILIGLNVLDLLFFVLLDLNDNAVSHLPVHIRIVDGIFQAASTRTAGFSVVNISLLHPAVQVSYMIMMYISVFPIAISIRRTNVYEEKSLGVYHSPDEDLEGTNENSAWSYVGTHLRRQLSFDLWYVFLGLFILAITEGPRIQKNDFDVYAVLFEIVSAYGTVGLSLGYPNVNASLCSQFTTGGKLIMIAMQIRGRHRGLPYGLDRAVLLPSESRFEKEAEEAHPVLARSATGASTGTALSATRSHLRSRRMSTNRGQGNLITQFLHPGPMIPHEDSLTNLSRHTRSFATDERPPMGEDMRRRNTEPVEDDTTSSSSETAAPPRRVFTTPAH
7E-142	483	2.3	2E-139	475.2	1.2	2.1	2	F2T190_TRIRC	Uncharacterized protein	TERG_08577	Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) (Athlete's foot fungus)	852	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Trichophyton, Trichophyton rubrum (Athlete's foot fungus) (Epidermophyton rubrum), Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) (Athlete's foot fungus)	559305	>tr|F2T190|F2T190_TRIRC Uncharacterized protein OS=Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) GN=TERG_08577 PE=4 SV=1MDTVKAAIERWKPSLEMREKLWAIKRKTPVLKDLHYNFICLHYAWIIGVTLVGSIILYPGGNMSYIDALFFASGSATQSGLNTIDVNKLYTYQQVWLWMGSMIANPIVIHSAVVFVRLYWFEQRFQHVVREAKALRRSRSRSRATTREPDDANDLHRAEAGVRGRDIVVLRNTDGHAQGRFLDAPKKEPETTSESDSSIQPAEGQGETAIKGNGQSTSSTSSKTNETLLAPSYFPGDARIQWSVPPSDNERHITFLEHQRRQTGALRIPSPREYDRGGMPEALDETDGADLARNATVQSDPPAEPTGTSLPTSPGPINQHITIDEPNITRTRKATQSRGGERDRDRDGDETSTIRRVTSRRSMVPSFMRSRTLEQLQQDAPYLSWEPTIGRNSAFVDLSETQREELGGIEYRALKTLAIVLIGVYFFFFHLLGIVCLIPWILNTRWGEIVRAAGQGRPWWAVFSAGSAFNDQGFTVTPDSMLSFYDAVFPMLLMTFLILIGNTGFPCMLRFVIWFFSMIVPKGSGVWEELKFLLDHPRRCFTLLFPSSANWWLFWVLVLLNGVDLIFFVVLDLNDPDVTRIPGGIRFVDGLFQAAATRTAGLSVIGLTTLHPAIQVSYMIMMYISVFPIAISVRRTNVYEERSLGIYSNPDEYSEDEKEPSFVGAHLQRQLSFDIWYIFLGLFVISIIEGTRLDNPKDLGFSLFAVLFEVVSAYGTVGLSLGYPDTNASFSAQFHTLSKLVIIAMEIRGRHRGLPYALDRAVLLPSEALHRKEDDDASKRLRRRSSNVSALSSATGQASGLFRDDGGLMARLQQQQPSSSGGGAVGSSSDAPPPPTASSARGAKRLSTHQEAA
1E-141	482	4	9E-140	475.9	2.4	2.1	2	E4US81_ARTGP	High-affinity potassium transporter	MGYG_04290	Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	860	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Microsporum, Arthroderma gypseum (Microsporum gypseum), Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	535722	>tr|E4US81|E4US81_ARTGP High-affinity potassium transporter OS=Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) GN=MGYG_04290 PE=4 SV=1MDTVKAAIERCKPSPEVREKLWAIKRKTPVLKDLHYNFICLHYAWIIGVTLVGSIILYPGGNMAYIDALFFASGSATQSGLNTIDVNLLFTYQQVWLWMGSMIANPIVIHSAVVFVRLYWFEQRFQHVVREAKALRRSRSRSRAPTRDGNDSNDAHRAEAGVRGRDIVVIRNNDGLAQGRFMDTPKKEPETTSDSGSSTQPAEGQGESTANGQTTTHDESPNKSNQTLLAPSHFPGDARIQWSVPSDNERHITFLEHQRRQTGALRIPSPREYDRGGMPEALDETDGSELARNATVQSDPSAEQTGTGTSLPTSPGPVNQHITIDEPNITRTRKATHSRGGDRDRDRDRDGDETSTIRRVTSRKSMVPSFLRSRTQEQLQQDAPYLSWEPTIGRNSAFVDLSETQREELGGIEYRALKTLAIVLIGVYFFFFHLLGIICLVPWILNTHWGSIVTSYGQGRPWWAVFSAGSAFNDQGFTITPDSMLSFYDAVFPMLLMTFLILIGNTGFPCMLRFVIWFFSIIVPEGSGVWEELKFLLDHPRRCFTLLFPSSANWWLFWVLVLLNGVDLIFFVILDLNDPDVTRIPGGIRFVDGLFQAAATRTAGLSVISLTTLHPAIQVSYMVMMYISVYPIAISVRRTNVYEERSLGIYSDPDEYSENEKEPSFVGAHLQKQLSFDIWYIFLGLFVISIIEGTRLDNPKDLGFSLFAVLFEVVSAYGTVGLSLGYPTSNTSFSGQFHTLSKLVIIAMEIRGRHRGLPYALDRAVLLPSEALHRKEADDAKRLLRRRGSNVSAMSSATGQASGMYRDDVGVMARLHQTQTQQQHQGLGQSSGGGKGVSSEVPPPTASSVQAKRLSTHQAA
1E-141	482	2.8	1E-139	475.3	1.3	2.1	2	D4ARQ0_ARTBC	Potassium uptake transporter, putative	ARB_06793	Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) (Trichophyton mentagrophytes)	858	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Arthroderma, Arthroderma benhamiae (Trichophyton mentagrophytes), Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) (Trichophyton mentagrophytes)	663331	>tr|D4ARQ0|D4ARQ0_ARTBC Potassium uptake transporter, putative OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) GN=ARB_06793 PE=4 SV=1MDTVKAAIERWKPSLETRERLWAIKRKTPVLKDLHYNFICLHYAWIIGVTLVGSIILYPGGNMSYVDALFFASGSATQSGLNTIDVNKLYTYQQVWLWMGSMIANPIVIHSAVVFVRLYWFEQRFQHVVREAKALRRSRSRSRAPTREPDDNNDLHRAEAGVRGRDIVVLRNTDGHAQGRFLDAPKKEPETTSESDSSIQPAEGQGETTAANGTGQSTSNTSSKTNETLLAPSHFPGDARIQWSVPPSDNERHITFLEHQRRQTGALRIPSPREYDRGGMPEALDETDGADLARNATVQSDPPAELAGTSLPTSPGPINQHITIDEPNITRTRKATHSRGGERDRDRDGDETSTIRRVTSRRSMVPSFMRSRTLEQLQQDAPYLSWEPTIGRNSAFVDLSETQREELGGIEYRALKTLAIVLIGVYFFFFHLLGIVCLIPWILNTHWGEIVRAAGQGRPWWAVFSAGSAFNDQGFTITPDSMLSFYDAVFPMLLMTFLILIGNTGFPCMLRFVIWFFSMIVPKGSGVWEELKFLLDHPRRCFTLLFPSSANWWLFWVLVLLNGVDLIFFVVLDLNDPDVTRIPGGIRFVDGLFQAAATRTAGLSVIGLTTLHPAIQVSYMIMMYISVFPIAISVRRTNVYEERSLGIYSDPDEYSENEKEPSFVGAHLQRQLSFDIWYIFLGLFVISIIEGTRLDNPKDLGFSLFAVLFEVVSAYGTVGLSLGYPDSNTSFSAQFHTLSKLVIIAMEIRGRHRGLPYALDRAVLLPSESLHRKEEDDASKRLRRRSSNVSAFSSATGQASGLFRDDGGLMARLHQQQQQQQQPPSSGGGGVGSSSDAPPPTASSARGAKRLSTHQEDA
1E-141	482	7.3	8E-141	479.3	0.6	2.1	2	Q0CAU4_ASPTN	Putative uncharacterized protein	ATEG_09190	Aspergillus terreus (strain NIH 2624 / FGSC A1156)	827	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus terreus, Aspergillus terreus (strain NIH 2624 / FGSC A1156)	341663	>tr|Q0CAU4|Q0CAU4_ASPTN Putative uncharacterized protein OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) GN=ATEG_09190 PE=4 SV=1MYSAILRGASSSIHRLTEVKARIPFLKNVHVNFILLHYTYIISMTFLSSIIIYPGTELAYIDALFFSAGAATQSGLNTVDFNLLHTYQQIVLYWVSMLTTPIFIHTILVFVRLYWFEKRFQHVARDARALRQSRSRMRTISQDKDSMSHGREEMGVGGRSIVVLRNTLRNQGTAQEPGSPKRSPPSDSGSASSGAPGESARTSGDEQDEEQDESPGTSLRMRFGSLRVPAQLSPEQHIAFLENQRRNTGALRIPSPREYDRGGVPQVLDEGNAEVTRTGSRQSDEPRSPRDAEESDHVGPMVGPHITINEPDMIRTKTRNSTFPRMDTRPTVRETKDPGDPSSPLTRIATRRPTITGVFRSLTHERERTTLPYLSWNATVARNSNFVDLTEEQRDELGGIEYRALKTLAVVLISYYVFFHLLGIICLVPWILTTRWGSVVTEIGQGRPWWAIFTAASSFNDVGFSITPDSMMGFADAIFPLLLNGFLIVIGNTGFPCMLRLIIWALSKFTRKETPLWEELKFLLDHPRRCFTLLFPRNATWWLFAILVALNGIDLIFFIILDLNNPTVTDFPVGIRILDGLYQATCTRTAGFSVVSLADLHPAVQVSYMIMMYISVFPIAISLRRTNVYEEKSLGIYPGADDDDDSENQTTPNYIGAHLRRQLGFDLWYVVLGLFIICIVEGGRLQRKDEYAFQIWSVLFEVISAYGTVGLSLGYPGVNASFCSQFQVISKLVIIAMQVRGRHRGLPYALDRAILLPSEALNQKEIVDAERRMRRRASSLAQTSTFDYANSQAREDGASTGLDRKDGPSQGEPIMRRQSTFRSQQSR

3E-141	481	3.9	3E-141	480.9	2.7	2	1	R7YMB5_CONA1	Uncharacterized protein	W97_02269	Coniosporium apollinis (strain CBS 100218) (Rock-inhabiting black yeast)	900	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Chaetothyriomycetidae, Chaetothyriales (black yeasts), Herpotrichiellaceae, Coniosporium, Coniosporium apollinis, Coniosporium apollinis (strain CBS 100218) (Rock-inhabiting black yeast)	1168221	>tr|R7YMB5|R7YMB5_CONA1 Uncharacterized protein OS=Coniosporium apollinis (strain CBS 100218) GN=W97_02269 PE=4 SV=1MFGPWVEVWRWLRPSLPKFEKGGISKPNFKNLRTPHFNFITLHYIYIIFMSILASVIIYGPGGMPYIDALFFGSGAATQSGLNTIDV NKLYLSQQLTLMFVASVCNPIIINTFVVFVRLYWFEKRFQHVAAEARHVRRTRERSRTMSEARRDIDNDLEERGVSKREINIVLGETDN NKWPNQYGKDGTTERDAEPSSGTSSSSSREEHESPGEKIFDPTLGKFVSPPSPTSQPAAPSAEHPPPFHRDIVFADEVSRADTEKEE TSNLERLPQPMSAEQHIAIVEAQRNPKDKGVLRIPGPRDFDRGDTIQRVDEDEKSDLNRVVSHESTSEPEPHQFLRNQRTTSINEEGD APKKSSSDDHPLKRNITFDQPAHPRRNSKAGWSAFSFNKRTATAGTGDDSALGIRQRQRTRTFASFVTNRSQEKDPMPYLSWTPTI GRNSQFVDLTEEQREELGGIEYRSLKTLAIILIIYYVGFHLLGMVCLLPWINHSRYVPYLHEQGVDPDFWGVFTPASLFNDLGFTLTAD SMVTFQRAVFPLLLGSFLIIIGNTGFPCMLRFIIWLASLVTPVGSGVWEELKFLLDHPRRCFTLLFPSKATWWLFWVLIILNLTDLFFFIVL DINDSTVTDLPVGVRILVGWFQAASTRTAGFAVINLAELHPAVQVSYLIMMYISIFPIAISLRRTNVYEEKSLGIFHSGEAEEPAAANGKE QSYVSQHLRRQLSFDLWYVFLGFFIIAIIEGSRLENVKGDEAYFTLFSILFEIVSAYGTVGLSLGFPGFNTSFSGQFHTLSKLVIIAMEIRG RHRGLPYALDRAILLPSESLQQKEAEDANRRAQMRRNSIMSQMVPPPVGDMAGSGLQREASANPAIAHSGRRMSGTNLSRFLSGA LNAGPTIPKDKRT	
7E-141	480	9.6	2E-140	478.3	2.8	2	2	E3Q8C1_COLGM	Trk family potassium uptake protein	GLRG_02304	Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) (Maize anthracnose fungus) (Glomerella graminicola)	918	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum graminicola (Maize anthracnose fungus) (Glomerella graminicola), Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) (Maize anthracnose fungus) (Glomerella graminicola)	645133	>tr|E3Q8C1|E3Q8C1_COLGM Trk family potassium uptake protein OS=Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) GN=GLRG_02304 PE=4 SV=1MLEASRGWLLAQLWAAKPSFISKKPHFNFISAHYIWICSLTILGSVLIYATAGGQMAYIDALFFASGANTQAGLNTIDVNLLNTFQ QACLYFFTMTSNPITIHSSVVFLRLYWFEKRFQGIVREARQRRNTMSKSKSRARDELSQAERGRLNVRNIKVMHTNGHRSRMTNDGI LLSTKEDEDGRVSPGSNGIGPAPAQQSPRDQTPDRASDHHDDDAHGTDLSQGRITFAQHVFRSDGTEPEVKLPPPHSPAHLAILERQ RNGPEETLRIPNPRDAERGMKPKRVEDNAAPEPEDERDDGIPHTRVAAGETNDMSHGLGNNAFRRPTIKIEEPERPREPERSVKDEI ADEAEVIGRTIFPFSLRKPNLHRKGDEKTRGEDGTSETPLARVRSRTFDTIRTALTRDKIEDMPYLSFTPTMGRNSAFPGLTLEQREEL GGIEYRSLRTLAVILLCYFWGFSLFAVTCFLPWIYTSSNAKYAGLVESSGVSKAWWGIFTANSAFNDLGLTLTPDSMNSFNDATFILLI MSFLIIIGNTGFPIMLRVIIWIMSKIVPKGTGLWEELRFLLDHPRRCFTLLFPAGATWWLFIIILGLNVLDLLFFVLLDLNDNAVSHLPVHIR VLDGIFQAASTRTAGFSVVNISLLHPAVQVSYMIMMYISVFPIAISIRRTNVYEEKSLGVYHSPDEDVEGTNENSAWSYVGTHLRRQLS FDLWYVFLGLFILAITEGRRIQAKDFDVYSVLFEIVSAYGTVGLSLGYPNINASLCSQFTTGGKLIMIAMQIRGRHRGLPYGLDRAVLLPS ESRFEKEAEEAHPVLVRSATGASTGTALSAARSHLRSRRMSTNRGQGNIITQFLHPGPVIPHEDSLTDLSRHTRSFAVDEHPPMGEN MKRRNTEPAEDDITSSDSETAGPPRRVFTTPAH	
7E-141	480	8.4	4E-140	477.2	3.8	2	2	R0JSU2_SETT2	Uncharacterized protein	SETTUDRAFT_42817	Setosphaeria turcica (strain 28A) (Northern leaf blight fungus) (Exserohilum turcicum)	859	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Setosphaeria, Setosphaeria turcica (Northern leaf blight fungus) (Exserohilum turcicum), Setosphaeria turcica (strain 28A) (Northern leaf blight fungus) (Exserohilum turcicum)	671987	>tr|R0JSU2|R0JSU2_SETT2 Uncharacterized protein OS=Setosphaeria turcica (strain 28A) GN=SETTUDRAFT_42817 PE=4 SV=1MFGPWLTLVSCLQKYTPSWLKALKPHANFITLHYAYIIGWALIGSVIMYGNGRIPYIDALFFASGAATQSGLNTIDVNKLSLYQQIT LYLMTCMCTPIFIHSSVVVVRLYWFEKRFQNIVLERGNRSGRSRTLSKAKSEMKNKLDRDAGREEQAVGAREIRVMRGSNGHAHGG TIENEYAFSDGQDSTGNGIRPRRSSSSEDEMPPFVRPETPAQNPAGIVWADNLNKPSKRLSKDSLEDSPANRLPQSNKERSIAFVEA QRNPTARNKLRIPGPRDFDQGLTPEAVKGEEEELDRTTSRVSQESRLNSPRNRERSNSLPHVLNGDDRPLKNHITIDVPDRQQRPNG HSVYSRTRTNDADANGPSPSMHLHNRSRTRTFASFLSRDKEEDEDPVPYLSWTPTLGRNSNFVDLTEEQREELGGIEYRALKLLAVIL TVFYLGWHTIGVICLAPWINHNAHYRGIVEAIGVNPTWWGFFTSASLFNDLGFTLTPDSMVSFQLAIWPLVLGTFLIIIGNTGFPCMLRF TIWVYSKLVPRSSAVWEELRFLLDHPRRCFTLLFPSKANWWLFWILVILNGVDLIFFIILDLDDPTVTSLSGGYRFLAGLFQAASTRTAG FAVVNIADLHPAVQVSYLIMMYISIFPIAMSIRQSNVYEEKSLGVWTGDDAEDGKLSYLSHHVRLQLSFDLWFVFLGFFFISIIEGPRLEN TNEYAFSLFSVLFEIVSAYGTVGLSQGFPNTNTSFSAQFKPLSKLIIIAMQIRGRHRGLPYALDRAILLPSETLHQKENEEATRRARRGS NAVDMGPGMPPGSFSRTGTMLSRRSTASGDRMVQETRPEQLKRILSGAFSAGPTGSSYREKAA	
8E-141	479	8.2	1E-140	479.1	5.7	1	1	Q9HPA9_HALSA	TRK potassium uptake system protein	trkH2 VNG_1721G	Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	558	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halobacterium, Halobacterium salinarum (Halobacterium halobium), Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	64091	>tr|Q9HPA9|Q9HPA9_HALSA TRK potassium uptake system protein OS=Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) GN=trkH2 PE=4 SV=1MSRANANRRRDLATIARDVGGLVLIAAGLMSASVLVAAGFQEWYAALGFLLAGGLSATVGGLARRRFADAPAPKMKHGMVIAA GGWFAIAVVGALPFLFTAWLTPPAAMARFVPTDATWTAVSVGNTTTLSSLAYFRQPLHALFESMSGWTGSGLTMAIHEPSLPRSIQ WWRSLTQWVGGVGVVVLTVSILARPGSGSYALYRSEAREKKIHPSVVSTVRTVWKLVVGYTVVGVAVLFVAIRASDYGAALPVWDA AWQALNHTMTGLTTGGFSVTDNSIATYDAPVIEAALLPIMVAGAIAFPIHYRLLADRDHGVLRGDLQTRWLFVLLGGGVVVLAAQNVA AVPVTPDAVTQWTPAIGDVPVLSPAQADAARDATFQWVSALTCTGFQSAPIGNWIAGGKILVVGAMTIGGAAGSTVGGIKIIRAYTAV RGFIWQFSRVFLPSNAVVTARIDGRTLDRDAMEQEFSEAAIVALLWVVLLFATSLVLVNLAGPSFSYADALFEVASAQGNVGLSSGIT GPDMSPIAEAMFLFNMWIGRLEIIPVLVFARAAISGLDP	
1E-140	479	4.3	2E-140	478	3	1.1	1	M1W6Q6_CLAP2	Probable potassium transporter TRK-1	CPUR_01462	Claviceps purpurea (strain 20.1) (Ergot fungus) (Sphacelia segetum)	828	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Claviceps, Claviceps purpurea (Ergot fungus) (Sphacelia segetum), Claviceps purpurea (strain 20.1) (Ergot fungus) (Sphacelia segetum)	1111077	>tr|M1W6Q6|M1W6Q6_CLAP2 Probable potassium transporter TRK-1 OS=Claviceps purpurea (strain 20.1) GN=CPUR_01462 PE=4 SV=1MHTSVVFLRLYWFEKRFRSWAREVRARRRTLTKSKSQTRNDMHLAEQGVNGRDITLVPHNGRKQRITNDGILLEDGNVQLPN SSLMQHKGDESDTTTVTEGHSPLTDHAVVDDLDDNAQEQRAIRVRRESRNSGHNVPGPTAITFADTVKRSDGLRNDETKFSQNRSH AEHIAILERQRNPDDDEVLRIPGPRETERGLGPRRLLAGDINEDDDHYGLHRSITADSRQGGGTADLGRLRERQPTIIISEPEKNRRDE MGDRVKAIGGTLDAFRFRKPRIFNDSQNKHHEDNEPKSVRATRTRTLDTIRSVLSNSKTEDMPYLSYTPTMGRNSNFVGLTLEQREE LGGIEYRSLRTLAVVLLMYFWGFHLVILICLLPYILHNDHYGKVVDADGVSRTWWAFFTSNSAFMDVGFTLTPDSMISFNTSEFVLMIT CFFILIGNTAFPVMLRFIIWVCAKLAPVGSGLWEELRFLLDHPRRCFTLLFPSGPNWWLFCILLLLNAIDLLFFMVLDLGSQPVTQISVKN RVVIGLFQAASTRTAGFSAVSLGDLNPAMPVLYLIMMYISVFPIAISIRRTNVYEEKSLGMYESHDVDNEDAPALSYVGSHLRRQLSFDL WYVFLGFFVITICEGPKIVAQKFSLFDILFEVVSAYGTVGLSMGAKGINASLCSDFTVVGKLVIVAMQIRGRHRGLPYGLDRAILLNSEE KFRGEPEEQAPPAFAHSNTVLSQATTSGMQRQGTSMSRTRSKSRERSRGNGSVVRSFLHPGPVVRRSDGPGHQRAGSTDTQGAP LSPMGTFSEARPEDETVELGRVSSAGSRPQQRRDDAVPGA	
2E-140	478	2.2	2E-140	478.4	1.6	1.9	1	E9F100_METRA	Cation transporter	MAA_05949	Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	921	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium robertsii, Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	655844	>tr|E9F100|E9F100_METRA Cation transporter OS=Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) GN=MAA_05949 PE=4 SV=1MFQTTISYVWGQLKAAKPAFISKKPHFSFITVHYFWIIGATIVGSIAMFVGGKGELAYIDALMFASGANTQAGLNPVDVNRLNGF QQAMIYLFSVTSNPITLHGFVVFLRLYWFEKRFRSWAREIRSRRRTLTKSKSKARNDVHLAEQGVNGRDITLMPQNGRKQRITNDGIL LDDGHETQHNAEVANKSDESDTTTATDDQPKLSEPNHPEKSDGSPPDHGAGENRTTSLPGHTAITFADTVKRSDGLGDEETKFPQR RTNAEHIAILERQRNQDDDEVLRIPGPRDAERGLGPRRLEASDMDEDDHRLARSLTAETFPGGVAQPGRIRERQSTIVIAEPEKHHRR EEIEEKAKAIGGTMDALRFRKPRIFNRSQNKHHEDEEDGRRTRPVRTRTLDNIRSVLSSSKTEDMPYLSYTPTMGRNSNFVGLTLEQR EELGGIEYRSLRTLAIVLLVYFWGFHLVILTCLLPFILHNDHYGDIVVADGVSRTWWGFFTSNVAFMDVGFTLTPDSMISFNTSAFCLM VMWFFIIIGNTGFPVMLRFIIWVAAKLAPVGSGIWEELRFLLDHPRRCFTLLFPSGPNWWLFWILVVLNAVDLLFFMVLDLGGEPIAKLS VSNRVVIGFFQAASTRTAGFSAVAMSEIHPAIPVLYLIMMYISVFPIAISIRRTNVYEEKSLGMYQPNHVEDDQDASALSYVGTHLRRQL SFDLWYVFLGFFIITISEGAKIVAGRFLSFDILFEVVSAYGTVGLSMGAAGVNASLCSQFSVVGKLVIVAMEIRGRHRGLPYGLDRAILLP SESRFRKEAEEQEAALARTNTALTHATASGVQHQDINLTRTRSKSREHVRANSNIVAQLLQPGPAVHREGPSHQRMSSKDSHGHPF GSMRTFSEPHPDDEQMDELAPLPSSGSKPWNRRVDSAPVS	

2E-140	478	4.1	2E-140	478.2	2.9	1.8	1	N1JQK2_BLUG1	Potassium ion transporter	BGHDH14_bgh05208	Blumeria graminis f. sp. hordei (strain DH14) (Barley powdery mildew) (Oidium monilioides f. sp. hordei)	835	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Erysiphales (powdery mildews), Erysiphaceae, Blumeria, Blumeria graminis (Powdery mildew) (Oidium monilioides), Blumeria graminis f. sp. hordei (Barley powdery mildew) (Oidium monilioides f. sp. hordei), Blumeria graminis f. sp. hordei (strain DH14) (Barley powdery mildew) (Oidium monilioides f. sp. hordei)	546991	[illegible] GN=BGHDH14_bgh05208 PE=4 SV=1METSANPMRKPLSALWNVTDVKNPHFNFITLHYFLIIGMSLIGSVCIYSSKNIRYIDALFLASGSATQTRKSRRTMNKTFSKAKTTDICYDLEERGQSKHKTRPVQAISQEATGIQPLESQDEPSTKNTEINDKTRRTLDEHDISREALGLRPSDTQNETMTRQIKFADQVKVENNFIGIVRLPGPRSHEEHIAVLQRQRNPEKGDVLRIPGPRDADAGASPHNVYTNQRSSGDLRNRGEDNEDENENETQQVTINTRQDSNISGTSQSRINSFKGVFTEKRAAAKSILEIFRLRKPATLKNNYLHNRHPKPLQNLRSVLSRDKDDTIPYLSWQPTIGRNSAFLDLSVEQREELGGIEYRSLKALAVVLVSYFWGFSFFGLICLIPWIYKAKPYSEVVMASGQGRVWWGVFTANSAFMDLGFTLTPDSMISFRSASWPLLIMSFLIIIGNTAFPIMLRVIIWVFARFSPTGSGVEQELQFLLEHPRRCFTLLFPAKTTLWLTMMLIFLNAVDLVFFIILDLGNTIVTKLPVRLRVLDGLFQAISTRTAGFSVVDLSLLHPAIQVSYLVMMYISVLPIAISVRRTNVYEERSLGIYSSPADEDENTEHSYVATHLRHQLSFDLWYISLGFFIISISEGTRLQSGDPRFTMFAVLFEIVSAYGTVGLSLGFSGINASFSAEFGMVAKLVIIAMQIRGRHRGLPNELDRAIILPSEKLQQKAEEDLARCTLRRRNSNATDVATGLSKTLSRGQATEILGAVFQPGPPLPRSYRNLHSDDSNLRQRPSFLANNLRERSPDSTALSKSRSNTKSVSSINSTKQIYEEVIGPSLSSRSHND
2E-140	478	8.3	8E-139	472.8	4.2	2.1	2	E9CSR7_COCPS	Potassium ion transporter	CPSG_00626	Coccidioides posadasii (strain RMSCC 757 / Silveira) (Valley fever fungus)	831	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Coccidioides, Coccidioides posadasii (Valley fever fungus), Coccidioides posadasii (strain RMSCC 757 / Silveira) (Valley fever fungus)	443226	[illegible] GN=CPSG_00626 PE=4 SV=1MSISRFASRLSRKLAYLKSKIPWINTLKFNFIFIHYAYIIGVTIIGSVYLYPGGNLAYTDALFLAAGSATQSGLNTIDLDRLSTYQQVGLWLGSMIANPIVIHSSVVFIRLRWFEKRFQHVVQEAKMMRRTRTRTRSRAPSAGSASSASSDMNRLEMGVRGRKITVLRDNEGQALGHFIEPKSKSQEANSIADSSGASNGGDAQMGPENDSDRSKTTEVPAGISTDSHIRSPMEHGPDHYITFIENQRRPTQALRIPSPREFDRGGVPETIDDFGDEPSRSRTVQSDQEPEISPLKQQQSRGQHITIDEPNIARSRRATTFPRTSSRVLADGETADVGEPALHHRRKQRRGTLASILFFGTKDEAREAPYLSWQPTLGRNSAFVDLTEEQKNELGGIEYRALKALAYVLIAYFVFFHVLGIISLVPWILHTRWGIFPIRAAVGRPWWAVFIAGSAFNNQGFSLTPNSLASFYDAIFPLLLMTFLIIIGNTGFPCMLRFIIWCFWKIFPKRTAVWEEFHFLLDHPRRCFTLLFPSSATWWLFWVLVVLNVIDLVLFIILDLNDTAVTSIPGGLRFVDGLFQAAATRTAGLSIISLSELHPGVQVSYMIMMYISIYPIAISLRKTNVYEEKSLGIYYGDEEDELISDKDPSYVAAHLRRQLGFDIWYIFLGLFIISIVEGSRVANDPQFTMFGILFEVVSAYGTVGLSQGYPGTNTSLSAQFKVISKLVIIAMMIRGRHRGLPYQLDRAILLPSEALHEKELRDATMRVRRRGSTISAMAGAARCASRASRDGYGTSTGWQQGPSGSPWTLGARSPQANTNARLPIHHEERSS
2E-140	478	5.1	2E-140	477.8	3.5	2.1	2	A0A0C4DMU7_MAGP6	Potassium transporter 1 (Uncharacterized protein)	MAPG_01112	Magnaporthiopsis poae (strain ATCC 64411 / 73-15) (Kentucky bluegrass fungus) (Magnaporthe poae)	924	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Magnaporthiopsis, Magnaporthiopsis poae (Kentucky bluegrass fungus) (Magnaporthe poae), Magnaporthiopsis poae (strain ATCC 64411 / 73-15) (Kentucky bluegrass fungus) (Magnaporthe poae)	644358	[illegible] GN=MAPG_01112 PE=4 SV=1MVSRRDVKDWLVAQFKNLKPSFLGKTAHFNFISAHYLYIVGQSFLGSILVYASGNGAISYIDSLFFASGASTQAGLNPIDVNQLNTFQQAVLYLQAMMCTPITINTCVVFLRLYWFEKRLMHIVKEARRRRGTISKSRSKSVFERTDDAEQGVNVDDIRVMHGGGNTRITNDGILLPPVSEESRPDGSGSGPSLRLPDEDVDPLTPLPVNGRPRDIKFAAAVKRSGAFDDGAMNLPTPRTTEEHLAILERQRNEDETLRIPGPRDVERGMAPERVDNSSSSSSGEDNEPETDRQSLQPRRPSGDSEHQAPQPRPQTIMIEEPAKPPRRDEMAEDLEVIKNVFSPLYTFRTPRMFRRKKPQQNEDEDDETRGRQQNLRPQSSKRQLSGLRRVLSHDQGIEGTPYLSWTPTIGRNSNFAGMSEDQRDEVGGIEYRSLKALAKVLVSYFLGFSIFAVVCLLPWIHLSDQYGAVVDAAAQSRTWWGFFTANSAFMDLGFTLTPDSMVSFNTAVFPLLIMSFLIIIGNTGFPVMLRFIIWLTSRIIPQNSGLWEELRFLLDHPRRCFTLLFPAAATWWLFGILLLLNGIDLIFFIVLDLGSGVVNDMPTGMKILNGVFQAASTRTAGFASVVNISQLHPAVQTSYLIMMYISIFPIAISVRRTNVYEESSLGIYGGSGMEEEGNNGSDLSYVGSHLRRQLSFDLWYIAMGFFLLSLSEGDRLQKGDFAMFAVLFELVSAYGTVGLSLGYTGVNASLVSQFTTFGKVVIIAMQIRGRHRGLPYGLDRAVLLPSDSRNKNEEALAEARLQDARLARRMSGVSTGTHFTGVHYQGTPSMQRMRSRSIDRTNSNILSQLLHPGPHPHHTPHHHNAATFTSMRSVSTSHLDDVENDHLGVGRHPVRRVETFGQTTSASPRPAAVSPRPAAVSPKP
4E-140	477	10.9	2E-139	474.6	5.2	2.1	2	F0XUE6_GROCL	Potassium ion transporter	CMQ_4515	Grosmannia clavigera (strain kw1407 / UAMH 11150) (Blue stain fungus) (Graphiocladiella clavigera)	930	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Ophiostomatales, Ophiostomataceae, Grosmannia, Grosmannia clavigera, Grosmannia clavigera (strain kw1407 / UAMH 11150) (Blue stain fungus) (Graphiocladiella clavigera)	655863	[illegible] PE=4 SV=1MDSLRDIVLQELKSLRPSFLSKNPHFNFISVHYFWIVGLTVIGSILLYGPGRGKLKYIDALTFAAGGSTQAGLNTVDVNTLDTFQQVVLYVICSLANPITINSFVVFLRLYWFEKRFQHIVHDTRLRRGTISKSKAKAVDDLYLAERGVNGRHITVLHNDLNSRIANDGAFLSPVPSVNTEENAARLAENGGAEDDGNHPHHRPRSDDAHARMSITEQFELRRPEIKFATTVKRSDGLGDQDVKVSQRVSDEEHIAILERQRNLEDDEVLCIPGPRDAERGVLPSRVVRRNSNERDETNPHGGSATREHSPNSVRSSPLPETVVNPSVSTAGEDHATEVAVSDGTGGGHPIMKPAITIQEPEKPPLRDDFTEDARAFVNVFTSFRARVNPFVKKKKGAGKDKNHNAFPFRFTRRPTLHSLRQALTRDKDEDTAPYLSWQPTVGRNSAFIGMSDEQREELGGIEYRSLKTLALVLFVYFWGFWLLGTVCLIPWIMLSKRYGAVVDAADQGRVWWGFFTAQSSFMDLGFTLTPDSMNSFNTAVFPLLLMSFLIVIGNTGFPVMLRLMIWVGSILVPRGSGLYEELTFLLDHPRRCFTLLFPSGATWWLFWLLVILNGIDLLFYCVLDLGSGPIAEMSAGSRVLDGLFQAFSTRTAGFSCVNLATLHPAVQASYMIMMYISVFPIAISVRRTNVYEENSLGIYVESDELDESANGNDLEFVGAHLRRQLSFDLWFLSVGFFILTISEGTRLQKNDFSMFAILFEVISAYGTVGLSLGYPTVNASLCSQFSVIGKLVIIAMMIRGRHRGLPYGLDRAILLPSESLNQKEDALTDGRNAPCVMTAAGRRGSVTSMGTQAATLRVTTSNRDRGRSRSRDHGNGHIFAQFLHPGPPIKHGPVVRPHSRRSFSDSAMEESTAQTTGIEVPGQDGRAQP
5E-140	477	6.8	5E-140	476.9	4.7	2	2	B2WLZ9_PYRTR	High affinity potassium transporter protein	PTRG_11009	Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis)	857	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Pyrenophora, Pyrenophora tritici-repentis, Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis)	426418	[illegible] GN=PTRG_11009 PE=4 SV=1MFTPWITAIAWLKQRTPSSLKALAPHANFITLHYAYIIGWTLIGSVILYGGGRIPYVDALFFASGSATQSGLNTIDINTLDLYQQITMYLMTSLCTPIFIHSSVVVVRLYWFEKRFQNIVLERGNRSGRTRTLSRRKSEMQEGGDRDVSHEEKSVGAREIRVMRGSNGHAHGGHIENEFAFSDGMDSTGNGIRARRRSSSSEDEMPPFVRPTTPVRNTSAIVWADNLSTPKDRDSDRKMSVEESPGGRLPQSNKEKSIAFVEAQRNPTARNKLRIPGPRDFDQGLTPEAVKGDDEELDRVQSRPSHESHPHPRFERANSLPHAANGDDRPFKNHITIDVPDRVNGPTGHSIYDRTGTVDADTGPTAGMHLRNRTRSRTIASFLSRSKDEDEEPVPYLSWTPTIARNSNFVDLTEEQREELGGIEYRALKLLAMILTIFYLGWHTIGVICLVPWITHTARYSGVVEAVGINPVWWGFFTSASLFNDLGFTLTPDSMVSFQLAVFPLIIGTFLFIIIGNTGFPCMLRFTIWMYSKMVPKTSSMWEELRFLLDHPRRCFTLLFPSKANWWLFWILVIMNGVDLIFFIILDLGDPTVTSLSPGHRFLAGLFQAASTRTAGFAVVNIADLHPAVQVSYMIMMYISIFPIAMSIRQSNVYEEKSLGVWASSGEGEEEENSSYLSHHLRLQLSFDLWFVFLGFFFISIIEGPRLENTNEYAFSLFSVLFEIVSAYGTVGLSQGFPGVNTSFSGQFKPLSKLIIIAMQIRGRHRGLPYALDRAILLPSETLHQKENEDATRRARRSSTAVDMSGGMGDGLSRTTTGISRRSTASGGIGQSQSRPKQLKRILSGAFSAGPTGQFKRA

7E-140	476	3.2	1E-139	475.7	2.2	1.2	1	E9DSM0_METAQ	Potassium transporter	MAC_00618	Metarhizium acridum (strain CQMa 102)	937	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium acridum, Metarhizium acridum (strain CQMa 102)	655827	>tr|E9DSM0|E9DSM0_METAQ Potassium transporter OS=Metarhizium acridum (strain CQMa 102) GN=MAC_00618 PE=4 SV=1MFQTTLSYVWGQLKAAKPAFLSKKPHFSFITVHLFVEVRVDLLTSINLEDFWIIGATIVGSIAMFVGGKGELAYIDALMFASGANTQAGLNPVDVNRLNGFQQAMIYLFSVTSNPITLHGCVVFLRLYWFEKRFRSWAREIRSRRRTLTKSKSEARNDAHLAEQGVNGRDITLMPQNGRKQRITNDGILLDDAHETQHNAEVANKSDESDTTTATDDQPKLTEPSPLEKSDDSPQEHGAGESRRTSLPGHTAITFADTVKRSDGLGDEGTKFPQRRTNAEHIAILERQRNQDDDEVLRIPGPRDAERGLGPRRLEASDMDEDDNRLARSPTAETIPGGAAQPGRIREIRQSTIVIAEPEKHHRREEMEEKAKAIGGTMDALRFRKPRIFNSSQNKHHEDDEDARPARPVRTRTLDNIRSVLSSSKTEDMPYLSYTPTMGRNSNFVGLTLEQREELGGIEYRSLRTLAIVLLVYFWGFHLVILTCLLPFILHNDHYGDIVVADGVSKTWWGFFTSNVAFMDVGFTLTPDSMISFNTSAFCLMVMWFFIIIGNTGFPVMLRFIIWVAAKLAPVGSGIWEELRFLLDHPRRCFTLLFPSGPNWWLFWILVVLNAVDLLFFMVLDLGGEPIAKLSVSNRVVIGFFQAASTRTAGFSAVAMSEIHPAIPVLYLIMMYISVFPIAISIRRTNVYEEKSLGMYQPHHIEDDQDASALSYVGTHLRRQLSFDLWYVFLGFFIITISEGAKIVAGRFSLFDILFEVVSAYGTVGLSMGAAGVNASLCSQFSVVGKLVIVAMEIRGRHRGLPYGLDRAILLPSESRFRKEAEEQEAALARTNTALTHATASGIQHQDINLTRTRSKSRERVRANSNIVAQLLQPGPAVHREGPPHQRMGSKDSHGHPFGSMRTFSEPHPDDEQMDELAPLPSSGSRPWNRRVDSAPVS
1E-139	475	8.7	1E-137	468.8	5.1	2.1	2	J3K852_COCIM	Trk family potassium uptake protein	CIMG_06445	Coccidioides immitis (strain RS) (Valley fever fungus)	818	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Coccidioides, Coccidioides immitis (Valley fever fungus), Coccidioides immitis (strain RS) (Valley fever fungus)	246410	>tr|J3K852|J3K852_COCIM Trk family potassium uptake protein OS=Coccidioides immitis (strain RS) GN=CIMG_06445 PE=4 SV=2MSISRFASRLSRKLAYLKSRIPWINTLKFNFIFIHYAYIIGVTIIGSVYLYPGGNLTYTDALFLAAGSSTQSGLNTIDLDRLPTYQQVGLWLGSMIANPIVIHSSVVFIRLRWFEKRFQHVVQEAKMMRRTRTRTSRAPSAGSAGSDMNRLEMGVRARKITVLRDNEGQALGHFIEPKSKSQEANSIADSSGASNGGDAQMGPENDSDRSKTTEVPAGISTDSHIRSPMEHGSDHYITFIENQRRPTQALRIPSPREFDRGGVPETIDDFGDEPSRSRTVQSDQEPEISPLKQQRSRGQHITIDEPNIARSRRATTFPRTADVGEPAPDHRRKQRRGTLASILFFGTRDEAREAPYLSWQPTLGRNSAFVDLTEEQKNELGGIEYRALKALAYVLIAYFVFFHVLGIVSLVPWILHTRWGIFPIRAAVGRPWWAVFIAGSAFNNQGFSLTPNSLASFYDAIFPLLLMTFLIIIGNTGFPCMLRFIIWFFWKIFPKRTAVWEEFHFLLDHPRRCFTLLFPSSATWLLFWVLVVLNVIDLVLFIILDLNNPAVTSIPGGLRFVDALFQAAATRTAGLSIISLSELHPGVQVSYMIMMYISIYPIAISLRKTNVYEEKSLGIYYGDEEDELISDKHPSYVVVAHLRRQLGFDIWYIFLGLFIISIVEGSRVANDPQFTMFGILFEVVSAYGTVGLSQGYPGTNTSLSAQFKVISKLVIIAMMIRGRHRGLPYQLDRAILLPSEALHEKELRDATMRMRRRRGSTISAMAGTARCASRASRDGYGTSTGWQQGPSGSPWTLGSRSPQANTNARLPIHHEERSS
2E-139	475	18.1	2E-138	471.2	7.6	2.1	2	G0SHF9_CHATD	Putative uncharacterized protein	CTHT_0069880	Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719)	970	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Chaetomium, Chaetomium thermophilum, Chaetomium thermophilum var. thermophilum, Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719)	759272	>tr|G0SHF9|G0SHF9_CHATD Putative uncharacterized protein OS=Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) GN=CTHT_0069880 PE=4 SV=1MGSFKDWVVGQIKGLRPSFMSHKPHFNFITAHYFYILGLTFIGSILLFAGGRGNISYTDALFFGACASTQAGLNVVDINKLNTFQQIVIYIIPMLANPITINSFVVFLRLYWFEKRFQHIVQESRLRRGTISRAKSKAKSLPGDLEKGVNGRKITVMLNGHRSRMTPDGTLLEDDPVPSEKSKLERRASDPLSRTSSSWKIESDAHRHPDIKFSRTVTKSDGMSDDVLKLPPLRSEQEHIAILERQRKDDDEVLRIPNPRDVERGVLPKRVVAGEDDEPDPLSPARGEFSHDVCDEPQHLTFDGRQQAITIEEPDRRKLEQSGSDDSLIDARAAVRALSWFRIPLPRFLKRGKARLHDNKHPAGLASAALKGRRRSLQTLRTVLSRDKVEGTPYLSWEPTIGRNSAFPDLTEEQREELGGIEYRSLKTLAVILVCYFWVFSILGVIGLLPWILHVQKYGQVVTAAGVSKVWWAFFTANSAFMDLGFTLTPDSMNSFNTATWPLLFMSFLIIIGNTGFPIMLRFIIWSLSLVTSVGTGLYEELRFLLDHPRRCFTLLFPSAATWWLFGVLIVLNVVDVILFIVLDLGAEPVIALSPGLKVLNGLFEAVSTRTAGFSSVNLGLLHPAVQSSYMIMMYISVFPIAISVRRTNVYEEQSLGVYTPYDLDDQGNQSDMSYVGTHLRRQLSFDLWYIFVGFFILNITEGSKLMANRFSGFAILFEVVSAYGTVGMSLGYSGGNESLSSQFSVIGKLVIIAMMIRGRHRGLPYGLDRAILLPSESLSATEASAPAPISVEPEIPRISRLYSRTSAVTGGPDIGSSARHKSFTSADPRNLLASILHPGPPLPSMGPAETIRRAESIRRMSIDPSLVSGLERLERQKSATTTFSQLPQDPAGASGAGASAAGDATAEVTSTAATSGTDYLHVDQQPWVTRITSRRTEPGASTSRRDRGRGESISSLSAIQRPKTSGPVH
2E-139	475	9.4	6E-139	473.1	3.9	2.1	2	U1GCL6_ENDPU	Uncharacterized protein	EPUS_07049	Endocarpon pusillum (strain Z07020 / HMAS-L-300199) (Lichen-forming fungus)	875	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Chaetothyriomycetidae, Verrucariales, Verrucariaceae, Endocarpon, Endocarpon pusillum, Endocarpon pusillum (strain Z07020 / HMAS-L-300199) (Lichen-forming fungus)	1263415	>tr|U1GCL6|U1GCL6_ENDPU Uncharacterized protein OS=Endocarpon pusillum (strain Z07020 / HMAS-L-300199) GN=EPUS_07049 PE=4 SV=1MSSSFRAVWDRIKPLIPDLFTKGRLNFITIHYLYISGMALTGSVIIYAIGGMPYIDALFFGSGGATQSGLNTIDVNKIHTGQQFLLYMLSMLCNPIFIHSSVVYVRLYWFEKRFKHVVEEARNLRRSKSKGRSVSKAKNDPELGRKEKGVRGRSIVVLHDGHTFDGSLEEEKSKANAAEESLSSSSARNESVTSSNDTAQGEIPSERQGALGADGAVPEIIQPPQRHNMDHHAIFLENQRSPKDKSTLRIPSPREFDRGGKPEDVGDEENAALTRKATGRLDQPHLGPVDFGRTPVSANHITINEPKISRSREKASPFPRLETEKNGSRSSSAQPSASLFSKVRSRRASDIKGLISANTTFFKSKEEEPKEQAPYLSWVPTVVRNSTFVNLNEEQREELGGIEYRALKTLAVVLIAYFFLFHAFGVICLTPWIMESATYGSVVTSFGQGRPWWGVFTAGSAFNDLGFTLTPDSMISFGTAVFPLLLMTFLIIIGNTGFPCMLRFVIWFTSKLVPRGTGLWEELQFLLDHPRRCFTLLFPRAATWWLFAIVIALNALDLIFFVILDLNDETVSRMPGFQKFTNGLFQAASTRTAGFSVVNLSLLHPAIQVSYLIMMYISVFPIAISMRRTNVYEEKSLGIYGERPANGDGDDSEPSYIGAHLRKQLSFDLWYVFLGLFIIAIVEGDRLENTNEYAFTLFSVLFEIISAYGTVGLSLGYPTINASFSGEFRTVSKLVIIAMQIRGRHRGLPYELDRAVLLPSESLQEKEAAEASRMLQRRMTSLSDTSKRDLSRMQSPASQSQTPFTPFTPSPPQDNALTSAVTVSNDDMKERLANIESLHNEKPSGPVRSGLGNAMFRLASPMHKQVPEGGETKQD
2E-139	475	10.8	9E-139	472.5	4.3	2.1	2	H1VCD1_COLHI	Trk family potassium uptake protein	CH063_09114	Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)	921	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum higginsianum, Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)	759273	>tr|H1VCD1|H1VCD1_COLHI Trk family potassium uptake protein OS=Colletotrichum higginsianum (strain IMI 349063) GN=CH063_09114 PE=4 SV=1MLQDTRGWLLAQLRAAKPSFISKKPHFNFISAHYFWICGLTVLGSILIYASAGGQMPYIDALFFASGANTQAGLNTIDVNLLNTFQQICLYFFTMTSNPITIHSSVVFLRLYWFEKRFQGVVREARQRRNTMSKSKSRARDELSQAERGRLSVRNIKVMHTNGHRSRMTNDGILLDMKEGEDGRISPSGNGFVPITITPAQHSPRDQTPDSASEHNDDAHSTDVSQGRITFAQHVFRSDGTEPEVKLPPPHSPAHLAILERQRNGPEETLRIPNPRDAERGMKPKRVEDDAAPEPEDERSNSVPHTNAATGGANDLPDAVGGNGGRRPTIKIAEPERPREPERSVKDEIAEEAEVIGRTIFPFALRKPRLFQKDDKKTHEDGDGAPENPIARVRSNTFDTIRTALTRDKVEDMPYLSFTPTMGRNSAFPGLTLEQREELGGIEYRSLRTLAVILLCYFWGFSIFAITCFLPWIYTSSNAKYANVVESAGVSKAWWGIFTANSAFNDLGLTLTPDSMNSFNDASFILMIMSFLIIIGNTGFPIMLRVVIWILSKIVPKRTGLWEELRFLLDHPRRCFTLLFPAGATWWLFIIIGLNVLDLLFFVLLDLNDNAVSHLPVHVRIVDGIFQAASTRTAGFSVVNISLLHPAVQVSYMIMMYISVFPIAISIRRTNVYEEKSLGVYHSPDEDMEGTNENSAWSYVGTHLRRQLSFDLWYVFLGLFILAITEGHRIQKNDFDVYSVLFEIVSAYGTVGLSLGYPNVNASLCSQFTTGGKLIIIAMQIRGRHRGLPYGLDRAVLLPSESRFEKEAEEAQPVLVRSATAASTGTALSATRSNLRSRRMSTNRGQGNLITQFLHPGPMIPHEDSLTNLSRRSRSFGTDDHPQMGNNMRRRNTEPVEDDTTSSDSETAAPPRRVFTTPAR

2E-139	475	5.4	2E-139	474.8	3.7	2	1	S3C9I9_OPHP1	Potassium transporter 1	F503_05254	Ophiostoma piceae (strain UAMH 11346) (Sap stain fungus)	942	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Ophiostomatales, Ophiostomataceae, Ophiostoma, Ophiostoma piceae, Ophiostoma piceae (strain UAMH 11346) (Sap stain fungus)	1262450	SV=1MESCKDIIFGQLKALRPSFLAKKPHFNFITSHYFYIIGLTILGSVLIYGPGKGNIRYIDALAFSAGGATQAGLNTINVNLLTTYQQVVI FVIAGVANPITINSFVVFLRLYWFEKRFQHIVSEARLRRGTISKSKSKAMGDLSRLENGVAGRRITVVHNGPQSRLANDGTYLGPMAAA TTDGAVNTANGNASNGAANGTATGNHDTLQPSFTFSEPLEARRQEIKFAPTVKRSDGLDDDFTKLPPRLTDEEHIAILQRQRNIPNDD EVLYIPGPRDAERGVLPSRVVRGESDEDEEPALPTGLRARQYSNDSSNSMHLAASSSATANGKSSQNGGDGQKDIDVDDSERGRP RLPQAITIQEPEKPSRLEHLNEDAEAAAHVVSSLRPRLHGLYEKRSNGQAGVDDTGNLRRTASARTNRRPTLTNLKMAFSRDKEEDP APYISWEPTIGRNSAFLGLTEEQREELGGIEYRSLKTLALVLLGYYWGFWLLGVVCLLPWILTTDTYGAVVTAASQSRVWWGFFTPH SAFMDLGFTLTPDSMNSFNTAIFPLLLMSFLIVIGNTGFPVMLRFVIWVTSHIVPQGSGVYEELKFLLDHPRRCFTLLFPSGATWWLFW LLVVLNGIDLLFFIILDLGNGPIFALPAGIRILDGLFQAFSTRTAGFSCVNLAEVHPAVQASYMIMMYISVFPIAISVRRTNVYEEKSLGVYP GSDVEEPANGTDLEYVGAHLRRQLSFDLWFLSVGFFILTISEGGRLQKNEFSMFSVLFEVVSAYGTVGMSLGYATGNESLCSQFSVV GKLVIIAMMIRGRHRGLPYGLDRAILLPSESLNAKEAAAAEIELARGISFMTAATRRNSGGSIPTHATGARGTSMNQDHRRSRSIDRVN SNILTQFLHPGPPKHNLHNPPPSRRSLSDAVAADDSTAHASGIDFADQIWRTRSQQQNP
4E-139	474	1.3	7E-139	472.9	0.9	1.3	1	C1H952_PARBA	Potassium transporter	PAAG_07293	Paracoccidioides lutzii (strain ATCC MYA-826 / Pb01) (Paracoccidioides brasiliensis)	879	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Paracoccidioides, Paracoccidioides sp. 'lutzii', Paracoccidioides lutzii (strain ATCC MYA-826 / Pb01) (Paracoccidioides brasiliensis)	502779	>tr|C1H952|C1H952_PARBA Potassium transporter OS=Paracoccidioides lutzii (strain ATCC MYA-826 / Pb01) GN=PAAG_07293 PE=4 SV=1MPPQFGFKKAVARAYWSSIDALSTALKVLGTIKSRIPIISSIRINFISIHYAYIISCSIVCSVVLFSIGNMSYIDALLFGAGSSTQSGLN PIDVNLLFTYQQVGVYFTSMITNPIVINTAVVFIRLFWFEKRFQHVVREAKTLRRSKSRSRTMTREVGEQGDRNHNREEMGVRGRHIV LVRNSDTGQPRTQVAVPDAVEKSSPESTSESDVSPTINPDSVTNGDWISQNTAGTQNRGSESNVKRSTAPDDTDEDGNLRAPPHLS PEHHIAFLEHQRRETGALRIPSPREYDRGGVPQSIDDDIDDTDLKPTHTSQSEQPSNPAQLSQFQQQLQSSPGQHITIDEPDVVRVRS RTATLPRISSRYGPSTATAGPDENFPKPTRRGTLTSIFRSASAQDADVDSSPYLSWQPTIGRNSAFVDLTEAQRDELGGIEYRALKALA AVLLIGYFFFFHLLGVVCLVPWIMQQTRFGDIVKAAGQGRPWWAIFTAGSSFNDQGFTLTPNSMISFFDAIFPLLLMAFLIIVGNTGFPC MLRFIIWVFSHLVPHGGPLWEELRFLLDHPRRCFTLLFPRAATWWLFGFLVLLNVVDVIFFVILYLNNSEISKIPGGIRFVDGLFQAAAT RTAGLSVVNLAEVHPAVQVSYMIMMYISVFPIAISVRRTNVYEEGSLGIYSSPYVHKEDGDEAFEAKEFNYVGAHLRRQLSFDLWFIFL GLFIIAIVEAGRLDNTGEDSFSMFAVLFEIVSAYGTVGLSLGYPGTNTSLCAQFKPLSKFIIIAMEIRGRHRGLPYELDRAILLPSESLQRR ELVDANKRSKRPGSQVSVHSGVTGQGQPQTTNPQQDIGSSSGYQRDGPHGSRWSEANSLAPTGAVTMTPRLATHHEIA
7E-139	473	0.7	1E-138	472.1	0.5	1.3	1	C1GEW0_PARBD	Uncharacterized protein	PADG_05796	Paracoccidioides brasiliensis (strain Pb18)	880	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Paracoccidioides, Paracoccidioides brasiliensis, Paracoccidioides brasiliensis (strain Pb18)	502780	>tr|C1GEW0|C1GEW0_PARBD Uncharacterized protein OS=Paracoccidioides brasiliensis (strain Pb18) GN=PADG_05796 PE=4 SV=2MSPQFGFKKAVARAYCNSIDALSTTLKVLGTIKSRIPIISSIRINFISIHYAYIISCSIACSVVLFSIGNMSYIDALLFGAGASTQSGLNP IDVNLLFTYQQVGIYFTSMITNPIVINTAVVFIRLFWFEKRFQHVVREAKTLRRSKSRSRTMTREAGEQGDRDHNREEMGVRGRHIVLV RNSDTGQPRTQFTVPDIVEKSSPESTSESDISPTINPDSVTNGDGISQNAAGTTQNRGSESNVKRPTAPDATDEDGNLRAPPHLSPE HHIAFLEHQRRETGALRIPSPREYDRGGVPQSIDDDIDGADLKPTHTSQSEQPSNPAQLSQFQQQLQSSPGQHITIDEPDVVRVRSRT ATLPRISSRYGPSTATAGPDENLPKPTRRGTLTSIFRSTSAQDADIDSSPYLSWQPTIGRNSAFVDLTEAQRDELGGIEYRALKALAVL LIGYFFFFHLLGVVCLVPWIMQQTRFGDIVKAAGQGRPWWAIFTAGSSFNDQGFALTPDSMISFFDAIFPLLLMAFLIIVGNTGFPCML RFIIWVFSHLVPHGGPLWEELRFLLDHPRRCFTLLFPRAATWWLFGFLVLLNVVDVIFFVILYLNNSEISKIPGGIRFVDGLFQAAATRT AGLSVVNLAEVHPAVQVSYMIMMYISVFPIAISVRRTNVYEEGSLGIYSSPYVDKDDGDEAFEAKEFNYVGAHLRRQLSFDLWFIFLGL FIIAIVEAGRLDNTGEGSLSMFAILFEIVSAYGTVGLSLGYPGTNTSLCAQFKPLSKLIIIAMEIRGRHRGLPYELDRAILLPSESLQRRELV DANKRSKRPGSQVSVHSGVTGQGQPQTTNPQQDIGSSSGYQRDGPHGSRWSEANSLAPTGAVTMTPRLATHHEIA
7E-139	473	14.2	7E-139	472.8	4.1	2.1	2	G2X0H2_VERDV	Low-affinity potassium transport protein	VDAG_03751	Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	924	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, mitosporic Plectosphaerellaceae, Verticillium, Verticillium dahliae (Verticillium wilt), Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	498257	FGSC 10137) GN=VDAG_03751 PE=4 SV=1MLDNTRAWLLGQVRAAKPSFISKQPHFNFISAHYFWIVSLTILASVLMYATAGGQLAYIDALFFASGANTQAGLNTVDVNLLNTF QQICIYIFTMTSNPIVIHSSVVFLRLYWFEKRFQNMVRDARARRVTISKSRAKAHLDMNQAEMGVAGRNIRIMPNSGSRITNDGIILDKK VENGGRESPSSNHTAVPSSSDTDDSRRSGANGHSERPSSGDTAARSSYTPRTARGDDIELDSIHGPRRLSHAEHLAILERQRRGYD ETLRIPNPRDVEKGIKPKRVEEGDAPEAEEEEDPNQPGIRSPGNTRPNTPPEGVNPRNRQPTIKIFEPQKPSERRQRPAQQNEESPE RDTMDELAEKATVIGNVLDSVMFRKPRIFQRGQKKYHVDSDEDENDGPRPGPKHRTRTLDVLRGALTGEKADDAPYLSWTPTLGRN SQFPGLSLEQREELGGIEYRSLRTLALLLVCYFWGWSIFALVCLLPWIKSPSNNEYAQVVDAAGMSRTWWGFFTANSAFLDLGLTLT PDSMVSFNQSQYVLMIMVFLIIIGNTGFPVMLRSIIWVMARLVPRGSGLWEELRFLLDHPRRCFTLLFPASATWWLFWILIGLNAIDLLF FVLLDLNDNVVSDMPVHLRIVNGLFQAACTRTAGFSSVNLSLLHPAVQVSYMMMMYISVFPIAISIRRTNVYEEKSLGVYNSAEDDETI NDASAMSYVGTHLRRQLSFDLWYVFLGLFILSITEGSKIKKNEFNVYSILFELISAYGTVGLSLGYPNVNASLSSQFTTGGKLVIIAMQIR GRHRGLPYGLDRAVLLPSEARFADEALETQNGLTRQMTAVTNRTGADLQRGRSRDRGIISSFLHPGPAVPREDRNLARRVSFDAGV SASGANGTEGPDLRRRHTVAVEDADTDEDEEIAPAARARRVFTTPMG
2E-138	472	4.7	2E-138	471.8	3.2	2.1	2	G1X277_ARTOA	Uncharacterized protein	AOL_s00007g386	Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) (Nematode-trapping fungus) (Didymozoophaga oligospora)	883	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, Orbiliomycetes, Orbiliales, Orbiliaceae, Orbilia, mitosporic Orbilia auricolor, Arthrobotrys oligospora (Nematode-trapping fungus) (Didymozoophaga oligospora), Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) (Nematode-trapping fungus) (Didymozoophaga oligospora)	756982	>tr|G1X277|G1X277_ARTOA Uncharacterized protein OS=Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) GN=AOL_s00007g386 PE=4 SV=1MIDFSKIDWSAWFELIRPPRLNFITLHYFYIIGCAIVGSILIFPLKNLPYVDCLFFTTGSSTQSGLNTVDLNTLTTYQQVVLILVPWIT NPIIINTGVVFIRLYWFEKRFETVVAQSKTLVSSRRTMSRRKSEGPDQAERGVAGRKITVLLNSAKKTGPSEKTEDQTTSGNKDLQEF RKNFGFNGPNRPINFPGLRSHSRSRSDGNHQLAMRHSKPGGLFSDTINDNDDDFAIEDDDETPPRPPMSAIPANTELSGILEKGGET SAPGHISFAEPKPRHRKDSEVIVVPSPFDVENRGSGIAHRFVDGGSEDEERGPKDEEQTLPPVPETPGLVKRAITIDEPTMTRETMHS NARQRIRTATSRGSTDQNYFLTPVSPGVHRVVSNNFHRRRGSSPSRKSTKNAEPAPYLPHTLTIGRNSQFNYGELSEEEKDELGGVE YRSLRTLGYILVAYFLFFQVFGIICLLPWIHTQLKYAAVVDAAHQNRTWWAIFTSSSAFTDLGFTLTPDSMLSFQTATWPLLLLSYLIIIG NTGFPCMLRFIIWVLWKICPENWVAKESLHFLLTHPRRCFTLLFPSRATWWLFGVLVIMNATDVILFIVLDLNNPDITALSVNNRILDAYF QAVSTRTAGFAVVNLANLHPAVQVSYLIMMYISVFPIAISVRKTNVYEERSLGIYADHEENDNPNDHSFVGAHLRRQLSFDLWYVFLGL FAICISEGTRISSREDYAFTQFACLFEVISAYGTVGLSLGYPNVNTSFSGQFNTFSKIVIMAMMVRGRHRGLPYELDRAILLPSESLQQK EEEDVTLRLQRRTETQERAERRSLRAMSRGPSAENVNGGISNGTVNGGATNGGTANGGATNGNAKSGDGTGVTTGFQMQRAAT

2E-138	472	0.2	2E-138	471.7	0.1	1.7	1	U7PWF4_SPOS1	Uncharacterized protein	HMPREF1624_03264	Sporothrix schenckii (strain ATCC 58251 / de Perez 2211183) (Rose-picker's disease fungus)	943	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Ophiostomatales, Ophiostomataceae, Sporothrix, Sporothrix schenckii (Rose-picker's disease fungus), Sporothrix schenckii (strain ATCC 58251 / de Perez 2211183) (Rose-picker's disease fungus)	1391915	>tr|U7PWF4|U7PWF4_SPOS1 Uncharacterized protein OS=Sporothrix schenckii (strain ATCC 58251 / de Perez 2211183) GN=HMPREF1624_03264 PE=4 SV=1MDNLKNILVAQLKALRPSFLNKKPHFNFITVHYFYVIGLALLGSVLIYGPGRGNIAYIDALAFASGGATQAGLNTVNVNLLTTYQQV VIFVIAGIANPIVIHSFVVVLRLYWFEKRFQHIAREARLRRGTLSKSKSKYVNDSSRLEDGVNGRHITVIHDGARSRLANDGTYLGPMAS AATDGPAPRDRTNGDAQHHAEDANGTEGENGSAAANGDTVPPKSTLTEPLETRRPEIKFAPTVKRSDGIDDDLTKLPPRLTDEEHIAI LERQRRNQDDDEVLRIPGPRDAERGILPSTIVRGESDDGDAPSPVLQRRNRRLSDASVASLDLDTKPTSQANGTQYRDNSKQTDGS RDSADERRGRPRLAQAITIQEPEKPSRLDELSVDAHAAAHVFTAFRPHRPRGVSSGDDENNLHQTASARPKRRQRMDSFKRVFSRD KEGDPAPYLSWEPTLGRNSAFLGLSEEQREELGGIEYRSLKTLALVLIGYYWGFWLLGVISLVPWILKSSTYGAVVDEASQSRVWWG FFTPHSAFMDLGFTLTPDSMNSFNTAIFPLLLMAFLIVIGNTGFPVMLRFVIWVLSNLVPRGSGVYEEFKFLLDHPRRCFTLLFPSGAT WWLFWLLVMLNGIDLLFFIVLDLGNGPIFALPPGIRVLDGLFQAFSTRTAGFSCVNLANVHPAVQASYMIMMYISVFPIAISVRRTNVYE ENSLGVYNGSEIDDPVHGTDLEYVGAHLRRQLSFDLWYLSIGFFILTISEGARLQANEFSMFAVLFEVVSAYGTVGMSLGYSGGDESL CSQFSVVGKLVIIAMMIRGRHRGLPYGLDRAILLPSESLNAKEAAAAEAQLARGLSFTTAATRRGSAVSLPTQAATLRGSSTNRDRRR SRSIERVNSNLLTSFLHPGPPKHNNLHVPPPPRRSFSEANIDETLAQSSGIDFANHSTFRSQQQ
2E-138	472	11.4	2E-137	468.4	4.8	2.1	2	M2WNW9_DOTSN	Uncharacterized protein	DOTSEDRAFT_72906	Dothistroma septosporum (strain NZE10 / CBS 128990) (Red band needle blight fungus) (Mycosphaerella pini)	973	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Mycosphaerellaceae, Dothistroma, Mycosphaerella pini (Red band needle blight fungus) (Dothistroma pini), Dothistroma septosporum (strain NZE10 / CBS 128990) (Red band needle blight fungus) (Mycosphaerella pini)	675120	>tr|M2WNW9|M2WNW9_DOTSN Uncharacterized protein OS=Dothistroma septosporum (strain NZE10 / CBS 128990) GN=DOTSEDRAFT_72906 PE=4 SV=1MSTTMERPTTANSHESQGDQREPWYHDAFAPIIEVGLWLKSIVPSQLKLKWPKFNFIAVHYGYMIGMTILFSVMIYGNHPHGIG LQYIDALFFAAGTATQSGLNTLNFNQLNTYNQVTMMLGCCLCTPVFINTIVVLVRLYWFEKRFEHIVKEARAVKKAGTISRTKSQMRGD KEKDPGALEVGSVRQKPIQILNNTLQLSADASKDPKKQEEARKFREKMGLQVSDGSTDATPAGSQSGGSNTYPSEPSDSDDTIGVPD IQVRKASRGLSFDTPTPKDHDRPETPQSPQSPFMGLNPRLNRDREITFADEVKTGRQSPELARIPEHRDISRHIEFLERQNQKRNEAG ALRIPGPRERDAGEDVKQLEADRELHRIQTNMSNAGSMRSRSVDARSEVSHDDRPIRRGITIDEPDHPAHRDRNDDDATFTKDDKRS SGVSKRRSHRGFNLSDGPRTLSKTLTQFTNSRSRAKDEDPMPYLSWTATTGRNSAFLGLTQEQREELGGIEYRSLKTLAMILVCYYV GFHTLGMLVFLPWMAAGYHNAPVIRDGQNPLWWGIFTPASMFNDLGFTLTVDSMISFNDSVLALLFGSFLIIIGNTGFPCMLRFIIWFL SKFIASYGSPWWEELRFLLDHPRRCFTLLFPSKATWWLFWVLVGLNVIDLIFFIILDLNDPTVTILPVGFRVLNGWFQAVSTRTAGFAS VNLANLHAAIQVSYLVMMYISVFPIAISVRRTNVYEEKSLGIFGGEEDAGDGDQSYVSQHLRRQLSFDLWYIFLGLFIIAIVEGDRITNSS EPAFTTFSVLFEIVSAYGTVGLSLGYPNVDFSFSGEFRTLSKLIVAMMLRGRHRGLPYALDRAILLPSEKLQQKEAAEAERQMLRRAS TFAEGQPELFNRSKTWEDGELDKYGLPAQHSIDHTNGAGHGHDPEYVGIRQTNTGRTNGSQQGGGKSHQRVRSLSKAILSGLNPA PTFNNKWD
3E-138	471	4.7	1E-137	469	0.2	2	2	T0KXC3_COLGC	Trk family potassium uptake protein	CGLO_03095	Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	913	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	1237896	>tr|T0KXC3|T0KXC3_COLGC Trk family potassium uptake protein OS=Colletotrichum gloeosporioides (strain Cg-14) GN=CGLO_03095 PE=4 SV=1MLDDARGWLLAQLRAAKPSFISKKPHFNFISAHYFWICGLTILGSILIYATAGGQMAYIDALFFASGANTQAGLNTIDVNLLNTFQ QICLYVFAMTSNPITIHSSVVFLRLYWFEKRFQTVVREARQRRNTISKSMSRARGDDLNQAERGRGLSVRNIQVIHRRRRGRMTNDGIV YDMKDDEDGRISPGSNGFVPIPGTPAHRSSGEQTPNTAPGSQDDANDVDASQNRITFARNVFRSDGTEPEVKLPPPSSPAHLAILER QRNDQNGETLRIPNPRDVEKGIEPKRVEHGDAPEPEDDRDHNHEHSAASEANGMANDVGNVGRRQTIKIEEPERPRDHHHEPPVKD ELADEAEAIGRAIFPFSFRRHRKKQPQDDATSENALTRVRSRVDTFRSALSRDKQDDMPYLSFTPTLGRNSAFPGLTQDQREELGGIE YRSLRTLAVILLCYFWGFSLFAVACLLPWVHTSSNDKYGNYIESNGVSKAWWAIFTANSALNDLGLTLTPDSMNSFNDVPFILLIMSFLI IIGNTGFPVMLRFVIWVLSKVVPKGGLHQELRFLLDHPRRCFTLLFPAGATWWLLTILIGLNVLDLLFFVLLDLNDNAVSHLPVGLRIVD GLFQAASTRTAGFSVVNISLLHPAVQVSYMIMMYISVFPIAISIRRTNVYEEKSLGVYHHPDEDVDTANENSAMSYVGTHLRRQLSFDLW YVFLGLFILAITEGPRIQKKDFDVFSVLFEIVSAYGTVGLSLGYPNVNASLCSQFTTGGKLIIIAMQIRGRHRGLPYGLDRAVLLPSESRF EKEAEEAPLPVLVRSATGASTGTAVSASRSHLRSRRQSTNRGNINILTQFLHPGPPMVPHEDSFTSRRSRSFEVGDHHLPIAEEMRR RATEPAEDDSTSTDSEVMNTTRRVNTTPAR
4E-138	470	4.1	4E-138	470.4	2.9	1.4	1	A6QSP4_AJECN	Putative uncharacterized protein	HCAG_00400	Ajellomyces capsulatus (strain NAm1 / WU24) (Darling's disease fungus) (Histoplasma capsulatum)	629	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain NAm1 / WU24) (Darling's disease fungus) (Histoplasma capsulatum)	339724	>tr|A6QSP4|A6QSP4_AJECN Putative uncharacterized protein OS=Ajellomyces capsulatus (strain NAm1 / WU24) GN=HCAG_00400 PE=4 SV=1MALRSAVDSIGTRVPFLSTIRLNFLSLHYGYIITCSLVASVILYAPGNMTYIDALLFATGATTQSGLNPIDTNLLLTYQQTPRSEWP AASPCTQPAQEHHITIDEPNAARMRSRINPRRSSTYRPSEPDADFIPPERTRSRTFSGLFRSSSQGPDIGSSPYLSWQPTIGRNSAFV DLTEAQRNELGGIEYRALKLLVVVLICYFFFFHLLGIVSLVPWILKTERFGNIVKEAGLGRPWWAVFASASAFNDQGFALTPDSMMSFY DAIFPLLLLSFILVGNTAFPCMLRFTIWMLSHLVPFGSPAWEELRFLLDHPRRCFTLMFPGAATWWLFGVLVVLNGLQLIIFIILDLNNP EFNSIPIGIRFVDGFFQAASTRTAGLAVVNLANIHPAVQVFFLIMMYISVFPVAISVRRTNVYEEGSLGIYSYPDDDEDETLGSKNVSYIG AHLRRQLSFDLWYIFLGLFLISIIEVNRLDQKGENFFSMFAVMFEIVSAYGTVGLSLGFPNSNTALAGHFRPLSKLIIIAMEIRGRHRGLP YELDRAILLPSESLNRKESMDANKRLRRRGSNMSTFSVATRQQSMPRVPLKGTRSSSAYQRGGWLGSRPEPTPSQIGAANTGPPLR PHQEGV
5E-138	470	6.3	8E-138	469.4	0.3	2	2	L2FUA1_COLGN	Potassium ion transporter	CGGC5_1078	Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	912	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	1213859	>tr|L2FUA1|L2FUA1_COLGN Potassium ion transporter OS=Colletotrichum gloeosporioides (strain Nara gc5) GN=CGGC5_1078 PE=4 SV=1MLGDARGWLLAQLRAAKPSFISKKPHFNFISAHYFWICGLTILGSILIYATAGGQMAYVDALFFASGANTQAGLNTIDVNLLNTFQ QICLYVFAMTSNPITIHSSVVFLRLYWFEKRFQTVVREARQRRNTISKSMSRARGDDLNQAERGRGLSVRNIQVIHRRRRGRMTNDGIV YDMKDDEDGRISPGSNGFVPIPGTPAHRSSGEQTPNTVPGSQDDANDVDASQNRITFARNVFRSDGTEPEVKLPPPSSPAHLAILER QRNDQNGETLRIPNPRDVEKGIEPKRVEHGDAPEPEDDRDHSHDHSAASGANGMANDVGNVGRRQTIKIEEPERPRDHHEPPVKDE LADEAEAIGRAIFPFTFRRHRKKQPQDDATSENALTRVRSRVDTFRSALSRDKQDDMPYLSFTPTLGRNSAFPGLTQDQREELGGIEY RSLRTLAVILLCYFWGFSLFAIACFLPWVHTSSNDKYGNYIESNGVSKAWWAIWTANSALNDLGLTLTPDSMNSFNDVPFILLIMSFLII GNTGFPVMLRFVIWVLSKVVPKGGLHQELRFLLDHPRRCFTLLFPAGATWWLLTILIGLNVLDLLFFVLLDLNDNAVSHLPVGLRIVDG LFQAASTRTAGFSVVNISLLHPAVQVSYMIMMYISVFPIAISIRRTNVYEEKSLGVYHHPDEDVDTANENSAMSYVGTHLRRQLSFDLW YVFLGLFILAITEGPRIQKKDFDVFSVLFEIVSAYGTVGLSLGYPNVNASLCSQFTTGGKLIIIAMQIRGRHRGLPYGLDRAVLLPSESRF EKEAEEAPLPVLVRSATGASTGTAVSASRSHLRSRRQSTNRGNINILTQFLHPGPPMVPHEDSFTSRRSRSFEVGDHHLPIAEEMRR RATEPAEDDSTSTDSEVMNTTRRVNTTPAR

7E-138	470	4.7	1E-137	469.2	3.2	1.2	1	A0A016PN48_GIBZA	Fusarium graminearum chromosome 4, complete genome (Uncharacterized protein)	FG07279.1 FG05_07279 FGRRES_16803	Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	933	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	5518	>tr|A0A016PN48|A0A016PN48_GIBZA Fusarium graminearum chromosome 4, complete genome OS=Gibberella zeae GN=FG07279.1 PE=4 SV=1MAAEARASIWARLKAVKPPFVSKKPHFNFISIHYTWIIGATLCASVIIYGSGRGQTSYIDSLMFASGANTQAGLNPIDVNLLNTFQ QVVVYFFTLTSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATISKAKTRPRNDDRQNEEGVNGRHITIVPPQGRRQRITNDGILL DGSEAYQSQAIVDDDDDNDHQRRQPPPASSDESDTVSAGRSNSIELSPLEKPGQAHHDNRDEWKEEQSRTQNTPSGIKFAETVKRS DGVDDDLTKFPQRRTHAEHIAILERQRNQDNEVLRIPGPRETERGLGPRRLEEDDGDDDNNTIAMTRTVESRPDHATIDSRGPPGRR PTIVIAEPKRPLKHELTDDARAIGGTLDAIRMRKPRILNRGQKETHDDGDSTMSRAFRTRTIDTIRSALTNDHTKDMPYLSYTPTMGRN SNFVGLTLEQREELGGIEYRSLRTLAVILLSYFWGFQLIAVTFLLPWILHTEKYGRIVEASAVSRTWWGFWTANSAFNDLGLTLTPDSM NSFNTSEYIMMIMWFFVIIGNTGFPVMLRFVIWVLSRLVPTNTGLWEELRFLLDHPRRCFTLLFPSSANWWLFWILVALNAIDLLFFVVL DLNSGPVAQLPVHTRIADGLFQAASTRTAGFSCFSLSDLHPALPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYSSKKDDDEEESASAL NYVGTHLRRQLSFDLWYVFVGFFLLAISEGGSLKAKDFNLFDILFEVISAYGTVGLSMGVPNVNASLCSQFTVVGKLIIVAMQIRGRHR GLPYGLDRAVLLPSEARFQKEAEENQPILIRTRTNASMGAASGMEPPSSPGFPGRRGSASRFRERANSRIISQFLYPGPVIPSNEIHG HKRATSNNSNNTRDFPRFNTEPVFEEEKDEVPPLRPIESHQFTPRRAETG
7E-138	470	1.7	9E-138	469.3	1.2	1.1	1	A0A0J9WHV4_FUSO4	Uncharacterized protein	FOXG_02137	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	874	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9WHV4|A0A0J9WHV4_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_02137 PE=4 SV=1MFASGANTQAGLNPIDVNLLNTFQQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRPRNEREAE EGVNGRHITVVPYQGRPPRITNDGILLDGNDVIQSQAIADDDDDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKPDQGFGDGREA NEGQSRSQNAPTGIKFAETVKRSDGVDDDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNN TIAMTRTVESRPDHATLDSRAPTGRRPTIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMGRAFRTRTI DTIKSALSNDHTKDMPYLSYTPTMGRNSNFVGLTLEQREELGGIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAIS RTWWGFWTANSAFNDLGLTLTPDSMNSFNTSEYVMMIMWFFIIIGNTGFPVMLRFVIWVLAQIVPKGTGLWEELRFLLDHPRRCFTL LFPSSANWWLFWILAALNAIDLLFFVVLDLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAIPVLYMIMMYISIFPIAISIRR TNVYEEKSLGVYHNKKDEDEEESASALNYVGTHLRRQLSFDLWYVFVGFFLLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVP NVNASLCSQFTVVGKLIIVAMQIRGRHRGLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMGTTSGMEPPISPGLPGRRGSM GRIRERANSRIISQFLYPGPVIPSNEIHGHKRATSNNSNNLRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAETNPMP
8E-138	469	4	8E-138	469.4	2.8	1.6	1	J3NR25_GAGT3	Potassium transporter 1 (Uncharacterized protein)	GGTG_03730 GGTG_03730	Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	937	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Gaeumannomyces, Gaeumannomyces graminis, Gaeumannomyces graminis var. tritici, Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	644352	>tr|J3NR25|J3NR25_GAGT3 Potassium transporter 1 OS=Gaeumannomyces graminis var. tritici (strain R3-111a-1) GN=GGTG_03730 PE=4 SV=1MVTRGDVKDWLVAQVKNLKPSFLGKTAHFNFITAHYLYIVGQLFVGSILLYASGNGAISYIDSLLFSSGASTQSGLNPIDVNMLNT FQQAVLYLQAMMCSPITVNTCVVFLRLYWFERRLMHIVKEARRRRGTLSKSRAKSVFERTNDAEQGVNVGDIRVMHGRGNTRITND GILLPPVSEESGQNGSGSGPSLRLPDEDVDPLTPQPVDGRPRDIKFAATVKRSDAFDDDPMNLPTARTTEEHLAILERQRNEEETLRI PGPRDVERGMAPQRVDNSSSSSSNEDNEPETNHGAANARRTSVDSRHQAPQPQLRPQTIMIEEPTKPQKRDEMAEDLEVIKNVFSP VYTFRTPRIFRSKNEPQHGGQDDEARGRQRQTPPQSSKRQLSGLRRVLSHDQATEGTPYLSWTPTIGRNSNFAGMSEEQRDEVGG IEYRSLKALVKVLIGYFVGFSLLGVVCLLPWIRLTDQYGSLVDAVSQSRTWWGFFMANSAFMDLGFTLTPDSMISFNTAVFPLLLMSFL IIIGNTGFPVMLRFMIWFTSRIIPQESGLWEELRFLLDHPRRCFTLLFPSGATWWLFGILILLNGIDLIFFIVLDLASGPVHDMPTGIKILNG VFQAASTRTAGFASVNISQLHPAVQTSYLIMMYISIFPIAISVRRTNVYEESSLGVYGSSGMEEEGNNGSDLSYVGSHLRRQLSFDLW YIATGFFLLSLSEGDRLQKGDFSMFAVLFELVSAYGTVGLSLGYTGINASLVSQFTPFGKVVIIAMQIRGRHRGLPYGLDRAVLLPGDS RNKNEEALAEAKLHDARLARRMSGISTGTHFTGVHYQGTPSVHRMRSRSIDRTNSNILSQLLHPGPHHTPPHHHNAATFTSMRSMST PHLDDLENDHLGVGRHPMRRAETLRAEALGQAPSASPRPPSASPRPAGVNLRPAAGTPRI
9E-138	469	3.7	2E-137	468.5	2.5	1.3	1	C0NT93_AJECG	Putative uncharacterized protein	HCBG_06373	Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus) (Histoplasma capsulatum)	847	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus) (Histoplasma capsulatum)	447093	>tr|C0NT93|C0NT93_AJECG Putative uncharacterized protein OS=Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) GN=HCBG_06373 PE=4 SV=1MALRSGVLKVRRAYWSSLEAFIKTLDSIGTRVPVLSTIRLNFLSLHYGYIITCSLVASVILYAPGNVTYIDALLFATGATTQSGLNPV DTNLLLTYQQVGLWFVSMITNPIFINTFVVFIRLFWFERRFQHVVHEAKALRRIKSRQRTLTREALTKDRRETSHNRDRGNIGVRGKEI VLLRDSGTGQAQGCSAAHDIEKKTDAASTSESDRSPKPSPGGEPSSPQGEDQARGENRGDAADTMEPPISDKNDKGVELGASKYL SPEHHIAFLAHQRRHTCALRIPSPREYDRGGVPQTVDDDADGEDLTQVQTSRSEWPATPPCTQPPQEHHITIDEPNAARMRSRINPR RRSTYRPSEPDADFIPPERTRSRTFSGLFRSSSQGPDIGSSPYLSWQPTIGRNSAFVDLTEAQRNELGGIEYRALKLLVVVLIGYFFFF HLLGIVSLVPWILKTERFGNIVKEAGLGRPWWAVFTSASAFNDQGFALTPDSMMSFYDAIFPLLLLSFLILVGNTAFPCMLRFTIWMLS HLVPFGSPAWEELRFLLDHPRRCFTLMFPGAATWWLFGVLVVLNGLQLIFFIILDLNNPEINRIPIGIRFVDGFFQAASTRTAGLAVVNL ANIHPAVQVFFLIMMYISVFPVAISVRRTNVYEEGSLGIYSYPDDDEDETLGSKHVSYIGAHLRKQLSFDLWYIFLGLFLISIIEVNRLDQK GENSFSMFAVMFEIVSAYGTVGLSLGFPNSNTALCGHFRPLSKLIIIAMEIRGRHRGLPYELDRAILLPSESLNRKESMDANRRLRRRG SNMSTFSVATRQQSMPRVPLKETRSSSAYQRGGWLGSRPESTSSHQEGV
1E-137	469	1.7	1E-137	469	1.2	1.3	1	A0A0J9UH19_FUSO4	Uncharacterized protein	FOXG_02137	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	936	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9UH19|A0A0J9UH19_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_02137 PE=4 SV=1MLDETRASVWARLKAVKPPFMSKKPHFNFISVHYTWIIGATLLASVIIYGAGRGQTSYVDSLMFASGANTQAGLNPIDVNLLNTF QQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRPRNEREAEEGVNGRHITVVPYQGRPPRITNDGILLD GNDVIQSQAIADDDDDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKPDQGFGDGREANEGQSRSQNAPTGIKFAETVKRSDGVD DDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNNTIAMTRTVESRPDHATLDSRAPTGRRP TIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMGRAFRTRTIDTIKSALSNDHTKDMPYLSYTPTMGRN SNFVGLTLEQREELGGIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAISRTWWGFWTANSAFNDLGLTLTPDSM NSFNTSEYVMMIMWFFIIIGNTGFPVMLRFVIWVLAQIVPKGTGLWEELRFLLDHPRRCFTLLFPSSANWWLFWILAALNAIDLLFFVVL DLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAIPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYHNKKDEDEEESASAL NYVGTHLRRQLSFDLWYVFVGFFLLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVPNVNASLCSQFTVVGKLIIVAMQIRGRHR GLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMGTTSGMEPPISPGLPGRRGSMGRIRERANSRIISQFLYPGPVIPSNEIHGH KRATSNNSNNLRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAETNPMP

1E-137	469	1.7	1E-137	469	1.2	1.3	1	F9FB72_FUSOF	Uncharacterized protein	FOXB_03624	Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	936	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	660025	>tr|F9FB72|F9FB72_FUSOF Uncharacterized protein OS=Fusarium oxysporum (strain Fo5176) GN=FOXB_03624 PE=4 SV=1MLDETRASVWARLKAVKPPFMSKKPHFNFISVHYTWIIGATLLASVIIYGAGRGQTSYVDSLMFASGANTQAGLNPIDVNLLNTF QQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRPRSEAREAEEGVNGRHITVVPYQGRPPRITNDGILL DGNDVIQSQAIADDDDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKPDQGFGDGREANEGQSRSQNAPTGIKFAETVKRSDGVD DDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNNTIAMTRTVESRPDHATLDSRAPTGRRP TIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMGRAFRTRTIDTIKSALSNDHTKDMPYLSYTPTMGRN SNFVGLTLEQREELGGIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAISRTWWGFWTANSAFNDLGLTLTPDSM NSFNTSEYVMMIMWFFIIIGNTGFPVMLRFVIWVLAQIVPKGTGLWEELRFLLDHPRRCFTLLFPSSANWWLFWILAALNAIDLLFFVVL DLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAIPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYHNKKDEDEEESASAL NYVGTHLRRQLSFDLWYVFVGFFLLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVPNVNASLCSQFTVVGKLIIVAMQIRGRHR GLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMGTTSGMEPPISPGLPGRRGSMGRIRERANSRIISQFLYPGPVIPSNEIHGH KRATSNNSNNLRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAETNPMP
5E-137	467	4.7	8E-137	466.2	3.3	1.2	1	K3V0P4_FUSPC	Uncharacterized protein	FPSE_01099	Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	933	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Fusarium pseudograminearum (Wheat and barley crown-rot fungus), Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	1028729	>tr|K3V0P4|K3V0P4_FUSPC Uncharacterized protein OS=Fusarium pseudograminearum (strain CS3096) GN=FPSE_01099 PE=4 SV=1MAAEARASIWARLKAVKPPFVSKKPHFNFISIHYTWIIGATLCASVIIYGSGRGQTSYIDSLMFASGANTQAGLNPIDVNLLNTFQ QVVVYFFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATISKAKTRPRNDDRQNEEGVNGRHITIVPPQGRRQRITNDGILLD GSEAYQSQAIVDDDDDNDHQRRQPLPASSDESDTVSAGRSNSIELSPLEKPDQAYRDNRDEWKEEQSRTQNTPSGIKFAETVKRSD GVDDDLTKFPQRRTHAEHIAILERQRNQDNEVLRIPGPRETERGLGPRRLEEDDGDDDNNTIAMTRTVESRPDHATIDSRGPPGRRP TIVIAEPKRPLKHELTDDARAIGGTLDAIRMRKPRILNRGQKETHDDGDSTMSRAFRTRTIDTIRSALTNDHTKDMPYLSYTPTMGRNS NFVGLTLEQREELGGIEYRSLRTLAVILLSYFWGFQLIAVTFLLPWILHTEKYGRIVEASAVSRTWWGFWTANSAFNDLGLTLTPDSMS SFNTSEYTMMIMWFFIIIGNTGFPVMLRFVIWVLSRLVPTNTGLWEELRFLLDHPRRCFTLLFPSSANWWLFWILVALNAIDLLFFVVLD LNSGPVAQLPVHTRIADGLFQAASTRTAGFSCFSLSDLHPALPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYSSKKDDDEEESASALN YVGTHLRRQLSFDLWYVFVGFFLLAISEGGSLKAKDFNLFDVLFEVISAYGTVGLSMGVPNVNASLCSQFTVVGKLIIVAMQIRGRHRG LPYGLDRAVLLPSEARFQKEAEENQPILIRTRTNASMGAASGMEPPSSPGFPGRRGSVSRFRERANSRIISQFLYPGPVIPSNEIHGHK RATSNNSNNTRDFPRFNTEPVFEEEKDEVPPLRPIESHQFTPRRAETG
6E-137	467	2.8	8E-137	466.2	1.9	1.1	1	W7LZQ3_GIBM7	Uncharacterized protein	FVEG_05299	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	875	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	>tr|W7LZQ3|W7LZQ3_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_05299 PE=4 SV=1MFASGANTQAGLNPIDVNLLNTFQQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRPRSEAREAE EGVNGRHITVVPYQGRPPRITNDGILLDGNDVIQSQAIADDDEDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKSDQGFGEGGEV NEGQSRSQNAPTGIKFAETVKRSDGVDDDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNN TIAMTRTVESRPDNATLDHRAPTGRRPTIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMGRAFRTRTI DTIKSALSNDHTKDMPYLSYTPTIGRNSNFVGLTLEQREELGGIEYRSLRTLALILMSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAIS RTWWGFWTANSAFNDLGLTLTPDSMNSFNTSEYVMMTMWFFIIIGNTGFPVMLRFVIWVLAQIVPKGTGLWEELRFLLDHPRRCFTL LFPSSANWWLFWILAALNAIDLLFFVVLDLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAVPVLYMIMMYISIFPIAISIRR TNVYEEKSLGVYHNKKDEDEEESASALNYVGTHLRRQLSFDLWYVFVGFFFLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVS NVNASLCSQFTVVGKLIIVAMQIRGRHRGLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMATASGMEPPTSPGLPDRRGSIG RIRERTNSRIISQFLYPGPVIPSNEIHGHKRATSNNSNNLRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAEANPMP
6E-137	467	0.6	6E-137	466.5	0.4	1.7	1	G9P4F5_HYPAI	Uncharacterized protein	TRIATDRAFT_30674	Hypocrea atroviridis (strain ATCC 20476 / IMI 206040) (Trichoderma atroviride)	942	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Hypocreaceae, Trichoderma, Hypocrea atroviridis (Trichoderma atroviride), Hypocrea atroviridis (strain ATCC 20476 / IMI 206040) (Trichoderma atroviride)	452589	>tr|G9P4F5|G9P4F5_HYPAI Uncharacterized protein OS=Hypocrea atroviridis (strain ATCC 20476 / IMI 206040) GN=TRIATDRAFT_30674 PE=4 SV=1MFDSARAYVAAQLRGVRPSVLTKHPHFNFITIHYFWIIFATLLSGVLIYAGGKGQLHFIDALMFGSGANTQAGLNPVDVNNLNGF QQSWIYTFSLFSNPITLHGCVVFLRLYWFEKRFQNWVQEAKLRRRTISKSKSKARNDLSQLENGLGVNGRRITVVPENTRAQRMTND GILLDKIEEAEPKLNPSSNASDTTTASDDLQKSAELEEDIGPLDQPRRRDISGADQSRQKNDTASGFPSPEQHLTTAITFADTVKRSDG VDDNPTKFPQRRPNAEHIAILERQRNQDNEVLHIPGPRDIERGLGPRRLEEGDHQEDDDQQIARQATFDSRINEPSDPYGQQQTAITF TEPEHPRREELKNDAKAIGGTVDSLRFRKPRFLNRSQDKVHEDGEHRPRSRTPHPHPVRTKTMDTIRSVLSRDKTVDDMPYLSYTPT MGRNSNFLGLTLEQREELGGIEYRALRTLALVLLFYFFVFHILGAVCLLPYILANQHYGNVLTEDSIGKTWWAFWTSNMAFMDVGFTL TPDSMNSFAKSEWILMSMWFFIIIGNTGFPVMLRFMIWAASKLTPKGSGLWEEFRFLLDHPRRCFTLLFPSNATWWLFWILILLNAIDL LFFIVLDLGAEPITALPLHNRVVIGLFQAASTRTAGFSAVSMSELHPAMPVLYLIMMYISVFPIAISIRRTNVYEEKSLGVYHDRTEEDPD AEASALDYVGTHLRRQLSFDLWYVFLGFFLLAITEGGKIVGGRFDLFSVLFEIVSAYGTVGLSMGVPNVNASLCSQFSVPGKLIIVAMQI RGRHRGLPYGLDRAVILPSEARLKREQEEADATLARTSTAVSTGAATGLQRQPTTGQSRSRSRERANSNLISKLLHPGPVVPPEHLG RPRGRSIEAYQRSKSVDVTNALSEPSDAHLEPPREEDDELEQISSSDLPPNKPRRTESSAF
7E-137	466	4.8	1E-136	465.7	3.3	1.2	1	G9N9T8_HYPVG	Uncharacterized protein	TRIVIDRAFT_195596	Hypocrea virens (strain Gv29-8 / FGSC 10586) (Gliocladium virens) (Trichoderma virens)	890	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Hypocreaceae, Trichoderma, Hypocrea virens (Gliocladium virens) (Trichoderma virens), Hypocrea virens (strain Gv29-8 / FGSC 10586) (Gliocladium virens) (Trichoderma virens)	413071	>tr|G9N9T8|G9N9T8_HYPVG Uncharacterized protein OS=Hypocrea virens (strain Gv29-8 / FGSC 10586) GN=TRIVIDRAFT_195596 PE=4 SV=1MFDETRAFIAAQIKGAKPAFVGKKPHFNFITVHYFWIISATLLCAILIYAGGKGELHFIDALMFGSGANTQAGLNPVDLNNLNGFQL SWIYTFSLFSNPITLHSCVVFLRLYWFEKRFQHWVQEARLRRRTLSKSKSKARNDLSQLESGLGVNGRNITIVPHGDKANRITNDGILL DQIPEVDPKPIAKSDESDTTTVSDDLHKSVDLDDIGPLDQPSKKDASHAIPDENDSAPGPPPENPPHLTTAITFADTVKRSDGVGSDPT KFPQRRPNAEHIAILERQRNQDNEVLRIPGPRETERGLGPRRLEEDDQQEDEDRPIARQMTAQSRDEPSGIYGRQPTITIAEPEHHKR DELKDDVAAAGNVVDSLRFRKPRFFNRSQDKIHEDGEESRHTRSRTPHPHPVRTKTMDTIRSVLTRDKADDMPYLSYTPTMGRNSN FLGLTLEQREELGGIEYRALRTLALVLIFYFFIFHVLGVVCLLPYILLNQHYGAVLEADDIGKTWWAFWTSNMAFMDVGFTLTPDSMNS FATSEWVLMSMWFFIIIGNTGFPVMLRFMIWVASKLTPRGTGLWEEFRFLLDHPRRCFTLLFPSNANWWLFWILILLNVIDLVFFIVLDL GAEPITAYPLKNRVVIGLFQAASTRTAGFSAVSMSELHPAMPVLYMIMMYISVFPIAISIRRTNVYEERSLGVYHDRSNEDDSEASALDY VGTHLRRQLSFDLWYVFLGFFLIAITEGGKIVGGRFDLFAVLFEIVSAYGTVGLSMGVPNVNASLCSQFSVVGKLIIVAMQIRGRHRGL PYGLDRAVILPSEARLKREQEESEAALARTNTAVSTGATTGLQRQATTGRSRSRSRDRANSSLLTQLLHPGPVVPQDQFLRCQATTS HTSRDG

1E-136	466	2.9	1E-136	465.8	2	1.3	1	W7M969_GIBM7	Uncharacterized protein	FVEG_05299	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	937	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	[illegible] PE=4 SV=1MLDETRASVWARLKAVKPPFVSKKPHFNFISVHYTWIIGATLVASVIIYGAGRGQTSYVDSLMFASGANTQAGLNPIDVNLLNTFQQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRPRSEAREAEEGVNGRHITVVPYQGRPPRITNDGILLDGNDVIQSQAIADDDEDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKSDQGFGEGGEVNEGQSRSQNAPTGIKFAETVKRSDGVDDDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNNTIAMTRTVESRPDNATLDHRAPTGRRPTIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMGRAFRTRTIDTIKSALSNDHTKDMPYLSYTPTIGRNSNFVGLTLEQREELGGIEYRSLRTLALILMSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAISRTWWGFWTANSAFNDLGLTLTPDSMNSFNTSEYVMMTMWFFIIGNTGFPVMLRFVIWVLAQIVPKGTGLWEELRFLLDHPRRCFTLLFPSSANWWLFWILAALNAIDLLFFVVLDLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAVPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYHNKKDEDEEESASALNYVGTHLRRQLSFDLWYVFVGFFFLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVSNVNASLCSQFTVVGKLIIVAMQIRGRHRGLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMATASGMEPPTSPGLPDRRGSIGRIRERTNSRIISQFLYPGPVIPSNEIHGHKRATSNNSNNLRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAEANPMP
1E-136	465	3.5	1E-136	465.3	2.4	2	2	N4VCY8_COLOR	Potassium ion transporter	Cob_06515	Colletotrichum orbiculare (strain 104-T / ATCC 96160 / CBS 514.97 / LARS 414 / MAFF 240422) (Cucumber anthracnose fungus) (Colletotrichum lagenarium)	917	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum orbiculare, Colletotrichum orbiculare (strain 104-T / ATCC 96160 / CBS 514.97 / LARS 414 / MAFF 240422) (Cucumber anthracnose fungus) (Colletotrichum lagenarium)	1213857	[illegible] LARS 414 / MAFF 240422) GN=Cob_06515 PE=4 SV=1MLDDARGWLLAQLRAAKPSFISKKPHFNFISAHYLWICGLTLLGSILMYATAGGQMPYIDALFFASGANTQAGLNTIDVNLLNTFQQICLYFFTMTSNPITIHSSVVFLRLYWFEKRFQTVVREARLRRNTISKSMSRARGDDLSQLERGRNQDFNRHNIKIVHGNGQSNRITNDGILLDMKDEDDGRVSPGSNGFVPIPGTPAYRSGEHTPNTIPESHDGTHDADPSQGRITFAQHVFRSDGTEPEVKLPPPSSPAHLAILERQRNGHDEETLRIPNPRDAERGMKPKRVEDGDAPEPEDDRDYGSHDHSAIGTNGTANGLGAGGRRQTIKIEEPERPRDQERHVKEEVAEEAEVIRRAIFPFSFRRFFRRNNDKRDQHDDSTTETPLTKVRSRVDTIRSAWTRDKVEDMPYLSFTPTLGRNSAFPGLTQEQREELGGIEYRSLRTLAVILLGYFWGFSLFAVACFLPWIYTSSNDKYVKIVESAGVSKAWWGIFTANSAFNDLGLTLTPDSMNSFNDVPFILMIMWFLIIIGNTGFPVMLRVIIWVLSKVVPKGGLHQELRFLLDHPRRCFTLLFPAGATWWLFWILIGLNVVDLLFFVLLDLNDNAVSHLPVHLRIVDGLFQAASTRTAGFSVVNLSLLHPAVQVSYMIMMYISVFPIAISIRRTNVYEEKSLGVYHNPDDDMEGTNENSAMSYVGTHLRRQLSFDLWYVFLGLFILAITEGHRIQAKDFDVYSVLFEIVSAYGTVGLSLGYPNVNASLCSQFSTGGKLIIIAMQIRGRHRGLPYGLDRAVLLPSESRFEKEAGEQPPVLVRSATAASTGTALSASRSHLRSRRQSTNRGNVNLITQFLHPGPPMSSLEDSFVRRSRSFEVGEHHLPIAEEMRRRNTEPIDDETTSSDSLEVPSQPRRVATTPAG
1E-136	465	2.7	1E-136	465.3	1.8	1.3	1	S0DXS4_GIBF5	Probable potassium transporter TRK-1	FFUJ_03182	Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	937	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella fujikuroi (Bakanae and foot rot disease fungus) (Fusarium fujikuroi), Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	1279085	[illegible] A-6831) GN=FFUJ_03182 PE=4 SV=1MLDETRASIWARLKAVKPPFVSKKPHFNFISVHYTWIIGATLLASVIIYGAGRGQTSYVDSLMFASGANTQAGLNPIDVNLLNTFQQIVVYFFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRPRSEAREAEEGVNGRHITVVPYQGRPPRITNDGILLDGNDVIQSQAIADDDDDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKPDQGFGDGREANEGHSRSQNAPTGIKFAETVKRSDGVDDDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNNTIAMTRTVESRSDHATLDPRAPTGRRPTIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHEDSESTMGRAFRTRTIDTIKSALSNDHTKDMPYLSYTPTMGRNSNFVGLTLEQREELGGIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAISRTWWGFWTANSAFNDLGLTLTPDSMNSFNTSEYVMMIMWFFIIGNTGFPVMLRFVIWVLAQIVPKGTGLWEELRFLLDHPRRCFTLLFPSSANWWLFWILAALNAIDLLFFVVLDLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAIPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYHNKKDEDEEESPSALNYVGTHLRRQLSFDLWYVFVGFFFLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVPNVNASLCSQFTVVGKLIIVAMQIRGRHRGLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMATTSGMEPPTSPGLPGRRGSMGRIRERANSRIISQFLYPGPVIPSNEIHGHKRATSNNSNNLRDFPRFNTEPVLEEEKDDVPPLRTIESHSGGPRRAETNPMP
2E-136	465	3.4	2E-136	465.2	2.3	1.7	1	C7YR25_NECH7	Predicted protein	NECHADRAFT_104185	Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	943	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium solani species complex, Nectria haematococca, Fusarium solani subsp. pisi (Nectria haematococca), Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	660122	[illegible] GN=NECHADRAFT_104185 PE=4 SV=1MLDGARASFWARLKAVKPPFVSKKPHFNFISVHYTWIIGATLIASIAIYAAGRGTTQYVDALMFASGANTQAGLNPIDVNLLNTFQQVVVYVFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRTTISKSKSRARSEVRQAEEGVNGRHITVVPHQGRPPRITNDGILLDGDAMIQSQAIEDDDDDDHMPPKPPPASSDESDTATVSAGRSNSMELSPLEKPDQAFEEDRDRRMEGQGQPQNAPAGITFAETVKRSDGIDDELTKFPRRTHAEHIAILERQRNQDNEVLRIPGPRETERGMGPRRLDDGDARDGDDDTIAMTHTRDSRQDQATIDSGLPRERRPTIVIAEPERPIREELADDAKAVGGTLDSLRFRKPRIFNRGQKQVHEDNESGGPVRAFRTRTLDTIKSAWSNDHTKDMPYLSYTPTMGRNSNFVGLTLEQREELGGIEYRSLRTLALILLCYFWGFQFLAATFLLPFILHNDHYGKIVDDDAISRTWWGIWTANSAFNDLGLTLTPDSMNSFNTSEYTMMIMWFFIIGNTGFPVMLRFIIWVLAQIVPKGTGLWEELRFLLDHPRRCFTLLFPSSANWWLFWILVALNAIDLLFFVILDLNSGPVAQLPVHTRIADGLFQAAATRTAGFSCFSMSDLHPAMPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYGNKRDEDEETESPSALNYVGTHLRRQLSFDLWYVFVGFFLLAISEGTSLKEKKFNSFDVLFEVISAYGTVGLSIGVPNVNASLCSQFTVVGKLIIIAMQIRGRHRGLPYGLDRAVLLPSESRFQKEAEENQPILIRTRTNASIGTASGVDPQAGFAASGRRGSFGRIKERANSRIISQFLFPGPVIPSDEIHGHKRTTSNTSQNAARAFPRANTEPVYDEEKDQVPPLRAIESHHHHHPQPRRADTTPML
7E-136	463	20.8	5E-135	460.2	6.8	2.1	2	A0A0B1PEF3_UNCNE	Putative component of the trk1p-trk2p potassium transport system	EV44_g1416	Uncinula necator (Grape powdery mildew)	906	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Erysiphales (powdery mildews), Erysiphaceae, Erysiphe, Uncinula necator (Grape powdery mildew)	52586	[illegible] GN=EV44_g1416 PE=4 SV=1MGYFSKSTRNCLSALSRAIISKDFNFSFITVHYIVIIVVFLVGSICIYSTGNIDYIDALFLSCGASTQAGLNTVDLNSLKTWQQFVLYMIPIITNPIVMNTSVVFLRLWWFEKKFQHVVRESRRNRRSIMKTFSRAKTNDQNFNNQERGIKGQKIVVIHGAPANENTNTNTSLGTYADLDENVNAKAKTKADADADNDVDSKENLKLELDQVTPLVVQNKDEKLSEIQKQMRSWNNFGGGKKAETLPEGQVSDTTQRQIKFADHVHVEGDINKAGRLSVHRIQEEHIAFLQRQRDEGDGEILRIPGPRDAEAGVAPHNIYYDVDPIDKKTKSRSNINEETKNYPEDSFSRRNSTYQSFSMSSTADYANMAQIPHGNSWLRKPSLLRSDTLQTQRKISIQTFKSVLTRDKEDLAPYLSWQPTIGRNSAFLDLTEQQRDELGGIEYRSLKTLAVILVSYFFGFSLLGIICLVPWIIRNSSFSEVVKADGQGKVWWAIFTANSAFTDLGFTLTPDSMISFQLATWPLTVMSFLITIGNTGFPIMLRIIIWVCSRITPNGSGAQQELRFLLDHPRRCFTLLFPATATLWLTLVLIILNTVDVAFFISLDLGKDFVKHLPMRIRILDGFFQAVSTRTAGFSIVDLSMIHPAVQVSFLIMMYISIFPIAISVRRTNVYEEQSLGIYSLSNRLEEDGEDDQTYISTHLRQQLSFDLWYICLGLFIIAVAEGARLQSGDSRFTLFSIIFEIVSAYGTVGLSLGYRNINASLSSEFGVVGKIVIIAMQIRGRHRGLPHELDRAIILPSETLQQKEEEDLARIALLRRTSNATDITNTLKKSTSKVQANGILSAVFYPGPPIPRGYRNLHRDDNHFQRSHSEAPSIDRERASSLTQKGSVSFRLDGKRNLNEEMLN

2E-135	462	2.2	3E-135	461	1.5	1.1	1	C1H2U6_PARBA	Potassium transport protein	PAAG_05089	Paracoccidioides lutzii (strain ATCC MYA-826 / Pb01) (Paracoccidioides brasiliensis)	742	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Paracoccidioidales, Paracoccidioides sp. 'lutzii', Paracoccidioides lutzii (strain ATCC MYA-826 / Pb01) (Paracoccidioides brasiliensis)	502779	>tr|C1H2U6|C1H2U6_PARBA Potassium transport protein OS=Paracoccidioides lutzii (strain ATCC MYA-826 / Pb01) GN=PAAG_05089 PE=4 SV=2MRTYQQVVIYIIPLLGNLSIINLVVVLVRLYWFETRFKDIVRLSHHCSFDRRHSVESSDERGRDTTTLREKLATGKIRDIRVPRPRS GISSRSKTSPSETEGMRLRATVANVNNPNSNTIIDLNSNRNDNRNIIQNKNDDDGIALTGNMNEKEENVTKEMGGSITSTTIPVSASAP PSNTQPVMIDQNNSSLDNNKTERSVPPTHISFSVETNLERRERALRIPGPREFESGQTVREVDDDDLIKIVSTEEPPSSGPSGDHNRR RLPTMERILSRAVSVEHAASNAFILGKASHKRSRSRSSNTGSRSSSKARQSHNMPYLSYQPTIGRNSRFLDLTDEQRDELGGIEYRSL RLLAKIVFGYYVFWHVLGAICLIGWIHNSDHKYRDYLRSVGQSPTWWAIYSGMTTFNNLGYTLTPDSMISFRTATFPILLMTLLIYIGNT AYPCMLRLIIWLLFKLSPRNSRIREPLNFLLDHPRRCFTLLFPSSPTWMLFFSLVFLNFIDVLLFLVLDLHNEEVLGVPSMWNRFLAALF QAASARTTGTNTFSISKVHPAVQFMLMVMMYISAYPIAISVRRTNIYEETSLGLYDSTSEEIDESNTTASYLGTHLKKQLAFDLWYVFLG MFILMVTEGPKLADKADPEFVIFSVFFEAVSAYGNVGLSLGHTAINSGLTTRFTVLGKLVICALMIRGRHRGLPYELDRAIILPSERNPTE SSSPRQVAVSTALKSADTTIAVSSRSRTT
5E-135	460	3.1	5E-135	460.4	2.1	1.4	1	A0A0F9XQF7_TRIHA	Uncharacterized protein	THAR02_05428	Trichoderma harzianum (Hypocrea lixii)	938	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Hypocreaceae, Trichoderma, Trichoderma harzianum (Hypocrea lixii)	5544	>tr|A0A0F9XQF7|A0A0F9XQF7_TRIHA Uncharacterized protein OS=Trichoderma harzianum GN=THAR02_05428 PE=4 SV=1MFDETRAFIAAQIKGAKPAFVSKTPHFNFITVHYFWIIFATLLSSILIYAGGKGELHFIDALMFGSGANTQAGLNPVDLNNLNGFQL AWIYTFSLFSNPITLHTCVVFLRLYWFEKRFQHWVQEARLRRRTLSKSKSKARNDLSQAENGLGVNGRHITIVPRGERANRITNDGILL DKIEEAEPKPVAKSDASDTTTVSDDLHKSVSLDDIDPLEQPRQKDTSHSISDEYGSAPGPQPENPPYLSTAITFADTVKRSDGLGSDPT KFPQRRPNAEHIAILERQRNQDNEVLRIPGPRETERGLGPRRLEEDDQQEDEDRPVARQRTIEFRNDEPSGIHGRQPTITIAEPEHHK RDELKDDAAAAGNVVDSLRFRKPRVFNRSQDKLHEDGEEPRHNRSRTPHPRPVRTKTMDTIRSALTREKVDDMPYLSYTPTMGRNS NFLGLTLEQREELGGIEYRALRTLALVLIFYFWIYHILGVVCLLPYILHNQHYGNILAADDIGRTWWAFWTSNMAFMDVGFTLTPDSMN SFATSEWVLMSMWFFIIIGNTGFPVMLRFMIWVASKLTPRGTGLWEEFRFLLDHPRRCFTLLFPSNANWWLFWILILLNVIDLVFFIVL DLGAEPITAFPLRNRVVIGLFQAASTRTAGFSAVSMSELHPAMPVLYMIMMYISVFPIAISIRRTNVYEEKSLGVYRDRGDEDAEEASAL DYVGTHLRRQLSFDLWYVFLGFFLLAITEGGKIVGGRFDLFAVLFEIVSAYGTVGLSIGVPGVNASLCSQFSVIGKLIIVAMQIRGRHRG LPYGLDRAVILPSEARLKKEQEESEAALARTNTAVSTGATSALQRQATTGRSRSRSRDRANGNLITQLLHPGPVVPPDPFLRPRGRSV EGHQRSMSADVTGALPEPAGAHLHPSIEEDDELHQLSSNDFPHKPRRIESSAF
8E-135	460	4.6	8E-135	459.6	3.2	1.8	1	G0RD60_HYPJQ	Predicted protein	TRIREDRAFT_120752	Hypocrea jecorina (strain QM6a) (Trichoderma reesei)	934	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Hypocreaceae, Trichoderma, Hypocrea jecorina (Trichoderma reesei), Hypocrea jecorina (strain QM6a) (Trichoderma reesei)	431241	>tr|G0RD60|G0RD60_HYPJQ Predicted protein OS=Hypocrea jecorina (strain QM6a) GN=TRIREDRAFT_120752 PE=4 SV=1MLDDTRAFIAAQLKAAKPAFVSKTPHFNFITVHYFWIIFATLLSSVLIYAGGKGQLHFIDALMFGSGANTQAGLNPVDVNNLNGFQ QSWIYTFSLLSNPITLHTCVVFLRLYWFEKRFQHWVQEARLRRRTLSKSKSKARNDLSQLENGQGVNGRHITIVPRGGERTNRITND GILLDKIPEADPKPVGRSDESDTTTVSDDLHKSDDLDDISPLDQPHPQGNSQNTDQNSSAAGGRPENHPLTTAITFADTVKRSDGVGS DPTKFPQRRSNAEHIAILERQRNQDNEVLRIPGPRETERGLGPRRLEEDDQQEDEDRPIGRQTTADSRNSESNNIHGRQPTITIAEPE HHRRDEIKEDARAIGGTLDALRFRKPRMFNRSQDKLHEDNESRHRSRTPNPRPVRTKTMDTIRSALTREKVDDMPYLSYTPTMGRNS NFLGLTLEQREELGGIEYRALRTLAIVLMVYFFAFHVLAVVCLLPYILANQHFGNILKEDSIGRVWWAFWTSNMAFMDVGFTLTPDSM NSFATSEWVLMAMWFFIIIGNTGFPVMLRFMIWVASKFTSRGTGLWEEFRFLLDHPRRCFTLLFPSNANWWLFWILVLLNVIDLVFFIV LDLGAEPITQFPLRNRVVIGLFQAASTRTAGFSAVSMSDLHPAMPVLYMIMMYISVFPIAISIRRTNVYEERSLGVYHDRSNDDDSEASA LDYVGTHLRRQLSFDLWYVFLGFFLLAITEGGKIVGGRFDLFAVLFEIVSAYGTVGLSMGVPGVNASLCSQFSVPGKLIIVAMQIRGRH RGLPYGLDRAVILPSEARLKREQEESEAALARTNTVVSTGATTGLQRQATTGRSRSRSRERANSSLITQLLHPGPVVPQEVIRPRGRS VEGHQRSRSVDVTGALPEPSSAHLQPRIEEDDELRHMSSYEFPHKARRIESSAF
1E-134	459	0.2	2E-134	458.5	0.1	1.2	1	D5GFS8_TUBMM	Whole genome shotgun sequence assembly, scaffold_31, strain Mel28	GSTUM_00007057001	Tuber melanosporum (strain Mel28) (Perigord black truffle)	589	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, Pezizomycetes, Pezizales, Tuberaceae, Tuber (truffles), Tuber melanosporum (strain Mel28) (Perigord black truffle), Tuber melanosporum (Perigord truffle)	656061	>tr|D5GFS8|D5GFS8_TUBMM Whole genome shotgun sequence assembly, scaffold_31, strain Mel28 OS=Tuber melanosporum (strain Mel28) GN=GSTUM_00007057001 PE=4 SV=1MSEVGVWRAESVCIVYPFYNIYLLPLSWKLTTVLSHLEKVVLRAADGSALPTQTTQTSSINDTGTTPHSPEAPTSGRIVWDVPA SHSTQNAHQSEEEKAHYYDTSRSTAGAIRRSSVDTIHEITDTGDITRVDTGPASSSSRRVRALSRENSLSRNRPSFRKSRDDPPAPYL SYNPSVGRNSRFYDLTEEQRNELGGIEYRSLKTLAWILIAYYAFIHVFGVIMLVPYLLRSLKYGKILDDFGVNKSWWGAYTAMSCFANV GFLLTPDSMVSFQRASLVLIVSGFLIIAGNTGFPLLLRFTIWCLFKLCPDRYPDKRDELNFLLDHPRRCFTLLFPSGPTWWLFWILIILNIA DTVLFIVLDLQTPVVESIPAGYRVLNALLQAVSTRTAGVSSVPIGSLHPGIQCSYLIMMYISVLPLAISIRRTNVYEEHSLGIYIPSAEAREA QEEKRDEGTYIKAHIRRQLEFDLWYVFLGFLLAITEGGKIVGGRFDLFAVLFEIVSAYGTVGLSMGVPGVNASLCSQFSVPGKLIIVAMQIRGRH RGLPYGLDRAVILPSEARLKREQEESEAALARTNTVVSTGATTGLQRQATTGRSRSRSRERANSSLITQLLHPGPVVPQEVIRPRGRS VEGHQRSRSVDVTGALPEPSSAHLQPRIEEDDELRHMSSYEFPHKARRIESSAF
3E-134	458	22.7	2E-132	451.6	9.9	2	2	M7NSX9_PNEMU	Uncharacterized protein	PNEG_01488	Pneumocystis murina (strain B123) (Pneumocystis carinii f. sp. muris)	761	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Pneumocystidomycetes, Pneumocystidales, Pneumocystidaceae, Pneumocystis, Pneumocystis murina, Pneumocystis murina (strain B123) (Pneumocystis carinii f. sp. muris)	1069680	>tr|M7NSX9|M7NSX9_PNEMU Uncharacterized protein OS=Pneumocystis murina (strain B123) GN=PNEG_01488 PE=4 SV=1MMGGTIEKLKTSQVVVPKINFLRLHYIYILSAILISTFLIYIPKNIKFVDALFLGCSAATQAGLATLDIDTLSTYQQVILYVVSILTTSIFI HSLTAVVRFFLIRSKFDNIVQQARSQSLRRNQNLSHPFLSYSEIEERGVGDRAIHVLLRWESANENEFHPTPLRRTSISFGNANSQPKL QDHERKNEVHRYLEGSSCLNNTSNSNNSIHKEDNTDIKLQKSESIIPREERQVSSDIRFGDLPVPVRQSIDVTKDNELHIVQEPFEQEN EFNNKLRKSKSVEPQSVSATNEPLTPITRLPTYDNNYYLRMRKSTTADRSISKVSTFDRYISNTFWKKRDSSPLSQRTSKSFPYLSYQ PTIGRNSAFVTLTKEQRDELGGIEYRALKLLCWILVCYYLIFHSFAAILFLIFSIYAKSYHKAINEASESSVWWAFFTSASLFNNFGMALN PTSLIEYRQSKFILIFGSFLIVAGNTAFPILLRFFIWLITFILPKDSLHKESLHFLLDHPRRCFILLFPSKVTMWLFALLVMLSITDAILFMVLD FNNPSLAEIGPIYLKILNSLFQSFSTRTAGFTVVNLLTLHTAVLVSYMFMMYISVFPVAVSIRKTNVYEERSLGIYTIDDDSAQNSSFVGT HIKHQLSFDLWYIFLGLFIICIVENTNIKDESLPNFSVFSILFEIISAYCTVGLSLGHSDIDSSFSSKLSTISKLVIISLQIRGRHRGLPYALDR AVLLPTEKMERVEEEDYRRKTRGPIINNENL
5E-134	457	12.5	1E-131	448.8	2.7	2	2	F2PLY3_TRIEC	Potassium uptake transporter	TEQG_01939	Trichophyton equinum (strain ATCC MYA-4606 / CBS 127.97) (Horse ringworm fungus)	708	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Trichophyton, Trichophyton equinum (Horse ringworm fungus), Trichophyton equinum (strain ATCC MYA-4606 / CBS 127.97) (Horse ringworm fungus)	559882	>tr|F2PLY3|F2PLY3_TRIEC Potassium uptake transporter OS=Trichophyton equinum (strain ATCC MYA-4606 / CBS 127.97) GN=TEQG_01939 PE=4 SV=1MFSLTKWPRVSRPSFIVVHYVYIVVLCLVGMVMIYPLKNITAIDALFQGVSAGTMTGLNTLDLNKLNTYQQLVLYICPILGNLGFIN FVVVLVRLYWFESKFKEIVRFSRLPSTERSHHIEHGPRSRRATTASATATEIPPAISSEPAEAEETEGLKHRNPHAPDEEAQDDPKPAT VEQQLPATGPGHISFSTDTFKPREKVLRIPGPREFEAGYRAHEVDEGADGDELTKATSVDPSIAGASSVRERGKLGRILSHATSVERA ASSAFVLGSASRPRSRSRSVSRSLRPLSRTGSRASQAPYLSYTPTIGRNSQFLNLTEEQRIELGGIEYRSLKLLAKIVGGYFFGFLLLG SICLVIWIYATDASHRQYLAKVGINPVWWAFYSSMTTYNNLGFALTPDSMISFRSSTFPIVVMAFLILVGNTAYPCMLRFIIWCMFHISP KGSAIREPLNFLLDHPRRCYTLLFPSRTTWTLLGSLVLINGVDIMLFMILDLKNPEVTAIDTTWHRLCAASFQSISSRTAGATTFALSKIH PAVQFSLMVMMYISVFPVAISMRKTNTYEESSLGLYESDEEIDENSDSSSYLGQHIKKQLAFDLWYVFLGVFLVTIAEGDKIADLTDPAF QIFAIFFEVVSAYGNVGLSLGHPTINAGLAGKFTVVSKLVMCAMMVRGRHRGLPYALDRAIVLPGEQERKEQARTDSQVVPNTS

1E-133	456	11.3	8E-132	449.6	3.1	2.1	2	Q3Y3Z0_NEUCR	Trk-1	trk NCU06449	Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987)	975	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora, Neurospora crassa, Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987)	367110	[illegible] 987) GN=trk PE=4 SV=1MERLRSITQEKWAWICHHIGFRPRKLMTEGHFQYQTVHYTLIIGLTIVGSILIYASHRGQVAYVDALFFAAGACTQGGLNTIDVNLI NTFSQAVIFLLAMLTNPISIGYYTVSLRRYWFEKKLQTIVQDAKQRRGTISKSKSQMRTDFLSQAERGVAGREITVMHGSGSPRMTND GILLGSFQKPTYDSRAPPDQRDPDQPEDTRRQPEIRFAGTVKKSDGLGLDAIKLPRSDEEHIAILERQRNRDDEVLRIPGPRDMERGA KPRRVDDSAEEDDREPAQRAPMVTLNGRAQAITIEEPDRNKLYETLTEDFVDDAKMFTHSFVPQLNHLKFRKNTRAPTRNRGDEEAD PKLQRSNSRMSRRPSLSAMRSAFTKDKMEPTPYLSWEPTLGRNSQFHDLTEEQREELGGIEYRVLKLLQKIILCYFFGFFLLGLVGLL PWILHEDRWGQVVDQAGQSRVWWAFFTANSAFMDLGLTLTPDSMNSFNTAVWPLLLMIFLIIIGNTGFPVMLRFIIWVMSIVVPRDS GLYEEVRFLLDHPRRCFILLFPSGATWWLFFIILGLNITDVVFFVVLDLGSGPVDALPGIKVLNGFFEAASTRTAGFSCINLAVLHPAV KVSYMIMMYISVLPIAMSIRRTNVYEEKSLGIYNNPEGEEESASPSSDLSYIGSHLRRQLSFDLWFIALFFFMLAISEGTRIMDGETDMF ALMFEVISAYGTVGMSLGFSTGNASLSAIFSTTGKVFIIMTLIRGRHRGLPYGLDRAIVLPKELNSSSSEDDGVERQRSHTSAMSTGRD AWSTTSRTSRRRHWRQRSNDIGNQIFGALLHPGPPRAAMPLDGHRPHHVPHAQTWHPVHFGSVGKARPLNRDSHHGSVGSQGVT GLGGGGGGNGVGSGGGDGINPNGWHSMRRRATNPEQHREETIHEGFPFPSDSDRRPESDQNTLTDPPRLGVGVDHNLKLMKRKS EPSFPSTPTDFSE
2E-133	455	9.4	2E-133	454.7	6.5	1.2	1	T5AG23_OPHSC	Potassium transporter	OCS_02748	Ophiocordyceps sinensis (strain Co18 / CGMCC 3.14243) (Yarsagumba caterpillar fungus) (Hirsutella sinensis)	918	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Ophiocordycipitaceae, Ophiocordyceps, Ophiocordyceps sinensis, Ophiocordyceps sinensis (strain Co18 / CGMCC 3.14243) (Yarsagumba caterpillar fungus) (Hirsutella sinensis)	911162	[illegible] GN=OCS_02748 PE=4 SV=1MLDSARDYVWAQLKAVKPAFVSKKPHFNFISVHYFWIIGATIVASIAIYASGRGGLAYIDALMFASGANTQAGLNPVDVNKLNGV QQAMIYLFAMLSNPITLHACVVFLRLYWFEKRFRSWVRDIRSRRPTLTKSKSEAGADVERDAPAQGVNGRHITIMPQDGRTHRITNDG ILLDDDISPRSAAVAKSDESDSSTMSDEKQLEAGVVAQQSHCGSTQESGALDKELAPEEPRSAPTAISFANTVKRSDGMGEDALKAP ERLPNAEHIAILERQRNQDNEILRIPGPRDAERGLGPRRLQMGDPQDDDEHGLPRSRTVDSRIGVAWADARNARGRQSTIVIAEPER HRGDDMADDARAVAGAMDTLRFRKSRLMNSAQKKVHDDGESRSSRMVGTRTLSNLRSVLSRDKEEDMPYLSYTPTIGRNSNFVGL TLEQREELGGIEYRSLRTLALILLFYFWGFQLVILTFLLPFIWHDTYYGNIVEAAGVSKTWWAFFTSNVAFMDVGFTLTPDSMISFQRS EFALVVMWFFIIIGNTGFPVMLRFLIWVAAKLVPRRSGLWEELRFLLDHPRRCFTLLFPSGPNWWLFWIILVLNALDLLFFIVLDLGSEPI SKLPLKNRVVIGFFQAASTRTAGFAAVNMSDLHPAMPVLYMIMMYISVFPIAISIRRTNVYEEKSLGVYQEASADDDNDASALSYVGSH LRRQLSFDLWYVFLGFFILAISEGDNIMAHKFDMFAVLFEVVSAYGTVGLSMGATGINASLSSQFSVVGKLVIIAMQIRGRHRGLPYGL DRAVLLPSESRFRKEAEEAEAVFARVNTGVSAATTSGLQRQRTNPASRRSMSRERANGNLILQFLHPGPAMQRDSTASYQTGTSVD SYGPSLNPRTHTEPANESEAAEATPSSPERLHQPRRTETSAF
2E-133	455	10.8	1E-131	449.2	2.6	2.1	2	G4UNA7_NEUT9	Potassium transport protein TRK1/TRK2 (Fragment)	NEUTE2DRAFT_90308	Neurospora tetrasperma (strain FGSC 2509 / P0656)	975	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora, Neurospora tetrasperma, Neurospora tetrasperma (strain FGSC 2509 / P0656)	510952	[illegible] / P0656) GN=NEUTE2DRAFT_90308 PE=4 SV=1MERLRSTAQEKWAWICHHIGFRPRKLMTEGHFQYQTVHYTLIIGLTIVGSILIYASHRGQIAYVDALFFAAGACTQGGLNTIDVNLI NTFSQAVIFLLAMLTNPISIGYYTVSLRRYWFEKKLQTIVQDAKQRRGTISKSKSQMRTDFLSQAERGVAGREITVMHGSGSPRMTND GILLGSFQKPTYDSRAPPDQRDPDQPEDTRRQPEIRFAGTVKKSDGLGLDAIKLPRSDEEHIAILERQRNRDDEVLRIPGPRDMERGA KPRRVDDSAEEDDREPAQPTPMVTLNGRAQAITIEEPDRNKLYETLTEDFVDDAKTFTHSFVPQLNHLKFRKNTRAPTRNRGDEEAD PKLQRSNSRMSRRPSLSAMRSAFTKDKMEPTPYLSWEPTLGRNSQFHDLTEEQREELGGIEYRVLKLLQKIILCYFFGFLLLGLVGLL PWILHEDRWGQVVDQAGQSRVWWAFFTANSAFMDLGLTLTPDSMNSFNTAVWPLLLMIFLIIIGNTGFPVMLRFIIWVMSIVVPRDS GLYEEVRFLLDHPRRCFILLFPSGATWWLFFILIGLNICADVVFFVVLDLGSGPVDALPGIKVLNGLFEAASTRTAGFSCINLAVLHPAV KVSYMIMMYISVLPIAMSIRRTNVYEEKSLGIYNNPEGEEESASPSSDLSYIGSHLRRQLSFDLWFIALFFFMLAISEGTRIMDGDTDMF ALMFEVISAYGTVGMSLGFSTGNASLSAIFSTTGKVFIIMTLIRGRHRGLPYGLDRAIVLPKELNSSSSEDDGVERQRSHTSAMSTGRD AWSTTSRTSRRRHWRQRSNDIGNQIFGALLHPGPPRAAMPLDGHRPHHVPHAQTWHPVHFGSVGKARPLNRDSHHGSVGSQGVT GLGGGGGVNGVGSGGGDGINPNGWHSMRRRATNPEQHREETIHEGFPFPSDSDRRPESDQNTLTDPPRLGVGVDHNLKLMKRKS EPSFPSTPTDFSE
3E-133	455	9.9	7E-133	453.1	1.6	2.1	2	F7W2Y7_SORMK	WGS project CABT00000000 data, contig 2.23	SMAC_02211	Sordaria macrospora (strain ATCC MYA-333 / DSM 997 / K(L3346) / K-hell)	1009	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Sordaria, Sordaria macrospora, Sordaria macrospora (strain ATCC MYA-333 / DSM 997 / K(L3346) / K-hell)	771870	[illegible] DSM 997 / K(L3346) / K-hell) GN=SMAC_02211 PE=4 SV=1MERLRGVVQDKWMRIRHSIGFQPRKLVTEKHFKYQTVHYTLIIGLTIVGSILIYASHRGKIAYVDALFFAAGSCTQGGLNTIDLNLI NTFSQIVIFFLTMLTNPIAIGYYTVSLRRYWFEKKLQTIVQDAKLRRGTISKSKSQMRADMLSQAERGERGVGGRQITVMHGSGSPRM TNDGIMLGSFNKPTYDSRAAPDQRDPDHPEDARRQPEIRFAGTVKKSDGEGLDAIKLPPLRTDEEHIAILERQRNRDDEVLRIPGPRD MERGAKPRRVDDSAEEDDRAPAQPTPMVMVNGRPQQTITIEEPDRNKLHETHTEDIVDDAKTFSHSFVPQINHLKFRRNTRTSTVNR VDEEEVDPKLQRTNSRMSRRASLSAMRSAFTRDKMEPTPYLSWEPTLGRNSQFHDLTEEQREELGGIEYRVLKLLQKIILCYFFGFYL MGLVGLLPWILKEDHWGQVVDAAGQSRVWWAFFTTNSAFMDLGYTLTPDSMNSFNTAVWPLLLLCFLIILGNTGFPVMLRFIIWVMS IVVPRDSGLYEEVRFLLDHPRRCFILLFPSGATWWLFFIILGLNITDVVFFVVLDLGTGPVVDLPAGIKVLNGFFEAASTRTAGFSCINLA ALHPAVKVSYMIMMYISVLPIAMSIRRTNVYEEMSLGIYNNPEHEEGEGENASPSSDLSYIGSHLRRQLSFDLWFIALFWFMLAISEGP RIMNGETDMFALMFEIISAYGTVGMSLGYSSGNASLSAIFSTAGKVFIIMTLIRGRHRGLPYGLDRAICLPKDLNSKSSSEDDRIDRQRS HASAMSTGRDAWSTTSRTSRRRHWRQRSNDIGGHIFGALLHPGPPRTATPDGHRHHHGPHPQNWHSVQFGSAGTNARHSNRDS HHGSIGSGGPGGPGPIFAGNSVFGGNGGNNGGNGGGINPNGWHSMRRRATNPEQHHEETIHEGFQFPPDASGGGGGDRRPASDQ TDQTNVSSDQNTLTEASRQLGLDGQHNPKLMKRKSEPSFPSTPTSFSE
3E-133	455	3.1	4E-133	454.1	2.1	1.1	1	C0NH13_AJECG	Low-affinity potassium transporter	HCBG_02635	Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus) (Histoplasma capsulatum)	723	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus) (Histoplasma capsulatum)	447093	[illegible] 2454 / RMSCC 2432) GN=HCBG_02635 PE=4 SV=1MRTFQQVVIYVVPLIGNLSVINLVVVLVRLYWFETRFKDIVRLSRQRLLDRPRSNRLQSSESGGRDSITLRNRLTAARIRDIRVLRP EPRIGSSKTAASESEGLRLRARILSRIPNNNANSESDSRIGTVPNENENENAKSCTVEIDDSTTSTSTPNPPASPSDPTPVMVDRTSPS LKKNSIERSAPPAHISFSAETNMEPRGRALRIPGPREFESDDLAKSITIEEPPMTGPSGENERRRLPTMGRLLSHAVSVERAASNAFIL GNSSRKRSRSRSSNPLNRSSSRADRVPLDMPYLSYQPTIGRNSRFLGLTDDQRDELGGIEYRSLKLLAKIVFSYYVFWHVFGVVCLIG WIHNSDRKYRDYIQSVGQSPTWWAIFSGMTTYNNLGFTLTPDSMTSFRNATFPIFIMTFLMYIGNTGYPCMLRLVIWLMFKISPRGSAI REPLNFLLDHPRRCYTLLFPSSPTWMLFFSLVFLNFIDVLLFLVLDLHNEEVLAVPSSWNRFLAAVFQAASARTTGTCTFNVSKVHPAV QFMLMVMMYISVFPIAISVRKTNTYEENSLGLYDPQSDEIDESNSTASYVGAHMKKQLAFDLWYVFFGMFLLMITEGSKLADKADPDF AIFSIFFEAVSAYGNVGLSLGHPSINSGLSTKFSVLGKLVICALMLRGRHRGLPYELDRAIILPSERNLTESSATKDGGPVTTTQTSTNAT IGSLLRTRIAEIV

3E-133	454	9	3E-133	454.4	6.3	2.1	2	G4N766_MAGO7	Potassium transporter 1	MGG_06469	Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	870	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Magnaporthe, Magnaporthe oryzae (Rice blast fungus) (Pyricularia oryzae), Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	242507	>tr|G4N766|G4N766_MAGO7 Potassium transporter 1 OS=Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) GN=MGG_06469 PE=4 SV=1MARLKDFLKAQAKSLKPAFFSKQPHFNFISAHYFYILAQTILASVLLYASGGAALSYIDALVFGSGAATQSGLNPVDVNLLNTFQQTVVYLVCMMCSPITINSFVVFLRLYWFEKKFQDLVKDARKRRSTFAQTRSKAKSVDHRQLNDMENGVNGRNITVMRNNGDTRITNDGLLLSPIPEPRPNGMPNTPKSSRDTDPTDDGLDSQDREFPQLRTTEEHVAILERQRNEGETLRIPGPRDVELGMAPERVEHSADEDAMPRSPRSPHRRPRSMESADGRAPGPRQQTIVIQEPTKPPAREEMAEEFEAIKNTLDPFKLRVPRIFKNKNPRLHEDDSDEEQEQTHLPERLRRRSTFGSVRKAFTQDKVEDTPYLSWTPTVARNSNFPGMSEEQREEMGGIEYRSLKSLAKVLVFYFMGFSVLGVVCLLPWILLTERWGVIVDQAGQSRTWWGFFTANSAFMDLGFTLTPDSMVSFNTATFPLLLMSFLIIIGNTGFPIMLRFLIWGFSLMVPRGSGLWEELRFLLDHPRRCFTLLFPAGATWWLFWILLALNGIDLIFFIVLDLDSGPVFEMPTGIKILNGIFQAASTRTAGFASVNLSQLHPAVLTSYIIMMYISVFPIAISVRRTNVYEESALGIYTNAEDDEQVSHIGSHFRRQLSFDLWFIFLGYFILSISEGTRLQSGDITMFAVLFEVVSAYGTVGLSLGYTNVNTSLVGQFSTVGKLVIVAMQIRGRHRGLPYGLDRAVLLPGDSRNVTEEKKEAAHADNSLDTQFQLHRRASGMSTATQGVGSSVRRGRSRSMTRVNSNVLVQLLHPGPAPIPHGPPMRRRSAADMEEEEYHEMYERSTSSIRRAETIAQVPIPSTGIPARH
3E-133	454	17.1	3E-133	454.2	11.9	1	1	TRKH_HAEIN	Trk system potassium uptake protein TrkH	trkH HI_0723	Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd)	487	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Haemophilus, Haemophilus influenzae, Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd)	71421	>sp|P44845|TRKH_HAEIN Trk system potassium uptake protein TrkH OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) GN=trkH PE=3 SV=2MRILSIIRIIGILVMCFSGTMLVPAFVALIYGDGGGKAFMQAFMLSLIAGTLLWWPCHHHKQELRSRDGFLIVVAFWLVLGSLATLPLLLFDSPHLTIASAVFEAFSGLTTTGATVMTGLDNLPKSILFYRQFLQWLGGMGIIVLAVAIIPLLGIGGTQLYRAESSGPLKDQKSLPKISEVAKALWIIYASLTVLCAIAYWLSGMNLFDAIGHSFSTISNGGFSTHDASIGYFNQASIYWVTTIFMLIGGVNFSLHISAFLALGKRNIWRNYWKDPEFRFFLTMQIIFIGIVSLSLYGYGLVSDINEAVTKGALQLTSMSMTAGYTIFDIDNLPPFIGLLLVISAVIGGCGGSTTGGLKAIRTLILWKQIDRELHSLIHPNLVQPIRIGKNRLAPRMIESIWAFFIIFILVYWGCVFAVILCGMNTFDAMGAVFATLTNAGPGLGFIHESFIGVPESAKLVFSFAMICGRLEMFSLIVLFIPSYWKK
4E-133	454	5.2	5E-133	453.6	3.6	1	1	C5GXC3_AJEDR	Potassium uptake transporter	BDCG_09110	Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) (Blastomyces dermatitidis)	624	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Blastomyces, Ajellomyces dermatitidis (Blastomyces dermatitidis), Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) (Blastomyces dermatitidis)	559297	>tr|C5GXC3|C5GXC3_AJEDR Potassium uptake transporter OS=Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) GN=BDCG_09110 PE=4 SV=1MPSNNSNSDKDKDNENENDNRNEAVPNVNENAKISTVENDGTTIFPSTPDLSASPDPQPLMLDQISSSPDKNNTERSAPSAHISFSAETNMEPRGRALRIPGPREFESGQTVREVDDDDLMKSITIEESLSAGPSGETERRRLPTMGRLLSHAASVERAASNAFILGNSSRKRSRSRSSNPLNRSSSKSERALLDMSYLSYQPTIGRNSKFLDLTDEQRDELGGIEYRSLKLLAKIVFCYYVFWHIFGVICLIGWIHNSDRKYSDYVRSVGQNPTWWAIFSSMTAYNNLGFTLTPDSMISFRNATFPIFIMTFLIYIGNTGYPCMLRLIIWIMFKISPRDSAIREPLNFLLDHPRRCYTLLFPSSPTWMLFFSLVFLNFIDVLLFLVLDLQNEEVLAVPSSWNRFLAALFQAASARTTGTSTFNVAKVHPAVQFMLMVMMYISVFPIAISVRKTNTYEENSLGLYDPQSDEIDESNSTASYVGAHMKKQLAFDLWYVFFGMFILMITEGSKLADKSDPEFAIFSVFFEAVSAYGNVGLSLSHPSISSGLTTKFSVLGKLVICALMLRGRHRGLPYELDRAIILPSERNLTDSSSTKDGGAITTALPSANTTIGPLSRVRTAEIV
4E-133	454	2.9	4E-133	454	2	1.8	1	B6K1F6_SCHJY	Potassium ion transporter Trk2	SJAG_02883	Schizosaccharomyces japonicus (strain yFS275 / FY16936) (Fission yeast)	715	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae, Schizosaccharomyces, Schizosaccharomyces japonicus (Fission yeast), Schizosaccharomyces japonicus (strain yFS275 / FY16936) (Fission yeast)	402676	>tr|B6K1F6|B6K1F6_SCHJY Potassium ion transporter Trk2 OS=Schizosaccharomyces japonicus (strain yFS275 / FY16936) GN=SJAG_02883 PE=4 SV=1MKKNLRRLLTDKLSFRNIWRYLRSRTSFLELHYAFIVGNIILGSVILYCSGHLRYIDALMLVSGACTQSGIAPVNLSSLSTYQQVTLFIFSAFTNVIAVNLGLSCFKLFFYHKRYDAVMLNNRLHMTYTKNTITEPATQNKSVGKRKIRVLLEQGNQFHRSVAPQNFRDEEERQWEMNRPVTHDYEADLGTSSSPYGSRYDGSRNPSLTTVVSNPEPERTITFFGGETRQRTASEDTEKSRESPSIRRDYAIQNHRRRKLSLASLPARFTRSFTSAVSRRFQPRNRNRVRSDETVRESLPYLSYTPTIGRNSAFYALSPEEREELAGMEYRALQSLVVILVAYLAFFYIFGFVSLLVFIYVAKVSYRLLTDRRINHGWWAFFTSSSMFHNVGYTLTDDSLNSFQKAIFPQLLGTALLFAGNNLFPVLLRMCIWVSRRLLPKNSQYVQSLTFLLEHPRRSFTLLFPPDTTRVLFWQIFWLNAITFALFLLLNVNNAYVRTIPVGYRIVNSIFQNACTRSGGFTVVDVALIAPAVITVYMFMMYISAYVALSIRRTNVYEERSLGIYTPPESTNENGDGSQNHHRSFLLTHVRRQLSHDLWYLFLGFFIICIVEGGRLERAEEPSFNLFAVLFEVVSGYGTVGLSLGYPNAPSLSAEFKILSKLVMIALEIRGRHRGLPNQLDKAVLMPSDKNFDKEEEDFLRKNGQPSLRHLRPPQD
5E-133	454	34.4	8E-133	453	23.8	1.2	1	O83176_TREPA	K+ transport protein (NtpJ) (Trk family potassium (K+) transporter, membrane protein)	TP_0140 TPANIC_0140	Treponema pallidum (strain Nichols)	575	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema pallidum, Treponema pallidum subsp. pallidum (syphilis treponeme), Treponema pallidum (strain Nichols)	243276	>tr|O83176|O83176_TREPA K+ transport protein (NtpJ) OS=Treponema pallidum (strain Nichols) GN=TP_0140 PE=4 SV=1MRPMHIGNLTHLTMLVLCLAIRLCDQFLPFSVQFFTIVGDVGILVLVWSSLASSLNKEKYVRTFLRQYTVPVFLGLLITLLTFVRASVTLTTASGDLYTTLTHIQNITLGIFALIAFKAQKKFAERAVSNPSQTLIVSFLVVIFIGTHLLMFPGATPHSQPLPMLTALFTATSAVCVTGLSVIDVATQLSTWGKAILAALIQIGGLGFMVFSFFGMITIKKKMSLESRLVASHLVSDSDMGSLSHNLKLIIFSTFFIEALSALFLFVGFSQTEGYTIQSLGNAYFHAISAFCNAGFSLYPNSLESFVSNPWITFPIAFTIILGGISFVVIDEVLCRVHGSIKNIFFKGKNILGSLSLNTFVVLKATVLLLAVSFVGIYLLEHTHSMKVYQVGTQYLAAFFQAVTLRTAGFSTIPFSNLRTATLFFMTFIMFVGGASGSTAGGIKLNTAAAIIASFRSFIHHDPKPRIRNLVIQGKQVERSFLILGFGICTVCLAGFCLSLTDNIPFIYLLFESVSAFATVGLSVGITANLSTAGLMILLILMFTGRVGTLTILTAASKEEQDMSVEYACGDLAIG

8E-133	453	19.4	1E-130	445.7	7.9	2.2	2	A0A099P107_PICKU	Uncharacterized protein	JL09_g2079	Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)	1173	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Pichiaceae, Pichia, Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)	4909	[illegible] SV=1MSVLFCIPMFMHPDFHGNPIQGEYPFASFVTSVAVGYFIWDLFYCCIVHYDLFGFEFLFHAFGALLVFGTTYIPFCQPFLCSFLVFEASTPFVQLHWMFTRAPKGMFSPTAITINGVFLISTFFFSRILWGVYYATYKSFVLCWPLRNEYPSLLIPTVYLLNGGFQFLNFMWFSKMFKLAKRMVSPPPPQSKKTNTRTTYLPFTDSLINRRILTRKSYILPIDAYSASPASRIGTRLAKDHPNTSPFWKTARLASGHDFLSLESSSSLDIRGWFSGDGYESPPSNIGAQKTNTNTDSISAGGSIIPLEATFGERMRRSIYKLEGKLFPVTKRIVPNFIIAHYLYIVLLIILGSVVVYGQKNMSFVDCLFTIASASTQGGLATQQVNDMELYQQITIYFCCFFTSTIFVHGSLTLVRLYWYEKIFDNIKETSMMQYKKRRSKTIANMRLEAHARSQTFANKQYRDSHNASEGLTTRIKRHHDSTNTSAKLSNEKGNVVNLCGDNTVSISPQFPNIKFGDLPKPVKNDLQQSNYESMTSSVQQDMRRSKGNTTHKRKPMHYKMHKKLIKNKKRNQEKMALPHLNTSTNDFEMVELKQFLNESTMKQGTANFERSFSSPIQIRSGVPNDYFLYSTGSLKPFLRLKKIPKSNTLDYQLPSTTETKKDHFSENYGFKFLKRDLSKVFCKTETGANLEGLSDEEFIINYTFDVPSNYLSWTPTIGRNSNFIALTRKQKIELGGVEYQATMLLSKIIFVYYFGLNVLGSIMMVAYVTSKKEYANVIKADGVAPAWWGLFTSMSSLCNLGLTLNATNLMIVAQNAYVQIISAILILCGNTALPICLRIIIWTMKKFTRPLTLFHDSLCFLLDHPRRCFTLLFPASATWWLAVVLITLNLADWMVFIVLDFDRSTLNYLPRGYQILCGLFQSISTRTAGFNVVVNLATLNPAIQLGYMVMMYISVLPLAISIRETNVYEEQSLGIYHDQKVHPSEANTTWKYVAEHLRKQLSFDLWFLFIAIFIICICEAGKIQSDPNFGIFQIMFEVVSAYGTVGLSLGYPNTNTSLSGKFSRISKLVIVATLIRGRHRGLPDKIDRAILLSDDKINALDDLESYRYTAGNDTTHLSHTANLRSDVISERELTPEKADFSHKQLTGQITHLLSKTVDYVLTISNIKYFTTHQP
1E-132	453	2.8	2E-132	452	1.9	1.1	1	F0U7F0_AJEC8	Low-affinity potassium transporter	HCEG_01779	Ajellomyces capsulatus (strain H88) (Darling's disease fungus) (Histoplasma capsulatum)	723	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain H88) (Darling's disease fungus) (Histoplasma capsulatum)	544711	>tr|F0U7F0|F0U7F0_AJEC8 Low-affinity potassium transporter OS=Ajellomyces capsulatus (strain H88) GN=HCEG_01779 PE=4 SV=1MRTFQQVVIYVVPLIGNLSVINLVVVLVRLYWFETRFKDIVRLSRQRLLDRPRSNRLQSSESGGRDSITLRNRLTAARIRDIRVLRPEPRIGSSRTAASESEGLRLRARILSRIPNNHANSESDSRIGTVPNENENENAKSCTVEIDDSATSTSTPNSPASPSDPTPVMIDRTSASLKKNSIERSAPPAHISFSAETNMEPRGRALRIPGPREFESDDLAKSITIEEPPMTGPSGENERRRLPTMGRLLSHAVSVERAASNAFILGNSSRKRSRSRSSNPLNRSSSRADRVPLDMPYLSYQPTIGRNSRFLGLTDDQRDELGGIEYRSLKLLAKIVFSYYVFWHIFGVVCLIGWIHNSDRKYRDYIQSVGQSPTWWAIFSGMTTYNNLGFTLTPDSMTSFRNATFPIFIMTFLMYIGNTGYPCMLRLVIWLMFKISPRGSAIREPLNFLLDHPRRCYTLLFPSSPTWMLFFSLVFLNFIDVLLFLVLDLHNEEVLAVPSSWNRFLAAVFQAASARTTGTCTFNVSKVHPAVQFMLMVMMYISVFPIAISVRKTNTYEENSLGLYDPQSDEIDESNSTASYVGAHMKKQLAFDLWYVFFGMFLLMITEGSKLADKADPDFAIFSIFFEAVSAYGNVGLSLGHPSINSGLSTKFSVLGKLVICALMLRGRHRGLPYELDRAIILPGERNLTESSATKDGGPVTTTQTSTNATIGSLLRTRIAEIV
1E-132	452	11.4	3E-132	451.3	1.3	2.1	2	E4UQ87_ARTGP	Potassium transporter 1	MGYG_02180	Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	711	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Microsporum, Arthroderma gypseum (Microsporum gypseum), Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	535722	>tr|E4UQ87|E4UQ87_ARTGP Potassium transporter 1 OS=Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) GN=MGYG_02180 PE=4 SV=1MFSSRVWPRVSAPSFIMVHYVYIVVLGLVGMVMIYPQKNISAIDALFQGMAAATMTGLNTVDFKGLSIFQQLVLYISPVLGNICFINFIVVLVRLYWFESKFKEIVRFSRLPSAERTHRVEHGLKTHKTIGLATAIEEPTVLLPEPVEAKEAEGLKHRNSHIPDEVLDEKEQDGSKPTVVEKQLPITGPGHVSFSTDTFKPREKALRIPGPREFEAGHRAHEVDEEADGDELTKATSIDPSLVGATSVRDRGKLERILSHAASVEQAASSAFVLGSASRPRSRSRSVSRSLRPLSRTGSRGSQAPYLSYTPTIGRNSQFLNLTEEQRIELGGIEYRSLKLLAKIVGGYYFGFLLLGSVLLIIWAYTADPSHRKYLLENGIHPVWWAFYSCMTTYNNLGFALTPDSMVNFRSSTFPMLFMTFLIIAGNTAYPCMLRLIIWCMFRISPKTSAIREPLNFLLDHPRRCYTLLFPSRATWMLLGTLVLLNGLDIMLFMILDLKNPEVTAIDTTWHRLCAAAFQSTASRTAGATTFALSKIHPAVQFSLMVMMYISVFPVAISMRNTNTYEESSLGLYESEEEVDENTNSSSYLGQHIKKQLAFDLWYIFLGVFLIITIAEGDKIADLTDPAFQVFAIFFEVVSAYGNVGLSLGHPTINAGLSGKFTIVSKLVMCAMMVRGRHRGLPYELDRAIVLPGERHRREEQSRAGSQVVSNN
2E-132	452	10.6	4E-132	450.6	1.6	2	2	U4L699_PYROM	Similar to Low-affinity potassium transport protein acc. no. P28584	PCON_12479	Pyronema omphalodes (strain CBS 100304) (Pyronema confluens)	805	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, Pezizomycetes, Peziza les, Pyronemataceae, Pyronema, Pyronema omphalodes, Pyronema omphalodes (strain CBS 100304) (Pyronema confluens)	1076935	[illegible] CBS 100304) GN=PCON_12479 PE=4 SV=1MDRNGVGERLSRPYHFNFITLHYMYLIGMTLVGSLIVWAGQNMPYIDALFFASGACTQSGLNTIDVNTIKIYQQVVIWFLPFVTTPIFINTVVVYIRLYWFEKRFKNIVSLSRQPSKARTMSQGAKRDTSSALEQGVGGRNIRVLHRDPAVTESSALENNDSGLISPLTGTAPSSIRGVELEKMSESEKSSSTMTEPMSNALLQPPGAEGASSATSPPPTRGSNLQFELPTPRDNAANAAGAQSNTHIAFLENQKAPNRGKALRIPGPREFEQGGRATEVDDDDTYTLHPARTADEQVAGPFRSHSFAQAATNASSFVRRRTTLANILPPVASVLSNAMSPGTAIYRKSSIRNMLPRKPTLETQNAPYLSYQPTIARNSQFVDLTDEQRDELGGIEYRSLKLLGKILLGYYILFHLFGVIGFIGWIYKADPKHMNYLNSLGVSPAWWAIFTAETTLNDVGFTVTPDSMISFQKDVWVLLLGTFLIIIGNTGFPCMLRFIIWVMFKLSPKNSRIREPLNFLLDHPRRCFTLLFPPRETWILFWVLVFLNGADVILFIVLDLKDPDVQHIEVGYRIVAALFQAASTRTAGTSVISIAAVHPAVQVSYMIMMYISVFPIAISVRKTNVYEEKSLGLYGGEEEVDDGTSSSYVGIHFRKQLSFDMWYIFLGLFIITIAEGGHIENTTEYTFTTFSCLFEVISAYGTVGLSLGYPNFNPSFSGRFSVIGKLVIIAMQIRGRHRGLPYELDRAVLLPKEQHDTEHISIRRRSSNISQSRSSVAATGSAPLMPDFAQGLTSRRVPSQAIEDE
2E-132	452	35.5	3E-132	451.2	24.6	1.2	1	H6KSX8_TREPD	Trk family potassium (K+) transporter, membrane protein	TPECDC2_0140	Treponema pallidum subsp. pertenue (strain CDC2)	575	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema pallidum, Treponema pallidum subsp. pertenue (Yaws treponeme), Treponema pallidum subsp. pertenue (strain CDC2)	491079	[illegible] (strain CDC2) GN=TPECDC2_0140 PE=4 SV=1MRPMHIGNLTHLTMLVLCLAIRLCDQFLPFSVQFFTIVGDVGILVLVWSSLASSLNKEKYVRTFLRQYTVPVFLGLLITLLTFVRASVTLTTASGDLYTTLTHIQNITLGIFALIAFKAQKKFAERAVSNPSQMLIVSFLVVIFIGTHLLMFPGATSHSQPLPMLTALFTATSAVCVTGLSVIDVATQLSTWGKAILAALIQIGGLGFMVFSFFGMITIKKKMSLESRLVASHLVSDSDMGSLSHNLKLIIFSTFFIEALSALFLFVGFSQTEGYTIQSLGNAYFHAISAFCNAGFSLYPNSLESFVSNPWITFPIAFTIILGGISFVVIDEVLCRVHGSIKNIFFKGKNILGSLSLNTFVVLKATVLLLAVSFVGIYLLEHTHSMKVYQVGTQYLAAFFQAVTLRTAGFSTIPFSNLRTATLFFMTFIMFVGGASGSTAGGIKLNTAAAIIASFRSFIHHDPKPRIRNLVIQGKQVERSFLILGFGICTVCLAGFCLSLTDNIPFIYLLFESVSAFATVGLSVGITANLSTAGLMILLILMFTGRVGTLTILTAASKEEQDMSVEYACGDLAIG
5E-132	450	1.8	5E-132	450.4	1.2	1.6	1	J5K1D9_BEAB2	Trk family potassium uptake protein	BBA_01122	Beauveria bassiana (strain ARSEF 2860) (White muscardine disease fungus) (Tritirachium shiotae)	937	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Cordycipitaceae, Beauveria, Beauveria bassiana (White muscardine disease fungus) (Tritirachium shiotae), Beauveria bassiana (strain ARSEF 2860) (White muscardine disease fungus) (Tritirachium shiotae)	655819	[illegible] PE=4 SV=1MLDNFRSNVWAQLKAIKPAFVSKNPHFNFITTHYFWIVGATIIGSICIYAGGKGHLAYIDALLFASGANTQAGLNPVDVNLLTTFQQVVIYVLVMMSNPITLHGSVVFLRIYWFEKRFQGWVREVRSRRPNLTKSKSQAANEVHRAEEGVNGRHITVVPANGKAQRMTNDGILIDSASIALPDPAHRGNEDSSTTTATDSPITATPGYSHHTQDSDDGLPSTHGTATPVAELHARADSAGEHTHGPTAITFADTVKRSDGLEEDATAFTQRRPNAQHIAILERQRNEDDNDVLRIPGPRDIERGQVPTRLEEFERDENLGSRATRVNSNSNSKPSQAEGSYQGLRGRHPTITIAEPERRPQEELSDDVKAFTGALDAFRFRKPRIFNRSGQSTHHEGEQEQPPRPTRTWTLERIRSALHRDSGKVEDMPYLSYTPTMARNSNFVGLTLEQREELGGIEYRSLRTLAFVLLGYFWGFQLFGLVTLLPFILHNEYYGKIVEGNGISRIWWGFFTPNVSFMDVGFTLTPDSMNSFVKSEYVLMIMCFLIILGNTGFPIMLRFIIWVLTKIVPRRSGLWEELKFLLDHPRRCFTLLFPSGPNWWLFWILISLNAIDLLFFIVLDLGKEPISQLPLHNRVVVGLFQAASTRTAGFSAVSLAELHPAMPVMYMIMMYISVFPIAISIRRTNVYEEKSLGVYDNNEGAEQEASALSYVGTHLRRQLSFDLWFVFLGFFILCISEGSKIQAKRFDVFSVLFEVVSAYGTVGLSMGAVGVNASLCSQFSVVGKLIIAALQIRGRHRGLPYGLDKAVLLPSEARFKKEAEEEAEAVLARMGTAPSATTTGLQRLPSVARGRTMSRGRDSNIIAKFLHPGPVVQRDPGPARQRSRSNESHALTLERNRTYTAPQADTEEALERMASGQSSKQMQPMRAETSQRTPWRP

2E-131	449	1	2E-131	448.7	0.7	1.5	1	G3J5B8_CORMM	Potassium ion transporter (Trk1), putative	CCM_01486	Cordyceps militaris (strain CM01) (Caterpillar fungus)	942	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Cordycipitaceae, Cordyceps, Cordyceps militaris (Caterpillar fungus), Cordyceps militaris (strain CM01) (Caterpillar fungus)	983644	>tr|G3J5B8|G3J5B8_CORMM Potassium ion transporter (Trk1), putative OS=Cordyceps militaris (strain CM01) GN=CCM_01486 PE=4 SV=1MLDNFRRAAWAQLKAIKPAFVSKNPHFNFITAHYFWIVGATIVGSICLYIGGTGHLAYIDALLFASGANTQAGLNPVDVNLLTTFQ QTVIYVLVLMLSNPITLHGSVVFLRIYWFEKRFQGWVREVRSRRPNLTKSKSQAVDETHRAEQGVNGRHITVVPPNGKAQRMTNDGIL LDSSATAPADLPRRVNEDSDTTTTATDSPSATTPGHSQHTRDSDDGMPSTHGTATPVAGMRARADSAGEHVHGATAITFADTVKRS DGLEEDATEFAQRRPNLQHIAILERQRNEDDNDVLRIPGPRDIERGQVPTRLEEFERDEALGPQISRLVSNPGSKVAQGEGTYQGLR GRHPTITIAEPDRRQRELADDAKALTGTLDAFRFRKPRLFNRSGQSSHHEEDEDQPPRPTRTWTLERIRSALHRDSSKIDDMPYLSYT PTMARNSNFVGLTLEQREELGGIEYRSLRTLAFVLLGYFWGFQLFGVVTLLPFIMNSEKYGKIIEDDGVSRVWWGFFTPNVSFMDVG FTLTPDSMISFVRSEYVLMISCFLIILGNTGFPVMLRFIIWTLTKIVPRHSGLWEELQFLLDHPRRCFTLLFPSGPNWWLFWILISLNAVD LLFFLVLDLGKEPISLLPLHNRVVVGLFQAASTRTAGFSAVNLSDLHPAMPVLYMIMMYISVFPIAISIRRTNVYEEKSLGVYDHNEGAE QEASALSYVGTHLRRQLSFDLWFVFLGFFILCITEGSKIQAGRFDVFSVLFEVVSAYGTVGLSMGAVGVNASLCSQFSVVGKLIIAALQI RGRHRGLPYGLDKAVLLPSEARFKKEAEDAEAVLARMNTAPSATTTGLQRLPSVARGRTVSRGRDSNIIAKFLHPGPVAQRDGDVAR QRSRSTESRALALERNHTLTEPPAEADEELERLPSGASSKRMQPMQPMRADTAPAAHPTPWRP
2E-131	449	8.2	5E-130	443.7	0.9	2	2	B2AXA7_PODAN	PaTRK-1 low-affinity potassium transport encoded by the Patrk-1 protein (Podospora anserina S mat+ genomic DNA chromosome 7, supercontig 1)	PODANS_7_9900	Podospora anserina (strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) (Pleurage anserina)	939	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora, Podospora anserina (Pleurage anserina), Podospora anserina (strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) (Pleurage anserina)	515849	>tr|B2AXA7|B2AXA7_PODAN PaTRK-1 low-affinity potassium transport encoded by the Patrk-1 protein OS=Podospora anserina (strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) GN=PODANS_7_9900 PE=4 SV=1MERFKQWIATKPFTAQRCKQFIYTRPRWLFECIFPQNQGFPFIRYHCRWPCLSPVALTVLIVMADYLIISLALIGALITWGAGKHS GGTAEIRFIDALFFTAGASTQAGLNTVDINLLTTFQQAIFYLWPMMANPITVNSLVVQLRLYWFEKKFQHITQNARLVRVPLAKSFTKSR TKAKQQDGDVEKGVNGRKITVMLNGKKSRINNDGTLLGDAKNKGRHGLGLTAANRTATDGGLDGPLDKADRHTGPAVTSSMTEPRR PALKFADTVTKSDGLGEDFLKLPRIRSDEEHIAIVERQKKGDDEVLRIPNPRDVERGLGPKRVEAGDNEDELLSPHAEAFNLDGEPRA QAADGRHPAITIEEPDRRKLQETDSDEFMDDVRAAAHTFGFLKPHFPRHKKKQDDVEKEPVIPGPSQNRRRQSMQTLRTAFSNNKA EGTPYLSWEPTVGRNSLFPELTEEQREELGGIEYRSLKTLARVLTVYFWGYTALGVVGLLPWILQATQYGQVVEAAGQNKVWWAFF TSQSAFMDLGFTLTPDSMNSFSTATWPLLWMSFLIVIGNTGFPIMLRFMIWVLSLIVPKNSGMYEELRFLLDHPRRCFTLLFPSKATW WLLGFLVLLNGLDVMFFIVLDGPVASMSDGQKVLNGIFEAASTRTAGFSCVNLSLLHPAVQVSYMIMMYISVFPIAISVRRTNVYEENA LGIYSHGEEEEHSKANHNDWSHVGTHARRQLSFDLPFIALGLFILAISEGPRIMNPEDAANGFTMFSMLFESISAYGTVGMSLGYSTIN ASLSAEFSDVGKLVIICLMIRGRHRGLPYGLDRAILLPSDALNAKDAMAADTEGRLARQISRMSVATHRSDTTHNQRGLGHVLAAILHP GPPVPPEPPMEAIHRRSTDPGSDAEPQPMRVTSRRTEPGVVRRSVSHLFSPRPRTAGGHEDD
2E-127	435	3.7	4E-125	427.7	0.3	2	2	R1GLK6_BOTPV	Putative potassium transporter protein	UCRNP2_6380	Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	1036	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Neofusicoccum, Neofusicoccum parvum, Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	1287680	>tr|R1GLK6|R1GLK6_BOTPV Putative potassium transporter protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_6380 PE=4 SV=1MAEYRHYAIPDEQWEDFPNNLPPDTRVEGMNREHHLIKPQDDLEISEFNVSARDGHPVLIRSYRPSDKKADELIPLVIYLHGGGF VTGGLETDDRSCRAVALRCGVVVLNVEYRLAPENKFPIGWQDSYDVAASPAAQKQLSVDPTKGFILGGTSAGANFTAGLSHFFAGH DDPTESSEKLSPPLTGLMFIAPSVCHPSARPEQYAERILSVDEITDAPGLTRKSIDYFAAKYGAPPSDRRLSPLRFPSHAGLAQKALFQ VCGWDPRRDEGLLFEQLLKEAGVQTRLLVYSGLPHGFWTTCPDLPVSKAWEEDLVEAEVGLVSWSNSPWGKRPRSYVIESLNEAR PPNRPDAYIIVLGILALIVIYPYGNVPAVDAYFFGVSATTESGLNTIDVKALKTYQQLVLYFIPTVTNIGFVNIIVVVVRLYWFEKRLKQIAV EKDIEAQVQRSSGRRILGKLADGGVGEDASSAGKPRKESQDHRQETAIDDNKRVENAADAQKIAPAQIVFAEGTRPPRNEKALRVPS PRERERGRPLEEVNDVMSDEDDDKIMRITTADYEPTGLTRRRTRVGMSGITSATSIERVASSMFVLGSDPNAHRPQSRRSGSMSRH SMTRMPYLSRQATIGRNSRFYNLSAEDREQLGGIEYRSLKLLLKIVTAYFFGLHIFGAICLAGWIQTADSKYRDYLAECGQDKTWWGI YSAQTMVNNLGYTLTPDSMITFQDATFPMLVMTFLAFAGNTIYPCLLRLLIWTMAKLLPRNSSMQEPLNFLLDHPRRCYTLLFPSRPT WILFGILFVMNFVDTLLIVVLDLHNPAVNNLPGGPRVLAALFQAASSRHTGTATFNLANVHPGVQFSLLVMMYVSVFPIAIAVRSSNTYE ERSLGVYAPDPEPEDSTSAVSYLRNHLQNQLSFDLWYVFLGIFCITIAEADRIMDQADPAFQVFPIFFEVVSAYGNVGLSLGYPTVLTS LSGQFTTFSKLVICAMMIRGRHRGLPYALDRAIQLPADVLSEHDGKSVSVAWSEVEKIDEKANLKRAHTS
2E-126	432	7.1	1E-123	422.7	2.1	2	2	E9DDA8_COCPS	Potassium uptake transporter	CPSG_08070	Coccidioides posadasii (strain RMSCC 757 / Silveira) (Valley fever fungus)	718	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Coccidioides, Coccidioides posadasii (Valley fever fungus), Coccidioides posadasii (strain RMSCC 757 / Silveira) (Valley fever fungus)	443226	>tr|E9DDA8|E9DDA8_COCPS Potassium uptake transporter OS=Coccidioides posadasii (strain RMSCC 757 / Silveira) GN=CPSG_08070 PE=4 SV=1MWYPTLRMPHLNFIRIHYVYILALSIVGTIVLYPIKNMRGIDAFFQAVSGSTVTGLNTVDLKEMSLYQQITVWFLPMLGNMCFVNV VVVYVRLHWFEKKFKDIVQLSRLPSSERSRAQLLSVSPKAQSSDDTAYPHNIRVLRPDPAHEEADLVNLRQRPAAKRDESSDSPTAE DQSPSSENNNAERPPAQPGHITFSSDTFDKPNRGKALRIPGPREFEKGYKVQEVDDEDDADMTKSIDDPFGAGPSDAYRKLPAMER LLSHAASFEHAASSAFIIGGSSRSRSRSRSRGPMNRVSSRGAATQALPYLSYNPTVGRNSKFLGLTEDQKEELGGIEYRSLRLLLKIAG GYYVIGHIIGAIGLIAWIWNSNPKYRDYVRGECAVNPTWWAFYSSMTTFNNLGFTLTPDSMISFRDSTFPMLWMTFLIYVGNTAYPCM LRLIIWIAFKLTPESSSIKEPLNFLLDHPRRCYTVLFPSKVTWLLFGSLVLINGFDVILFLILDLHYPEVTAIQSGWHRFCAALFQTASART TGTSSFAVANVHPAAQFSLMVMMYISVFPIALSVRGTNTYEESSLGIFDSTEELVEMKRTSYLGVHIKMQLAFDLWYVFLGVFVLAIAE GSKIADPNNPGFNMFSIFFEVISAYGNVGLSLGHPDVNTALTGRFGIVGKLVICAMMIRGKHRGLPYEVDRAIILPGEKRIVEEDARIEA MSHNLSRRHTN
3E-126	431	25.9	4E-126	430.9	18	1.1	1	TRKG_ECOLI	Trk system potassium uptake protein TrkG	trkG b1363 JW1358	Escherichia coli (strain K12)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli (strain K12)	83333	>sp|P23849|TRKG_ECOLI Trk system potassium uptake protein TrkG OS=Escherichia coli (strain K12) GN=trkG PE=1 SV=1MNTSHVRVVTHMCGFLVWLYSLSMLPPMVVALFYKEKSLFVFFITFVIFFCIGGGAWYTTKKSGIQLRTRDGFIIIVMFWILFSVIS AFPLWIDSELNLTFIDALFEGVSGITTTGATVIDDVSSLPRAYLYYRSQLNFIGGLGVIVLAVAVLPLLGIGGAKLYQSEMPGPFKDDKLT PRLADTSRTLWITYSLLGIACIVCYRLAGMPLFDAICHGISTVSLGGFSTHSESIGYFNNYLVELVAGSFSLLSAFNFTLWYIVISRKTIKP LIRDIELRFFLLIALGVIIVTSFQVWHIGMYDLHGSFIHSFFLASSMLTDNGLATQDYASWPTHTIVFLLLSSFFGGCIGSTCGGIKSLRFLI LFKQSKHEINQLSHPRALLSVNVGGKIVTDRVMRSVWSFFFLYTLFTVFFILVLNGMGYDFLTSFATVAACINNMGLGFGATASSFGVL NDIAKCLMCIAMILGRLEIYPVIILFSGFFWRS

8E-125	427	6.4	2E-122	418.4	1.9	2.1	2	J3KHW4_COCIM	Trk family potassium uptake protein	CIMG_00852	Coccidioides immitis (strain RS) (Valley fever fungus)	718	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Coccidioides, Coccidioides immitis (Valley fever fungus), Coccidioides immitis (strain RS) (Valley fever fungus)	246410	>tr|J3KHW4|J3KHW4_COCIM Trk family potassium uptake protein OS=Coccidioides immitis (strain RS) GN=CIMG_00852 PE=4 SV=2MWYPTLRMPHLNFIRIHYVYILALSIVGTIILYPIKNMRGIDAFFQAVSGSTVTGLNTVDLKEMRLYQQITVWFLPMLGNMCFVNV VVVYVRLHWFEKKFKDIVQLSRLPSSERSRAQLLSVSPKAQSSDDTAYPHNIRVLRPDPAHEEADMVNLRQRPAAKRDESSDSPTAE DQSPSSENNNAERPPVQPGHITFSSDTFDKPNRGKALRIPGPREFEKGYKVQEVDDEDDADMTKSIDDPFGAGPSDAYRKLPAMER LLSHAASFEHAASSAFIIGGSSRSRSRSRSGPMNRVSSRGAATQALPYLSYNPTVGRNSKFLGLTEDQKEELGGIEYRSLRLLLKIAG GYYVIGHIIGAIGLIAWIWNSNPKYRDYVRGECAVNPTWWAFYSSMTTFNNLGFTLTPDSMISFRDSTFPMLWMTFLIYVGNTAYPCM LRLIIWIAFKLTPEGSSIKEPLNFLLDHPRRCYTVLFPSKVTWLLFGSLVLINGFDVILFLILDLHYPEVTAIQSGWHRFCAALFQTASART TGTSSFAVANVHPAAQFSLMVMMYISVFPIALSVRGTNTYEESSLGIFDSTEELVEMKRTSYLGVHIKMQLAFDLWYVFLGVFVLAIAE GSKIADPNNPGFNMFSIFFEVISAYGNVGLSLGHPDVNTGLTGKFGIVGKLVICAMMIRGKHRGLPYEVDRAIILPGEKRIVEEDARIEA MSHNLSRRHTN
3E-124	425	7.7	3E-124	424.6	5.4	1	1	G3AJW9_SPAPN	Putative uncharacterized protein	SPAPADRAFT_59429	Spathaspora passalidarum (strain NRRL Y-27907 / 11-Y1)	412	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Spathaspora, Spathaspora passalidarum, Spathaspora passalidarum (strain NRRL Y-27907 / 11-Y1)	619300	>tr|G3AJW9|G3AJW9_SPAPN Putative uncharacterized protein OS=Spathaspora passalidarum (strain NRRL Y-27907 / 11-Y1) GN=SPAPADRAFT_59429 PE=4 SV=1MPDHKSRLEGLAINPAWWAFFTAQSAFNDLGFTLTADSMLSFNQSALVLVVCSFFIVIGNTGFPVFLRFIIWLLFKTAKPLSLYKE SLGFLLDHPRRCFTLLFPSAPTWWLFAILVILNGFDLVIFCIVDLKDKPFETIPMGYRVLGGLFQAFCTRTVGFTVMDLSELHAAVQVSY MLMMYISVMPLAISIRRTNVYEEQSLGVYARENNQSDIENGTPSNYVGAHLRNQLSYDIWYIFLGLFVICLAEGGRLRQQDFRFSVFAI LFEIISAYGTVGMSLGYPTVNTSLSGQFTVISKLVIIAMMIRGRHRGLPYTIDRAIMLPDAEMRKHDRMQETHALQRSNTLEQSATHTLR RVATQGGSGGPIDAGQNLLGRVYTNVQDYRRRRHERKEAKKLTSRNPNYIVTTVSNI
4E-124	424	3.2	3E-122	418.2	0.5	2.1	2	S7ZDY8_PENO1	Uncharacterized protein	PDE_03450	Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	669	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium oxalicum, Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	933388	>tr|S7ZDY8|S7ZDY8_PENO1 Uncharacterized protein OS=Penicillium oxalicum (strain 114-2 / CGMCC 5302) GN=PDE_03450 PE=4 SV=1MWKPPVNYLTLHYAWIIFMGLLSLMIIYPYGNLKAIDAYFFGASASTESGLNTVDVKELKTYQQVYIYLIPIFTNLGFINILVVVFRV RWFEKHLKEVAPRYLRPEPPIEGDTEAQGNGITSVSIDPKRVATDAEGTGSSISVNDEAGTRESKISPIRTPAIQFAEDSRPSANKDKA LYIPPPWRRDRGTSFSEVDEKYDTEDDNGKEETERDLKRQKSTRSMASRSRTRTVERAVSSIFVLGNAPAPTQGSERRTQIEQRTFD LPNISSQATIGRNSQFYNLTAEDKARLGGIEYRSLKLLLKIVTGYFFGLHLFGAICLVGWILHCDPKYRAYLADCGQGNVWWGFYSAQ SMVNNLGFTLTPDSMVTFRDATFPMLLMSFLAFAGNTCYPCLLRFIIWTMYKLSPENSSMKEPLSFLLDHPRRCYTLLFPSRPTWILFG ILFAMNFTDVLLIIVLDLHNPAVNALAPGPRIVAAIFQAANARHTGGATFNLADVNPAVQFSLLVMMYIAIFPIAISIRASNVYEENSLGIYE SSSDPDESNGKSYIMKHIQNQLSFDLWYIFLGVFCISIAESGKIADNSIPAFSIFSVLFEVTSAYANVGLSLGYPTASTSLSGQFTIFSKLV ICFMMIRGRHRGLPYKLDRAVVLPSERDDEGYQTTNRSRAYYD
4E-123	421	0.2	4E-119	407.9	0.1	2	2	C5G9S4_AJEDR	Potassium transporter	BDCG_00726	Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) (Blastomyces dermatitidis)	678	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Blastomyces, Ajellomyces dermatitidis (Blastomyces dermatitidis), Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) (Blastomyces dermatitidis)	559297	>tr|C5G9S4|C5G9S4_AJEDR Potassium transporter OS=Ajellomyces dermatitidis (strain ER-3 / ATCC MYA-2586) GN=BDCG_00726 PE=4 SV=1MWKPPLNFITIHYAYIISLSISSLIVLYPYGNLKAIDAYFFGASGCTESGLNTYDVKDLKTYQQLFIYVIPIISHLGFVNIAVVLSKPVR NAELGIAPSQVQHRDDVEAKAFKTPKDVRKYTSSNANPDTTTPTATSTPGNANETDESQAAQPTKPTGASISFAADVRGYDKSKALYV PPPQERDRGRPMVEVDEIFSDDDEIAKTNDSNARRRSLSARRRIMGSSRIASTSTLEKVASSIFVLEGRPSTSNKQPPLQPSLSQHLDL PLSSHATLGRNSQFRNLTAEDREKLGGIEYRSLKLLLKIVTAYFFGLHLFGAICLLGWILHSDPKYREYLRECGQSPVWWAFYSSQTMI SNLGFTLTPDSMVSFRDAEWPMILMSFLAYVGNTFYPCFLRFIIWTMSLIVPKTSSLKEPLNFLLKHPRRCYTLLFPSGTTWALFSGLF VLNFVDIVLIITLDLDNPAVNDLPIGKRILASLFQAASTRHTGTSPFNLAKVNPAVQVSILVMMYVAILPIALSIRASNTYEQRALGIYPQDR DLDEYNGKTYILAHIKNQLTFDLWYIFLGVFCICASESKKIMDPNEPAFSVFAIFFEVTSGYGNVGLSLGHPSVNTSLSGQFSVFSKLVV CAMMLRGRHRGLPSQLDRAVMLPSDRLVDDDDKVETIETKYSTKIKRYHTH
1E-122	419	4.6	3E-120	411.3	1.9	2	2	E9FCC7_METRA	Potassium transport protein, high-affinity	MAA_09926	Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	690	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium robertsii, Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	655844	>tr|E9FCC7|E9FCC7_METRA Potassium transport protein, high-affinity OS=Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) GN=MAA_09926 PE=4 SV=2MWHPPVNFITLHYAWILSMGLLSFPVLYTYGNLAAIDAYFFGASASTESGLNTVDVKNLALYQQLYLYFIPILTNMCFINIVVVVVR LHWFNQHLDRFGPALIRVKRRKSGNGGVHSDPEVAEPTQASSSTASAALSNIPSHVGDQLGNQRTNQPSANDNDDGIGEIRPERET HNHALELSLEPTEKPTQHIAFHPSVWDKPTNSRRDSTLYIPGPRERDRDADSTPTRRSSDADAEDSQRRLTRARSFDRAASAAGSIFII GRTPTVPQLSRAATLHRAAADQMPYLSRRATIGRNSRFHNLTSRDRQELGGIEYRSLQLLLKVVVVYFFGMHIFGAIGLVGWILHANP KYDAYLQQCGQNSIWWAFYTAQSMMDNLGFTLTPDSMISFREAEWPLFLSTFLTLAGNTLYPVFLRLVLWTMSKTVSQKSATQESL QFLLNHPRRCYTLLFPRGTTWALFGIIFILNFMDAFFILILDLNNAEVASLPPGPRVMAAIFQAGSSRHTGASVFNLANVSPAVQFSLLIM MYISAFPIALSIRASNTYEEKSLGIYQVDTEEDLDENSGRSYLVRHLQSQLSFDLWYIFLGIFVLSISEAGKIEHLAQPSFGLFPIFFEAVS AYGNVGLSLGYPGINASLSTEFSTFGKLVICAMMIRGRHRGLPYTLDRAIMLPDEHLIGAATRERITREDE
2E-122	419	1.6	4E-118	404.4	1.8	2	2	G2X362_VERDV	Low-affinity potassium transport protein	VDAG_04847	Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	702	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, mitosporic Plectosphaerellaceae, Verticillium, Verticillium dahliae (Verticillium wilt), Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	498257	>tr|G2X362|G2X362_VERDV Low-affinity potassium transport protein OS=Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) GN=VDAG_04847 PE=4 SV=1MTIIIGAWKPRLNFIGIHYAWILFCSLLAFPVMYSYGNLTAVDALFFGCSGSTESGLNTVDVKDLKTYQQVYIYVIPIITNLMFINAM VVPVRLFWFRRLLKQAGPANAAAAARDDDEEKMSEQKVQGANQGADQDQDAAAAPSPTLPKASRSPTITFYDRPSDAKHQASEQH RLRPAPRQSDIDQPDPRHGVNHQDNDVSGITNLPSAATTSTVTCRRAFSDADDTDDIKPVQRTQSARLRHYTEGPVLHAAKSIEKAAA SAFILGDARPRPVSRSRSRSRNLDLPKLSRYATVGRNSNFYNLTEADRELLGGIEYRALKILLKFVFGYFIGLHVLGVVCLLPWIHNAPA KYTDWLEESSVGKTWWAFYSAQTMVDNLGFTLTPDSMATFKDATWPMLVMTFLAFAGNTCYPVLLRLIIWIVYKMVPRNSQSRETL QFLLDHPRRCYTLLFPSRPTWILFYIIFALNFIDVVLIIVLDLDNPAVNDLPMGPRILSALFQAASARHTGTSTLNLANVNPAVQFSLLTMM YIAIFPIAISVRASNTYQDRALGIWSTEHNLDEHNGISYVLVHVRNQLTFDLWYIFLGTFLICIAESKRIMDLDEPSFSVFPVLFEVTSAYG NVGLSLGGPFGYTSMVGHYTVFSKVVVCAMMIRGRHRGLPYALDRAITLPNDTVLSDTADDPDELAKGSKLACVMNTLPTY
6E-122	417	10.4	7E-120	410.2	7.2	2.1	1	R4X8Y4_TAPDE	Potassium transport protein	TAPDE_001770	Taphrina deformans (strain PYCC 5710 / ATCC 11124 / CBS 356.35 / IMI 108563 / JCM 9778 / NBRC 8474) (Peach leaf curl fungus) (Lalaria deformans)	701	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Taphrinomycetes, Taphrinales, Taphrinaceae, Taphrina, Taphrina deformans (peach leaf curl fungus), Taphrina deformans (strain PYCC 5710 / ATCC 11124 / CBS 356.35 / IMI 108563 / JCM 9778 / NBRC 8474) (Peach leaf curl fungus) (Lalaria deformans)	1097556	>tr|R4X8Y4|R4X8Y4_TAPDE Potassium transport protein OS=Taphrina deformans (strain PYCC 5710 / ATCC 11124 / CBS 356.35 / IMI 108563 / JCM 9778 / NBRC 8474) GN=TAPDE_001770 PE=4 SV=1MELEERGVGGREIRVLFDSARNQQVYSADDRRNPSQDPLDRGVKSKPSFSTVGDRRSISSMMPRRTSTKQDEALDSLIDADR PPTRGSTDKISDSTISKMSESSTSEPDSKERSPSQDEPPSSNVRRTPSIVSQAIVDDEDEKEVKVEDGNDEQLRGNADIRFAELPVPR KAHNEDSGHLRTGSMGLPSRNNGTENPLSRARTADPASRIGSAILDFGQRTMTLDGPARANRMHRRRPSSVVRPAAGRSTTIERTIT TAFRRRRDSSPSGRSARVRDMTLPYISFQPTIGRNSAFKSLSKEQRAELGGIEYRATRALCWVLVAYFFGFHIFGFVCYLAFIYSAQQ YIPAVLETGAARGWWSLFTSASTFNDLGLTLTSTSFIPFQNAAFLLLMSSFLIVIGNTGFPCMLRFVIWLLYRLWPAESPVKEEFAFLLD HPRRCFTLLFPSSATWWLFAILVGLNGLDLLLLFIILDLGNDEITNIPVGYRIIDGLFQAFCTRTAGFTSVNLAGLHSAILVSYMIMMYVSSS TSNILAYNVRYISVFPVAISIRKTNVYEERSLGIYSAEDEEEGAGQSFVGTHIRRQLGFDLCIIENPEIQNASLQSFNIFNVLFEIVSAYGT VGLSIGYPGVDYSFSGEFHTLSKLVIIALQIRGRHRGLPLKLDRAVLLPSEKLIASEEEDAVLRSGRSFSRSMQTGTRERED

															>tr|G7XE17|G7XE17_ASPKW Ankyrin repeat-containing protein OS=Aspergillus kawachii (strain NBRC 4308) GN=AKAW_03290 PE=4 SV=1
7E-122	417	5.5	6E-120	410.4	0.8	2	2	G7XE17_ASPKW	Ankyrin repeat-containing protein	AKAW_03290	Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	645	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus kawachii (White koji mold) (Aspergillus awamori var. kawachi), Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	1033177	MPPRESVVDNPKSPLRRCHHYIYIISWALLSSLILYCAGGISYVDALLLASGAATQTGLNTVDLNRLHVVQQVTLLVVSMVTNVIFVHSLLVVIRLYWFRKRFKRAINEAKMMCRAQRNTLNQRLADVENGPSRSFSRERPAEDTPLLSTVTEESLTASPSESPGGRRYGATGSMSPHITFCETDAEHEVKQRRRTYSGTWSRRSFPEIDSPQRRRSFSEMQNDMPPLPSLMWQSSIASYSDWNEAQKEELGGIEYRALKTLFIILVCYYVVIHLLGALLFLVWILPNKHYGQILADNGLSRPWWAIFTAGSAFNDLGFTLTPNSMGSFNTAVFPLLVMTFLIVLGNTGFPCMLRFIIWTLSQFTTYGSPLDDELQFLLDHPRRCFTLLFPSTETWRLAAVLLLINAIDLIIFYTLQEFPHPSPISAGLRLVNGLFQIASTRTAGFTIASLGTLHPAVQVSFVGMMYISAFPIAIAMRKTNVYEERSLGIYNEEYDEHDKPHQSDSLGAHIQRQLGFDLWFVMLGFFFVAVAEGKRLQENRTDIAFSLFPILFEIVSAYGTVGLSMGYPGTETSLCREFNGLSKVIVIAMQVRGRHRGLPHALDHAILLPCDLVEPDEQGRRPEWWWKRWIRKKSSDLGNLFTHD
9E-122	417	17.2	2.6E-58	207.2	0.9	3	3	K5UJS8_PHACS	Uncharacterized protein	PHACADRAFT_214314	Phanerochaete carnosa (strain HHB-10118-sp) (White-rot fungus) (Peniophora carnosa)	874	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Phanerochaetaceae, Phanerochaete, Phanerochaete carnosa, Phanerochaete carnosa (strain HHB-10118-sp) (White-rot fungus) (Peniophora carnosa)	650164	>tr|K5UJS8|K5UJS8_PHACS Uncharacterized protein OS=Phanerochaete carnosa (strain HHB-10118-sp) GN=PHACADRAFT_214314 PE=4 SV=1MWATARSHCNFYRIHLLCFIILPIIFAGIFVASNGRFTTVYIDALFVCVSAATGTGLSTIDLSSLTAWQQTILVILEIAGNQVFVCWIVVFIRRYYFRKHLDHVVSVEQELRRPWAHRDPQHSSHLLRELSRHTRLTPGLPRNEELKTLERKNLDQSAEGRIRPDMVRRVDIALRPVDPMGVPTRPVTPDSTITRRRATLNDMRGDDLGEVYPSSDVGFGGFPGPREVFTRTSQRLFPRLHRRFQNTLTMPRTSTFIPQDAHGIDSQHIASSIRPVPYLSFQVDVGKNSTFKDLSEEEMLELGGVEYSALNALMWIVPLYYFGLLAIAIIIITPYMALASQYKDVFLPPMQHRKISPIWFSIFQVVGAWANTGMSLVDQNMIPFKMAYPLIFVLFFCVLAGNTAYPVFLRLMIWSLYKLFPKKSPTCKALKFLLDHPRRCFITLFPAHQTWLLLFVLFLMNMVLFVGDLVLNIDNPATDAIPVGTRIALAVLSSGAVRSAGFQAVAVSSLTPATQVLYVIMMYIAIYPIAMSVRSTNVYEENSLGIYPDDDDDDDKFNEKTLKVKEKRVQIWGRHLVRHVQKQLSFAHQTWLLLFVLFLMNMVLFVGDLVLNIDNPATDAIPVGTRIALAVLSSGAVRSAGFQAVAVSSLTPATQVLYVIMMYIAIYPIAMSVRSTNVYEENSLGVYPDDDDDDDDDKFNEKTLKAKEKRVQIWGRHLVRHVQKQLSFDIWWLALSLWLICIVERNGIMDPSKPWFNVFAILFEIVSGYGTVGLSLGIPTANYSLSGVFHILSKLIICAVMLRGRHRGLPVALDRAVMLPHEFKRRYEDSEAAQAQAASPHQIVGHLPEESVGAGAMGHKADGSSAEDSEKTVV
1E-121	416	5.9	7E-120	410.2	0.9	2	2	G3Y6I7_ASPNA	High-affinity potassium uptake transporter	ASPNIDRAFT_45611	Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	701	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	380704	>tr|G3Y6I7|G3Y6I7_ASPNA High-affinity potassium uptake transporter OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) GN=ASPNIDRAFT_45611 PE=4 SV=1MDRASVAGWEPFSFQHARSRSRTIYFNQQSRLIPKTTFAFSSAVLPPELLRPGVSRMPPRESVVDNPKSPLRRCHHYIYIISWALVSSLILYCAGGLSYVDALLLASGAATQTGLNTVDLNRLHVVQQVTLLVVSMVTNVIFVHSLLVVIRLYWFRKRFKRAIHEAKMMCRAQRNTLNQRLADVENGHYRTFSRERPSEEEPLLSTVTEESTTASPSESPGGRRYGATGSTSPHITFCETDAEHEVKQRRRSYSGTWSRRSLPEIDSPQRRRSFSEMQNDMPPLPSLMWQSSIASYSDWNEAQKEELGGIEYRALKTLFVILVCYYVIIHLLGALLFLVWILPNRHYGQILAENGISRPWWAIFTAGSAFNDLGFTLTPNSMGSFNTAVFPLLVMTFLIVLGNTGFPCMLRFIIWTLSQFTTYGSPLDDELQFLLDHPRRCFTLLFPSTETWRLAAVLLLINAIDLIIFYTLQEFPHPSPISAGLRLVNGLFQIASTRTAGFTIASLGTLHPAVQVSFVGMMYISAFPIAIAMRKTNVYEERSLGIYNEEYDEHDKPHQSDSLGAHIQRQLGFDLWFVMLGFFFVAVAEGKRLQENRTDIAFSLFPILFEIVSAYGTVGLSMGYPGTETSLCREFNGLSKVIVIAMQVRGRHRGLPHALDHAILLPCDLVEPDEQGRRPEWWWKRWLRKKSSDLGNLFTHD
2E-121	415	5.5	2E-116	399.1	1.9	2.5	2	C6HFE4_AJECH	Potassium ion transporter	HCDG_04667	Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	836	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	544712	>tr|C6HFE4|C6HFE4_AJECH Potassium ion transporter OS=Ajellomyces capsulatus (strain H143) GN=HCDG_04667 PE=4 SV=1MALRSGVLKVRRAYWSSLEAFIKTIDSIGTRVPVLSTIRLNFLSLHYGYIITCSLVASVILYAPGNVTYIDALLFATGATTQSGLNPIDTNLLLTYQQVGLWFLSMITNPIFINTFVVFIRLFWFERRFQHVVHEAKALRRIKSRQRTLTREALTKDRRETSHNRDRGNIGVRGKEIVLLRDSGTGQAQGCSAAHDLEKKTDAASTSESDRSPKPSPGGEPSSPQGEDQARGENRGDAADTMEPPISDKNDKGVELGASKYLSPEHHIAFLAHQRRHTCALRIPSPREYDRGGVPQTVDDDADGGDLTQVQTSRSEWPATPPCTQPPQEHHITIDEPNAARMRSRINPRRRSTYRPSEPDADFIPPERTRSRTFSGLFRSSSQGPDIGSSPYLSWQPTIGRNSAFVDLTEAQRNELGGIVSLVPWILKTERFGNIVKETGLGRPWWAVFTSASAFNDQGFALTPDSMMSFYDAIFPLLLLSFLILVGNTAFPCMLRFTVWMLSHLVPFGSPAWEELRFLLDHPRRCFTLMFPGAATWWLFGVLVVLNGLQLIFFIILDLNNPEFNRIPIGIRFVDGFFQAASTRTAGLAVVNLANIHPAVQVFFLIMMYISVFPVAISVRRTNVYEEGSLGIYSCPDDDEDETLGSKDVNYIGAHLRKQLSFDLWYIFLGLFLISIIEVNRLDQKGENSFSMFAVMFEIVSAYGTVGLSLGFPNSNTALCGHFRPLSKLIIIAMEIRGRHRGLPYELDRAILLPSESLNRKESMDANKRLRRCGSNMSTFSVATRKQSMPCVPLKETRSSSAYQRGGWLGSRLESTSSQIGAANTGPPLRPHQEGV
2E-121	415	5.5	2E-116	399.1	1.9	2.5	2	F0UP43_AJEC8	Potassium ion transporter	HCEG_06117	Ajellomyces capsulatus (strain H88) (Darling's disease fungus) (Histoplasma capsulatum)	836	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain H88) (Darling's disease fungus) (Histoplasma capsulatum)	544711	>tr|F0UP43|F0UP43_AJEC8 Potassium ion transporter OS=Ajellomyces capsulatus (strain H88) GN=HCEG_06117 PE=4 SV=1MALRSGVLKVRRAYWSSLEAFIKTIDSIGTRVPVLSTIRLNFLSLHYGYIITCSLVASVILYAPGNVTYIDALLFATGATTQSGLNPIDTNLLLTYQQVGLWFLSMITNPIFINTFVVFIRLFWFERRFQHVVHEAKALRRIKSRQRTLTREALTKDRRETSHNRDRGNIGVRGKEIVLLRDSGTGQAQGCSAAHDLEKKTDAASTSESDRSPKPSPGGEPSSPQGEDQARGENRGDAADTMEPPISDKNDKGVELGASKYLSPEHHIAFLAHQRRHTCALRIPSPREYDRGGVPQTVDDDADGGDLTQVQTSRSEWPATPPCTQPPQEHHITIDEPNAARMRSRINPRRRSTYRPSEPDADFIPPERTRSRTFSGLFRSSSQGPDIGSSPYLSWQPTIGRNSAFVDLTEAQRNELGGIVSLVPWILKTERFGNIVKETGLGRPWWAVFTSASAFNDQGFALTPDSMMSFYDAIFPLLLLSFLILVGNTAFPCMLRFTVWMLSHLVPFGSPAWEELRFLLDHPRRCFTLMFPGAATWWLFGVLVVLNGLQLIFFIILDLNNPEFNRIPIGIRFVDGFFQAASTRTAGLAVVNLANIHPAVQVFFLIMMYISVFPVAISVRRTNVYEEGSLGIYSCPDDDEDETLGSKDVNYIGAHLRKQLSFDLWYIFLGLFLISIIEVNRLDQKGENSFSMFAVMFEIVSAYGTVGLSLGFPNSNTALCGHFRPLSKLIIIAMEIRGRHRGLPYELDRAILLPSESLNRKESMDANKRLRRCGSNMSTFSVATRKQSMPCVPLKETRSSSAYQRGGWLGSRLESTSSQIGAANTGPPLRPHQEGV
6E-121	414	2.1	6E-119	407.2	0.4	2	2	G4N084_MAGO7	Potassium transporter	MGG_09119	Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	677	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Magnaporthe, Magnaporthe oryzae (Rice blast fungus) (Pyricularia oryzae), Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	242507	>tr|G4N084|G4N084_MAGO7 Potassium transporter OS=Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) GN=MGG_09119 PE=4 SV=1MVKLIGAIGAWRPKLDFIALHYIWIIFCAILGFIVLYPHGNVPAIDALFFGASASTESGLNTIDLKELKMYQQLYLYVIPMITNLGFINPFVVAVRIYWFRKKLKQMRPSISRPDPEAVVLALRGHEDAKPRQEEPRPRSPSLDLAVEDEEDDEKKTRLDGKPIGPEAPDTTYFIPPPRERDSGQPFVVVDPRNDDEIRPAPAEHMDSEAGVRLRRPMTARDGPALTTARSLQHAASSVFVLGPNKAGRRNSVSSRAPATSNLPALSRQVTVGRNSKFYNLTPEDEEKLGGIEYRALKVLLKVTIAYFFGLHLLGIVCLVPWIHNAPAKYTDWLAQNGLDKTWWGFYSAQTMVDNLGFTLTPDSMVTFRDATWPMLIMTFLAFAGNTLYPVLLRLTIYVMSKVVPARSSTKEALQFLLDHPRRCYTLLFPSGPTWVLFVIAALNLIDVVLIIVLDLDNPAINDLPMGPRVLSALFQAASSRHTGTSTLNLALINPAVQFSLLVMMYIAILPIAISIRASNTYEEKSLGMYKDQELPDESDASSYVVVMHFRNQLSFDLWYIFLGTFCICVAESQKISDPAEPAFSVFSIFFECVSAYGTVGLSLGHPSVSASLSSQFGIFGKLVICAAMIRGRHRTLPYAIDRAIMLPGEGSDDGTGPQGDALLRGATARSEKEATD

7E-121	414	4.5	6E-119	407.1	1.8	2	2	E9EGI0_METAQ	Cation transporter, putative	MAC_08978	Metarhizium acridum (strain CQMa 102)	690	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium acridum, Metarhizium acridum (strain CQMa 102)	655827	>tr|E9EGI0|E9EGI0_METAQ Cation transporter, putative OS=Metarhizium acridum (strain CQMa 102) GN=MAC_08978 PE=4 SV=1MWHPPVNFITLHYAWILSMGLLSFPVLYTYGNLAAIDAYFFGASASTESGLNTVDIKNLALYQQLYLYFIPILTNMCFINIVVVVVRL HWFNQHLDRFGPALIRVKRRKSGNGGVHSDPEVAEPTEVSSSTASAALSNIPSHVGDQLDSQGTRQPSKNDNDGGVGEIRPEPETH NHALELSLEPTEKPTQRIAFHPSVWDKPTNSRRDSTLYIPGPRERDRDADATCSPRPSDADAEDSRRRLTRAKSLDRAAGAAGSIFIIG RTPTVPQLSRAPTLHRAAADRMPYLSRRATIGRNSRFHNLTSRDRQELGGIEYRSLQLLLKVVVIYFFGMHIFGAIGLVGWILHADPKY DAYLQQCGQNRIWWAFYTAQSMMDNLGFTLTPDSMISFRQAEWPLLLSTFLTLAGNTLYPVFLRLVLWTMSRMVARKSVTQESLQF LLNHPRRCYTLLFPRGTTWALFGIIFILNFMDAFFILILDLNNAEVASLPPGPRVVAAIFQAGSSRHTGASVFNLANVSPAVQFSLLIMMY ISAFPVALSIRASNTYEEKSLGIYRVGTEEDLDENRGRGSYLVRHLQSQLSFDLWYIFLGIFVLSISEAGKIEQLAQPSFGLFPIFFEAVSA YGNVGLSLGYPGINASLSTEFSTFGKLVICAMMIRGRHRGLPYTLDRAIMLPDEHLIGAATRERITREDE
2E-120	412	13.7	3E-117	401.7	3	2	2	K1X6X3_MARBU	Cation transporter	MBM_01518	Marssonina brunnea f. sp. multigermtubi (strain MB_m1) (Marssonina leaf spot fungus)	659	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Dermateaceae, Marssonina, Marssonina brunnea, Marssonina brunnea f. sp. 'multigermtubi', Marssonina brunnea f. sp. multigermtubi (strain MB_m1) (Marssonina leaf spot fungus)	1072389	>tr|K1X6X3|K1X6X3_MARBU Cation transporter OS=Marssonina brunnea f. sp. multigermtubi (strain MB_m1) GN=MBM_01518 PE=4 SV=1MWKPPMNFITFHYMYIIVLSILGYIIIYPHKNMPSTDAFFFGVSAATESGLNTIDVKDLKLYQQLVVLYFFPILGNIGFINIVVVLVRL MWFEKRLRKADSESRAHDAENGTVALPVRDCEAQADLFGSSHRKEESGNETSVNQPAKHINFGPEPEQLREKSARDANQDPERLM SDEEGASRPKSALSGTELGRSFKLRKTATHSSQISNSAAVAHVASSIFVVGASGTERDDGQTPRLKFRIPFLSRQATVGRNSNFHRLT IEDRLRLGGIEYSSLRLLLKIVLGFFFGLHIFGAICLVIWIQYAPAKYTDYVQESGQNKIWWAFYSAQTMANNLGFTLTPDSMISFRDAT FPMIVMTFLAYAGNTFYPILLRLVIWMGSKLVSKTSSLREPLQFLLDHPRRCYTLLFPSHPTWVLFGILVVLNVVDVLLIILLDLDNETVTV LPPGPRVLAAIFQSASARSTGTATFNLAEVNPAVQFGLLVMMYISVYPIAISVRASNTYEEKSLGIYSDKRVDVDEQDPRSYLVMHLQN QLSFDLWYIFFGIFCITIAEEQKIADPNNPAINVFSIFFEVVSAYANVGLSLGHPSVLTSLSGKFTPFSKLILCAMMIRGRHRGLPYQLDR AILLPNERLAAIDDSSEETANVDVNMFLMKRHHTQ
2E-119	409	6.3	8E-118	403.5	1	2.1	2	A2R8F4_ASPNC	Aspergillus niger contig An16c0220, genomic contig	An16g06940	Aspergillus niger (strain CBS 513.88 / FGSC A1513)	817	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain CBS 513.88 / FGSC A1513)	425011	>tr|A2R8F4|A2R8F4_ASPNC Aspergillus niger contig An16c0220, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=An16g06940 PE=4 SV=1MLPRPLGTSSSTTVPTIRTQMTTTSPTGALLAMATMLPVHERQGSHRCTGNCLLNNKLEFLRPAGDDCQEMSMLQITGLCRVL SPELTVGELLLTFESQFDEFPRYGGKQRVRVDQTMDRASVAGWEPFSFYHARSRSRTIYFNQQSRLIPKTTFAFSSAVLPPELLRPG VSRMPPRESVVDNPKSPLRRCHHYIYIISWALVSSLILYCAGGLSYVDALLLASGAATQTGLNTVDLNRLHVVQQVTLLVVSMVTNVIF VHSLLVVIRLYWFRKRFKRAIHEAKMMCRAQRNTLNQRLADVENGHYRTFSRERPSEEEPLLSTVTEESTTASPSESPGGRRYGPTG SMSPHITFCETEAEHEVKQRRRSYSGTWSRRSLPEIDSPQRRRSFSETQNDMPPLPSLMWQSSIASYSDWNEAQKEELGGIEYRAL KTLFVILVCYYVIIHLLGALLFLVWILPNRHYGQILAENGISRPWWAIFTASAFNDLGFTLTPNSMGSFNTAVFPLLVMTFLIVLGNTGFP CMLRFIIWTLSQFTTYGSPLDDELQFLLDHPRRCFTLLFPSTETWRLAAVLLLINAIDLIIFYTLQEFHPPSPISAGLRLVNGLFQIASTRT AGFTIASLGTLHPAVQVSFVGMMYISAFPIAIAMRKTNVYEERSLGIYNEEYDEHDKPHQSDSLGAHIQRQLGFDLWFVMLGFFFVAV AEGKRLQENRTDIAFSLFPILFEIVSAYGTVGLSMGYPGTETSLCREFNGLSKVIVIAMQVRGRHRGLPHALDHAILLPCDLVEPDEQG RRPEWWWKRWLRKKSSDLGNLFTHD
5E-119	407	0	2E-117	402.2	0	2	2	C7ZL87_NECH7	Putative uncharacterized protein	NECHADRAFT_54501	Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	668	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium solani species complex, Nectria haematococca, Fusarium solani subsp. pisi (Nectria haematococca), Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	660122	>tr|C7ZL87|C7ZL87_NECH7 Putative uncharacterized protein OS=Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) GN=NECHADRAFT_54501 PE=4 SV=1MWLPPINFLTLHYAYIILMCLLAIPILYPYGNLKAIDCFFFGASSSTESGLNTVDVKELKTYQQLYIYFVPMLTNLGFVNIIVVVVRLH WFRSHLKRLAPQLHPRRQPGSSEADPEIPDTSTIKAPDTAGKLPVAVASGNDAGTTGESPSQAPVMSPDSERPLARTTTITFDTSTE KHKDDTTLYIPSPQDRERDDRIKPVSSATSNNEGPALRLRRRFSDRDGIQMTAARSMDRVADVAASILLLGSETKPRPRPPTPTPQKP PALNDTPFLSRQATIGRNSQFRNLTSDDLEVLGGIEYRSLKLLLKIVIAYFFGMHLFGVICLIGWIQTANPKYTDYLESIGQDKNWWAIY SAQTMVDNLGFSLTPDSMISFRDAKFPMILMSFLAFAGNTLYPVFLRLVIWIMAKVTPKHSSTQEPLAFLLDHPRRCYTLLFPSQPTWI LFAIIFALNFVDVLLIILLDLHNPEVASLSLDARIPAAIFQAASARHTGTATFNLANVDPAVQLSLLVMMYIAVFPIALSIRSSNTYEEKSLGL WKDEESPDEENSKTYLVTHMKNQLGFDLWYIFLGTFCIIIAESDRVANVDEPAFSVFSILFEVTSAYGNVGLSLGYPTVSTSLSGMFNT FSKVVMCLMMIRGRHRGLPYALDRAIMLPDGQILEDPPKSS
2E-118	406	0	4E-115	394.8	0	2	2	A0A0J9V0W1_FUSO4	Uncharacterized protein	FOXG_06579	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	676	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9V0W1|A0A0J9V0W1_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_06579 PE=4 SV=1MWRPPINFLTLHYAWIISMSLLALPILAPYGNISVTDAYFFGASASTESGLNTVDVKDLKTYQQLYIYFIPIITNLGFINIGVVIVRLY WFKKHLKRRAPQLFSPRRRDASGENVEDGKIVEEKAQNDLPAVTAPSNNLEQHATTDTPVPRTTTITFDPSIDQRRDSATLYIPGPQD RDRGHPIIAKTGNEHYDSDNSDDDRITPVPTAASGEPSSSMRRRLPRRISTGDGLQMTATRSMDRVAGIASSLLMMGSETTRPRRQS SSSVSQQQPALNDRPFLSRQATIGRNSEFQNLTSHDRELLGGIEYRSLKLLLKIVTAYFFGVHLFGAICLLGWIQTANPKYREYLQSTG QDKNWWAFYSAQTMVDNLGFTLTPDSMISFRDAKWPMILMSFLAFAGNTLYPVFLRLIIWTMSKLLPKHSSTQEPLGFLLNYPRRCY TLLFPSKPTWILFGIIFSLNFIDVLLIIILDLDNPEVASLPLDSRIPAAIFQAASARHTGTATFNLANVNPGVQLSLLVMMYIAVFPIALSIRLS NTYEEKSLGIWEPEGSLNERNGKSYLMQHIKNQLGFDLWYIFLGTFCICVAEATRIADVKDPAFTIFSILFEVTSAYGNVGLSLGYPTVS TSLCGKFGTFGKVVICLTMIRGRHRGLPYALDRAVMLPDEHLLETPADSTE
3E-118	405	10.1	5E-116	397.6	2.6	3.1	2	C5FPM9_ARTOC	Potassium transport protein 1	MCYG_04453	Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) (Microsporum canis)	692	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Arthroderma, Arthroderma otae (Microsporum canis), Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) (Microsporum canis)	554155	>tr|C5FPM9|C5FPM9_ARTOC Potassium transport protein 1 OS=Arthroderma otae (strain ATCC MYA-4605 / CBS 113480) GN=MCYG_04453 PE=4 SV=1MFSSGVWPRLSRPSFILVHYVYIVALCLVGMVMIYPLKNMSAIDALFQAVGAATMTGLNSVDFKGLTIYQQVVLYISPLLGNICFIN FIVVLVRLYWFESKFKEIVRFSRLPSTERSHHVESGLRGHRVVGLSTAPDLPIKPSEETETKDGEGLKQRTSHVPEEEGREDSKPTVV EKQLPTTGTGHVSFSTDTFRPREKALRIPGPREFEAGHRAHEVDEEADGDELTKATSIDPSLVGAPSLRERGKLERILSHATSVEQAA SSAFVLGSASRPRSRSRSISRSLRPLSRTGSRGSQVPYLSYTPTIGRNSQFLNLTEEQRIELGGIEYRSLKLLAKIVGGYYFGFLLLGSIL LIIWIYAANPVHRQYLAENGIHPVWCLTPDSMVNFRSNTFPMLFMTFLILVGNTAYPCMLRFIIWCMFRLSPKASAIHEPLNFLLDHPRR CYTLLFPSRTTWVLLGTLVSLNGLDIMLFMILDLRNPEVTAIDTVWHRLCAASFQSTASRTAGATSFALSKIHPAVQFSLMVMMYISVF PVAMSMRKTNTYEESSLGLYDSEEEVDETTDSSSYLGQHIRKQLAFDLWYIFLGVFLITIAEGAKIADLNDPAFQIFAIFFEVVSAYGNV GLSLGHPTINAGLSGKFTTVSKLVMCAMMVRGRHRGLPYELDRAIVLPGERRRKEEQARAEGLVASVKE

5E-118	404	4.8	1E-112	386.7	0.9	2.1	2	M7WVH0_RHOT1	Potassium ion transporter	RHTO_04771	Rhodosporidium toruloides (strain NP11) (Yeast) (Rhodotorula gracilis)	1013	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Pucciniomycotina, Microbotryomycetes, Sporidiobolales, Rhodosporidium, Rhodosporidium toruloides (Yeast) (Rhodotorula gracilis), Rhodosporidium toruloides (strain NP11) (Yeast) (Rhodotorula gracilis)	1130832	>tr|M7WVH0|M7WVH0_RHOT1 Potassium ion transporter OS=Rhodosporidium toruloides (strain NP11) GN=RHTO_04771 PE=4 SV=1MRRRLSLDRHPSTAARFPPFLERSSVWNRISAFSSAHLNFYRLHLLAFTFLPLIASGIFFASNGPTQANQIPYIDALFMCTSAMTL TGLNTALFANLTVWQQFILFFLMSIGSTSFVSMITIIIRRHFFRNKFEYMVANDEEARTRVNEVGEGEAARHGRSYHAFDDAHQPTRP WYTHLLPGRRGGELPAAPRANGSLGEELGGQWTAKDRERSRRRTEKLRTDMIKRVDTPVRVNEMSVSGWLGGEKTGDAKEGEEG RDDPNVDGGRAKNPIHEVREAQSPQGLPHALPREPSVDRGEGNLPLAVQAARASTDEGSADAAGHARAIQIDESTRPDRRARERRN SDSVAATPTRAAGASLPRTHTLDHRHLGHVGASLPAQPHPSSPARQQRDLEVGRTRTIDFRDPDGAGDLRLRRNRTQALDPDYPIRR RMSQSSLHDADPRAFTRTVTLDQAAMHSDFGGFPNPLFAAASFAKDKIPGLRNVLDRTATLPRTTTMRSTHSQGRSPSRRRESDGE FKPVSYISFDAIVGRNSKFHGLTTAQQEELGGVEYRALTVLLRIVFAYWLGVQLLAVLAVAPWLATTQPWKSTISAAGPNPTWFSFFQ VWSAYSNCGMSLDDASMVPFQKAYGLVIVQGLLILAGNTAFPVFLRLLIWIVSKAVPSRSRTRETLQFLLDHPRRCFIYLFPSYQTWFL VFMLVCLNGIDWASFLVLDIGNPQIEALPTGVRVIDGLFQAVAVRTAGFAIVSLSTVAPALQLLYVIMMYIAVYPIAVSIRSTNVYEEKSM GVYDEDFEEDPDEAEARFDKSHSATQYIGYHARKQLAFDLWWLALAVWLICIVERHRISSTDWPEVTIFSLIFEIVSAYGTVGLSLGNN RTATSLAGVLSTMSKLIVCAVMLRGRHRGLPIAIDRAVLLPSDLEKHWDDTLSINSREDAPGELGRRTRTSFSSHTAVAGGGLQAVEP LTDEDRRHRLRRTSGVRQDDTNGDAEAEVGRSSSLNGSKEGIAGSAASHEP
6E-118	404	0.3	9E-118	403.3	0.2	1.2	1	A1CIS2_ASPCL	Cation transporter, putative	ACLA_052500	Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	701	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus clavatus, Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	344612	>tr|A1CIS2|A1CIS2_ASPCL Cation transporter, putative OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) GN=ACLA_052500 PE=4 SV=1MWRPPVNFITLHYAYIITLGILGIAVLYPYGNLRAVDAYLFGVSSSTESGLNPFVGPIDRSRGRGSLTRNVTKCSVDLKELKTYQQ LFLYFVPIVSNPGFVNVLVVIVRLYWFEKHLKTLAPTLLRPDWHEKDAESHAKVNEDSKVERWATPCRAAHIDLSDKLFSEAVRRGQG MITNNGIPGDDNTIRNKHISFADDSRALYIPSPRERDRGITLIKLRFPPGTHRRTGSEEAEIESIHRRSASGGTPLERIASTMSALGAYPS RSQERQVKRTVSLSKDPELTGLSSQASLGRNSRFYDLTTEDRERLGGIEYRSLRLLLKISLGYFVGLHVLGVICLVPWIQHADPKYRDY LRECGQGKIWWAFYTAQTMVDNLGYSLTPDSMISFRDAAWPMFIMSFLAYAGHTMYPCFLRLIIWVTFKSVPRDSSLREPLSFLLNY PRRCFTLLFRSRPTWVLFGILFVLNFVDVLLIVVLDLHNPAVNTLPGGQRVLAAIFQAASSRHTGTSSFNLADVNPAVQFSLLVMMYISI FPIAISIRASNTYEESALGLYPSDTEMDEDHGVNYVMAHLRNQLSFDLWYIFLGIFCVCATEARRIMDPAEPAFNVFAVFFEVVSAYGN VGLSLGYPGVSTSFCGQFSVFSKLVLCAMMVRGRHRGLPVQLDRAILLPGEKLVGDDRVDARSHSDDRPTILNSFRRRYHTK
9E-118	403	0.7	6E-115	394	0.4	2	2	A0A0J9V0C4_FUSO4	Uncharacterized protein	FOXG_06683 FOXG_07247	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	638	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9V0C4|A0A0J9V0C4_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_06683 PE=4 SV=1MSLLALPILAPYGNISVTDAYFFGASASTESGLNTVDVKDLKTYQQLYIYFIPIITNLGFINIGVVIVRLYWFKKHLKRRAPQLFSPR RRDASGENVEDGKIVEEKAQNDLPAVTAPSNNLEQHATTDTPVPRTTTITFDPSIDQRRDSATLYIPGPQDRDRDRITPVPTAASGEP SSSMRRRLPRRISTGDGLQMTATRSMDRVAGIASSLLMMGSETTRPRRQSSSSVSQQQPALNDRPFLSRQATIGRNSEFQNLTSHD RELLGGIEYRSLKLLLKIVTAYFFGVHLFGAICLLGWIQTANPKYREYLQSTGQDKNWWAFYSAQTMVDNLGFTLTPDSMISFRDAKW PMILMSFLAFAGNTLYPVFLRLIIWTMSKLLPKHSSTQEPLGFLLNYPRRCYTLLFPSKPTWILFGIIFSLNFIDVLLIIILDLDNPEVASLPL DSRIPAAIFQAASARHTGTATFNLANVNPGVQLSLLVMMYIAVFPIALSIRLSNTYEEKSLGIWEPEGSLNERNGKSYLMQHIKNQLGFD LWYIFLGTFCICVAEATRIADVKDPAFTIFSILFEVTSAYGNVGLSLGYPTVSTSLCGKFGTFGKVVICLTMIRGRHRGLPYALDRAVMLP DEHLLETPADSTE
1E-117	403	5.7	3E-115	394.9	3.5	2	2	A0A0J9WVI6_FUSO4	Uncharacterized protein	FOXG_16842	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	681	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9WVI6|A0A0J9WVI6_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_16842 PE=4 SV=1MLRPPINFLTLHYAYIILMGLIALPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVVVRLFW FKRHLKRLTPQNLDNSPGIPDVDIESARHESKVPADTTENSAEVTNEPNGKAKATDDHIEEDATIANEDRRVARTMTITFDPSTEKHKE DAALYIPGPRARDRGYPIAPRSHEAARHPDDSDDDDAIKPVPNKILNNGSSSMRRRRRFSSDDGLEITVSRSMDRVAGVAASFLALGS QTAPQPRVISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREVLGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQY ADILQASGQDKTWWGIYSAQTMVDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKTSPTQESLAFLL NYPRRCYTLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVASLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISI RASNAYEEKSLGLWEEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSAYGNVGLSLGY PTVSTSLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIAEN
1E-117	403	5.8	6E-116	397.4	1.4	2	2	W7MU37_GIBM7	Uncharacterized protein	FVEG_12850	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	678	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	>tr|W7MU37|W7MU37_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_12850 PE=4 SV=1MLLPPINFLTLHYAYIILMGLIAIPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVIVRLFWF KRHLKRLAPQMLDNSTGITDVDIESTHNEPKVLADTTENSAEATDDLIEEDPTVANEDRRVARTMTITFDQSTEQHKD DDALYIPGPRARDRGYPIAPRAARHPEDSDDDDVIKPVPNRNQNDGSSSMRRRRRFSSDDGLKVTASRSMDRVAGVAASLLVLGSQ TAPQPRPISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYAD ILQASAQDKTWWGIYSAQTMYDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKTSPTQESLAFLLTYP RRCYTLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVSSLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISI RASNAYEEKSLGLWEEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSAYGNVGLSLGY PTVSTSLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIAEN
2E-117	402	6	1E-116	399.7	1.3	2	2	F9GAT2_FUSOF	Uncharacterized protein	FOXB_15764	Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	655	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	660025	>tr|F9GAT2|F9GAT2_FUSOF Uncharacterized protein OS=Fusarium oxysporum (strain Fo5176) GN=FOXB_15764 PE=4 SV=1MAAIDAWFFGASASTESGLNTIDVKALKTYQQVYIYLVPILTNLGFINIIVVIVRLFWFKKHLKRLAPQSPRDDRPSTTDVDVEGAH DLSKEVPETSGNSTAVSANTVDRPPANLNAQEQGPRTTTITFDPSTEQHKENTTLYIPGPRARQPIVARNTGDKFDHDGSDDEDRPK SISRVASNTSTIRRRHRLSREDSLQITAAKSMERVAGVAASVLVMGSQTTPPRPRSVVSTTNQQLALNEVPFLSRQATIGRNSQFHNL TERDREVLGGIEYRSLILLLKIVTAYFFGIHLFGAICLIGWIHTADPKYGKVLQEAGQGKTWWGFYSAQTMVDNLGFTLTPDSMISFRD AKWPMILMSFLAFAGNTLYPCFLRLAIWIMSKVVPKNSSTHESLSFLLDHPRRCYTLLFPSRPTWILFGIIFALNFIDILLIIILDLHNPEVSS LPLSARIPAAIFQAASARHTGTATFNLANVNPAVQLSLLIMMYIAIFPIAISIRVSNTYEEKSLGIWEQEESLNEANGKSYLLTHMKNQLGF DLWYIFLGTFCICIAESGRIADVNDPAFSVFSVLFEVTSAYGNVGLSLGYPTVSTSLSGMFGVFGKVVICFTMIRGRHRGLPYALDRSIM LPSEQALESSAQSQQDAVLGDSKTQQRS

2E-117	402	5.8	5E-116	397.5	1.4	2	2	W7NEH3_GIBM7	Uncharacterized protein	FVEG_12850	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	660	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	>tr|W7NEH3|W7NEH3_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_12850 PE=4 SV=1MGLIAIPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVIVRLFWFKRHLKRLAPQMLDNSTGITDVDIESTHNEPKVLADTTENSAEATDETNGKAKATDDLIEEDPTVANEDRRVARTMTITFDQSTEQHKDDDALYIPGPRARDRGYPIAPRAARHPEDSDDDDVIKPVPNRNQNDGSSSMRRRRRFSSDDGLKVTASRSMDRVAGVAASLLVLGSQTAPQPRPISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQSSAQDKTWWGIYSAQTMYDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKTSPTQESLAFLLTYPRRCYTLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVASLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWEEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSAYGNVGLSLGYPTVSTSLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIAEN	
3E-117	401	2.9	3E-115	394.8	0.5	2.1	2	F0U8D8_AJEC8	Potassium transporter	HCEG_00258	Ajellomyces capsulatus (strain H88) (Darling's disease fungus) (Histoplasma capsulatum)	680	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain H88) (Darling's disease fungus) (Histoplasma capsulatum)	544711	>tr|F0U8D8|F0U8D8_AJEC8 Potassium transporter OS=Ajellomyces capsulatus (strain H88) GN=HCEG_00258 PE=4 SV=1MWKPPLNFITIHYAYIVTLSISSLVVLYPYGNLKAIDAYFFGASSCTESGLNTYDVKDLKTYQQLFIYVIPIISHHAFINIAVVLVRLHWFRKRLDEIAPTQVRHRHDVEAKAYKPLENGKKYTSNDQHITDATALNVISTGEHTNETDKPQAQTAEPTGRSISFAADVRGYDKSKALYVPPPQERDRGRPMVEIDEIFSDDDEITKTNDSNVRGSLPARRKIMGSSRITSTTTLERVASSIFVLEGRPSTRQKQPPLQHSLSEHLHLPLSSHAALGPNSQFRNLTAEDRETLGGIEHRSLKLLLKIVTVYFFGLHLFGAVCLLGWILHSDPKYRKYLKECAQSPVWWAFYSSQTMISNLGFTLTPDSMISFRDAEWPMILMSFLAYVGNTFYPCFLRFIIWTMSLIVPKTSPLKEQLNFLLKHPRRCYTHLFPSGTTWALFAVLFILNFVDIILMITLDLHNPAVNDLPWGKRILASLFQAASTRHTGTASFNLANVNPAVQVSILVMMYIGIFPIALSTRASNTYEQRALGIYPQDRELDEYNGKAYILAHIKNQLTFDLWYIFLGFFCICASESKKIMDPNEPAFSVFAMLFEVTSGYGNVGLSLGYPGINTSLSGKFSVFGKLIMCAMMLRGRHRGLPSQLDRAVMLPSDRLVDGDERENTTEIRNSTKIKRHHTH	
1E-116	400	6.1	1E-115	396.6	2.4	2	2	S0EKU2_GIBF5	Probable potassium transporter TRK-1	FFUJ_11478	Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	648	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella fujikuroi (Bakanae and foot rot disease fungus) (Fusarium fujikuroi), Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	1279085	>tr|S0EKU2|S0EKU2_GIBF5 Probable potassium transporter TRK-1 OS=Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) GN=FFUJ_11478 PE=4 SV=1MPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVIVRLFWFKRYLKRLAPQALDYSPAIPDVDIESAQHESKVLADTNENSAKTTDEPNGKAKATNDCIEEDAALANEDRRVARTTAITFDPSTERHKEDDALYIPGPRARDRGYPIAPRSHEAAQHPDDSDDDDAIKPVPNETQNNGSSSMRRRRFSNDDGLKVTASRSMDRVAGVAASFLVLGSQIEPQPRPISSHSNQQPAINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQSSAQDKTWWGIYSAQTMYDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSNLVQKTSPTQESLAFLLTYPRRCYTLLFPSGPTWILFGIIFALNFTDILLIIVLDLSNPEVASLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWEEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSAYGNVGLSLGYPTVSTSLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIAEN	
1E-116	400	3.2	2E-116	398.8	0.8	1.9	1	R0KJS0_SETT2	Uncharacterized protein	SETTUDRAFT_108086	Setosphaeria turcica (strain 28A) (Northern leaf blight fungus) (Exserohilum turcicum)	673	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Setosphaeria, Setosphaeria turcica (Northern leaf blight fungus) (Exserohilum turcicum), Setosphaeria turcica (strain 28A) (Northern leaf blight fungus) (Exserohilum turcicum)	671987	>tr|R0KJS0|R0KJS0_SETT2 Uncharacterized protein OS=Setosphaeria turcica (strain 28A) GN=SETTUDRAFT_108086 PE=4 SV=1MWKPPINFITLHWAYILTVGILAFPVIYPYGNLSAIDTYYFGVSASTSSGLNPIDVKALKTYQQVWFYFTPIVTNLGFINIIVVIVRLRWFRQKLKDIPAAHIRPRSSLGKSTDPRIQVLANVADTRALESGLASEATVAEKKIEAGAEQSDASAAPRITFAPDPRHVVNEKGALRIAGPRDGDNDHTIASMSDDEDEDQIKPIAESSNPLRRAISETRSMSKATSVDRAVSSIFVLGSTPGVTSARRSEDNRSRQPSIDLKSLSREELGGVEHRALQVLLKIVVVYFFGLHLFGAICLIPWIHLAPAKYKDYLASQGQDKTWWAIYSAQTMIDNLGLTLTPDSMISFRDATWPMLIMSFLAFAGNTFYPVFLRLVIWIMWKLAPQDSSLSESLRFLLDHPRRCYTLLFPSAATWILAAILFILNFLDTLLIVILDLNNPEVNVLPGGPRVLAALFQSASSRHTGTASFNLANVNPAVQFSLLVMMYISVYPIAISIRMSESYEESSVGLYAADESLDEKNDSKTYMINRMRNQLSFDLWYIFLGVFCICTVESKRITNPNDPAFSVFSIFFEVVSAYGNVGLSLGYPTNLASLSGEYTVFGKVVICAMMLRGRHRGLPYALDRAINLPSDLVTEDEADKYKDDETESAAVSQIVHEETRLERGRRLMRSLTQ	
1E-116	400	8.5	2E-110	379.1	2.4	2.1	2	M7XWF8_RHOT1	Potassium ion transporter	RHTO_04767	Rhodosporidium toruloides (strain NP11) (Yeast) (Rhodotorula gracilis)	1049	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Pucciniomycotina, Microbotryomycetes, Sporidiobolales, Rhodosporidium, Rhodosporidium toruloides (Yeast) (Rhodotorula gracilis), Rhodosporidium toruloides (strain NP11) (Yeast) (Rhodotorula gracilis)	1130832	>tr|M7XWF8|M7XWF8_RHOT1 Potassium ion transporter OS=Rhodosporidium toruloides (strain NP11) GN=RHTO_04767 PE=4 SV=1MRRRVSLNRHPSTAPRIPGFLQRSSVWSRISAFSSAHLNFYRLHLLVFTFVPLIASGIFFASNGPSNENQISYVDALFMCTSAMTVTGLNTVVLSALTVWQQVMLFLLMTIGSTSFVSILVIVIRRQFFRNKFEYMVANDAEARKRVNEVGEQEAARAGRAYRAFDASHRPGHTPWYSDFLPGQHSAVPSPRPSPFNSAAPTRQDGEDEERQRKKKKRKVAKLRTDMIKRVDVPVRVNKMNVSGWLGDEKHEGEERMDEEVHEMKKVREAHAAEEEAPAEARGAERTQDLPEVFSDDDQDEEEVPPVQRHDGELADSPRPASPEPVERANGVAGHTRAIQIDTSSRPDRGTRGRRSSDSVAAAASRAPGAGFPRTRTFDHRHLDGITESPSPLQSPSSPTFRNRDLDVGRTRTIEFRDPSEAGDLRLRRNRMHAVDPDYPVTRRMSQSNLRDRTFIRTTTVDQAAMHSGFGGFPNPIYAAASLAKSKIPALRNAVERTSTMPRTTTMLSTHSHGGTSSGGVKHEGTGNFKPVSYITFDAVVGRNSKFHGLTTAQQEELGGVEYRALTVLLRIVFAYWLGVQLLSVLVLAPWLSTSERWAPITRESNANPTWFTFFQVWSAYSNLGMSLVDTSMIPFQRAYWLIIVQGFLILAGNTAFPVFLRLLIWTVYKVMPSRSRTRETLQFLLDHPRRCFIYLFPSHQTWFLVFMLVCLNGIDWASFLILDIGNPEIEALPTRVRVLDGLFQAFAVRAAGFSIVPLASVAPALQLLYVIMMYIAVYPIAVSIRSTNVYEEKSMGVYDDDFDEDPDLMEARFDKSHSATEYISYHARKQLAFDLWWLGLAVWLICIVERHRIGSTDWPEVTIFTLIFEIVSAYGTVGLSLGNGRNNASLAGVLSTLSKLIICAVMVRGRHRGLPIAIDRAVLLPSDLEKHGDDTATTFSFDNLAREPSLRTRWTRTSFSSHTAVAGGGLQAVEPLTDEHRFERSRRFSDDQHDVGNGELAPGSSPSDSKDSALDGKEPSLSTADDAPQGMKGEGPPIDRNQTGWV	
1E-116	400	7.6	3E-115	395.2	3.3	2	2	A0A0D2YJX6_FUSO4	Uncharacterized protein	FOXG_16842	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	663	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0D2YJX6|A0A0D2YJX6_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_16842 PE=4 SV=1MGLIALPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVVVRLFWFKRHLKRLTPQNLDNSPGIPDVDIESARHESKVPADTTENSAEVTNEPNGKAKATDDHIEEDATIANEDRRVARTMTITFDPSTEKHKEDAALYIPGPRARDRGYPIAPRSHEAARHPDDSDDDDAIKPVPNKILNNGSSSMRRRRRFSSDDGLEITVSRSMDRVAGVAASFLALGSQTAPQPRVISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREVLGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQASGQDKTWWGIYSAQTMVDNLGFTLTPDSMISFRTAKWPMILMSFLALGSQTAPQPRVISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREVLGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQASGQDKTWWGIYSAQTMVDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLGIWVMSKLVPKTSPTQESLAFLLNYPRRCYMLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVASLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWDEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSAYGNVGLSLGYPTVSTSLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIIEN	

1E-116	399	5	7E-116	397.1	1.3	2	2	M2SPW3_COCSN	Uncharacterized protein	COCSADRAFT_142759	Cochliobolus sativus (strain ND90Pr / ATCC 201652) (Common root rot and spot blotch fungus) (Bipolaris sorokiniana)	671	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Bipolaris, Cochliobolus sativus (Common root rot and spot blotch fungus) (Bipolaris sorokiniana), Cochliobolus sativus (strain ND90Pr / ATCC 201652) (Common root rot and spot blotch fungus) (Bipolaris sorokiniana)	665912	>tr|M2SPW3|M2SPW3_COCSN Uncharacterized protein OS=Cochliobolus sativus (strain ND90Pr / ATCC 201652) GN=COCSADRAFT_142759 PE=4 SV=1MWKPPINFITLHYAYILSFGILTMIIVYPYGNMKAIDAYYFGVSASTSSGLNPFDVKALKTYQQVWFYITPIITNLGFINIVVVIVRLR WFKQKLKGIPAANKRPKSSRHSVDPRIQILADVSEKRDLEGGPPAETVSETKPEVSGNQQKDETPNTAHITFAPDPRYTVNEKGTLHV AGPREGESAQPSIPMSDDEDDDQIKPVGEFNNRLRRRLSETRSISKATSIDRAVSSIFVLGSTPSGRRSEEKSRQPSIDLASLSPEELG GVEYRALRVLLKVVVAYFFGLHLFGAICLIPWIHLSPLKYKEYLASQGVDKTWWAIYSSQTMIDNLGLTLTPDSMISFRDATWPMLVMS FLAFAGNTFYPCFLRLVIWIMWKIAPNESSTKESSRFLLDHPRRCYTLLFPSTATWILTAILVFLNFVDTLLIVTLDLDNTEVNVLPAGPRI LAALFQSASSRHTGTSTFNLANVNPGVQFSLLVMMYISVYPIAISIRMSETYEDKSVGLYAADESPDDNTDSKTYLINHLRNQLSFDLW YIFMGVFCICCSESKRIMSHEDWAFSVFSIFFEVVSAYGNVGLSLGYPTNLASLSGQFSVFGKLVICAMMLRGRHRGLPYGLDRAINLP NDLVTKDEQERYKDFDTQGTITSDGMERKEEGKFKKGKRLMKSLTQ
2E-116	399	6.9	2E-116	399.1	4.8	1.6	1	B2W9V0_PYRTR	Potassium transport protein 1	PTRG_06758	Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis)	693	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Pyrenophora, Pyrenophora tritici-repentis, Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis)	426418	>tr|B2W9V0|B2W9V0_PYRTR Potassium transport protein 1 OS=Pyrenophora tritici-repentis (strain Pt-1C-BFP) GN=PTRG_06758 PE=4 SV=1MWKPPINFITLHYAYILSFGVLAMAIMYPYGNLSAIDTYYFGVSCSTESGLNPLLLVLRSVDLKALKTYQQIFLYIVPIITNLGFINILV VVVRLRWFSQKLKGITAAHRRPVSRNETSEQQGQIAANISETRDIEGGLTGETVSEKRPVVQTESSQEGAKDESKDEANLPHIKFAPD PRLRANEKGALYIPGPRERDNGEPITMTSDDEDEDQIKPIADSSYAMRRTKSNTRSMRSTRSMSKATSVDRVVSSMFVLGSTSSATR SESKPRREPLDLSSLTPEELGGVEYRALRVLLKITIGYFFGLHIFGVICLLPWIHLAPSKYQDLLASHGVDKTWWAFYSAQTMVNNLGL TLTPDSMISFRDTVWPMIVMSFLAFAGNTFYPCFLRLLIWTINKLSPSGSSLQESTRFLLDHPRRCYTLLFPSTATWILATILIILNFIDTLL IIVLDLDNSEVNVLAVGHRILAAIFQSASSRHTGTSTFNLANVNPAVQFSLLVMMYISVYPIAISIRMSESYEEKPVGLYAAEESLDEDKG SKTYLINHMRNQLSFDLWYIFLGVFCICIGESKRIMNNADPAFSVFAVFFEVVSAYGNVGLSLGYPTNATSLSGHFNVFGKVVICFMML RGRHRGLPYALDRAINLPSDIVGGDDEQEKYRDKEDEDVTSVAEARPVGAEPKFARGRKMMRALTQ
2E-116	399	2.9	2E-114	392.2	0.5	2.1	2	C0NV51_AJECG	Potassium transporter	HCBG_06815	Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus) (Histoplasma capsulatum)	680	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus) (Histoplasma capsulatum)	447093	>tr|C0NV51|C0NV51_AJECG Potassium transporter OS=Ajellomyces capsulatus (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) GN=HCBG_06815 PE=4 SV=1MWKPPLNFITIHYAYIVTLSISSLVVLYPYGNLKAIDAYFFGASSCTESGLNTYDVKDLKTYQQLFIYVIPIISHHAFINIAVVLVRLH WFRKRLDEIAPTQVRHRHDVEAKAYKPLENGKKYTSNDQHITDATALNVISTGEHTNETDKPQAQTAEPTGRSISFAADVRGYDKSK ALYVPPPQERDRGRPMVEIDEIFSDDDEITKTNDSNVRGSLPARRKIMGSSRITSTTTLERVASSIFVLEGRPSTRQKQPPLQHSLSEH LHLPLSSHAALGPNSQFRNLTAEDRETLGGIEYRSLKLLLKIVTAYFFGLHLFGAVCLLGWILHSDPKYRKYLKECAQSPVWWAFYSS QTMISNLGFTLTPDSMISFRDAEWPMILMSFLAYVGNTFYPCFLRFIIWTMSLIVPKTSPLKEQLNFLLKHPRRCYTHLFPSGTTWALFA VLFILNFVDIILMITLDLHNPAVNDLPWGKRILASLFQAASTRHTGTASFNLANVNPAVQVSILVMMYIGIFPIALSTRASNTYEQRALGIY PHDRELDEYNGKTYILAHIKNQLTFDLWYIFLGFFCICASESKKIMDPNEPAFSVFAMLFEVTSGYGNVGLSLGYPGINTSLSGKFSVFS KLIMCAMMLRGRHRGLPSQLDRAVMLPGDRLVDGDERENTTEIRNSTKIKRHHTH
2E-116	399	3.1	1E-113	389.9	2.5	2.1	2	K3VZY8_FUSPC	Uncharacterized protein	FPSE_06649	Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	654	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Fusarium pseudograminearum (Wheat and barley crown-rot fungus), Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	1028729	>tr|K3VZY8|K3VZY8_FUSPC Uncharacterized protein OS=Fusarium pseudograminearum (strain CS3096) GN=FPSE_06649 PE=4 SV=1MYRPPINFLTLHYAYIIFMGLMALPILYPYGNMAAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIIVVIVRLHW FKRHLRRLAPQMLDGEQNNDVEDAYNESNLKTDTTGKSTTDGPSIATGTPNETTDPNDKQPNRERFATRTTTISFDVSTEAHTGNTA LYIPGPRARDRDRIKPVNSATSNNASSSMRRRRLSNDGLQITASKSIDRVANVAASLLLLGSETAPRPRSVNSTSIQQPALNDIPQLSR QATIGRNSHFKNLTEHDREVLGGIEYRTLKLLLKIVTCYFFGLHLFGAICLVGWIHTADSKYTDILAAAAQDKTWGFYSAQSMMDNLGF TLTPDSMISFRDAKWPMILMSFLAFAGNTLYPVFLRLTIWIMSKITPKTSPTQESLTFLLNHPRRCYTLLFPSGPTWILFSIIFALNFIDILLI ILLDLKNAEVASLPLSARIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWDHEESLNEQNGK SYLLTHMKNQLGFDLWYIFLGTFCICIAEQTRIADVKDPAFSVFSILFEVTSAYGNVGLSLGYPTVSFSLCGKFGVFGKVVICFMMIRGR HRGLPYALDRAIMLPSSQSPEKSR
2E-116	399	3.3	1E-114	393.2	0.5	2.1	2	A0A0J9UYU9_FUSO4	Uncharacterized protein	FOXG_06577	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	728	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9UYU9|A0A0J9UYU9_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_06577 PE=4 SV=1MGKPFINFFTLHYVYILAAGLVAFTVIAPYGNIDVIDALFFGISACTESGLNPVDVKDLKTYQQLVIYIIPTISHMAVINIVVVVVRLH WFERRLEQVAPHLIRSKARSAQIKNPSVPATHDCLHIGQLGSTTADPSLPSRSSTTEPRESLRDDQCDDLVPEQHADVEQGRRIAFSH TLPDHRTDATTIYAPPLRGRHRKRSFSRTRQSRPESTGHLENDTALMSIPHDTLSATRVGTREETNSRSAARMTTRASPDSRPRVRD HFGLEHTASIERVTSSVFVLGQTRSRSRGLNRGRRDASRPRAPYTHVSDLPQLSSRVTIGRNSQFHGLTVEERETLGGMEYRSLKLL FWISMGYFLALHILGVICLIPWIQHAPAKYTDYLDEVGQNKIWWAFYSAQTMANNLGFTLTPDSMAHFRDATFPMIIMTFLAYAGYNFY PIFLRLIIWTFYKLVPKNSALRGPLAFLLEHPRRCCMLLFPSRPTWILLGILLFINFFDVLLLIVLDLDNPSVTELPLARRILAAIFQAASSRH TGTSTFDLSKLNPAAQFSLLVMMYISVYPIALTIRASNTYEERSLGTYAPEQVNPDESTGRKYLVSHMRNQLSFDLWYIFLGIFLICIAES EKIMDTSQPEFSVFPVFFEVTSAYCNVGLSLGHPAVQTSFSGTFSVYGKLVICAMMIRGRHRGLPYEIDRAIELPSERLVDDEDERGP SRRPLLLSDAGSQAG
3E-116	398	2	3E-116	398.1	1.4	1	1	W7MU41_GIBM7	Uncharacterized protein	FVEG_12850	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	577	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	>tr|W7MU41|W7MU41_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_12850 PE=4 SV=1MLDNSTGITDVDIESTHNEPKVLADTTENSAEATDETNGKAKATDDLIEEDPTVANEDRRVARTMTITFDQSTEQHKDDDALYIP GPRARDRGYPIAPRAARHPEDSDDDDVIKPVPNRNQNDGSSSMRRRRRFSSDDGLKVTASRSMDRVAGVAASLLVLGSQTAPQPR PISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQASA QDKTWWGIYSAQTMYDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKTSPTQESLAFLLTYPRRCYT LLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVSSLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNA YEEKSLGLWEEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSAYGNVGLSLGYPTVST SLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIAEN

3E-116	398	3.5	7E-114	390.4	2.4	2.1	2	A0A098DJT0_GIBZA	Fusarium graminearum chromosome 2, complete genome (Uncharacterized protein)	FG03834.1 FGRRES_03834	Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	654	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	5518	>tr|A0A098DJT0|A0A098DJT0_GIBZA Fusarium graminearum chromosome 2, complete genome OS=Gibberella zeae GN=FG03834.1 PE=4 SV=1MYRPPINFLTLHYAYIIFMGLMALPILYPYGNMAAIDAWFFGASSSTESGLNTIDVKELKTYQQLYIYFIPILTNLGFINIIVVIVRLHW FKRHLKRLAPQMLDGEQNNDIEDTYNESNLKTDTTWKSTSDGPSLATETPNETIDPSDKQPNRERLAARTTTISFDVSTDAHTGNTSL YIPGPRARERDRIKPVNSVMSNNASSSIRRRRLSNDGLPITASKSIDRVANVAASLLLLGSETTPRPRSVNSTSIQQPALNDIPQLSRQA TIGRNSHFKNLTEHDREVLGGIEYRTLKLLLKIVTCYFFGLHLFGAICLVGWIHTADSKYTDVLAAAAQDKTWGFYSSQSMLNNLGFTL TPDSMISFRDAKWPMILMSFLAFAGNTLYPVFLRLTIWIMSKITPKTSPTQESLTFLLNHPRRCYTLLFPSGPTWILFSIIFALNFIDILLIIL LDLKNDEVASLPLSARVPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWDEEESLNEQNGKS YLLTHMKNQLGFDLWYIFLGTFCICIAEQTRIADVKDPAFSVFSILFEVTSAYGNVGLSLGYPTVSFSLCGMFGIFGKVVICFMMIRGRH RGLPYALDRAIMLPSSQSPEKSR
4E-116	398	9.6	1E-111	383.1	0.3	2.1	2	K1VPX2_TRIAC	Uncharacterized protein	A1Q2_03057	Trichosporon asahii var. asahii (strain CBS 8904) (Yeast)	1048	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Tremellomycetes, Tremellales (jelly fungi), Tremellales incertae sedis, Trichosporon, Trichosporon asahii, Trichosporon asahii var. asahii, Trichosporon asahii var. asahii (strain CBS 8904) (Yeast)	1220162	>tr|K1VPX2|K1VPX2_TRIAC Uncharacterized protein OS=Trichosporon asahii var. asahii (strain CBS 8904) GN=A1Q2_03057 PE=4 SV=1MPTLPRYLKKPSWWEQSMAVFFASLNFYRVHMMCFTFIPLIFSGIFYACNTEFHIKYVDCLFLCVSSMCVTGLATVDLSSLSTFQ QFLMYFQMLIGSLIFVSIIMLSVRKRFFRLKFKHVMEEQRSKRRFDLAKTFTNFPTTTGQMTSALRRRFTRHHDDTEEENHSVPPTPA DTIREKDHAKPKKKGPIKLTTDMIRRVDGGGVGMVNPMGWYDANTPTPGNQTPETNRSVSPPPMSRASSDGREPSQTGSISDPQTL RNDSDHSDKGKEEYRSSSEGKKTERPSDDLQTAPSLLKNFGEELRTAPTRTEDSIDSEPSRPPPSPRHKHVPVAYKPTPAEDDAFPR SKTIAFDEPEDGMDHELHFSNTRDPWGTGPSNFPRSATIRSDNSRFPRSGTTGSGFPRTSSLSRTGSRLVDSKMTGFGGFPTPLEIA SDLFHKVFPKAHSKVKRTITMPRTETISGHQSNQEGRDVPYISFAATVGRNSNFQDLTEEQREELGGAEYRALKILWWIVSVYWVFM PLAGATIIAPYIAAGNRYDWVFNEQHKHVRIPWFAFFQSTSSFSNTGMSLVDQSMVPFQKAYLMAAVQALLILFGNTCFPILLRFIIWSI YKLAPTGSHVREPLKFLLDHPRRCFVYLFPSTHTWFLLLVVLTLTIIDWVSFMVLDIGTPDIEALPVGTRIAAGLFQSVAVRAAGFGIVP MNSLAPSVKVLYIIMMYISVYPIAMSVRATNVYEERSLGLFDDDDSDEEDEEEHEASETRGAHAVAKYVGWHARRQLAFDMWWIALA LWLVCIIERNNLNRTDNAEWFNTFNVIFELVSAYGTVGLSLGAGSNNYSLSGELRTLSKLVIIVVMIRGRHRGLPVAIDRAVMLPRDFQE EDERQLESRLRRSRSRMTSTFGDRDQVLSQTGSGFPRTFTMQSTPATNIVPPSPMIARRDSSVGNPSSPGMAPQHVRSFSNTSDTP SPMSPQSPGLHFALQNPPRHIRSHSHSSNTASSPPISGANPNSLNINGLDTVEETGLSRLPTLTLSTSNIPRSSSPDGDAPPLTA
5E-116	398	4.6	1E-114	393.3	1.2	2.1	2	A2Q9W1_ASPNC	Aspergillus niger contig An01c0310, genomic contig	An01g09300	Aspergillus niger (strain CBS 513.88 / FGSC A1513)	709	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain CBS 513.88 / FGSC A1513)	425011	>tr|A2Q9W1|A2Q9W1_ASPNC Aspergillus niger contig An01c0310, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=An01g09300 PE=4 SV=1MWKLQANFITLHYAYILFLGLLGLVVLYPYGNLRAIDAYFFGVSSSTESGLNTVDVKDMKLYQQLFIYFVPIVSNLGFINILVVVVRL LWFEKRLKEIAPGVLDRKSNPSSSNAARYDPEAHPRALSEPSTSENGPVDSTEKKEVDDGQRLVGSRIGHVVPESIANRDIGQEALA MYDLKTTARIHTLLVYRGVSPLRTLPRRSTFLHRENATEEVIEEDDEDAETERRNSENTDELSENGRSATGGLPFERVASSLFVIGKQP SRAREPSLRPAISLSKDANLPELSVQATLGRNSQFHNLTAADRERLGGIEYRSLRLLLKIVIGYFVGFHVFGVVCLVPWILHSNRKYRD YLHECGQNEVWWAIYSAQTMTSNLGLTLTPDSMISFNDAVFPMLVMSFLAYAGNTLYPCCLRLIIWAMSKCTPESSSLKEPLEFLLKY PRRCYLLLFRSKPTWILFGIIFVLNFVDVLLILVLDLDNPAVNDLAPGPRVAAAIFQSASSRHTGTASFNLADVNPAVQFSLLVMMYISVF PIAISVRASNIYEERSIGVFSSETDMDEADGKRYVLMHMRNQLSFDLWYIFLGIMCICIAESGKIMDPTKPAFSVFAIFFEVVSAYGNVG LSLGYPTASTSFSAQFDIFSKIVICAMMIRGRHRGLPYQLDRAILIPNNRLVEDDKVETRPSISLPRIRSMDPTDSRYMKMKKAHTR
5E-116	398	31.9	3E-114	391.6	15.8	3	2	L0PH96_PNEJ8	I WGS project CAKM00000000 data, strain SE8, contig 275	PNEJI1_000744	Pneumocystis jiroveci (strain SE8) (Pneumocystis pneumonia agent)	745	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, Taphrinomycotina, Pneumocystidomycetes, Pneumocystidales, Pneumocystidaceae, Pneumocystis, Pneumocystis jiroveci (Pneumocystis pneumonia agent), Pneumocystis jiroveci (strain SE8) (Pneumocystis pneumonia agent)	1209962	>tr|L0PH96|L0PH96_PNEJ8 WGS project CAKM00000000 data, strain SE8, contig 275 OS=Pneumocystis jiroveci (strain SE8) GN=PNEJI1_000744 PE=4 SV=1MGGTIEKLKTIQILLPKVSIYIAVMILIGTFLIYLQSNIQYIDAFFLATSAATQAGLVTLDINTLSVYQQVVLYIIPMLTTPIFIHSLTAIVR LFLIRIQQARTQSLRKNQCLNNVFMSYSEIEERGVGDRPIHVLLRRESVIENETQSMPFCKIGTSFGNIVSPIRMNELERRNDVDSKRG GPLNSAGMDSSFNANRQHNKDENFVTEFQKYECVSLQQERHGNSDIRFGDLPVPVRSSIDGPKDDELYIVPDRFEQENQFNNKLQK SKSVEPQSVSIINEGLTNITRLSTYDNNNYYLRMRKSITIDRSISKVSTFDRYISNAFWKKRDSSPFSQRTNKSFPYLSYQPTIGRNSAF VTLTKEQRDELGGYYVLIHVFAAICFLLFSVFAKSYKEAIIDSLASPSWWAFFTSASLFNDFGMTLNATSMVKYRQSNFVLILGSFLIIAG NTAFPILLRFFIWIITFTLPKNSLHREVDIILISLHFLLDHPRRCFTLLFPSRVTFWLFALLIILNIADTLIFIALDFNNPSLEEIGPTHLKVLNCL FQSIATRTAGFTVVSLSTLHTAVLVSYMFMMYISVFPVAVSIRKTNVYEERSLGIYSNDDDSQNASFVGTHIRQQLSFDLWYIFLGLFIC IVENKKIKDESIPSFNVFSVLFEIISAYCTVGLSFGSPDINSSFSSKFSIIGKLVIISLQIRGRHRGLPYTLDRAVILPTEKMGRVEEEDYQR KTKVPVINNDNLYHS
1E-115	397	4.8	1E-115	396.4	3.3	1	1	A0A0J9W8N3_FUSO4	Uncharacterized protein	FOXG_16842	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	516	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9W8N3|A0A0J9W8N3_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_16842 PE=4 SV=1MTITFDPSTEKHKEDAALYIPGPRARDRGYPIAPRSHEAARHPDDSDDDDAIKPVPNKILNNGSSSMRRRRRFSSDDGLEITVSR SMDRVAGVAASFLALGSQTAPQPRVISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREVLGGIEYRSLKLLLKIVVVYFFGLHI FGAVCLVGWIHTADKQYADILQASGQDKTWWGIYSAQTMVDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLGIWVM SKLVPKTSPTQESLAFLLNYPRRCYMLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVASLPLSQRIPAAIFQAASARHTGTASFNLAN VSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWDEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAF SVFSVLFEVTSAYGNVGLSLGYPTVSTSLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIIEN

2E-115	396	4.6	6E-113	387.4	2.8	2	2	N1RU99_FUSC4	Low-affinity potassium transport protein	FOC4_g10003209	Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	678	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. cubense, Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	1229665	>tr|N1RU99|N1RU99_FUSC4 Low-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 4) GN=FOC4_g10003209 PE=4 SV=1MLRPPINFLTLHYAYIILMGLIALPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVVVRLFW FKRHLKRLTPQNLGNSPGIPDVDIESARHESKVPADTTENSDEVTNEPNGKAKATDDRIEENATIANEDRRVARTMTITFDPSTEKHKE DAALYIPGPRARDRGYPIAPRSHEAARHPDDSDDDDAIKPVPNEIQNNGSSSMRRRRRFSSDDGLKFTDSRSMDRVAGVAASFLVLG SQTAPQPRAISSDSNRQPVINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQY ADILQSSGQDKTWWGIYSAQTMVDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLGIWVMSKLVPKTSPTQEFLLNYP RRCYTLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVASLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISI RASNAYEEKSLGLWDEEKPLDEKHSKTYLLTHMKNQLGFDLWYIFFGTFCICISESTRIADVNEPAFSVFSVLFEVTSAYGNVGLSLGY PTVSTSLSGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQITKN
3E-115	395	0.7	4E-115	394.6	0.5	1.1	1	Q4WQP5_ASPFU	Potassium uptake transporter, putative	AFUA_4G13540	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	522	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Neosartorya fumigata (Aspergillus fumigatus), Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	330879	>tr|Q4WQP5|Q4WQP5_ASPFU Potassium uptake transporter, putative OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=AFUA_4G13540 PE=4 SV=1MQKRRHPRSMPIVPQKPKQRICTQVLYMIISRSSINVNTNTLSTSDHFAHVDDDHQTDIARHRTLVSGIPLERVASSMFVLGSYP SRSQERQTRRITSLARDPELPQLSSQASLGRNSKFYNLTPEDREALGGIEYRSLRLLLKITLGYFVGLHVFGVICLVPWIQYADPKYRD YLKECGQGNVWWALYTSQTMVDNLGFTLTPDSMISFRDAAFPMFIMSFLAYAGHTMYPCFLRLVIWIMFKCSPKHSSNREPLSFLLN YPRRCYTLLFRSRPTWVLFGILFVLNFVDVLLIVLLDLHNPAVNTLSGKHRILAAIFQAASARHTGTSSFNLAEVNPAVQFSLLVMMYISI FPIAISIRASNTYEERALGLYPSNEDELDENNGINYVTTHMRNQLSFDLWYIFIGIFCICATEARRIMDPSEPGFSVFAIFFEVVSAYGNV GLSLGYPNVTTSFCGQFSVFSKIVICAMMIRGRHRGLPVQLDRAILLPGERIAGDDGLDESFAARQSQTLNSFRRYHTK
5E-115	394	2.8	2E-114	392.6	1.3	1.8	1	M2ULC2_COCH5	Uncharacterized protein	COCHEDRAFT_1205887	Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis), Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis)	648	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Bipolaris, Cochliobolus heterostrophus (Southern corn leaf blight fungus) (Bipolaris maydis), Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis)	701091	>tr|M2ULC2|M2ULC2_COCH5 Uncharacterized protein OS=Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) GN=COCHEDRAFT_1205887 PE=4 SV=1MWKPPINFITLHYAYILSFGILAMIIVYPYGNMRAIDAYYFGVSASTSSGLNPFDLKALKTYHKNLKEFIHIAAAHKRPKSSRHSVDP RIQVLADVSEKRDLEGGPPAGSVSKMKPEVSGNQQKDETPNNNHITFAPDPRYTVNEKGTLHVAGPREGESAQPSVPMSDDEDDD QIKPVGEFNNRLRRRLSETRSISKATSIDRAVSSIFVLGSTPSGRRSEEKSRQPSIDLTSLSPEELGGVEYRALRVLLKVVVGYFFGLQL FGVICLIPWIHLAPLKYKEYLASQGVDKTWWAIYSSQTMINNLGLALTPDSMISFRDATWPMLIMSFLAFAGNTFYPCFLRLVIWIIWKI SPNDSSTKESSRFLLDHPRRCYTLLFPSTATWILAAILIFLNFVDTLLIVTLDLDNTEVNVLPAGPRILAALFQSASSRHTGTATFNLANVN PGVQFSLLVMMYISVYPIAIGIRMSESYEDKSVGLYAADESPDDNTDSKTYLLNHLRNQLSFDLWYIFMGVFCICCSESKRIMSREDWA FSVFSIFFEVVSAYGNVGLSLGYPTNLASLSGQFSVFGKLVICAMMLRGRHRGLPYALDRAINLPNDLVTEDEQERYRDFDTQGTITN DGTDRKEEEKFEKGKRLMKSLTQQFN
6E-115	394	0.7	7E-115	393.8	0.5	1	1	A0A0J9V0V5_FUSO4	Uncharacterized protein	FOXG_06577	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	639	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9V0V5|A0A0J9V0V5_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_06577 PE=4 SV=1MVDDADARIAPHLIRSKARSAQIKNPSVPATHDCLHIGQLGSTTADPSLPSRSSTTEPRESLRDDQCDDLVPEQHADVEQGRRI AFSHTLPDHRTDATTIYAPPLRGRHRKRSFSRTRQSRPESTGHLENDTALMSIPHDTLSATRVGTREETNSRSAARMTTRASPDSRP RVRDHFGLEHTASIERVTSSVFVLGQTRSRSRGLNRGRRDASRPRAPYTHVSDLPQLSSRVTIGRNSQFHGLTVEERETLGGMEYR SLKLLFWISMGYFLALHILGVICLIPWIQHAPAKYTDYLDEVGQNKIWWAFYSAQTMANNLGFTLTPDSMAHFRDATFPMIIMTFLAYA GYNFYPIFLRLIIWTFYKLVPKNSALRGPLAFLLEHPRRCCMLLFPSRPTWILLGILLFINFFDVLLLIVLDLDNPSVTELPLARRILAAIFQA ASSRHTGTSTFDLSKLNPAAQFSLLVMMYISVYPIALTIRASNTYEERSLGTYAPEQVNPDESTGRKYLVSHMRNQLSFDLWYIFLGIF LICIAESEKIMDTSQPEFSVFPVFFEVTSAYCNVGLSLGHPAVQTSFSGTFSVYGKLVICAMMIRGRHRGLPYEIDRAIELPSERLVDDE DERGPSRRPLLLSDAGSQAG
1E-114	393	5	1E-114	392.7	0.5	2	2	J3P4U0_GAGT3	Uncharacterized protein	GGTG_08526 GGTG_08526	Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	702	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Gaeumannomyces, Gaeumannomyces graminis, Gaeumannomyces graminis var. tritici, Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	644352	>tr|J3P4U0|J3P4U0_GAGT3 Uncharacterized protein OS=Gaeumannomyces graminis var. tritici (strain R3-111a-1) GN=GGTG_08526 PE=4 SV=1MWRPSVNFISLHYLWILFCSFLAFPILSPYGNLAAVDVFFFGCSSSTESGLNTIDVKELKTYQQLFIYVIPIITNLCFVNVMVVVIRL YWFQKRMKTLKPVPPSASVDDTEAQAGETKAMVTSPDSDALPLVRSNHFVQPIANKDAAVGGEGIKLEPEPEPEPEPVPSQRVTSIK FDADTALPRRISTEDAVALRIPGPRERDSGHPIVKVATDGRSSASQLDEDQESIKPTSHASSAGPSRRRTFHTARRLSLTHSIEKTASS LLVLGPTPTIDRPRPPSSLSTRPRVADLPQLSRQVTVGRNSNFYNLTERDREVLGGIEYRSLKLLLKIVSSYFIGLHLFGIICLLPWIHANA GSKYTDWLDQNGLDWSWWAIYSAQTMTDNLGFTLTPDSMVSFKDATWPILVMTFLAFAGNTCYPIFLRLIIFTMSKLVPKKSATKGH LQFLLDHPRRCYTLLFPSKPTWVLFGILVALNFVDVLLMIVLDLKNPAVTDLPIGPRILSALFQAASARHTGTATFNLSLVNPAVQFSLIC MMYIAVFPIAISIRASNTDENHALGIYSGESNLNELSGVDYVTAHIRNQLSFDLWYIFLGTFCICIAESERIMDPKDPAFSVFPVFFEVVSA YGNVGLSLGHPTVNTSLCGQFTPFSKVVICAMMIRGRHRGLPNSIDRAIMLPGEDRPGEAPLSQYGGHSGRPAAKDQ
1E-114	393	1.8	1E-114	392.9	1.2	1.9	1	B8NBH0_ASPFN	Ankyrin repeat-containing protein, putative	AFLA_045450	Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	787	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus flavus, Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	332952	>tr|B8NBH0|B8NBH0_ASPFN Ankyrin repeat-containing protein, putative OS=Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167) GN=AFLA_045450 PE=4 SV=1MPPYPEPQADSSPLRLHHHYFYIIIWALVASIILYIPGGLSFVDALLLASGAATQTGLNPIDLKDLHISQQITLWLVPMVTNVVFLHT LLVLIRIYWFRKRFKSAIREAKAVCHSQRQRMNQALDYEARRPIGLNRTITDTTDTTTTAFDSSDRDDEEQPLLGSTDDEISPGASPKT QVGDQSPVGYQTFKPAAIGPSSPRITFYESDRDYEARQKRRSSFSRRRSFSEAVNEAFPRTDSPNTPVLPSLMWQHSIASYSDWDE DQKEELGGIEYRALKTLMVILVGYFLAFHLLGIILFIPWIMMDSKYGGMVKDMGLNRPWWAVFTAGSAFHDLGYTLSPDSMASFRNAA FPLLVMTFLVVIGNTGFPCMLRLIIWLISKFTTYGSPLDDEVHYLLEHPRRCFTMLFPGSETWRLAGVLLLLNALDLFVFYTLQEVSSTF NPFSPGLRLVDGLFQIASTRTAGFSITSLGTLHPAVQVSFVVMMYISAFPIAIAIRKTNVYEEKSLGIYDDEDKPNPHGLAAHIQRQLGFD LWYVMLGFFLISVTEGKRIQQTHGRDFAFSLFPLLFEIVSAYGTVGLSLGYPKTETSLSAQFNPMSKLIIIAMQVRGRHRGLPHALDHAI LLPCDFIDRIIDCTPLLIATFQGHEHVARLLLDNGADIECKDEEDYTPLIWAAIQGHKGLVSLLLERGADMNCEDEDSNTPLIHAAKNGDK VVVKLLLEKGPPDLERKNWHRMTALACADANEHQDVVSLLLEYGAKREQLPPPDLSVILSYYSASYTNEDDENV

2E-114	393	1.4	2E-114	392.6	1	1.4	1	C8VFW2_EMENI	Potassium ion transporter (Eurofung)	ANIA_05636	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	673	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Emericella nidulans (Aspergillus nidulans), Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	227321	>tr|C8VFW2|C8VFW2_EMENI Potassium ion transporter (Eurofung) OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) GN=ANIA_05636 PE=4 SV=1MWKISINFILLHWLAVFYPYGNVSAIDSYFFGVSSSTESGLNPYANLGLYIWVVDLKDLKTYQQLFLYFIPIVSNLGFINILIVVIRLHWFEKRLKEIAPSVLRQRPEVSAIKTTQFDQEAQSVSNAEPTKPAGNQGVQENKASEKVRETSIQAGASTKGSLEESQPAVSFSYTSKALYIPPPRDRDRGCPIIEIDHTPNKDDSANDTDIAVGDVRARRRLSDASIHQVGVLTFAQTSRKHRDTGTAVSLSKDMSLPGLSSQATLGRNSQFLNLTTRDREHLGGVEYRSLRLLLKIAIGYFLGIHLIGAVCLAAWIQNADMKYRNYLDECALNPVWWAFYSAQTMSNNLGLTLTPDSMVSFQEATFPLFVMSFLAYAGNTLYPCFLRLVIWTMFKLVPGESSLREPLNFLLKYPRRCYVLLFRSRPTWALAGIIFILNFVDILLILLDLDNPAVNSVPAGPRVIAAIFQAASARHTGTASFSLADVNPAVQFSLLVMMYIAVYPIAITVRASNTYEEKSLGIYSPEPETDENGKGYILTHMRNQLSFDLWYIFLGIFCICVAESKRIMNPAEPGFSVFAIFFEAVSAYGNVGLSLGYAGVSTSFSAQFSTFSKLVVCALMIRGRHRGMPSQLDRAVLLPSDRLVEDDSVTMYSSKGLWLEPRSLKVRRYHTR
3E-114	392	2	9E-114	390	0.2	2	1	Q2TZT0_ASPOR	Na+/K+ transporter	AO090011000734	Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	666	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus oryzae (Yellow koji mold), Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	510516	>tr|Q2TZT0|Q2TZT0_ASPOR Na+/K+ transporter OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=AO090011000734 PE=4 SV=1MPPYPEPQADSSPLRLHHHYFYIIIWALVASIILYIPGGLSFVDALLLASGAATQTGLNPIDLKDLHISQQITLWLVPMVTNVVFLHTLLVLIRIYWFRKRFKSAIREAKAVCHSQRQRMNQALDYEARRPIGLNRTITDTTDTTTTAFDSSDRDDEEQPLLGSTDDEISPGASPRTQVGDQSPVGYQTFKPAAIGPSSPRITFYESDRDLEARQKRRSSFSRRRSFSEAVNEAFPRTDSPNTPVLPSLMWQHSIASYSDWDEDQKEELGGIEYRALKTLMVILVGYFLAFHLLGIILFIPWIMTDSKYGGMVKDMGLNRPWWAVFTAGSAFHDLGYTLSPDSMASFRNAAFPLLVMTFLVVIGNTGFPCMLRLIIWLISKFTTYGSPLDEELHYLLEHPRRCFTMLFPGSETWRLAGVLLLLNALDLFVFYTLQENPQSNPFSPGLRLVDGLFQIASTRTAGFSITSLGTLHPAVQVSFVVMMYISAFPIAIAIRKTNVYEEKSLGIYDDEDKPNPHGLAAHIQRQLGFDLWYVMLGFFLISVTEGKRIQQTHGRDFAFSLFPLLFEIVSAYGTVGLSLGYPKTETSLSAQFNPMSKLIIIAMQVRGRHRGLPHALDHAILLPCDVHQDQHGEWWWKRWLKRKSSNISNFFSHGDANEDIERLAL
5E-114	391	0.7	5E-114	391.1	0.5	3.1	2	A0A0J9WN28_FUSO4	Uncharacterized protein	FOXG_19345 FOXG_19711	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	1444	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9WN28|A0A0J9WN28_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_19345 PE=4 SV=1MGPLYPERNQRIAAWAHAAAVASDPPAPTNPEARNLHDQENAQRIELQDLHCEGKQTYSSLVLLWLAWQSTGVVYGYIGTSPLYVFSSTFAQQPTWHDLVGALSIIIWSLTIIVTIKYCFIVLSANDGGQGGTFAVYTLLARHASIVRTDPNGPRSLIDGLDRRTDTELSRAGRCLRNFIETSRGAKIGLKLIGIMGVSMTLADSVLAPAQSVLGAVQGIQVVSPELGRPAIVGVTCSILILLFLLQPLGTSKIGTFFAPIVLIWLLFNLGVGIYNLIEYDHTVLKAFSPYFAFAYLYGSSGWKSLSGLLLAITGVESLFAALGAFGKRAIQLSWLLIAYPSLLLAYAGQAAYISFDETGIAFTNPFFYTVPRPTLYFSVVIAVLAAIVASQAMITSSFQLISQLIRLSYFPHIKIIYTSRRFRGHVYMPFANWLLMIGTVVVTAIYNNTTSLGYAYGTCAITVCFLTTCMVSLVALIIWRVHLLVVLLIFLVFILLDGVYLSAALSKVPQGAWLALVLSFLLSALLSLWRWGKEQQWAAECQDRITPPERPISQNSSHNTSRASSRDIRDNSSACQLAYDNILFAPGLGIFFDKVGGPSDHIPEVFTHFVHKFRTRPQVVIFFHMRSLSQPTIPADQRFVIARVNSNIPSCYHIVLRHGYMDDVLTSNLTRIVIGELMVFIMRDSFEPSEDELPSDIRQELESLRAAEDTQTVYLIGKQILRVQKKDDVYILAAGLVAFTVIAPYGNIDVIDALFFGISACTESGLNPVDVKDLKTYQQLVIYIIPTISHMAVINIVVVVVRLHWFERRLEQVAPHLIRSKARSAQIKNPSVPATHDCLHIGQLGSTTADPSLPSRSSTTEPRESLRDDQCDDLVPEQHADVEQGRRIAFSHTLPDHRTDATTIYAPPLRGRHRKRSFSRTRQSRPESTGHLENDTALMSIPHDTLSATRVGTREETNSRSAARMTTRASPDSRPRVRDHFGLEHTASIERVTSSVFVLGQTRSRSRGLNRGRRDASRPRAPYTHVSDLPQLSSRVTIGRNSQFHGLTVEERETLGGMEYRSLKLLFWISMGYFLALHILGVICLIPWIQHAPAKYTDYLDEVGQNKIWWAFYSAQTMANNLGFTLTPDSMAHFRDATFPMIIMTFLAYAGYNFYPIFLRLIIWTFYKLVPKNSALRGPLAFLLEHPRRCCMLLFPSRPTWILLGILLFINFFDVLLLIVLDLDNPSVTELPLARRILAAIFQAAASSRHTGTSTFDLSKLNPAAQFSLLVMMYISVYPIALTIRASNTYEERSLGTYAPEQVNPDESTGRKYLVSHMRNQLSFDLWYIFLGIFLICIAESEKIMDTPKPAFSVFAISFEVVSAYGNVGLSLGYPTASTSFSAQFDIFSKIVICAMMIRGRHRGLPYQLDRAILIPNNRLVEDDKVETRPSISLPRIRSMDPTDSRYMKMKKAHTR
6E-114	391	2.6	2E-112	385.9	0.5	2	2	G7X5Z9_ASPKW	Cation transporter	AKAW_00121	Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	714	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus kawachii (White koji mold) (Aspergillus awamori var. kawachi), Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	1033177	>tr|G7X5Z9|G7X5Z9_ASPKW Cation transporter OS=Aspergillus kawachii (strain NBRC 4308) GN=AKAW_00121 PE=4 SV=1MWKLQANFITLHYAYILFLGLLGLVVLYPYGNLRAIDAYFFGVSSSTESGLNTVDVKDLKLYQQLFIYFVPIVSNLGFINILIVVVVRLLWFEKRLKEIAPGVLDRKSNPSNYDSTRYDPEAHPRRQSEPTTSETVPGDSTEKDVDDGQRSVGSKIGHVVPERPRSTGRVRPENDSSDPHPAGLSRSISFADTTKALYIPSPQERDRGVPIAEVQRGPGEDVIEEEDEDAETERRNSENTDDLSENGRSATSGLPFERVASSLFVIGKQPSRAREPSLRPAISLSKDANLPDLSVQATLGRNSQFHNLTAADRERLGGIEYRSLKLLLKIVIGYFVGLHVFGVVCLVPWILHSNRKYRDYLDECGQNDVWWAIYSAQTMTSNLGLTLTPDSMISFNDAVFPMLIMSFLAYAGNTLYPCCLRLLIWGMSKCIPESSSLKEPLEFLLKYPRRCYLLLFRSKPTWILFGIIFVLNFVDVLLILVLDLDNPAVNDLPGGPRVAAAIFQSASSRHTGTASFNLADVNPAVQFSLLVMMYISVFPIAISVRASNIYEEKSIGVFSSETDMDEGDGKRYVLMHMRNQLSFDLWYIFLGIMCICIAESGKIMDPTKPAFSVFAISFEVVSAYGNVGLSLGYPTASTSFSAQFDIFSKIVICAMMIRGRHRGLPYQLDRAILIPNNRLVEDDKVETRPSISLPRIRSMDPTDSRYMKMKKAHTR
9E-114	390	13.1	3E-109	375.3	4.5	2.1	2	V2Z059_MONRO	Potassium transporter	Moror_17780	Moniliophthora roreri (strain MCA 2997) (Cocoa frosty pod rot fungus) (Crinipellis roreri)	885	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Marasmiaceae, mitosporic Marasmiaceae, Moniliophthora, Moniliophthora roreri, Moniliophthora roreri (strain MCA 2997) (Cocoa frosty pod rot fungus) (Crinipellis roreri)	1381753	>tr|V2Z059|V2Z059_MONRO Potassium transporter OS=Moniliophthora roreri (strain MCA 2997) GN=Moror_17780 PE=4 SV=1MSSTTLGTRLWRFIKKHLNFYRVHILFFTFTPLIFSAIFYASNGQNHISYIDALFNCVSAITVCGLATVDLSSLTPWQQVILFIQMCLGTPVVVSWVMVYIRKHYFETKFEHIIRSAAARESVAVPFTEERKNTKWPRRLISFFYRERGIPIMKEDTQSDHDEKERANGGSTKRVRTDMIRRMDDAPKLVNPSGWISEGDRIPMKRNATIQSTSQDRRLSFVTPLPSMDTTSSRLAPLPRKMSRRLSDPGTPTVPTVNSAPLHRFETIAPQSRPHSPTLPQSPTLETQPSAVNHPVSPISSTLPRTQTVEFNLPRRRPRRGTSVGRDAELPASDSVQPEDRRSLHRMSMQNAPFTSHPTTHTYNSHISISQATKHSGFGGFPMPHEIVQALIKEFFPGLRRKLTRTVTIPLTHTIASQHGANVPPGAKPVPYISFEAVVGRNSAFPMLSEDQLEELGGVEYRALNALLWIVAGYHILVQLIAFVIVVPYISQAKWRDDFNPPALHRPVAPAWFALFQMVSAYTNTGTSLVDTSMVPFQTAYIMIIAIVILILAGNTAFPIFLRFTIWILTKLVPKASRANETLHFLLDHPRRCFIYLFPSHQTWFLLTVVIGLTLTDWFFFLVLDIGTTEFESIPVGIRFIVGLLQATAVRAAGFGIVPLAALAPAVKVLYVIMMYISVYPIAMSVRSTNVYEEQSLGVYRGEESDDEDEFQAAGPRVTVWSRYLAMHARKQLAFDMWWLCLGLFLVCIIERSSLDDENSATWFNIFSIIFEMVSAYGTVGLSLGAPMVNYSFSGTLRPLSKLIFCVIMLRGRHRGLPVAIDRAVMLPQDIQKYDEVEARSMNMGDRDDFFARSSTIRNSDFPNGGHVMSEKQPSIMEEARSNID

1E-113	390	5.8	1.4E-74	260.8	3.2	2.1	2	A6R6P9_AJECN	Putative uncharacterized protein	HCAG_05307	Ajellomyces capsulatus (strain NAm1 / WU24) (Darling's disease fungus) (Histoplasma capsulatum)	711	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain NAm1 / WU24) (Darling's disease fungus) (Histoplasma capsulatum)	339724	>tr|A6R6P9|A6R6P9_AJECN Putative uncharacterized protein OS=Ajellomyces capsulatus (strain NAm1 / WU24) GN=HCAG_05307 PE=4 SV=1MRTFQQVVIYVVPLIGNLSVINLAVVLVRLYWFETRFKDIVRLSRQRLLDRPRSNKLQSSDSRGRDSISLRNRLTAARIRDIRVLRP EPRIGSSRTAASESEGLRLRARILSRIPNNNANSESDSRNGTVPNENENENVKSCAVEIDDSTTSTSTPDPPASPSDPTPVVIDRTSAS LKKNSIERSAPPAHISFSAETNMEPRGRALRIPGPREFESGQTVREVDDDDLAKSITIEEPPMAGPSGENERRRLPTMGRLLSHAVSV ERAASNAFILGNSSRKRSRSRSSNPLHRSSSRADRVPLDMPYLSYQPTIGRNSRFLGLTDDQRDELGGIEYRSLKLLAKIVFSYYVFW HVFGVVCLIGWIHNSDRKYRDYIQSAGQSPTWWAIFSGMTTYNNLGFTLTPDSMTSFRNATFPIFIMTFLMYIGNTGYPCMLRLVIWL MFKISPQGSAIREPLNFLLDHPRRCYTLLFPSSPTWMLFFSLVFLNFIDVLLFLVLDLHNEEVLAVPSSWNRFLAAVFQAASARTTGTST FNVSKVHPAVQFMLMENSLGLYDPQSDEIDESNSTASYVGAHMKKQLAFDLWYVFFGMFLLMITEGSKLADKADPDFAIFSIFFEAVS AYGNVGLSLSHPSINSGLSTKFSVLGKLVICALMLRGRHRGLPYELDRAIILPSERNLTESSATKDGGPVTTTQTSTNATISSLLRTRIAE IV
3E-113	389	10	5E-111	381.1	3.4	2.1	2	U5GY44_USTV1	Uncharacterized protein	MVLG_00116 MVLG_00116	Microbotryum violaceum (strain p1A1 Lamole) (Anther smut fungus) (Ustilago violacea)	1302	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Pucciniomycotina, Microbotryomycetes, Microbotryales, Microbotryaceae, Microbotryum, Microbotryum violaceum (strain p1A1 Lamole) (Anther smut fungus) (Ustilago violacea), Microbotryum violaceum (strain p1A1 Lamole) (Anther smut fungus) (Ustilago violacea)	683840	>tr|U5GY44|U5GY44_USTV1 Uncharacterized protein OS=Microbotryum violaceum (strain p1A1 Lamole) GN=MVLG_00116 PE=4 SV=1MWDTTHYQKSNQVKEEIPVNASEPSHFEPKDTEPVSHVADLDRTLNGIRTKMCQGLVVLDPKERKSVENAVRSLAALGLDNDA ALLAVQQAYDKADAQAEERFLLDAIETANESLPGRAQILRLPSLLRHDTRQLALDLKSLTEHRRAHQCAHLKGKHGAPTSTAQDFDPT SKAQLSKHGEVHSSVLRGLVQSMGAARLEAVSGVARSIRWTGQGTFSRFSTANETNNIGYIEDGRKEVRMQLRARQYTVFAKIPMF GSIDGNVTSAMPLKIGSLVCFGSKRGIIALAYCFALAETDSLALLSNVVLQELRVSRSLSLARHPSTAPHVPSLFRKSASLSGLSEWMS RHLNFYRHLATLVLLHLDARVVPCCAMNSRPWRSHLVRSVHMLFFLFMPLVSSGIFYASNGATKVAYIDALFMTVSASTVTGLNSALL GPMTRWQQTILFINMCVGSTVFVSLVTIVIRLSFFRRKFEYMVEHDPAARQRVNRVGAEEAQLEGRSFRPFPTHLRASDIEFATHSPA GSSPIWTREEKKEGGANNKNNNKKKKKKKKKGPLRTDMITRVDVPVRVNQMNVTGWLSDEAKAAEELATTTQAGGTIKAGEFGGVI TAEPEAAEEPVASSAPHTTAIHIDDSTKPDRSHRHVRRTSDPIAHAPASLSPTHQSVGLPRVKTLDTHHAHDHRHGSLTSPASPDFPR SRTIEFRDNGDSNLRMRRTRTGAQDVDVRRRQSQGNLRDIEAHTLTRTGTNAPDALNTGFGGFPNPIVVAADYARKRIPVFNTVVER NLTLPPTKLSYISFDAVVGRNSKFRGLTSAQQEELGGVEYRALQLLLRIVFAYWIGLQLIAVLVLAPWLTYSERYRPVLEDPQWAVSPT WFVFFQVWSAFSNNGMSLVDASMVPFQQAYPLIVVMSILILGGNTAYPVFLRICIWIIFKLVPRRSRTRETLQFLLDHPRRCYIYLFPSH QTWFLVFVLVILNSIDWISFIVLDIGNTEIERLPVGIRIIDGLLQAFAVRAAGFAIVTLSAVAPALQLLYVVMMYVAVYPIAVSIRSTNVYEE KSMGVFEEEEDEDDVEARFEKSHSASQYISYHARKQLAFDMWWLVLAVWLICIIERRLIGDLEYPEVTIFTIMFEVASAYGTVGLSLGT SRKNTSLSGILRTLSKLVLCAVMFRGRHRGLPVAIDRSILLPSEIKTAETGSTRGDGASARRGSRSSCASSGRDEDGPGGEGGLETVE PETDEARTERVRHESGRENSGDEAYGFEYTKPPTEPRSRREDESSELAHKSDFNEGVVSNDSDNTISETR
4E-113	388	7.3	4E-101	348.4	0.6	3.1	3	Q2H6K0_CHAGB	Putative uncharacterized protein	CHGG_05715	Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	841	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Chaetomium, Chaetomium globosum (Soil fungus), Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	306901	>tr|Q2H6K0|Q2H6K0_CHAGB Putative uncharacterized protein OS=Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) GN=CHGG_05715 PE=4 SV=1MDRLKDMLVGQIKALRPAFISKQPHFNFISAHYFYVIGLALVGSVIVFGAGKGNIAYIDALFLASCTTTQAGLNTVDLNILNTFQQIV LYLWPMLANPITINSFVVFLRLYWFEKRFQHIARAERLRRGTLSKAKSKAGLDNADAEKGVNGRKITVMLNGARSRITNDGMLLEGNR SLANEQRRVPSPQPPNQTKTNSPDETSEPRKPEIKFAHTLTKSDGLGEDAVKLPPARSDHEHIAFLERQRKGDDEVLRIPNPRDAERG MLPKRVEAGDDEEPDVGDAPAGASAPTAAADNRQQAITIEEPDRNKLQQSDSDELLEDAKAAAHALSFLKLRKPRFLSRTNSKSHGT EADSSATATAARTRSRRQSFQSMRTAFSREKVEGTPYLSWEPTIGRNSAFPDLTEEQREELGGIEYRSLKTLALVLTGYFWIYSAIGVI GLVPWILNMDSYGEIVDQAGVSRTWWAFFTSSSAFMDLGFTLTPDSMNSFNTAVWPLLLMSFLIVIGNTGFPVMLRFIIWVLSHITPA GTGLYEELRFLLDHPRRCFTLLFPSGATWWLFWLLVIMNGLDVMFFIVLDLGKGPVVDLPAGLKVLNGLFEAVATRTAGFSCVNLAAL HPAVQFSYMVMMYISVFPIAISVRRTNVYEEKSLGVYSSHDVEEQPGQSDLSYVGSHVRRQLSFDLCVNASLCSQFSVVGKLVIIAMM VRGRHRDLPYGLDRAILLPSEALNAREAADADARMARIQSHASVATGGPRGSSVGRRKSMNGDRGNILASLLHPGPAVPVDPVMTEI HRTKSTEPNDEELDSHATRVTSRRTEPGVSRRHDPALYIHRPRTSAGEED
1E-112	386	1.2	2E-109	376.2	0.3	2.1	2	A0A098DM18_GIBZA	Fusarium graminearum chromosome 2, complete genome (Uncharacterized protein)	FG04057.1 FGRRES_04057_M	Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	772	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	5518	>tr|A0A098DM18|A0A098DM18_GIBZA Fusarium graminearum chromosome 2, complete genome OS=Gibberella zeae GN=FG04057.1 PE=4 SV=1MPACSPLSEKTIHTLVYKLYPRLANGTRPRQTSFSRVSFSRLRRLTPNRRTMWRPNLNFVKLHYIYIIVMGLSSFLFIYPNGKLSAI DAYFLGVSASTVTGLTTIDVPVLRTYQQLYLYFIPLVCNTVVINIIVVVARLIWFRKYLKKAAPALLSRRRAADPDPKEDPEIGAEIPVSEQ PGHRPSIARAVTDRVPRNTAEKDVLPQIEARSQTLPAPDQNSQRSVEDGTPPVKDDKVTEHGTKITFDPSTDHHPRHEHQDATLYIPG PRARDQGLPFVELNSGRPFSRDARDDDTIEPISRTYSNSIRTLRHRRSGLNLSQVRSVERVATVASSLFVIGNTAQGPKERPLARAPTL AVGDFPNLSREVTIGRNSIFHNLTSEDREELGGIEYKSLKLLLKIIVGYYAFLQFLGAVCLIGWVNHAPSKYVDYIAKCGQNRFWWAIFS AQTMVANLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPILLRFIIWSASRVIPKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALLA ILTLLNVADVLFIILLDLDNPTVTVLPGWQRFCAAVFQAVSSRHTGTATFNLANVNPAVQLALLVMMYVSVYPISIVVRSSNTYEERSLGI YEDEQQPDEEDGGSYFVTHLRNQLSFDLWYICLGLFCITIAEHKKIMNGNDIAFTMWPILFEGVSAYCNVGLSLGYPTISASFCTEFST FSKLVICAMMIRGRHRGLPYALDRAIVLPTEKSMGDETTSTRTRSRSHESHEHHE
1E-112	386	0.6	2E-112	386	0.4	1.1	1	B8NS11_ASPFN	Potassium uptake transporter, putative	AFLA_052420	Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	574	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus flavus, Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	332952	>tr|B8NS11|B8NS11_ASPFN Potassium uptake transporter, putative OS=Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167) GN=AFLA_052420 PE=4 SV=1MCFTNILVVIVRLYWFEKRLRETAPTAFRPSSRSVTSKEYDYDQEAQPRKLNTIRVRDPEQTAGERINAENEHLADSSKSQTVP EDSLTPEISEYAENDDAKSEIRRRLRDTSNPLERVASSLFVLGSQPSRTQGSQLREAVSLSKSSNLPSISAEATLGRNSKFYNLTAEDR ERLGGIEYRALKMLLKTVLGYFFGLHIIGAICLVGWIQYAGPKYREYLKECGQNHIWWAFYAAQTMANNLGFTLTPDSMVSFQDATFP MLIMTFLAYAGNNLYPVFLRLIIWTTYRCTPKNSSLREPLDYLLKYPRRCYTLLFRSKPTWVLFGIIFVLNFVDVLLIVVLDLHNPAVNTLP GGPRVLAAIFQAASARHTGTSSFNLADVNPAVQFSLLVMMYISVFPIAISMRASNTYEERSLGLFSSDGEVVDESNTTNYVLSHVRNQ LSFDLWYIFLGIFCICVAESNRIMNPSEPGLTVFAIFFEAISAYANVGLSLGYPGVSTSLSGQLSTFSKVVVCLLMIRGKNRGLPYQLDR AIRLPNERLVDDQVDSESVNLYTDGKLDPLDIRDLKVKRHHTK

3E-112	385	8.4	3E-108	372.1	1.7	2.1	2	I4YG41_WALSC	TrkH-domain-containing protein	trk2 WALSEDRAFT_31613	Wallemia sebi (strain ATCC MYA-4683 / CBS 633.66)	1015	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Basidiomycota incertae sedis, Wallemiomycetes, Wallemiales, Wallemiales incertae sedis, Wallemia, Wallemia sebi, Wallemia sebi (strain ATCC MYA-4683 / CBS 633.66)	671144	>tr|I4YG41|I4YG41_WALSC TrkH-domain-containing protein OS=Wallemia sebi (strain ATCC MYA-4683 / CBS 633.66) GN=trk2 PE=4 SV=1MNNSGKDNDELASDGTEKPNPVKVRDWLHDAWKGSFNFYRIHMLVFTIAPLIFGAIIYAGDTNHGFAYIDTLFVATSAFTVTGLSTIELSHFNGFQQAVLFFCMSIGSVSTVSIVMVIIRRFYFRKRFEHVIMTENKRKAQRRPSWYEVATSSARETASGIRSRFRQSSQRPSDHSERPSTPNNISPSSSSSSSSEFKTPIKPAGGTKLNRVARSLGIGTSAHHDPDSIPPIGDKQKKKRRFTPSMIRRVDAPALINRMAPGGWISDKASAKSMSPPHSPMQSHQDIKNQYKNADNEHALDTDSESEEEDAEKMAGQQQQQQQRKRSSVTLQASGRPSRIGRGESFGSRSIDRPSQDPQPQPIIVDHGNSQVDEEKFPRSATIGFREPDLSINRQRTAGTNLDRSNTYQSGRSRSIAPSGYFPRTTTKPYSTRDRNFGGFPGPLTLITRFVDKIFPQFRSRLDRSVTIPYTHTYTSQPEGTIGGLGSRGKHAPYITFDAIVGRNSVFKDLTDEQLDELGGAEYLALKILTVILIFYYFFFQLIGLTIIAPYINEIPRFRNTVEEEAPNLNPVWYTAFNTVSAYSNTGMSLVDSSLQKFQTAYGMYLPISFLILLGNTCFPIMLRFIIWLGTKVVRKESQEYRGLHFLLDHPRRAFLYLFPSHQTYFLLSMVVIMVVTDWVCFLLLDIGTPSIEEIPLGTRFACGFMQATAVRAAGFNIVNLANLSPSVQLLYLIMMFVSVYPIALSVRGTNVYEEMSLGIYSNDDQSSEEPNEDNVDSTASPSRGKLWGSYFGWHVKKQLSFDIWWLAFVLFLLCIIERGKILDEEKSYFTIFSILFEVVSAYGTCGLSLGVSDKNYSLSGEMRTLSKLLLMVVMIRGRHRGLPNAIDRAVVLLPSDLRETDQQMADQQSQAEALRRTRSMATSFSAARNNTFYRELENNYRGPPFPMPQSNEEDDKLATINEQTQQPTPSLSPESTNVGLPADLSPKHENKPDIPALSEEPEDRSHSPSQSQANKDD
6E-112	384	10.6	2E-111	382.6	5	2.1	2	E3RUY1_PYRTT	Putative uncharacterized protein	PTT_12924	Pyrenophora teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)	663	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Pyrenophora, Pyrenophora teres, Pyrenophora teres f. teres, Pyrenophora teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)	861557	>tr|E3RUY1|E3RUY1_PYRTT Putative uncharacterized protein OS=Pyrenophora teres f. teres (strain 0-1) GN=PTT_12924 PE=4 SV=1MAILYPYGNLSAIDAYYFGVSCSTESGLNPVDLKALKTYQQIFMYIVPIITNLGFINIVVVVVRLRWFSQKLKGITAAHRRPVSRNETSEQQGQVSANVSETRDLEGGLTGETVSEKKPVVQTESSQEEAKDESKDEANVPHIKFAPDPRLRTNEKGALYIPGPRERDNGEPITMTSDDEDEDQIKPITESSYAMRRTKSNTRSMRSTRSMSKATSVDRVVASMFVLGSTSSVTHSEIKPRREPLDLSSLTPEELGGVEYRALRVLLKITVGYFFGLHIFGVICLLPWIHLAPSKYQDYLATHAVGKTWWAIYSSQTMVDNLGLTLTPDSMISFRDTFWPMLVMSFLAFAGNTFYPCFLRLVIWTINRLSPSGSSLQESTRFLLDHPRRCYTLLFPSTATWILATILIILNLFIDTLLIIVLDLDNREVNVLAIGHRILAAIFQSASSRHTGTSSFNLANVNPAVQFSLLVMMYISVYPIAISIRMSESYEEKPVGLYAGEESLDEDKGSTTYLISHMRNQLSFDLWYVFLGVFCICIGESKRIMNNEDPAFSVFAIFFEVVSAYGNVGLSLGYPTNATSLSGHFNVFGKVVICFMMLRGRHRGLPYALDRAINLPSDIVGGEEESERYRDKDDEDVTSVGEARPGRVEAKLARGRKMVRALTH
2E-111	382	1.2	2E-109	375.8	0.3	2.1	2	W7MHE8_GIBM7	Uncharacterized protein	FVEG_16760	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	724	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	>tr|W7MHE8|W7MHE8_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_16760 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNLVTINIIVVVVRLIWFRRYLKNAAPALLSRRRPVDLDPKEDPENGADNPLSEVLDNRPGLARSVTERVHKNAAERDALPPIEARSRTDPAPDHPTQQRPVDILSPTIKEERVKEEDQHETRITFDPSTDRHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPIGILRRRRSAGLSLAKVRSVERVANVASSLFVIGNPTQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWVQNAPKKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKVVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPAFTMWPMLFEGVSAYCNVGLSLGYPTINSSFCTEFSTFSKLIICAMMIRGRHRGLPYALDRAIVLPTEKSLGAETITQSHESHEPHEHRE
4E-111	382	1.3	4E-109	374.7	0.3	2.1	2	F9FCW8_FUSOF	Uncharacterized protein	FOXB_04246	Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	717	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	660025	>tr|F9FCW8|F9FCW8_FUSOF Uncharacterized protein OS=Fusarium oxysporum (strain Fo5176) GN=FOXB_04246 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLIWFRRYLKNAAPALLSRRRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIKARSRTDPAPNHPHQRPVDILSPTIKEEKVKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWVQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPAFTMWPMLFEGVSAYCNVGLSLGYPTINSSFCTEFTTFSKLIICAMMIRGRHRGLPYALDRAIVLPTEKSLGAETITQPHESHESHEHRESALWIISISEYKTA
4E-111	382	1.2	4E-109	374.8	0.3	2.1	2	A0A0J9VL84_FUSO4	Uncharacterized protein	FOXG_11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	723	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9VL84|A0A0J9VL84_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLVWFRRYLKNAAPALLSRRRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWVQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPAFTMWPMLFEGVSAYCNVGLSLGYPTINSSFCTEFTTFSKLIICAMMIRGRHRGLPYALDRAIVLPTEKSLGAETITQPHESHESHEHRE
5E-111	381	2.3	2E-109	375.7	0.5	2.1	2	K3W0N7_FUSPC	Uncharacterized protein	FPSE_05220	Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	701	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Fusarium pseudograminearum (Wheat and barley crown-rot fungus), Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	1028729	>tr|K3W0N7|K3W0N7_FUSPC Uncharacterized protein OS=Fusarium pseudograminearum (strain CS3096) GN=FPSE_05220 PE=4 SV=1MGLSSFLFIYPNGKLSAIDAYFLGVSASTVTGLTTIDVPVLRTYQQLYLYFIPLVCNTVVINIIVVVARLIWFRKYLKKAAPTLLSRRRAADPDPKEDPEIGAGIPVSEQPEHRPSIARAVTDRVPRNTAEKDVLPQIEARSQTLPAPDQNSQRSVEDGTPPVKDDKVAEHGTKITFDPSTDHHPRHEHQDSTLYIPGPRARDQGLPFVELNSGRPFSRDTRDDDTIEPISRTYSNSIRTLRHRRSGLILSQVRSVERVATVASSLFVIGNTAQGPKERPLARAPTLAVGDFPNLSREVTIGRNSIFHNLTSDDREELGGIEYKSLKLLLKIIVGYYAFLQFLGAVCLIGWVNHAPSKYVDYIAECGQNRFWWAIFSAQTMVANLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPILLRFIIWSASRVFPKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFAILTLLNVADVLFIILLDLDNPTVTVLPGWQRFCAAVFQAVSSRHTGTATFNLANVNPAVQLALLVMMYVSVYPISIVVRSSNTYEERSLGIYEDEQQPDEEDGGSYFVTHLRNQLSFDLWYICLGLFCITIAEHKKIMNGNDIAFTMWPILFEGVSAYCNVGLSLGYPTISASFCTEFTTFSKLVICAMMIRGRHRGLPYALDRAIVLPTEKSMGDETTSTRTRSRESHEHHE

6E-111	381	14.7	7E-111	380.5	10.2	1	1	Q5V40 6_HAL MA	TRK potassium uptake system protein	trkH3 rrnAC0 755	Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) (Halobacterium marismortui)	564	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Haloarcula, Haloarcula marismortui, Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) (Halobacterium marismortui)	272569	>tr|Q5V406|Q5V406_HALMA TRK potassium uptake system protein OS=Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) GN=trkH3 PE=4 SV=1MSRRNGGLFPTDLQTIARDIGSLLLMEAGLMTITAAVALGFQEFYAAFGFFTAAGMTAGVGGLANRGFSDAPAPQMKHGMVIA AGGWLLVAAFGSLPFLLTAWFTPPAVMDTFVPVGTDTSTWAPIRVGGTTTLSSLAYFRNPLHAFFESMSGWTGSGLTMAIHEPSLPR AVQWWRSFIQYVGGVGVIVLTVSILSRPGSGSYALYQSEAREEKIHPSVVSTVRTVWKLVVGYTVLSFALLFGAILASDSEYAESLPL WEVAWQALNHAMTGLTTGGFSVTDNSIATYNSPLVETVLLPIMILGAIAFPVHYVVLHDRQVRELVTDLQTRWLFILLTVGVVGLSVQN AWSVPATTEAFATQSFLPVSVPMLNAAQLDAVRDSTFQWVSALSCTGFQSAPIGRWLAGGKVLVAGAMVLGGAAGSTVGGIKIIRG YTIVRGIIWQFSRVFLPTNAVITARIGNRTLDRESMEREFSEAAIVTLLWLIILIISSVVLTNVAGPAFGYADALFEVASAQGNVGLSSGIT GPSMPAIAEGMFVLNMWVGRLEIIPILVFIRAGLYGLDP
6E-111	381	1.5	5E-109	374.6	0.4	2.1	2	S0EH4 1_GIBF 5	Probable potassium transporter TRK-1	FFUJ_0 9488	Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	724	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella fujikuroi (Bakanae and foot rot disease fungus) (Fusarium fujikuroi), Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	1279085	>tr|S0EH41|S0EH41_GIBF5 Probable potassium transporter TRK-1 OS=Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) GN=FFUJ_09488 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNLVTINIIVVVVRLI WFRRYLKNAAPALLSRRRPVDLDPKEDPENVADNPLSEVFDKRPGLARSVTERVHKNVAERDALPPIEARSRTDPAPDHPTQQRPVD ILSPTIKEETAKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNNGRRFSRDTRDEDVIEPISRTQSTPVGTLRR RRSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKII IGYYVFLHCLGAVCLIAWVQNAPQKYVEYIDKCGQNRIWWAVYSSQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLL RLVIWATSKAVSKRSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRH TGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGFLCISIAEH KKIMDGNDPAFTMWPMLFEGVSAYCNVGLSLGYPTINSSFCTEFTTFSKLIICAMMIRGRHRGLPYALDRAIVLPTEKSLGAETITQPH EPHESHEHRE
2E-110	379	2.4	4E-109	374.9	0.3	2	2	N4UY0 2_FUS C1	Low-affinity potassium transport protein	FOC1_ g10010 409	Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	695	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. cubense, Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	1229664	>tr|N4UY02|N4UY02_FUSC1 Low-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 1) GN=FOC1_g10010409 PE=4 SV=1MGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLIWFRRYLKNAAPALLSRR RPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHET RITFDPSTDHHPRHEQQESTLYIPGPRARDQGTPTIHSFSQDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVATVASSLFVIGN PAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWVQHAPNKYVEY IDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQEPLHFLLNHPR RCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYP ISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPAFTMWPMLFEGVSAYCNVG LSLGYPTINSSFCTEFTTFSKLIICAMMIRGRHRGLPYALDRAIVLPTEKSLGAETITQPHESHESHEHRE
3E-110	379	2.4	4E-109	374.9	0.3	2	2	A0A0J 9VKW8 _FUSO 4	Uncharacterized protein	FOXG_ 11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	705	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9VKW8|A0A0J9VKW8_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLVWFRRYLKNAAPALLSR RRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHE TRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERV ATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAW VQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQ EPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQM ALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPAFTMWPML FEGVSAYCNVGLSLGYPTINSSFCTEFTTFSKLIICAMMIRGRHRGLPYALDRAIVLPTEKSLGAETITQPHESHESHEHRE
4E-110	378	5.5	1.2E-93	323.7	1.6	2.1	2	C1GBD 4_PAR BD	Uncharacterized protein	PADG_ 04935	Paracoccidioides brasiliensis (strain Pb18)	706	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, mitosporic Onygenales, Paracoccidioides, Paracoccidioides brasiliensis, Paracoccidioides brasiliensis (strain Pb18)	502780	>tr|C1GBD4|C1GBD4_PARBD Uncharacterized protein OS=Paracoccidioides brasiliensis (strain Pb18) GN=PADG_04935 PE=4 SV=2MRTYQQVVIYIIPLLGNLSIINLVVVLVRLYWFETRFKDIVRLSRQCSFDRRHSVESSDERGRDTTTLREKLATGKIRHIRMSRFRS GISSRSKTSPSEAEGMRLRATVANVNNPNSNNIIDLNSDRNDNTNIIQNKNDDDGITLNGNMNEKEENATKEMGGSITSTTIPVPVSPS APPSNTQPVMIDQNNSSLDNNKTERSVPPTHISFSVETNLERRERALRIPGPREFESGQTVREVDDDDLIKVVSTEEPPSSGPSGDHD RRRLPTMERIFSRAVSMEYAASNAFILGKASHKRSRSRSSNPGSRSSSKARQSHNMPYLSYQPTIGRNSRFLDLTDEQRDELGGIEY RSLRLLAKIVFGYYVFWHVFGAICLIGWIHNSDHKYRDYLRSVGQSPTWWAIYSGMTTFNNLGYTLTPDSMISFRAATFPIFLMTFLIYI GNTAYPCMLRLIIWLLFKLSPRNSRIREPLNFLLDHPRRCFTLLFPSSPTWMLFFSLVFLNFIDVLLFLVLDLHNEEVLGVPSMWNRFLA ALFQAASARTTGTNTFSISKVHPAVQFMLMVMMYISAYPIAISVRRTNIYEETSLGLYDSTSEEIDESNTTASYLGTHLKKQLAFDLCGN VGLSLGHTAINSGLTTRFTVLGKLVICALMIRGRHRGLPYELDRAIILPSERNPTESSSPRQVAVSTALKSADTTIAVSSRSRTT
6E-110	377	3.3	6E-110	377.4	1.5	1.5	1	Q0C90 2_ASP TN	Putative uncharacterized protein	ATEG_ 09832	Aspergillus terreus (strain NIH 2624 / FGSC A1156)	677	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus terreus, Aspergillus terreus (strain NIH 2624 / FGSC A1156)	341663	>tr|Q0C902|Q0C902_ASPTN Putative uncharacterized protein OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) GN=ATEG_09832 PE=4 SV=1MATEADDNNKYLESARDYTTVLVGPSHMPPNREPQVETSPLRLRHHYFYIIFWILLASLLLYLPGGLSYIDALLLASGAATQSGLN PVDLNRLHLLQQITLWIVPMATNVVFMHSLLVLIRLYWFRRRFRRAIRDAKALCHAERGRWNQHLLDSESPTLVGLTRTVPEPEPRTS QESAVLSEPEDQERHLLTSSPESKPANGSSGPHITFDDTDRDYELKKNRRHTYSSYPVNGNRRASISSTRTRNSHDIYGSTMPNLPPL MWQSSIASYSQWNEAQKEELGGIEYRALKTLMVILVSYFLVFHIVGMLVFMLWISLSPQYDSTLAEIKVNKFWWATFTSGSAFNDLGY TLSPDSMASFRYASFPLLTMAFLIVMGNTGFPCMLRLIIWALSKMTSYGTPLDEELHYLLEHPRRCFTLLFPRADTWRLAAVLLLLNAID LVIFYALQEAARLDPGMSAGAKFVNGLFQIASTRTAGFTITWLSRLHPAIQVSFLVMMYISAFPIAIVMRKTNVYEEKSLGIYYDDTPMP HAQQGLMSHIQRQLGFDLWYVMLGFFLIAVAEGKRLQEHPNDRAFSLFPILFEMVSGYGTVGLSLGYPGTDTSLCAQFSWVSKLIIIA MEVRGRHRGLPHALDHAILLPCEQQEDAQGEWWWKRWLKRRTSISHLFSHEADELERLL

1E-109	377	2.3	2E-108	372.4	0.4	2	2	N1RGY2_FUSC4	Low-affinity potassium transport protein	FOC4_g10007955	Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	705	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. cubense, Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	1229665	>tr|N1RGY2|N1RGY2_FUSC4 Low-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 4) GN=FOC4_g10007955 PE=4 SV=1MGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVIVRLIWFRRYLKNAAPALLSRRR PVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPPQRPVDILSPTIKEEKVKEGDQHETR ITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVAT VASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWV QHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWAISKAVSKQSSLQE PLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMA LLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPAFTMWPMLF EGVSAYCNVGLSLGYPTINSSFCTEFTTFSKLIICAMMIRGRHRGLPYALDRAIVLPTEKSLGAETITQPHESHESHEHRE
2E-109	376	5.4	4E-109	374.9	0.5	2.1	2	C7ZHJ0_NECH7	Putative uncharacterized protein	NECHADRAFT_69883	Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	663	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium solani species complex, Nectria haematococca, Fusarium solani subsp. pisi (Nectria haematococca), Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	660122	>tr|C7ZHJ0|C7ZHJ0_NECH7 Putative uncharacterized protein OS=Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) GN=NECHADRAFT_69883 PE=4 SV=1MWRPELNFVKLHYLYIIFLGLTSFAILYPAGNISAIDAYFMGASASTVTGLATLDVKELQTYQQLYLYFVPMFSNLVFINIIVVVVRL FWFNRHLKKAGFPALPSPARTVIEDTLPRIGERSRTEPPPSKAPHRLAPPRAAVDAEKLAEDEDEEEGEESRRANQLEPRITFDPSTD HHPRHEATLYIPGPHDEIETIYRTHSTPGSNLRRRRSAGLRMSEARSMERVATVASSMFVIGGARETRRERLTTAPTMAAGDFPQLS REVTVGRNSMFHNLSSKDREELGGIEYRSLKLLLKIILMYFFGLHFIGMICLIGWIQYAPSKYAEHIAESGQNKIWWAIYSAQTMVDNLG FTLTPDSMISFNDAPAPMLIMSVLALAGHTFYPVVLRFILWSISKLLPEESSLHEPLSFLLNHPRRCYTLLFPSGPTWALLGVLALLNIVD MLFIILLDLDNEAVSTLPGWPRFAAAVFQAVSSRHTGTTSFNLAAVNPAVQMSLLVMMYVSVYPISIVVRSSNTYEERSLGLYEPSIQP DEQNGGSYFVTHLRNQLSFDLWYICLGLFCVCIAESKRIMNGNDPAFTMWPILFEGLSAYCNVGLSLGYPTIASSFCSEYSTFSKLVIC AMMIRGRHRGLPYALDRAIVLPDEKSLGTQFVDEEDHDHHE
5E-109	375	9.4	1E-108	373.3	1.6	2.2	2	E4V781_ARTGP	High-affinity potassium transporter	MGYG_08871	Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	674	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Microsporum, Arthroderma gypseum (Microsporum gypseum), Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)	535722	>tr|E4V781|E4V781_ARTGP High-affinity potassium transporter OS=Arthroderma gypseum (strain ATCC MYA-4604 / CBS 118893) GN=MGYG_08871 PE=4 SV=1MVNLEAVLRWPHINFVTLHYAYIIFMSVLSLAILYPAGNMAAIDAYFFGASSATESGLNTMDLKELYTYQQLYVYFIPMFTNLGFIN SVVVLVRFLWFRKHLSKLAPQLRDNKKSTSSKSNDVDAEAGHIPGTVDNDAETKSPGEQKAEEKKDEDDAATAEFLKSRTINFEPSA DNHPKNDETLYIPGPRDRDRGITNAVYQSPFEISVAESSAAGGLRRRFVDGLPLAESNTIGRVANIASSAFVLGPDHRHRRGSISSNVS QQREVQARNSLALSQHASLGRNSDFYNLTREDREKLGGIEYRSLKLLLKIVFTYYFGLHLFGAICLVGWIQYADPKYRAVLAASSQNIH WWAFYSAQTMVDNLGFTLTPDSMISFRDAQWPMFIMSLLAFAGNTLYPVFLRLVIWTISKLAPKNSSIQEPLSFLLDHPRRCYTLLFPS RPTWILFGIIFAMNFIDTLLILVLDLKNPEVASIPLGPRILAAIFQAASARHTGTAAFNLANVNPAVQFSLLVMMYIAIFPIAISMRSSNTYED KSLGIYERPNRLDESSGTDYLLKHMRNQLSFDLWFIFLGAFCICIAESERIADTSIPAFSVWTVFFEVTSAYGNVGLSLGYPDVSYSLSG KFSLFSKLVVCVIMIRGRHRGLPYALDRAIILPNGDGDIDVVETDDIYS
5E-109	374	4	5E-109	374.3	2.8	2	2	E9DWG6_METAQ	Cation transporter, putative	MAC_01964	Metarhizium acridum (strain CQMa 102)	608	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium acridum, Metarhizium acridum (strain CQMa 102)	655827	>tr|E9DWG6|E9DWG6_METAQ Cation transporter, putative OS=Metarhizium acridum (strain CQMa 102) GN=MAC_01964 PE=4 SV=1MRCPPLNFIALHYAYIFVMGLLSIPFLYLYGNISAIDAYFMGSSTSTESGLNVVNLNELKLYQQLYLYFATLFTQMGFVNILLVVVR LYWFNKHLDNFGPAFLHARRSGPDSQEDARLEYGESKATSPGTDVVAETGTSGKLTGPRLKSKEETTRYGGDNHRQHRLQTLGPL RESRSIDRAAALASSIFVIGREPTPSLISRELTRRRRASDDMPYLSTGASIGRNSRFYNLTRQDRSELGGIEYRSLKLLLKIVVAYYFGVH LIGAIGLVAWILHADSKYAAHLDEFAQDKIWWAFYTSQTAVCNLGFTLTPDSMVFFQDSPWVMFWLSLLTFAGNTLYPVFLRFILWTM SKVTPRGSSIQEPLQFLLTHPRRCYALLFPGGTTWALFGIIIGLNFLGTLILLVLDLHNPEFTHLTLAQRVAAAFFQSAAARHTGAASFTL SNLSPGAQFTLLVMMYISAFPIAMSIRSSNIYEEKSLGYYAQDPTYNEDRGASYLLQHMQKQLGFDLWYIFLGLFCLSVSEASKLADPS EPAFSFFAIFFEVVSAYGGVGLTMGYPDITSALSTEFSTFGKVVMCAMMLRGRHRGMPYGLDRAIMLPVERLVEHSA
7E-109	374	21.2	1E-108	373.4	14.7	1.2	1	Q9CKV7_PASMU	Trk system potassium uptake protein	trkH PM1498	Pasteurella multocida (strain Pm70)	487	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Pasteurella, Pasteurella multocida, Pasteurella multocida subsp. multocida, Pasteurella multocida (strain Pm70)	272843	>tr|Q9CKV7|Q9CKV7_PASMU Trk system potassium uptake protein OS=Pasteurella multocida (strain Pm70) GN=trkH PE=3 SV=1MRILSIIRIVGILVMCFSLTMLAPAFVALLYGDGGGKAFMQTFVMSAIVGMLLWWPCHHHKEELRSRDGFLIVVAFWLVLGSIGAI PFMLFEKPHLSFSSAIFESFSGLTTTGATVIEGLDQLPKAILFYRQLLQWLGGMGIIVLAVAIIPLLGIGGTQLYRAESSGPLKEQKLRPRI AEVAKLLWILYFSLTVLCAIAYWFAGMNAFDAIGHSFSTVANGGFSTHDASMGYFNNATIYLITTFFMLIAGVNFNLHISALTYLGKQSL WKNYWKDPEFRFFVAIQVLFILLFSLSLYFYDVLTNLSDAFIQGSLQLTSMSMTAGYSIFDMNNLPAFSAMLLVIASVIGGCGGSTTGG LKTIRVLILWLQVKRELRSLVHPNLVQPIKLGQNILPIRMLESIWAFLMIFILVYWVCVFAVILCGMDVFDAMGSVFATLTNAGPGLGVIH QDFLNVPESAKIVFAFAMICGRLEIFSLLVLFTPTFWKE
8E-109	374	19.8	7E-107	367.4	5.9	2.1	2	M5GFM1_DACSP	Uncharacterized protein	DACRYDRAFT_114599	Dacryopinax sp. (strain DJM 731) (Brown rot fungus)	845	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Dacrymycetes, Dacrymycetales, Dacrymycetaceae, Dacryopinax, Dacryopinax sp. (strain DJM 731) (Brown rot fungus)	745407	>tr|M5GFM1|M5GFM1_DACSP Uncharacterized protein OS=Dacryopinax sp. (strain DJM 731) GN=DACRYDRAFT_114599 PE=4 SV=1MAPHTTRPPGRIRIIWTKFVNSLNFFRIHAIYFTLTPIIMACIIFAVNGEYHMEFVDALFLSYSAITTTGLASINVSSATALQQFLIMS QMLLGQLVTVSWVMVYVRRRFFMKKFEHLVRLSRSRTQATTNAETTALRNRFPTIFARARTSSIRPPPRMGDKKKHKGPLSLAMIKR LSSAPQKVDPSGRLVSNLEKTRTRTAEDPGLRFTSQPILLSPQQMTGTSNGFPHRYDRSYFRDDEDLEGPNFIEPEEEDLPPRPLRS PGQETHFARSQTIEIREPNIDRMPRTQTVDFREPHRPPIERLNSRATTFDGRSYQSRRRSSMSGEPFNSSHRDYRDQGFGGWPGPN RLIARLHKKLFPKMHLSLSRTMSVALSETLPTTTHQSTYLSFQAVVGRNSNFFGLTSDQLEELGGVEYRALGLLLWLIPSYMLLIYLSVF AACAITAGLHNNYAYVFDAQQGPVNPVWFGCFQTFAAFSNAGMSLVDTSMVPFQTAYAMIFFMIIAILGGNTAFPVFLRLMIWIISKLT SNTTPMAETLRFLLDHPRRCFVYLFPSPQTWLLTLVLLLNSIDWICFGLLDIGNPYVETIPVGVRVTDGLFQAISVRAAGFAIVQLALLS PAVKLLYMTMMYISAYPIAMSVRSTNVYEEKSMGVYDDESMDENDAPTGEWKSYLAWHIKRQLAFDIWWIFLAMLVICITERGKILDP TNPSVDIFPIMFEVVSAYGTNGMSLGVSYDNFSLAGSFSPLSKVVLCLVMLRGRHRGLPLAIDRAVVLPWEFEQKKEDEQPEQDDPP AAQENEVPEPEEHELGQVSGSSESEPSSTTLRSDEQASPQQTGSTVPPHPQ

1E-108	373	11.9	6E-106	364.4	2.7	2.1	2	R9AGZ3_WALI9	Low-affinity potassium transport protein	J056_004285	Wallemia ichthyophaga (strain EXF-994 / CBS 113033)	1011	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Basidiomycota incertae sedis, Wallemiomycetes, Wallemiales, Wallemiales incertae sedis, Wallemia, Wallemia ichthyophaga, Wallemia ichthyophaga (strain EXF-994 / CBS 113033)	1299270	>tr|R9AGZ3|R9AGZ3_WALI9 Low-affinity potassium transport protein OS=Wallemia ichthyophaga (strain EXF-994 / CBS 113033) GN=J056_004285 PE=4 SV=1MSNDDIDNDDGGGDEALSKRASTKLSWISSKLIGSLNFYRIHMIVFTIAPLIIGAILYAGDDHHDYAFIDTLFVATSAFTVTGLSTIELSHFNGFQQGVVFFCMCVGSVSTVSIIMVIIRRFYFRKRFMHVIMTDKQKKAQRRPSWYAAATSSARETASGIRSRIRSTVHRSSEISPSFSRSQSSGPPNPPTAPSNAQRPSSSDQESSSSSDFKTPIKPAGGTKLNKVVRSLGIGTSNNTQSDNVPQHGSSDQKKKRRFTPSMIRRVDGPALINRMAPGGWISDKASAKSVSPPSSPVQSQNDMRSRYRDADNEHALDTDSESDEENAATVRQPPRNRSSVTIARPPWVHSQSRSRDSQGSKSLERPSQDQQPQPIIVDHGNAQQDEEKFPRSATIGFREPEFSMNRQRTMGTNFDRSNTYQSGRSRSIAPSGYLPRTTTKPYSTRDRDFGGFPTPITLVSRLVDRFFPNLRSKLDKSVTIPHTHTFTSQAGGTVGGPGSRGKYAPYISFDAIVGRNSVFKDLSDDQIDELGGAEYLALKILTVVLIFYYLFFQLAGLTIIAPYINEIPRFERIVDEESPGLDTVWFTAFNTISAYSNTGMSLVDSSLQRFQQAYGMYLPMSFLILIGNTCFPIVLRFIIWLGTKVVVKKDSHEYQGLHFLLDHPRRSFLYLFPSHQTYFLLSMVVIMVVTDWVCFLLLDIGTPSIEQIPIGTRFACGFMQSTAVRAAGFNIVNLADLSPSVQILYMIMMFVSVYPIALSVRGTNVYEEMSLGVYNNDDQSSEEPNENNVEPTVSESRGKLWGSYFGWHVKKQLSFDIWWLAFVLFLCCILERGKILDTTKPYFSIFSILFEIVSAYATCGLSLGVNERSYSLSGEMRTLSKLLLIVVMIRGRHRGLPNAIDRAVLLPSDVQETDQQMADQQSQAEDLRRTRSQTTSFSAARNNTFYRELENNYRDGDEGLATINEQTHHPTLSPESTRLSSPSELSPKHESPPHITSNDQDSQNTQVNKEE
2E-108	372	8.2	7E-106	364	1.5	2.1	2	S7Q6N9_GLOTA	Uncharacterized protein	GLOTRDRAFT_111153	Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) (Brown rot fungus)	917	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Gloeophyllales, Gloeophyllaceae, Gloeophyllum, Gloeophyllum trabeum (Brown rot fungus), Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) (Brown rot fungus)	670483	>tr|S7Q6N9|S7Q6N9_GLOTA Uncharacterized protein OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_111153 PE=4 SV=1MQSRVDTLPKAEDQPKKDFWRYLRSHLNFYRVHLIVFTFTPILFSGILYASNGEYPISYIDALFNCISAMAVCGLATVDLSQLTGWQQAILFIQMCLGSPVLVSWVMVYIRRYFFAKTFEHMVEAEAAKRTKVKIDVEATIIPWHSKMVNMLRRRKRLTSVKEESEESTPKERKPSSVKKLRTDMIRRMDDAPKLVDPSGWISEGRTESTLHTPARGPAVDTREVQTEGQNHQLSFADRPSVSPDRSSTISSSSSEHHEEQTEGATTPDRSRKGRRLSDPGMARRFRSASVTANEENFRRYPTVNVAAYTSREPDPLPRTQTVEFAPEPRRQRFTSVDRERGRRASVISEQSTAYRRPSIEPTDTQDERRPGRRPSVTLRPTMSTSHTFPRYPTGVRTKHRGFGGFPMPHEILSRVFRYFFPEVQQKLHRTMTMPRTQTIASTRGEVPAGVKPVPYISFDAIVGRNSAFYELTNDELEELGGVEYRALNALLWIVPVYHICVQAISFIVIAPYMSESRWSSDFKPPALHRNLPPPWFALFQVVSAYTNTGTSLVDQSMIPFQTAYPMIFFVIFLILAGNTAFPIFLRLMIWTMTKVVPPRSRLNETLHFLLDHPRRCFIYLFPSHQTWFLLIVLVTLTCTDWVSFLVLDIGTPVIEAIPAGTRVIVGLLQATAVRAAGFSAVSLSALAPAVKVLYVIMMYISVYPIALSVRSTNVYEEQSLGVFEEDDESENDVEFQTTGPRVAVWSRYLAWHARKQLAFDMWWLGLALVLLCIIERHNIDAEDNQSWFNIFSIIFELVSAYGTVGLSLGLPTANYSFSGAFRPLSKLIICIVMIRGRHRGLPVAIDRAVMIPPEFRAQPDEGTMAEQRSLRSVVSRTSAYRQPPPNAGHMEEIPMADIPEDAVMTDDIDHVRTKST
4E-108	372	11.6	3.9E-77	269.2	0.9	3.1	3	C9SCA9_VERA1	Low-affinity potassium transport protein	VDBG_02833	Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) (Verticillium wilt of alfalfa) (Verticillium albo-atrum)	818	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, mitosporic Plectosphaerellaceae, Verticillium, Verticillium alfalfae, Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) (Verticillium wilt of alfalfa) (Verticillium albo-atrum)	526221	>tr|C9SCA9|C9SCA9_VERA1 Low-affinity potassium transport protein OS=Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) GN=VDBG_02833 PE=4 SV=1MLDNTRAWLLGQIRAAKPSFISKQPHFNFISAHYFWIVSLTILASVLMYATAGGQLAYIDALFFASGANTQAGLNTVDVNLLNTFQQICIYIFTMTSNPIVIHSSVVFLRLYWFEKRFQNMVRDARARRVTISKSRAKAHLDMNQAEMGVAGRNIRIMPNSGSRITNDGIILDKKVENGGRESPTAPNGHSERPSSGDTAARSSYAPRTARSDDIELDSIHGLRRLSHAEHLAILERQRRGHDETLRIPNPRDVEKGIRPKRVEEGDGPEAEEEEDPNQPGIRSPGNTRPNTPPEGNEESPERDTMDELAEEATVIGNVLDSVMFRKPRIFQRGQKKYHVDSDEDENDNPRPGPKHRTRTLDVLRGALTGEKADDAPYLSWTPTLGRNSQFPGLSLEQREELGGIEYRSLRTLALLLVCYFWGWSIFALVCLLPWIKSPANNEYAQVVDAAGMSRTWWGFFTANSAFLDLGLTLTPESMVSFNQSHATWWLFWILIGLNAIDLLFFVLLDLNDVVSDMPVHLRIVNGLFQAACTRTAGFSSVNLSLLHPAVQVSYMMMMYISVFPIAISIRRTNVYEEKSLGVYNGAEDDETINDASAMSYVGTHLRRQLSFDLWYVFLGLFILSITEGSKIKKNEFNVYSILFELISAYGTVGLSLGYPNVNASLSSQFTTGGKLVIIAMQIRGRHRGLPYGLDRAVLLPSEARFADEAFETQNGLTRQMTAVTNRTGADLQRGRSRDRGIISSFLHPGPAVPREDRNLARRVSFDAGVSASGANGMEGPDLRRRHTVAVEDADTDEDEEIAPATRARRVFTTPMG
8E-108	371	8	1E-107	370.1	5.6	1	1	F8PSW3_SERL3	Putative uncharacterized protein	SERLA73DRAFT_105229	Serpula lacrymans var. lacrymans (strain S7.3) (Dry rot fungus)	689	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Boletales, Coniophorineae, Serpulaceae, Serpula, Serpula lacrymans, Serpula lacrymans var. lacrymans, Serpula lacrymans var. lacrymans (strain S7.3) (Dry rot fungus)	936435	>tr|F8PSW3|F8PSW3_SERL3 Putative uncharacterized protein OS=Serpula lacrymans var. lacrymans (strain S7.3) GN=SERLA73DRAFT_105229 PE=4 SV=1MQRTATVEFAPNVARHYPATLTTISSRGRQGRETPLGSDSDFSTGHRIEERERDGSRPPRRPSIPPNSRIPVARYPTTHTNRSARSRRASQLQSFSTQPYEPPNPPLPQKHSGFGGFPMPHEILAMILRWLFPGVEKRLHRTVTIPVTTTLTGGGLGRTVSLGPGGRTYSVHGSGLDAGGSISGAIGEDAKPVAYISFDAIVGRNSAFHLLTNEQLEELGGVEYRALNALLWLVAGYHLGSQLISFIVIAPYISRSEWKSDFVPPQLFKPVSQAWFSIFQVVSAYTNTGTSLVDQSMVPFQTAYPMIFFMIFCILAGNTAFPIFFRLLIWIISKLVPSTSRAKETLHFLLDHPRRCFIYLFPSHQTWFLLTVLLMLNLTDWFFFMVLDIGNPAIESIPLGTRFVAGLLQAVAVRAAGFGIVTLAALSPAVKVMYVVMMYISVYPIALSVRSTNVYEEQSLGIYRDDDESEEEQTFPAQGPRMTVWSRYLAMHARKQLAFDMWWLALALFLVCIIERGNLNDSKQQSWFNIFTIIFELVSAYGTVGLSLGQPAQNYSFSGALSPLSKLIICIVMLRGRHRGLPVAIDRAVMLPSEFQKTKDDPDFGLAHDDRQSARRLSRHFNMDGPLDAEDPDYNNPDINGKANSGEYDETENGMEERLRRVVGGKSSQDAMIEAGREKAHEDDKMMST
1E-107	370	3.6	1E-107	370	2.5	2.1	2	G7DW42_MIXOS	Uncharacterized protein	Mo01502E5Q_01502L969D_RAFT_97190	Mixia osmundae (strain CBS 9802 / IAM 14324 / JCM 22182 / KY 12970)	1019	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Pucciniomycotina, Mixiomycetes, Mixiales, Mixiaceae, Mixia, Mixia osmundae, Mixia osmundae (strain CBS 9802 / IAM 14324 / JCM 22182 / KY 12970)	764103	>tr|G7DW42|G7DW42_MIXOS Uncharacterized protein OS=Mixia osmundae (strain CBS 9802 / IAM 14324 / JCM 22182 / KY 12970) GN=Mo01502 PE=4 SV=1MSKLASRATQTISSAWSDAKEPGASWMEAAASHLNFYRVHFVFFVLNPLMWSLIMYASNGPNHIRYIDCLFNCVSATCVCGLNSSLLGVMTGWQQVILFIQMIEGSIVTVSIVTIMIRRHFFRKAFKELIKLDEKSCRRVEDVEQAQKRRQGTFLHRVLHPGHHPSPEEPIMMDKPLRASPSSSLSPPGDSETLEKSPSTDRARAKKTHDDIVEKLRLREQERMQQAQADKERREQEKRKKKKTGPVTVGMIKRTDEPPKVNMMSVGGWLSDHPTAEGPAGEIQDAQALARETSQTGNGHVPSQPVTADNSANISRAASPALNSADFGSRDRSGQASPFDPSSPSSGANKQRRRNSDPATASRTPNLEVPRTNTIAHFAESPHPPHHTLNFAEPSQEAYGRRQSVYEPEQTIRQRHPTAASHNLNLERTMTRRSLARHETMPRSVTRQATMTQGFGGFPNPLAEGVRVLRRAADQAIRKTMTMPQTYSRTGTVQSAHSTGAISAATTNRNYLSFDPQVRRNSHFVKLTAAQEEELGGVEYRALSVLLKIVIGYYLGVHLIACLILAPYLTYGAPQYASNFTQTGGYTSPVWYIFFNVWSAFSNTGMSLLDSSLTLFQDAYLLLIVTIFLILAGNTAFPVFLRLTIWILAKCSPRQSRYRETLDFILDHPRRCYIYLFPTYQTIYLAVVVLLLTCIDWLSFLVLDIGNDYLGAIPLHTRVIDGLLQSAAVRAAGFQVVNLAATAPAVQLLYVIMMYVAVYPIALSIRATNVVYEDKALGIYDDDDDESEVDAEFEQKKDTKGYLAYHARRQLAFDLWYVVLAAWLICIIEKHNIQNVDLPWFSIFSIIFEIVSAYGTVGLSLGSPVLGTSLSGSFSQLSKIIICMVIIRGRHRGLPIAIDRSIMLPNALDMQAKSDAEGASLHRTKSWRRASLVPELTSDSRTRQDSMPGEHVYPPTFSDQGGIVEDEKTQRQRQQSVPATGISFANPHAARDARTLQNGKDQSSSESSGSGLSVEEKASL
1E-107	370	2.9	2E-107	369.6	2	1	1	G2Y3H1_BOTF4	Uncharacterized protein	BofuT4_P003700.1	Botryotinia fuckeliana (strain T4) (Noble rot fungus) (Botrytis cinerea)	402	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Sclerotiniaceae, Botrytis, Botryotinia fuckeliana (Noble rot fungus) (Botrytis cinerea), Botryotinia fuckeliana (strain T4) (Noble rot fungus) (Botrytis cinerea)	999810	>tr|G2Y3H1|G2Y3H1_BOTF4 Uncharacterized protein OS=Botryotinia fuckeliana (strain T4) GN=BofuT4_P003700.1 PE=4 SV=1MISFNTAIWPLLLMSFLIIIGNTGFPIMLRFIIWVTTLWVPRNSAVWEELRFLLDHPRRCFTLLFPSKATWWLFWILVILNGVDLLFFIILDLGNSVVTNLPVNIRVLDGWFQAASTRTAGFGVVNLAELHPAIQVSYLIMMYISVLPIAISVRRTNVYEEKSLGIYGSPTEENEDEGEPSYVGAHLRRQLSFDLWYIFLGLFIISIAEGGRLQGTDPSINMFSVLFEIVSAYGTVGLSLGYPGIDASLSAEFNVVSKLVIIAMQIRGRHRGLPYELDRAILLPSEHLAEKEALDAAQRVYRRNSNATAVSNGADLATVNTGVQRANTERQGPPTNFLSSLLHPGPTIPNSHRNQGTTHVRRHSIATPERGRSVSPKASGGIFSKWNSSDKHQNNVDKKISE

8E-107	367	15.1	2E-103	356.4	5.3	2.1	2	F4RTR8_MELLP	Putative uncharacterized protein	MELLADRAFT_89551	Melampsora larici-populina (strain 98AG31 / pathotype 3-4-7) (Poplar leaf rust fungus)	946	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Pucciniomycotina, Pucciniomycetes, Pucciniales (rusts), Melampsoraceae, Melampsora, Melampsora larici-populina, Melampsora larici-populina (strain 98AG31 / pathotype 3-4-7) (Poplar leaf rust fungus)	747676	[illegible] GN=MELLADRAFT_89551 PE=4 SV=1MVNRNTSSPPPCLNNFNNFTFNNHNNNNNNNNNNNNNRQSISGHRSHHRLSINRTTSFKSDQNFIRRLFDRLQYAIEPHLNFYRAHLLAFIFLPLLFGIIILLANRLNPPDSSTLQPARFIDCVFMSYSAMTMTGLNTIPLASINRFQQVILYILMTIGSTTSVSIMMIFIRLRYFKLRFRHILSTRQPSRPFISSPVDAHPLGNICPPRPKEAVSPRTLNTDIHGTPQEFFESKHIEPEQSPSNLNVLLPKPVAPVISDLEPNTTSIARIPLRRNSDTVLRQVSFSPARGRLHSTPKKLSAFPRSVTLGDEPKSVLRNPQWRFPAVAQSPILEATAMPVQVEFLIDEEQHLHQQEGAVRAGSLANDGPRYRRPRPRLGSKIERDSLHNRYTKTVSTGAHHGRTPSYASNAFSGNVPTTPIRRKPSLASQQDFGGFPNPFQILISRLFSWIRKCLRQKSSENNSNKLQFVRTTSLAINHPGVQDEKNHWWLSDVFDSIKKVKVVSYINFNAIVGRNSNFLTLTSAQEEELGGVEYRALSILLKILIGYWILVQFGAIIIILPWLETNDRYKPIFEAPDGTSIAWYAIWITCSSFTNGGMSLIDAGFTVFQDAYLLIFVCSFLILAGNTAFPIFLRFSIWFLSKIAPSRPSNSAGSCTKEVLGFLLDHPRRCFVYLFPARQNWYLLGSIVVLNIISWVAFLVLNIGNPEIEKIPPGTRLLAGLLQSLSVRAAGFSVVSIAALAPAVQVLYIIMMYIAVYPIAMSIRSTNVYEERSLGIFEQPGGGAVGERRGSNETIQSQHRNWWEGSRSYLSFHARQQLAFDIWWLFLALWIICIVERHQIIGDRNPWFNVFSILFELVSAYGTIGLSLGVPFSSTSLCGQFSRLSKLVVILVMIRGRHRGLPIAIDRAVLLPVDYNNQDEYQDENREEIGDENEEEEEEGQRNV
1E-106	367	16.7	3E-102	352.2	7	2.1	2	M2QLW3_CERS8	Uncharacterized protein	CERSUDRAFT_118212	Ceriporiopsis subvermispora (strain B) (White-rot fungus)	911	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Gelatoporia, Ceriporiopsis subvermispora (White-rot fungus) (Gelatoporia subvermispora), Ceriporiopsis subvermispora (strain B) (White-rot fungus)	914234	[illegible] PE=4 SV=1MPSFRPLRRLSRRCHNVWKYIWGHLNFYRVHILFFTFTPLIMSGIFFASNGEFRISYIDSLFNCVSAMTVCGLATVDLSTLTPFQQFLLFLQMILGSPVSVSWVMVYIRRNFFARKFEHIVKRNLARRMANQTNSPVQVKMVPLWRRALGLLFHRGRASTKTKVTNESSSSSSHEHNRPSGARLRPDMIRRMDDAPKLVNPSGLISEGRPQVTHVQSFVNRDPPVQPDRVRPRHLSFSQAEANKADTIDDSESTSGSSGLRGEHEWQQQEEHQLQTVQENPRTLGPPSALQPFLRSQSLAPTSTNHMPRTQTVEFASPPHMSRDAAHHENESYLQPIDHNGSDHFSSHDHRSFRRPTMSIPRTATAHTYRSRRTLHKGFGGFPMPHEIISSIMRRLFPTLERKLTRTITMPRTRTIASHHAAQAGARPVSYISFEAVVGRNSVFHSLTTEQLEELGGVEYRALTALLWIVGGYHVLLQLLAFVIIAPYISAPRWAADFVPPMLHRTVSPVWFSAFQVVSSYTNSGMSLEDQSMVPFQRAYPMIVVMIILILAGNTAFPVFLRFLVWVLSKIAPRKSRSNETLHFLLDHPRRCFVYLFPAHQTWFLVTVLISLNFTDWVFFLILDIGNSAITSIPAGVRVIIGLLQAVAVRASGFGTVALSALAPAVKVLYVLMMYVSVYPIAMSVRSTNVYEEKSLGIFEDESSSLDEEAFNPTGNRVTVWSRYLAMHMRKQLSFDMWWLGLALFLVCIIERSSIDNPDKQSWFNIFTILFELVSAYGTVGLSLGVPYANFSFSGALTPLSKVIVCGVMLRGRHRGLPVAIDRAVMLPIEFGDHFEQDEEVAEQEDDIVEPDTEMGQMPSGNVETIHEKQEHPRGDQESPDRHADTHESSHELQQRTNTRHTYEEAELGEH
5E-106	365	13.7	6E-106	364.3	9.5	1.1	1	E4NQC7_HALBP	Trk-type K+ transport system, membrane component (Trk-type k+ transporter, membrane component)	Hbor_22390_C499_17244	Halogeometricum borinquense (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3)	553	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Halogeometricum, Halogeometricum borinquense, Halogeometricum borinquense (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3)	469382	>tr|E4NQC7|E4NQC7_HALBP Trk-type K+ transport system, membrane component OS=Halogeometricum borinquense (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3) GN=Hbor_22390 PE=4 SV=1MAPSRRPTVAGWPADVAIIARDVGSLLALESALMTVSVLVALVFQEWYVAFAFFTAGGVTAAFGLGARVAFEDAPDPRMKHGMIIAAAGWLMTAVFGSLPFLFTAYFLPPEVAASYVPAGVDYATSSIQYFRNPLHALFESMSGWTGSGLTMAVNEPSLPRAIQWWRSLIQWVGGVGVIVLTVSILARPGSGSYALYRSEAREEKIHPSVVSTVRTVWKIFVGYTLVSVTVLFVAIRLSDYGSSLPLWEAGWQALNHAMTGLSTGGFSVTNNSITTYDSPLIEFVLLPVMSLGAIAFPVHYVVLRDRDFSELLGDLQTQWLLIAFIVGVVVLGIQNVVSIPFTTKAFEGGANWLGIGSLINPVVADAFRDSTFQWISALSCTGFQSAPIGKWSAGGKLILSGAMVIGGAAGSTVGGIKIIRAYTISRGIAWQFRRVFLPANTVVSIQMDGRRLDRTEMEREFSEAAIVSLLWVILLVVSSLLLVNLAGPNFTYADALFEVASAQGNVGLSTGITGPTMNPLAEGMFLLNMWVGRLEIIPILVFARAILYGLEP
1E-105	363	0.1	2E-102	353.1	0	2	2	T5A557_OPHSC	Potassium transport protein, high-affinity	OCS_06588	Ophiocordyceps sinensis (strain Co18 / CGMCC 3.14243) (Yarsagumba caterpillar fungus) (Hirsutella sinensis)	589	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Ophiocordycipitaceae, Ophiocordyceps, Ophiocordyceps sinensis, Ophiocordyceps sinensis (strain Co18 / CGMCC 3.14243) (Yarsagumba caterpillar fungus) (Hirsutella sinensis)	911162	[illegible] 3.14243) GN=OCS_06588 PE=4 SV=1MRSLAFNFITLHYAWVVFMGLLSLPILLPYGNLAAIDAYFFGASASTMSGLNTHDCKDLALYQQLYIYFVPLLTNLGFVNIMVVVVRLYWFNKRIDKLGHALIRARRRLAPDASPALDALGLAPESGATRSASASTHQDNESPLQRSPLQRSEPSVSQDWVHEEKTTLARLSGRRKTTTLGRDADVDTLTSKDRDEIGGVEYRSLKLLLKVVTVYFFGIHLLGGFGLLGWIQYADAKYTNNLREIGQDQKWWAFYTAQSMMDNLGFSLTPDSMAPFRDAVWPLLLMSFLGLAGETLYPVFLRFILWTLSRLAPRGSPMRESCRFLLKHPRRCYTLLFPSGTTWALLSIISALNAFDTLLIVVLDRHNPQVAGLDVGKRIAAALFQAVASRHAGMTPYTLADVHPAVQVSLLVMMYISAYPVALSVWTSNAYEERPVGLYAAEARYDENKGLSYLVRHMQQQLSFDLWYIFIGIFLLAVSESSKIQDSNEPASPQTCQLSLSFEIFPIFFEVVSAYANVGISLGHASTTASLSARFSVVGKLVICAMMIRGRHRALPSKLDRAVMLPDEHLLEGPEEEASRPMMDRTSWP
2E-105	362	5.3	8E-102	350.7	1.2	2	2	S7ZG48_PENO1	Uncharacterized protein	PDE_04188	Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	713	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium oxalicum, Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	933388	[illegible] PE=4 SV=1MEKIRRKSIRSYLPHVRFLTVHYAYFIIVTLVCSGILWGSSTPAHSLRYIDALYLAVSAMTLAGMNTVNLSTLNTFQQLLLFFLIMSGSAIWVSIGVVLTRKRAFERRFSELVKAERLERKARSQIGLGRSLARSHSISRQPTMPEEHPWASGILPIVRSPSRTEPFQSASALDSRISQNEGRSLRPRGMGLNEKAGSRSTLEGDYDSLTAREANVEATSGTLEIQKSNADTGTHVAFSPSSEAVQDEQAHSLRHRMLSPYTNVLDRTNTLGELERGSSADQTLGGDLHADILRKLNRNSSFYNLTEKERQRLGGAEYRAICLLAIIIPIYFFLWQLLGGLGLGAYLANNKASVTESNGLNPWWTGFFFAVSAFNNSGMSLLDANMVPFQTSPYILITMGLLILAGNTCYPIFLRCIVKAIHLMLPKHAYFDQFRDTLTFLLNHPRRVYTTLFPSAHTWWLLLSVIVLNGIDWLAFEVLNLDNPSVTSIPTGARVLDGLFQALCVRSGGFYLINIGGLQLGTQMIYVVMMYISVYPVVITMRHSNVYEERSLGIYADDLSAENREDNSSSDDSTSALSMAPTASRFYFIRHQLRSQLAYDLWWIALAVIIVCIVEAGQFTKDPVTFSALNIIFETVSAYGCVGISTGLPDQLYSFSGGWHTLSKLVLCAVMIRGRHRGLPVAIDKAIMLPSDKLMRAEEEDAQIRLERTMSRR
3E-105	362	2.8	3E-105	362	2	1	1	A0A080WIJ9_TRIRC	Uncharacterized protein	TERG_11998	Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) (Athlete's foot fungus)	321	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Trichophyton, Trichophyton rubrum (Athlete's foot fungus) (Epidermophyton rubrum), Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) (Athlete's foot fungus)	559305	>tr|A0A080WIJ9|A0A080WIJ9_TRIRC Uncharacterized protein OS=Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) GN=TERG_11998 PE=4 SV=1MTTYNNLGFALTPDSMVNFRASTFPMLLMTFLILVGNTAYPCMLRFIIWCMFHISPKASAIREPLNFLLDHPRRCYTLLFPSRTTWTLLGTLVLLNGLDIMLFMILDLKNPEVTAIDTTWHRLCAASFQSTASRTAGATTFSLSKIHPAVQFSLMVMMYISVFPVAISMRKTNTYEESSLGLYESEEEVDENSDSSSYLSQHIKKQLAFDLWYIFLGVFLITIAEGDKIADLADPAFQIFAIFFEVVSAYGNVGLSLGHPSINAGLSGKFTTISKLVMCAMMVRGRHRGLPYELDRAIVLPGERHKQEQARTDSQVVSSNS

7E-105	361	10.6	4E-103	355	2.7	2.1	2	A0A060STZ6_PYCCI	Uncharacterized protein	BN946_scf184907.g12	Pycnoporus cinnabarinus (Cinnabar-red polypore) (Trametes cinnabarina)	961	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Trametes, Pycnoporus cinnabarinus (Cinnabar-red polypore) (Trametes cinnabarina)	5643	>tr|A0A060STZ6|A0A060STZ6_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184907.g12 PE=4 SV=1MPSLPGRLLDKSKLADFQAYIVRHLNFYRVHLLFFTFTPLIFSGIFYASNGEFHIDYIDCLYNCVSAMTVCGLATVDLSSLTSFQQA LLFIQMCLGSPVVVSWTMVYIRRSFFARKFQRIVEAELARRAARKMHAPVNVKIEPWWQKLWTMLKWRRGTRLRSFSDISVQEVGP VKTRGRIHLRPDMIRRVEGAPKLVDPSGWISERVSEQQNQDDASPHRKSERDDHRRPSTSAASSSVMHTHSADSENKREDAHAQE GETAGERPPAETSPRNVTTALNHGTTPILRTQTINRPATRGPQLAHTQTVEFAATPAPHRRSLSMERRFSRIPQSPAESDTEHERRS MARPTMSRTRISNPTMSRPTMSRPTISRPTMSRPTMSRPTMSRPMSMPRTGTITTSGSQGFAPRRNVHKGFGGFPMPHEILSRLFG RAFPQLERKLTRTITIPRTRTIASERGTLPPGTRPVPYISFEAVVGRNSVFQSLTREQLEELGGVEYRALTALLWIVAAYHIGLQLLAFVV IAPYMSMNRWKADFLPPALHRPISSTWFSAFQVVSSYTNTGTSLVDQSMVPFQQAYPMIAFMILLILAGNTAFPVLLRFQIWILTKVVP RGSRLNETLHFLLDHPRRCFIYLFPSHQTWFLLIILFALNVTDWFFFLVLDIGNPAVDSIPLGVRFIIGLLQAAAVRAAGFATVSLAALAPA VKVLYVLMMYVSVYPIAMSVRSTNVYEEKSLGIFPDEDDLTPDEAFSSTAGNRASVWGRYLAMHARKQLSFDMWWLGLALFLVCIIE KDGLEDQSNNDWFTIFNIVFELVSAYGTVGLSLGVPYANYSFSGALRPLSKLIICAVMLRGRHRGLPVAIDRAVMLPYEFKEGLQDGY GEENYGDYAMEDYEMTRTGTVESASEDGRDVDTGRRYQDQQDGQTGMADEPKAPVDGATQHYQQQVGVQGEEDCSTEQQASG H
1E-104	360	5.3	2E-103	356.2	2.1	2	2	Q0CSV0_ASPTN	Putative uncharacterized protein	ATEG_03234	Aspergillus terreus (strain NIH 2624 / FGSC A1156)	686	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus terreus, Aspergillus terreus (strain NIH 2624 / FGSC A1156)	341663	>tr|Q0CSV0|Q0CSV0_ASPTN Putative uncharacterized protein OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) GN=ATEG_03234 PE=4 SV=1MWPKPQLNFITLHYAYIIFLGLLALPVLYPYGNLRAIDSYFFGVSASTESGLNTVDVKELKLYQQLFIYFIPIVSNLGFVNILVVCVRL WFFRKRLDEIGNPPFDFMMGKLQDCTPDQSTIHEKQNPDHDRNEQPEEPNTDHEAPEDENARSTSTKPLQPGDLNRTISFADTEKAL YIPSPQERDRGHPIIEVDRDTIADDTGNFEKSYPRLRRSLSIRNDTTLERVASSMFVLGKQHSRSQGPRMSQAISLSKDSNLPGLSTQA TLGRNSQFHNLTAEDRERLGGIEYRSLKVLLKIVVGYFFGLHLFGIICLVGWVQYAPAKYRDYIASCGLNQVWWFVETYTMLVVKRSD FVGFTLTPDSMISFNDATFPMLVLTFLAFAGNTLYPCFLRLIIWVLFKCVPNNSSLKEPLDFLLKYPRRCYMLLFRSRPTWVLFGIIFALN FVDVLFIITLDLDNPAVNSLAPGPRILAALFQAASARHTGTATFNLANVNPAVQFSLLVMMYISIFPIAISVRASNSYEERALGIYDSGDEL DENNGSKYVLAHMRNQLSFDLWYIFVGLFCIIATESKRIMDPAEPAFNVFAIFFETVSAYANVGLSLGYPTVSTSLCGQFSTFSKVVICA MMIRGRHRGLPNQIDRSILLPSERLVEDDHIDAKPPPWHTADRVTWMDSRQPKVRRYYTK
1E-104	360	9.8	1E-104	360.1	6.8	1.9	1	Q59X77_CANAL	Uncharacterized protein	TRK1 CaO19.8233	Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)	874	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Candida, Candida albicans (Yeast), Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)	237561	>tr|Q59X77|Q59X77_CANAL Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=TRK1 PE=4 SV=1MLYRVSGFYKRHTRNFTNIDYGYYIRNFIHHIASKIYPYAKVVLPNFRAAHYFYILTLVILGSILVYPVKTCAYIDVLFFTAGASTQA GLNTVNVNDLSLYQQIVLYLLATLATPIFIHGSLLFVRLYYFERHFDNIKERSLMDYRMRKSATLARLGSAPTMSSTRLNTFNNQVLGFQ EREAEKGSSLSPQSSSSQTSQPVSTAYNDQGGNDIEHHSEPSDSDDDESGNGPVTFQEKIHFEEPQRPRSQRRHSRTDSGIKFSAL PHPRRRKSIDPEDMYRSINMLQEHKKNQEAKSKGIQFLNIGSPVRRKSRSSNIEAFPEEDTNPSRDDEITPATNSVGTGNNDEDEDDIL IIKPPIEIENSDGANPIFTKKKKLASQIQFKETPGKAKKWITTKTRKHYNPWTSKLKKTLSNSSKKGSLSVVPTDTEDDSEDEEYASIDSE TSDISDNEHAADNAEGSDVDSVGSYEEDEDEDEHNSDDDDGEGERRLGNGASLTKAQSHLVLPSKDETGGKKYTKRSNTLDTPQ QNTSDGRKIRKKAPKRKTPRTQRNASFNQHSNVSIGDGSIENVDTNDSYQRLSRTMSGNYLSWTPTVGRNSTFIKLTDEQKEELGGI EYRAVKLLIKIIVVYYVGFNIIPGVMLSIWIYCMPHYKNLMISSSISPAWWAFFTSQSSFNDLGLTLTSNSMMSFNQNAFVQILCSFLIVIG NTGFPILLRFIIWVMFKTARPLSLYKESLGFLLDHPRRCFTLLFPSVPTWWLFFILVVLNGFDLVIFCILDLHDDTFKGVDMGYRVLNGLF QAFCTRTVGFSVMDLSQLHAATQVSYLIMMYISFCPIAISVRRTNVYEEQSWGYMPRRMQRVLMRVRHQTMLGRI
1E-104	360	9.8	1E-104	360.1	6.8	1.9	1	Q59XC5_CANAL	Uncharacterized protein	TRK1 CaO19.600	Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)	874	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Candida, Candida albicans (Yeast), Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)	237561	>tr|Q59XC5|Q59XC5_CANAL Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=TRK1 PE=4 SV=1MLYRVSGFYKRHTRNFTNIDYGYYIRNFIHHIASKIYPYAKVVLPNFRAAHYFYILTLVILGSILVYPVKTCAYIDVLFFTAGASTQA GLNTVNVNDLSLYQQIVLYLLATLATPIFIHGSLLFVRLYYFERHFDNIKERSLMDYRMRKSATLARLGSAPTMSSTRLNTFNNQVLGFQ EREAEKGSSSSPQSSSSQTSQPVSTAYNDQGGNDIEHHSEPSDSDDDESGNGPVTFQEKIHFEEPQRPRSQRRHSRTDSGIKFSAL PHPRRRKSIDPEDMYRSINMLQEHKKNQEAKSKGIQFLNIGSPVRRKSRSSNIEAFPEEDTNPSRGDEITPATNSVGTGNNDEDEDDI LIIKPPIEIENSDEANPIFTKKKKLASQIQFKETPGKAKKWITTKTCKHYNPWTSKLKKTLSNSSKKGSLSVVPTDTEDDSEDEEYASIDS ETSDISDNEHAADNAEGSDVDSVGSYEEDEDEDEHNSDDDDDGEGERRLGNGASLTKAQSHLVLPSKDETGGKKYTKRSNTLDTPQ QNTSDGRKIRKKAPKRKTPRTQRNASFNQHSNVSIGDGSIENVDTNDSYQRLSRTMSGNYLSWTPTVGRNSTFIKLTDEQKEELGGI EYRAVKLLIKIIVVYYVGFNIIPGVMLSIWIYCMPHYKNLMISSSISPAWWAFFTSQSSFNDLGLTLTSNSMMSFNQNAFVQILCSFLIVIG NTGFPILLRFIIWVMFKTARPLSLYKESLGFLLDHPRRCFTLLFPSVPTWWLFFILVVLNGFDLVIFCILDLHDDTFKGVDMGYRVLNGLF QAFCTRTVGFSVMDLSQLHAATQVSYLIMMYISFCPIAISVRRTNVYEEQSWGYMPRRMQRVLMRVRHQTMLGRI
4E-104	358	9.8	1.4E-52	188.3	0.1	2.4	2	A1CT00_ASPCL	Cation transporter, putative	ACLA_081250	Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	641	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus clavatus, Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	344612	>tr|A1CT00|A1CT00_ASPCL Cation transporter, putative OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) GN=ACLA_081250 PE=4 SV=1MPTTLDEAKDLSPIRLHHHYFYLAFWIVLASAITYGIGDIDFIDALAFASGAATQSGLNPIDLNRLHVLQQLVLWIVAMVTNVIFVNS LLVCIRLYWFRKRLRGVVREAQTISLVHRRKGQEGLESSASHISIESNNRNNDLAYTSADDDGSKQPLLRGYHGELRRLSSTNYEVVK QIAGLTELHVTFDETERQPRHHRTYSSSESYRCPSEGRASLHRSSYDMDSSLSALPALMWQSSIASYSDWNERQKDQLGGIEYRAL KRLLVILLYYFLAFHIVGILLLISWAWLNPQYGQYLSENGINSSWWAIFTAASAFNDLGFTLTPDSMESLNGAPFPLLIMSFLIVIGNTAFP CMLRLIIWLLSKFTSHDTYLREELQFLLDHPRRCFTLLFPSAESWRLLGVLIMLNGFDLIVFCTLSNVASTRTAGFSITPLADIHPAIQVSF LVMMYISAFPTAITIRKTNVYSEKSLGVYDDDSDSESDHGPHTRSGLAVHIQRQLGFDLWYVMLGFFLIAVAEGHRLQTGAGDSSFSL FAVLFEIVSAYGTVGLSLGYPLTGTSFCAQFNWVSKLVIVAMQVRGRHRGLPNALDHAILLPYELHREGEGGSGWLGGWLKKRASNL STLLSQARGPDDDEESVLHY

4E-104	358	13.9	4E-103	354.9	5.2	2.1	2	J4G0W1_FIBRA	Uncharacterized protein	FIBRA_01258	Fibroporia radiculosa (strain TFFH 294) (Brown rot fungus) (Antrodia radiculosa)	920	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Polyporaceae (bracket fungi), Fibroporia, Fibroporia radiculosa, Fibroporia radiculosa (strain TFFH 294) (Brown rot fungus) (Antrodia radiculosa)	599839	>tr|J4G0W1|J4G0W1_FIBRA Uncharacterized protein OS=Fibroporia radiculosa (strain TFFH 294) GN=FIBRA_01258 PE=4 SV=1MPSLPSRRLSRKSWNWLSNIWRYFRGHLNFYRVHILVFLFAPLIFSAIIYAANGEFHIAYIDCLFNSVSAFAVCGLASIDLSRMTPF QQALLFIQLSLGNIVVVSWVMVYIRRSFFAKKFQRFMEADMARKLSRQSHKHVEVKLVPWWRRAANIVFGQTKLDSGDANDSGSSS TPDHRGAQTSRLRPDMIRRMDDAPRRINPSGWISEARMDTRGHATSEAPHGDVSSSPQFLTFSDIESPAPVDGPALQGSPRSASVT ELESDVSDSKHHGAGDEEEEQNRRRVLSDPQVPPMMSELHKSGQGDRLPRSISVSVASPNRQGYLPRTQTIEFAATPRPLRSARSF GEFGGRVNSLAQQGTITDYSTPHDRRSMHRPTISMPHTFESRASLHSHPPRVMDTGFGGFPMPFEILSRLFRHFFPKLERKLTRTVT MPRTRTIVSQHGSVAPGARPVSYISFEAVVGRNSTFKRLTHEQLEELGGVEYRALGALLWIVGGYHLVTQLMAFTIIAPYVSIPRWSA DFKTPQLFRNTSPIWFSAFQVASAYTNAGMSLVDQSMLPFQEAYPMIVAMIFVILAGNTAFPIFLRFTIWILSKLVPRQSRLNETLHFLL DHPRRCFIYLFPSHQTWFLLTILTILNTTDWFAFLVLDLGNSVIGSIPVGVRVIDGMLQAVAVRAAGFGIVPLAALAPAVKVLYVIMMYIS VYPVAMSVRSTNVYEEKSLGVFEDDQSSVDVNFNPAGNRVTVWSRYLAMHMRKQLAFDMWWLAVALVLICIVERDSLENPANATW FNIFNVLFETVSAYGGVGLSLGVPYDNFSLSGAFSPLSKLIICAVMLRGRHRGLPVAIDRAVMLPSDFDVVEPPPTSETPAYHDEESAP AKLSSPESPRSRRLSVLRTLSEAPSRDTPDRDEQDRPVGNGDVSA
4E-104	358	1.8	1.3E-98	340.1	0.2	2.1	2	A1C8P3_ASPCL	Cation transporter, putative	ACLA_044000	Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	708	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus clavatus, Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	344612	>tr|A1C8P3|A1C8P3_ASPCL Cation transporter, putative OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) GN=ACLA_044000 PE=4 SV=1MNRIYKFLKNHRPRVRFLTLHYAYFTTTCFIGSIILWASSHPLGSLRYIDALFLAFSAMTLTGLNTVNLSTLNLFQQLLLLFLIMLGS TIWVSIAVLLTRRRAFERRFGDIIREQRLRRWKTSGSLRAGLNRSLTRSLGQLGSSSTNVAQESEKGDGLRATGTLDRRPTGRHDSG VGDETVASVLESTPRHLASYDAKEHFSLLNRASTGDRRPSFLHTMNSDDGNHVNFAADVRPHGRPSSAYSRIIPAGRRLSKENIRHC RHPDPHMCPEHGHLSFLRHFGRNATAPELTDEERDRLGGIEYRAVCLLTVIVPLYFVLWQVIGGLAVAAYVARNKAGVTERNGMNP WWAGFFFGISAFNNSGMSLVDANMVPFRSSIFMLITMGLLILAGNTCYPIFLRCILYGMKHLLPKHKYFREMRATLRFVLKYPRRCYTN LFPAQHTWWLLCLVIVLNGIDWAAAFEILNIDNPAVTSIPLGPRVLDGLFQALCVRNSGFFIANISTLQLGMQLIYLVMMYISVYPVVITMR NSNVYEERSLGIYADDSARSQRASRSPPASRTRPRAPSSIPKKSPSRRLYFVQQQLRAQLAYDLWWIALAVIVICIVEAGNFTRHPVTY SAFNIIFETVSAYGTVGLSTGLPDETYSFSGGWHTLSKLVLCAVMLRGRHRGLPVAIDKAILLPAEHLMLAERedTRIRRDRTRSWNR GMV
1E-103	357	14.7	2.6E-97	335.8	2.1	2	2	Q5KK04_CRYNJ	Potassium transport protein, high-affinity, putative	CNC04730	Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) (Filobasidiella neoformans)	810	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Tremellomycetes, Tremellales (jelly fungi), Tremellaceae, Filobasidiella, Filobasidiella/Cryptococcus neoformans species complex, Cryptococcus neoformans (Filobasidiella neoformans), Cryptococcus neoformans var. neoformans, Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) (Filobasidiella neoformans)	214684	>tr|Q5KK04|Q5KK04_CRYNJ Potassium transport protein, high-affinity, putative OS=Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) GN=CNC04730 PE=4 SV=1MPSIRPSLSTLPSYLALPSRRTKWKALIVGSLNFYRIHLITFTVVPLITSSIMFACNTEYHISYIDCLFCCMSAMTVTGLATVDLSTL SPFQQVILFLQMIIGSLSFVSIVMILVRQYFFRQTFKHVLQERERRRTRLTKTITRVATAAPPISAIRKRFGAGFRQFDKGDTELKNGSPE RSAPSSLELKAVSHSPKKPEDHHHKHWKKGHQKLRPDMIKRVQGGGVGLVNPMGWYDVERAEIATPAPTPELRSDTPLPSGKTVAA DGKDLSQALEAVVVSGVAQARQSAGEAEQEVSEVENKEPKTKLSEAEAGAKVADKVSTGSNEGDRTPTPPPSPARHKIPYAGLQLT DGAGRSTGGGTEGKDAPYISFSATVGRNSRFQGLTTEQMDELGGVEYRALRVLLYIVVGYVIFMPLAGFVIIAPYISAGNRYDYVFNE QPRNVGIPWFALYQSISAFTNTGMSLCDMSMLPFQRAYLMIVGRSLFSVAHALLIPWTKFIWVIYKCVPESSRVRESLKFLLDHPRRCF VYLFPSTQTWVLALVMLTLTLIDWVSFLVLDLGTEAIMSLPIGTRIAAGFLQSAAVRAAGFSIVPLGDLAPAVKVLYVVMMYISVYPIALS VRSTNVYEEKSLGLFGDEVEEDDLSEEGSGAHAVAKYIGWHARRQLAFDIWWLAFALWLVCIIERGHIDNDQEWFSIFNIIFELVSAYA TVGLSLGVPYDNYSFCGGFRKLSKLVVIIVMLRGRHRGLPVAIDRAVMLPKDFTTAEETAFEEERSRRASRMGSMFNEDVFDMRRGS YGGDVPNYRASDPAS
2E-103	356	1.3	9E-101	347.2	0	2.1	2	S0DIE9_GIBF5	Related to TRK1-Potassium transporter I	FFUJ_01611	Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	763	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella fujikuroi (Bakanae and foot rot disease fungus) (Fusarium fujikuroi), Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) (Bakanae and foot rot disease fungus) (Fusarium fujikuroi)	1279085	>tr|S0DIE9|S0DIE9_GIBF5 Related to TRK1-Potassium transporter I OS=Gibberella fujikuroi (strain CBS 195.34 / IMI 58289 / NRRL A-6831) GN=FFUJ_01611 PE=4 SV=1MLDSFTSRWKDLREEHPRLDAVVTQAGGLVPPINFITIHYAYFIFGSLFFSLIFWLSSEPSQSIPYVDCLFLVVSSFCDTGLNTVNL SEITTWQQVLLYLLFIIGSALWVSFWTVMVRKQAFEKRFEDIVRTEREARKRRAALRRAKPLGRFLPFAKARTTPVSTETSSTLTGLGT VQRTATEKPDPNDLFKTTAPMRRAVTAPPDSISDSDDNDSNTTQVAAPARNAPMTPNTGDHIQFADNLSPRSAGRDSVSIYRRNENE EPNRRPSTSDSVNSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKILAVTVPLYAFMWQAVCGIALGAWISINR PSAATVNDVNPWWCGIFLSSSAFNNAGMSLNDAGMGAFQDAYFVLIVVGILVLAGNTGYPLLLRFFLWCSLRLLQLTTEPKTLGPWK ETIEFILKYPRRVYTTLFPSGATWWLFTVIVTINTIDWVAFEVLNIGNDVVEAMPVSDRIIAGWFQAIAVRAAGFAVVSIGSLYPAVQLLY MIMMYISVYPVSITMRHSNVYEERSLGIYEDDPQVVEAENGNGSENGNHLLPTISEEPEKPALRRRVTAAAQKTVKKSMTFHGVGVR PPPKGPDDNSRISFIGQQIRGQLAHDMWWLILPVIVIMIETDHFLEQPLAYSVFNVLFEVVSAYGCVGLSMGLPGKSYSMAGGMHRG SKFVLCLVILRGRHRGLPVALDKAVRLPGEKLVREEEEDSKIRRTKTMNRIASRESRVM
2E-103	356	2	2E-99	343.1	0.1	2.1	2	K3UHP9_FUSPC	Uncharacterized protein	FPSE_08550	Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	762	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Fusarium pseudograminearum (Wheat and barley crown-rot fungus), Fusarium pseudograminearum (strain CS3096) (Wheat and barley crown-rot fungus)	1028729	>tr|K3UHP9|K3UHP9_FUSPC Uncharacterized protein OS=Fusarium pseudograminearum (strain CS3096) GN=FPSE_08550 PE=4 SV=1MFEFIKNRWQDLREEHPRLDAVATKVWMVVPPINFITIHYAYFIFGSLIFSVIFWGSSQPSQSIDYIDCLFLVVSSFCDTGLNTVNL SQLTTWQQVLLFILFIIGSALWVSFWTVMARKHAFEKRFEDIVRTEREARKRRTALRRSKPLGRFISFDKYKTSPASTGTSGILPGLGT KQKTETEKTDTNTNDLFTTTKPIRRAVTAPEEPISSDSDDNDSNRTHVAASSRIPPPTPSSGDHIQFASNLSPRSGGRDRDSVSIYRRN DDTELDRHPSRASVADSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKVMSVTVPLYGFAWQAICGIALGAWI NNNRPSAATVNAQNPWWCGIFLSASAFNNAGMSLNDAGMAAFQDGYFVLIVVGLLILAGNTAYPLLLRFFLWCSLRLLQLTTQPKTL GPWKETIEFILKYPRRVYTTLFPSGATWWLFLVIFVINTIDWVAFEVLNIGNKVVESMPVSDRIIAGWFQAIAVRAAGFAVVSIGSLYPA VQLLYMIMMYVSVYPVSITMRHSNVYEERSLGIYEDDPQVLEAENGTGHLRTISEAPEKPALRRRVTAAAQKTVKKSMTFHGVGVRP PPKGPDDNSRISFIAQQMRGQLAHDLWWLILPVLIIMIETDHFNQQPLAYSIFNVLFEVVSAYGCVGLSVGAPGQSYSLAGGMHRGS KFVLCLVMLRGRHRGLPVALDKAVRLPGENLAREEEEDSKIRRTNTMFRMASRESRAV
3E-103	355	9.8	2E-100	346.1	4	2.1	2	S7Q5S4_GLOTA	TrkH-domain-containing protein	GLOTRDRAFT_77591	Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) (Brown rot fungus)	775	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Gloeophyllales, Gloeophyllaceae, Gloeophyllum, Gloeophyllum trabeum (Brown rot fungus), Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) (Brown rot fungus)	670483	>tr|S7Q5S4|S7Q5S4_GLOTA TrkH-domain-containing protein OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_77591 PE=4 SV=1MPRLNFFRIHLLLFVVCSLIFSAILWASNGCFKINYVDALFLCVSSVTGTGLYTIDLSSLTAWQQTIMVILELIGNPVAVSWVLVYV RRRYFVNHLHHVIRAEIERTKSRNQMATNKVDEEQAPRRRSREPDATQLDRPEVVVASTRSGPGLVRRLDTAPRRIGAMDFVEGAG VISPWPRPMMYHRMLIVRPRCQAMEKLRVLSTIRARTSNCPHAGRRNKARQVNASGIQSSIHTQRTRSLRRQESDFGGFAGPTEFVS KLMKRTAPNLHTQLTRTITMPHTTTVTGMDDRGEEGAHRGATKQVPYISFNATVDRNSRFLQLTEDNLQELGGVEFRALNALLWIVPI YYMGILAVSLVVVAPYMSLSRWTSNFLPPQQHRVINPVWFSMFQVVAAWANTGMSLVDQNMIPFQTAYPMIFFLILCILAGNTAYPILL RFMIWILSKCVHRRSRAYETYQFLLDHPRRCFIYMFPSRQTWFLLLMLLFLNCTDWFFFLILDIGNPAISTIPVGTRNILGLLQACAVRTA GFQSVILSALAPAVKVLYLIMMYISVYPVAMSVRSTNVYEKQSLGIYDEEAEVDDDDDQFNNGSRVAIWGKYIFLHVRRQLAFDLWWL AFALFLLCIIEAHNLNDPSKATWFNIFQLTFELVSAYGTVGLSLGIPTANYSFAGALRTLSKLILCAVMLRGRHRGLPVALDRAVMLPSEF RPKEKEKEVSNPTDLDQDTPKTYPSQDARREGAASSHDLTEKIDQRQKQNRDSLGTFLPDPDAAIQFE

4E-103	355	14.2	2E-101	349.1	5.3	2.1	2	B0D8N6_LACBS	Predicted protein	LACBIDRAFT_296383	Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) (Bicoloured deceiver) (Laccaria laccata var. bicolor)	893	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Tricholomataceae, Laccaria, Laccaria bicolor (Bicoloured deceiver) (Laccaria laccata var. bicolor), Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) (Bicoloured deceiver) (Laccaria laccata var. bicolor)	486041	[illegible] GN=LACBIDRAFT_296383 PE=4 SV=1MPSLFTPSTFATTDTNSSGWWRKIRKQLNFYRVHILCFTFTPLIFSAIFFASNGRYKVSYIDALFNCVSAMTVCGLATIDLSELTGWQQTILFIQMCLGSPVFVSWVIVLIRKYFFARKYQHVLKAAVARKDAQAAEDSAKRRNSWSNRIHTYVHSGKKLSVVAEEPLQAKKKVEREESKGFIGKLRPDMIRRMDDAPKLVNPSGTVSEGTPLAIRKIPTAHTHTDFPRQISFVTPSALESVHDHSGIAKRSRRLSDPGKSSGLPSPLKQRPGEGEALNHAGKRFRRSQTVEFSLRTPDHGLSKPVLDPVPESSSARQTLAPHASMTTFTTHPTQHTHHSPRHIQESKNRGFGGFPMPFEIISSIFAKLFPKLNQKLTRTLTTPVTIPLVSNREGGVEGGKQVPYISFDAVVGRNSAFYLLTSDQMDEIGGVEYRALNSLLWIVPFYHIGIQLFCFTIIAPYISTKRWSSIFVPPEQLRPIPTTWFAAFQVVSAYTNTGTSLVDQSMVPFQRAYPMVILVSFLILAGNTSFPIFLRFLIWMLSKLVPKKTRFGETLHFLLDHPRRCFIYLFPSHQTWFLLTIVLLLTITDWFFFLILDIGNPVIEEIPLNVRVLAGLMQAIAVRAAGFAIVPLAALAPAVKVLFVIMMYISVYPIAMSVRSTNVYEEKSLGIFDAHEEESDGESEFQASGPRMTVWSRYLAMHARKQLAFGRQIQCISKYQNANIFIVDMWWLAGALFLVCIIERGNIMNPDNQSWFTIFNIIFELVSAYGTVGLSLGIPTDNFSLSGAFHPLSKLVVCLVMLRGRHRGLPVAIDRAVLLPDEFEKTDEDMADDRSQHSHTMREEGTLGSRQSRHLDEDEGLWQRAPRSNDEDDYAILPTARLAEAAAGQVPP	
1E-102	354	1.7	4E-100	345.3	0	2.1	2	W7MF12_GIBM7	Uncharacterized protein	FVEG_09483	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	763	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	[illegible] PE=4 SV=1MLDSITSRWKDLCEEHPRFDAVVTQAGRLVPPVNFITIHYAYFIFGSLFFSLIFWLSSEPSQSIPYVDCLFLVVSSFCDTGLNTVNLSEITTWQQVLLYLLFIIGSALWVSFWTVMARKQAFEKRFEDIVRTEREARKRRAALRRAKPLGRFIPFAKARTTPVSTETSNTLTGLGTVQRTATEKPDPNDLFKTTAPMRRAVTAPPDSISDSDDNDSNTTQVAAPARNAPMTPNSGDHIHFADNLSPRNAGRDSVSIYRRNENEEPNRRPSTSDSVNSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKILAVTVPLYAFMWQAVCGIALGAWISINRPSAATVNAINPWWCGIFLSSSAFNNAGMSLNDAGMGVFQDAYFVLIVVGILVLAGNTGYPLLLRLFLWCSLRVLQLTTEPKTLGPWKETIEFILKYPRRVYTTLFPSGATWWLFTVIVAINTIDWVAFEVLNIGNDVVEAMPVSDRIIAGWFQAIAVRAAGFAVVSISGLYPAVQLLYMIMMYISVYPVSITMRHSNVYEERSLGIYEDDPQVLEAENGNGNENGNHLLPTISEEPEKPALRRRVTAAAQKTVKKSMTFHGVGVRPPPKGPDDNSRISFIGQQIRGQLAHDMWWLILPVIVIMIIETDHFLEQPLVYSVFNVLFEVVSAYGCVGLSMGLPGKSYSMAGGGMHRGSKFVLCLVILRGRHRGLPVALDKAVRLPGEKLVREEEEDSKIRRTKTMNRIASRESRVM	
2E-102	353	2	5E-100	344.8	0	2.1	2	A0A0D2Y4V4_FUSO4	Uncharacterized protein	FOXG_11308	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	765	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	[illegible] 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11308 PE=4 SV=1MLDSITSRWKDLREEHPRLDAVATQAGRLVPPINFITIHYAYFIFGSLFFSLIFWLSSEPSQSIPYVDCLFLVVSSFCDTGLNTVNLSEITTWQQVLLYLLFIIGSALWVSFWTVMARKQAFEKRFEDIVRIERAARKRRAALRRAKPLGRFLPFTKARTTPVSTETSNTLTGLGTVQRTATEKPDPNDLFKTTAPMRRAVTAPPDSISDSDDNDSNTTQVAAPARNAPMTPNSGDHIQFADTLSPRSAGRDSVSIYRRNENVEPNRRPSTSDSVNSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKILAVTVPLYAFMWQAVCGIALGAWISINRPSAATVNAINPWWCGIFLSSSAFNNAGMSLNDAGMGAFQDAYFVLIVVGILVLAGNTGYPLLLRFFLWCSLRVLQLTTEPKTLGPWKETIEFILKYPRRVYTTLFPSGATWWLFTVIVTINTIDWVAFEVLNIGNDVVEAMPVSDRIIAGWFQAIAVRAAGFAVVSISGLYPAVQLLYMIMMYISVYPVSITMRHSNVYEERSLGIYEDDPQILEAENGNGNENGNHLLPTISEEPEKPALRRRVTAAAQKTVKKSMTFHGVGVRPPPKGPDDNSRISFIGQQIRGQLAHDMWWLILPVIVIMIIETDHFLEQPLVYSVFNVLFEVVSAYGCVGLSMGLPGKSYSMAGGGMHRGSKFVLCLVILRGRHRGLPVALDKAVRLPGEKLVREEEEDSKIRRTKTMNRIASRESRVM	
2E-102	353	1.2	7E-100	344.3	0	2.1	2	F9FTI3_FUSOF	Uncharacterized protein	FOXB_09714	Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	767	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	660025	[illegible] SV=1MLDSITSRWKDLREEHPRLDAVATQAGRLVPPINFITIHYAYFIFGSLFFSLIFWLSSEPSQSIPYVDCLFLVVSSFCDTGLNTVNLSEVTTWQQVLLYLLFIIGSALWVSFWTVMARKQAFEKRFEDIVRIERAARKRRAALRRAKPLGRFLPFTKARTTPVSTETSNTLTGLGTVQRTATEKPDPNDLFKTTAPMRRAVTAPPDSISDSDDNDSNTTQVAAPARNAPMTPNSGDHIQFADTLSPRSAGRDSVSIYRRNENVEPNRRPSTSDSVNSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKILAVTVPLYAFMWQAVCGIALGAWISINRPSAATVNAINPWWCGIFLSSSAFNNAGMSLNDAGMGAFQDAYFVLIVVGILVLAGNTGYPLLLRFFLWCSLRVLQLTTEPKTLGPWKETIEFILKYPRRVYTTLFPSGATWWLFTVITINTIDWVAFEVLNIGNDVVEAMPVSDRIIAGWFQAIAVRAAGFAVVSISGLYPAVQLLYMIMMYISVYPVSITMRHSNVYEERSLGIYEDDPQVLEAENGNGNENGNHLLPTISEEPEKPALRRRVTAAAQKTVKKSMTFHGVGVRPPPKGPDDNSRISFIGQQIRGQLAHDMWWLILPVIVIMIIETDHFLEQPLVYSVFNVLFEVVSAYGCVGLSMGLPGKSYSMAGGGMHRGSKFVLCLVILRGRHRGLPVALDKAVRLPGEKLVREEEEDSKIRRTKTMNRIASRESRVM	
2E-102	353	1.8	7E-100	344.3	0	2.1	2	N4UM14_FUSC1	High-affinity potassium transport protein	FOC1_g10013048	Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	767	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. cubense, Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	1229664	[illegible] GN=FOC1_g10013048 PE=4 SV=1MLDSITSRWKDLREEHPRLDAVATQAGRLVPPINFITIHYAYFIFGSLFFSLIFWLSSEPSQSIPYVDCLFLVVSSFCDTGLNTVNLSEITTWQQVLLYLLFIIGSALWVSFWTVMARKQAFEKRFEDIVRIERAARKRRAALRRAKPLGRFLPFTKARTTPVSTETSNTLTGLGTVQRTATEKPDPNDLFKTTAPMRRAVTAPPDSISDSDDNDSNTTQVAAPARNAPMTPNYGDHIQFADTLSPRSAGRDSVSIYRRNENVEPNRRPSTSDSVNSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKILAVTVPLYAFMWQAVCGIALGAWISINRPSAATVNAINPWWCGIFLSSSAFNNAGMSLNDAGMGAFQDAYFVLIVVGILVLAGNTGYPLLLRFFLWCSLRVLQLTTEPKTLGPWKETIEFILKYPRRVYTTLFPSGATWWLFTVIVTINTIDWVAFEVLNIGNDVVEAMPVSDRIIAGWFQAIAVRAAGFAVVSISGLYPAVQLLYMIMMYISVYPVSITMRHSNVYEERSLGIYEDDPQVLEAENGNGNENGNHLLPTISEEPEKPALRRRVTAAAQKTVKKSMTFHGVGVRPPPKGPDDNSRISFIGQQIRGQLAHDMWWLILPVIVIMIIETDHFLEQPLVYSVFNVLFEVVSAYGCVGLSMGLPGKSYSMAGGGMHRGSKFVLCLVILRGRHRGLPVALDKAVRLPGEKLVREEEEDSKIRRTKTMNRIASRESRVM	
6E-102	351	5.2	3.2E-97	335.5	0.8	2.1	2	V5FVD9_BYSSN	Uncharacterized protein	PVAR5_2300	Byssochlamys spectabilis (strain No. 5 / NBRC 109023) (Paecilomyces variotii)	918	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Thermoascaceae, Byssochlamys, Byssochlamys spectabilis (Paecilomyces variotii), Byssochlamys spectabilis (strain No. 5 / NBRC 109023) (Paecilomyces variotii)	1356009	[illegible] GN=PVAR5_2300 PE=4 SV=1MVQMSWKAIRPYLPRARFLTLHYVYFISMSLLASLIFWGASTPSRSVSYIDSLFVTTSAMTVTGLTSLNLSTLNTFQQILLYLLNMCGSAITVSIAVVLVRKQAFEKRFSDIVAEQRRRRRELRRRTKIRRATPLQEAPSGQIIVGSMNTATDHPHVENKTASWQSPVDLLRGRLRLFGRKDADSMDEKTKQLSVSETAVGGEPLSTCQQEKQNNPSVRNSPHVTFSNDVRRPSREHPQEPSHQSLAPVYSNTTDPLNSLHNVEDGSTLEDEDDLHLRFLGSLGRNSTFYNLDDDERDKLGGVEYRAIQMLLYIVPLYFIIWQFIGGLAVGAYLSRNRTGVVKTYSQNPWWAGFFLATGAFTNSGMSLIDAGMTPFQTSKFLLLTLSLLMLAGNTCYPIFLRWSLRAIQWMLPDTDYGRYYRETLQFLFDHPRRCYTTLFQSKETWWLFASVVGMNALDWILFEILNYDNPVVDSIPLGSRILDGLFQSLAVRTTGFSIISISSLQIGLQLVYVVMMYISVYPVVITMRNSNVYEERSLGIYDEDTADMQEQEEEAGVTGTPNSSTSQLPTFRASGRMYFIRQQLRAQLAYDMWWMVLAAIIICIIEAGNFKRDPITFSAFNIIFETVSGYGCVGLSTGLPDQPYSFSGAWHTLSKLIMCAVMLRGRHRDLPVAIDRAILLPGEHLSRAEEEDAKIRMQNTLTRPSLLISIIAIALTDFADKVRFQIYELRAQMSSKATTKHTQAAAKGAEIKRLQEEALRKLPLNTLYTALYIRNDPPIPNDFHWAFYFHTSPRGGTEYQVKGVGDGWIADHVSVGGIFKSNFLCVLIQITTVPQTAHAQVDQILRSYDEHLNSIPNITCRVWLLNMAQLLTQEGLLNCENIEALQQECFGIGNQYMWEAAMAQQPRPVVKSSVCS	

7E-102	351	7.9	3E-98	338.9	3.6	2.1	2	E6ZPT4_SPORE	Related to potassium transporter TRK-1	sr15310	Sporisorium reilianum (strain SRZ2) (Maize head smut fungus)	1173	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Ustilaginomycotina, Ustilaginomycetes, Ustilaginales, Ustilaginaceae, Sporisorium, Sporisorium reilianum, Sporisorium reilianum (strain SRZ2) (Maize head smut fungus)	999809	>tr|E6ZPT4|E6ZPT4_SPORE Related to potassium transporter TRK-1 OS=Sporisorium reilianum (strain SRZ2) GN=sr15310 PE=4 SV=1MLESVASNSQATATDSRSKLRSFGRWCGKNLNFYRVHVLVFTFTPLIAAAIFYACNGETHINFIDALFCCVSAMTVTGLVTINIST ANGGQQAILFILMCIGNISAVSVTMIWIRRSFFRKKFDRVVRRSAKVRKRMHDVEEQERRERRHNIAKIQRMVGLKSSDSATTISDTED HDQSSSTSSGQIELRRIDKSKQKSKGKRKPLRADMIRRIDGPAFLINSAGDPSKTIPDHHHAALLNSNESQPPLTTEQVGSPRIAAAAA PQPGASILASDHGRQGSVASDDPNAQPNIRIALPHDTIQPGANSISSPTSPAPARKRFSIPRFDHRHDPDADSDEEAVAEEEEEQIQTP SSPPLRARFPDHHELGRGRRVSDPLQPQLRRGSDTGLVQAYARHEKLDMFPRAQTVEFAVPSDYRSALTETQQREPGYTTGQAFG GASGLRQRNTTFNRTVTGRSYVSGRLSNGRSGVPLARTQTSSKQRGFGGFPTPFEIAGMAIKKAVPGVQERFQRTMTMPRTATFTS VNSGGGPSESAIRPTPYLSFDATVTGNSRFEALTEAQRDELGGVEYRALDLLAKLVPAYWLIVNLGMVTLVAPYISSSAFKKYRPVFE AQGSEKPDYTWFWFFQVVSAYSNTGMSLIDTSMTQMQDAYFLLIPMGFLILAGNTGFPILLRFFIWMISVCVPSSSRIYETLRFLLDHP RRCFVYLFPSSQTWFLLFVLVLFNSIDWLAFLILDIGNPVIERITLSIRVFDGLFQSIAVRAAGFTVVSLLALAPAVQFLYVIMMYLSAFPL ALSVRSTNVYEEKSLGVYVDEPAEPGVVPLESNNAKVWGSFLASHARRQLAFDIWWLGFALWLICIIERNDIQDPNSNGWFTIFSCLF ELTSAYGTVGLSLGTPFDNFSLSGRFHTLSKLVVCAVMIRGRHRGLPVAIDRAILLPSELEQEDMMDDDLSHIDDAWDRDSTFVVDPA GSAAVPRGSMSVVDRQRSNSGSRVDGESSGDYKPPSSGVSFAINPVKARRSSMPPSSMEPLSPKQQAELVHEPRRSFTLTLPPSSL PLHHQAPNGVGLPTSSISSSGVLGPMMVSSPGQLTAIDEMPSGVGTTPVNQSRAESPSVTGQGQHGSPSSAETLGSSSSGSVKGK EKQHGEVDTERQMAQRAGCSSPGGQHDPVTGES
9E-102	351	2	3E-99	342.5	0	2.1	2	N1RQ98_FUSC4	High-affinity potassium transport protein	FOC4_g10007108	Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	765	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. cubense, Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	1229665	>tr|N1RQ98|N1RQ98_FUSC4 High-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 4) GN=FOC4_g10007108 PE=4 SV=1MLDSITSRWKDLREEHPRLNAVATQAGRLVPPINFITIHYAYFIFGSLFFSLIFWLSSEPSQSIPYVDCLFLVVSSFCDTGLNTVNL SEITTWQQVLLYLLFIIGSALWVSFWTVMARKQAFEKRFEDIVRIEREARKRRAALRRAKPLGRFLPFTKARTTPVSTETSNTLTGLGT VQRTATEKPDPNDLFKTTAPMRRAVTAPPDSISDSDDNDSNTTQVAAPARNAPMTPNSGDHIQFADNLSPRSAGRDSVSIYRRNENV EPNRRPSTSDSVNSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKILAVTVPFYAFMWQAVCGIALGAWISINR PSAATANAINPWWCGIFLSSSAFNNAGMSLNDAGMGAFQDAYFVLIVVGILVLAGNTGYPLLLRFFLWCSLRVLQLTTEPKTLGPWKE TIEFILKYPRRVYTTLFPSGATWWLFTVIVTINTIDWVAFEVLNIGNDVVEAMPVSDRIIAGWFQAIAVRAAGFAVVSISGLYPAVQLLYM IMMYISVYPVSITMRHSNVYEERSLGIYEDDPQVLEAENGNGNGNENGNHLLPTISEEPEKPALRRRVTAAAQKTVKKSMTFHGVGVR PPPKGPDDNSRISFIGQQIRGQLAHDMWWLILPVIVIMIIETDHFLEQPLVYSVFNVLFEVVSAYGCVGLSMGLPGKSYSMAGGMHRG SKFVLCLVILRGRHRGLPVALDKAVRLPGEKLVREEEEDSKIRRTKTMNRIASRESRVM
1E-101	350	6.5	1E-99	343.8	0.9	2.1	2	K2RZV7_MACPH	Cation transporter	MPH_04517	Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	723	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Macrophomina, Macrophomina phaseolina, Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	1126212	>tr|K2RZV7|K2RZV7_MACPH Cation transporter OS=Macrophomina phaseolina (strain MS6) GN=MPH_04517 PE=4 SV=1MRVRPSLLAPVRRLARFVRRNLPPLNFITLHYTYFIVTCLLSAVIFWGASTPARSVSFTDSLFLCVSAMTLAGLNPVNLSDLNTFQ QVMLFLLIIAGSAIFVSAFVVHVRRKAFEAKICKVAEEQKQKRGRHRFSLSRPISRRSSRGRSRSAIDGQKHPGMMLIEASSETNAIGT GDISSSAVGDDDVIQKETDLNFGGSSKDDHVSFSPEALQNMSRDSRPRRHSHRLLSMQGVGARSNASLHGRPGVTGHSSIYATRSQ AVEDEGHDDRERTLTEKDESINVPKNFPSSGLSGFIGRNSQFHHLTEEERQALGGAEYKAIKFLSVIVPLYFVLWQLLSCIGLGAYVAI NRPSTALTNGLNPWWVGAFNAVSAFNNSGMSLLDANMTAFQTAYYMLLTMGLLILAGNTCYPIFLRLIIWTIRKLLPTSEGWDDLRHT LQFLLDHPRRCYTNLFPSQHTWWLLLSVITLNAIDWAAFEILNIGNKAINDLPTAAEIIDGLFQAFAVRSGGFYVVPIPSVRISLQVLYVIM MYISVYPVVITMRNSNVYEERSLGIYADDPYLDTPEENEKRSVFGFIQQRFMGSGDNGEQTKSYFVRQQLRAQLAHDLWWLVLAVFV IMIIEGGQFERDPANFSVFNVIFETVSGYGCVGVSMGVPYDSFSFVGSWHTLSKLVLCAVMLRGRHRGLPVAIDKAVLLPSEAQYQAE EEDAQLRMERTISRRDIV
1E-101	350	1.6	9E-98	337.3	0	2.1	2	A0A098D3H5_GIBZA	Fusarium graminearum chromosome 1, complete genome (Uncharacterized protein)	FG01407.1 FGRRES_01407	Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	764	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium sambucinum species complex, Gibberella zeae (Wheat head blight fungus) (Fusarium graminearum)	5518	>tr|A0A098D3H5|A0A098D3H5_GIBZA Fusarium graminearum chromosome 1, complete genome OS=Gibberella zeae GN=FG01407.1 PE=4 SV=1MFEFIKNRWQDLREEHPRLDAVATKVWMVVPPINFITIHYAYFIFGSLIFSVIFWGSSQPSQSIDYIDCLFLVVSSFCDTGLNTVNL SQLTTWQQVLLFILFIIGSALWVSFWTVMARKHAFEKRFEDIVRTERERARKRRAALRRSKPLGRFISFDKYKTSPASTGTSGILPGLGT KQKSETEITDTNTNTNDLFTTTKPIRRAVTAPGEPISSDSDDNDSNRTHVAASSRIPPPTPSSGDHIQFASNLSPRSGGRDRDSVSIYR RNDDTELDRHPSRASVADSDESEDFLLHWKKILGSHNTSKRGQFYDLSSDEREALGGCEYRALKVMSVTVPLYGFAWQAICGIALGA WINNNRPSAATVNAQNPWWCGIFLSASAFNNAGMSLNDAGMAAFQDGYFVLIVVGLLVLAGNTAYPLLLRFFLWCSLRLLQLTTQPK TLGPWKETIEFILKYPRRVYTTLFPSGATWWLFLVIFVINTIDWVAFEVLNIGNKVVESMPVSDRIIAGWFQAIAVRAAGFAVVSIGSLYP AVQLLYMIMMYVSVYPVSITMRHSNVYEERSLGIYEDDPQVLEAENGTGHLPTISEAPEKPALRRRVTAAAQKTVKKSMTFHGVGVRP PPKGPDDNSRISFIAQQMRGQLAHDLWWLILPVLIIMIIETDHFNQQPLAYSIFNVLFEVVSAYGCVGLSVGAPGQSYSLAGGMHRGS KFVLCLVILRGRHRGLPVALDKAVRLPGENLAREEEEDSKIRRTNTMFRMASRESRAV
1E-101	350	15.8	1.6E-97	336.5	6.3	2.1	2	K5VPL0_PHACS	Uncharacterized protein	PHACADRAFT_211077	Phanerochaete carnosa (strain HHB-10118-sp) (White-rot fungus) (Peniophora carnosa)	916	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Phanerochaetaceae, Phanerochaete, Phanerochaete carnosa, Phanerochaete carnosa (strain HHB-10118-sp) (White-rot fungus) (Peniophora carnosa)	650164	>tr|K5VPL0|K5VPL0_PHACS Uncharacterized protein OS=Phanerochaete carnosa (strain HHB-10118-sp) GN=PHACADRAFT_211077 PE=4 SV=1MSPLSQQRKDLWEHRFSSLGHYIRTHLNFYRVHILFFTFAPLIASGIFYASNGEHHISYIDALYNCVSAVTVCGLATIDLSSLTPW QQVILFILMCMGSPVVVSWVMVYVRREFFASKFRHVVETELARRVANKVDAPVEIHLVPWWKRATRVLTGRNLSTIPEATSSTGSTT RERELDKDKERNHAAVNRLRPEMIRRMNDAPKLINPSGYISEGHTPEIPSAGLPDPPHPLSLGTSEFEVLAEDTLQETKEEARRQLNH SSISCSEDSIDREKGKHELQGSPSKNNAPTSGQTFMPRIRQNTGEDGLPHTQTIEFALGPRPDRDQNEQGTDPLAPTEFRFPNPSSP RMRRTSLPRIGTLPHTATMPRTGTLPRTATTHTYRSMRTKHRGFGGFPMPDQIVSRVMNYFFPGLRRQLTRTLTVPRTQTIVSQRAG SVVGPDVRAVPYISFEAVVGRNSAFQQLTRDQIEELGGVEYRALTALLWIVGGYHILSQLLAFTVIAPYMSLSRWHSDFVPPAEHRPV SSTWFSLFQVVSSYTNTGMSLVDQSMVPFQTAYPMILFMVFLIFAGNTTFPIFLRFTIWIISKLVPHNSRLSETIHFLLDHPRRCFIYLFP SHQTWFLLSVVLALNLTDWFFFLVLDLGNPAVTVVPTGVRVIIGLLQAAAVRCAGFAAVSLSALAPAVKVLYVLMMYVSVYPIAMSVRS TNVYEEKSLGVFEDDDASIGEEGFTPTGHRATIWSRYLAMHMRKQLSFDMWWLGLALFLVCIVEKDNLENPDNLSWFTIFTIVFELVS AYGSVGLSLGLPYANYSFSGALRLPSKLIVCAVMLRGRHRGLPVAIDRAVMLPFEFRASDMHDEEPQDVASPRRNSQDSPYANGTH NDTGNPPFEKLQRRSWHTASPDSAQLRRPTSKDTQLDAH

6E-101	348	3.6	2.6E-60	213.8	0.1	2.1	2	C6H6X1_AJECH	Low-affinity potassium transporter	HCDG_02172	Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	688	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	544712	>tr|C6H6X1|C6H6X1_AJECH Low-affinity potassium transporter OS=Ajellomyces capsulatus (strain H143) GN=HCDG_02172 PE=4 SV=1MRTFQQVVIYVVPLIGNLSVINLVVVLVRLYWFETRFKDIVRLSRQRLLDRPRSNRLQSSESGGRDSITLRNRLTAARIRDIRVLRP EPRIGSSRTAASESEGLRLRARILSRIPNNNANSESDSRIGTVPNENENENAKSCTVEIDDSATSTSTPNSPASPSDPTPVMIDRTSASL KKNSIERSAPPAHISFSAETNMEPRGRALRIPGPREFESGGNEPFLSNIGKLCVSARIADMVPNRTNDDLAKSITIEEPPMTGPSGENE RRRLPTMGRLLSHAVSVERAASNAFILGNSSRKRSRSRSSNPLNRSSSRADRVPLDMPYLSYQPTIGRNSRFLGLTDDQRDELGGIE YRSLKLLAKIVFSYYVFWHVFGVVCLIGWIHNSDRKYRDYIQSVGQSPTWWAIFSGMTTYNNLGFTLTPDSMTSFRNATFPIFIMTFLM YIGNTGYPFLDLHNEEVLAVPSSWNRFLAAVFQAASARTTGTCTFNVSKVHPAVQFMLMVMMYISVFPIAISVRKTNTYEENSLGLYD PQSDEIDESNSTASYVGAHMKKQLAFDLWYVFFGMFLLMITEGSKLADKADPDFAIFSIFFEAVSAYGNVGLSLGHPSINSGLSTKFSV LGKLVICALMLRGRHRGLPYELDRAIILPGERNLTESSATKDGGPVTTTQTSTNATIGSLLRTRIAEIV
7E-101	348	8.9	9E-101	347.2	6.2	1.1	1	D4GVN4_HALVD	TRK potassium uptake system protein TrkH	trkH1 HVO_1056 C498_13474	Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) (Halobacterium volcanii)	553	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Haloferax, Haloferax volcanii (Halobacterium volcanii), Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) (Halobacterium volcanii)	309800	>tr|D4GVN4|D4GVN4_HALVD TRK potassium uptake system protein TrkH OS=Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) GN=trkH1 PE=4 SV=1MPRRGRTVSGWPADLAVIGRDVGSLLAMESALMTASVLVAVGFREWYAALAFLAAGGATAFVGLGARKAFADAPAPRMKHG MIIAAAGWFATAAFGSLPFFLTAHFAPQGVFTALVPAGVDYAQSSLVYFRDPLHALFESMSGWTGSGLTMGIHEPSLPRTIQWWRSL IQWVGGVGVIVLTVSILSRPGSGSYALYRGEAREEKIHPSVVSTVRTVWKIFVGYTLLSVVVLFVAIRASDYGATLPLWEVAWQALNH AMTGLSTGGFAVTDGSIGTYDSPLIETVLLPIMALGAIAFPVHYAILKNRDVDRLWGDLQTRWLLVLFAVGAVALAVQNLVSLPATAGS AFVETADYFGLAGVAGGPESDAVRDAAFHWVSALTCTGFQAAPLGAWSDGGKILLSGAMTLGGAAGSTVGGIKIIRGYTISRGIRWQ FSRVFLPESAIVNIEMNGRRLSRTEMDREFSEAAIVSMLWVLLLVGSSVLLVNLAGPEFTYADALFEVASAQGNVGISTGITGPWMNP WAETMFLFNMWVGRLEIIPVLVFARSAIYGLNP
7E-101	348	11.4	3.1E-94	325.6	4.7	3.1	3	Q2H9T7_CHAGB	Putative uncharacterized protein	CHGG_03017	Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	698	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Chaetomium, Chaetomium globosum (Soil fungus), Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	306901	>tr|Q2H9T7|Q2H9T7_CHAGB Putative uncharacterized protein OS=Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) GN=CHGG_03017 PE=4 SV=1MWKPELNYITLHYAWIIFAGLLALVVIYPYGNISAMDAWFFGASASTESGLNTVDIKDLKTYQQVYTYVIPIITNLGFINIIVITVRLR WFEKRFKAVASSSKLSGRSEDIEVQIQAAVPERPKDQSSNTEPAEQNPTHEKPKADELVETASSGPQGPRVTFGEDVKEPRADSTLY IPPPRERDDGTKACLSWRNRRLTDWNHAGHSFVERNHVADEEDGNEAGSGHDLKGSPANMPLPDEDAIKPAMPGGVSRRRGYQH EDEPSMSRSRTVEQAVTSLFVLGKTVTGSSRQSAPTLTSHPAEMPYLSKQATLGRNSSFHRLTAQDRERLGGIEYRALKLLQKIVTEC AQDKTWWAFYSAQTMVNNLGFTLTPDSMITFRDATWPMLVTSFLAYGGETFYPVFMRLIIWIMSKLVPKQSSLKEPLQFLLNHPRRC SMLLFPSRPTWILFGILFAMNFVDVLLIIVSDLDNPAVNVLPMGPRILAALFQAASARHTGTAAFNLAEVNPGVQFTLVVMMYIAIFPIAIS IRASNTYEERSLGIYEQQVALDESNGKSYVMMHIRNQLSFDLWYIFLGTFWICFAEAPRIMDNNDPAFSVFSIMFEVVSAYANVGLSLG HPSVSTSLSGKFTTASKVAICAMMIRGRHRGLPYAVDRAVLLPGEPEYRGFAGHGGGPAEGGGGASLPKGRRAASRELSRGE
1E-100	347	7.6	5.2E-98	338.1	3.5	2.1	2	M2RLB5_CERS8	Uncharacterized protein	CERSUDRAFT_111935	Ceriporiopsis subvermispora (strain B) (White-rot fungus)	762	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Gelatoporia, Ceriporiopsis subvermispora (White-rot fungus) (Gelatoporia subvermispora), Ceriporiopsis subvermispora (strain B) (White-rot fungus)	914234	>tr|M2RLB5|M2RLB5_CERS8 Uncharacterized protein OS=Ceriporiopsis subvermispora (strain B) GN=CERSUDRAFT_111935 PE=4 SV=1MWIHIRKKLNFYRIHLLLFLLVPLIFSAILWACNGEFSIPFLDSLFICVSAATGTGLTTVDLSSLTAFQQAILFVLELVGNQVFVAWIV VIVRRQYFLDHLEHIVAAELERKSIRHDTQSSERPTPSVLRRIISRKKLHGTSHDQESFHSNDLTQLKTISRESGGKIRPEMVRRIDVAP HLITPMGIQAHAEPSTSFVSDAVVLQATGLDSEQLPRLNSRRSITHPSPSTTPRTHLHEDDFGGFPGPRQIGSRLLQKLFPGLHHKLRR TVTMPRTETLIPSAVRPSSDIATIPAKRVPYITFPVTVGRNSSFQGLTAENIEELGGVEYAALTSLLWIVPLYYLGLLAISFIVIAPYMALPR WKGVFLPPMQHRKINTTWFSAFQVMGAWANTGMSLVDQNMVPFQTAYPMTVFLVICVLAGNTAIPVFLRFLIWILTKILPHNSRTLES LHFLLDHPRRCFIYMFPSSQTWLLFAILVLLNGLDWFFDLLLNIGNPVMDAIPVGNRLLLALLQASAVRSAGFQPVPMASLVPATQVLY VIMMYIAVFPIAMGVRSTNVYEEKSLGIWHQGQDDQEEESPVGESRVAIWGKYLMRHVRIQLSFDMWWLGLSLFLLCIVERDGLTNT QNATWFNIFALIFEEVSAYGTVGLSLGIPTANYSFSGALRKLSKLIIIAGMLRGRHRGLPVALDRAVLLPHEFLPTEKRPAVPGTPLELPD TPNGLASPGIDGMASPTLETETDRKFGGMRQPRGRTLSFAEEIAEH
1E-100	347	8.6	1.1E-97	337	2.5	2.1	2	A0A0D1CKG8_USTMA	Chromosome 14, whole genome shotgun sequence	UMAG_04423	Ustilago maydis (strain 521 / FGSC 9021) (Corn smut fungus)	1220	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Ustilaginomycotina, Ustilaginomycetes, Ustilaginales, Ustilaginaceae, Ustilago, Ustilago maydis (Corn smut fungus), Ustilago maydis (strain 521 / FGSC 9021) (Corn smut fungus)	237631	>tr|A0A0D1CKG8|A0A0D1CKG8_USTMA Chromosome 14, whole genome shotgun sequence OS=Ustilago maydis (strain 521 / FGSC 9021) GN=UMAG_04423 PE=4 SV=1MLEHISPRSLPTAARTTLRSLSRWCGSNLNFYRVHVLVFTFTPLLAACIFYACNGETHISFVDGLYVCVSAMTVTGLVTFNISTAN PGQQAILFILMCIGNISAVSITMIWIRRSFFRKKFDHVVRRSAKVRKRMHDVEEQERRERRHNIAKIQRMVGLKSSDSVTTISDTEEHDR TDTSSSSQIELRRLEKNKQKSKAKRKPLRADMIRRIDGPAFLINSAGDPSNTIPDSANTTPFTNDPHASLTQEPASLRSTTPPPAQAAV GILNAQQDHHASVTSDDPSHQPSIRISLPHHSLPSDEFTQHKATADPTQPPRQTFSLPRCDHRHDPDADTDSDQASLTHQGDTHFTQ PPLSPPLRARFPDHQIPGRARRVSDPPQSQFRRGSDTGLVHTYATHEKHDMFPRAQTVEFAIPSNYRSPIDAQQREQSYTTGHGVN PTGGLRHRNTTFNRTVTSRSYVSGRLSNGRSGVPLARTQTSAKQRGFGGFPTPFEIAGMALKKAAPGVQERFQRTMTMPRTATFTS VRSGGGLTETANKAAPYLSFDATVTGNSRFHALTETQRDELGGVEYRALDLLAKLVPAYWLIVNLGMVTLVAPYISSNAFRKYRPPFE AQGNNRPDNTWFWFFQVISAYSNTGMSLIDTSMTQMQDAYFLLIPMGFLILAGNTGFPILLRFFIWTISVCVPSNSRIYETLRFLLDHP RRCFVYLFPSSQTWFLFFVLVLFNSVDWLAFLILDIGNPVIESITLSIRIFDGLFQSIAVRAAGFTVVSLLALAPAVQFLYVIMMYLSAFPL ALSVRSTNVYEEKSLGVYVDEPADPGLAPQESDNPKVWGSFLASHARRQLAFDIWWLGFALWLICIIERNDILDPNSNGWFTIFSCLF ELTSAYGTVGLSLGTPFDNFSLSGRFHTLSKLVVCAVMIRGRHRGLPVAIDRAILLPSELEQEDMLDDDLSHLGDSWDRDSTFVSDPL VPTPGAPRPSMNGPDQQRSNSIGSVAGESNSGMSSVRRTPSGVSFAVHPLASKPRRSSSMSPMAMEPLSPKQQAELALQEPRRSL TLTLPPSSLPAHYAGPTLGVGGFAHHLGGLGGALPPSSSSNASTVGGVLGAMMVSSPGQLTAIDEMPSGLGAMPTSESRCESPAGV NASAAASNAQSQAHVLPTTFCTNVESTSSTSSGSGGSGCSVKGKERAAMRIADEDRERLVAQHAGCSTPDGRHDPVDGQD
1E-100	347	8.6	6.3E-97	334.5	0.7	2	2	N1PIL1_DOTSN	Uncharacterized protein	DOTSEDRAFT_175094	Dothistroma septosporum (strain NZE10 / CBS 128990) (Red band needle blight fungus) (Mycosphaerella pini)	649	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Mycosphaerellaceae, Dothistroma, Mycosphaerella pini (Red band needle blight fungus) (Dothistroma pini), Dothistroma septosporum (strain NZE10 / CBS 128990) (Red band needle blight fungus) (Mycosphaerella pini)	675120	>tr|N1PIL1|N1PIL1_DOTSN Uncharacterized protein OS=Dothistroma septosporum (strain NZE10 / CBS 128990) GN=DOTSEDRAFT_175094 PE=4 SV=1MANLKHRTRSHAREIKDSLMRLNFYRLHLLYFLAVIIISSGVLYGSGTSAYHLPYIDAISLTTSAMCNVGLNTVNLGDLNRFQQTVL FILMLMGDLTIVTISVVVVRRYFFSRSIDKLVKDSTTGRRLAEDIERQHGQQNGAPASHKAPTRPQNQHRTDRASWTSSRENDRLVPR SHLRGYGSFWTPWSGDNLSNAWKTIRPGKVRNLAEKHRYLSFEPDLDYKGRFISLSQEQRDELGGVEYRALRVLTWLLPAYTAFWI LLIVVIATPYVATSSAGDTVRTSQPGNLDPSWWAIFTAVSSYSNTGLNLLNQNMIPFARNYLLLIVFGTATIVGNTLYPVLLRLLIWSVAK LVPRHSELHHSLSFLLQHPRRCYLLLFPRNNTWILFAVQVFINLIAWVLWIILQLDQSAIEAIPPGQRVMNGLFQSVELRAGGMYIITGE VSPALQFFYMIIMYLSMYPLIVSLRESNVYEERSLGQDDTTKFGRKSDDKSAPKSQIGLHIRKQLAYDIWWLLLAIFLICIVEHNPLSSGA PGYTIFSIMFEVVSAYGTVGLSLGVPYDDYSFCGAWHVLSKLILLTVMIRGRHRILPLAVDRAVLLPGQDLMDRLDREVEGPNGRRRH EIEARIREDEGGEQAEQAGNKHQQDPE

1E-100	347	12.1	1E-100	347	8.4	1.4	1	I3R3G2_HALMT	Potassium transporter Trk (Trk potassium uptake system protein)	trkG HFX_1056 BM92_03925 C439_05200	Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (Halobacterium mediterranei)	553	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Haloferax, Haloferax mediterranei (Halobacterium mediterranei), Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (Halobacterium mediterranei)	523841	>tr|I3R3G2|I3R3G2_HALMT Potassium transporter Trk OS=Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) GN=trkG PE=4 SV=1MPRRGRMVAGWPADLAVIGRDVGSLLAMESLLMAVSVLVAIGFGEWYAALAFFIAAGATAGVGLGARKAFDEAPAPRMKHGM IIAAAGWFATAAFGSLPFFLTAHFAPDSVFTALVPAGVEYTQSSLVYFRNPLHALFESMSGWTGSGLTMGIHEPSLPRTIQWWRSLIQ WVGGVGVIVLTVSILSRPGSGSYALYRGEAREEKIHPSVVSTVRTVWKIFVGYTVLSVVVLFVAIRASNYGSALPLWEAGWQALNHA MTGLSTGGFAVTDNSIGTYNSPLIETVLLPIMALGAIAFPIHYTILRNREVDKLWTDLQTRWLLAIFAVGVAGLTIQNLVSLPTTAGSAFV ETADYFGLSGIIGGPETDAIRDSAFHWVSALSCTGFQAAPLGQWSDGGKLLLSGAMTLGGAAGSTVGGIKIIRGYTISRGIQWQFSRV FLPESTVVNIEMNGRRLSRSEMDREFSEAAIVSMLWVLLLVASSVLLVNLAGPEFTYADALFEVASAQGNVGISTGITGPSMNPYAEA MFLFNMWIGRLEIIPVLVFFRSVLYGLNP
2E-100	346	1.8	1.3E-97	336.8	0	2.1	2	C7YWM3_NECH7	Putative uncharacterized protein	NECHADRAFT_74352	Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	760	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium solani species complex, Nectria haematococca, Fusarium solani subsp. pisi (Nectria haematococca), Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	660122	>tr|C7YWM3|C7YWM3_NECH7 Putative uncharacterized protein OS=Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) GN=NECHADRAFT_74352 PE=4 SV=1MLSSIKTRWEELLEEHPKLEAVVSQVSRFIPPINYITIHYAYFIFGSLFFSVIFWGSSEPSRSVRYIDALFLVVSSFCDVGLNTVNLS EITTWQQVLLYLLFILGSALWVSFWTVMARKHAFEKRFEDIVMAEREMRKRRAAAKPTPALKKFFTFDKFKSSPPATTTLPGLGTRQR TMMEKSDPDELMATTLPMRRARSAPEDSISSDSEDNDSNTTTVAAHPTLSPGANDHITFASSMARPNGRRGSVSIYSHNDDDNNRG LPGARRPSTAESAKSDESEDFLLHWKKILGAHNTSKRGQFYDLSSDEREALGGCEYRALKVLAVAVPLYGFLWQFLCALALGGYINN HRPEAAAVNSVNPWWCGIFLSSSAFNNAGMSLLDANMSAFQDAYFVQIVVGILILAGNTAYPLLLRLSLWCCLQVLKLTTPATAHGP WKETIEFILKYPRRVYTTLFPSRATWWLFAVIATINTIDWVAFEVLNIGNPVVEDMPVSDRVIAGWFQAVAVRAAGFAVVSIAKLYPAV QLLYMIMMYVSVYPVSITMRHSNVYEERSLGIYEDDPQMLEEENGNTLPTIAEEPEKTPLRRRVTAAVHKTAHKTVKRSMTFHGVGVI APPKGPDDNSRISFIGQQIRGQLAHDMWWLILPVIIIMIIETDNFLDKPLEYSVFNILFEVVSAYGCVGLSMGVANNSYSLAGGMHTGSK LILCMVIIRGRHRGLPVALDKAVRLPGEKLHKEEEEDSRIRRTKTMDRIASRESRVI
3E-100	346	7.6	3.4E-98	338.7	0.9	2	2	T0KWM9_COLGC	Uncharacterized protein	CGLO_03467	Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	669	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	1237896	>tr|T0KWM9|T0KWM9_COLGC Uncharacterized protein OS=Colletotrichum gloeosporioides (strain Cg-14) GN=CGLO_03467 PE=4 SV=1MTNPSRHPHGDENGISDEAHDAPTPRSSPRSGIRSFLPPLNFITLHYAYFIGTSLLASAVFYASSNPRGSISYVDALFLVVSAITEA GLNTVNLSQMTVWQQVMLWLLIVVGSTIWVSIWTVLARKHVFEKRFREIVEAERERDQVREGEGCLPIAHGPGKKAAEASGAGVVG DGVSTRVRAVDNHVTWEAENITRRSTASVSSKTKPTRPWLSILSASKEGRNAQFHSLTAAERSRLGGHEYRALRLLSVVVPLYSVLW QVLGAVALGAWIANNMPTTATSNGANPWWAGIFFAISAFNNSGMSLLDANVVPFQQAYFVLITMGLLILAGNTAYPLFLRLIFWSALK VLRLTTAEGACVELKSTLEFILKYPRRVYTNLFPSRPTWWLFFMVVLINGIDWVAFEVLNIGNPVIEAIPVGARVLDGLFQALAVRSGGF YLIPISSAYPGLQVLYVIMMYISVYPVVITMRHSNVYEERSLGIYADDEEQHPNPFQPSEKSHHTAGSNVIADFFRQNLSFAGVGAARP AAGPNGYESRTSFVSQQIRGQLAHDLWLLTLAVLLIVIIETSHFLEDPVHFSVFNVVFEVVSAYGCVGISVGLPNDAMSFAGGWHAGS KLVLCLVMLRGRHRGLPVALDRAVRLPGQRLLEDEEEDWRLRRARSRGVDSRGI
4E-100	345	5.1	1.7E-95	329.8	0	2	2	N1PUG3_DOTSN	Uncharacterized protein	DOTSEDRAFT_70137	Dothistroma septosporum (strain NZE10 / CBS 128990) (Red band needle blight fungus) (Mycosphaerella pini)	731	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Mycosphaerellaceae, Dothistroma, Mycosphaerella pini (Red band needle blight fungus) (Dothistroma pini), Dothistroma septosporum (strain NZE10 / CBS 128990) (Red band needle blight fungus) (Mycosphaerella pini)	675120	>tr|N1PUG3|N1PUG3_DOTSN Uncharacterized protein OS=Dothistroma septosporum (strain NZE10 / CBS 128990) GN=DOTSEDRAFT_70137 PE=4 SV=1MAPFTAPNLGPLQNPARWIRKHLLPPLNFITIHYTYFIVSCMVSAVIIWGSSSPAHSVEFIDALFLSISAMTEAGLNTVNLSSLNTF QQIWLFLQIFFGSAIFVSAVVVHFRKAAFEKKFQHVLAEREKRRQVQRGRSQSRGHRCGWSFSSRTMQDHQDEEILVEESKECQESI VDKGNPKDVHEELTMSSRVQYGGSKVDSTAPDLPGKELGTNAGTSGHHAGLHFSGDTIFDRQHSPVSPGKRSHSLFRMQGVGVDT STSFEPAGTAPSEAHNNSSTKPKIHGDFGGYINTLGGWIGRNSQMYGLTEKEREQLGGYEYRAVKVLSWLVPTYLLLMQLLGALGCA TWVAYNRPDAPLKNGLNPWWVGAFNAVSAFNNSGMSLLDANMTAFQTGDYILLTMGFLILAGNTCYPIFLRLIIWVMWKLVTRFTES QPWQEHARTLQFLLDHPRRCYTNLFPRRHTYWLLASVVILNGIDWAGFEILNIGNEYIEILPVGVRVIDGLFQAVAVRSGGFYVVSISQ VRISLQVLYVVMMYISVYPVVITMRNSNVYEERSLGIYAEDAEQEEEPHHSEDGFLGRFTGHLAGHHHRKESNTHFIRHQLRAQLAHD MWTVVVALFLIMIIEGGQFERDQGTFSVFNFLFEIVSGYGCVGISVGVPWENYSFCGTWHKGSKLILCVVMLRGRHRGLPVAIDKAVL LPGEKTVETEEADGMRRLEMERLRTQSRGREVV
6E-100	345	5.3	9.7E-98	337.2	0.3	2	2	E3QJ66_COLGM	Cation transporter	GLRG_06048	Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) (Maize anthracnose fungus) (Glomerella graminicola), Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) (Maize anthracnose fungus) (Glomerella graminicola)	672	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum graminicola (Maize anthracnose fungus) (Glomerella graminicola), Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) (Maize anthracnose fungus) (Glomerella graminicola)	645133	>tr|E3QJ66|E3QJ66_COLGM Cation transporter OS=Colletotrichum graminicola (strain M1.001 / M2 / FGSC 10212) GN=GLRG_06048 PE=4 SV=1MSFQPPRPTALEQDGRDRDDGRAEFRRSTSSGLRSFLPPLNFITLHYAYFIGTTLLASVIFYVSSSPHGSIGYVDSLFLVVSAMT EAGLNTVNLSEMTVWQQVMLWLLIIVGSSVWVSIWTVLARKHVFEKSLREVVQASDEERDRQHGRLPIFNGRDAASRGKGGASMT GVMERGVSSQARAGDNHITIDTPENLTRRSTHSVSSSTKPTRPWLSFLSSAKEGRNSQFHSLTASERSRLGGHEYRALRLLSVVVPV YSILWQVLGSLAIGAWIANNMPTVATSNGANPWWAGIFFAVSAFNNSGMSLLDANMVPFQQAYFVLITMGLLILAGNTAYPLFLRLIF WSALKVLRLTTGEEIHVELKSTLEFILRYPRRVYTNLFPSRPTWWLFFMVVLTNGIDWMAFEVLNIGNPVIEAIPVGARVLDGLFQAIAV RSGGFYVIPIASAYPGLQVLYVIMMYISVYPVVITMRHSNVYEERSLGIYADDDDDDDPASRSSTDEKKHGGGNGLLTKLIRDNLSFAG VGAANPKRADGLESRTSFVSQQIRGQLAHDLWLLTLAVLIIVTIETSHFLEDPVHFSVFNVVFEVVSGYGCVGISVGLPKDAMSFSGG WHAGSKLVLCLVMLRGRHRGLPVALDRAVRLPGQRLLEDEEEDWRLRRARSGRGVESKAV
7E-100	344	5.1	4.5E-95	328.4	1.1	2	2	B6QTE2_PENMQ	Putative uncharacterized protein	PMAA_003710	Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333)	692	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Trichocomaceae, Talaromyces, Penicillium marneffei, Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333)	441960	>tr|B6QTE2|B6QTE2_PENMQ Putative uncharacterized protein OS=Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333) GN=PMAA_003710 PE=4 SV=1MVHILDVIRAHRPRLRPRFLTIHYTYFIGMCMLTSVIFWGASTPARSVRYIDALFFAVSAMTETGLNTINLSTLNMFQQVILCFLSIV GSTIWVSIAIVLVRRRAFEKRFSDIVEEQRRPRNRKDSLSSRRPNSASIYRPFASHNLGLLRFRSFRTEPKGQPNTMQPDHDNRDPER NLATLAPLGAETVLKKENASHYGGQPEQEQGQHQDDTAPNHITFAANMRGQSPTAYQRHLNPPYENALSQAESQEESHNTEALDPR SHFLEMFGRNSSFHHLSEAERRRLGGVEYRAICLLSVIVPLYLFLWQFLGALAVGAYMARNHGDLSRQNRLNPWWIGIFFAISAFNNS GMSLLDANVVPFQNSRFFLITVGLLILAGNTCYPIFLRWCLVVIKKFTPNTDYFTQYHETVTFLLQHPRRCYTTLFPSTYTWWLLCLVIV LNCTDWVAFEVLNYDNPAIDSIPLGSRILDGLFQAICVRSGGFYVVSIASLQISLQVLYVVMMYIAVYPVVITMRNSNVYEERSLGIYADD PSANEGDHSQSSSSADSQNPLLRWVPRGRAYFVEHQLRLQLAHDLWWLGLAVIISIIEAGNFTRDPLTYSVFNIIFETVSAYGCVGLS TGLPNEAYSFSGGWRTLSKLVLCAVMIRGRHRGLPVAIDKAILLPSEHMGKAEDEDADNIRSERSLSRARRYM

1E-99	343	5.9	9.1E-98	337.3	0.2	2.1	2	S3BTU4_OPHP1	Impb mucb samb family protein	F503_06218	Ophiostoma piceae (strain UAMH 11346) (Sap stain fungus)	1412	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Ophiostomatales, Ophiostomataceae, Ophiostoma, Ophiostoma piceae, Ophiostoma piceae (strain UAMH 11346) (Sap stain fungus)	1262450	PE=4 SV=1MPVKNMPPSRPAFAARHPRLTAVAGVARSLLPPLDFITIHYAYFIVTPLVFSLIFWGSSTPALSISYTDSLFLVVSAMTESGLNTVN LSQMTTWQQAILFLLIILGSSIWVSIWTVAFRRHVFELRFDTIVSADRERRMLRNCPATTAPPNPRSWGRIASIFYKGQGKIRCNADILP LSALSTSPPAKGDSSPDIQVSVRRMEQLDAGVTRTTALESGTTASGHISFADRQKATSSSGACTPQTDRKAARRLALSTHRGSTIADE KHDGVFDGSASFLSGHPIGRNAQFHGLTREEREELGGCEYRALKLLCVIVPLYFVLWQVLGCIALGAWINCHMASTATANGINPWWL GIFNGASAFNNSGMSLLDANMVPFQNAYFVLITMGMMILAGNTAYPVLLRLILWSGLKIANRATRHDQLSETKETVKFILQYPRRVYTN LFPARPTWWLLFMILLLNCIDWVAFELMNLGNPLVDNIPTGPRILDGLFQAIAVRSGGFYIVPMSEVYIGLQVLYVIMMYISVYPVVITMR HSNVYEERSLGIYYDDPSVAAAQGDASSEDGRDASKSPFHEIGRAIGRAFMPWHRAGVAPQATHKGQTNETRISFISQQIHGQLAHD LWLLVLAVLVITTIETSHFLADPVSNSVFNVIFEVVSAYGCVGISMGVPNAAYSFSGGWHSASKIVLCLVMIRGRHRGLPVALDRAVRL PGEQLHRDEEEDYHIRRSQNIPAEETGKLVGTVATGSSADSTEPKTILSVPSDSLEHGSLKYSLLGPSLLKAGQETVDQAKLPQVSDII YNASKGSKYFDREEERDKVLSSKIEQILAKKARLERLDLSHDLRIVDGLVAQYEASRDLSQYIVHVDCDAFYAAVELLDRPELADVPFA VGGGVLTTCNYAARKFGCRSGMAGFVAKKLCPQLVLLKPDFTKYTAKAQEIRQILADYDPRFESASIDEAYLNVTQYCAENGMEPAA AVEKLRLEVAEQTKVTVSAGIAANTRLAKICSNMNKPNGQYVLPNDRTAILEFMADLPCRKVNGVGRVFERELAAVGVKTCGDVYKH RMFLSRLFGEKACSFLVEAHLGLGRTRVQPAEDYERKSVGTESTFSSMSDPSELRHKLQLIAGELEKDLQRASCKGRTLVLKVKLHTF EVYTRQSIVPRAIHLADDLYNFALPMLTKLEQEMPGMTLRLMGLRCTHLVSTKRPDAIAFFGIKPSSGSAVSGGSSIPVTPVARGAGEE ADELAGAGGEWEVWPGEEFGGQEMPTSTGGSDVLSNSHEDPHPHIGTGDTAAIFAPTVSSPVPLSRLNIPNPIGSNTTVRAVSPEE WWSCPVCLRPQAADERQFNSHIDSCLSRRTILEAVQESGMGGQAPAESARLSPEKRNTGLGPEKKRGRPTANATVGKDPRQKKICF RSL
1E-99	343	17.3	2E-99	342.9	12	1.1	1	M9WYP4_MANHA	Trk system potassium uptake protein	trkH MHH_c04700	Mannheimia haemolytica M42548	494	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Mannheimia, Mannheimia haemolytica (Pasteurella haemolytica), Mannheimia haemolytica M42548	1316932	SV=1MQFFSIIRIVGILVMCFSFTMLVPATVALIYGDGGGRAFLEAFALNFMVGTLLWWLCRDNKNELRSREGFLIVVLFWVVLGLLGA VPFIILENPDLNVAESIFESFSGLTTTGATVITGLDSLPKAILFYRQFLQWLGGMGIIVLAVAIIPLLGIGGMQLYRAEMPGPLKEQKMRP RIAETAKALWLIYLSLTILCAVAFWLAGMTVFDAISHSFSTVSIGGFSTHDASIGYFNNAAISYITVFFLLLSACNFALHFAVIDRIRDAQSR KKGGILSRLYWGDYEFRFFLMVQLGLFLVCTLVLVGYGYFDNTSVTIEQALFQSVSISTTAGFTTNDFSQWSSFLPTLLVLSSFIGGCA GSTGGGLKVIRVLLLYLQSKREIHRYIHPNVIQPIKLGNHVLSERVVDGIWAFFSAYFFVFVICWLATIACGMETFDALNAVIASLNNLGP ALGSVSSNFTQVPDSAKLVLTFAMVCGRLEVFTLLVILSPVFWKD
3E-99	342	4.8	1.5E-95	330	1.8	2.1	2	M9MDH5_PSEA3	Na+/K+ transporter	PANT_11d00054	Pseudozyma antarctica (strain T-34) (Yeast) (Candida antarctica)	1134	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Ustilaginomycotina, Ustilaginomycetes, Ustilaginales, Ustilaginaceae, mitosporic Ustilaginaceae, Pseudozyma, Candida antarctica (Yeast) (Trichosporon oryzae), Pseudozyma antarctica (strain T-34) (Yeast) (Candida antarctica)	1151754	>tr|M9MDH5|M9MDH5_PSEA3 Na+/K+ transporter OS=Pseudozyma antarctica (strain T-34) GN=PANT_11d00054 PE=4 SV=1MLERIAAGPRAAAVRAKCRSAARWCGRNLNFFRVHVLVFTFVPLIAAAIFYACNGETHIDFIDALFCCVSAMTVTGLVTINISTAN GGQQAILFILMCIGNISAVSVTMIWIRRHFFRRKFDHVVRRSAKVRKRMHDVEEQQRRERRHNIAKLQRMVGLKASDSATTLDDTEDA DRTDSSSSGHIELRRIEKKQSKSKPKRKPLRADMIRRIDGPAFLINSAGDPSNTIPDHHILAGPLTSEPATAAAVASAQPGASILSTTSES DRRDEPAEPDQQQPSIRISLPHDPSQVAEPGTTDSAPRRRLSIPRFSGRHDPEADSDEEAVADEELHDTADVPMPQSPPLRARFPDH QPLGRGRRVSDPPQSHFRRGSDTGLMATYNAHEKHDMFPRAQTVEFAVPSDYRSPADPALRESSGYTTGTHFHRPGAGMRQRNA NFNRTVTGRSYASGRTGYGRGVPLARTQTSAKQRGLGGFPTPLEIAGLAIKKAMPGVQERFQRTMTMPRTSTFTSVRSGGGLTDG GSKTAPYLSFDATVTGNSRFHALTEAQRDELGGVEYRALDLLAKLIPAYWLMINLGMITIVAPYINSGAFAKYRPAFEQQGANRPNYT WFWFFNVVSAYTNTGMSLIDTSMTLMQDAYFLLIPMAFLILAGNTGFPIVLRFFIWIVSLCVPKGSSVYETLRFLLDHPRRCFVYLFPSS QTWFLAFVLVVFTSIDWLAFLILDINNPTIESIKLDIRVFDGLFQSIAVRAAGFTVVSLLTLAPAVQFLYVVMMYLSPFPLALSVRSTNVYE EKSLGVYGDEPTDPGNLPQESGNPKVWGSFLASHARRQLAFDIWWLGFALWLVCIIERDDIQDPNSNGWFTIFSCLFELTSAYGTVG LSLGTPFDSFSLSGRFHTLSKLVVCAVMIRGRHRGLPVAIDRAILLPSELELEDMLDDDVSHLDEWERDSTFVDPTAPRPSMSTEVYH QRSGSTGSGGENGMSAVQRVQSGVSFALGPRGRRGSVPPGAEYGGSLSPKQHAEVHEPRRSFTMTLPPSAMPLHASGAGMAGT GMVASPGQLTAIDEMPAGLTPLSESRAQTPTRGENPPSFHSESSAGESSTSSKGKQRLDEQETQLARQAGSSTPRGMHDPLTGAE
3E-99	342	2.6	3.7E-94	325.4	0.1	2	2	M2LWN9_BAUCO	Uncharacterized protein	BAUCODRAFT_389945	Baudoinia compniacensis (strain UAMH 10762) (Angels' share fungus)	781	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Teratosphaeriaceae, Baudoinia, Baudoinia compniacensis, Baudoinia compniacensis (strain UAMH 10762) (Angels' share fungus)	717646	>tr|M2LWN9|M2LWN9_BAUCO Uncharacterized protein OS=Baudoinia compniacensis (strain UAMH 10762) GN=BAUCODRAFT_389945 PE=4 SV=1MARMLQLKAPNLGPLNKPLRWMGRQLPPLNFISVHWAYFCIVCLNAAWIFYVSNTETKVTFTDSLFLSVSAMTEAGLNTVNLSE LNTFQQFILFFLIILGSAIFVSAWIVQVRKVTFERKFRDFLAAQRRRRERSRSRSRVRARTWSRRRSGSATRGVEAGKALEEKDHLEP ATENQSITGNETGQIPRQYSALDGIVDAEGRGRDMTPPARRGGAEMNDNAVSDGEEETLPGDNASSNRGPTPGITFAGDTRFGPTS PIQDGMLQPRRRRNSNIFNFQGVGARPDANLSPTTPSQPTSTAGQPANMPAQPHGRSLGDISQYFESATGWIARNSQFHGLSEKER EKLGGCEYRAISLLSWLVPVYFVLWQFLGAIGCAAWVAHNAASTARMNGLNPWWVGAFNAVSAFNNSGMSLLDANMTAFQRSYY MLITMSMLILAGNTCYPIFLRLIIWCMWKFVTSGLFKGEEWDERAQTLRFLLDHPRRCYTNLFPAQHTWWLLFALVMLNGIDWAAFEV LNIGNSQLNSGLPTNIRVIDGLFQAFAVRSGGFYVVAIPSVRISLQALYVVMMYISVYPVVITMRNSNVYEERSLGIYAEDQEDDDEDKD GAKSETGNVMATGTANSDGFFLRRAKTIRSTILPTKPGESNSHFVRHQLRAQLAHDAWWIVLALILIMIIENPLFVENPSVFSVFNFLFEI VSAYGCVGISVGLPWAAYSFCGSWHTLSKLILCAVMLRGRHRGLPVAIDRAVLLPGEETWRAEEEDGRIRIARTMSRGRGEMAV
4E-99	342	9.6	5.5E-96	331.4	4.4	2.1	2	I2FVS2_USTH4	Related to potassium transporter TRK-1	UHOR_06912	Ustilago hordei (strain Uh4875-4) (Barley covered smut fungus)	1175	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Ustilaginomycotina, Ustilaginomycetes, Ustilaginales, Ustilaginaceae, Ustilago, Ustilago hordei (Barley covered smut fungus), Ustilago hordei (strain Uh4875-4) (Barley covered smut fungus)	1128400	>tr|I2FVS2|I2FVS2_USTH4 Related to potassium transporter TRK-1 OS=Ustilago hordei (strain Uh4875-4) GN=UHOR_06912 PE=4 SV=1MSGSIASSPRAAAARTKLKSMARWCGKHLNFFRVHVLVFTFTPLIAAAIFYACNGETHVNFIDCLFVCVSAMTVTGLVTINISTTN GGQQAILFFLMCIGNISAVSITMIWIRRSFFRNKFDNVVRRSAKVRKRMHDVEEQQRRERRHNIAKIQRMVGLKSSDSATTISDTEDPD RTDSSSSGHQIELRRITEKNKQKNRRKRKPIRADMIRRIDGPAFLINSAGDPSNTVPEPASLLQLGERPSPITRGPEQITSAQPSGGGIL TSDRDRQASITSGHQQQQQQQPSIRISLPRDAVNATDSASTKDEGANRVDSPPRRRLSIPRFSGRHDPDADSDEGPSRQETPRSPLL RARFPDDQVAGRTRRGSDPANSRLRRGSDTGLMHTYARHEKPDMFPRAQTVEFAVPSDYRTSIDPQYRESGYTTGQNLNNSSGLR QRTTTFNRTVTGRSYLSGRLSNGRSGVPLARTQTSSKQRGLGGFPTPFEIAGMAIKRVVPGVQERLQRTMTMPRTATFTSIRSGGGL TESGAKPAPYLTFDATVTGNSRFHALTEAQRDELGGVEYRALDLLAKLVPAYWLFVNLFMITMVAPYINSRAFAKYQTVFEAQEADRP NYTWFWFFQVISAYSNTGMSLIDTSMTQLQDAYFLLIPMGFLILAGNTAFPILLRFFIWVISLCVPSGSRIYETLRFLLDHPRRCFVYLFP SSQTWFLFFVLLLFNSIDWLAFLILDIGNPVIESITLSIRVFDGLFQSIAVRAAGFTVVSLLVLAPSVQFLYVIMMYLSAFPLALSVRSTNVY EEKSLGVYVDEGPVEAGAPPEESNNAKVWGSFLASHARRQLAFDIWWLGFALWLICIIERNDIQDPNSNGWFTIFSCLFELTSAYGTV GLSLGTPFDNFSLSGRFHTLSKLVVCAVMIRGRHRGLPVAIDRAILLPSELEAEDMLDDDLSHMGDTWERNGAYLAEPTIAPRPSMNS VGRERSGSNASGGAGGAAGDDPDMSSVKRSASGVSFAINPQTKMRRSSIPPTAMESLSPKQLAEAAAGGESRRSFTLTLPPSSLPL HHGGAAHVAPSTGVLGPMMASSPGHLTAIDEMPSGFGATPLSESRAESPAGQGDQPPSFHTNASSGSPNPSSDGSVKGKEKAAVE EAEEKQKKESEMAQRAGCSTPSGRHDPLTLEP

5E-99	342	4.4	3.9E-96	331.9	0.2	2.1	2	L2G3V9_COLGN	Cation transporter	CGGC5_6987	Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	768	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	1213859	>tr|L2G3V9|L2G3V9_COLGN Cation transporter OS=Colletotrichum gloeosporioides (strain Nara gc5) GN=CGGC5_6987 PE=4 SV=1MGFVAAAKRLLARNPLNRFLPPLNFITLHYAYFIIVCLLSSVIFWASSDAEFKVSYTDSLFLVVSAMTEAGLNTVNLSQLTTWQQTI LFLLLLLGSTIWVSIWTILARKHVFEKRFDEIVRAERARKLSRQGSTISLALPRLPLTLPKLQLALSFGKAQTVPPPDQPFKGTGSRIPET HPPPDYKDSDTTEGPPQFRRAMSTPDVNTRDKNTPKDVEDVADSQNPGHITFDDTPHPNATQATSTGVSVQGDGVALPSRRPAKA PTDSADIDLDARHFLKHRSASRNGQFHDLSSAERDHLGGCEYRALKVLATIVPAYFFMWQFLTSLALGAWMNNYMPNTARANGINP WWLGIFNAVSAFNNSGMSLLDANMIPFQEAYYVLITMGLLILAGNTAYPLFLRLIIWGMLRILNLATPQEAFADFKATLEFILKYPRRVYT NLFPSRASWWLFFMLLWLNSVDWVAFELLNIGNSVIEKIPTGSRILDGLFQALAVRSGGFYVVPISGLFIGLQLLYVIMMYISVYPVVIT MRHSNVYEERSLGIYSDDMESTSEPDPEAGVPLLPMGSRPPTLARTTSFGAASAHPSVLARRLSRSGPVSDARRAFKSTFMSFHGV GVAPPKPGAPGTPGPDQPRPESRISFISQQVRGQLAHDLWWLVLATLIITIIETSKFIKDPVTFSVFNIIFEVVSAYGCVGISVGLPTDAF SFCGAWHTGSKLILCLVMLRGRHRGLPVAVDHAVRLPGRQLHRDEEEDHQIRRSRTIEIER	
5E-99	341	6.8	5.7E-97	334.7	2.1	2.1	2	V5EV95_PSEBG	Uncharacterized protein	PSEUBRA_SCAF11g01174	Pseudozyma brasiliensis (strain GHG001) (Yeast)	1180	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Ustilaginomycotina, Ustilaginomycetes, Ustilaginales, Ustilaginaceae, mitosporic Ustilaginaceae, Pseudozyma, Pseudozyma brasiliensis (strain GHG001) (Yeast)	1392244	[illegible] GN=PSEUBRA_SCAF11g01174 PE=4 SV=1MLRTITSSSQATAARNRLGSFGRWCGKNLNFYRVHVMVFTLVPLIAAGIFYACNGETHVKFIDCLFVCVSAMTVTGLVTFNISTA NGGQQAILFLMCFGNISAVSVTMIWIRRSFFRKKFDRVIRRSAKARKRVHDVEEQERRDRRHNIAKIQRMVGLKSTDSATTISDTEDQ DRTDTSSSDQIELRRMEKNKQKSKAKRGPLRADMIRRIDGPAFLINSAGDRVNSVPEHSNEHRNSLPREASSVGSPRIPAAQPGASIL NTDQERQSSIVSDGQGQQPNIRIALPHETNASDAAGEKSTESRASNSERKGFSIPRFDHRHDPDADSDEEAIADEEEEEEEEIQEEAL RSPPLRARFFPDHQIHGRSRRVSDPPGFASRRGSDSGLAQAYSKHEKHDMFPRAQTVEFSVPSDYRSPVDFQRGQGYTTGMNVNG PGGLRQRTTTFNRTVTTRSGVSGRLSTGRTGVPLARTQTSSKQRGFGGFPTPLEIAGMAIKKAVPGVQERLQRTMTMPRTSTFTSV RSGGGITESGNKPAPYLTFDATVTGNSRFHALTETQRDELGGVEYRALDLLAKLVPAYWLIVNLGMVTLVAPYISSNAFRKYRPPFDE QGENKPDYTWFWFFQVISAYSNTGMSLVDTSMTRMQDAYFLLIPMGFLILAGNTGFPILLRFFIWTISICVPSTSRIYETLRFLLDHPRR CFVYLFPSSQTWFLFFILLLFNCIDWLAFLILDIGNPVIESITLSIRVFDGLFQSIAVRAAGFTVVSLLALAPAVQFLYVIMMYLSAFPLALS VRSTNVYEEKSLGVYVDEPADPGTAPSESKDAKVWGSFLASHARRQLAFDIWWLGFALWLICIIERNDIVDPESNGWFTIFSCLFELT SAYGTVGLSLGTPFDNFSLSGRFHTLSKLVVCAVMIRGRHRGLPVAIDRAILLPSELEQEDMMDDDLSHLDDTWDRDSTFVADPTAAT TVPVFAGGAVERQRTTSNASSKNGMSSVKRSQSGVSFALSPATNARRSSMPPAAMEPLSPTTAPAEFGVQEPRRSFTLTLPPSSLP LHHQSIYSSGGPPPSHSTGGGILGGMMVSTPGPLTAIDETPSGLGATPMSESRSESPRPPAGPAQRDNLTPSSLDTKASSEASTASV KGKERESPQSAVDEDKERRVAQSAGCSTPNGRHSPVSGAD	
6E-99	341	12.1	6.8E-96	331.1	4	2.1	2	S8FPZ8_FOMPI	Uncharacterized protein	FOMPIDRAFT_112253 2	Fomitopsis pinicola (strain FP-58527) (Brown rot fungus)	906	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Fomitopsis, Fomitopsis pinicola, Fomitopsis pinicola (strain FP-58527) (Brown rot fungus)	743788	[illegible] PE=4 SV=1MPSISSRPLRTSGFNRLKDAWSFAVAHLNFFRIHILVFTFTPLVFSGILYACNGRYHIAYIDCLFLCVTSMTVCGLATVNLSSLTPF QQFLLFAQMCLGSPVTVSWVMVYIRRRYFAKKFQHILEAEMSRKASEKAHRRIVVRVVPLWRRMLDFFLPDTTAEKDVDQSSDDSSE EHRSSRLRVDMIRRTDNAPQLVNPSGWISAGRTELSASNPGTQQRGQQKNADEYELQSPQRYLAFADIDNPSLVDNAMRTVDKRFD RSEPLSPVGEAPDSAGLSDAQSFQTAQSNDMRSETFSRTQTIEFANSPRPAREARSDRGFSQPRETSYSNWDDYGSSRDRRSMRG PTLSYPQSYPQSTTTHHSKRTHTLHSGFGGFPMPHEIFTSLMHRFFPKLERKLTRTMTIPRTRTFVSQQSGAPSGRPVTYISFDAVVG RNSEFKALTTEQLEELGGVEYRALGALLWIVGGYHILIQVLSWVVIAPYMSMSRWRDDFGTPPLYKDVSPVWYVFSAFQVVSAYTNT GMSLQDQSMVPFQRAYLMIFIIFLILAGNTAFYSSTSRRWVLSLVVPQESRIKETLHFLLDHPRRCFVYLFPSHQTWLLFIILLGLNLTD WFCFLVLDLGNPEIMSIPVGVRVVIGTLQACAVRAAGFATVNLANLAPAVKVLYVIMMYISVYPIAMSVRSTNVYEERSLGVFEDDEES VDEEFNSTGNRVTVWSHYLAMHMRRQLSFDMWWLGVALVLVCIIEKDGLEDASNATWFNIFRTLFEIVSAYGTVGLSLGVPYDNFSF SGALRPLSKLIICAVMLRGRHRGLPVAIDRAVMLPAEFSQASQNRLDDIASNNVRRSSMSMQLDGMNRDADERSQFRKPRVRSPSTIL TNGPESPQSPPNPASPQSLTQQQQNDHVETQ	
8E-99	341	6.6	1.8E-96	333.1	2.9	2.1	2	R9P3Z1_PSEHS	Uncharacterized protein	PHSY_003593	Pseudozyma hubeiensis (strain SY62) (Yeast)	1209	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Ustilaginomycotina, Ustilaginomycetes, Ustilaginales, Ustilaginaceae, mitosporic Ustilaginaceae, Pseudozyma, Pseudozyma hubeiensis, Pseudozyma hubeiensis (strain SY62) (Yeast)	1305764	>tr|R9P3Z1|R9P3Z1_PSEHS Uncharacterized protein OS=Pseudozyma hubeiensis (strain SY62) GN=PHSY_003593 PE=4 SV=1MLDNFLTSSSQATAPRTRLRSVGRWCGKHLNFYRVHVLVFTFTPLIAAAIFYACNGENHIKFIDSLYVCVSAMTVTGLVTFNISTA NGGQQAILFILMCFGNISAVSVTMIWIRRSFFRKKFDRVVRRSAKVRKRMHDVEENERKERRHNIAKIQRMVGLKSSDSATTVSDTED QDRTDSSSSGHIEMRRIEKNRQQKSKGKRKPLRADMIRRIDGPAFLINSAGDPSNTIPDPAAAEASNQPTGAALTEEPEPLSSPIFAPA QPGVSILNSEHDRRPSVFSDDPNHQTSIRISAPNDTVPSTNTKEDQVDPNPAQPPRKRFSIPRFDHRHDPDADSDEEAVADQEEEEL EHAPHSPPLRARFPDHASPGRSRRVSDPPQSHFRRGSDTGLLHTYKTHEKPDMFPRAQTVEFAVPSDYRSAADSQQQPTQGYTTG NAINPGGGLRQRNTTFNRTVTGRSYVSGRLSNGRTGVPLARTQTSSKQRGFGGFPTPLELAGMAIKKAAPGVQERFQRTMTMPRT STFTSVRSGGGLTETATKPAPYLSFDATVTGNSRFHSLTEAQRDELGGVEYRALDLLAKLVPAYWLIVNLGMVTLVAPYISSSAFRKY RPPFESQGENKPDYTWFWFFQVISAYSNTGMSLVDTSMTQMQDAYFLLIPMGFLILAGNTGFPIFLRFFIWLISLCVPSTSRAYETLRF LLDHPRRCFVYLFPSSQTWFLLCVLVLFNSIDWLAFLILDIGNPVIESITLSIRVFDGLFQSIAVRAAGFTVVSLLALAPAVQFLYVVMMYL SAFPLALSVRSTNVYEEKSLGVYVDEHAEPGAVPHESNNPKVWGTFLASHARRQLAFDIWWLGFALWLICIIERNDIQDPSSNGWFTI FSCLFELTSAYGTVGLSLGTPFDNFSLSGRFHTLSKLVVCAVMIRGRHRGLPVAIDRAILLPTELEQEDMMDDDLSQYDETWDRDSTF VTDPTAPTPGAPRASMNVPTTNRQRSDSNEGSAAGESNSGMSSVKRTQSGVSFAINPLAAKARRSSVPPTAMEPLSPKQQAEVAA QEPRRSFTLTLPPSSLPMHHASPHHHGGLGGMPPSSSSNNNTSVAGGIMGGPMVVSSPGQLTAIDEMPSGLGATPISESRSESPA VAAGVSGREERTQASPPSFHTNAESSSSSSSDGSLKGKEKATSAVDEKRERQVAEKAGCSTPNGRHDPVSGGD	
1.3E-98	340	4.4	1.9E-98	339.6	3	1.1	1	M5C2M0_THACB	Low-affinity potassium transport protein	TRK1BN14_07741	Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)	617	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Cantharellales, Ceratobasidiaceae, mitosporic Ceratobasidiaceae, Rhizoctonia, Rhizoctonia solani, Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)	1108050	[illegible] 7/3/14) GN=TRK1 PE=4 SV=1MPSRHSNGTIPTPHRPDYDVTPHPANLSPPVTDELHLGPLMESPGRIDDQGGILLHPDTDRDQAIEDESEAIDHVTSGHERHPS EAVTHREPGTGTGEFPRIQTIEFVNTPHLPSHQSGYGGFPMPHELAGRFIKRVFPQTMTLTRRNSQFHDLTQEEQEELGGVEYRALG ALLWIIAAYHIGIQLFGFVVFAPYSSMPKWAPVFREQQHRFVPPTWFSAFQAVSAYTNTGMSLIDQSMIPFQTAYPMIIITFFMILAGNT AFPICLRFFIWLLSKVVGKRSHETLSFLLDHPRRCFIYLFPSHQTWFLLIVLVTMVITDWVSFMVLDIGNEVFEAIPVGTRIAIGLLQAGAV RAAGFATISLSALAPAVKVLYVTMMYVAVYPIALSVRATNVYEEQSLGVYLDGEGDEEEPNGPSSVSAWGSYLAWHARRQLSFDMW WLAVALWLLCIIERGEIMNPESEHWFDIFTIIFELVSAYGTVGLSLGLPTANYSFSGALRPLSKLVICLVMLRGRHRGLPHAIDRAVVLP WELMGRQGQNRSYSGLDTLGNRQSMAGEPGSSLEGHSTSRAPTATHGGVDLKHRTNTILSPVHEVLTPVTSVTGTPRATFSALGP GEN	

1.5E-98	340	4.4	1.3E-95	330.2	0.2	2.1	2	T0LW67_COLGC	Uncharacterized protein	CGLO_07710	Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	768	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	1237896	>tr|T0LW67|T0LW67_COLGC Uncharacterized protein OS=Colletotrichum gloeosporioides (strain Cg-14) GN=CGLO_07710 PE=4 SV=1MGSVAAAKRLLAHNPLNRFLPPLNFITLHYAYFIVVCLLSSVIFWASSDAEFKVSYTDSLFLVVSAMTEAGLNTVNLSQLTTWQQTILFLLLLLGSTIWVSIWTILARKHVFEKRFDEIVRAERARKLSRHGSTISLALPRLPLTLPKLQLALSFGKAQTVPPPDQSFKGTGSRIAETHPPPDFQDSDTTEGPPQFRRAMSTPDVNTRDKHTTKDVEDIADSQNPGHITFDDTPHPNATQATSTGVSVQGDGVALPSRRSAKAPTDSADIDLDARHFLKHRSASRNGQFHDLSSAERDHLGGCEYRALKVLATIVPAYFFMWQFLTSLALGAWMNNYMPNTARANGINPWWLGIFNAVSAFNNSGMSLLDANMIPFQEAYYVLITMGLLILAGNTAYPLFLRLIIWGMLRILNLATPQDAFTDLKATLEFILKYPRRVYTNLFPSRASWWLFFMLLWLNSVDWVAFELLNIGNSVIEKIPTGSRILDGLFQALAVRSGGFYVVPISGLFIGLQLLYVIMMYISVYPVVITMRHSNVYEERSLGIYSDDMETTSEPDPEAGMPLLPMGSRPPTLARTTSFGAASARPSVLARRLSRSGPVSDARRAFKSTFMSFHGVGVAPPKAGAPSIPGPDQPRPESRISFISQQVRGQLAHDLWWLVLATLIITIIETSKFIKDPVTFSVFNIIFEVVSAYGCVGISVGLPTDAFSFCGAWHTGSKLILCLVMLRGRHRGLPVALDHAVRLPGRQLHRDEEEDHQIRRSRTIEIER	1237896
1.6E-98	340	2.1	7.8E-95	327.6	0	2	2	G2R780_THITE	Uncharacterized protein	THITE_2116861	Thielavia terrestris (strain ATCC 38088 / NRRL 8126) (Acremonium alabamense)	730	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Thielavia, Thielavia terrestris, Thielavia terrestris (strain ATCC 38088 / NRRL 8126) (Acremonium alabamense)	578455	>tr|G2R780|G2R780_THITE Uncharacterized protein OS=Thielavia terrestris (strain ATCC 38088 / NRRL 8126) GN=THITE_2116861 PE=4 SV=1MSRWPHHLDDAESGAASACSKFRAWLPPLNFITIHYAYFIVVCLVASLVFWGSSDPARRISYADSLFLVVSAMTEAGLNTVNLSQMTTWQQTMLFLLIILGSSIWVSIWTVVARKHVFEKRFQDIVRAERMRRASRAGSAVSLPKLQRFLSFRKLPTTIPLQSPLVSQGGEHPEPKEGPPPSEPATGQIEPAAAAAAASIDAQLAVAAAAPREAALSPARVVFVHTPRPSEAVSTTAREHSEPSQLTRRSRNGKDGSQDDGKDDFSIRHLLAHRPGGRNAQFHGLTREERERLGGCEYQALRVLSVIVPLYFFLWQLLGCLALGAWINKYQPEPPLKNGINPWWLGIFNGVSAFNNSGMSLLDANMIPFQNSYFVLITMGLMILAGNTAYPIFLRLIIWSALKVLRTTGEETHVELKSTLEFILRYPRRVYTNLFPSRPTWWLFFMVVMTNGIDWMAFEVLNIGNPVIEAIPIGARVLDGLFQAFAVRSGGFYVIPIASAYPGLQVLYVIMMYISVYPVVITMRHSNVYEERSLGIYADDDAPSRSSVDEKKHAGGNGLLIQLIRDNLSFAGVGAAKPKRADGLESRTSFVSQQIRGQLAHDLWLLTLAVLIIVTIETSHFLEDPVHFSVFNVVFEVVSGYGCVGISVGLPKDAMSFSGGWHAGSKLVLCLVMLRGRHRGLPVALDRAVRLPGQRLLEDEEEDWRLRRARSGRGMEDKAV	1173701
2.6E-98	339	8	2E-96	332.9	1.3	2	2	A0A066XFJ1_COLSU	Putative cation transporter	CSUB01_11506	Colletotrichum sublineola (Sorghum anthracnose fungus)	668	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum sublineola (Sorghum anthracnose fungus)	1173701	>tr|A0A066XFJ1|A0A066XFJ1_COLSU Putative cation transporter OS=Colletotrichum sublineola GN=CSUB01_11506 PE=4 SV=1MSSQPQGPEALHHDGQDRDVSRGGSRRLTSSGLRSLLPPLNFITLHYAYFIGTTLLASVIFYVSSSPHGSIGYVDSLFLVVSAMTEAGLNTVNLSEMTVWQQVMLWLLIIVGSSVWVSIWTVLARKHVFEKSLREIVQASEEEGVQHHDRLPTFNGGDAAPRSKGEASVTGVMGPGTSNQARAMGNHMTIDASENLTRRSTHSVSSSTKPTRPWLSFLSSAKEGRNSQFHSLTASERSRLGGHEYRALRLLSVVVPVYSVLWQVLGSLALGAWIANNMPTVATSNGANPWWAGIFFAVSAFNNSGMSLLDANMVPFQQAYFVLITMGLLILAGNTAYPLFLRLIFWSALKVLRLTTGEETHVELKSTLEFILRYPRRVYTNLFPSRPTWWLFFMVVMTNGIDWMAFEVLNIGNPVIEAIPIGARVLDGLFQAFAVRSGGFYVIPIASAYPGLQVLYVIMMYISVYPVVITMRHSNVYEERSLGIYADDDAPSRSSVDEKKHAGGNGLLIQLIRDNLSFAGVGAAKPKRADGLESRTSFVSQQIRGQLAHDLWLLTLAVLIIVTIETSHFLEDPVHFSVFNVVFEVVSGYGCVGISVGLPKDAMSFSGGWHAGSKLVLCLVMLRGRHRGLPVALDRAVRLPGQRLLEDEEEDWRLRRARSGRGMEDKAV	1173701
2.6E-98	339	9.1	1.1E-93	323.8	3.1	2.9	2	G3XTK0_ASPNA	Uncharacterized protein (Fragment)	ASPNIDRAFT_130818	Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	617	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	380704	>tr|G3XTK0|G3XTK0_ASPNA Uncharacterized protein (Fragment) OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) GN=ASPNIDRAFT_130818 PE=4 SV=1ILFLGLLGLVVLYPYGNLRAIDAYFFGVSSSTESGLNTLVDHLLYYVTFDVKDMKLYQQLFIYFVPIVSNLGFINILVVVVRLLWFEKRLKEIAPGVLDRKSNPSSSNAARYDPEAHPRALSEPSTSENGPVDSTEKKEVDDGQRLVGSKIGHVVPESISFADTTKALYIPSPRERDRGVPIAEVQRGPERRNSENTDELSENGRSATGGLPFERVASSLFVIGKQPSRAREPSLRPAISLSKDANLPELSVQATLGRNSQFHNLTAADRERLGGIEYRSLRLLLKIVKGAYKQLRHSLLCDQAIYSAQTMTSNLGLTLTPDSMISFNNAVFPMLVMSFLAYAGNTLYPCCLRLIIWAMSKCTPESSSLKEPLEFLLKYPRRCYLLLFRSKPTWILFGIIFVLNFVDVLLILVLDLDNPAVNDLAPGPRVAAAIFQSASSRHTGTASFNLADVNPAVQFSLLVMMYISVFPIAISVRASNIYEERSIGVFSSETDMDEADGKRYVLMHMRNQLSFDLWYIFLGIMCICIAESGKIMDPTKPAFSVFAIFFEVVSAYGNVGLSLGYPTASTSFSAQFDIFSKIVICAMMIRGRHRGLPYQLDRAILIPNNRLVEDDKV	380704
4.5E-98	338	6.1	1.7E-94	326.5	0.5	2.1	2	L8G1S9_PSED2	Uncharacterized protein	GMDG_02197	Pseudogymnoascus destructans (strain ATCC MYA-4855 / 20631-21) (Bat white-nose syndrome fungus) (Geomyces destructans)	734	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Leotiomycetes incertae sedis, Pseudeurotiaceae, Pseudogymnoascus, Pseudogymnoascus destructans, Pseudogymnoascus destructans (strain ATCC MYA-4855 / 20631-21) (Bat white-nose syndrome fungus) (Geomyces destructans)	658429	>tr|L8G1S9|L8G1S9_PSED2 Uncharacterized protein OS=Pseudogymnoascus destructans (strain ATCC MYA-4855 / 20631-21) GN=GMDG_02197 PE=4 SV=1MSDSLRSRSRGHQENMQENERMRRGQSHLPPLNFITVHYAYFIVTCLVCSLIFWGASSPAQSISYTDSLFLVVSAMTEAGLNTVNLSTMTSFQQTMLFLLILIGGSIFVSIGTVLVRKRAFDSRFKHVVKLQKERRRGHRRSFSISAMRSGPILRRLRSRRGLEEAVDDDLPKSWADSSSRNATAGKSMSDPMETGRNGTPGVVVTAESAADEDGHREATHLSGDHISFMPHDSSSTRESRRVLSSVGPGPHLSSTSLRGPFAGTRGRQGKEVKMEEEKEKEEDPPDSWFPGYLTRHTTGRNGQFFGLSRAERDHLGGVEYRAIQLLAWIVPIYFVLWQLLGCLGLAAYVAHNKASVAQENGINPWWLGIFNGASAFNNSGMSLLDENMIPFQTSIYMLTTMGLMILAGNTAYPLFLRLILWSMLKLLTRIYPSEDQCADYKTTLRFILTYPRRVYTNLFPSSQTWWLLLMLIVLNGIDWAAFELLNIGNSTTSTIPERFRILDGLFQALAVRSGGFYVTSIANLRIGLQVLYVIMMYISAYPVVITMRHSNVYEERSLGIYAQDEPYSPGGPRIGTPASQLRRALSKAITSPFPSGAYNAHDFMWQQIRGQLAHDLWWLVVAILLISCIEVANFEKDPVTYSVFNIMFEVVSAYGCVGISPGLPNKSYSFSGGLHTCSKLILCAVMLRGRHRGLPVALDRAVRLPTAAGDDDELEEEDSVVRRTRHIHHGGGD	658429
7.3E-98	338	15.9	1.1E-97	337	11	1.2	1	B8F7W0_HAEPS	Trk system potassium uptake protein	trkG HAPS_1924	Haemophilus parasuis serovar 5 (strain SH0165)	488	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Haemophilus, Haemophilus parasuis, Haemophilus parasuis serovar 5 (strain SH0165)	557723	>tr|B8F7W0|B8F7W0_HAEPS Trk system potassium uptake protein OS=Haemophilus parasuis serovar 5 (strain SH0165) GN=trkG PE=3 SV=1MRIVGILVMCFSFTMLVPAFVALIYDDGGGRAFLEAFVLNLSVGTALWWFCRKYKQELRSREGFLIVVLFWVVLGSLGAVPFILLENPDLNFSESIFESFSGLTTTGATVITGLDQLPKAILFYRQFLQWLGGMGIIVLAVAIIPLLGIGGMQLYRAEMPGPLKEQKMRPRIAETAKALWLIYLSLTVLCAVAYWLAGMNGFDAISHSFATVAIGGFSTHDASIGYFNSPMIDLITVLFLLISSCNFALHFAVFDQFNDRYKGNNKSNFLGLYWKDYEFRFFITVQLALFVICFGVLLIYNYFDDHSVTFIQALFQSVSISTTAGFTTNDFSQWPSFLPLLLVLASFIGGCAGSTGGGLKMFRVLLLYLQGKREIHRFIHPNVIQPIKLGKHVLSERIVEGVWAFFSAYFFVFVVCWLATIACGMETFDALNAVIASLNNLGPALGTVSSNFTQIPDSAKWVLTFAMVCGRLEVFTLLVILSPSFWID	557723
1.4E-97	337	7.7	9.3E-93	320.8	0.9	2.1	2	S3D9Y8_GLAL2	Uncharacterized protein	GLAREA_06962	Glarea lozoyensis (strain ATCC 20868 / MF5171)	746	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Helotiaceae, Glarea, Glarea lozoyensis, Glarea lozoyensis (strain ATCC 20868 / MF5171)	1116229	>tr|S3D9Y8|S3D9Y8_GLAL2 Uncharacterized protein OS=Glarea lozoyensis (strain ATCC 20868 / MF5171) GN=GLAREA_06962 PE=4 SV=1MSPKTLTTRLRQKTNAFFEDDRTKNIQKYLPPLNFITIHYAYFITTCLIFSLIFWGSSNPTHSISYLDSLFLVVSAMTEAGLNTVNLSQMTTFQQVLLWILIVIGSAIFVSISTVLTRKRVFEKRFDYVVKAQREARRLRRRSMSQMREVPVIERLNSQRKTEEPVVKSDFESRHSGPRDPTNGLFETPAGNQSGLGAVRESEETDEMVKVGGQDVVDEGVHDRRGSVTTVVDEGVRDRRGSIVTTTGPTLRLAPTSPALSNTRVINFVGVGEHPNASSTSYRLPHSRGGITQRGRSNTATTGQQSLHDLHYPSYLTKTVTGRNSQFHGLSRDEREHLGGVEYRAITLLAYIVPIYFVMWQLLGCVGLGAYMAHNKASVAEMNGINPWWLGIFNGASAFNNSGMSLLDANMIPFKNSVYTLLTMSLMILAGNTAYPLFLRLIIWSGLKIMNLFYPLESQHPETKATLRFILRYPRRVYTNLFPSTPTWWLLFMVVCLNGIDWVAFEVLNIGNAAVEDIPKQFRVLDGLFQAFAVRSGGFYVIAIPSLRIGLQFLYVVMMYISVYPVVITMRHSNVYEERSLGIYADDPPLEKEGTYSKLKRTLTNSVNPSHGVGVGAQQFINQQIRSQLAHDIWLLIVSILLIVILETPNFARDPITYSVFNIMFEVVSAYGCVGISTGLPDQAYSFSGGWRRASKFILIIVMLRGRHRGLPVALDRAVRLPGEFGRGEEEDWEVRRGRREGELGV	1116229

1.5E-97	337	0.1	1.9E-92	319.8	0	2.1	2	A0A0C4EZY2_PUCT1	Uncharacterized protein	PTTG_06393	Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)	1330	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Pucciniomycotina, Pucciniomycetes, Pucciniales (rusts), Pucciniaceae, Puccinia, Puccinia triticina, Puccinia triticina (isolate 1-1 / race 1 (BBBD)) (Brown leaf rust fungus)	630390	>tr|A0A0C4EZY2|A0A0C4EZY2_PUCT1 Uncharacterized protein OS=Puccinia triticina (isolate 1-1 / race 1 (BBBD)) GN=PTTG_06393 PE=4 SV=1MAGSIVRSSIDYQVEGRMNDDVPFQPSPFLVFLRQDKISATHYQSVSSGDGRTLIGLLQSRRRTIEESLHPNLATSSPGPARLVHMQKNRPEDAFNQGDTQDLRGRPMTPLTDDAIQLANSSHQMPSSPPSSILPPINLRARSHRSRRTIFRRFSSRRTFRWLRRWIGCDLNFYRCHLLAFIFIPFIFAIIFYLAHTLNQPEVEKPAFIDCLFMCHSAMTMTGLNTIMLSSINRFQQALLYILMSIGSTTMISMIMIYIRLRAFKERFKAIINSSTPLTISHPIPINGTPPQLKFPTISLRGDPDHVPALDKSRSVSAEEAQKLESQCIASFADPDLMESLPTHPLTRAEDRIEHLAPNLPSPTAHLESLQHPSPGAVPVVESPEPSPASVRRPNRTGEFVRRPILLRRNSDGGVVGARSSASDIEPHLDSSLRSNPLLSILKSSPLILDNLLSHHLTFEKSTRQNTRANRSRDLFPRSTTLDQASSFPRNRVSQSQSRDRSLTFALQRTPANSDHHAVADRGRPTLRGLMADDIQVSPFSHIDTLHPQRHDHHTLLPGQLGWIAGMEPESAGPQTEAQTFQQWKMGGVSRGEAPEHDSDGLRRRPKPARSTSAVQGTHHHRGQSGSVPAGSHRHRPSQHSISGHSALGPTCRRRSSFTGLPRTSSTTDFGGFPNPAFVLLKRLGKALRPAQNSQHSLEFVRTSSLAAPAFDQNERHKLAEWLFGRGAGMISERIRDVKTVSYIKFNVRSSLCEIPCVSGILFSNPSYFNFSHKPPAFLYSSRIQGSRGPAGLLITLPGYGAAPAVPLSKAQSQKWRSHFQEEELGGLEYRALSMLLKVVIGYWTIFQLMAILILIPYLETPRGNRRFSEVFDGPGGTDRVWYAIWITCSAFTNGGMSLIDAGFTVFHGGYLLMLVCSALIVAGNTGYPIILRAIIWTLSKICPESTPEEHKKVGGGKKRCFVYLFPSRQTWYLFFILLLLTFIDWFFFLILDIGNPKIESIPIGTRIIVGLLQSLSVRAAGFSTIALGDLAPAVQVLFTIMMYIAVYPIAISIRATNVYEERSLGIFHVEDEPDQDSDDEDEMRAHDRGRDGRRTVPSEHPLNLDHFPHSFSSALDETPNSNTSLRNKTQKPRLSHSHRFSSNPDRRHSRLERSENTHSYDRQADCDSRNSTPSYLALHIRKQLAFDIWWLALAVWCICIAERSKIVTAQATDSASFSIFSIMFEIVSAYGTIGLSVGLPDSPTSMVGGFSSFSKLVVIAVMLRGRHRGLPIAIDRAVILPYDKSKPDDQDRAEEEELVEDVEDQTPSEERPEIQERIFNQKLPDLESQ
2.2E-97	336	7.6	3.7E-94	325.4	1	2	2	G3XQN3_ASPNA	Uncharacterized protein	ASPNIDRAFT_171029	Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	681	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7)	380704	>tr|G3XQN3|G3XQN3_ASPNA Uncharacterized protein OS=Aspergillus niger (strain ATCC 1015 / CBS 113.46 / FGSC A1144 / LSHB Ac4 / NCTC 3858a / NRRL 328 / USDA 3528.7) GN=ASPNIDRAFT_171029 PE=4 SV=1MLPPFNFLTLHYVYFIATSLICSVIFWGSSTPRRSVSYTDSLFLCISAMTGAGLNTVDLSSLNSFQQSILFALLLLGHAILISITVLFVRMGAFQAKFKGISLERARKALQQQLVGQDTILEPIQESVASEEHYQLAKIDGATLDVKHAVTAGAAPADKCNDVRDDDQIRWVDDDQVTLSHMRARQKHHHHHRVFPMVGVGARLDLNNHPRDAAPRMTQNDGDTDLPALKGLIKGTQKYFRSKGSIARNSQFHGLTPEERERLGGVEYKAVSLLLVIVALYWILFLICGIIGMGTWIAVNHPDIPRSNGLSPFWTGAFFAVSAFVNSGMSLLDANMTAFQTNAYPLLTMAFLILSGNTLYPCFLRFIIWAMRCLIPDKPSWATWKVTLDFILDHPRRVYTNLFPRRHTWYLLGTIIILNAIDWAGFEVLSIGNKEIESLPTGYRVLDGLFQACAVRAGGFYVVTIANLRQGLLVLYVLMMYVSAYPVLVTMRNTNVYEERSLGIYAHDNTDDETEEKASPNMLIQLVRHHLLGRQDASTPEASRSYFVHQQLRSQLSHDLWWIALAVFLIAIAESGNYSRMPVAYSTLNIIFEVVSAYGCVGISVGFPSSNASFCSSWHTISKLILAAVMLRGRHRGLPVAIDRAVMLPNESLEWAEEEDAAMRREQSRAWGSDKMPVGSV
2.3E-97	336	2.3	2.1E-91	316.3	0.3	2	2	M3AZW7_PSEFD	Uncharacterized protein	MYCFIDRAFT_203372	Pseudocercospora fijiensis (strain CIRAD86) (Black leaf streak disease fungus) (Mycosphaerella fijiensis)	643	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetidae, Capnodiales, Mycosphaerellaceae, Pseudocercospora, Pseudocercospora fijiensis, Pseudocercospora fijiensis (strain CIRAD86) (Black leaf streak disease fungus) (Mycosphaerella fijiensis)	383855	>tr|M3AZW7|M3AZW7_PSEFD Uncharacterized protein OS=Pseudocercospora fijiensis (strain CIRAD86) GN=MYCFIDRAFT_203372 PE=4 SV=1MRLVAIFQPLKRPFRYLRRLLPPLNFITIHYAYFILTCLISAIILWAADTDRDLRFIDALFLAVSAMTLAGLNTVNLSTLNTFQQFWLFLLIIIGSAVLVSAFVVQIRKRAFETKFKDVVLKERQRRMERRSRSRSRAGSRRGQPDAQDHQDLVQPVDTAQDASADMGDAEKASKSEISVEGPAILETPPKNHGNIGRYFHSTSGWIGRNSEFHGLTDKERQHLGGYEYRAVCFLAWLVPIYLVLMQLLGCLGCAAWIARNRPETTTANGLNPWWVGAFNAVSAFNNSGMSLLDANMTAFQTGYYLLITMGFLILAGNTCYPIFLRLIIWTIYKVVQRLAPRSEEWADRAKMLKFLLDHPRRCYTNLFPSRHTWWLLASVVALNLIDWIGFEVINIGNKAIEQLPLGVLVIDGLFQAFAVRSGGFYVVAISQVRIGLQVLYVVMMYISVYPVVITMRNSNVYEERSLGIYAEDLPENDGRANDQPGFLRQLTQHFVSGGASNSESNSSFVRQQLRAQLAHDAWTIFLALFAIIIIETAQFDRDPNVFSVFNFLFEIVSGYGCVGISQGIPWDAYSFCGTWHTASKLILCGVMLRGRHRGLPVAIDRAVLLPGEEIEQAEEDDGRIRLQRTISRGRSTLQQQDV
2.9E-97	336	6.2	3.8E-97	335.3	4.3	1.1	1	B8P1H3_POSPM	Predicted protein	POSPLDRAFT_98377	Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	732	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Postia, Postia placenta, Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	561896	>tr|B8P1H3|B8P1H3_POSPM Predicted protein OS=Postia placenta (strain ATCC 44394 / Madison 698-R) GN=POSPLDRAFT_98377 PE=4 SV=1MIRRMDDAPRLVNPSGWISEGRSEPLTIDPAGNNDAGRYLAFADIDNEELVNSAMPIQSPAGPTQGFALDAERSSESEDIDDEDETLVSIGCSDLAVSDILTEMNELPRSLSINIASQNRSPIMPRTQTVEFAQTPLPLREARSLDRAQRQHLDSIAQGRSYTGNFSSHSRGRGSMRRPTLSLQQSMNSQHSGRRSSMHVPAMHSGFGGFPMPHQIASRLFRRLFPRLEHKLTRTLTLPRTRTIASQHGSLAPGARAVSYISFEATVGRNSRFRALTRDQQEELGGVEYRALSALLWIVGGYHILTQLLGFMVISSYMSISRWSDDFKIHQLYRNISPVWFSAFQVVSAYTNAGMSLEDESMVPFQRAYPTILAMIFLILAGNTAFVGLQFLLSYSQLTPTGSLFFCVLRYHPRRCFIYLFPSHQTWFLLTILIALNATDWFFFLVLDLGNSAVTSIPIGVRIIDGLLQAVAVRAAGFSVVTLSELVPAVKVLYVIMMYVSVYPVAMSVRSTNVYEEKSLGVFEDEDESIDVDETFTPSGNRMTVWSRYLGMHMRKQLSFDMWWLGTALFLICIIEKDKLQDDANATWFNIFRILFETVSAYGGVGLSLGVPYDNYSFCGAFNPLSKLIICAVMLRGRHRGLPVAIDRAVMLPMEFHPDFQRSNIDGQEDRFDYQPASPNGNARSDAVSEKSPRSYRRNTPMSAGQEHARGGTLSPREANPQIARLQDEEAL
3.4E-97	335	7.3	6.9E-93	321.2	0.3	2	2	C7YXY8_NECH7	Putative uncharacterized protein (Fragment)	NECHADRAFT_12230	Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	543	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium solani species complex, Nectria haematococca, Fusarium solani subsp. pisi (Nectria haematococca), Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	660122	>tr|C7YXY8|C7YXY8_NECH7 Putative uncharacterized protein (Fragment) OS=Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) GN=NECHADRAFT_12230 PE=4 SV=1FLSKLSFITSHYAYFIIVCLIASLIFWGSSSGTSYVDSLFLVVSAMTATGLTTVNLSKATTGQQVLLFLLIIFGSRIWISICIVYSRKRRFNKRFDEIVREARMRRRDRSPPRLAPSPSPPPEGEITGDARTREKDDDEVPYLSWTPTIGRNSQFYKLTSEQRDELGGIEFRALKLLLRILLLYLFLWQFLGCISLGSWINNNKPALENSPNLWWLGIFNGVSAFNNSGMSLLDASMVPFQRSYFVLITMGLMILAGRTAFPIFLRLILWSLVKIMRGLVTWYLLWPRGVTWYLLSVLIFLNSVNWVGFLLFNLNNPEIESIPTGPRVLAGLFQALSIRFGGFHITNIANLHIGLQVLYVIAMLVLAYPIRLGVRRTNVYEERSLGIFNPRNDHDSTQDGGQNTLIDELRRFRRQLNRGSVRHDAWALMLAVVIITTIESGQFRRDPVHYSVFNIMFEVVSAYGCVGVSVGLPDADCSFSGGWHVASKVILCAVMLRGRHRGLPEAIDRAILLPSEGRFSREEE
3.4E-97	335	7.2	1E-93	324	1.2	2	2	G7XK79_ASPKW	Potassium transporter	AKAW_05491	Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	728	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus kawachii (White koji mold) (Aspergillus awamori var. kawachi), Aspergillus kawachii (strain NBRC 4308) (White koji mold) (Aspergillus awamori var. kawachi)	1033177	>tr|G7XK79|G7XK79_ASPKW Potassium transporter OS=Aspergillus kawachii (strain NBRC 4308) GN=AKAW_05491 PE=4 SV=1MTSRGWRQLLSRSILAMLPPFNFLTLHYVYFIATSLICSVIFWGSSTPRRSVSYTDSLFLCISAMTGAGLNTVDLSSLNSFQQSILFALLLLGHAILISITVLFVRMGAFQAKFKGISLERARKAFEQQGILHGRAHKVEHQAISLQCAREALGQQLVGDDTKAYDHQPQSTSLEPILEHYQLAKLDGATVDVKHAVTAGAAPAENCDSVRSDDQIQWVDDDQVTLSHMRARQKHHHHHRVFPMVGVGARLDLNNHPRDAAPIMAHNDEETDLPALKGLIKGTQKYFRSKGSIARNSQFHGLTPEERERLGGVEYKAVSLLLVIVALYWVLFLLCGIIGMGTWIAVNHPDIPRANGLSPFWTGAFFAVSAFVNSGMSLLDANMTAFQTNAYPLLTMAFLILSGNTLYPCFLRFIIWAMRCVIPDKPSWATWKVTLDFILDHPRRVYTNLFPRRHTWYLLGTIIILNAIDWAGFEVLSIGNKEIESLPTGYRVLDGLFQACAVRAGGFYVVTIANLRQGLLVLYVLMMYVSAYPVLVTMRNTNVYEERSLGIYAHDNTDDETEEKASPNMFIQLVRHHLLGRQDASTPEASRSYFVHQQLRSQLSHDLWWIALAVFLIAIAESGNYSRMPVAYSTLNIIFEVVSAYGCVGISVGFPSSNASFCSSWHTISKLILAAVMLRGRHRGLPVAIDRAVMLPNESLEWAEEEDAAMRREQSRAWGSDKMPIGSV

3.6E-97	335	0.9	1.5E-90	313.5	0.6	2.1	2	H0EPJ7_GLAL7	Putative Low-affinity potassium transport protein	M7I_4578	Glarea lozoyensis (strain ATCC 74030 / MF5533)	661	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Helotiaceae, Glarea, Glarea lozoyensis, Glarea lozoyensis (strain ATCC 74030 / MF5533)	1104152	>tr|H0EPJ7|H0EPJ7_GLAL7 Putative Low-affinity potassium transport protein OS=Glarea lozoyensis (strain ATCC 74030 / MF5533) GN=M7I_4578 PE=4 SV=1MAKTFSRSRTTEQNIDSEEMGVRGRSIVVMHNMTASNGMSTDRSRTEEFAHHMEKINAIEEEPARSSNDSDGTKRQPSANGA RSKSPGAADRPSTGIKFADQHKPSEKTIAYYGELNNGIVDEEERRPSHRSPEEHIAILERQRKQDDGAVLRIPGPRDADAGVAPQAVDD SDVISRTMSRRASTLQSHTADTDAVALNGDDHPTFDNEAAKPRNITIAEPEKEPAGERATKDTSDEGAPYLSWEPTVGRNSAFVDLT EDQREELGGIEVQSAGNFVPKNSGIWEELKFLLDHPRRCFTLLFPAGATWVLFLILCLGLNGLDLLFFIILDFGNSVVTQLPVHIRFLDGW FQAASTRTAGFAVVNLALLHPAIQVSYLIMMYISVLPIAMSVRRTNVYEEDSLGVYGSSEEENSDAAEPSYIGAHLRRQLSFDLWYIFL GFFIITISEGSRLQSGDPGFSMFSVLFEIVSAYGTVGLSLGYTNINASFSAEFGVIAKLVIIAMQIRGRHRGLPYELDRAILLPSEQLAKRE ADAAARARRNSDLTQVNTRGTKLDRTASRATSSRGGQNFFSGLLHPGPTIPNNNLGAIRTRPVRERRHSIATTPMRRGLSRSISPTAT GIMARENHAMGMALGGDGAESRGRTEGRRSFFKDGVNPAPAPDAQ
4.1E-97	335	7.6	2.9E-95	329.1	1.2	2	2	N4URW6_COLOR	Cation transporter	Cob_12650	Colletotrichum orbiculare (strain 104-T / ATCC 96160 / CBS 514.97 / LARS 414 / MAFF 240422) (Cucumber anthracnose fungus) (Colletotrichum lagenarium)	657	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum orbiculare, Colletotrichum orbiculare (strain 104-T / ATCC 96160 / CBS 514.97 / LARS 414 / MAFF 240422) (Cucumber anthracnose fungus) (Colletotrichum lagenarium)	1213857	>tr|N4URW6|N4URW6_COLOR Cation transporter OS=Colletotrichum orbiculare (strain 104-T / ATCC 96160 / CBS 514.97 / LARS 414 / MAFF 240422) GN=Cob_12650 PE=4 SV=1MAISTRDVHDDHDLHDFDEPAVQPAAKSTLRSLLPPLNFITLHYAYFIGTSLLASAVFYASSNPHGSISYVDSLFLVVSAITEAGLN TVNLSAMTVWQQVMLWLLIIVGSSIWVSIWTILARKHAFEKRSREIVEAERARGDRDGCLPVHRPGKGRAGASGTEILVQGDARVRG ADHVAFGTGNITRRSTPSVSSVQKPARPWLGILSASKEGRNAQFHSLTAAERSRLGGHEYRALRLLSVVVPLYSVLCHLLGSLALGA WIANHMPAVATSNGANPWWAGIFFAVSAFNNSGMSLLDANVVPFQQAYFVLLTMGFLILAGNTAYPLFLRLIFWTALKVLRFTTSEGT LAELKTTLEFILRYPRRVYTNLFPSRPTWWLFFMVLLTNGIDWMAFEVLNIGNPVIEAIPVGARVLDGLFQALAVRSGGFYVIPISSAYP GLQVLYVIMMYISVYPVVITMRHSNVYEERSLGIYADDDSRPASYEASEKKHLASGGIVANFVRENLSFAGVGAAKPAGPDGKESRTS FVSQQIRGQLAHDLWLLTLAVLVIVIIETSNFLADPVHFSVFNVVFEVVSAYGCVGISVGLPNDAMSFAGGWHAGSKLVLCLVMLRGR HRGLPVALDRAVRLPGQRLLEEEEEDWRLRRARSRGVDDGGI
4.7E-97	335	15.9	1.1E-93	323.8	5.1	2.1	2	A8N5R3_COPC7	Potassium transporter	CC1G_12095	Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) (Inky cap fungus) (Hormographiella aspergillata)	919	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Psathyrellaceae, Coprinopsis, Coprinopsis cinerea (Inky cap fungus) (Hormographiella aspergillata), Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) (Inky cap fungus) (Hormographiella aspergillata)	240176	>tr|A8N5R3|A8N5R3_COPC7 Potassium transporter OS=Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) GN=CC1G_12095 PE=4 SV=2MADLAPVTDSEHDSNRGLWRRCTKHLNFYRIHILVFTFTPLFFSVIFYLSNGEVKISYVDSLFNCVSSMAVCGLATVDLSSLTPW QQVILFIQMCIGNPIVVSWLIVFSRKRYIERRCSNALASYIDQREKVENVDMKKRSPWARFMRSLGFLTPNHSVNDTDTELGEKPRAG RSIDPANIRRLEAAPRPVNPSGQYTDQDAYAIEITPPTERNSPVPLSRESTPSSSSAESSTGKRSQFDDYDDPTASEGPGLPRTVTFQ ESEVTSRIRHRTGKYNEGDDIVTEHLRSEDPGTRQSSNQGIPRTMTHQSTRPSLRTYTTNVSVISQAPRKNQGFGGFPMPWTVLSSL FHWLFPDLGRKLHRTITMPVTATIASGAGSTKPGPSYIIPDDEPVIVGKNSDVQASNSQLKNLAYHEYKALILLLWIIAFYHVGVQLIGFA IAAPYISTSRWKEAFVPPQLVRPVNSVWFSAFQTVSAYTNTGSSLVDQSMLPFQSAYVLILVMIFLIYAGNTCFPIFLRFVIYCLWKLTG PTSRVGPTLEFLLDHPRRCYIYLFPSHQTWFLLTVVIGLTLLDWIFFLILDIGNAVLDEIPTNIKVLDGFMQAVAVRAAGFSIVPLAAIAPA VKVLYVVMMYISVYPIAMSVRSTNVYEANSLGIFPELEDEEENEENFNNQGPRVQVWGRYLMMHIRQQLSFDMWWIVLAIFLICIVES GNLQDPAKSEWFTIFNLLFELVSAYGIVGLSLGIPDGNYSFSGALRPLSKLIICVVMIRGRHRGLPVAIDRAVLFPKEFRREQLGADNFE DGVSLSGLTASMDQDQDAASTGYSRSRLSRHRTLSQTISVQRSPTQVSIQLPSKDLTHSPQVHWDNPSPRVARQSSRQSRQADAIS EITPSSSNSTEARIGRQGRPARRSTVDSAKSTPY
5.7E-97	335	6.1	6.2E-95	328	0.3	2.1	2	F9GAT3_FUSOF	Uncharacterized protein	FOXB_15765	Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	898	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	660025	>tr|F9GAT3|F9GAT3_FUSOF Uncharacterized protein OS=Fusarium oxysporum (strain Fo5176) GN=FOXB_15765 PE=4 SV=1MSRWDDFVDDHSWVSRILSVRKYLPPLNFITIHYAYFIVVCLISSVIFWQSSDPASPISYTDSLFLVVSAMTEAGLNTVNLSALTT WQQTMLFLLIMLGSTVWVSMWTVLARKHVFKKRFDDIVRAERVRRLSQRGSSMSLTLPKLRKAISFRKAQTVPVPDQNLPAIGNRAL KSKLDPEVDRLQVAKAMPKSRRALSLPDLDLMEPPRASAGPEPEPRSPDTPDRHIVFVDTLHRAEGSNATSTGTSYFNERRPTRRNG AAKTPADQDRVELSIRHFLGSRSSSRNGQFHSLTSEERENLGGCEYRALKALGVLVPLYYFLWQFLGCVALGAWMNNNMPDTAKAN GINPWWLGVFNGVSAFNNSGMSLLDANMIPFQNAYFVLITMGLMILAGNTAYPLFLRLIVWIGLKLLKAVTKCDANDDLKATFEFILKYP RRVYTNLFPSRPTWWLFFMLIWLNSIDWVAFEIMNIGNSVIESIPTGSRILDGLFQALAVRSGGFYVVPISQVVIGLQVLYVIMMYISVY PVVITMRHSNVYEERSLGIYSGDGFSTSDADLEAAAPLFSADGHDSESHIHASTTNGALSTAPTLVRRLSRSSAAVDIGHALQRTFTW NGVGAPPAMRGNKSYNGPTPNRPGGSSSKRNSRIGFISQQIHRQLAHDIWWLVLAVLVITTIETSYFMADPVAFSVFNIIFEVVSAYGT VGISVGIPRDAYSFSGAWHTDSKLVLCLVMLRGRHRGLPVALDHAVEWTPSRLLSQSRSLVLNESLVELKNRREGRLVLELREEDAV EPEVDSISHGSGLARKTVRRIEIFRLLLFWLCLATASPSCDEFALMPLAIRLWDWRAVEDGDTRGPTSPAIWTKIRPWVAIADKIVAGEI SISIESGSKKEVPLYEEN
7.9E-97	334	1.5	1E-96	333.9	1.1	1	1	A5E1G9_LODEL	Putative uncharacterized protein	LELG_03456	Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) (Yeast) (Saccharomyces elongisporus)	367	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Lodderomyces, Lodderomyces elongisporus, Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) (Yeast) (Saccharomyces elongisporus)	379508	>tr|A5E1G9|A5E1G9_LODEL Putative uncharacterized protein OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) GN=LELG_03456 PE=4 SV=1MFIWKYRGSLVFLRFIIWVLFNTARPLSLYKESLGFLLDHPRRCFTLLFPLLPTWWLFFILVVLNGFDLVIFCILDLRNAIFDGIPMG YRVLNGLFQAFCTRTSGLSIMDLSQLHAATLVSYMIMMYISVLPIAISVRRTNVYEEQSLGVYAPDEGTKEADEKVPANYVGAHLRNQL SYDLWYVFLGLFIICIAEGHRIQKQDIRFLVFPILFEIVSAYGTVGMSLGYPDSSTSLSGQFNVISKLVIIAMMIRGRHRGLPYAIDRAIMLP DADMRRHDRMQENHALKRHQTMERTGTLGRVATMTGNPMDGGNNLLTRVLTNVNDFIDARRRNSAAQSNFDEPSDSSEENSIHAV DPHYHVTTVDHV
8.9E-97	334	18.4	6.2E-68	238.9	1.4	3.1	3	K5W2Z2_AGABU	Uncharacterized protein	AGABI1DRAFT_127169	Agaricus bisporus var. burnettii (strain JB137-S8 / ATCC MYA-4627 / FGSC 10392) (White button mushroom)	877	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Agaricaceae, Agaricus, Agaricus bisporus (White button mushroom), Agaricus bisporus var. burnettii, Agaricus bisporus var. burnettii (strain JB137-S8 / ATCC MYA-4627 / FGSC 10392) (White button mushroom)	597362	>tr|K5W2Z2|K5W2Z2_AGABU Uncharacterized protein OS=Agaricus bisporus var. burnettii (strain JB137-S8 / ATCC MYA-4627 / FGSC 10392) GN=AGABI1DRAFT_127169 PE=4 SV=1MADLSVRWFPNAWTKVKHELNFFRIHVIYITVTPIVLAAILYAANGRYHITYVDALYNSYSAMTNCGLATVNLSSMTAFQQVLLLV QMNIGNIVFVSWFVVYFRRQYFRKQLQHILKAEVVRRSKSSSREDVERQRSRRMSSRLSSVPEESDGRRTERRDASRRRKKKIRPE MIRRLDGTPQLVNPSGWISEKVAGKSAPIQGPADRGVVDSDEQEKELSSSKSELSESNDGQQRQMVDVGVSGMYYRNYLKEWRHF DASFSAPFDIVVESRHYGTQSLPRQQTIEFAPVQHPNQGEIQLEPAADMRSLRGSVTRNDLQVSPGADETPSRNRGFGGFPMPFAIL NSIISKLFPRFQRHLSRAVTMPATTSFVSTQTAQPMPPHAKAVPYISFNAIVGRNSEFRNLTNEQLEELGGIEYRALNVLLWLIGLYFFG LQVLGFVIVVPYMYQQRWGSTFEAPPLTRHVTPGWFSAYQISSSFTNTGSSLVDQSLLPYQRAYLLLIIQWMLILLGNTGFPVLFVLYH FDFTHTYSHILPFQRLRFIIWSMTKWIPRESRLNETLHFLLDHPRRCYIYLFQSHQTWFLFAIIVIFTGLQWFFFMLLDIGQRGVEDIPLN VRFSAGLFQAVAVRAAGFVIIQINTLAPAVQVLYLIMMYITVIPIALSVRSSNVYEEQALGVYKPEDDPEVLFETAGGSRMRIWGRYFAM HARRQLAFDLWWLAIALFLICIIERRNLNNPDNTGWFNIFTLIFETVSAYGPVGLSFGVPYDNFSLSGAFATLSKLIICITMIRGRHRNLPS ALDRSILLPTEFKRTETHESDHASQASQGTSTSRIASRHSRDGTMHDNSGDPNTILHRRATRHTSMPSILGPEPTDPMHRT

1.3E-96	334	3.2	3.4E-94	325.5	0	2.1	2	F7VM75_SORMK	WGS project CABT00000000 data, contig 2.1	SMAC_07388	Sordaria macrospora (strain ATCC MYA-333 / DSM 997 / K(L3346) / K-hell)	729	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Sordaria, Sordaria macrospora, Sordaria macrospora (strain ATCC MYA-333 / DSM 997 / K(L3346) / K-hell)	771870	>tr|F7VM75|F7VM75_SORMK WGS project CABT00000000 data, contig 2.1 OS=Sordaria macrospora (strain ATCC MYA-333 / DSM 997 / K(L3346) / K-hell) GN=SMAC_07388 PE=4 SV=1MAHSAGNESASSRLRAMLPPVNFISIHYAYFIVVCMFASLIFWASSNPAHSISYPDSLFLVVSAATETGLNTVNLSEMTTWQQILL FLLIIFGSAIWVSIWTVLARKHVFETRFKDVVRADRLRRANRPSLGSLSRLRFMPSQGRRSLNVIPSPAINDTPDVVGKSTSSPVNLDD PILNVHEHHTQCTGTTGFSDKNESQCSPTLAHIAFAESPHSSPEKHPPTGISTAAQYGYLGSLNNATRRIGSHRHEPMEPERNEKGEF SVRSLFARAAGRNAQFHDLSREERRVLGGCEYRALRVLAVVIPLYFFLWQLIGCIALGAWINHHRPEPPLRNGINPWWLGIFNGASAF NNSGMSLLDLNMIPFQDSYYVLVTMGLLILAGNTAFPIFLRLILWGLLQVLAVATGETEFHELKETLQFILDYPRRVYTNLFPQRQTWW LVFMLILLNSVDWVAFELLNIGNPAVESLSKGSRVIDGLFQAVAVRSGGFYVIAIPSLYIGVQVLYTIMMYISCFPVVITLRHTNVYEERSL GIYSGDPVQPSDIESGSHGPSGVTGLARQLSHSGTSAIGRVFHHTFTWHGVGVRTPSTNPAANSRISFIGQQIQGQLAHDMWWLGVA VLVIVTIETSNFLADPVTFSVFNVIFEVVSAYGCVGISVGLPNANYSFSGGWHTASKVVLCAVMLRGRHRNLPVALDRAVRLPGDEMH DEEEEDHRLRRSVTIRGVGFNEG
2.4E-96	333	2.1	3E-67	236.6	0	2.3	2	A0A0D2XE06_FUSO4	Uncharacterized protein	FOXG_02137	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	861	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0D2XE06|A0A0D2XE06_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_02137 PE=4 SV=1MLDETRASVWARLKAVKPPFMSKKPHFNFISVHYTWIIGATLLASVIIYGAGRGQTSYVDSLMFASGANTQAGLNPIDVNLLNTF QQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRPRNEREAEEGVNGRHITVVPYQGRPPRITNDGILLD GNDVIQSQAIADDDDDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKPDQGFGDGREANEGQSRSQNAPTGIKFAETVKRSDGVD DDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNNTIAMTRTVESRPDHATLDSRAPTGRRP TIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMGRAFRTRTIDTIKSALSNDHTKDMPYLSYTPTMGRN SNFVGLTLEQREELGGIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAISRTWWGFWTANSAFNDLGLTLTPDNVC SSSAPLVYYHANLRQLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAIPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYH NKKDEDEEESASALNYVGTHLRRQLSFDLWYVFVGFFLLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVPNVNASLCSQFTVV GKLIIVAMQIRGRHRGLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMGTTSGMEPPISPGLPGRRGSMGRIRERANSRIISQF LYPGPVIPSNEIHGHKRATSNNSNNLRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAETNPMP
2.4E-96	333	10	5.9E-95	328	1	2.1	2	C7ZND9_NECH7	Putative uncharacterized protein	NECHADRAFT_94790	Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	675	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium solani species complex, Nectria haematococca, Fusarium solani subsp. pisi (Nectria haematococca), Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) (Fusarium solani subsp. pisi)	660122	>tr|C7ZND9|C7ZND9_NECH7 Putative uncharacterized protein OS=Nectria haematococca (strain 77-13-4 / ATCC MYA-4622 / FGSC 9596 / MPVI) GN=NECHADRAFT_94790 PE=4 SV=1MRKYLPPLNFITIHYAYFIIVCLISSVIFWRSSDVASPVSYTDSLFLVVSAMTEAGLNTVNLSALTTWQQTILFLLIMLGSTIWVSM WTVLARKHVFEKRFDDIVRIEYARKLSQRGSGISLTLPKLRKAISFRKAQTVAKAMPRPRRALSLPDLDPAEPPGPDNTDRHIFFVDTP HRAEDSSATSTGTSYFSQNRPTRRNGVPKTPADQDRVELSIRHFLGSRSSSRNGQFHSLTSEERENLGGCEYRALKALAVLVPLYFF LWQFLGCVALGAWINNYMPDTAKANGINPWWLGIFNGVSAFNNSGMSLLDANMIPFQNAYFVLITMGLMILAGNTAYPLFLRLIVWT GLKLLKAVTSDDAYDDLKATLEFILKYPRRVYTNLFPSRPTWWLFFMLTCLNSIDWVAFEIMNIGNPVIESIPTGSRILDGLFQALAVRS GGFYVVPISQIYIGLQVLYVSMMYISVYPVVITMRHSNIYEERSLGIYSGDGSSMPDADPEAAAPLHTFNTNDIQPMGPNLRTFTWNGV GAPPAISSSRRNSRLGFISQQIHGQMAHDIWWLVLAVLVITTIETSHFMADPVAFSVFNIIFEVVSAYGTVGISVGIPRDAYSFSGAWHT GSKLVLCLVMLRGRHRGLPVALDHAVRLPGEHLHRDEEEDHQIRRTMMGPRMNLNP
5.7E-96	331	2.5	1.3E-94	326.9	0.2	2	2	E9EXG7_METRA	High-affinity potassium transporter	MAA_04716	Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	668	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium robertsii, Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	655844	>tr|E9EXG7|E9EXG7_METRA High-affinity potassium transporter OS=Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) GN=MAA_04716 PE=4 SV=2MRWPSLNFITLHYAYIFVMGLLSIPFLYLYGNISAIDAYFMGSSASTESGLNVANLNELKLYQQLYLYFATVFTQMGFVNILVVVV RLYWFNKHLNSFGPALLHARRRGGTDSQEDSRLEYGEPKASPPDTSGVAETRASGKVCEKDGVQLAADNNGAIRGPCQDLESEAR VSYSSFVEEAIDASAPHISFDSSADKLRHPRSDSVLYVPGPRDRDLEITRYGEDDNGQYRLQTLGPLRESRSIDRAAALASSLFVIGSE PPPSSISRELTRRRRASDDMPYLSTGASIGRNSRFYNLTRQDRNELGGIEYRSLKLLLKVVVAYYFGVHLIGAIGLVGWILHADSKYAA HLDEFAQDKIWWAFYTSQTAICNLGFTLTPDSMVFFQDSPWVMFWLSLLTFAGNTLYPVFLRSILWTMSKITPRGSSIQEPLQFLLTH PRRCYALLFPGGTTWALFGIIIGLNFLGTLILLVLDLHNPEFTHLTPAQRVAAAFFQSAAARHTGAASFTLSNLSPGAQFTLLVMMYISA FPIAMSIRSSNIYEEKSLGYYAQDPTYNEDRGASYLFQHMQKQLGFDLWYIFLGLFCLSVSEATKLADPNQPFTEADLFPSGGVGLTL GYPDITSALSTKFTTFGKVVMCAMMLRGRHRGMPYGLDRAIMLPDERLVERSA
9.6E-96	331	3.2	1.2E-92	320.4	0.1	2.1	2	A0A0C4E588_MAGP6	Uncharacterized protein	MAPG_07654	Magnaporthiopsis poae (strain ATCC 64411 / 73-15) (Kentucky bluegrass fungus) (Magnaporthe poae)	679	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Magnaporthiopsis, Magnaporthiopsis poae (Kentucky bluegrass fungus) (Magnaporthe poae), Magnaporthiopsis poae (strain ATCC 64411 / 73-15) (Kentucky bluegrass fungus) (Magnaporthe poae)	644358	>tr|A0A0C4E588|A0A0C4E588_MAGP6 Uncharacterized protein OS=Magnaporthiopsis poae (strain ATCC 64411 / 73-15) GN=MAPG_07654 PE=4 SV=1MRHGDGRADNAAIPTHVRGRLRGLLPPLTFITCHYAYFVGVCLASSVIFWGSSSGGGFRVGYVDSLFLVVSAMTGTGLNTVNL SQLNTWQQMMLFLLIMFGGPIWVSIWTVLARKRAFERRFHDIVVAAAGERARGGPHCCATTTPAAAADCLLSRVASRSRPRSIRPTV ENSRAGDAGVSSSPRRPRSTHGGNKTPADAAVRLVETGGLSFLDRTPAGRNGQFYSLSSEEREQLGGTEYRALKVLAAVVPLYFAL WQLIGCLALGAWMTLNRPGVALANGIDPWWLGIFNGVSAFNNSGMSLLDANMIPFEQATFVLLTMALMILAGNTAYPIFLRLIFWAWL ELLKRTTREDALADFKATLEFILRYPRRVYTNLFPSRPTWWLLFMVVLLNSIDWVAFEVLNLGNPVIESIPKGARVLDGLFQAVAVRSG GFYVVPIAKVYIGLQILYVIMMYVSAYPVVITMRHSNVYEERSLGVYAGEQEPSRLDPEAGNTHAVSQGSAVDTNESKRRPVVELGQA LQRAFSPWHGVGVVAPSTSAPTRMSFISQQIHGQLAHDIWWLVLAVLVITTIETAHFLRDPVAWSVFNVIFEVVSAYGCVGISVGVPY DNFSFCGGWHPSAKLVLCLVMLRGRHRGLPVALDGAVRLPGEQLHRDEEEDHQIRRTVSMTTGRRLSIGV
1E-95	331	1.3	9.6E-93	320.7	0	2	2	J3PC97_GAGT3	Uncharacterized protein	GGTG_11120 GGTG_11120	Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	792	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Gaeumannomyces, Gaeumannomyces graminis, Gaeumannomyces graminis var. tritici, Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	644352	>tr|J3PC97|J3PC97_GAGT3 Uncharacterized protein OS=Gaeumannomyces graminis var. tritici (strain R3-111a-1) GN=GGTG_11120 PE=4 SV=1MRIRHGFTSHDGAVSKILGRAKRLLPPLTFITCHYAYFVGVCLIASVVFWGSSSENFRVSYVDSLYLVISAMTEAGLNTVNLSQLN TWQQVILFVLIILGSSIWVSIWTVLARKHAFERRFDDIVKVARAKRALGAVSPGLVLRRIMSIPRSARSNVPTPGLGDPLQLPTHSSKRP NGLGITSNEGPGPLSPPISREPIPKRASRDSVSAIAPPAETVATPTPAAEKNPDDAVTPLPAPGSPAPGPSDTASPRNPESGRIVFADG VRDAPLRRRPVPKMATGPPQSETGSAQPKTLREFLDNTPALRNGQFHDLSSDERDQLGGCEYRALKVLAMIVPVYFVMWQLLGCLA LGAWINNNMPDTATANGIRPWWLGVFNGVSAFNNSGMSLLDANMIPFQQAYFVLITMGLMILAGNTAYPLFLRLIIWSVLWLLRRATN ENECAELKATLEFILKYPRRVYTNLFPSGPTWWLLFMVILLNSVDWVAFELLNFGNPVIESIPVGPRVLDGLFQALAVRSGGFYVVPPA KLYIGLQVLYVIMMYISVYPVVITMRHSNVYEERSLGIYAGDEAALADPEAGPAWPGFSEPLVQGATPSVARGKSRPGLDVGHALRRT FTPWHGVGAWPGAWPAGERAQGTAAATPGSATTTTAAWPSRISFISQQIHGQLAHDIWWLVLAVLVIATIETSHFLGDPVSWSVFNI IFEVVSAYGCVGISVGVPFDSFSFSGGWQPGSKLVLCLVMLRGRHRGLPVALDRAVRLPGEQLHAEEDEDHRIRRSMSFSVSRRAS VDI

1.3E-95	330	3.5	1.6E-93	323.3	0.9	2.7	2	D4AKR6_ARTBC	Uncharacterized protein	ARB_04909	Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) (Trichophyton mentagrophytes)	630	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Arthroderma, Arthroderma benhamiae (Trichophyton mentagrophytes), Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) (Trichophyton mentagrophytes)	663331	>tr|D4AKR6|D4AKR6_ARTBC Uncharacterized protein OS=Arthroderma benhamiae (strain ATCC MYA-4681 / CBS 112371) GN=ARB_04909 PE=4 SV=1MVMIYPLKNMTAIDALFQGVGAATMTGLNSVDFKELTIYQQVVLYISPILGNICFINFIVVLVRLYWFESKFKEIATEIAAISSEPAEA GEPEGLKHRNAHPPDEKVQEDPKPATVEKQLPTTGPGHVSFSTDTFRPREKALRIPGPRQFEAGHRAHEVDEETDGDELTKATSVD PSIVGASSVRERGKLGRILSHATSVEQAASSAFVLGSASRPRSRSRSVSRSLRPLSRTGSRGSQAPYLSYTPTIGRNSQFLNLTEEQR IELGGIEYRSLKLLARIVGCYYFGFLLLGSICLVIWIYAADPSHRQYLAKNGIHPVWCMTTYNNLGFALTPDSMVNFRSSTFPMLLMTFLI LVGNTAYPCMLRFIIWCMFHISPKASAIREPLNFLLDHPRRCYTLLFPSRATWTLFGTLVLINGVDIMLFMILDLKNPEVTAIDTTWHRLC AASFQSTAARTAGATAFSLSKIHPAVQFSLMGELLLCPCYLGMCAANIFGSDDVYFCLSGSYQTNTYEESSLGLYESDKEVDENSDSS SYLGQHIKKQLAFDLWYIFLGVFLITIAEGNKIADLTDPFVSGNVGLSLGHPTINAGLSGKFTTVSKLVMCAMMVRGRHRGLPYELDRA NELFEQSQ
2.1E-95	330	20.2	2.7E-95	329.2	14	1.1	1	C9R2F5_AGGAD	Trk system potassium uptake protein	D11S_0581	Aggregatibacter actinomycetemcomitans serotype C (strain D11S-1) (Actinobacillus actinomycetemcomitans)	487	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Aggregatibacter, Aggregatibacter actinomycetemcomitans (Actinobacillus actinomycetemcomitans) (Haemophilus actinomycetemcomitans), Aggregatibacter actinomycetemcomitans serotype C (strain D11S-1) (Actinobacillus actinomycetemcomitans)	668336	>tr|C9R2F5|C9R2F5_AGGAD Trk system potassium uptake protein OS=Aggregatibacter actinomycetemcomitans serotype C (strain D11S-1) GN=D11S_0581 PE=3 SV=1MHFLSILRIVGILVMCFSCTMLLPAFVALLYGDGGGKAFIQSFVMSAIAGVILWWACHHHKEELRSREGFLIVVAFWVVMGSLGA IPFMLFEDPYLTVSSAFFESFSGLTTTGATTIVGLDNLPKAILFYRQLLQWLGGMGIIVLAVAIIPLFGIGGMSLYRAEISGPLKENKMRP RITETAKTLWIIYASLTLLCAFSYWLAGMSPFDAISHSFSTVSIGGFSTHDRSMAYFASSTVNIITVVFLLISACNYVLHFNAFSQLGKRNI FLSYFRDPEFRFFMLIQFSLVLICFAMLLANHHFDETFQNLEQALFQSVSISTTAGYTTSSFEQWPLFLPILLLFASCIGGCAGSTGGGL KVVRVLVLYLQAKRELKRLIHPNLVYPIKLGKRVLDERVIQSIWAFFSAYLLVFVICLLGVISCGVETFDAFNAVIACLNNVGPALGTVSS NFVGIPDSAKWILTLAMVCGRLEIFSLLVLFTPAFWKS
3.8E-95	329	0.7	7E-91	314.6	0	2.1	2	B2AMV2_PODAN	PaTRK-2 Potassium transporter encoded by the Patrk-2 protein (Podospora anserina S mat+ genomic DNA chromosome 5, supercontig 5)	PODANS_5_5260	Podospora anserina (strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) (Pleurage anserina)	730	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora, Podospora anserina (Pleurage anserina), Podospora anserina (strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) (Pleurage anserina)	515849	>tr|B2AMV2|B2AMV2_PODAN PaTRK-2 Potassium transporter encoded by the Patrk-2 protein OS=Podospora anserina (strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) GN=PODANS_5_5260 PE=4 SV=1MSRRRRELAQNHPRAVVLISRCRSWLPPLNFITIHYAYFISVCLVSSLVFWGSSSPAWSISYTDSLFLVVSAMTEAGLNTVNLSQ LTTWQQSLLFFLIIFGSSIWVSIWTVMTRKHAFEQRFRDVIQSERRRRTSHGGSALSLGRLPNFRSSRRSLSSHTAQHQPAAYRLSSI DNQHVSLPQTNRPEADATTNFGRACINVEASENTNPTHIAFVDTHLPNMQVHDGIKATSTAAQHVPLDNQPVYRSVLAHGRPEEGTK CHSGMRSFLTHRSSNRNAQFYDLTNEEREQLGGCEYRALKVLALLVPVYFVLWQSLGCIALGAWINNNQAEPPLRNGINPWWLGIF NGASAFNNSGMSLLDANMIPFQNSYFVLVTMGLMILAGNTAYPVFLRLIVWSLLRLLSLVTREEEYNPLKDTLKFILQYPRRIYTNLFPA RATWWLLFMLVLLNSIDWVAFEVLNIGNPPIESIPPGSRVLDGLFQAIAVRSGGFYVVPIPSVYIGLQVLYVIMMYISAYPVVVTMRHSN VYEERSLGIYVEDDALDSDPEQSPLTHHGPPPSRVSPQGGLSALHRAFSWTVTWHGVGARPPSSLRRPESRISFISQQIHGQLAHDL WWLSLAILVIVTINTSNFMADPINFSVFNVIFEVVSAYGCVGISVGVPHDSYSFCGGWHPVSKLLLCVVMLRGRHRGLPVALDRAVRL PGEELEQEEEEDHQIRMSMGGNRRVSSEA
4.8E-95	328	2	5.5E-90	311.6	0.5	2.1	2	B2WL29_PYRTR	Potassium transport protein 1	PTRG_10689	Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis)	734	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Pyrenophora, Pyrenophora tritici-repentis, Pyrenophora tritici-repentis (strain Pt-1C-BFP) (Wheat tan spot fungus) (Drechslera tritici-repentis)	426418	>tr|B2WL29|B2WL29_PYRTR Potassium transport protein 1 OS=Pyrenophora tritici-repentis (strain Pt-1C-BFP) GN=PTRG_10689 PE=4 SV=1MRSSSPWLRLGDPNDNDNYSGSENENNDNSEEDMPDAIDELRNPRQAKDDFYQYLKEEVFKLNFYRAHMLYFVVVIGISSVIV YGQGLANGPEEVGGAHLTFTNALFLCCSAMTTTGLNPVNLGDLSGFQQATFAVLMIIGNIPFVSTAVVLIRRALFRRKMADVVKHSHT MRRLVQDVEENGQTNHEHDGSGAANLRQRTNAEGNKQTTGKQARSNKSSEVAIKPVPQRRTYHYETGFGFIPTPWETKLARGFFG GIINRLVGELKPEHHDYVSFKPHLDSKGRFRDLSEEERMELGGVEYRALQALLLILVGYQIFWYLVGFTFFLPYAYRGNIKGVLYELQP GGINPEWWGVFATITEFANGGLNVLNANFVPFSGYPYILLVAGVLAFAGQTQFPILLRITIWAMQKMAPKGSRFKNTMGFLLQHPRRC FIYLFGSRETLYLFATQTVIDITAWLCFEILNIGMPDIEALPTGTRILDGLFQATGLRTSGAYAVTISSLAPACLVAYLVIMYISIYPMTLTLR KTNTYEEQSIGLDQHSRNAAGISSHLQRQLAYDIWFQFLVFFLICTIERGRILRADPGFTIFSILFEVTSAYGTVGLSMGVPGKDYSLCG DFAGLSKVVLLFAMVRGRHRGLPLAIDRSILLPGEELMRRMDWEFSAKGVEDPGEERELRGDIEGSGVKKGWGKGEQDPEDERGT KSGSNSGQQDEGVVAELSSHESYHFQAKFEGI
6.7E-95	328	8.8	1.9E-89	309.9	0.4	2	2	B8MZ2_ASPFN	Potassium transporter, putative	AFLA_083170	Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	676	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus flavus, Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	332952	>tr|B8MZ28|B8MZ28_ASPFN Potassium transporter, putative OS=Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167) GN=AFLA_083170 PE=4 SV=1MAVVPPFNFITLHYAYFIVTSLVCSVIFWGASNPLRSVSYADALFMCVSAITGAGLNTVDLSSLNTFQQAILFALLMLGHAILISITV LFVRKRAFESKFKGISNRLAQYRESRPTSDLNVPLDEADFKVVNVQPSNMNAGHGDKAPGMTEVSPVENSTDLTSDDHIHWAEDDQI TIGARRRSHHQSHRVFPMVGVGARPDLNNHPKDAIPNLPLREESDILRLKGIIQGTQKYFASRGFISRNSQFYGLTPDERERLGGVEY KAVSFLAVIVAVYWLMFLIIGMIGVGGWLEANHPDISRENGLSPFWTGAFFAVSAFVNSGMSLLDANMTALQKNVYPLLTMGLLILAG NTLYPCFLRFIIWSMRCMIPDQPAWKTWEVTLDFILDHPRRVYTNLFPRRHTWYLLGTIIVLNAIDWAGFEILAIGNQEIEQLPPGYRVL DGLFQALAVRSGGFYVVTISGLRQGLLVLYVLMMYVSAFPVLVTMRNTNVYEERSLGIYAHDDPESESEGQAKPGLFMSLVRHHLLG RQDVPSAEVSRSYFVHQQLRSQLSHDIWWIALAVLFISIAESPNFNRDPVSYSTFNIIFEVVSAYGCVGVSVGIPGRNSSFCSGWHTIS KLILAAVALRGRHRGLPVAIDQAVMLPNDSLAWAEEEDAALRREKTRAWGVDKMPVGAV

2E-94	326	4.4	1.1E-91	317.2	0.1	2.1	2	G4UVR4_NEUT9	TrkH-domain-containing protein	NEUTE2DRAFT_115623	Neurospora tetrasperma (strain FGSC 2509 / P0656)	723	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora, Neurospora tetrasperma, Neurospora tetrasperma (strain FGSC 2509 / P0656)	510952	>tr|G4UVR4|G4UVR4_NEUT9 TrkH domain containing protein OS=Neurospora tetrasperma (strain FGSC 2509 / P0656) GN=NEUTE2DRAFT_115623 PE=4 SV=1MESTHSRLRTMLPPINFISIHYAYFIIVCLFASLIFWGSSNPAHSISYADSLFLVVSAMTETGLNTVNLSEMTTWQQILLFLLIIFGSAIWVSIWTVLARKHAFEKRFEDVVRAERLRRANRSSSVNLSRLRFMRFQGRRSLNVIPPPAMTETLDLVSISTPSPGKSNNPILDVHAHHTHYTGTAKLSDNNTPQRSSTLAHIAFAETPHSSPENHPPTGISTAAQHGYLVSQNNTARRIAPQRQEHMETEGDAKGDFSVRSLFARAAGRNAQFHGLSREERRVLGGCEYRALRVLAVIVPLYFFLWQFIGCMALGAWINRHRPEPPLRNGVNPWWLGIFNGASAFNNSGMSLLDLNMIPFQDSYYVLVTMGLLILAGNTAYPIFLRLILWGILQILDVATMETELCELKETLQFILDYPRRVYTNLFPQRQTWWLVFMVILVNSVDWVAFELLNMGNPAVESLSKGSRVVDGLFQAVAVRSGGFYVIAIPSLYIGVQVLYTIMMYISCFPVVITLRHTNVYEERSLGIYSGDPISPDIESGLHGRSGVTSLTRHISHSGTSAIGQVFRHTLTWHGVGVRTPLTNSAADSRISFISQQIQGQLAHDMWWLAAAVLVIVTIETSNFLADPVTFSVFNVIFEVVSAYGCVGISVGLPSANYSFAGGWHTASKIVLCAVMLRGRHRNLPVALDRAVRLPGDDLHEEEEEDHRLRRSVTIRGVESGEG
2E-94	326	0.7	2.2E-94	326.1	0.5	1	1	A0A0D2XRT3_FUSO4	Uncharacterized protein	FOXG_06685 FOXG_06577 FOXG_07249	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	326	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0D2XRT3|A0A0D2XRT3_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_06685 PE=4 SV=1MANNLGFTLTPDSMAHFRDATFPMIIMTFLAYAGYNFYPIFLRLIIWTFYKLVPKNSALRGPLAFLLEHPRRCCMLLFPSRPTWILLGILLFINFFDVLLLIVLDLDNPSVTELPLARRILAAIFQAASSRHTGTSTFDLSKLNPAAQFSLLVMMYISVYPIALTIRASNTYEERSLGTYAPEQVNPDESTGRKYLVSHMRNQLSFDLWYIFLGIFLICIAESEKIMDTSQPEFSVFPVFFEVTSAYCNVGLSLGHPAVQTSFSGTFSVYGKLVICAMMIRGRHRGLPYEIDRAIELPSERLVDDEDERGPSRRPLLLSDAGSQAG
2.1E-94	326	0.7	9E-93	320.8	0.3	2	2	G1XRE1_ARTOA	Uncharacterized protein	AOL_s00193g140	Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) (Nematode-trapping fungus) (Didymozoophaga oligospora)	524	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, Orbiliomycetes, Orbiliales, Orbiliaceae, Orbilia, mitosporic Orbilia auricolor, Arthrobotrys oligospora (Nematode-trapping fungus) (Didymozoophaga oligospora), Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) (Nematode-trapping fungus) (Didymozoophaga oligospora)	756982	>tr|G1XRE1|G1XRE1_ARTOA Uncharacterized protein OS=Arthrobotrys oligospora (strain ATCC 24927 / CBS 115.81 / DSM 1491) GN=AOL_s00193g140 PE=4 SV=1MTLAGLNTVDLSSLNTFQQFILFLELLLGSSVFVSIVIVHIRRFAFEKRFAQIAADRNRSGGHSKEVAPHGGEIPDTKTVEAVPCTVHNDLDINIHGQPSAIRLHNRSSAGQPDDLHVTQSGPLDHAKAHRSDLDQEQRFHLGGLEYRAIYLLSWIVPAYFILWQLLSCISLGAWIATYKADVTRANGLNPWWVGAFNTVSAFNNSGMSLLDANMVAFQDSYFVIVTMSFLILAGNTCFPIFLRLILWTLFKILPEDGYFHETKRALGFLLRHPRRCFTHLFPPQHTWWLLTAVIFLNGTDWVAFEVLNIGIPEIEKLPLPARIIDGLFQALAIRSGGFYVVPIAATRISLQALYVIMMYIGVYPVVITIRRSNEYLYRSLGIYEGDDEEKADDDTIYELRQEKIKPFLGFFTSQLKAQLSNDLWFLIFGIWVIVVIEAKRIEADPKNFSFFNICFEAVSGYGTVGVSTGFPDVNYSFAGEFKSLSKLVMCLIMLRGRHRGLPISLDKAVQLPSDVNPPPNDEK
2.4E-94	326	7.6	2E-92	319.7	2.7	2.1	2	M2RAM0_CERS8	Uncharacterized protein	CERSUDRAFT_110026	Ceriporiopsis subvermispora (strain B) (White-rot fungus)	793	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Gelatoporia, Ceriporiopsis subvermispora (White-rot fungus) (Gelatoporia subvermispora), Ceriporiopsis subvermispora (strain B) (White-rot fungus)	914234	>tr|M2RAM0|M2RAM0_CERS8 Uncharacterized protein OS=Ceriporiopsis subvermispora (strain B) GN=CERSUDRAFT_110026 PE=4 SV=1MTLSFNWTRIWQRIEEEANFFRIHLLYFLLVPLVAAGIFYGANGEFHIPFIDALFLCYSALTVTGLATVNLSTLTPFQQVILYILQLAGDVTVIAWVMVLIRKHYFHQHVLDVHRKKLTLGKIMRNFSLLGGGSGSPDVPKIEVQGGSIPLPESAPHSQPGTQRIKATEGIGAALAGGGGTGLGLGIALGMTMQPEHDRLSLPDRELQESPTPMSPSSDARPSMDGQDTLGERHSSISSHMSPMSRFDSRTQRAPQFVESDLRRRKPIPRRRTIIAPTMPFVPYDPSVPTNQLPFGQRPKDQGLGGFPGPIDLVKRIAQRMFPHLYKHVERTFANGPSPTARGHTRKWLSETLLGNLVIGRNSEFNTEDLTDEQLEELGGIEYRALRFLSYLVILYFIGVQLITFTLIAPWLNTTHKYDDVFDSQFRLVNKSWFVLFQVAGAYTGGGMSLVDVGMVPFQRAYLMIFAMIFAILAGNHGLPIFLRLLIWLSTKFVKDGSKRDQALHFLLDHPRRCFLYLFPSHVTWFLVVALVIFTAIEWSSFIVLNIGLDVVESLPPGTRAVAGLFQSFAVRASGFAIVSLSSLAPSFQFLCIIMMYIAVYPVALSIRSTNVYEEKSLGVFEIPPEDEDDEPVINEKASRRERIGKYLGWHLRRQVAFDIWWLVCAIFLICIIERGKIMDDVNAPWFNVFRIIFELVSAFGGIGLTLGIPTENFAFSGALGPLSKLVVIIIMLRGRHRGLPVAIDRAILLPEDLVPNKPADARSQNPTSPAVNGPQDDLAEKGRMSTTVEKPT
2.5E-94	326	8.6	8.6E-86	297.8	4.1	2.1	2	G2X4Q9_VERDV	High-affinity potassium transport protein	VDAG_05141	Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	688	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, mitosporic Plectosphaerellaceae, Verticillium, Verticillium dahliae (Verticillium wilt), Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	498257	>tr|G2X4Q9|G2X4Q9_VERDV High-affinity potassium transport protein OS=Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) GN=VDAG_05141 PE=4 SV=1MAGYSDRGLGIQRQHPRTKSLSCCSCRRKLCLVLFSLFRLVAESTAFCCRLVPLCFLIFAGKPCAFSPYVRPLFRVSAPKDNRPRAFLFSPAFGPLLSLKPGMWKPRFNFIRIHCRVDVKDLKTYQQVYLYVVPIITNMMFLNAIVVPVRLFWFRQRLRQAGIAREVARNDEEEARPATRRESQETAVIDEQAPALAPAPSPPFSAPQRTTTITFDDKAIASGYSRSEKQVLRIPNPRESDRGAPITEIEPGLRRSYTEEDPDAIKPLPEFRSGRSRRSSFHAEGTILSAATSIEKAATSAFILGKVQLAPRRQADRETLGGIEYRALKLLLKFVFGYFFGLHFFGAICLLFWIHNAPSKYLDVLAESGVGATWWAFYSAQTMSNNLGFALTPDSMASFKDATWPLLVMTFLAFAGNTCYPVFLRCIIWLTSLMVPKNSQTRETIQFILDHPRRCYTLLFPSRPTWILFGIVVILNFVDVVLIIVLDLDNPAVNDLPVGPRILSSLFQAASARHTGTATLSLVDVNPAVQFSLLTMMYIAVFPIAISVRASNTYEERTIGIWAREENLNEDNGVSYVMVHVRNQLTFDLWYIFLGTFLICIAESTLIMDVAEPTFSIFAVLFEVTSAYKVVICAMMIRGRHRGLPYALDRAITLPSEHTLSDESSSADQIPKSLSLGRTQSSGARSAP
3.2E-94	326	1.4	5.4E-89	308.4	0.5	2.1	2	E3RXG3_PYRTT	Putative uncharacterized protein	PTT_14075	Pyrenophora teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)	720	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Pyrenophora, Pyrenophora teres, Pyrenophora teres f. teres, Pyrenophora teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)	861557	>tr|E3RXG3|E3RXG3_PYRTT Putative uncharacterized protein OS=Pyrenophora teres f. teres (strain 0-1) GN=PTT_14075 PE=4 SV=1MRSSSPWLRLGDSNDNDNYNGSENENNSNELNMPDAIDELRNPRQAKDEFYQYLKEEVFKLNFYRAHMLYFIVVIGASSVIVYGQGLANGPEEICGAHLTFTNALFLCCSAMTTTGLNPVNLGDLSGFQQATFAVLMVIGNIPFVSTAVVLIRRALFRRKMADIVKHSHTMRRLVQDAEENRQTNHEQDGSGAANLRQRVNAERSQQATGKQARSNKTSEVTKKTLSRRRTYHYETGFGFIPTPWETNLARGFFSGIIDRMVGELKPEHHDYVSFKPHLDSKGRFRELSEEDRMELGGVEYRALQALLLILVSYQIFWYLLGFTFFLPYAYRGNIKSVLYESQPGRINPGWWGVFATITEFANGGLNVLNANFVPFSGYPYVLLVAGVLAFAGQTQFPIFLRITIWAMKKLAPKGSRLKNTMDFLLQHPRRCFIYLFGTRETLYLFATQTVIDITAWLCFEILNIGIPEIEALPTGTRILDGLFQATGLRTSGAYAVTISSLAPACLVAYLVIMYISIYPMTLTLRKTNTYEEQSIGLDQHSRSAAGISPHLQRQLTYDIWFQFLVFFLICTIERGRILRADPGFSIFSILFEVTSAYGTVGLSMGVPGKDYSLCGDFAGLSKVVLLFAMVRGRHRGLPLAIDRSILLPGEELMRRMDWEFSAKGVEDATEERELRGDIEGSGVKKGNGKGEQDPEDERGGNSGSKGGRQEGGAVAELSS

1.2E-93	324	6.3	1.6E-91	316.7	1.1	2.1	2	S7RZ88_GLOTA	TrkH-domain-containing protein	GLOTRDRAFT_135024	Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) (Brown rot fungus)	755	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Gloeophyllales, Gloeophyllaceae, Gloeophyllum, Gloeophyllum trabeum (Brown rot fungus), Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) (Brown rot fungus)	670483	>tr|S7RZ88|S7RZ88_GLOTA TrkH domain containing protein OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_135024 PE=4 SV=1MDVSWNYFRLHLVFFTVHPVLWSAVLYAANGRYPVSYLDSFFLCFSAQTVTGLTTVNLSSLTAFQQAILYWLMVSGSYTTTSW VMVMARRYYFVQKCAHVIKKDPSRLNKRFERLRSKTMDVWRSTTNAPGVSEKSPDRGNGVTTAVHSPPASGPVSEQDLTTQVHHE AEPSYTNTLVGVPLERTQSPSSIGSFQPTTVAFAEADGPRRQVLRTATGLTNRSARRPPRLQTHAPTILAPKSPTESTHERGFGGFAG PLTLTGKLAARVAPGVVRALERKLTLPAHGAVLTPASQSTLVGAGDEERKRAESRDWLDDVGALHAKTVSYLKKGALWVGRNSFFD AEHLSDEQLEEIGGVEYRAIKFLSWLVPAYFIGTQLCTFIIYTAYLESVHTYDSVFAALFRPVPKAWFSAFQALSAYTGAGMTLVDQGM VPFVSSYTMIISLGMLIMAGNMLMPVFLRLIVWIIFRMLPEGSSTREPVQFLLDHPRRCYLYLFPSHQTWFLVAVFMFLTAIEWAGFELF DVGLPVVDNIPRGPRVLAGLFQSLGVRASGFSIVSIGSLAPATTLLYIVMMYISAYPIAMSIRSTNVYEERSLGVFQATAEDEAEEPKGEI FSKYLGWHVRRQLAYDLWWLAAAVLLICIVERGNIMNPENDTWFNQFSILFEIVSAYATVGLSMGIPTQNYSFSGALKPLSKLVICAVM LRGRHRDLPVAVDRAVLLPQEFSRVSTAGRNHIIPENEDFTVLSPVDEPHHTAA
1.6E-93	323	20.1	5.5E-93	321.5	14	1.7	1	I2B579_SHIBC	Trk system potassium uptake protein	trkH1 EBL_c05580	Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	495	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Shimwellia, Shimwellia blattae (Escherichia blattae), Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	630626	>tr|I2B579|I2B579_SHIBC Trk system potassium uptake protein OS=Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) GN=trkH1 PE=3 SV=1MYPTRYSELRQKISRGRVITHFCSFLVFLYSFSMFPPMLVALLDKDRSFFIFLATFGICFCGGGLAFLATRGNDLELKTRDGFVVI VMFWLLFSLISAMPLAMDDALNLTLASALFEGVSGITTTGATVINDVGALPRAMLYYRAQLNFLGGLGVIVLAVAVLPLLGVGGMKLYQ SEMPGPLKEERLTPRIADTSRSLWLTYSILGLCCMLAYMAAGMTAFNALCHALSTVSLGGFSTHSASIGFYNSNVVEMVAGVFSLLSA VNFTLWFVAFSRRSLRPLLRNAELHFFLSVVLVVVLITAWQVWHVGMYNIPDSLVHAFFLVSSVITDNGLATGDYAQWPSHTIMFLMV MSFFGGCVGSTCGGIKALRFLILFKQSRRELHQLAHPRAQIGLRIGGVIINDRILSSVWSFFFLYVGFSILFVWILNMMGYDLVTSFATV AACINNMGLGFGSTVSSFDVLNDGAKYLMCLAMILGRLEIFPILILFSRFFWRT
1.6E-93	323	8.1	1.1E-91	317.3	2.1	3	3	E4ZJV0_LEPMJ	Similar to potassium transport protein 1	LEMA_P068930.1	Leptosphaeria maculans (strain JN3 / isolate v23.1.3 / race Av1-4-5-6-7-8) (Blackleg fungus) (Phoma lingam)	716	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Leptosphaeriaceae, Leptosphaeria, Leptosphaeria maculans complex, Leptosphaeria maculans (Blackleg fungus) (Phoma lingam), Leptosphaeria maculans 'brassicae' group, Leptosphaeria maculans (strain JN3 / isolate v23.1.3 / race Av1-4-5-6-7-8) (Blackleg fungus) (Phoma lingam)	985895	>tr|E4ZJV0|E4ZJV0_LEPMJ Similar to potassium transport protein 1 OS=Leptosphaeria maculans (strain JN3 / isolate v23.1.3 / race Av1-4-5-6-7-8) GN=LEMA_P068930.1 PE=4 SV=1MQDPMEELRDPRKAKDDFLHYMRHEFFRLNFYRAHMLYFIVVIAISSLIVYGQGRANGPKEVGGEHLTYMNALFLTCSAMTTTG RIKPPRYRKRQIADIHVGLNPVDLGDLSGFQQAVFAILMFIGNIPFVSTFVVLIRRKLFRKKMAHVVKHSRTMRRLVQDIEDNRHTGRGE ADSSGTLRQRASRGPSRWANGTKEERDCSPKMQPLSKRRTYHYQTGFGFIPTPWETKIARNFFRRIFDRLTSELKPERHDYVSFKP RLDSKGRFLDLSEQDRMELGGVEYRALQALLLILIGYQVFWYSLGTVLLVPYAYRSHIQAVLHEAQPGRLNPGWWAFFCTVTEFANG GLNVLNSNFVPFSGYPYILIVAGLLAFAGQTQFPTFLRMLIWTMKKISPQQSRFRNTLEFLLQHPRRCFIYLFPSRETWYLFVIQVVIDIT AWLCFVILNIGMPDIEALSLRRRFLDGSFQATGLRTSGAYIIAFSSLAPACLVVYLVIMYISSYPMVLTLRKTNTYEEQSIGLQKHDSSTV GIASHLQKQLAYDIWFQFLSFFLICVIERGHILRKDPGFDVFSILFEVTSAYGTVGLSTGIPGKDYSLSGSFASLSKVVLLFVMVRGRHR GLPLAIDRSILLPGEELMRRLDQEYSARVVPDAHDMADLATNIALSGKPRTPCGKGEQDPELLRNPSSRTDVHEDRDARERGNVDAT TASMTDTSRP
3.8E-93	322	2.7	1.3E-87	303.8	0	2.1	2	U1GSZ0_ENDPU	Uncharacterized protein	EPUS_08433	Endocarpon pusillum (strain Z07020 / HMAS-L-300199) (Lichen-forming fungus)	817	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Chaetothyriomycetidae, Verrucariales, Verrucariaceae, Endocarpon, Endocarpon pusillum, Endocarpon pusillum (strain Z07020 / HMAS-L-300199) (Lichen-forming fungus)	1263415	>tr|U1GSZ0|U1GSZ0_ENDPU Uncharacterized protein OS=Endocarpon pusillum (strain Z07020 / HMAS-L-300199) GN=EPUS_08433 PE=4 SV=1MSQLTKCIDHRLPAPVRRVWHTFIRPALPDWSFITIHYLYFILMCLVSSLLFRVTSTPSKNVSYVDSLFLVTSAMTEAGLNTVNLS QLNTFQQVLLFFLIVLGSAIWVSIATVHIRKRAFEQKLQELADNKKKRLRLSRSLRTSLSKTGKDTGDRRIAAIASGALRGTALVEGDGR PKDDCNLNADEHITFDLPLQQKADDEHVSLDNLKELSHSAYRGHSSPLSLDANLDSDKHRPATARYDSYDVRSPAAKSSVADNVRILE TQRSPAHGCDIDSTTIPLQRRHTRIFSGYGVGARPSLSSHPRNATLDISPTRSIDDEERAFGRRMQSLTFFDKYLKGFNGLIGRNSQFH GLSEKDRRKLGGLEYDALVLLSYLVPTYFFLFQLAGAIGMGAWMQSNRPDVALKNGLDPFWTGSFFAISAFNNSGMALLDANAVALQ TSYYCLLTLGFLILAGNTCFPPFLRLIIWTGKVCIPRSWNDSKWDKRRQVLQFLLDHPRRCYTHLFPSAQTWWLVGTLVVLNGIDWVA FEVLNIGNPAIESIPTHFRVLDGLFQAFAVRSGGFYVVSISQLRPALLCLYIYMMYLSALPVTLTLRNTNVYEERSLGIFAEEIANTQASP PQPPPRRDSTSERLASTLRRHITGQVSTSADSPTITTATTWSRRDFLQQQLRGQLSHDLWWLALAIFLITIIETSQLSRDPINFSVFNIIF ECVSAYGCVGISVGVPWDNYSFCGAWHTGSKLVLCAVMLRGRHRGLPVAIDRAVLVPDQRLGWAEEEDAVARRKRTRSIGGGDAV TTTTRRRSSGSVSRNALREREG
4.9E-93	322	10.6	1.6E-89	310.1	1.2	2.1	2	A0A0A2L4P8_PENIT	Potassium transport protein, high-affinity	PITC_032220	Penicillium italicum	868	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium italicum	40296	>tr|A0A0A2L4P8|A0A0A2L4P8_PENIT Potassium transport protein, high-affinity OS=Penicillium italicum GN=PITC_032220 PE=4 SV=1MLSHLPAASQSRPYHSGRSKPETEEGIPRPSPSLPTTSDADLPHLTPSKTVHMTQITEKPETKRVATAACTVSFSNPRPWEILR EGQTTHKGDVFSVARIAGIMAAKRTPDIVPLCHPGIGITGVEVSVELVGPAQQRDHGGMHIVASVSCFGRTGVEMEAMTATMGAALT VYDMLKAVDKGMLILRKWWRVTGNAIMAVLPPLNFLTLHYFYFIATCLIASIIFYLTSTPWLNVAYVDSIFLCVSAMTGAGLNTVDLSAL NSFQQAVLFILLILGHAILISLTVLLVRKRAFEAKFKGVSDERERERQSSLNPSDVQLQDREPAHGSTGADLSENTEGHSCKPRAKTSVL VQVKPGEPLSRDEQQWVDDDQKTIGGTPRHHHHRVFPMAGIGARPDLHNHPRDAVPNVPLVAEDSVSGFKGLLRGTQKYMASKGL VSRNSQFHGLTPAERDELGGVEYKAVSFLSVVVFLYFILFIIFGMVGVGGWLEVNDPAVTRTNGLSPFWTGAFFAVSAFVNSGMSLL DANMTALQLNAYPLLTMGLLILAGNTLFPCFLRFIIWTMRIMLPDRPKWQSWRITLDFILEHPRRVYTNLFPARHTWYLLGTIIILNGIDW AAFELLSIGNKDIESLPTEYRVLDGLFQAIAVRAGGFYVVTIADLRQGLLVLYVLMMYVSAYPVTLTMRNTNVYEERSLGIYAHDESPDS PANTSRSNVVMDLIRHHLGRPGLSETSRGYFVHQQLRSQLSHDLWWIALAVLLIAIRESDHYESQPVAFSTFNIIFEVVSAYGCVGVSL GFPGKNYSFCGAWHNVSKLILAAVALRGRHRGLPVAIDKAIMLPSESLAWAEEEDAAMRRDRDRSRAWAQEHGPVGSV
4.9E-93	322	20.2	7E-93	321.2	14	1.1	1	B0URK7_HISS2	Trk system potassium uptake protein	HSM_0442	Histophilus somni (strain 2336) (Haemophilus somnus)	487	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Histophilus, Histophilus somni (Haemophilus somnus), Histophilus somni (strain 2336) (Haemophilus somnus)	228400	>tr|B0URK7|B0URK7_HISS2 Trk system potassium uptake protein OS=Histophilus somni (strain 2336) GN=HSM_0442 PE=3 SV=1MHILSILRIVGILVTCFSITMLIPAFIALIYGDGGGKAFILSFFYNLSAGVGLWWLCRAHKASLRSREGFLIVTMFWVLLSLLAVIPFM LFDELTLSLADAVFESFSALTTTGATVILGLDHLPKSILFYRQLLQWIGGMGLIVLVVAIIPLLGIGSGHLYRAESSGPMKDQKALPRIGEV AKLLWFLYCILTIFCAFAYWVAGMSWFDAISHSFSTVSNGGMSNYDASLGYFDNPAIYLISAGFMLISGCNFALHIRALTNWKYQPVW KIYARDPEFRFFCAIQGIFIFLLSLGLYLTYENYSVFDAFSQGALQSVSMAMTSGYTLFDLNQLPAFLGMLLVFMAILGGCAGSTTGGLK MIRVLVVWLQIKREFKHLVHPHLVIPIKLGKMLLVQRVIDGIWGFLIAFFLTYWVCVFAVILCGMNAADAMLSVFATLTNVGPGLGIISQS FSQVPDNAKYVFSFAMAAGRLEIFSLLLLFTPTFWKS

															>tr|A8Q87|A8Q87_MALGO Uncharacterized protein OS=Malassezia globosa (strain ATCC MYA-4612 / CBS 7966) GN=MGL_3219 PE=4 SV=1
5.7E-93	322	8.2	1.4E-90	313.6	3.6	2.1	2	A8Q87_MALGO	Uncharacterized protein	MGL_3219	Malassezia globosa (strain ATCC MYA-4612 / CBS 7966) (Dandruff-associated fungus)	916	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Ustilaginomycotina, Malasseziomycetes, Malasseziales, Malasseziaceae, Malassezia, Malassezia globosa, Malassezia globosa (strain ATCC MYA-4612 / CBS 7966) (Dandruff-associated fungus)	425265	MRPRSWRKDVRSSWNRCLASVIRFADVYMNYFRVHMLYFVFMTLFWSAIMYASNPKDHYVPYTDCLFLCASAVTVTGLVTVPVSQLTLWQQIILFCLASCGNLVIVSTTTVLVRRHWFAKRFHKELERSFTLRKQVEDVHAREVEERTQEIKRLRRFFHLRTQDSMQDHRRQPFTSRKQPPHKLHAGMVHRVQGPAVQVNPTGQHTTRVDHVEVPESAGATGILSGSTAPESAASALHGRLDAGKLFRSSSLRHSIDDLFRARPLTKSATHGGPDDEQPMKRRRFSFNDMSSRYYKASDVASGARLPRVQTVDPASIHHDTSSLKSLRVRPAMRMPQHAHTWAFGDASEKHLHADMSDDENDDDDDDDTRGPKDLRSLPGHALHRTMTQKRDTGLGGFPNVLDFAVSLVESSHLRQRMHVPTVRTMTTMQPALSGDDSARDTRFAPYLTFDATVTGNSHFRNLTGAQRRELGGVEYRALNLLAWLIPVYWLTIVCITIVFTAPYLASGPGAQYREALQKPKPPHNSTWFWIFQTVSSVTNLGMSLRDDSLTGTMSKAYMVLIPQMILIVVGNTGFPVMLRFVIWCMSRCVSRRSKMYETLMFLLDHPRRCFLYLFPSQNTWLLFAVLLILTLVDWFLLMICDLNLRHGFASNGTWVLASLFQSVSTRSSGFQTFTVSQLSPAEQLLEVLMMYIAAFPLMMTMRSTNVYEDRSLFVEETNEDAKSEKLEPDSQAIWGRFLGTHIRNQLAYDLWWVMLALWVVLLCEKGKIDSAEFSNMSVFGIIYELMSAYGTVGMSYGATSKSASLAGDMSVLSKLVITAVMIRGRHRNLPSAVDRAVMLPHDLHHHDNVQDVKRDDPVDSMNKVPSRTSSVHEQATDTPASTSEAGMPPRLHTHFVDEPIIMNDGPTVESPKSM
															>tr|M4R774|M4R774_BIBTR Trk system potassium uptake protein OS=Bibersteinia trehalosi USDA-ARS-USMARC-192 GN=WQG_3210 PE=3 SV=1
5.8E-93	321	21.2	1.1E-92	320.5	14.7	1.4	1	M4R774_BIBTR	Trk system potassium uptake protein	WQG_3210	Bibersteinia trehalosi USDA-ARS-USMARC-192	495	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Bibersteinia, Bibersteinia trehalosi (Pasteurella trehalosi), Bibersteinia trehalosi USDA-ARS-USMARC-192	1171377	MQFLSILRIVGILVMCFSFTMLVPAFVALIYGDGGGRAFVESFVLTFFIGSVLWWFCRKNRQELRSREGFLIVVLFWVVLGSLGAVPFIILEQPNLNVSESIFESFSGLTTTGATVITQLDSLPKAILFYRQFLQWLGGMGIIVLAVAIIPLLGIGGMQLYRAEMPGPLKEQKMRPRIAETAKALWLIYLSLTILCAGAFWLAGMDVFDAISHSFATVAIGGFSTHDASIGYFNSNLINYITVFFLLVSSCNFALHFAIFDQMREKQSRNSKTKILGLYWKDYEFRFFITIQLALFAICFVVLLAHNYFEGDTATTLSQAMFQSVSISTTAGFTTNDFSSFPSFLPLLLVLASFIGGCAGSTGGGLKMFRVLLLYLQGRREIHRFIHPNVIQPVKLGKHVLSERIVEGVWAFFSAYFFVFVVCWIASIACGMETFDALNAVIASLNNLGPALGTVSSNFTKVPDSAKWVLTFAMVCGRLEVFTLLVILSPTFWRD
															>tr|E9EAQ5|E9EAQ5_METAQ Potassium transporter, putative OS=Metarhizium acridum (strain CQMa 102) GN=MAC_06953 PE=4 SV=1
6.4E-93	321	14.7	7.4E-90	311.2	3	2	2	E9EAQ5_METAQ	Potassium transporter, putative	MAC_06953	Metarhizium acridum (strain CQMa 102)	629	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium acridum, Metarhizium acridum (strain CQMa 102)	655827	MSLRNAQHGTCTLLAAAWRRVVGLGSQHVNFVSLHYAYFIFVSLLSSVVFWLLSEPKFSVAYVDSLFMVVSGVTETGLNTVDLSKLTTAQQVLLCLLMICGSAVWVSIWLISARKRSFCRLLAQNGVSQPQLDRRQSVNVPYPGAYQNAPDSDAHETKATEGDAGQFGRLPVQTTCFNSTTPLGSRNTRLLNLGSEQVLHQPMEPRPNPLAFLTSKNIGRNGDFINLTSEEKIQVSSIEHKVLQLLSLVVPLYFTLWQVLGCVGLGAWIATNQARPALENGINPWWLGIFNGVSAFNNSGMSLLDANMVPFQAAYYVLVTMGLLILAGNTAYPIFLRFILWSVYKVLNVFSQGPLVTEWQSTLEYILRYPRRVYTNLFPTQHTWWLAFMVVMLNGIDWAAFELLNIGNPVISAIPSGPRIMDGLFQAVAVRSGGFYIVPIAKTHIGLQVLYVIMMYISVYPVIITMRNSNVYEERSLGMFAAESTKDEEYVDPYAKALRSFRTRRLFISQQIRGQLADDIWLLALATFIITVMEAPHFAEDPVSYSVFNIIFEIISAYGCVGISVGSPGANYSFCGGWRAGSKLVVCLVMLRGRHRTLPASLDYAVRPAGKDIREEAFEEDTEGRRRPS
															>tr|V5GAX5|V5GAX5_BYSSN Potassium transporter, putative OS=Byssochlamys spectabilis (strain No. 5 / NBRC 109023) GN=PVAR5_7903 PE=4 SV=1
7.1E-93	321	14.4	3.3E-91	315.7	2.1	2	2	V5GAX5_BYSSN	Potassium transporter, putative	PVAR5_7903	Byssochlamys spectabilis (strain No. 5 / NBRC 109023) (Paecilomyces variotii)	707	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Thermoascaceae, Byssochlamys, Byssochlamys spectabilis (Paecilomyces variotii), Byssochlamys spectabilis (strain No. 5 / NBRC 109023) (Paecilomyces variotii)	1356009	MDVLPPFNFLTLHYTYFIAAVLICSVVFWGAATPSGSISYVDALFLCASAMTGAGLNTVNLSTLNTFQQLILFLLIVFGSAILVSSFVLFVRKRAFERKLKGIIKDRQSTSLHQRSRLNIPLSRLHRTTPSLQEASDINPDLENPYPDSKQPVAQSVYISPNEPSTPGPGAPGPGNSGPVHECSQQDEDHIQWIDDDQVTIGGTRRPRRHSHRRVFPMAGVGARPDLNNHPRDILPDPLLYEGRRPSLIETALKGTQKYFLSKGFISRNSQFYGLTPSERERLGGVEYRAVSFLSIIVPLYFVLFHIFGIVGVGSWISMNRPHIARENGLSPFWVGAFFATSAFGNSGMALLDANMTALQTSAYCLVTMGMLILAGNTLYPCFLRFIIWSMRRLLPNRESWQEWRVVLDFILDHPRRVVTNLFPARHTWYLLGTIIFLNGIDWMGFEVLSIGNNEIDKLPSGYRVLDGLFQALAVRSGGFYVVTIADLRQGLLVLYVLMMYVSAFPVLVTMRNTNVYEERSLGIYADDNQLRDPEVQAKTANPLVSLLKHHLLPNHQETAVDLEASRGYFVRQQLRSQLSHDIWWIALAVLFIAIAESANFEKDPVSFSTFNIIFEVVSAYGCVGISVGFPNQNYSFSGSWHPISKLILTAVMIRGRHRGLPVAIDKAVMLPSESLAWAEEEDAALRIERSRTWSVGKMQPSGATAVNFASMNDVAKWILISTMLFGRLEVFTLLVLFTPTFWRE
															>tr|E6WHL0|E6WHL0_PANSA Trk system potassium uptake protein OS=Pantoea sp. (strain At-9b) GN=Pat9b_0197 PE=3 SV=1
8E-93	321	14.5	1.1E-92	320.5	10	1.2	1	E6WHL0_PANSA	Trk system potassium uptake protein	Pat9b_0197	Pantoea sp. (strain At-9b)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. (strain At-9b)	592316	MHFRAITRIVGLLVILFSVTMILPGLVALIYRDGAGRAFSQTFMMAIVIGSLLWWPNRKQKTELKPREGFLIVVLFWTVLGSVGAMPFMFAEQPHLSVTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTVACAVALWLAGMPVFDAIGHSFSTIAIGGFSTHDASIGYFNSPTINTIVAIFLLISGCNYGLHFSLLSGRSLKVYWRDPEFRMFIGVQLTLVVICTVVLWFHDVYSSGLQTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRILLLFKQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFLVSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADNFASMNDVAKWILISTMLFGRLEVFTLLVLFTPTFWRE
															>tr|D8MKX2|D8MKX2_ERWBE Trk system potassium uptake protein OS=Erwinia billingiae (strain Eb661) GN=trkH PE=3 SV=1
9.2E-93	321	13.4	1.5E-92	320.1	9.3	1.3	1	D8MKX2_ERWBE	Trk system potassium uptake protein	trkH EbC_02470	Erwinia billingiae (strain Eb661)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Erwinia, Erwinia billingiae, Erwinia billingiae (strain Eb661)	634500	MHYRAITRIVGLLVILFSGTMIVPGLVALIYRDGAGRAFTQTFFMALLIGSMLWWPNRKQKKELKPKEGFLIVVLFWTVLGSVGAMPFIFAEHPNLSITDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTVVCALALWLAGMPLFDAIGHSFSTIAIGGFSTHDASIGYFNSPTINTIIAIFLLISGCNYGLHFSLLSGRNLRVYWRDPEFRMFIGVQLTLVVICTIVLWFHDVYHSGLQTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRILLLFKQGNRELKRLVHPNAVYTIKLGQRALPERILEAVWGFFSAYALVFLLSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADNFTTMNDTAKWILILTMLFGRLEVFTLLVLFTPTFWRE
															>tr|W7MTB7|W7MTB7_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_12850 PE=4 SV=1
9.8E-93	321	5.3	6.2E-91	314.8	1.1	2	2	W7MTB7_GIBM7	Uncharacterized protein	FVEG_12850	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	619	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	MLLPPINFLTLHYAYIILMGLIAIPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVIVRLFWFKRHLKRLAPQMLDNSTGITDVDIESTHNEPKVLADTTENSAEATDETNGKAKATDDLIEEDPTVANEDRRVARTMTITFDQSTEQHKDDDALYIPGPRARDRGYPIAPRAARHPEDSDDDDVIKPVPNRNQNDGSSSMRRRRRFSSDDGLKVTASRSMDRVAGVAASLLVLGSQTAPQPRPISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQASAQDKTWWGIYSAQTMYDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKTSPTQESLAFLLTYPRRCYTLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVSSLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWEEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSA

1.1E-92	321	6.3	1.3E-87	303.8	1.5	2.1	2	A1CNJ6_ASPCL	Cation transporter, putative	ACLA_019220	Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	691	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus clavatus, Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)	344612	>tr|A1CNJ6|A1CNJ6_ASPCL Cation transporter, putative OS=Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1) GN=ACLA_019220 PE=4 SV=1MIVRLRRTWVQPLGRCITAVLPPFNFLTLHYAYFIATPLICSIIFWGAATPSRSIDYADALFMCVSAMTGAGLNTVDLSSLNTFQQ SILFALLILGHVILISITVLLVRKRAFQLKIKSFSDECVRKGFFRHASKPGASNEGADNTHDLQTREVHETAGTKAFDAESRSEEPAHTTD DDRIRWVDDDQVTVGHPQSRHHHHHHRVFPMAGVGARLDLNNHPRDVARTVPLADADDDMTRPGGSLKGTQKYFSSSGSISRNS QFHGLTPEEREQLGGVEYKAVSVLSVIVALYWGLFLIIGIVGMGGWLEANHPEIPRANGLSPFWTGAFFAVSAFVNSGMSLLDANMT ALQTNVYPLLTMGMLILAGNTLYPCFLRYIIWAMRRLVPNHPSWDTWKITLDFILDHPRRVYTNLFPVRHTWYLLGTIIILNGIDWAGFEI LAIGNREIETLPAGYRILDGLFQAIAVRSGGFYVVTISELRQGLLVLYVLMMYVSAFPVLVTMRNTNVYEERSLGIYASDETLGPSGEKS PSIVMSLIRHHLLGRQDVSTTEASRSYFVHQQLRSQPSHDIWWIALAVLFIAIAESSHYTDDPIAYSTFNIIFEVVSAYGCVGISVGFPGK NYSFCGSWHTISKLILAAVTLRGRHRGLPVAIDQAVMLPNESLAWAEEEDAVLRREQTRAYGSEKMPMGIV
1.1E-92	321	15.7	2.8E-92	319.2	10.9	1.5	1	A7MRG0_CROS8	Trk system potassium uptake protein	ESA_pESA3p05484	Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	458	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cronobacter, Cronobacter sakazakii (Enterobacter sakazakii), Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	290339	>tr|A7MRG0|A7MRG0_CROS8 Trk system potassium uptake protein OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=ESA_pESA3p05484 PE=3 SV=1MLVALFCKDRSYFSFLMTFVIFFVPGCAAWLATRRHIAPLKTRDGFLIIVLFWILFSLISAMPFWLDNALGLNAAQALFEGVSGITT TGATIINDVSGLPKAYLYYRAQLNFIGGLGVIVLAVAVLPLLGIGGMKLYQSEMPGPFKEERLTPRLADTSRTLWFTYVLLGAACAVAY RIAGMPWFDALCHGLSTVSLGGFSTRNESIGFYDSYPVELVAGLFSLLSAVNFTVWFVAFTRRTLKPFRRNAELHFFLLVTLIIVLLTA WQVWHEGMYDLTGSLVHAFFLASSMITDNGLATSDYASWPAHTIVMLLLASFFGGCVGSTCGGIKALRFLILFKQSRNEVHQLAHPR AILSLHVGQSVVNERVLRSVCSFFFLYMLASILFIWALTLMGYDLLSAFGTVAACINNMGLGFGVTAASFDTLSDGAKYLMCLAMILGRL EIYPFLILLSRFFWRA
2E-92	320	5.3	5.7E-91	314.9	1.1	2	2	W7N4Z2_GIBM7	Uncharacterized protein	FVEG_12850	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	601	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	>tr|W7N4Z2|W7N4Z2_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_12850 PE=4 SV=1MGLIAIPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVIVRLFWFKRHLKRLAPQMLDNST GITDVDIESTHNEPKVLADTTENSAEATDETNGKAKATDDLIEEDPTVANEDRRVARTMTITFDQSTEQHKDDDALYIPGPRARDRGYP IAPRAARHPEDSDDDDVIKPVPNRNQNDGSSSMRRRRRFSSDDGLKVTASRSMDRVAGVAASLLVLGSQTAPQPRPISSDSNRQPAI NDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQASAQDKTWWGIYSA QTMYDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKTSPTQESLAFLLTYPRRCYTLLFPSGPTWILF GIIFALNFIDILLIIVLDLSNPEVSSLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNAYEEKSLGLWEE EKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSA
2E-92	320	13.9	9.7E-89	307.5	2.8	2.1	2	U1G6B3_ENDPU	Uncharacterized protein	EPUS_08359	Endocarpon pusillum (strain Z07020 / HMAS-L-300199) (Lichen-forming fungus)	701	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Chaetothyriomycetidae, Verrucariales, Verrucariaceae, Endocarpon, Endocarpon pusillum, Endocarpon pusillum (strain Z07020 / HMAS-L-300199) (Lichen-forming fungus)	1263415	>tr|U1G6B3|U1G6B3_ENDPU Uncharacterized protein OS=Endocarpon pusillum (strain Z07020 / HMAS-L-300199) GN=EPUS_08359 PE=4 SV=1MRDPWEEVQHPQKAKQHFLAYLRDDVFRFNFYRLHMFYFIVVILIFSIIVYGEGLANGSTKVNGTKLRYIDALFLCCSAMTTTGLN TVNFGSLTSFQQAMLCVLLLIRNVVFVSTFVVVIRRHFFRRKLAHVVEHSKSGRKVLRDIERQERYQSSRSKRSPSTELTPNGQISSHE RRGSLRKRLTTNPAESRNRSSGYDQRYHHQNGYGWMPAPWEIASVRNAFHHPFKKLASWGVRDQSYLAFDVNLDEKGRFRALNE YERAELGGVEYRALGALLWILAAYNLFWLALGTAFLVPYSYRSSVVNVLHSTQLGSLNPGWFGFFACSTSFANGGLNLVNANFIPFQ SYYFILTVCGVLSLAGNTQFPILLRLVIWIMSKISPSGSNFRQTLTFLLDHPRRCFLYLFPGKETWYLFAIQLMIDCTGWILFETLNLGLP AVMAIPTKVRVFDGLFQATGLRTSGASIINMSYLAPALLIAYLIIMYISNFPIVMALRQTNTYGERSIGLDKGQTGRGLAMHLQKQLAYDL WFQLLAWFLICIFERGKIVAEQPGFSNFNVLFEVASAYGTVGLSTGVPYDTYSLSGAFQTTSKLILLAAMIRGRHRGLPLAIDRSILLPG EELMHKMDTEYKEDGELHSQDEAEVRRDEELSGRNDMSWGEGAEQDPERDNNGNISGDRDGESGSKTPNQNQKEKNRVDFQLS
3E-92	319	10.4	3.1E-92	319.1	2.7	2.2	2	G7EA49_MIXOS	Uncharacterized protein	Mo06412 E5Q_06412	Mixia osmundae (strain CBS 9802 / IAM 14324 / JCM 22182 / KY 12970)	1444	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Pucciniomycotina, Mixiomycetes, Mixiales, Mixiaceae, Mixia, Mixia osmundae, Mixia osmundae (strain CBS 9802 / IAM 14324 / JCM 22182 / KY 12970)	764103	>tr|G7EA49|G7EA49_MIXOS Uncharacterized protein OS=Mixia osmundae (strain CBS 9802 / IAM 14324 / JCM 22182 / KY 12970) GN=Mo06412 PE=3 SV=1MVIQAGRHWSDHFNFFRIHLVVFITLPLILSGIFYAINVEPNIAFIDCLYMCYAAMTMTGLQSVLFANMTRAQQGILFIQLVLGSIVT VSIVTIVVVRLRAYPAQSANTARSSRSGSTSLELARRKQDGKHVRLHTGLIRRTADEVRVNALSNAGNEATPMESRSLQCHERIPSGPT QLTFDETTRSPVLRHRRSDSTTHRPSIYRGLGGFENPAHSLYRVLTGQVSNAHAIGRTTTQISTHSHRHHLALAGTKPISYLSFDATIG RNSRYLDLAPEELAELVELEQRALRLLLIITTSYYFGLQLLFVAVLAPYFAVGNYSENFTQAEGTSSSIWFVIFNTWSAFGNNGLSLLDA NFTAFQSCYLLILSTSFLILAGNTCFPVFLRGIIWSLSKFVPSEHTRGALHFLLDHPRRCYLYLFPAKQTIWLATIVFVFTAIDWLSFLVLDI GNDLIDTIPLNVRVIDGLFQSTAVRTAGFSIVPLATTAPAVQVLFATMMYISAFPLTLSIRTTNVYDEQGRASEGSEEDRLAHHARKQLA FDIWWVVLAIWLICIIERHGINDPSQTSVGIFAIVFEVISAYGTVGLSLGAPGGTSLSGTFRTLSKLIIIAVMIRGRHRGLPNALDRSILLPA TIEALRLDQDQDEMNGECDGSNDSRLLDDSRSGSLTRPTPLRPKRSTRLHLTGHLIMRTPSLLLLVRRTSSTCSIDCAHAKAHLESDSA TLRTDHCREDCLAGGTSALKSRHRSRKSPHVPPVCDYFNCKHFTSLASEVVSLSTKRARAETDSSTMQQRPRAWASAGTPSSPLTA TATAMLAQRQVQVDMRDFPPERIRSFTVIAHIDHGKSTLSDRLLELTKTIPAIAGFSNSQVLDKLKVERERGITVKAQSATMIHRHTDGH RYLLQLIDSPGHVDFASEVHRGLSASQGALLLVDATQGIQAQTLSVLEAAQQRGISILGVLNKVDLGHAEPAKVEAEMRTLLGQSDEEI YHVSAKTGLGVKNLLSACVDHLPPPPRLEDNITPKALVFDSWYDGFRGVVSLLAVKSGSFAVGDKIASYYTKKTYTVTDLGIMHPDQV SLKPGQRLSTGQIGWLTCAMKDPLDAQLGDTFYLAGQPVEPFEQHSPLRSMIFGGIYSQDSRDFTRLEESVRRLALTDRSVQVSRES SLALGQGLRLGFLGALHMDVFRQRLEDEYDADVIVTKPFTTVKVIYKKGTEEMIDSPNDFPEVKLMSSGGIIDHIEEPIIRATIVTPDEFV GPVMVLCTNHRAQQDSMTYLDASASATGEGLSGRRVVMTYTMPLSSIVTTFYSSLKSITSGYASFDYDDAGWQASDLVKLTVLINAT PVDALAFVVHRSEVEREGRDIATRLRTVIPRQQYEVVIQTAVGSKIVARERIAPLRKDVTGHLYGGDITRRTKLLDQQKKGKKQLKARS VGNVVLPNEVFSRVLTK
3.1E-92	319	1.5	1.2E-90	313.8	0.7	2.2	2	M2UAB9_COCH5	Uncharacterized protein	COCHEDRAFT_1026404	Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis)	733	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Bipolaris, Cochliobolus heterostrophus (Southern corn leaf blight fungus) (Bipolaris maydis), Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) (Southern corn leaf blight fungus) (Bipolaris maydis)	701091	>tr|M2UAB9|M2UAB9_COCH5 Uncharacterized protein OS=Cochliobolus heterostrophus (strain C5 / ATCC 48332 / race O) GN=COCHEDRAFT_1026404 PE=4 SV=1MSSSWQPLDGHDDTDESIMTDPLEELQSPRKAKDDFIKYMKNEVFRLNFYRAHMLYFIVVIFLSSLVVYGQGRADGPKELGSAH ITYTDALFLCCSAMTTTGNPCHTNRLYSPINGETGLNPVDLGPLSGYQQATFAILMMVGNIPFVSAAVVLIRRALFRKKLADVVKHSHT MQRLVQDIEQNHQSDQVENNSSSSSNSNRGLRQRATVSQGHQSQGKQSHKQGPSKANIKPASRQRSYHYEAGFGFMPTPWETQF AQNLFHRFIDFFATELKPEQHDYISFKPHLDSRGRFRDLSEADRMELGGVEYRALQALLLILVGYQVFWYLLGITFLLPYAYRDNIKNVL YTAQPEQGIHPGWWGFFATVTEFANGGLNILNANFIPFSGYPYVLLVAAAVAFAGQTQFPILLRVTIWGLKKLAPTQSRFRNTMEFLL QHPRRCFIYLFPARETLYLFVTQFVIDVTAWLCFEILNIGMPDVEALSTGTRILDGLFQASGLRTSGAYIISLTSLAPACLVAYLVIMYISIY PMTMTLRKTNTYEERSIGLEESGNSATSVASHLQKQLAYDIWFQFLVFFLICCIERRHILNADPGFSIFSILFEVTSAYGTVGLSLGVPG KNYSLCGDFASLSKVVLLFAMLRGRHRGLPFAIDRSILLPGEELMHRMDQEYSAKGTEDPQQEAELRRDIERSGVKTLDNNGKGEQD PGDRRHSQPNNHTACESSSATVQAESDP

3.5E-92	319	18.8	8.9E-92	317.5	13	1.6	1	A6VLP0_ACTSZ	Trk system potassium uptake protein	Asuc_0512	Actinobacillus succinogenes (strain ATCC 55618 / 130Z)	487	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Actinobacillus, Actinobacillus succinogenes, Actinobacillus succinogenes (strain ATCC 55618 / 130Z)	339671	>tr|A6VLP0|A6VLP0_ACTSZ Trk system potassium uptake protein OS=Actinobacillus succinogenes (strain ATCC 55618 / 130Z) GN=Asuc_0512 PE=3 SV=1MHIFTIIRIVGILVMCFSFAMLAPAFIALIYGDGGGTAFIQSFFISLAVGASLWWSCHLHKEELRSREGFLIVVSFWVVLGSLAALPF MLFDEPNLTLASAFFEAFSGLTTTGATTITGLDNLPKAILFYRQFLQWLGGMGIIVLAIAIIPLLGIGGMQLYRAEMSGPMKEQKMQPRIA ETAKTLWFIYASLTVLCALSYYWAGMSGFDAISHSFSTVSIGGFSTHDASMGYFDSPTINMITVVFLLISACNFALHFRAFSEIREGNFF KIYLRDPEFRFIRIQIVLIALCSFALVRHHTADDWWVNVEQAVFQAVSISTTTGYTTADFTHWPSFIPMLLIIASFIGGCAGSVGGGLRV ARVLVLSLQGLRELKLFVHPNLVYPIKWGKVILDNRVISSIWSFFSAYVLLFVICLLSVIACGLEPFDAFNAVLACLNNLGPGMGIVSSNF VDVPDSAKWILTGAMVCGRLEIFTLLALFSPAFWRT
4E-92	319	17.2	5.4E-92	318.2	11.9	1.1	1	Q6DAP2_PECAS	Trk system potassium uptake protein	trkH ECA0211	Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica), Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pectobacterium, Pectobacterium atrosepticum (Erwinia carotovora subsp. atroseptica), Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	218491	>tr|Q6DAP2|Q6DAP2_PECAS Trk system potassium uptake protein OS=Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) GN=trkH PE=3 SV=1MHLRAITRIVGQLVILFSGTMVIPGLVALIYRDGAGRAFTQTFIVALAIGIMLWLPNRKQKHELKSREGFLIVVLFWTVLGSVGALP FLFAEHPNLGVTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKENKMRP RIADTAKTLWLIYLLLTIACAVALWLAGMPVFDAIGHSFSTVSVGGFSTHDASIGYFNSPTINTIIAIFLLISGCNFGLHFALLSGRSLKVY WRDPEFRMFIFVQLSLVAVCTIVLWFHHVYDSGMQTINQAFFQVVSMATTAGFTTDSIASWPLFLPVLLLCSAFIGGCAGSTGGGLKV IRILLLLFLQSGSRELKRLVHPNAVYTIKLGHRALPERILEAVWGFFSAYALVFIVSMLAVIATGVDDFSAFAAVAATLNNLGPGLGVVAENF TSMNDTAKWILILTMLFGRLEVFTLLVLFTPTFWRE
4.7E-92	319	22	2.3E-91	316.2	15.2	1.8	1	Q65W78_MANSM	Trk system potassium uptake protein	trkG MS0175	Mannheimia succiniciproducens (strain MBEL55E)	487	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Basfia, [Mannheimia] succiniciproducens, Mannheimia succiniciproducens (strain MBEL55E)	221988	>tr|Q65W78|Q65W78_MANSM Trk system potassium uptake protein OS=Mannheimia succiniciproducens (strain MBEL55E) GN=trkG PE=3 SV=1MHILSIVRIVGILVMCFSVAMLAPAFVALIYGDGGGKAFMQSFVISLIVGTTLWWSCHSHKQELRSREGFIIVVAFWVVLGSLASIP FMLFEYPDLTVASSFFEAFSGLTTTGATTIVGLDDLPKAILFYRQLLQWMGGMGIIVLAVAIIPLLGIGGMSLYRAEMSGPMKEQKMRP RIAETAKILWFIYASLTILCALAYYLAGMSPFDAISHSFSTVSIGGFSTHDASIGYFNDSWINLITVVFLWISACNFALHFRAFSEINKGGF FKIYRNDPEFRFFVSIQVILILICSAVMLSHSYFETTWENIEQVIFQSVSISTTTGYTTSDFSAWPSFVPMLLIIASFIGGCAGSVGGGVRV ARILVLYLQGKRELKLFVHPNLVYPIKWGKRILDERVIGSIWAFFSAYLLVFIICLLGVIACGVDVFNAFNAVLACINNLGPAMGIVNSNMV EIPDSAKCILTIAMVCGRLEIFTLLALFSPTFWKA
7.8E-92	318	8	4.1E-88	305.5	0.8	2.1	2	A0A0A2IC33_PENEN	Potassium transport protein, high-affinity	PEX2_042770 PEXP_071080	Penicillium expansum (Blue mold rot fungus)	690	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium expansum (Blue mold rot fungus)	27334	>tr|A0A0A2IC33|A0A0A2IC33_PENEN Potassium transport protein, high-affinity OS=Penicillium expansum GN=PEX2_042770 PE=4 SV=1MHAPLILRKWRRKTGNAIMAVLPPLNFLTLHYLYFIATCMIASIIFYLTSTPWLSVAYVDSIFLCVSAMTGAGLNTVDLSTLNSFQQ AVLFVLLILGHAILISLTVLLVRKRAFEAKFKGVSDERERERSTRNPSQVELQDREPVQGSTGADLSGENTDGLSCKPRAKTSVLVQIK PGESSSRDEQQWVDDDQKTIGGTPRHHHHRVFPMAGIGARPDLHNHPRDAVPNVPLVVEDSVSGFKGLLRGTQKYMASKGLVSRN SQFHDLTPAERDELGGVEYKAVSFLSVVVFLYFILFIIFGMIGVGGWLEVNDPEVTRTNGLSPFWTGAFFAVSAFVNSGMSLLDANMT ALQLNAYPLLTMGFLILAGNTLFPCFLRFIIWTIRIMLPDRPRWQSWRITLDFILEHPRRVYTNLFPARHTWYLLGTIIILNGIDWAAFELL SIGNKDIESLPSEYRVLDGLFQALAVRAGGFYVVTIADLRQGLLVLYVLMMYVSAYPVTLTMRNTNVYEERSLGIYAHDESPDSPANTS RSNVVMDLIRHHLGRPGPSETSRGYFVHQQLRSQLSHDLWWIALAVFFIAIRESDHYESQPVAFSTFNIIFEVVSAYGCVGVSLGFPG KNYSFCGAWHTVSKLILAAVALRGRHRGLPVAIDKAVMLPSESLAWAEEEDAAMRRDRSRAWGQDHGPVGSV
8.4E-92	318	8.3	6.9E-89	308	1.1	2.1	2	M7USF5_BOTF1	Putative cation transporter protein	BcDW1_1420	Botryotinia fuckeliana (strain BcDW1) (Noble rot fungus) (Botrytis cinerea)	935	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Sclerotiniaceae, Botrytis, Botryotinia fuckeliana (Noble rot fungus) (Botrytis cinerea), Botryotinia fuckeliana (strain BcDW1) (Noble rot fungus) (Botrytis cinerea)	1290391	>tr|M7USF5|M7USF5_BOTF1 Putative cation transporter protein OS=Botryotinia fuckeliana (strain BcDW1) GN=BcDW1_1420 PE=4 SV=1MTGEHGTWQVTSGETTARNSTDLEIESHEAYGRREKLRNDDREIPKIVIPHENETGTCTLDTESKQRKLDASKVRMGEGQLGV PKLQTEPRNLNSQTAPRTFGSFFAVHSPIATRPLKSLLPSRGDKEKTLPRSMRGSFFNSHPSREEMDKKPRSLKSFMGDEWYDRVM RCLSPILALFPPLNFITIHYTYFIVTLLITSLIFWGSSNPSKSISYVDSLFMVTSGMTEAGLNTVNLSTLTTFQQVILWLLIVVGSAIFVSVAT VRTRKRAFEVRFGEVVGRYKEERRRERMRSGSRDAMGSRRGDGNGLMRANWTFPSTSGGNGGEDALEMEEGLKVRPVGGEGD DNCMTAISEISPRGGIPKDMGDHITFAPNAYPVNGKGKANDVTVGSSNTETATPARSTNFQFPTSISENTIKHRVQETSTPIQQTQTG QQDLAPLQYPSYLNSNTTGRNAQFHGLSRAEREHLGGVEYRAISFLAWLVPLYFILWQLLGGIGLGAYMAYNKSNVALENGINPWWL GVFNAISAFNNSGMSLLDLNVIPFQTSVYTLLTMGLLILAGNTAYPLFLRLILYTLLKLLDTFPNVLSPFQHHKPTLLFILRYPRRVYTNLF PSRPTWWLLFMVITLNSIDWVAFELLNIGNSATQVIEPRYRVLDGLFQAIAVRSGGFYVISIPSLRIGLQFLYVIMMYISVYPVVITMRHS NVYEERSLGIYRGDVETDSHTSRWGRGMKRIRKSISGRDIGIPHTASSNSNITSTSPPDETTGTQFIHHQLRSQLSHDLWWLTLATFLI VCIESSSFEKDPITYSVFNVIFEVVSAYGCVGISTGLPDQDYSFSGGLRTASKVVLAVMVRGRHRGLPRALDRAVRLPGWEGEGLG GEGGGERGEEEAAIGECGEGGKERDGGKGKERERSEEGRGLRKRRFSRGVGGTEEV
1.3E-91	317	7.1	1.2E-87	304	2.4	2.1	2	S2KDK6_MUCC1	Uncharacterized protein	HMPREF1544_02766	Mucor circinelloides f. circinelloides (strain 1006PhL) (Mucormycosis agent) (Calyptromyces circinelloides)	825	cellular organisms, Eukaryota, Opisthokonta, Fungi, Fungi incertae sedis, Mucoromycotina, Mucorales (pin moulds), Mucorineae, Mucoraceae, Mucor, Mucor circinelloides (Mucor griseo-roseus), Mucor circinelloides f. circinelloides, Mucor circinelloides f. circinelloides (strain 1006PhL) (Mucormycosis agent) (Calyptromyces circinelloides)	1220926	>tr|S2KDK6|S2KDK6_MUCC1 Uncharacterized protein OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_02766 PE=4 SV=1MNRFTGALHRFWDTRIHFLELHYLYTLVITFLFSGLYYCEPGTDWNYIDALFMATTGCTDTGLNTIAMSAMSTYHMVLLYITSFL GSHVTVSFVVVMVRRYYFSKRFEKELEYNKKRKEEYKQQKLLREQQAQEQEEQQRLSSDGSSTTTNTTKASRKTDIITGPIRRRMSM LSIRSTPAHSSRKLSLFNIRKRGSYDTHATRTKDIVVHHPNYNYSDSNGSASPSDTNFSSIQMEHYPNSEDQQQQENDAANDGDDND NVECIASTHPCDTTPCNSKRNSAVSSDDNSSQEHGKTAISFLEDQDGKPVNNTSNTTNTNNNQQITFREDTNVLRERERRKLLQNRN DDHNIEQLPLHRTNSEYEIMRQPSAKHELTKNERYRIGGTEYRALEMLARIVPLYYLGFIISFGFFFRIYVAASTYAQEVLATSNPTGPV EPWFFSFFMSLSAFTNLGLNHLDASMAPFQNAPAPLILAILLILVGNTAFAILLRFIIWICYVLTPERKVMRRETFRYLLDHPRRCYTTLFP STQTWWLLIVLIAITLVELICFLALNYWLPVLAGISWGSRFLDGLFQSVATRNAGFSVISLADLNPGAQLVYIIAMYISVYPVAISMRNSNI YQERALGIFRGEDEEPVKFSDDDLAEAPFIKLKRHSTMTSIAQGTKKLLKGPDFFVITQIQRQLTSDICWVITGIFCICVIEAESIMSPSPV TIATVIYECVSAFGNVGASTGYPNTATSQAAQYRTLSKLVLIILMYRGRHRGLPASIDRSILLPSDALAEKEKEDEIRRRNTSVSLQVVND SATSTGVHGSPDHLIYTRSCTL
1.5E-91	317	14.5	2.4E-91	316.1	10	1.3	1	A8ACZ8_CITK8	Trk system potassium uptake protein	CKO_00192	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter koseri (Citrobacter diversus), Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	290338	>tr|A8ACZ8|A8ACZ8_CITK8 Trk system potassium uptake protein OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=CKO_00192 PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFVALVIGSLLWWPNRREKGELKSREGFLIVVLFWTVLGSVGAL PFIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFSTIAIGGFSTHDASVGYFDSPTINSIMAIFLLISGCNYGLHFSLLSGRSLKVY WRDPEFRMFIGVQLTLVVICTLVLWFHDIYNSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVI RILLLFKQGNRELKRLVHPNAVYSIKLGHRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNF ASMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE

1.6E-91	317	16.4	2.2E-91	316.2	11.4	1.2	1	G7LUB1_9ENTR	Trk system potassium uptake protein	BrE312_0227	Brenneria sp. EniD312	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Brenneria, Brenneria sp. EniD312	598467	>tr|G7LUB1|G7LUB1_9ENTR Trk system potassium uptake protein OS=Brenneria sp. EniD312 GN=BrE312_0227 PE=3 SV=1MQLRAITRIVGLLVILFSGTMFIPGLVALIYRDGAGRAFTQTFLVALAIGIVLWLPNRKQKHELKSREGFLIVVLFWTVLGSVGALP FLFAEHPNLGVTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIADTAKTLWLIYLLLTVACAVSLWLAGMPIFDAIGHSFSTVSVGGFSTHDASIGYFNNPTINSIVAVFLLISGCNFGLHFAVLSGRSLKV YWRDPEFRMFIFIQISLVAVCTLVLWFHNVYASGMQTLNQAFFQVVSMATTAGFTTDSIASWPLFLPVLLLCSAFIGGCAGSTGGGLK VIRILLLFLQGSRELKRLVHPNAVYTIKLGHRALPERILEAVWGFFSAYALVFIVSMLAVIATGVDDFSAFAAVAATLNNLGPGLGVVADN FTSMNDAAKWILILTMLFGRLEVFTLLVLFTPTFWRE
2.1E-91	316	16.2	1.5E-90	313.5	11.2	1.9	1	TRKH_SALTY	Trk system potassium uptake protein TrkH	trkH STM3986 STMD1.3	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella typhimurium, Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	99287	>sp|Q8ZLE2|TRKH_SALTY Trk system potassium uptake protein TrkH OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFVALAIGSILWWPNRREKGELKSREGFLIVVLFWTVLGSVGALP FIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPR IAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFSTIAIGGFSTHDASVGYFDSPTINTIAIFLLISGCNYGLHFSLLSGRSLKVYW RDPEFRMFIGVQLTLVVICTLVLWFHNIYDSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRI LLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFAS MNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
2.3E-91	316	2.6	5.8E-90	311.5	0.3	2.4	2	M2T5K7_COCSN	Uncharacterized protein	COCSADRAFT_155870	Cochliobolus sativus (strain ND90Pr / ATCC 201652) (Common root rot and spot blotch fungus) (Bipolaris sorokiniana)	713	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Bipolaris, Cochliobolus sativus (Common root rot and spot blotch fungus) (Bipolaris sorokiniana), Cochliobolus sativus (strain ND90Pr / ATCC 201652) (Common root rot and spot blotch fungus) (Bipolaris sorokiniana)	665912	>tr|M2T5K7|M2T5K7_COCSN Uncharacterized protein OS=Cochliobolus sativus (strain ND90Pr / ATCC 201652) GN=COCSADRAFT_155870 PE=4 SV=1MTDPLEELQSPRKAKDDFIKYMKNEVFRLNFYRAHMLYFIVVIFVSSLVVYGQGRADGPKELSSAHMTYTDALFLCCSAMTTTG KLCHTNWLYPSTDDETGLNPVDLGPLSGYQQATFAILMMVGNIPFVSAAVVLIRRALFRKKLADVVKHSHTMQRLVRDIEQNHQSDQ AENNRSSNSSNKGLRQRSTVSQDPQSQGKQSHNQDSSKVNIKPASRQRSYHYETGFGFMPTPWETQFAQNLFHRFIDFFATELKP EHHDYISFKPHLDSRGRFRDLSEADRMELGGVEYRALQALLLILVGYQIFWYLLGITFLLPYAYRENIKNVLYTAQPEGINPGWWGFFA TATEFANGGLNILNANFIPFSGYSYVLLVSATVAFAGQTQFPIFLRATIWGLKKMAPRQSRFRSTMDFLLQHPRRCFIYLFPARETLYLF VTQFVIDVTAWLCFEILNIGMPDVEALPTGTRILDGLFQASGLRTSGAYIISLSSLAPACLVAYLVIMYISIYPMTLTLRKTNTYEERSIGLE ESDNSATGVASHLQKQLAYDIWFQFLVFFLICCIERRHILNADPGFSVFSILFEVTSAYGTVGLSLGVPGKNYSLCGDFASLSKVVLLFA MLRGRHRGLPFAIDRSILLPGEELMHRMDQEYNAKGTEDPRQEAELRRDIERSGVKTLDNNGKGEQDPEHRRRSQPNNHTACESSS ATVQAESDP
2.7E-91	316	14.9	3.9E-91	315.4	10.3	1.2	1	A4WFX1_ENT38	Trk system potassium uptake protein	Ent638_3946	Enterobacter sp. (strain 638)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Enterobacter, Enterobacter sp. (strain 638)	399742	>tr|A4WFX1|A4WFX1_ENT38 Trk system potassium uptake protein OS=Enterobacter sp. (strain 638) GN=Ent638_3946 PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFAALVIGSMLWWPNRREKGELKSREGFLIVVLFWTVLGSVGAL PFIFAEQPNLTVTDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMR PRIAETAKTLWFIYVLLTVACALALWFAGMPAFDAIGHSFSTIAIGGFSTHDASVGYFDSPTINTIIAVFLLISGCNYGLHFSLLSGRSLKV YWRDPEFRMFIGVQLTLVVICTSVLWLHDVYSSAVTTVNQAFFQVVSMATTAGFTTDSISRWPLFLPVLLLCSAFIGGCAGSTGGGLK VIRILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADN FASMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRD
3E-91	316	1.6	3.6E-91	315.5	1.1	1	1	W7MTC8_GIBM7	Uncharacterized protein	FVEG_12850	Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	518	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium fujikuroi species complex, Gibberella moniliformis (Maize ear and stalk rot fungus) (Fusarium verticillioides), Gibberella moniliformis (strain M3125 / FGSC 7600) (Maize ear and stalk rot fungus) (Fusarium verticillioides)	334819	>tr|W7MTC8|W7MTC8_GIBM7 Uncharacterized protein OS=Gibberella moniliformis (strain M3125 / FGSC 7600) GN=FVEG_12850 PE=4 SV=1MLDNSTGITDVDIESTHNEPKVLADTTENSAEATDETNGKAKATDDLIEEDPTVANEDRRVARTMTITFDQSTEQHKDDDALYIP GPRARDRGYPIAPRAARHPEDSDDDDVIKPVPNRNQNDGSSSMRRRRRFSSDDGLKVTASRSMDRVAGVAASLLVLGSQTAPQPR PISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQASA QDKTWWGIYSAQTMYDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKTSPTQESLAFLLTYPRRCYT LLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVSSLPLSQRIPAAIFQAASARHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISIRASNA YEEKSLGLWEEEKSLDEKHSKTYLLTHMKNQLGFDLWYIFLGTFCICISESTRIADVNEPAFSVFSVLFEVTSA
3.3E-91	316	16.4	2.3E-90	312.9	11.3	1.9	1	B5RFL3_SALG2	Trk system potassium uptake protein	trkH SG3466	Salmonella gallinarum (strain 287/91 / NCTC 13346)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella gallinarum, Salmonella gallinarum (strain 287/91 / NCTC 13346)	550538	>tr|B5RFL3|B5RFL3_SALG2 Trk system potassium uptake protein OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFVALAIGSILWWPNRREKGELKSREGFLIVVLFWTVLGSVGALP FIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVSILPILGVGGMQLYRAEMPGPLKDNKMRPR IAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFSTIAIGGFSTHDASVGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVYW RDPEFRMFIGVQLTLVVICTLVLWFHNIYDSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRI LLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFAS MNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRN
4.2E-91	315	15.2	5.8E-91	314.8	10.5	1.1	1	B2VFE5_ERWT9	Trk system potassium uptake protein	trkH ETA_02490	Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Erwinia, Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	338565	>tr|B2VFE5|B2VFE5_ERWT9 Trk system potassium uptake protein OS=Erwinia tasmaniensis (strain DSM 17950 / Et1/99) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMIVPGLVALIYRDGAGRAFTQTFFMALMIGTLLWWPNRKKKSELKPREGFLIVVLFWTVLGSVGA MPFIFTEQPHLKLTDAFFESFSALTTTGATTLTGLDTLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKM RPRIAETAKTLWLIYVLLTVACALALWLAGMSAFDAIGHSFSTIAIGGFSTHDASIGYFNSPTINTIIAVFLLISGCNYGLHFSLLSGRNLRV YWRDPEFRMFIGVQITLVIICTLVLWFHDVYQSGMQTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLK VIRILLLFKQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFILSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADN FTSMNDTAKWILILTMLFGRLEVFTLLVLFTPTFWRE
4.7E-91	315	17.2	8.1E-91	314.4	11.9	1.3	1	A0A097QXT7_HAFAL	Trk system potassium uptake protein	AT03_02130	Hafnia alvei FB1	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Hafnia, Hafnia alvei, Hafnia alvei FB1	1453496	>tr|A0A097QXT7|A0A097QXT7_HAFAL Trk system potassium uptake protein OS=Hafnia alvei FB1 GN=AT03_02130 PE=3 SV=1MHFRAIIRIVGLLVILFSGTMIIPGLVALIYRDGAGRAFTQTFFVALTIGTLLWWPQRKQKHELKPREGFLIVVLFWTVLGSVGALP FLFSERPNLSVTDAFFESFSGLTTTGATTLVGLDNLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGLQLYRAEMPGPLKDNKMRP RIAETAKTLWFIYVLLTVACAVALWGAGMDVFDAISHSFSTIAIGGFSTHDASIGYFNSPTINTIIAVFLLISGCNFSLHFALLSGRSLKVY WRDPEFRMFIFVQLTLVAVCTLVLWWHNVYQTGLQTVNQAFFQVVSMATTAGFTTDSIAHWPLFLPVLLLCSAFIGGCAGSTGGGLK VIRILLLFLQGSRELKRLVHPNAVYTIKLGSRALPERILEAVWGFFSAYALVFIISMLAIIATGVDDFSAFAAVVATLNNLGPGLGVVADNF TSMNDAAKWVLVVTMLFGRLEVFTLLVLFTPTFWRN

5E-91	315	20.2	6.9E-91	314.6	14	1.1	1	A0A0F5F0W2_AVIPA	Trk system potassium uptake protein	Z012_04425	Avibacterium paragallinarum (Haemophilus gallinarum)	487	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Avibacterium, Avibacterium paragallinarum (Haemophilus gallinarum)	728	>tr|A0A0F5F0W2|A0A0F5F0W2_AVIPA Trk system potassium uptake protein OS=Avibacterium paragallinarum GN=Z012_04425 PE=3 SV=1 MHILSIFRIIGILVMCFSATMLVPAFVALIYGDGGGKAFLQAFLSSFLFGTLLWRACHQHKQELRSREGFLIVVVFWVLLSLLAVIP FLLFDELSMSFADAVFETFSAITTTGATVMSGLDNLPKSILFYRQFLQWIGGMGLIVLVVAVIPILGIGGTQLYRIESSGPLKDQKNLPRI AEVAKLLWLLYCLLTVISTLGYWWAGMSFFDALCHSFSTVSNGGMSTHDANLGYFKDSKIYFLAAIFMLAAGCNFGLHIMAFTHFKHQ SVLKTYWQDPEFRFFCLIQGGFILIMSFGLYLSYQDLSLVDAFAQGSAQLSSMSMTSGYTLFDINQLPPFLGMLLVISAVLGGCAGSTS GGLKMIRVLVIWLQFKRELKYLIHPNLVVPIKLGDNLLSINVIERIWAFLIAFFLTYWLCVFAAILCGMGAFDAMGAVFATLSNAGPGLGV VSSSFANVPDNAKYVFSFAMVAGRLEIFSLLVLFSPAFWRA
5.1E-91	315	13.9	1.8E-88	306.7	1.9	2	2	E9EK07_METRA	Cation transporter	MAA_00092	Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	623	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Clavicipitaceae, Metarhizium, Metarhizium robertsii, Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) (Metarhizium anisopliae (strain ARSEF 23))	655844	>tr|E9EK07|E9EK07_METRA Cation transporter OS=Metarhizium robertsii (strain ARSEF 23 / ATCC MYA-3075) GN=MAA_00092 PE=4 SV=1 MSLRNAQHGTCALLAAAWRRVSRLGSHHVNFVSLHYAYFIFVSLISSVVFWLLSAPKLSVTYVDSLFMVVSGVTETGLNTVDLS KLTTAQQVLLCLLMICGSAVWVSIWLVSARKRSFRRLLARNGLARPPLDRRQSVHVPYPGAYQNASDSEAREAKATEGDAEPFEGLS VQASRLSPPAPLGSRNRRLLNPGSEQALGEPLEEPTPNPLAFLTSKNMGRNGDFINLTAQERIQVSSIEHKALQLLSLIVPLYFTLWQV LGCLGLGAWIATNQPRPALENGINPWWLGIFNGVSAFNNSGMSLLDANMVPFQAAYYVLVTMGLLILAGNTAYPIFLRFLLWSVLKVL HVFPEGPIVTEWRSTLEYILRYPRRVYTNLFPTQHTWWLAFMVLMLNGIDWAAFELLNIGNPVISAIPFGPRIMDGLFQAVAVRSGGF YIVPIAKTHIGLQVLYVIMMYISVYPVIITMRNSNVYEERSLGLFAVESTKDEEYVDPYAKALRSFRTRRLFISQQIRGQLADDIWLLALAT FIITVIEAPHFAEDPVSYSVFNIIFEIISAYGCVGISVGSPGANYSFCGGWRAGSKLVVCLVMLRGRHRTLPASLDYAVRPAGKDIQEEV LEEHH
6.4E-91	315	12.1	6.7E-87	301.5	6.4	2.2	2	F9F5B5_FUSOF	Uncharacterized protein	FOXB_01590	Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	587	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum (strain Fo5176) (Fusarium vascular wilt)	660025	>tr|F9F5B5|F9F5B5_FUSOF Uncharacterized protein OS=Fusarium oxysporum (strain Fo5176) GN=FOXB_01590 PE=4 SV=1 MTISDMFGSIDVKDLKTYQQLYIYFIPILTNLGFINIVVVFVRLSWFKRHLKRFTPQNLDNSPGIPDVDIESAHHESKVPADTTENS AEVTNEPNDKAKATDDHIEEDATIANEDRRVARTMTITFDPSTEKHKEDDALYIPGPRARDRDDAIKPVPNEIQNNGSSSTLHRRRFSS DDGLKITVSRSMDRFAGVASSFLVLGSQTAPQPRALSSDSNRQPAINDVPLLSRQATLGRNSQFKNLTSHYREILGGIEYRSLKLLLKI VVAGQIVPSHRGIYSAQTMLDNLGFTLTPDSMTSFHTAKWPMILMSFLAFAGNTLYPVFLRLSIWIMSKLVPKATPTQESLAFLLNYPR RCYTLLFPSGPTWILFGIIFALNFIDILLIIVLDLSNPEVASLQLSQRIPAAIFQAASSRHTGTASFNLANVSPAVQLSLLIMMYIAVFPIAISI RASNAYAEKSLGLWDEEKSLDEKHSKTYLSMYMKNQLGFDLWYIFFGTFCTCISESTRIADVNEPAFSVSSALFEVTSAYGNVALSLG YPTVSTSLSAMFGTFGKAVICLMMIRGRHRGLLLYALDRAIMLPTGQITEN
6.5E-91	315	18.4	1E-90	314	12.7	1.3	1	E0SLG4_DICD3	Trk system potassium uptake protein	trkH Dda3937_02080	Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Dickeya, Dickeya dadantii, Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	198628	>tr|E0SLG4|E0SLG4_DICD3 Trk system potassium uptake protein OS=Dickeya dadantii (strain 3937) GN=trkH PE=3 SV=1 MHLRAITRIVGLLVILFSGTMFIPGMVALIYRDGAGRAFIQTFIVALVMGLLLWLPNRKHRHELKAREGFLIVVLFWTVLGSVGALP FLFVERPNLSVTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWMGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDHKMR PRIAETAKTLWLIYVLLTVLCALSLWLAGMSVFDAISHSFSTIAIGGFSTHDASIGYFNSPTINTIIAVFLLISGCNFGLHFAVLSGRSLRVY WRDPEFRMFIVVQMSLVVICTLVLWGHGVYKNGMETLNQAFFQVVSMATTAGFTTDSIASWPLFLPVLLLCSAFIGGCAGSTGGGLK VIRILLLFLQGSRELKRLVHPNAVYTIKLGQRALPERILEAVWGFFSAYALVFIVSMLAVIATGVDNFSAFAAVAATLNNLGPGLGTVADN FTSMNDAAKWILIVTMLFGRLEVFTMLVLFTPTFWRE
6.7E-91	315	16.8	2.4E-90	312.8	11.6	1.7	1	A6TGM7_KLEP7	Trk system potassium uptake protein	trkH KPN_04343	Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	463	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Klebsiella, Klebsiella pneumoniae, Klebsiella pneumoniae subsp. pneumoniae, Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	272620	>tr|A6TGM7|A6TGM7_KLEP7 Trk system potassium uptake protein OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=trkH PE=3 SV=1 MIVPGLVALIYRDGAGRAFTQTFFVALAIGSMLWWPNRKQKGELKSREGFLIVVLFWTVLGSVGALPFIFSEQPNLTVTDAFFES FSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIA CALALWFAGMPAFDAIGHSFATIAIGGFSTHDASVGYFNSPMINSIIAIFLLISGCNYGLHFSLLSGRSLKVYWRDPEFRMFIGVQLTLVI VCTLVLWLHNVYGSVLTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRILLLFKQGNRELKRLVH PNAVYSIKLGNRALPERILEAVWGFFSAYALVFIISMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFATMNPVAKWILIANMLFG RLEVFTLLVLFTPTFWRE
8.1E-91	314	14.2	1.2E-90	313.8	9.9	1.2	1	D2TUY6_CITRI	Trk system potassium uptake protein	trkH ROD_39061	Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter rodentium, Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	637910	>tr|D2TUY6|D2TUY6_CITRI Trk system potassium uptake protein OS=Citrobacter rodentium (strain ICC168) GN=trkH PE=3 SV=1 MHFRAITRIVGLLVILFSGTMIIPGLVALIYRDGAGRAFTQTFFVALAIGSMLWWPNRKEKGELKSREGFLIVVLFWTVLGSVGAL PFIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFATIAIGGFSTHDASVGYFDSPTINSIIAIFLLISGCNYGLHFSLLSGRSLKVY WRDPEFRMFIGVQLTLVVICTLVLWFHDVYNSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVI RILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNF ASMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
8.9E-91	314	12	3E-89	309.2	2.9	2	2	B6QBX9_PENMQ	Potassium transporter, putative	PMAA_066440	Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333)	719	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Trichocomaceae, Talaromyces, Penicillium marneffei, Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333)	441960	>tr|B6QBX9|B6QBX9_PENMQ Potassium transporter, putative OS=Penicillium marneffei (strain ATCC 18224 / CBS 334.59 / QM 7333) GN=PMAA_066440 PE=4 SV=1 MAKMSVPWRKPIRRMANLLPPLNFLTLHHSYFIAMGLLWSLIFWATASPAQSVSYIDALFLCVSAMTGAGLNSINLSTVNSFQQA ILFGLIILGHPILISSTVLFVRKRAFETRFRSIVHAVARNRSAVHQAIHLPRIAKKVLLADGDKPVPRTEDQVADNETHNNASARMSSETR TVNNDIRSQNNLNDADAIRWVDDDQLTVQSHSRNKVRHRVFPMAGIGARPDARDPKDAAPSFVADEERRHSLIESLTRSPQKFFLSR GLISRNSQFHGLTASEREKLGGVEYKAICLLSIIVPLYFVLFNVLGFIGLGTWLAVNRPNVARENGLNPFWTGSFLAISAFGNNGMSLL DLNMTALQTCSYVLLTMGFLILAGNTLYPCFLRFSIWTMRHVLPRTKWCEEWKIVLDFILDHPRRVYTHLFPKRHTWYLLATIILFNGID WAGFEVLSIGNTAVQSLGGYRVLDGLFQAFAVRAGGFYVVTIADLHQGLLVLYVLMMYVSAFPVLVTIRNTNVYEERSLGIYANDHLT EDQRHHASLGSFFGHIKGIVSPSSEGDNTQDSEQSTSHIDENNTSRSYFVRQQVRSQLSHDIWWICLAVLFITIAEAPHFKNDPVSYS TFNIIFEVVSGYGCVGISVGLPNQNYSFCGGWYTISKLILIAVMLRGRHRGLPVAIDKAVMLPDESLAWAEEEDAAMRLEGSRSRNAN HGATCEWKSEDIV
1.4E-90	314	14.6	3E-90	312.5	10.1	1.5	1	A0A0A0Z1I2_9ENTR	Trk system potassium uptake protein	PSNIH1_06565	Pantoea sp. PSNIH1	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH1	1484158	>tr|A0A0A0Z1I2|A0A0A0Z1I2_9ENTR Trk system potassium uptake protein OS=Pantoea sp. PSNIH1 GN=PSNIH1_06565 PE=3 SV=1 MHFRAITRIVGLLVILFSVTMIVPGLVALIYRDGAGRAFSQTFLMAIVIGSLLWWPNRKQKTELKPREGFLIVVLFWTVLGSVGAM PFIFAEQPHLSATDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMR PRIAETAKTLWLIYVVLTIACALALWLAGMPMFDAIGHSFSTIAIGGFSTHDASIGYFNSPTINTIVAIFLLISGCNYGLHFSLLSGRNLKVY WRDPEFRMFIGVQFTLVVICTLVLWLHNVYDSGWQTLNQAFFQVVSWATTAGFTTDSIARWPLFLPVLLLCSAFIGGMAGSTGGGLK VIRILLLFKQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFLLSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADN FTTMNDVAKWILILTMLFGRLEVFTLLVLFTPTFWRE

1.8E-90	313	8.3	1.2E-89	310.5	2	2	2	L2FC66_COLGN	Potassium transporter	CGGC5_14465	Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	591	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	1213859	>tr|L2FC66|L2FC66_COLGN Potassium transporter OS=Colletotrichum gloeosporioides (strain Nara gc5) GN=CGGC5_14465 PE=4 SV=1MWKPKLNFISLHSAIDAFFFGASGSTESGLNTIDVKDLKTYQQVYIYVIPMITNLMFINIVVVVARLYWFQQRLKNIAKERTLSRCA EDLEAGPPDQEAEARGRKSALDETHAEQKAVQTGPSESKQNETVDTGLAFGPRATTITFEENLPNRGQSTADNAVLHVPGPRDRDD GQSMIETRQDRESIDDIDAIRPVEPVASGLSRRRPHNMEGPAMCAARSMEKVASSVLVLGHSKSLDRESRRSDLSTRPRPPRTADLP YLSRQVTVGRNSQFFHLTERDRELLGGIEYRSLKLLLKIVFSYFIGLHVFGVICLLPWILHAPPKYKSWLLENGQGQVWWAFYSAQTM VDNLGFTLTPDSMSTFKDATWPMLAMTFLAFAGNTIYPVLLRLVIWIMSRVVNKKSATKEHLEFLLDHPRRCYTLLFPSRPTWILFGIVF LLNFIDVLLIIVLDLDNPAVNDLAMGPRILSALFQAASSRHTGTSTLNLSLVNPAVQFSLLCMMYIAIFPIAISIRASNTYEERALGVYEANS HLDENNGASYVVMTHVRNQLSFDLWYIFLGTFCICIAESQRIMDLNEPVRTIFTTILESQC
1.8E-90	313	20.7	4.6E-90	311.9	14.3	1.5	1	R4YJB2_OLEAN	Trk system potassium uptake protein	trkG OLEAN_C00160	Oleispira antarctica RB-8	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Oleispira, Oleispira antarctica, Oleispira antarctica RB-8	698738	>tr|R4YJB2|R4YJB2_OLEAN Trk system potassium uptake protein OS=Oleispira antarctica RB-8 GN=trkG PE=3 SV=1MNFSVIARVLGLLMMIFSFTLVPPMIVSWVYQDGTLSAFLYALLITFGIGFLVWLPVHNHRQELKTRDGFIITVLFWLVLAFSGSVP LYLAEQANLSYTDAFFESLSGWTTTGATVITGLDELPKSILWYRQQLQWLGGMGIIVLAVAVLPMLGIGGMQLFRAETPGPVKDSKLT PRITETAKALWYIYLSLTIACAAAYWFAGMTLFDAIGHSFSTVAIGGFSTHDASLGYFNSPTIEAIAMIFMLISVLNFGLHFYAWKNKSIV HYFLDSEFKFIFSIMLGGAALTVSALWLTDTYTLSNSVRNGLFQLVSIATTTGFSTVGFAEWPVFLPVLLFMMAFIGGCAGSTGGGMK VIRVLLIYKQGIREIRRLIHPNAIIPVKINKRTVNDRVLESVWGFFSVYILTYMVMMVALLATGLDHVTAFSAVGACLNNLGPGLGEVAAH YGNISDVAKWILSITMLLGRLEIFTFLVLMSPAFWRN
2.2E-90	313	12.7	3.4E-90	312.3	8.8	1.2	1	A0A089UBU4_9ENTR	Trk system potassium uptake protein	LH23_06300	Cedecea neteri	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cedecea, Cedecea neteri	158822	>tr|A0A089UBU4|A0A089UBU4_9ENTR Trk system potassium uptake protein OS=Cedecea neteri GN=LH23_06300 PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFVALAIGSLLWWPNRREKRDLKPKEGFLIVVLFWTVLGSVGAL PFVFAERPNLTVTDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGLQLYRAEMPGPLKDNKMR PRIAETAKTLWLIYVLLTIACALALWFAGMPAFDAIGHSFSTIAIGGFSTHDASVGYFNSPTINTIIAIFLLISGCNYSLHFSLLSGRSLKVY WRDPEFRMFIGVQLSLVLVCTLVLWFHNTYQSAWQTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLK VIRILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVAATLNNLGPGLGVVADN FASMNPVAKWILIVNMLFGRLEVFTLLVLFTPTFWRE
2.3E-90	313	14.2	3.4E-90	312.3	9.8	1.2	1	A0A0A1B467_9ENTR	Trk system potassium uptake protein	PSNIH2_16295	Pantoea sp. PSNIH2	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH2	1484157	>tr|A0A0A1B467|A0A0A1B467_9ENTR Trk system potassium uptake protein OS=Pantoea sp. PSNIH2 GN=PSNIH2_16295 PE=3 SV=1MHFRAITRIVGLLVILFSGTMIVPGLVALIYRDGAGRAFSQTFIMALIIGAMLWWPNRKQKNDLKPREGFLIVVLFWTVLGSVGAM PFIFAEHPNLSVTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMR PRIAETAKTLWLIYVLLTVACAVALWLAGMPMFDAIGHSFSTIAIGGFSTHDASVGYFNSPTINTIIAVFLLISGCNYGLHFSLLSGRNLRV YWRDPEFRMFIGVQFTLVVICTIVLWFHNVYASGWQTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGL KVIRILLLFKQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFLLSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVAD NFTSMNDVAKWILISTMLFGRLEVFTLLVLFTPTFWRE
2.4E-90	313	16.1	3.9E-90	312.1	11.2	1.3	1	TRKH_ECOLI	Trk system potassium uptake protein TrkH	trkH b3849 JW5576	Escherichia coli (strain K12)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli (strain K12)	83333	>sp|P0AF27|TRKH_ECOLI Trk system potassium uptake protein TrkH OS=Escherichia coli (strain K12) GN=trkH PE=1 SV=1MHFRAITRIVGLLVILFSGTMIIPGLVALIYRDGAGRAFTQTFFVALAIGSMLWWPNRKEKGELKSREGFLIVVLFWTVLGSVGAL PFIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMDAFDAIGHSFATIAIGGFSTHDASIGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVYW RDPEFRMFIGVQFTLVVICTLVLWFHNVYSSALMTINQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRI LLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFTS MNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
2.4E-90	313	16.1	3.9E-90	312.1	11.2	1.3	1	TRKH_ECO57	Trk system potassium uptake protein TrkH	trkH Z5371 ECs4777	Escherichia coli O157:H7	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli O157:H7	83334	>sp|P0AF28|TRKH_ECO57 Trk system potassium uptake protein TrkH OS=Escherichia coli O157:H7 GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMIIPGLVALIYRDGAGRAFTQTFFVALAIGSMLWWPNRKEKGELKSREGFLIVVLFWTVLGSVGAL PFIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMDAFDAIGHSFATIAIGGFSTHDASIGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVYW RDPEFRMFIGVQFTLVVICTLVLWFHNVYSSALMTINQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRI LLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFTS MNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
2.4E-90	313	16.1	3.9E-90	312.1	11.2	1.3	1	Q32A24_SHIDS	Trk system potassium uptake protein	trkH SDY_3896	Shigella dysenteriae serotype 1 (strain Sd197)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Shigella, Shigella dysenteriae, Shigella dysenteriae serotype 1 (strain Sd197)	300267	>tr|Q32A24|Q32A24_SHIDS Trk system potassium uptake protein OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMIIPGLVALIYRDGAGRAFTQTFFVALAIGSMLWWPNRKEKGELKSREGFLIVVLFWTVLGSVGAL PFIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMDAFDAIGHSFATIAIGGFSTHDASIGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVYW RDPEFRMFIGVQFTLVVICTLVLWFHNVYSSALMTINQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRI LLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFTS MNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
2.4E-90	313	12.5	2.9E-90	312.6	8.7	1.1	1	E1SUM4_FERBD	Trk system potassium uptake protein	Fbal_0015	Ferrimonas balearica (strain DSM 9799 / CCM 4581 / PAT)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Ferrimonadaceae, Ferrimonas, Ferrimonas balearica, Ferrimonas balearica (strain DSM 9799 / CCM 4581 / PAT)	550540	>tr|E1SUM4|E1SUM4_FERBD Trk system potassium uptake protein OS=Ferrimonas balearica (strain DSM 9799 / CCM 4581 / PAT) GN=Fbal_0015 PE=3 SV=1MEYRTITRIIGLLVALFSTTMLPPALIAVIYKDGGGTTFVQAFVLSLVLGLLLWYPNRDAKQELRSREGFLIVVLFWTVLGSIGAIPL VLADSPNLSFTDAMFEAFSALTTTGATVITGLDNLPKAILFYRHLLQWLGGMGIIVLAVAVLPMLGVGGMQLYRCETPGPVKDNKMTP RIAETAKALWYIYLTLTIACALAYWLAGMNLFDAVGHAFSTVSIGGFSSYDASMGHFDSRLINAICVVFLLIAGVNFSLHFTAFGRRGVN LKTYFRDTEVKVFLGFQLGVTAICFLVLLNSGIYDSPESTLDHAMFQAVSISTTAGFATQSFSEWPLFLPILLILASFIGGCAGSTGGGM KVVRIVLLLKQGGREVKRLIHPRAMYAIRLNNKAVGDRVIDAVWGFFAAYAGLFALFMVALIATGMDDITAFSATVACLNNLGPGLGAV ASHFGDITDTAKWLLVLAMLFGRLEIFTLLVLFSPAFWKS

3E-90	313	5.2	3E-90	312.5	3.6	1.3	1	G4T4T9_PIRID	Related to potassium transporter TRK-1	PIIN_00119	Piriformospora indica (strain DSM 11827)	861	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Sebacinales, Sebacinales group B, Piriformospora, Piriformospora indica, Piriformospora indica (strain DSM 11827)	1109443	>tr|G4T4T9|G4T4T9_PIRID Related to potassium transporter TRK-1 OS=Piriformospora indica (strain DSM 11827) GN=PIIN_00119 PE=4 SV=1MTVNGLSTINLSTLTGFQQALMYILMCAGHPIAVSLIIIQSRMWMFEEHLEPLVRKRREEREARKLRRGESKWSTRILTRIKTWTK RDEAKVDVELAETDGDSTSVKRGRLRASMIRRVNNAPQRINPSGLVMDSRMAEAVSQPPPTIEASPPILHESPRSMPTQISQESPPAI EIRQATGDNEASPGDSTVMYRSPTISLANRRPTRDIRQNSIMAEDKATTSAFPHSQTIEFSLSKPARTTSIDREAKRDFSSFSMQGHSE RKERQMSHPVDTMSRSYGGPGLDRYPSRVATTFPRTMTGASQRRKGSKHTGFGGFPTPYRLLIKFVSWMAPGLAERIRLRLTVPRT PSMAFKNTKSMAAETIEAALQTEHKLIEKDLEFLGGVEYKSLKLLRLIVLSYHIGIQVIGMAIIVGEASRKKWLPAFEAQPRFVPPAWFAV FQATSAYTNTGTSLMDLSMIPFQGATLMIITMFILILAGNTAFPIFLRLIIWGIKKATDANAPIQSQLHFLLAHPRRCFIYLFPSHQTWFLLT MIVTLTITDWVCFLVLDIGNPVTEAVPVGTRVLIGLLQASAVRAAGFATISISALAPAVKVLYVIMMYVSIYPVALSVRASNEYEERSLGIF VEPDNDSESSSLLSQEREFGKRTGVSRRKIWGEYLVWHAKQQLAFDMWWLALALWLICIIERGPLSDNTELRWFDIFTVIFELVSAYG TVGLSLGVPFDNFSTSGAFKPLSKLIMCAVMVRGRHRGLPVAIDRAIVLPSEYNKENAFMPPFEGFNSLGAGEMSHGRVSSIKPSNPP VEPEPHIPKMHLEAVPESGQPSPAMKPMQDGRPISPSALSFSTQDTREASTTRDGSTPQK
3.9E-90	312	16.1	6.5E-90	311.4	11.1	1.3	1	A8GCS4_SERP5	Trk system potassium uptake protein	Spro_1811	Serratia proteamaculans (strain 568)	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia proteamaculans, Serratia proteamaculans (strain 568)	399741	>tr|A8GCS4|A8GCS4_SERP5 Trk system potassium uptake protein OS=Serratia proteamaculans (strain 568) GN=Spro_1811 PE=3 SV=1MVKNKQILVVIHLCSFLVFLYSLSMIPPLLVALLYKEKSVFSFFYTLVIAGSLGGLGWFSTRQSRVQLRTQDGFLIIVLFWLLFSMV SALPLWMDDTLNISLTDAMFEGVSGITTTGASVLNDVSGLPKSFLYYRSQLNFIGGLGVIVLAVAVLPLLGIGGAKLYQSEMPGPFKEE RLTPRLADTSKNLWLIYLGLGLACTVAFRIAGMQWFDALCHGISTVSLGGFSTRNESLGFYDSSAVEMVGGIFSILAAVNFTLYFVVVG RRSLKPLYRNPELRFFLLVLSIIVAIVCFELYRSGMYGAKDSFVHGFFLTSSMMTDNGLATADYAKMPSHTIMLLLAASFFGGCVGSTC GGIKALRFLIMYKQSRHEINQLVHPNAIFTIKVGNAPIQDRVLRSVWSFFFLYVFFSCFFVWLLNLMGYDLVTSFATVAACINNMGLGF GETAAGFGTLSDAAKWLMCSAMLLGRLEIYPMLILCSRAFWRF
4.1E-90	312	10.4	1.7E-88	306.7	2.2	2.1	2	B8M0P0_TALSN	Potassium transporter, putative	TSTA_086560	Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum)	717	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Trichocomaceae, Talaromyces, Talaromyces stipitatus, Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium stipitatum)	441959	>tr|B8M0P0|B8M0P0_TALSN Potassium transporter, putative OS=Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) GN=TSTA_086560 PE=4 SV=1MTVPKRKAIRRMANLLPPLNFLTLHHAYFIVMGLIWSVIFWAAASPVQTVRYIDALFLCVSAMTGAGLNTINLSTVNSFQQAILFG LIVLGHPILISSTVLFVRKRAFESRFRSIVQAGERRRLAALQGVNLPKIEKRVLTGEGNNACPINGDSAGNRETTDGPIQLSSETGQTNT QTHSQSDMNDADAIRWADDDQLTIQSRSRNKIRHRVFPMAGVGARPDARDPKDAAPSFVADDERRSSLLEIITRNPQKYFASKGLISR NSQFHGLTASERDKLGGVEYRAICFLSIIVPLYFVLFNVLGFIGLGTWFAVNRPSVARENGLSPFWTGSFLAISAFGNNGMSLLDANMT ALQTCSYVLLTMGLLILAGNTLYPCFLRFSIWTMKHVLPRTKWCEEWNAVLDFILDHPRRVYTHLFPKRHTWYLLATIILFNGIDWAGF EVLSINNTAVEILGGYRVLDGLFQAFAVRSGGFYVVTIADLHQGLLVLYVLMMYVSAFPVLVTIRNTNVYEERSLGIYADDYLAEDQRY HARLGSFVGHTKAIISHGSNGKQSQKADSNPSTGQAGENNTSRSYFVRQQIRSQLSHDIWWICLAILFITIAEGPHFTKDPISYSTFNIIF EVVSGYGCVGISVGLPDQNYSFCGGWYTISKLILIAVMLRGRHRGLPVAIDKAVMLPDESLAWAEEEDAAMRLERARSRSVAQGPIY DEKTDDIV
4.5E-90	312	18.3	2.3E-89	309.6	12.7	1.8	1	A0A0F7JZ49_9GAMM	Trk system potassium uptake protein	AAY24_12305	Sedimenticola sp. SIP-G1	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, Sedimenticola, Sedimenticola sp. SIP-G1	1543721	>tr|A0A0F7JZ49|A0A0F7JZ49_9GAMM Trk system potassium uptake protein OS=Sedimenticola sp. SIP-G1 GN=AAY24_12305 PE=3 SV=1MKFSAIQRILGILLMLFSGTMLPPLAVSLWYDDGAYSAFLIAFVIILMVGGISWVMVSDQRRELRLRDGFMVVVLFWTVLGITGAL PLSLSDHPHLSLTDAVFESISGLTTTGSTVIIGLDELPRSILYYRQQLQWLGGMGIIVLAVAVLPMLGIGGMQLYRAETPGPMKDTKLTP RITETAKALWFIYMGLTIACLLGYWAAGMSLFDAIGHAFSTVAIGGFSTHDASIGYFDSTLIEMIAVLFLLLSGVNFALHFIAINRRNLRVY LVDSEFLFYLMVLLFVAVLVVVTLHTTGTYDSWGEAFTKGLFQAVSIGTTAGFTTADYSLWPGFIAILLLFASFIGGCAGSTGGGIKVIR FLLLIKQGMREITRLIHPSAQIPIRVGGKTITPRVVEAVWGFFALYVASFTFMYLALALTGLDLMTSFSAVAASINNLGPGLAGVGLNYAS INDPAKWILCFAMLLGRLEIFTLLVLLSPAYWRK
7.6E-90	311	13.9	1.1E-89	310.7	9.6	1.2	1	A7MQN7_CROS8	Trk system potassium uptake protein	ESA_03711	Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cronobacter, Cronobacter sakazakii (Enterobacter sakazakii), Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	290339	>tr|A7MQN7|A7MQN7_CROS8 Trk system potassium uptake protein OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=ESA_03711 PE=3 SV=1MHFRAITRIVGLLVILFSGTMIIPGLVALLYRDGAGRAFTQTFFVALAIGAALWWPNRHQKRELKSREGFLIVVLFWTVLGSVGAL PFIFSERPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFATIAIGGFSTHDASVGYFASPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVYS RDPEFRMFIGVQLTLVFICTLVLWFHDTYDSAITTLNQAFFQVVSMATTAGFTTDSIAKWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRI LLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFLVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFAS MNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
7.9E-90	311	16.9	2.4E-89	309.5	11.7	1.6	1	A0A090UJJ6_9ENTR	Trk system potassium uptake protein	trkH CIFAM_25_00210	Citrobacter farmeri GTC 1319	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter farmeri, Citrobacter farmeri GTC 1319	1114922	>tr|A0A090UJJ6|A0A090UJJ6_9ENTR Trk system potassium uptake protein OS=Citrobacter farmeri GTC 1319 GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFVALVIGSMLWWPNRREKGELKSREGFLIVVLFWTVLGSVGAL PFIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFATIAIGGFSTHDASVGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVY WRDPEFRMFIGVQLTLVVICTLVLWFHNIYSSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVI RILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNF ASMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE

8.3E-90	311	14.6	1.3E-89	310.4	10.1	1.3	1	A0A089PGI5_PLUGE	Trk system potassium uptake protein	ABW06_20145 ABW07_20735 ABW08_21095 ABW09_20915 ABW10_19735 ABW11_21715 ABW12_22115 ABW13_20715 LG71_05255 SS31_24840	Pluralibacter gergoviae (Enterobacter gergoviae)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pluralibacter, Pluralibacter gergoviae (Enterobacter gergoviae)	61647	>tr|A0A089PGI5|A0A089PGI5_PLUGE Trk system potassium uptake protein OS=Pluralibacter gergoviae GN=ABW06_20145 PE=3 SV=1MHFRAITRIVGLLVILFSGTMIVPGLVALIYRDGAGRAFTQTFFVALAIGSLLWWPNRREKGELKSREGFLIVVLFWTVLGSVAALPFIFAEQPHLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFATISIGGFSTHDASVGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVYGRDPEFRMFIGVQLTLVFICTLVLWFHDVYSSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLFSAFIGGCAGSTGGGLKVIRILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIISMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFASMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
1.1E-89	311	15.3	4.9E-89	308.5	10.6	1.7	1	Q48AT3_COLP3	Trk system potassium uptake protein	trkH CPS_0015	Colwellia psychrerythraea (strain 34H / ATCC BAA-681) (Vibrio psychroerythus)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Colwelliaceae, Colwellia, Colwellia psychrerythraea (Vibrio psychroerythus), Colwellia psychrerythraea (strain 34H / ATCC BAA-681) (Vibrio psychroerythus)	167879	>tr|Q48AT3|Q48AT3_COLP3 Trk system potassium uptake protein OS=Colwellia psychrerythraea (strain 34H / ATCC BAA-681) GN=trkH PE=3 SV=1MQYKNIIRILGLLVGLLSVTMLPPALISLIYRDGGGLPFILAFLWCICTGFLAWYPHRFEKTDLKAREGFLIVVLFWLVLASFSAIPLMLLEEPNLSTADAFFESFSGLTTTGATILNHIDDLPHAVLWYRQQLQWLGGMGIIVLAVAVLPMLGIGGMQLYRAETPGPVKDSKMTPRIADTAKHLWYIYLGLTIACALAYWLAGMSGFDAICHAFSTIAIGGFSTHDASMGYFNSPTINLVCVTFLLIAGVNFALHYAAVQSRSVRSYFFDPEFKVFIGIQIVLTVICFTVLLATGTYQDVDQALDQALFQSVSISTTAGFATTSFADWPTLLPMLLIFSSFIGGCAGSTGGGMKVVRVVLLYLQGLRELNKLVHPRAIFSIKLGRKVLPDRIVEAVWGFFSAYAAVFVICMLLLLAAGMDDITAFTAVAACINNLGPGLGEVAANFSSINDMSKWVLIMAMLFGRLEIFTLLVLFTPAFWRS
1.3E-89	310	15.7	1.3E-89	310.4	10.9	1.7	1	C5BCB8_EDWI9	Trk system potassium uptake protein	NT01EI_0154	Edwardsiella ictaluri (strain 93-146)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Edwardsiella, Edwardsiella ictaluri, Edwardsiella ictaluri (strain 93-146)	634503	>tr|C5BCB8|C5BCB8_EDWI9 Trk system potassium uptake protein OS=Edwardsiella ictaluri (strain 93-146) GN=NT01EI_0154 PE=3 SV=1MHFRAIIRIVGLLVILFSGTMFVPGLVALIYRDGAGRAFVETFFVALGIGMLLWWPQRKQKHELKPREGFLIVVLFWTVLGSVGALPFLFSERPNLSVTDAFFESFSGLTTTGATTLVGLDALPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGLQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVMLTIACAIALWGAGMDVFDAISHSFSTIAIGGFSTHDASIGYFNSPTINTIIAAVFLLISGCNFSLHFAFLSGRSPRVVYWRDPEFRMFIAVQLTLVSVCTLVLWLHNVYASGWQTFNQAFFQVVSMATTAGFTTDSIAKWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRILLLLFLQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFIISMLAIIATGVDDFSAFAAVVATLNNLGPGLGVVADNFTSMNDVAKWILVVTMLFGRLEVFTLLVLFTPTFWRN
1.7E-89	310	14.8	2.2E-89	309.6	10.3	1.1	1	I2BE28_SHIBC	Trk system potassium uptake protein	trkH2 EBL_c37430	Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Shimwellia, Shimwellia blattae (Escherichia blattae), Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	630626	>tr|I2BE28|I2BE28_SHIBC Trk system potassium uptake protein OS=Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) GN=trkH2 PE=3 SV=1MHFRAITRIVGLLVILFSGTMIVPGLVALLYRDGAGRAFTQTFFVTLAIGVLLWWPHRREKSELKPREGFLIVVLFWTVLGSVGSLPFVFAEQPNLTVTDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIGCAVALWFAGMPAFDAIGHSFATIAIGGFSTHDASVGYFNSPTINSIIAIFLLISGCNYGLHFSLLSGRSLKVYWRDPEFRMFIGVQFSLVVICTIVLWFHNTYGSVVQTVNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFILSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADNFTTMNPVAKWILIINMLFGRLEVFTLLVLFTPTFWRE
1.8E-89	310	1.5	4.9E-85	295.3	0.3	2.1	2	H6BVL6_EXODN	Putative uncharacterized protein	HMPREF1120_03231	Exophiala dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) (Black yeast) (Wangiella dermatitidis)	803	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Chaetothyriomycetidae, Chaetothyriales (black yeasts), Herpotrichiellaceae, Exophiala, Exophiala dermatitidis (Black yeast) (Wangiella dermatitidis), Exophiala dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) (Black yeast) (Wangiella dermatitidis)	858893	>tr|H6BVL6|H6BVL6_EXODN Putative uncharacterized protein OS=Exophiala dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) GN=HMPREF1120_03231 PE=4 SV=1MCNEKVKPLGRVSAQIRTLFDRHVRPSLPAASFINLHYLYFGVTCLLASIIFWGSSTPPRSVSYIDSLFLCISAMTEAGLNTVNLSTLNTWQQVILFLLIIIGSAIWVSIGVLYVRKRAFERKFAELAARRRKRLQRPRSFNFSFSKRKTSMSDADHVAAVASGAVRGRAIPNDQVDHEHKRSDSLSHHRSPSDERLRMSKTATGTDEGDNPERAGHIRFRADVAAGDHADYLPHPIRRHRTSFLEGSGVGAKGLDNHPRNARPVDYYNDHADESEVDGEFLSRSRKPINKYLDTVNGYLGRNSQFHHLSDKERKKLGGIEYDAICLLSWVVPVYFVLFQLLGALGVGAWIKVNRPGVSLKNGLDPFWTGAFFAISAFNNSGMALLDANATAVQTSYYVLLTLSLLILAGNTCFPPFLRLVLWTMKNLIPKSWNSAEWQVRRRTLEFCLDHPRRVYTNLFPKAQTWWLVFSVVMLNGIDWLAFELLNIGNPTTDSIPAHFRVLDGLFQAFAVRSGGFYVVSIAGLRSGLLVLYVLMMYISAFPVTMTIRNTNVYEERSLGLYAEDLPLSPHPQSAENGASDEKAAARPRSKNKLLHGLKKTMTMTHGQSISSPMNKATFPTSWTRQDFVRQQLRSQLGHDLWWIALAIFVITSIETGQFERDPVVFSTFNIIFEVTSAYGCVGISTGVPWNAYSFCGAWHTASKLVLCAVMLRGRHRGLPVSIDRAILLPDESLAWAEEEDAHKRRASFHSTTAAATATGLGMVPSRPSMSTREGLTRPRTASFGAPGPSVRQETERDVGDMV

2.1E-89	310	1.9	5.7E-67	235.7	0	2.4	2	N4TYS3_FUSC1	Low-affinity potassium transport protein	FOC1_g10013622	Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	887	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. cubense, Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	1229664	>tr|N4TYS3|N4TYS3_FUSC1 Low-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 1) GN=FOC1_g10013622 PE=4 SV=1MAHPGSPLSLFLGFCLRIFLNVTKVTNGLLFSLEDMLDETRASVWARLKAVKPPFMSKKPHFNFISVHYTWIIGATLLASVIIYGA GRGQTSYVDSLMFASGANTQAGLNPIDVNLLNTFQQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRP RSEAREAEEGVNGRHITVVPYQGRPPRITNDGILLDGNDVIQSQAIADDDDDDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKPD QGFGDGREANEGQSRSQNAPTGIKFAETVKRSDGVDDDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDND DTQDGDDDNNTIAMTRTVESRPDHATLDSRAPTGRRPTIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNES TMGRAFRTRTIDTIKSALSNDHTKDMPYLSYTPTMGRNSNFVGLTLEQREELGGIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEK YGRIVEGNAISRSFNDLGLTLTPDSMNSFNTSECMQLVSPSLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAIPVLYMI MMYISIFPIAISIRRTNVYEEKSLGVYHNKKDEDEEESASALNYVGTHLRRQLSFDLWYVFVGFFLLAISEGESLKAKDFNLFDVLFEVIS AYGTVGLSMGVPNVNASLCSQFTVVGKLIIVAMQIRGRHRGLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMGTTSGMEPPI SPGLPGRRGSMGRIRERANSRIISQFLYPGPVIPSNEIHGHKRATSNNSNNMRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAE TNPMP
2.1E-89	310	14.7	3.4E-89	309	10.2	1.3	1	G9YXV0_9ENTR	Trk system potassium uptake protein	HMPREF0880_00033	Yokenella regensburgei ATCC 43003	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yokenella, Yokenella regensburgei, Yokenella regensburgei ATCC 43003	1002368	>tr|G9YXV0|G9YXV0_9ENTR Trk system potassium uptake protein OS=Yokenella regensburgei ATCC 43003 GN=HMPREF0880_00033 PE=3 SV=1MHFRAITRIVGLLVILFSGTMIVPGLVALIYRDGAGRAFTQTFFVALAIGSLLWWPNRREKRELKSREGFLIVVLFWTVLGSVGAL PFIFAEQPNLTVTDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMR PRIAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFATIAIGGFSTHDASVGFFNSPTINTIIAVFLLISGCNYGLHFSLLSGRSLKV YWRDPEFRMFIGVQLTLVICTLMLWFHNVYGSALMTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLK VIRILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNF ASMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE	
2.4E-89	310	0	3.1E-89	309.2	0	1.1	1	M7T6I2_EUTLA	Putative cation transporter protein	UCREL1_7595	Eutypa lata (strain UCR-EL1) (Grapevine dieback disease fungus) (Eutypa armeniacae)	666	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomycota, Pezizomycotina, leotiomyceta, sordariomycota, Sordariomycetes, Xylariomycetidae, Xylariales, Diatrypaceae, Eutypa, Eutypa lata, Eutypa lata (strain UCR-EL1) (Grapevine dieback disease fungus) (Eutypa armeniacae)	1287681	>tr|M7T6I2|M7T6I2_EUTLA Putative cation transporter protein OS=Eutypa lata (strain UCR-EL1) GN=UCREL1_7595 PE=4 SV=1MTTWQQIMLWLLIVIGSSMWVSIWTILVRKHAFERRFREIVRRENERRLESRGSHSVLPLTERLRSLGRSQSRHITGGHGSVPE LEPGPVTRDTAGNILPISQPADGRLIGSKVPSSKDDPLTNGVNEEDVKPMPSPRSAPVGRADHVVFAADPRENAISTSVAPENTAIRR QVPSNNEELKGSTAFWRHGFLPSGKVKRNAQFHNLTSHERESLGGTEYRALKLLSVLVPMYWFIWQFLGSISLGAWIANNQPQPAK DNAIGPWWNGIFNGVSAFNNSGMSVLDANMVPYNSSYFVLIVMGLLILAGNTAYPIYLRLILWSGLKILNKATYPDQLVEWKTTLEYILK YPRRVYTNLFPSRQTWWLLFMLFVLNGTDWIAYEVLNLGNAALESTPLGPRIIDGLFQALAVRSGGFYVVPIPTLYIGLQVLYVIMMYIS VYPVVITMRHSNVYEERSLGIYGDDDSSEPEQQPPESSLPLSRHLSNRSTASRRQQAVGSVLRRTLTTAWGGVGAAPPSLPESGFD FVSHQVRSQLSHDIWWLVLAILVIVIIETRHFIEDPVHASVFNVVFEVVSAYGCVGITVGVPYDAYSFSGSWYPGSKLVLCLVMLRGRH RGLPVALDRAVRLPGDDLREEEGGDGGLRRYQTRGSVRSLSARRPSLGGGSRV	
2.5E-89	309	17.1	1.7E-88	306.7	11.9	1.9	1	A9MIW9_SALAR	Trk system potassium uptake protein	SARI_03673	Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica subsp. arizonae, Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	41514	>tr|A9MIW9|A9MIW9_SALAR Trk system potassium uptake protein OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=SARI_03673 PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFVALAIGSILWWPNRREKGELKSREGFLIVVLFWTVLGSVGALP FIFSESPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPR IAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFATIAIGGFSMHDASIGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVYW RDPEFRMFIGVQLTLVVICTMVLWFHNIYDSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRI LLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFAS MNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
2.8E-89	309	15.8	5.9E-89	308.2	11	1.5	1	L0MBV8_ENTBF	Trk system potassium uptake protein	D782_4306	Enterobacteriaceae bacterium (strain FGI 57)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, unclassified Enterobacteriaceae (miscellaneous), Enterobacteriaceae bacterium (strain FGI 57)	693444	>tr|L0MBV8|L0MBV8_ENTBF Trk system potassium uptake protein OS=Enterobacteriaceae bacterium (strain FGI 57) GN=D782_4306 PE=3 SV=1MHFRAITRIVGLLVILFSGTMILPGLVALIYRDGAGRAFTQTFFVALVIGSLLWWPNRREKGELKSREGFLIVVLFWTVLGSVGAL PFIFSEQPNLTITDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTVACALALWFAGMPAFDAIGHSFATIAIGGFSTHDASVGYFDSPTINTIIAIFLLISGCNYGLHFSLLSGRSLKVY WRDPEFRMFIGVQLTLVFICTLVLFFHNVYSSALTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVI RILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIISMLAIIATGVDDFSAFASVVATLNNLGPGLGVVADNFA SMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE
2.8E-89	309	15.1	3.9E-89	308.8	10.5	1.1	1	Q7CKU4_YERPE	Trk system potassium uptake protein	trkH y0468 YP_3285 YPO3762	Yersinia pestis	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia pseudotuberculosis complex, Yersinia pestis	632	>tr|Q7CKU4|Q7CKU4_YERPE Trk system potassium uptake protein OS=Yersinia pestis GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMFIPGLVALIYRDGAGRAFSETFFVAVSIGLLLWLPNRKQKHELKPREGFLIVVLFWTVLGSVGALP FLFSERPNLSLTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTIACALALWGAGMSVFDAISHSFSTIAIGGFSTHDASIGYFNSPTINTIIGIFLLISGCNFGLHFAVLSGRSLKVYW RDPEFRMFIFVQLTLVIVCTLVLWQHSVYKSGIETLNQAFFQVVSMATTAGFTTDSIAKWPLFLPLLLLCSAFIGGCAGSTGGGLKVIRI LLLYLQGSRELKRLVHPNAVYTIKLGRRALPERILEAVWGFFSAYALVFIISMLAIVATGVDEFSAFAAVTATLNNLGPGLGVVADNFTS MNPAAKWILVITMLFGRLEVFTLLVLFTPTFWRE
3.4E-89	309	15.3	5.8E-89	308.3	10.6	1.2	1	D2YTI0_VIBMI	Trk system potassium uptake protein	VMD_30640	Vibrio mimicus VM573	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio mimicus, Vibrio mimicus VM573	671076	>tr|D2YTI0|D2YTI0_VIBMI Trk system potassium uptake protein OS=Vibrio mimicus VM573 GN=VMD_30640 PE=3 SV=1MQFRSIIRIVGLLLALFSVSMLAPALVALIYRDGAGVPFVSTFFVLLLCGGLFWFPNRHHKHELKARDGFLIVVLFWTVIGSAGSLP FLLAADPNISVTDAFFESFSALTTTGATVIVGLDELPKAILFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDTKVTPRIA ETAKALWYIYLSLTIACAAAFWLAGMTLFDAICHSFSTIAIGGFSTHDASIGYFDSYAINLITVIFLLISSCNFTLHYAAFASGGVHPKYYW RDPEFRAFFVIQILLFVICFSVLLKHHAYDSFYQAFDQALFQTVSISTTAGFTTTGFSDWPLFLPVLLLFSSFIGGCAGSTGGGMKVIRV LLLTLQGAREMKRLVHPRAIYPIKLGGRALSQRVVDAVWGFFSAYALVFVVCMLALIATGMDELSAFSAVAATLNNLGPGLGEVAVHF ADVNDKAKWILIASMLFGRLEIFTLLILLTPTFWRS
3.6E-89	309	23.6	4.3E-89	308.7	16.4	1	1	M4U7T4_9GAMM	Trk system potassium uptake protein	PCNPT3_12510	Psychromonas sp. CNPT3	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Psychromonadaceae, Psychromonas, Psychromonas sp. CNPT3	314282	>tr|M4U7T4|M4U7T4_9GAMM Trk system potassium uptake protein OS=Psychromonas sp. CNPT3 GN=PCNPT3_12510 PE=3 SV=1MAFRSIIRIVGLLIGLFSLTMLPPVFVASIYQDGGGDDFLAAFAVTLFISFLLWAPNRHKKTELRVRDGFLIVVIFWITLGSVGAIPFL MSSRIEMSVASAFFESFSGLTTTGATVIEYLDSLPKSILFYRQMLQWFGGMGIIVLAVAILPMLGVGGMQLYRAETPGPIKDTKMTPRIA ETAKALWYIYLCLTVACMLAFWLAGMSLFDALGHSFSTVSIGGFSTHDASIGYFNSDIINTITVVFLLISGVNYALHFSAFSAPKFSLNIY KRDPEVRMFLYIQIILTSICFITLMNHQVYTSIERTFSQALFQAVSISTTAGFSTTSFSNWPLFLPVLLVLSSFIGGCAGSTGGGLKVIRILL LNLQGLRELKRLVHPKAVYKIKLANKAVPDRVIEAVWGFFSTYALVFIVCMLALAMTGMDELSSFSATVAMLNNLGPGLGQVAVHFNE VNESSKWIMIIAMLFGRLEIFTLLVLFTPVFWKN

3.7E-89	309	16.4	6.5E-89	308.1	11.3	1.3	1	U3U042_9ENTR	Trk system potassium uptake protein	E05_20110	Plautia stali symbiont	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, unclassified Enterobacteriaceae (miscellaneous), Plautia stali symbiont	891974	>tr|U3U042|U3U042_9ENTR Trk system potassium uptake protein OS=Plautia stali symbiont GN=E05_20110 PE=3 SV=1MHFRAITRIVGLLVILFSVTMILPGLVALIYRDGAGRAFSQTFMMAIVIGSLLWWPNRKQKSELKPREGFLIVVLFWTVLGSVGAMPFIFAEQPHLSVTDAFFESFSGLTTTGATTLVGLYSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTVACALALWLAGMPMFDAIGHSFSTIAIGGFSTHDASIGYFNSPTINTIVAIFLLISGCNYGLHFSLLSGRNLKVYWRDPEFRMFIGVQLTLVLICTLVLWFHNVYSSGWQTLNQAFFQVVSMATTAGFTTDSIARWPLFLRVLLLCSAFIGGMAGSTGGGLKVIRILLLCKQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFLVSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADNFTSMNDVAKWILISTMLFGRLEVFTLLVLFTPNFWRE	
5.3E-89	308	17.4	1.3E-88	307.1	12.1	1.5	1	A0A068R4F9_9ENTR	Trk system potassium uptake protein	trkG XPG1_2432	Xenorhabdus poinarii	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus poinarii	40577	>tr|A0A068R4F9|A0A068R4F9_9ENTR Trk system potassium uptake protein OS=Xenorhabdus poinarii GN=trkG PE=3 SV=1MVKKNQLLIVGHLCSFLVLLYSLSMLLPIFVALFYKEKSIFAFFETFLIGFVTGGIGWYFTRKTKAHPSTQDGFLIIVLFWLLFSLLSALPFVLDENLDINLVDAVFEGVSGITTTGATVLNNVSALPKSVLYYRAQLNFIGGLGVIVLAVAILPLLGIGGAKLYQSEMPGPFKEERLTPRLADSAKSLWVVYLLLGGLCSVSFAAAGMSWFDAICHGISTVSLGGFSTRNESLGYYDSAAIEMVGGIFSILSAVNFTLYFVALTRRSLKPLLKNAELRFFLLVLTVIILTTWLELYRSGMYGIKDAFVHGFFMTSSVMTDNGLSTSDYAQWPPHTILLLLAVSFFGGCVGSTCGGIKALRFMILTKQSVNEITQLIHPNSISTIKIGKSVVQERVLRSVWGFFFLYIFFSCFFIWALNLLGYDLVTSFATVAACINNMGIGYGATAQSFGDLDPIAKWMMCAAMLLGRLEIYPILILCSKAFWRF	
5.8E-89	308	13.5	2.1E-88	306.4	9.4	1.7	1	W0TMK2_9GAMM	Trk system potassium uptake protein	TBH_C0414	Thiolapillus brandeum	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, Thiolapillus, Thiolapillus brandeum	1076588	>tr|W0TMK2|W0TMK2_9GAMM Trk system potassium uptake protein OS=Thiolapillus brandeum GN=TBH_C0414 PE=3 SV=1MHLTVVQRILGLLLMLFSVTMLPPVLVSLGYDDGASQAFVTAFVITLVVGLISWLPVRRQHRELRLRDGFVVVVMFWTVLSATGALPFALAEHPRLSVTDAFFESISGLTTTGATVIVGLDDLPKSILYYRQQLQWLGGMGIIVLAVAVLPMLGIGGMQLYRAETPGPIKDSKLTPRITETAKALWYIYLGLTLACVLGYWLAGMTPFDAVAHAFSTVAIGGFSTHDASMGYFNNTAIYLVGVLFMFLAGVNFALHFSVVRQKSLKVYWRDSEFRFYLLLMVLVIVVTTGGLHYHATHGSFHENFVHGLFQAVSIGTTAGFTTAEWHNWPGFIAILLLFSSFVGGCAGSTGGGIKVIRFLLLIKQGMREITRLVHPNAQIPVRVGNKSIPPRVVEAVWGFFALYVASFTLMYLLLAATGIDLMTAFSAVAASINNLGPGLGNVGANYAGLHDPAKWILCFAMLLGRLEIFTLLVLLTPVFWRH	
6.2E-89	308	16.5	7.8E-89	307.8	11.5	1.1	1	A8GYG3_SHEPA	Trk system potassium uptake protein	Spea_0021	Shewanella pealeana (strain ATCC 700345 / ANG-SQ1)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella pealeana, Shewanella pealeana (strain ATCC 700345 / ANG-SQ1)	398579	>tr|A8GYG3|A8GYG3_SHEPA Trk system potassium uptake protein OS=Shewanella pealeana (strain ATCC 700345 / ANG-SQ1) GN=Spea_0021 PE=3 SV=1MQYRTIIRITGLLMGLFSLSLLPPALVAVIYKDGGGMAFIQAFVLCLILGFGLWYPNRAHRKDLRTREGFLLVVMFWVVLGSIGAVPFIFSGQPSLSLTDSFFESFSALTTTGATVIVGLDSLPKAILFYRHLLQWLGGMGIIVLAVAILPVLGVGGMQLYRAEMPGPVKDSKMTPRIAETAKALWYIYLALTVACAVAYWLAGMDTFDAICHSFSTIAIGGFSTHDASMGYFDSPTINMICVVFLLIAALNFSLHFAAFSRRGINLRVYFRDAEFKVLIAIQLVLTAICFVTLYGSGIYDSAEETFDYALFQAVSISTTAGFGTESFHAWPLFLPILLIFSSFIGGSGGSTAGGIKVIRVILLLLQGSRELKRLVHPRGMFSIRISGNALPDRVIDAVWGFFSAYALVFVVCMLILMALGMDAITAFSATAACLNNLGPGLGEVASNYASIGDGEKWVLLFAMLFGRLEVFTLLILFTPTFWKN	
7.2E-89	308	15.5	1.2E-88	307.2	10.7	1.2	1	Q9KNI3_VIBCH	Trk system potassium uptake protein	VC_2756	Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio cholerae, Vibrio cholerae O1, Vibrio cholerae O1 biovar El Tor, Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	243277	>tr|Q9KNI3|Q9KNI3_VIBCH Trk system potassium uptake protein OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) GN=VC_2756 PE=3 SV=1MQFRSIIRIVGLLLALFSVSMLAPALVALIYRDGAGVPFVSTFFVLLLCGGLFWFPNRHHKHELKARDGFLIVVLFWTVIGSAGALPFLLAADPNISVTDAFFESFSALTTTGATVIVGLDELPKAILFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDTKVTPRIAETAKALWYIYLSLTIACASAFWLAGMSLFDAICHSFSTIAIGGFSTHDASMGYFDSYAINLITVVFLLISSCNFTLHYAAFATGGVHPKYYWRDPEFRAFFVIQVLLFVICFSVLLKHHSYDSFYQAFDQALFQTVSISTTAGFTTTGFSDWPLFLPVLLLFSSFIGGCAGSTGGGMKVIRVLLLTLQGAREMKRLVHPRAIYPIKLGGRALSQRVVDAVWGFFSAYALVFVVCMLALIATGMDELSAFSAVAATLNNLGPGLGEVAVHFADVNDKAKWILIASMLFGRLEIFTLLILLTPTFWRS	
8.1E-89	308	15.5	1.3E-88	307.1	10.8	1.3	1	W8UQM6_YEREN	Trk system potassium uptake protein	trkH LC20_04960	Yersinia enterocolitica LC20	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia enterocolitica, Yersinia enterocolitica LC20	1443113	>tr|W8UQM6|W8UQM6_YEREN Trk system potassium uptake protein OS=Yersinia enterocolitica LC20 GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMFIPGLVALIYRDGAGRAFSETFFVALAIGLLLWLPNRKQKHELKPREGFLIVVLFWTVLGSVGALPFLFSERPNLSLTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIACALSLWGAGMSVFDAISHSFSTIAIGGFSTHDASIGYFNSPTINTIIGIFLLISGCNFGLHFAVLSGRSLKVYWRDPEFRMFIFVQLTLVIVCTLVLWQHNVYKSGLETLNQAFFQVVSMATTAGFTTDSIAKWPLFLPILLLCSAFIGGCAGSTGGGLKVIRILLLYLQGSRELKRLVHPNAVYTIKLGRRALPERILEAVWGFFSAYALVFIISMLAIIATGVDEFSAFAAVTATLNNLGPGLGVVADNFTSMNPAAKWILVITMLFGRLEVFTLLVLFTPTFWRE	
1E-88	308	6.3	1.1E-88	307.4	2.5	1.9	1	A7F5W3_SCLS1	Putative uncharacterized protein	SS1G_12991	Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum)	717	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Sclerotiniaceae, Sclerotinia, Sclerotinia sclerotiorum (White mold) (Whetzelinia sclerotiorum), Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum)	665079	>tr|A7F5W3|A7F5W3_SCLS1 Putative uncharacterized protein OS=Sclerotinia sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) GN=SS1G_12991 PE=4 SV=1MTEAGLNTVNLSTMTIFQQVILWLLIVVGSAIFVSVATVRTRKRAFEVRFGEVVGRQKEERRRERMRSGSREAVESRRGDVGVGVGDGSGFMKDNWKFPSIGGGKNGDEDIVEMNEGLKIRPAEGKTDENCMTAISEISPLGGIPKDAGDHITFAPDAYPGNGKGAKDITVGSSNDGTSTAARSTNFQTPTSTSETNTLKHRINEINTPLRHSQTGQQDLAPLQYPSYLNSNTTGRNAQFHGLSRAEREHLGGVEYRAISFLAWLVPAYFILWQVLGGIGLGAYMAYNKSNVALENGINPWWLGVFNAISAFNNSGMSLLDLNMIPFQTSVYTLLTMGLLILAGNTAYPLFLRLILYTLLKLLDTFPNFLSPFQHHKATLLFILRYPRRVYTNLFPSRATWWLLFMVITLNSIDWIAFELLNIGNSATQVIEPRYRVLDGLFQAIAVRSGGFYIISIPTLRIGLQFLYVVMMYISVYPVVITMRHSNVYEERSLGIYTNDIDPSHHTSRIGRRMKKIKRSFSGREITTSSSEVISNSAQKDKEETTGSQFIHHQLRSQLSHDLWWLTLATFLIVCIEASSFEKDPVTYSVFNVIFEVVSAYGCVGISTGLPDQDYSFSGGLKSASKVVLVAVMVRGRHRGLPRALDRAVRLPGWEGEGLGGEGGEHRGRDDGEEEVFGEDGGNGDGGREGDRDGAEGQGLRKRRFSRGVADLEEV	
1.2E-88	307	16.1	1.7E-88	306.7	11.1	1.1	1	B7VGL6_VIBTL	Trk system potassium uptake protein	VS_0043	Vibrio tasmaniensis (strain LGP32) (Vibrio splendidus (strain Mel32))	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio tasmaniensis, Vibrio tasmaniensis (strain LGP32) (Vibrio splendidus (strain Mel32))	575788	>tr|B7VGL6|B7VGL6_VIBTL Trk system potassium uptake protein OS=Vibrio tasmaniensis (strain LGP32) GN=VS_0043 PE=3 SV=1MQFRSIIRIVGLLLALFSVSMLAPALVALIYRDGAGVPFVTTFFVLLFCGATCWFPNRRYKHELKARDGFLIVVLFWTVIGSAGALPFLIADNPSVSVTDAFFESFSALTTTGATVIVGLDDLPKAILFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIAETAKALWYIYLSLTIACAVAFWLAGMSFFDAISHSFSTIAIGGFSTHDASMGYFNSPAINMITVVFLLISACNYSLHFAAFASGGVHPKYYWKDPEFRAFIFIQVVLFLVCFSLLLNHHSYDSYYDAFDQALFQTVSISTTAGFTTTGFSEWPLFLPVLLLFSSFIGGCAGSTGGGMKVIRILLLTLQGAREMKRLVHPRAVYTIKVGGSALPQRVVDAVWGFFSAYALVFVVCMLALIATGMDELSAFSAVAATLNNLGPGLGEVAMHFGDVNDKAKWVLIVSMLFGRLEIFTLLILLTPTFWRS	
1.7E-88	307	13.4	2.7E-88	306.1	9.3	1.2	1	E1SKS7_PANVC	Trk system potassium uptake protein	trkH Pvag_3445	Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea vagans, Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	712898	>tr|E1SKS7|E1SKS7_PANVC Trk system potassium uptake protein OS=Pantoea vagans (strain C9-1) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSVTMILPGLVALIYRDGAGRAFSQTFMMALVIGSLLWWPNRKKKTELKPREGFLIVVLFWTVLGSVGAMPFIFAEQPHLSVTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTVACALALWLAGMPAFDAIGHSFSTIAIGGFSTHDASIGYFHSGTINTIVAVFLLISGCNYGLHFAMLSGRNLRVYWRDPEFRMFIGVQLTLVLICTLVLWFHNVYASGWQTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRILLLCKQGNRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFLVSMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADNFTSMNDVAKWILISTMLFGRLEVFTLLVLFTPTFWRE	

1.9E-88	307	15.4	2.9E-88	306	10.7	1.1	1	Q7MQH7_VIBVY	Trk system potassium uptake protein	VV0031	Vibrio vulnificus (strain YJ016)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio vulnificus, Vibrio vulnificus (strain YJ016)	196600	>tr|Q7MQH7|Q7MQH7_VIBVY Trk system potassium uptake protein OS=Vibrio vulnificus (strain YJ016) GN=VV0031 PE=3 SV=1MQFRSIIRIVGLLLALFSVTMLAPALVALIYRDGAGVPFVTTFFVLLFCGTVCWFPNRRHKHELKARDGFLIVVLFWTVLGSAGALPFLIADNPSISITDAFFESFSALTTTGATVIVGLDELPKAILFYRQILQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIAETAKALWYIYLSLTIACAGAFWLAGMTPFDAISHSFSTIAIGGFSTHDASMGYFDSYAINLITVIFLLISACNYSLHFAAFASGGVHPKYYWKDPEFRAFIFIQALLFVICFLLLLAHHSYDSIYDAFDQALFQTVSISTTAGFTTTGFSDWPLFLPVLLLFSSFIGGCAGSTGGGMKVIRILLLTLQGARELKRLVHPRAVYTIKVGGNALSQRVVVDAVWGFFSAYALVFVVCMLALIATGMDELTAFSAVAATLNNLGPGLGEVAVHFADVNDKAKWVLVVSMLFGRLEIFTLLILLTPTFWRS
2.1E-88	306	18.5	3.9E-88	305.5	12.8	1.3	1	D3V3V9_XENBS	Trk system potassium uptake protein	trkG XBJ1_3217	Xenorhabdus bovienii (strain SS-2004)	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus bovienii, Xenorhabdus bovienii (strain SS-2004)	406818	>tr|D3V3V9|D3V3V9_XENBS Trk system potassium uptake protein OS=Xenorhabdus bovienii (strain SS-2004) GN=trkG PE=3 SV=1MVRKNQLLIVGHLCSFLVLLYSLSMLLPIFVALFYKEKSVFAFFDTLLIGLSIGSVGWYFTRKTKAQPSTQDGFLIIVLFWLLFSLLSALPFVLDKSLNINLVDAVFEGVSGITTTGATVLNDVSALPKSMLYYRAQLNFIGGLGVIVLAVAILPLLGIGGVKLYQSEMPGPFKEERLTPRLADSAKSLWLVYLLLGALCSVSFKVAGMSWFDAVCHGISTVSLGGFSTRNESLGYYDSAAIEMVGGIFSVLAAVNFTLYFVALTRRSLKPLLKNAELKFFLLVLAAVVCIIWLELYRSGMYGVKEAFVHGFFMTSSMMTDNGLATSDYAQWPSHTILMLLAVSFFGGCVGSTCGGIKALRFLILAKQSISEINQLVHPNAISTIKVGQSSVHERVLRSVWGFFFLYVFFSCFFIWALNLLGYDLVTSFATVAACINNMGVGYGATAQGFGDLDAIAKWMMCAAMLLGRLEIYPILILCSKAFWRF
2.3E-88	306	16.3	3E-88	305.9	11.3	1.1	1	A0A068QVS1_9ENTR	Trk system potassium uptake protein	trkH XDD1_3185	Xenorhabdus doucetiae	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus doucetiae	351671	>tr|A0A068QVS1|A0A068QVS1_9ENTR Trk system potassium uptake protein OS=Xenorhabdus doucetiae GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSVTMIIPGLVALIYRDGAGRAFSQTFIFALVIGLILWVPNREQKADLKPKEGFLIVVLFWTVLGSVGALPFIFSEKPNLSITDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPLGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIACALALWGAGMSVFDAISHSFSTIAIGGFSTHDASIGFFNSPVINTIIAIFLLISGCNFGLHFAVLSGRSLKVYWRDPEFRMFITIQLALLAICMLILWQHSVYESEWEALNHAFFQVVSMATTAGFTTDTFAHWPLFLPFLLLCSAFIGGCAGSTGGGLKVIRILLFLQSGRELKRLVHPNAVYTIKLGQRALPERIIEAVWGFFSAYVLVFISMLLLIATGVDEFSAFSAIAATLNNLGPGLGAVSDNFTTMNPMAKWILVVVTMLFGRLEVFTLLVLFTPTFWRE
2.7E-88	306	17.4	3.8E-88	305.6	12.1	1.2	1	D3UZ88_XENBS	Trk system potassium uptake protein	trkH XBJ1_0521	Xenorhabdus bovienii (strain SS-2004)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus bovienii, Xenorhabdus bovienii (strain SS-2004)	406818	>tr|D3UZ88|D3UZ88_XENBS Trk system potassium uptake protein OS=Xenorhabdus bovienii (strain SS-2004) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSVTMIIPGLVALIYRDGAGRAFSQTFIFALVIGLMLWVPNRNQKHDLKPKEGFLIVVLFWTVLGSVGALPFIFSEKPNLSVTDAFFESFSGLTTTGATTLIGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPLGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIACAIALWAAGMSIFDAISHSFSTIAIGGFSTHDASIGFFNSPAINTIIAIFLLISGCNFGLHFAVLSGRSLKVYWRDPEFRMFITIQLALLVICVLILWQQSIYESGLDALNHAFFQVVSMATTAGFTTVSFADWPLFLPFLLLCSAFIGGCAGSTGGGLKVIRILLFLQGSRELKRLVHPNAVYTIKLGQRALPERIIEAVWGFFSAYVLVFISMLLLIATGVDEFSAFSAIAATLNNLGPGLGAVSDNFTTMNPAAKWILVVTMLFGRLEVFTLLVLFTPTFWRE
3.4E-88	306	14.2	9.4E-88	304.3	9.8	1.6	1	D4GGS0_PANAM	Trk system potassium uptake protein	trkH PANA_0204	Pantoea ananatis (strain LMG 20103)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea ananas (Erwinia uredovora), Pantoea ananatis (strain LMG 20103)	706191	>tr|D4GGS0|D4GGS0_PANAM Trk system potassium uptake protein OS=Pantoea ananatis (strain LMG 20103) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSVTMILPGLVALIYRDGAGRAFSQTFMMALVIGSLLWWPNRKKKTELKPREGFLIVVLFWTVLGSVGAMPFIFAEQPHLSVTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIACALALWFAGMPAFDAIGHSFSTIAIGGFSTHDASIGYFQSGTINTIVAVFLLISGCNYGLHFSLLSNRNLRAYWRDPEFRMFIGVQLTLVLICTIVLWLHNVYDSGWQTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGSTGGGLKVIRILLLCKQGNRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFLISMLAIIATGVDDFSAFAAVAATLNNLGPGLGVVADNFTSMNDVAKWILISTMLFGRLEVFTLLVLFTPTFWRE
3.7E-88	306	19	8.3E-88	304.4	13.2	1.5	1	C4K7R6_HAMD5	Trk system potassium uptake protein	trkH HDEF_2037	Hamiltonella defensa subsp. Acyrthosiphon pisum (strain 5AT)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, ant, tsetse, mealybug, aphid, etc. endosymbionts, aphid secondary symbionts, Candidatus Hamiltonella, Candidatus Hamiltonella defensa, Hamiltonella defensa subsp. Acyrthosiphon pisum (strain 5AT)	572265	>tr|C4K7R6|C4K7R6_HAMD5 Trk system potassium uptake protein OS=Hamiltonella defensa subsp. Acyrthosiphon pisum (strain 5AT) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSGTMFIPGLVALFYRDGAGKAFTQTFFVALTIGFFLWFPNRRHKSELKAREGFLIVVLFWTVLGSVGALPFLFSERPNLSVTDAFFESFSGLTTTGATTLVGLDTLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKENKMRPRIAETAKTLWLIYVVLTMACAFCLWGAGMSIFDAICHSFSTIAIGGFSTHDASIGYFDNPVINTIIAIFLLISACNFGLHFGLLSGRSLKVYCHDPEFRTFIFLQFILVILCTFVLWIHNVYQTGLTALNQAFFQVISMATTAGFSTHSIAQWPLFLPMLLLCSSFIGGCAGSTGGGLKVIRILLLYLQGSRELKKLVHPNAVYTIKLGNKVLPDRVLEGVWGFFSAYVAVFICSMLAIIATGVDEFSAFSAVTATLNNLGPGLGVLRDNFTGINAEAKWILVLTMLFGRLEVFTLLVLFTPTFWRE
4.9E-88	305	16.6	4.5E-87	302	11.5	1.9	1	C7RAD6_KANKD	Trk system potassium uptake protein	Kkor_2622	Kangiella koreensis (strain DSM 16069 / KCTC 12182 / SW-125)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Kangiella, Kangiella koreensis, Kangiella koreensis (strain DSM 16069 / KCTC 12182 / SW-125)	523791	>tr|C7RAD6|C7RAD6_KANKD Trk system potassium uptake protein OS=Kangiella koreensis (strain DSM 16069 / KCTC 12182 / SW-125) GN=Kkor_2622 PE=3 SV=1MQYATIIRILGILLMIFSITMLPPAIVSAIYEDGGGSAFISTFLLSLITGLVLFWPKRKAKAELKIRDGFLIVVLFWTVLSTFGAVPFILAQSLPVSLADAVFESFSGLTTTGATVISGLDDLPHSILFYRQQLQWLGGMGIIVLAVAILPLLGIGGMQLYRAEMPGPMKDNKLTPRIAGTAKALWYIYLGMTIACALAYWIAGMTTFDAIAHSFSTVAIGGFSTHDASIGYFDSNAIELICAFFMFIAGINFALHFISVRTLTIRPYLKDPEFKGYFAILCIVILCCTSVLLYYQEYPFTDALVKSIFHSVSIATTAGFASADFATWPTLLPVLLIFASFIGASAGSTGGGMKVIRVLLLFKQGMREIKRLIHPNGIFLIKLGKASVNDRVVQAVWGFFATYVVLFVLLMLILLADGLDQITAFSAVAACMNNLGPGLGDVAVNYSGLSDLAKYVLSFAMLLGRLEIFTLLVLFTPYFWRR
5.5E-88	305	11.8	4.1E-63	223	0.2	3	3	B8P6T3_POSPM	Predicted protein (Fragment)	POSPLDRAFT_19535	Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	730	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Postia, Postia placenta, Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	561896	>tr|B8P6T3|B8P6T3_POSPM Predicted protein (Fragment) OS=Postia placenta (strain ATCC 44394 / Madison 698-R) GN=POSPLDRAFT_19535 PE=4 SV=1HLNFYRVHILVFTFTPLIFSGIQYGANGKYPVAYIDCLFNCVSAMSVCGLASIDLSRMTAFQQALLFIQMCLGNPVLVSWVMVYIRRSFFAKKFQHIMEANIAREMSEKTQSSVKVRMLPWWRRAIRRFLPRSRDVSRTSSENGERSSYEHRGSSFARVRPEMIRRMDDAPRLVNPSGWISEGRSEPLTIDPTGNNDLVRSAIPVQSPAGPAQGLALDAERSSESEDIDDEDDTSNRSPIMPRTQTVEFAQTPLPLREARSLDRAQRQHLESITQGRSYTGNFSSHSGRRGSMRGPTLSLQQSMNSQHSGRRSSMHVPAMHSGFGGFPMPHQIASRLFSRLFPKLEHKLTRTLTLPRTRTIASQHGSLAPGARAVSYISFEATVGRNSRFRALTRDQQEELGGVEFRALSALLWIVGGYHILTQLLGFMVISSYMSISRWSDDFKIPQLYRDISPVWFSAFQAVSAYTNAGMSLEDESMVPFQRAYPTILAMIFLILAGNTAFVGLQFLLHATDWFFFLVLDLGNSAVTSIPIGVRIIDGLLQAVAVRAAGFSVVTLSDLVPAVKVLYVIMMYVSVYPVAMSVRSTNVYEEKSLGVFEDEDESIDVDETFTPSGNRMTVWSRYLGQHMRKQLSFDMWWLGTALFLICIIEKDKLQDDANATWFNIFRILFETVSAYGGVGLSLGVPYDNYSFCGAFNPLSKLIICAVMLRGRHRGLPVAIDRAVMLPMEY

5.6E-88	305	21	9.2E-88	304.3	14.6	1.3	1	A0KEL5_AERHH	Trk system potassium uptake protein	trkH AHA_0143	Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Aeromonas, Aeromonas hydrophila, Aeromonas hydrophila subsp. hydrophila, Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	380703	>tr|A0KEL5|A0KEL5_AERHH Trk system potassium uptake protein OS=Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240) GN=trkH PE=3 SV=1MQILSIIRIVGLLVALFSSTMLLPALVAFGYRDGGGAEFVNSFFIALLLGAALWFPNRHQKKDLRSKEGFLIVVLFWVVLGSVGALPFLLGEVPGMTVSEAFFESFSGLTTTGATVLTGLDNLPKAFLFYRQLLQWLGGMGIIVLAVAILPLLGIGGMQLYRAEIPGPVKDNKVTPRIAETAKALWFIYLLLTSLCALAYWMAGMTLFDAICHSFSTLSVGGFSTHDASIGFFNSPAINLITVVFLLLASVNFALHFMVFAHKPVRLSNYLRDSELKVFLSIQCVLVLICFVSLLFHGHYATWQEALNHGLFQAVSLGTTTGYSTTSYAEWPSFLPMLLMFSAFIGCCAGSTGGGIKVMRFMILFLQGMRELKRLVHPRAIYTLKLGRRAVPERIVEAVWGYFATYIILFFIFMLLLLMTGLNEVTAFSAVAAAFTNVGPGLGEVSANFGKISATAQWILVVAMLFGRLEIFTLLVLFTPAFWRS
7.4E-88	305	18.4	3.3E-87	302.5	12.8	1.8	1	K8WA06_9ENTR	Trk system potassium uptake protein	OO7_15683	Providencia sneebia DSM 19967	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia sneebia, Providencia sneebia DSM 19967	1141660	>tr|K8WA06|K8WA06_9ENTR Trk system potassium uptake protein OS=Providencia sneebia DSM 19967 GN=OO7_15683 PE=3 SV=1MHFRAITRIVGLLVIIFSFTMIVPGIVALIYRDGAGRAFSQTFVAALIIGLMLWIPTRNSKHELKAKEGFLIVVLFWTVLGSVGALPFIFSERPNLSVTDAFFESFSGLTTTGATTLVGLDTLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIVCAIALWLAGMDVFDAISHSFSTIAIGGFSTHDASIGYFNSPAINTIIAVFLIISGCNFGLHFAVLTGRSLGIYWKDPEFKTFISFQLVLVIICTLVLLYHAVYDSFGQTLDQAFFQVVSMATTAGFTTDSFSGWPLFLPMLLLCAAFVGGCAGSTGGGLKVIRILLLFLQGSRELKRLVHPNAVYTIKLGQRALPERIIEAVWGFFSAYALVFIVSLLILIATGVDEFSAFSAIATTLNNLGPGLGSVADNFTSMNPVGKWILVVTMLFGRLEVFTLLVLFTPTFWRD
8.9E-88	304	20.2	1.6E-87	303.5	14	1.4	1	D3VAF4_XENNA	Trk system potassium uptake protein	trkG XNC1_1325	Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus nematophila (Achromobacter nematophilus), Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	406817	>tr|D3VAF4|D3VAF4_XENNA Trk system potassium uptake protein OS=Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6) GN=trkG PE=3 SV=1MVKKNQFLIVGHLCSFLVLLYSFSMLLPIFVALFYKEKSVFAFFETFIIGLVVSGGGWYLTRKTKAQPSTQDGFLIIVLFWLLFSLISALPFVLDESLNINLVDAMFEGISGITTTGATVLNDVSALPNSVLYYRAQLNFIGGLGVIVLAVAILPLLGIGGVKLYQSEMPGPFKEERLTPRLADSAKSLWVVYLLLGGLCSISFWVAGMSWFDAVCHGISTVSLGGFSTRNESLGYYDSSAIEMVGGIFSILSAVNFTLYFIALTHRSWKPLLKNAELQFFLLVLAIIVGIIWLELYRSGMYGVKDAFVHGFFMTSSMMTDNGLATSDYAQWPPHTVLMLLAVSFFGGCVGSTCGGIKALRFMILAKQSFSEVNQLVHPNSISTIKIGKSVVQERVLRSVWGFFFLYVFFSCFFIWALNLLGYDLVTSFATVAACINNMGIGYGATVQGFGNLDAVAKWMMCAAMLLGRLEIYPILILCSKVFWRF
9E-88	304	18.4	1.3E-87	303.8	12.8	1.2	1	Q8EKR6_SHEON	Trk system potassium uptake protein	trkH SO_0024	Shewanella oneidensis (strain MR-1)	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella oneidensis, Shewanella oneidensis (strain MR-1)	211586	>tr|Q8EKR6|Q8EKR6_SHEON Trk system potassium uptake protein OS=Shewanella oneidensis (strain MR-1) GN=trkH PE=3 SV=1MQYKTIIRIIGLLIGLFSITMLPPALIAIWYNDGGGTAFIQAFFVSLFIGFWLWYPHRRCKEELRTREGFLIVVLFWTVLGSIGALPFIFSSQPDLSWTDSFFESFSALTTTGATVIVGLDSLPKAILFYRHLLQWLGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIAETAKALWYIYLLLTISCAGAYWLAGMSMFDAICHSFSTIAIGGFSTHDASMGYFNSPVINLICVFFLIVSAVNFSVHFAAFSWRGINLKVYFRDTEFKVLVAIQLLLTAICFFTLYFYSDIYDTPEETLNHALFQAVSIATTTGFGTDSFNMWPLFLPMLLMFSSFIGGCGGSTAGGIKVIRVILLLLQGSRELKRLVHPKAMFSIRIGSKALPDRIVDAVWGFFSAYALVFVLCMLALMAMGLDDITSFSATAACLNNLGPGLGEVASNYASIGDGAKWVLVVAMLFGRLEIFTLLILFTPTFWKD
1E-87	304	5.2	8.9E-84	291.2	0.2	2.1	2	K2SMW4_MACPH	Cation transporter	MPH_04632	Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	716	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Macrophomina, Macrophomina phaseolina, Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	1126212	>tr|K2SMW4|K2SMW4_MACPH Cation transporter OS=Macrophomina phaseolina (strain MS6) GN=MPH_04632 PE=4 SV=1MRDPIEEVRNPGEAKEHFLQYLKNEVFHLNFYRMHMLYFIAVILVGSVIVYGAGLADDSNQINGDSLRYIDALFLCCSAMTTTGLNSVNLGSLTGFQQAVLCILLIIGTVPFVSSFVVVIRRHYFHRKLADVVQHSRSGRQMVRDLEEQDARKHRGIEEARQDRSTSRIRRRNVPTKHRDTSERRPLRDHSRQQRRYQSRNQEKPPNRRLYHHTSGFGAFPWPWEAHNVQRLFHYPFQRLRQEWQPHDRSYISFTATYDARGRFRNLSEHERAELGGVEYRALELLLTLLIAYQLFWYAVGTAFLVPYAYRDAIATILKTSQPGDLSPGWWGFFATVTSFSNGGLNVLNSNYIPFSGNALILVISGALTVAGNTQFPILLRLLIWTLSKSVPTASRLRQTCLFLLHHPRRCFIYLFPAKETWYLLAIQLSIDLAMWILYEILNIGLPPVEAAGPLGTRILDGLFQATGLRNSGAYIIAISSLAPALLVAYLVTMYISSFPIVMALRQTNTYEERSVGLDRRHPESGGGSEGRLGVHLRRQLAYDIWFQLLAWFLICVIERAKLIGSEPGFTIFSVLFEVTSAYGTVGLSTGVPYDQYSLSGAFGAGSKVVMLGVMLRGRHRGLPLAIDRSILLPGEELMHRMDREYGEYGQWSCECEAECRRDEEQSGLGSLGPGKGLSEQDPERLREDDAGSAREGGMSSSSRTEDEDYEPHFEMT
1.3E-87	304	17.3	1.8E-87	303.3	12	1.1	1	A0A0F5AQ07_9GAMM	Trk system potassium uptake protein	WN56_09790	Salinivibrio sp. KP-1	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Salinivibrio, Salinivibrio sp. KP-1	1406902	>tr|A0A0F5AQ07|A0A0F5AQ07_9GAMM Trk system potassium uptake protein OS=Salinivibrio sp. KP-1 GN=WN56_09790 PE=3 SV=1MQFRSITRIVGLLLALFSITMLAPALVAFIYRDGAGYPFVLTFFLLLAGGGLLWFPNRNYRHELKARDGFLIVVLFWTVIGSAGAVPLMLSEQPDLSVSEAFFESFSGLTTTGATVIVGLDELPKAILFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDTKMTPRIAETAKVLWYIYLTLTVSCALAYWLAGMSAFDAIGHSFSTVAIGGFSTHDASIGHFDSTAVNLITVVFLLISACNFSLHFAAFANNGLNLKFYLRDPEFRAFLVIQFLLWLVVFTMLSGHQVYESATETFTQALFQSVSISTTAGYTTTFTFAHWPLFLPVLLLFSSFIGGCAGSTGGGMKVIRILLLSLQGTRELKRLVHPRAVYTIKVGNKALRQQVVDAVWGFFSAYALVFVICMLALIATGIEELTAFSAVAATLNNLGPGLGEVAAHFGDINDTAKWVLILAMLFGRLEIFTLLVLFTPTFWRS
1.7E-87	303	17.6	2.6E-87	302.8	12.2	1.2	1	D3VBR1_XENNA	Trk system potassium uptake protein	trkH XNC1_3872	Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus nematophila (Achromobacter nematophilus), Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	406817	>tr|D3VBR1|D3VBR1_XENNA Trk system potassium uptake protein OS=Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6) GN=trkH PE=3 SV=1MHFRAITRIVGLLVIIFSVTMIIPGLVALIYRDGAGRAFSQTFIFALVIGLILWVPNRDQKRDLKPKEGFLIVVLFWTVLGSVGALPFIFSEKPNLSITDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIACAIALWAAGMSVFDAISHSFSTIAIGGFSTHDASIGFFNSPTINTIIGIFLLISGCNFGLHFAVLSGRSLKVYWRDPEFRMFITIQLALFIVCMLILWQYSVVYESGLETLNHAFFQVVSMATTAGFTTDSFASWPLFLPFLLLCSAFIGGCAGSTGGGLKVIRILLLFLQGSRELKRLVHPNAVYTIKLGHRALPERIIEAVWGFFSAYALVFAISMLLLIATGVDEFSAFSAIAATLNNLGPGLGTVAENFTTMNPMAKWVLVVTMLFGRLEVFTLLVLFTPTFWRE
2.1E-87	303	15.8	1.9E-85	296.7	4.8	2.1	2	S2JVC7_MUCC1	Uncharacterized protein	HMPREF1544_06441	Mucor circinelloides f. circinelloides (strain 1006PhL) (Mucormycosis agent) (Calyptromyces circinelloides)	866	cellular organisms, Eukaryota, Opisthokonta, Fungi, Fungi incertae sedis, Mucoromycotina, Mucorales (pin moulds), Mucorineae, Mucoraceae, Mucor, Mucor circinelloides (Mucor griseo-roseus), Mucor circinelloides f. circinelloides, Mucor circinelloides f. circinelloides (strain 1006PhL) (Mucormycosis agent) (Calyptromyces circinelloides)	1220926	>tr|S2JVC7|S2JVC7_MUCC1 Uncharacterized protein OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_06441 PE=4 SV=1MLPILRDIGGYIEWFYHNKIHFLQLHYLYILLLSFLGSTFFYFQPGTTYAYIDALFMSTSAVTNTGLNTINMSSLSTWQALIMYFGSFFGSHVMISIIIVYVRRHYFSKRFEDILIFNKAQRLREANRRKFEKNISEMEKQRRKSTGESIKGDKPLRRRLSFISVRSSTKDEDTMPQPVTARRKKSRFSAPRPLSTGVSHFDLMAHFKKKHSQGIDTNQPMQNLNDSASETQSEGGAYEVVHPREAHVKSISHETDMTDDDISMSTLRNNSNHSEDDTLPIRASSEADNHTYPLLNATTNLSISSSSHNPNTNTSHSILFVDDGRPHHPTDTTNDDDEEHNNTVSGNQGIAFAENIERQREIAARRRLEQDRRFEDILQRIAGDAADSASAPNANSAPTDQGIMMDIETEDEEMKRIMREPIHKSELTRQQRYRIGGAEYRAIDFLTILVPIYYLFCVLGFGFFLRIYVAASTYAQGVLETTNSTGPIDPWFYSFFLSLSSFNNLGLSLVDASMVPFQSAPCILILNMILILAGNTAYAIVLRLIIWILYKITPKTYIMRRETFRYLLDHPRRCYTTLFPATQTKWLLIVLIGITAVEFITFVALNYWLPVLSGLDWGARILDGLFQSVATRNAGYSVVDLMALNPGTQIVFIVAMYISVPVAISMRNSNVYQERALGIYSGQDDDDGEYDDSNAPTFIHRLKRQPTMSSIVTTSRKVLRKPDFFVMTQIQRQLTSEICWVICCIFAICVIESESIMSSSPITMSTVIYECVSAFGNVGASTGYPNTSASQAQQYHTLSKLVLIILMYRGRHRGLPAAIDRAVLLPSEQLEQKEQEDHLLRRRNTSISVGEGNGVPVKFYNRSRTL

2.1E-87	303	14.9	3.6E-87	302.4	10.3	1.3	1	Q2NWT0_SODGM	Trk system potassium uptake protein	SG0120	Sodalis glossinidius (strain morsitans)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Sodalis (tsetse S-endosymbionts), Sodalis glossinidius, Sodalis glossinidius (strain morsitans)	343509	>tr|Q2NWT0|Q2NWT0_SODGM Trk system potassium uptake protein OS=Sodalis glossinidius (strain morsitans) GN=SG0120 PE=3 SV=1MHFRTITRIVGLLVTLFSVTMIIPGLVALIYRDGAGSVFAQTFFCAQAIGLLLWFPNRRQKSELKSREGFLIVVLFWTVLGSVGALP FLFAEHPNLSVTDAFFESFSGLTTTGATALVGLDTLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVALTIACALALWGAGMPAFDAISHSFSTIAIGGFSTHDASIGYYHSPLINTIVAIFLLISGCNYGLHFAALSGRNLKVY WRDPEFRMFIAVQLTLVVVCILILWRYDVYANSLQTLNQAFFQVVSMATTAGFTTDGIAQWPLFLPILLLCSAFIGGCAGSTGGGLKVI RILLLYLQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFILSMVAVVATGVDNFSAFAAVAATLNNLGPGLGVVADNF TSMNAVAKWILILTMLFGRLEVFTLLVLFTPTFWRE	
2.3E-87	303	17.8	1.4E-86	300.4	12.3	1.8	1	A0A0F5V883_9GAMM	Trk system potassium uptake protein	KY46_18340	Photobacterium halotolerans	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	265726	>tr|A0A0F5V883|A0A0F5V883_9GAMM Trk system potassium uptake protein OS=Photobacterium halotolerans GN=KY46_18340 PE=3 SV=1MQIRSIIRIVGLLLALFSVTMLVPALIALLYRDGAGFPFVVTFFILLAGGAALWLPNRHHRRELKARDGFLIVVLFWTVIGSAGAVPF ILSKNPDLSFTDSFFESFSALTTTGATVIVGLDALPKAILFYRQMLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIA ETAKTLWYIYLTLTVACAGAFWLAGMDLFDAIAHSFSTVAIGGFSTHDASIGYYNSTAINMVTVVFLLISACNFSLHFAAFSNRGHNLRT YWRDPEFKAFLVIQLILLLICYGMLMKHQTYDTWWATLDQALFQTVSISTTAGFTTTGFSEWPLFLPVLLLFSSFIGGCAGSTGGGIKVI RVLLLFLQGVRELKRLVHPRAVYTIKVGNKALPQRVVDAVWGFFSAYALVFVICMLVLVGTGMDELTAFSAVAATLNNLGPGLGQVAV HFGEVNDAAKWTLIVAMLFGRLEVFTLLVLFTPTFWRN	
2.4E-87	303	20.4	3.9E-87	302.2	14.1	1.3	1	A6VR77_MARMS	Trk system potassium uptake protein	Mmwyl1_0013	Marinomonas sp. (strain MWYL1)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Marinomonas, Marinomonas sp. (strain MWYL1)	400668	>tr|A6VR77|A6VR77_MARMS Trk system potassium uptake protein OS=Marinomonas sp. (strain MWYL1) GN=Mmwyl1_0013 PE=3 SV=1MHFSVILRVIGLLVMVFSVSLIPPIIVSLIYSDGALNAFLYALGVNLLGGFLLWFPVRNERGELKIRDGFLVTVLFWTVLGLFGSVPF FLAETPDLTFTDALFESISGLTTTGATILTGIDALPQSILFYRQLLTWLGGMGIIVLAVAIMPMLGIGGMQLYRAETPGPVKDTKLTPRIAE TAKALWYIYATLTSVCALGYWIAGMSLFDAICHSFSTVAIGGFSTHDESIGYFNSVAIEMICTFFMIVSAFNFALHFYAWRHKSVWHYF KDPEARFFLLILSSTVILAILVLAMTSTYDWSTSIRYAVFESVSIATTSGFSTSDFASWPHFLPFLLIVTSFVGGCASSTGGGMKVIRILLIL KQGMREIKRLIHPNAVIPVKVGGKAINERVVSAVWGFFSAYLLVYVVLMIGLMATGLDQVTAWSAVAATLNNLGPGLGDVASSFTSVS DPAKWMLCFSMLLGRLEVFTLLVLFTPMFWQK	
2.4E-87	303	19.4	5.6E-87	301.7	13.5	1.5	1	B4EWE5_PROMH	Trk system potassium uptake protein	trkH PMI3553	Proteus mirabilis (strain HI4320)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Proteus, Proteus mirabilis, Proteus mirabilis (strain HI4320)	529507	>tr|B4EWE5|B4EWE5_PROMH Trk system potassium uptake protein OS=Proteus mirabilis (strain HI4320) GN=trkH PE=3 SV=1MHFRSITRIVGLLVILFSVTMIIPGIVALIYRDGAGRAFSQTFIVALIIGLMLWIPNRNNKSDLKPKEGFLIVVLFWTVLGSVGALPFIF SEQPHLSITDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRIA ETAKALWLIYVLLTIICALALWIAGMDVFDAISHSFSTIAIGGFSTHDASIGYFNSPTINVIIGVFLLISGCNFALHFSVLTGRSLNIYWRDPE FRMFIFIQLGLVIICSLILWLYSVYDSGWTTINQAFFQVVSMATTAGFATDSFAQWPTFLPLLLLCSAFIGGCAGSTGGGLKVIRILLLFL QGSRELKRLVHPNAVYTIKLGHRALPERIIEAVWGFFSAYALVFIISLMLLIATGVDEFSAFSAIATTLNNLGPGLGIVADNFTTMNPAAK WILVVTMLFGRLEVFTLLVLFTPTFWRD	
2.7E-87	303	14	3.8E-87	302.3	9.7	1.1	1	TRKH_VIBPA	Trk system potassium uptake protein TrkH	trkH VP0032	Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio harveyi group, Vibrio parahaemolyticus, Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	223926	>sp|Q87HN7|TRKH_VIBPA Trk system potassium uptake protein TrkH OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=trkH PE=1 SV=1MQFRSIIRIVGLLLALFSVTMLAPALVALLYRDGAGVPFVTTFFVLLFCGAMCWFPNRRHKHELKSRDGFLIVVLFWTVLGSAGS LPFLIADNPNISVTDAFFESFSALTTTGATVIVGLDELPKAILFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDTKMTP RIAETAKALWYIYLSLTIACAVAFWLAGMTPFDAISHSFSTIAIGGFSTHDASMGYFDSYAINLITVVFLLISACNFTLHFAAFASGGVHPK YYWKDPEFRAFIFIQVLLFLVCFLLLLKHHSYTSPYDAFDQALFQTVSISTTAGFTTTGFADWPLFLPVLLLFSSFIGGCAGSTGGGMK VIRILLLTLQGARELKRLVHPRAVYTIKVGGSALPQRVVDAVWGFFSAYALVFVVCMLGLIATGMDELSAFSAVAATLNNLGPGLGEVA LHFGDVNDKAKWVLIVSMLFGRLEIFTLLILLTPTFWRS	
2.7E-87	303	19	4.3E-87	302.1	13.1	1.2	1	Q5E8X4_VIBF1	Trk system potassium uptake protein	trkH VF_0027	Vibrio fischeri (strain ATCC 700601 / ES114)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Aliivibrio, Aliivibrio fischeri (Vibrio fischeri), Vibrio fischeri (strain ATCC 700601 / ES114)	312309	>tr|Q5E8X4|Q5E8X4_VIBF1 Trk system potassium uptake protein OS=Vibrio fischeri (strain ATCC 700601 / ES114) GN=trkH PE=3 SV=1MQFRSIIRIVGILLAVFSFFMLAPAFIAFIYRDGAGVPFVITFFLLLAGGGALWFPNRQHKHELKSRDGFLIVVLFWMVIGSAGALP FLFSGSPDISVTNAFFESFSGLTTTGATVLTGLDHLPKAILFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRI AETAKVLWYIYLTLTIACALAFWVAGMGWFDAISHSFSTIAIGGFSTYDASMGHFNSPVINAITVVFLLISACNFSLHFAAFASGGVHPK YYWRDPEFRAFIFIQILLFLTFLLLLKHNTYNSVGTAIDQALFQTVSISTTAGFTTTSFAEWPLFLPVLLLFSSFIGGCAGSTGGGMKVIR ILLLSLQGMREIKRLIHPRAIYTIKIGTKALPQRVVDAVWGFFSAYALVFVICMLALIATGIDELTAFSAVAATLNNLGPGLGEVAVHFGEV NDAAKWILIIAMLFGRLEVFTLLILFTPTFWRS	
3.3E-87	303	16.3	4.7E-87	302	11.3	1.2	1	Q7MZ95_PHOLL	Trk system potassium uptake protein	trkH plu4399	Photorhabdus luminescens subsp. laumondii (strain TT01)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Photorhabdus, Photorhabdus luminescens (Xenorhabdus luminescens), Photorhabdus luminescens subsp. laumondii, Photorhabdus luminescens subsp. laumondii (strain TT01)	243265	>tr|Q7MZ95|Q7MZ95_PHOLL Trk system potassium uptake protein OS=Photorhabdus luminescens subsp. laumondii (strain TT01) GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSVTMIIPGLVALIYRDGAGRAFSQTFIFALIIGLMLWIPNREQKHELKPREGFLIVALFWTVLGSVGALPFI FSEQPNLSITDAFFESFSGLTTTGATTLIGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRIA ETAKTLWLIYVLLTIACALALWAAGMSVFDAISHSFSTIAIGGFSTHDASIGYFNSPAINTIIAIFLLISGCNFGLHFAVLTGRSLTVYWRDP EFRMFISIQLVLVIICTLILWHHAVYKSGIETLNQAFFQVVSMATTAGFSTDSFARWPSFLPILLLCSAFIGGCAGSTGGGLKVIRILLFL QGSRELKRLVHPNAVYTLKLGRRALPERIIEAVWGFFSAYALVFIISLLLLIATGVDELSAFSAIAATLNNLGPGLGVVADNFTAMNPAAK WILVITMLFGRLEVFTLLVLFTPTFWRE	
3.5E-87	302	16.8	5.7E-87	301.7	11.6	1.3	1	H2IVW2_RAHAC	Trk system potassium uptake protein	Rahaq2_4264	Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Rahnella, Rahnella aquatilis, Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	745277	>tr|H2IVW2|H2IVW2_RAHAC Trk system potassium uptake protein OS=Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65) GN=Rahaq2_4264 PE=3 SV=1MHFRAITRIVGVLVILFSGTMIIPGLVALIYRDGAGRAFSQTFFVALAIGLFLWLPNRKQKSELKPREGFLIVVLFWTVLGSVGALP FLFSERPNLSLTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVLLTIACALALWGAGMPVFDAISHSFSTIAIGGFSTHDASIGYFHSGTINTIVAIFLLISGCNYGLHFAVLSGRNIKVYW RDPEFRMFIGVQFTLVIICTVILWIHNTYGSGLETLNQAFFQVVSMATTAGYTTDSISKWPLFLPLLLLCSAFIGGCAGSTGGGLKVIRIL LLYLQGSRELKRLVHPNAVYTIKLGNRALPERIIEAVWGFFSAYALVFIVSMLAIVATGVDNFSAFAAVTATLNNLGPGLGVVADNFASM NSVAKWILIVTMLFGRLEVFTLLVLFTPTFWRE	
4E-87	302	18.2	6.4E-87	301.5	12.6	1.2	1	A0A090IIS6_9GAMM	Trk system potassium uptake protein	trkH MVIS_4404	Moritella viscosa	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Moritellaceae, Moritella, Moritella viscosa	80854	>tr|A0A090IIS6|A0A090IIS6_9GAMM Trk system potassium uptake protein OS=Moritella viscosa GN=trkH PE=3 SV=1MQFRAILRIVGILVTIFSVTMIFPALIAAIYKDGGGLVFINSFAFCVTLGSIVWYQNRNYKKELKAKDGFLIVVLFWTVLGSVGALPFI LSEQPDLSVAGAFFESFSGLTTTGATVIVGLDELPKALLFYRQFLQWLGGMGIIVLAVAVLPVLGIGGMQLYRAETPGPVKDSKMTPRI AETAKALWYIYLCLTVFCAMAFWLAGMTIFDAIAHSFSTIAIGGFSTHDSSMGHFDSSIINMITVVFLLIAGMNFSLHFAAFSIKGFKPGTY LHDPELRTFLFVQLVLVAICFFILLSKGVYESPEMALDKAVFQAVSISTTAGFTTTSFQDWPLFLPVLLVFSSFIGGCAGSTGGGMKVV RILLLYLQGMREMKRLVHPRAVYKIKLGKKVLPDRVIDAVWGFFSAYALVFVICMLALIATGMDELSAFSAVVATLNNLGPGLGQVAVH FGDVNDSAKWILVVAMLFGRLEVFTLLILFTPAFWRS	

4.2E-87	302	11.3	6.5E-86	298.2	0.3	2.1	2	G3JM21_CORMM	Cation transporter, putative	CCM_07165	Cordyceps militaris (strain CM01) (Caterpillar fungus)	716	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Cordycipitaceae, Cordyceps, Cordyceps militaris (Caterpillar fungus), Cordyceps militaris (strain CM01) (Caterpillar fungus)	983644	>tr|G3JM21|G3JM21_CORMM Cation transporter, putative OS=Cordyceps militaris (strain CM01) GN=CCM_07165 PE=4 SV=1MGRGKVRNPTLLLQTDLPLEPAISCRKPGSFPLLRDPLHLTGERLGGFGDSMGTLVSLRSMSSHRLNFLTIHYCYFVVVCLLSSV VFWASSSPRGRISYVDSLFVVVSAMTEAGLNTVNLSTMTTWQQTILFLLIMLGGTIWVSIWTVFARRAVFYRRFVHTAWPTWACSPA RQTIRTAHAQGVKDPSSGSGPGSASSHSASPRVCSAAAEKDLDMALARTRGRPYYTLPQKPSSPRNEEDGLADGKSQRICGCEYRA LELLSIIVPVYFVLWQLLGCIGLGAWVHNHMPDTALANGINPWWLGVFNGVSAFNNSGMSLLDANMVPFQEAHFVLITMGLMILAGNT AYPIFLRLILWSAHKLLDLTTEADSFQSTKLAVQLLLKDPRRIYTNLFPSRLTWWLFFMLVCLNSIDWVLFELLNLNNPVVDSIPVGPRVL VGLFQALAVRSGGFYVVPIAQIAIGVQFLYVIMMYISVYPVVMTIRQSSVYTYSQRDGPGIELRDAAHSHLPKLSRAVSYPIEKRSLTTR HRVHLTFATPAERATWRGKPGHPVTTTTGVSPPLLYSEQLSNWPREKRPSHHARLLSLHGTPPPPTYDSHMSFIHQQIHGQLAQDI WWLVLAVLVIIIESSQFNADPINHSVFNIIFEVASAYGTVGISVGTPSGAYSFSGTWYTGSKLILCLVMLRGRHRGLPTALDHAIRLPE QHLNCKEYDMEDK	
4.4E-87	302	3.9	1.6E-86	300.2	0.2	2.1	2	R1EC21_BOTPV	Putative potassium ion transporter protein	UCRNP2_8280	Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	672	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Neofusicoccum, Neofusicoccum parvum, Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	1287680	>tr|R1EC21|R1EC21_BOTPV Putative potassium ion transporter protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_8280 PE=4 SV=1MRDPLDEVRNPHEAKEHFLQYFKKEIFHLNFYRMHMLYFIVVILIASVIVAMTTTGLNTVNLGSMTGFQQAALCVLLIVGNVPFVS SFVIIIRRHYFHRKLADVVQHSRSGRQMVRDLEEQDQESRVEHQVARRRKRINPNNNHNTSEERPLREAPKKTQRKQMSPEQRLYH HASGFGAFPWPWETHTAQRLFHYPFKRLQQEWEPRDRSYISFNAEYDERGRFRNLSERERAELGGVEYRALELLLALLVAYQVVW YALGTLFLVPYAYRPAVSRTLKTSQPGDLSPGWWGFFAVVTSFSNGGLNVLNSNYIPFSGDALILIVSGALTVAGNTQFPILLRLAIWT LSKSVPAASRLRQTCLFLLHHPRRCFIYLFPSRETWYLLAIQLLIDLAMWVLYELLNVGLPPVEAFPLGTRVLDGLFQATGLRNSGAYII AISSLAPALLVAYLVTMYISSFPIVMALRQTNTYEERSVGLDGRSSSSSASGGGLGMHLRRQLAYDLWFQLLGWFLICVVERRKLIAGS PGFGIFAVLFEVTSAYGTVGLSTGVPYDQYSLSGAFQTGSKLVMLAVMLRGRHRGLPLAIDRSILLPGEELMHRMDDEYGEFGRWSS EEERAVRHDEESGKRDLGPGKGLNEQDPERREDGSGSSRGEGTSKSRASEWEDEPHFEMT	
5.6E-87	302	15.1	8.7E-87	301.1	10.5	1.2	1	A0A097QP73_9VIBR	Trk system potassium uptake protein	JV59_39395	Vibrio coralliilyticus	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio coralliilyticus	190893	>tr|A0A097QP73|A0A097QP73_9VIBR Trk system potassium uptake protein OS=Vibrio coralliilyticus GN=JV59_39395 PE=3 SV=1MQFRSIIRIVGLLLALFSVSMLAPALVALIYRDGAGVPFVTTFFVLFICGAICWWPNRRHKHELKARDGFLIVVLFWTVIGSAGSIP FLLSDNPNVSVTDAFFESFSALTTTGATVIVGLDELPKALLFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPR IAETAKALWYIYLSLTIACALAFWLAGMTPFDAIGHSFSTIAIGGFSTHDASMGYFDSYAINMITVVFLLISACNYSLHFAAFASGGVHPK YYWKDPEFRAFIFIQALLFIVCFLILLNHHSYDSVYDAFDQALFQTVSISTTAGFTTTGFSEWPLFLPVLLLFSSFIGGCAGSTGGGMKVI RILLLTLQGARELKRLVHPRAVYTIKVGGTALSQRVVDAVWGFFSAYALVFVVCMLGLIATGMDELSAFSAVAATLNNLGPGLGEVALH FGDVNDKAKWVLIVSMLFGRLEIFTLLILLTPTFWRS	
5.6E-87	302	18.1	7.1E-87	301.4	12.5	1.1	1	A1S1J1_SHEAM	Trk system potassium uptake protein	Sama_0035	Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella amazonensis, Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)	326297	>tr|A1S1J1|A1S1J1_SHEAM Trk system potassium uptake protein OS=Shewanella amazonensis (strain ATCC BAA-1098 / SB2B) GN=Sama_0035 PE=3 SV=1MQYRTIIRITGLLMGLFSITMLPPALVAIYYKDGGGTAFIQAFVVSLILGFIFWYPNRKHKSELRTREGFLIVVLFWTVLGSIGALPFI FSSTPDLSWTDSFFESFSALTTTGATVIVGLDSLPKAILFYRHLLQWLGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIAE TAKALWYIYLLLTIACATAYWAAGMSVFDAICHSFSTIAIGGFSTHDASMGYFDSPTINMICVVFLIIAAVNFSVHFAAMSRRGINLRVYF RDTEFKILVAIQLLLTAICFATLYHSGIYDSPEETFDYALFQAVSISTTAGFGTESFHLWPLFLPMLLIFSSFIGGCGGSTAGGIKVIRVVLL LLQGSRELKRLIHPRAMFSIRIGKTALPDRVVDAVWGFFSAYALVFVICMLILMAMGLDDITAFSATAACLNNLGPGLGEVASNYASIGD GAKWVLVVAMLFGRLEIFTLLVLFTPTFWRT	
5.7E-87	302	14.6	1.1E-86	300.7	10.1	1.4	1	W0HNC8_9ENTR	Trk system potassium uptake protein	trkHSant_0260	Sodalis praecaptivus	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Sodalis (tsetse S-endosymbionts), Sodalis praecaptivus	1239307	>tr|W0HNC8|W0HNC8_9ENTR Trk system potassium uptake protein OS=Sodalis praecaptivus GN=trkH PE=3 SV=1MHFRTITRIVGLLVILFSVTMIIPGLVALIYRDGAGSAFAQTFFCAQAIGLLLWLPNRRQKSELKSREGFLIVVLFWTVLGSVGALP FLFAEHPNLSVTDAFFESFSGLTTTGATALVGLDTLPHAILFYRQMLQWFGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRP RIAETAKTLWLIYVALTIACALALWGAGMPAFDAIGHSFSTIAIGGFSTHDASIGYYHSPLINTIVAVFLLISGCNYGLHFAALSGHNLKVY WRDPEFRMFISVQLTLVVVCILILWRYDVYDSSLQTLNQAFFQVVSMATTAGFTTDSIAQWPLFLPILLLCSAFIGGCAGSTGGGLKVI RILLLYLQGSRELKRLVHPNAVYTIKLGSRALPERILEAVWGFFSAYALVFILSMLAVVATGVDNFSAFAAVAATLNNLGPGLGVVADNF TSMNAVAKWILILTMLFGRLEVFTLLVLFTPTFWRE	
6.2E-87	302	16.6	1.1E-86	300.7	11.5	1.3	1	H2FYV9_OCESG	Trk system potassium uptake protein	GU3_01835	Oceanimonas sp. (strain GK1)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Oceanimonas, Oceanimonas sp. (strain GK1)	511062	>tr|H2FYV9|H2FYV9_OCESG Trk system potassium uptake protein OS=Oceanimonas sp. (strain GK1) GN=GU3_01835 PE=3 SV=1MHIRSIIRIVGILVALFSVTMLAPALVAYIYRDGAGLDFFSAFVICLVLGLMLWFPNRNHHKELRAKEGFLIVVLFWTVLGSVGAIPF LLSEVPDMTVAEAFFESFSGLTTTGATVISGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGIGGMQLFRAEIPGPVKDNKVAPRIA ETAKALWYIYLVLTIACALLLWLAGMNLFDAICHSFSTVAIGGFSTYDASVGHFNSPMINLIIVVFLIIAGVNFSLHFAAFSSRGMRLSVYR LDPELKVFIGVQLVLTLICLSMLLAHRVYTDPWQALDQALFQSVSIATTAGFSTTGFAEWPLFLPVLLMFASCIGGCAGSTGGGIKVVRI MLLNLQGMRELKRLIHPRAVYRIKLGNKALADRVVEAVWGFFAAYALVFVLCMLALLATGMDELTAFTAVVATLNNLGPGLGEVAANF GTTTDGAKWIMVLAMLFGRLEIFTLLVLFTPAFWRS	
7.9E-87	301	13.8	1.3E-86	300.5	9.6	1.3	1	A8G8D5_SERP5	Trk system potassium uptake protein	Spro_0265	Serratia proteamaculans (strain 568)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia proteamaculans, Serratia proteamaculans (strain 568)	399741	>tr|A8G8D5|A8G8D5_SERP5 Trk system potassium uptake protein OS=Serratia proteamaculans (strain 568) GN=Spro_0265 PE=3 SV=1MHFRAITRIVGLLVILFSGTMFIPGLVALIYRDGAGRAFSQTFFVAVTIGLMLWWPNRKQKHELKPREGFLIVVLFWTVLGSVGAL PFLFSERPNLSLTDAFFESFSGLTTTGATTLVGLDSLPKAILFYRQMLQWMGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMR PRIAETAKTLWLIYVLLTIACALALWGAGMSVFDAIGHSFSTIAIGGFSTHDASIGYYASPTINTIIAIFLLISGCNYGLHFALLSGRSLKVY WRDPEFRMFIAVQLTLVVVCTAVLWGHGVYKTGMETVNQAFFQVVSMATTAGFTTDSIAKWPLFLPMLLLCSAFIGGCAGSTGGGL KVIRILLLYLQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFAAVTATLNNLGPGLGVVAD NFTTMPAPAKWILVLTMLFGRLEVFTLLVLFTPTFWRE	
8.6E-87	301	16.6	1.6E-86	300.2	11.5	1.3	1	F0LQJ1_VIBFN	Trk system potassium uptake protein	vfu_A00360	Vibrio furnissii (strain DSM 14383 / NCTC 11218)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio furnissii, Vibrio furnissii (strain DSM 14383 / NCTC 11218)	903510	>tr|F0LQJ1|F0LQJ1_VIBFN Trk system potassium uptake protein OS=Vibrio furnissii (strain DSM 14383 / NCTC 11218) GN=vfu_A00360 PE=3 SV=1MQFRSIIRIVGLLLALFSVSMLAPALVALIYRDGAGVPFVSTFFVLLLCGGVFWFPNRRHRHELKARDGFLIVVLFWTVIGSAGSL PFLLADNPNVSVTDAFFESFSALTTTGATVIVGLDNLPKAILFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDNKVTP RIAETAKALWYIYLSLTIACAGSFWMAGMTLFDAICHSFSTIAIGGFSTHDASIGYFDSYAINMITVVFLLISACNFTLHYAAFATGGVHP KYYWKDPEFRAFVVIQAILFAICFLMLLKHHSYDSLYDAFDQALFQTVSISTTAGFTTTGFADWPLFLPVLLLFSSFIGGCAGSTGGGM KVIRVFLLTLQGAREMKRLVHPRAIYHIKIGDSALPQRVVDAVWGFFSAYALVFVVCMLALIATGMDELSAFAAVAATLNNLGPGLGEV SMHFANVNDTAKWILVVSMLFGRLEIFTLLILLTPTFWRS	

1.2E-86	301	7.7	4.7E-48	173.3	1.3	3.1	3	S8E5F5_FOMPI	Uncharacterized protein	FOMPIDRAFT_55551	Fomitopsis pinicola (strain FP-58527) (Brown rot fungus)	823	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Fomitopsis, Fomitopsis pinicola, Fomitopsis pinicola (strain FP-58527) (Brown rot fungus)	743788	>tr|S8E5F5|S8E5F5_FOMPI Uncharacterized protein OS=Fomitopsis pinicola (strain FP-58527) GN=FOMPIDRAFT_55551 PE=4 SV=1MFTCISKSLRFYRIHLLLFTIVPLVAASIFWASNGEFKIRFVDALFVCVSAATGTGLSPVDLSGTTPWQQAVITLLEICGNLVFVAW VVVYFRRAYFIDHLKHIVAAEHGRKTARHETSASHASQGNSSRTIVDHLAVYGLNELHERQSSEFTPISRRTSKRTSAKGSPVIRPDMV RRLDIPPHPIDPTGNTSLGAYASGVQPPCLPNSKRAVDSDRCPSVRSIDASAQAPQPRHAHPESFGGFPYPWTILSRMFRRLLPTLH QKLRRTMTMPRTSTLLPQNGDPAAVLTGEETRRVPYISFSASVGRNSTFHNLTDENIEELGGVEYRALTALLWIVPLYYFGLLAFSFIII APYANLARWRWIFRIPEQHRNINPIWYMFSAFQVVGAWANTGMSLVDQNMVPFREAYPMITFLVLDVLAGNTAFPIFLRFLIWVLTKL LHRDSRTKEALHFLLDHPRRCFIYLFPANQTWVLLVVQSAIDVVLWVFNIALDLGNPATESISIGTRLIDALLQAAAVRSAGFQAIPVSTV VPAVQVLDVIMMYVAIYPIALRQVEPTPYFHLRVARASLTHHFLTRPNRSVRATNVYEETSLGIYEHVEETTYGLDDSPDSRVEIWGRY LWQHARRQLSFDIWWLVLSLFLICIVERTPLMDTSKASCFNIFAIIFELVSAYGTVGLSLGVPYANYSFSGALHTLSKLILCAVMIRGRHR GLPVALDRAVLLPHEFEKREDSAEKAQDLPVEDLTMLSEKRQQSDATSVAPEKDGLTEVLSTSNRASRIRTLNFADDQPKYGARLVD DHIDNITSDVPRSRIHDIDEKSPV
1.3E-86	301	18.5	3.3E-86	299.2	12.8	1.5	1	A0A068QQ86_9ENTR	Trk system potassium uptake protein	trkG XDD1_1265	Xenorhabdus doucetiae	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus doucetiae	351671	>tr|A0A068QQ86|A0A068QQ86_9ENTR Trk system potassium uptake protein OS=Xenorhabdus doucetiae GN=trkG PE=3 SV=1MVKKNQLLIVGHLCSFLVLLYSLSMLLPIFVALFYKEKSVFAFFETFIIGLVTGGIGWYFTRKTKAQPSTQDGFLIIVLFWLLFSLLS ALPFVLDKSLNINLVDAMFEGISGITTTGATVLNDVSALPNSVLYYRAQLNFIGGLGVIVLAVAILPLLGIGGAKLYQSEMPGPFKEERLT PRLADSAKSLWVVYLLLGGLCSASFWAAGMSWFDAVCHGISTVSLGGFSTRNESLGYYDSAAIEMVGGIFSVLSAVNFALYFVALTR RSLKPLLKNAELQFFLLVLAAIVAIIWIELYRSGMYGVKEAFVHGFFMTSSMMTDNGLSISDYAQWPPHTVLLLLAVSFFGGCVGSTCG GIKALRFMILTKQSVSEINQLIHPNAISTIKVGKSVVQERVLRSVWGFFFLYVFFSCFFIWALNLLGYDFMTSFATAAACINNMGIGWGV TAQGFGALDPIAKWMMCAAMLLGRLEIYPILILCSKAFWRF
1.4E-86	300	0.9	1.4E-86	300.4	0.6	2.3	2	R0IP48_SETT2	Uncharacterized protein	SETTUDRAFT_31045	Setosphaeria turcica (strain 28A) (Northern leaf blight fungus) (Exserohilum turcicum)	720	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Pleosporaceae, Setosphaeria, Setosphaeria turcica (Northern leaf blight fungus) (Exserohilum turcicum), Setosphaeria turcica (strain 28A) (Northern leaf blight fungus) (Exserohilum turcicum)	671987	>tr|R0IP48|R0IP48_SETT2 Uncharacterized protein OS=Setosphaeria turcica (strain 28A) GN=SETTUDRAFT_31045 PE=4 SV=1MASQTCDSATLGVARPLETIDEPDTSGPLSMSSFWQRLDDDGDDESVMTDPLNELQRPQKAKDDIVKYLKEELFKLNFYRAHM LYFVVVIALSSVIVYVQGLADGPEMPGGAHLHAMTTTGLNPVDLGSLSGYQQATFAVLMMIGNIPFVSTAVVLIRRALFRRKLADVVKH SHTMQRLVRDIEETPESDTLGSSSGSGRSLRQRTGTTQSQTSQSKQMGGNGSSTVKIKPVSRKQGYYYERDFGFLPAPWETRFVR NMFRRTIAVFATELRPEHHDYISFKPHLDSRGRFRELSEQDRMELGGVEYRALQALLLILIGYQVFWYLLGVTFLLPYAYRGNVKNILK ESQPGGIHPGWWSFFASVTEFANGGLNILNANFIPFSGNAYVLLVAGALAFAGQTQFPILLRVTIWGLKKIAPKESRVKNTLGFLLQHP RRCYIYLFPSRETLYLFFTQFMIDMTAWLCFEILNTGMADVEALPTGTRILDGLFQASGLRTSGAYIISMSSLAPACLVGYLVIMYISIYP MTLTVRKTNTYEERSLGLERGAGSAAGIASHLQKQLTYDIWFQFFVFFLICCIERQHLVDGDAGFSIFSVLFEVTSAYGTVGLSVGVPG QYYSLCGEFAGLSKVVLLLAMVRGRHRGLPFALDRSILLPGEELMRRMDQEYSAKGTEDPDQEAQLRSDIERSGVREVHGGQGEQD PEDRRAAQPHSDMGAESAS
1.4E-86	300	17.7	1E-85	297.5	12.3	1.9	1	I0DST7_PROSM	Trk system potassium uptake protein	S70_07680	Providencia stuartii (strain MRSN 2154)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia stuartii, Providencia stuartii (strain MRSN 2154)	1157951	>tr|I0DST7|I0DST7_PROSM Trk system potassium uptake protein OS=Providencia stuartii (strain MRSN 2154) GN=S70_07680 PE=3 SV=1MHFRAITRIVGLLVIIFSFTMVVPGIVALIYRDGAGRAFSQTFVTALVLGLLLWIPTRNSKHELKAKEGFLIVVLFWTVLGSVGALPF IFSEKPNLSITDAFFESFSGLTTTGATTLTGLDTLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRI AETAKTLWLIYVLLTIVCAIALWIAGMDVFDAISHSFSTIAIGGFSTHDASVGYFNSPAINTIIAVFLIISGCNFGLHFAVLTGRSLGIYWRD PEFKTFISFQLALVIICTLVLLYHSVYGSFGQTLDQAFFQVVSMATTAGFTTDSFAGWPLFLPMLLLCAAFVGGCAGSTGGGLKVIRILL LFLQGSRELKRLVHPNAVYTIKLGQRALPERIIEAVWGFFSAYALVFIVSLLLLIATGVDEFSAFSAIATTLNNLGPGLGTVADNFTSMNP AGKWILVVTMLFGRLEVFTLLVLFTPTFWRD
1.4E-86	300	17.8	3E-86	299.3	12.4	1.5	1	Q6LW04_PHOPR	Trk system potassium uptake protein	STY3574 PBPRA0066	Photobacterium profundum (Photobacterium sp. (strain SS9))	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium profundum (Photobacterium sp. (strain SS9))	74109	>tr|Q6LW04|Q6LW04_PHOPR Trk system potassium uptake protein OS=Photobacterium profundum GN=STY3574 PE=3 SV=1MQFRSIIRIVGLLLALFSVTMLAPALVAFIYRDGAGFPFVVTFFLLFTGGASLWLPNRHHRRELKARDGFLIVVLFWTVIGSAGALP FILSKTPDLSITDSFFESFSALTTTGATVIVGLDDLPKAVLFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIA ETAKALWYIYLALTISCAAAFWLAGMSVFDAIAHSFSTVAIGGFSTHDASMGYFNSPTINMITVVFLLISACNFSLHFAAFANGGIHLRTY WRDPEFRAFFGAQFILFAICFAMLLQHHSYDSYNDAFDQALFQTVSISTTAGFTTTGFSDWPLFLPVLLLFSSFVGGCAGSTGGGMK VIRMLLLFLQGVRELKRLIHPRAIYTIKVGNKALPQRVVDAVWGFFSAYALVFVVCMLALIATGIDELTAFSAVAATLNNLGPGLGEVAV HFGDINSSAKWVLIISMLFGRLEVFTLLVLFTPTFWRN
1.5E-86	300	15.1	2.6E-86	299.5	10.4	1.3	1	A0A0A7EC96_9GAMM	Trk system potassium uptake protein	OM33_03300	Pseudoalteromonas sp. OCN003	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas sp. OCN003	1348114	>tr|A0A0A7EC96|A0A0A7EC96_9GAMM Trk system potassium uptake protein OS=Pseudoalteromonas sp. OCN003 GN=OM33_03300 PE=3 SV=1MQYRTIIKILGQLVALFSITMIPPALVSLIYKDGGGVPFVLAFVFSIIIGLIAYYPNRKQRGDLKAREGFLIVVLFWLVLGSFGSLPLIF LEEPNLSIADSVFESFSGLTTTGATVLTGIEYLPKAILFYRQQLQWLGGMGIIVLAVAVLPMLGVGGMQLYRAETPGPVKDSKMTPRIA DTAKHLWYIYVSLTGACTLAYWAAGMNWFDAICHAFSTIAIGGFSTYDASIGHFNSPLINIICVVFLLIAAVNFSLHYAAVANKNFRVYW RDPELKVFLFIQTCLVLLCFFVLTSAGIYTSTDQAFDQALFQAVSISTTAGFATDSFSQWPLFLPILLIFSSFIGGCAGSTGGGMKVVRV FLLYLQGIRELNRLVHPRAIYSIKLGRKALPDKVVEAVWGFFSAYALVFVIIMLCLLATGMDNITAFSATAACLNNLGPGLGDVAAHFGDI TDTAKWILTLAMVFGRLEIFTLLVLFTPTFWRG
1.8E-86	300	21.1	3.1E-86	299.3	14.6	1.2	1	T2L4F1_9GAMM	Trk system potassium uptake protein	trkH HALA3H3_210008	Halomonas sp. A3H3	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas sp. A3H3	1346287	>tr|T2L4F1|T2L4F1_9GAMM Trk system potassium uptake protein OS=Halomonas sp. A3H3 GN=trkH PE=3 SV=1MSLRVILRILGLLLMLFSLTMLPPTLISLWFRDGVWSAFISGIAISVATGLLLYLPNRRSQKELRIRDGFIIAAMFWTVLALFGSLPL MLFGEGSLGVTDAVFESFSGLTTTGATVITGIDFLPESILYYRQQLQWLGGMGIVVLAVAILPTLGVGGMALYRTEIPGPLKDSKLTPRI TETAKALWYIYATLTLACMIAYMLAGMSVFDALSHSFSTVAIGGFSTHDASIGYFDSATIEMICVGFMLISAFSFSLHFIAWREKSLMHY FHDPEARFLMLFLLALSVVTVLSLWLTDTYDTARGLRHGVFQVVSVATTAGFSVADFSMWPGALPFLLFVAAFVGGCSGSTGGGMK VIRIILILKQGMREIMRLIHPNAVIAVKVGKVSVPDSIAQAVWGFFSVYVMLFFLMLVGVMATGVDQVTAWSTVGSALNNLGPALGESH THYGDMPSLAKWILVMAMLLGRLEIFTVLVLFTPAFWRR
2E-86	300	17.3	2.7E-86	299.5	12	1.1	1	A0A068R615_9ENTR	Trk system potassium uptake protein	trkH XPG1_3060	Xenorhabdus poinarii	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus poinarii	40577	>tr|A0A068R615|A0A068R615_9ENTR Trk system potassium uptake protein OS=Xenorhabdus poinarii GN=trkH PE=3 SV=1MHFRAITRIVGLLVILFSFTMAIPGLVALIYRDGAGSAFSETFIFALIIGLMLWIPNREQKADLKPKEGFLIVVLFWTVLGSLGALPFI FAEKPNLSITDAFFESFSGLTTTGATTLVGLDNLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRI AETAKTLWLIYVLLTVACAIALWAAGMSVFDAISHSFSTIAIGGFSTHDASIGFFNSQTINIIIAIFLLISGCNFGLHFAVLSGRSLKVYWRD PEFRMFITIQLALLAICVLILWQHSFYQSELDALNHAFFQVVSMATTAGFTTIKFHEWPLFLPLLLLTSAFIGGCAGSTGGGLKVIRILLLF LQGSRELKRLVHPNAVYTIKLGRRALPERIIEAVWGFFSAYALVFFISMLLLIATGVDEFSAFSAIAATLNNLGPGLGNFAENFVFMQPE AKWVLIVTMLFGRLEVFTLLVLFTPTFWRE

2.5E-86	300	12.1	3.5E-82	285.9	0.6	2.2	2	L2FE06_COLGN	Cation transporter	CGGC5_14015	Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	776	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	1213859	>tr|L2FE06|L2FE06_COLGN Cation transporter OS=Colletotrichum gloeosporioides (strain Nara gc5) GN=CGGC5_14015 PE=4 SV=1MAWQSWEKFKADHPATADRMVESWAAVRPYLPPVNFITVHYAYFILVGLIFAGIFHGISNPANSVSFIDSLFLVISAFTTSGLNTV DISKLSTAQQAIIALMMILGSPVFVSIFTIWLRARVFEKRFEDIVEAERNRRIKKTGTIVGMAGAMIGLPVMSSFKGTKRKQKKGRHERQ AEADAFQLTGYKSREKGHDRSQSQPANQESAPSGMLEPIEEGQRLNLSTSSTEPLSPKSNATPRRRPFSRDSGRVSISEGFDFKTFI HENKTSIGRNGQFFDLTEEQREYLGGVEYRALKILFTIVCVYFVLWQLLGAITLGAWSYTHSQSITAVNSQNSWWAGIFLAISSFNNAG MTLLDAGIAAFDNDAFVLTIVTILSLAGNAAFPAFLRATVYFCRFVLKMCVDEDEHVVWKEAFDFILKYPRRLYMMMFPAKANFVFVTM FSTIAVMDWVLLVVLSIGNSAIEAYPVGKRVGLALFQALAIPSSGFGVVGVSSLYFDVLVLWVIVMYISAYPEIIVMRNSNVYEERSLGIY TTEPEKPEDPDATANESTDELLPTFAEPAFGHALGPEQTAVSASGVSLSQVKSHFSTKPVKRIAAIGRRGTSFVGKQIQSRMNNFQG VGVTAKPRRLKRSAAINFDNPNAGSASTPEGHVSLVSQHLRGQLSHDIWAIAFSLFLVTLIETSHSIADPRSYSVFNFLFEIVSGYTNIGLS IGLPGHSFSFAGGWYTGSKLVMILMMIRGRHRGLPVALDHSVKLPGWDNVKKQNEDAEIRRSINEW
2.5E-86	300	10.9	2.1E-85	296.5	7.6	1.9	1	G4SWE8_META2	Trk system potassium uptake protein	trkH MEALZ_2483	Methylomicrobium alcaliphilum (strain DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomicrobium, Methylomicrobium alcaliphilum (Methylobacter alcaliphilus), Methylomicrobium alcaliphilum (strain DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z)	1091494	>tr|G4SWE8|G4SWE8_META2 Trk system potassium uptake protein OS=Methylomicrobium alcaliphilum (strain DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z) GN=trkH PE=3 SV=1MQAKVVLRSIGLMLMMFSTTLFLPLLVSYIYQDQAESLFWQSFLILLTAGAVLWFPFRNEKRQLYHRDGFLIVALFWMILGTMGA VPFILGDTPSLSITDAVFESVSGFTTTGATILEGLDDMPKSILFYRQLLQWFGGMGVIVLALAVLPVLGIGGMQLFRAEVPGPVKDSKLT PRIAGTAKALWVIYLGITIICAIAYRIAGMDWFDAIGHSFSTAANGGYSTHDDSIGFFKNPAIEIVAIFFMAVSGMNFALHFAALQSASLKV YLLDSEARTYLLLMILSGSVVGGILYYEGISDFSLFDAMRHGMFQIVSFMTTAGFSTTDFYNWPGPVPVMLVFIGFVGGCAGSTAGGL KVIRVMLLYKQGDREIQRLIHPNARIPVKVGKEVQQERIIEAVWGFFGLYVVSFVVIMLLMMAGGLDQVTAFSAVAACINNVGPGLGDV ATSFRTVSDPVKWLACFAMLLGRLEIFTILVLLSPKYWRY
2.6E-86	300	18.9	6.2E-86	298.3	13.1	1.4	1	F7YHW2_VIBA7	Trk system potassium uptake protein	VAA_00816	Vibrio anguillarum (strain ATCC 68554 / 775) (Listonella anguillarum)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio anguillarum (Listonella anguillarum), Listonella anguillarum serovar O1, Vibrio anguillarum (strain ATCC 68554 / 775) (Listonella anguillarum)	882102	>tr|F7YHW2|F7YHW2_VIBA7 Trk system potassium uptake protein OS=Vibrio anguillarum (strain ATCC 68554 / 775) GN=VAA_00816 PE=3 SV=1MQIRSIIRIVGLLLALFSVSMLAPALVALLYRDGAGVPFVTTFFVLLMCGGFFWFPNRRYRHELKARDGFLIVVLFWTVIGSAGSL PFWLADNPNVSVTDAFFESFSALTTTGATVIVGLDELPKAILFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDTKVTP RIAETAKALWYIYLSLTIACATAFWAAGMTLFDAICHSFSTIAIGGFSTHDASMGYFDSYAINLITVIFLLISACNFTLHYAAFATGGVHPK YYLKDPEFRAFALIQVILFAVCFSILLKHHSYDSFYDAFDQALFQTVSISTTAGFTTTGFADWPLFLPVLLLFSSFIGGCAGSTGGGMKVI RILLLTLQGAREMKRLIHPRAVYTIKVGGSALSQRVVDAVWGFFSAYALVFVACMLALIATGMDELSAFSAVAATLNNLGPGLGQVSV HFADVNDSAKWVLVVSMLFGRLEIFTLLILLTPTFWRS
2.6E-86	300	11.6	4.3E-82	285.6	0.5	2.2	2	T0L4X6_COLGC	Uncharacterized protein	CGLO_00035	Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	782	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	1237896	>tr|T0L4X6|T0L4X6_COLGC Uncharacterized protein OS=Colletotrichum gloeosporioides (strain Cg-14) GN=CGLO_00035 PE=4 SV=1MAWQSWEKFKADHPATADRMIESWAAVRPYLPPVNFITVHYAYFILVGLIFAGIFHGISNPANSVSFIDSLFLVISAFTTSGLNTV DISKLSTAQQAIIALMMILGSPVFVSIFTIWLRARVFEKRFEDIVEAERNRRIKKTGTIVGMAGAMIGLPVMSSFKGTKRKQKKGRHERQ AEADAFQLTGYKSREKGHDRSQSQPTNQDSAPHGMLEPIEEGQRLNLSTSSTEPLSPKSNATPRRRPFSRDSGRVSISEGFDFKTFI HENKTSIGRNGQFFDLTEEQREYLGGVEYRALKILFTIVCVYFVLWQLLGAITLGAWSYTHSQSITAVNSQNSWWAGIFLAISSFNNAG MTLLDAGIAAFDNDAFVLTIVTILSLAGNAAFPAFLRATVYFCRFVLKMCVDEDEHVVWKEAFDFILKYPRRLYMMMFPAKANFVFVTM FSTIAVMDWVLLLVLSIGNSAIEAYPVGKRVGLALFQALAIPSSGFGVVGVSSLYFDVLVLWVIVMYISAYPEIIVMRNSNVYEERSLGIY TTEPEKPEDPDATANESTDELLPTFAEPAFGHALGPEQTAVSASGVSLSQAKSHFSTKPVKRIAAIGRRGTSFVSKQIQSRMNNFQGV GVTAKPRLKRSAAINFDNPNAASASTPEGHVSLVSQHLRGQLSHDIWAIAFSLFLVTLIETSHSIADPRSYSVFNFLFEIVSGYTNIGLSI GLPGHSFSFAGGWYTGSKLVMILMMIRGRHRGLPVALDHSVKLPGWDNVKKQNEDAEIRRSISRSRTGLTI
2.7E-86	300	13.7	4.4E-86	298.7	9.5	1.3	1	W0LEZ9_9ENTR	Trk system potassium uptake protein	Z042_13410	Serratia multitudinisentens RB-25	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia multitudinisentens, Serratia multitudinisentens RB-25	1441930	>tr|W0LEZ9|W0LEZ9_9ENTR Trk system potassium uptake protein OS=Serratia multitudinisentens RB-25 GN=Z042_13410 PE=3 SV=1MHFRAITRIVGLLVILFSGTMFIPGLVALIYRDGAGRAFSQTFFVALTIGLMLWWPNRKQKNELKPREGFLIVVLFWTVLGSVGAL PFLFVERPNLSLTDAFFESFSGLTTTGATTLVGLDSMPKAILFYRQMLQWMGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKM RPRIAETAKTLWLIYVLLTIACALALWGAGMSVFDAIGHSFSTIAIGGFSTHDASVGYYASPAINTIIAVFLLISGCNFGLHFAVLSGRSLK VYWRDPEFRMFIAVQFTLVAVCTILLWWHGIYKSGMETINQAFFQVVSMATTAGFTTDSFAKWPLFLPMLLLCSAFIGGCAGSTGGG LKVIRILLLYLQGSRELKRLVHPNAVYTIKLGNRALPERILEAVWGFFSAYALVFIVSMLAIIATGVDDFSAFAAVTATLNNLGPGLGVVAD NFTTMPPPAKWILVLTMLFGRLEVFTLLVLFTPTFWRE
2.7E-86	299	0	8.5E-81	281.3	0	2.6	2	M7SE29_EUTLA	Putative cation transporter protein	UCREL1_10638	Eutypa lata (strain UCR-EL1) (Grapevine dieback disease fungus) (Eutypa armeniacae)	796	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Xylariomycetidae, Xylariales, Diatrypaceae, Eutypa, Eutypa lata, Eutypa lata (strain UCR-EL1) (Grapevine dieback disease fungus) (Eutypa armeniacae)	1287681	>tr|M7SE29|M7SE29_EUTLA Putative cation transporter protein OS=Eutypa lata (strain UCR-EL1) GN=UCREL1_10638 PE=4 SV=1MQLQQRWEDFGTRHPRIYDKLIAVARAVRPYLPPVNYITLHYAYFIGTTIVGTLIFWGASVPAYSVGWWDSMFMVMSALTASGL NTVNVSQLTTFQQVELCVLMIIGSQVLISYVTIAFRKHIFEKRFEDIVETERERRKKKMSGTGAVVGMTGAMFGLQVMSSFGKGRPRA NSRSSIPNAVASPTRKTFSEEEVPVPEAQIGGGARSSQQHHVGFLDPIQEGKSLEGQPTTTGHSIYQTQSHQTGATRRRPQTADSRA TGDGFNVQTFLKEQKRNIGRNGQFFNLSEDQREYLGGVEYRSLKFLSVFVLVYFVLCQFFGAIALGAWMWVHETDAAAVNAQNPW WAGIFLAISAYNNAGFTLLDAGFVPFQSSYFLLTVVTLLSLAGPAAFPVFMRLIIWSMSSLLNMFSKDKEYGVVWKEGFDFILKFPRRVY TSLFPAKDTWMFAATFGGFVIADWILILILSIGNPTMEAIPLGQRVFDALFQGFSIPSGGYAIVSPSAIYFDVQVLWLVVYYTAAYPHIIT MRNSNVYEERSLGIYEGDNAEEEQLHSATSSLFDVDADIPNEPGLPSTANNNNNNNNDNKNWDTLSRTTSTKSIKKLYTVGRRGTAF VGRQIQHRMTAFQGVGVAAAAPGTAAGPAIKPLRRAATVDFARASVHSLHDHVPATGPPSLVSQQVRGQLSHDVWWIALTLFLITLIE TRHSLADPATYSVFTILFEIVSGYTTIGISIGLPDQSYSFSGGLYTGSKIVMILVMLRGRHRGLPVALDRAVRLPGKKLAEYEEEDAEIRS MSAFSR
2.9E-86	299	14.3	4.9E-85	295.3	9.9	2	1	W0DYD0_9GAMM	Trk system potassium uptake protein	THIAE_09770	Thioalkalimicrobium aerophilum AL3	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Piscirickettsiaceae, Thioalkalimicrobium, Thioalkalimicrobium aerophilum, Thioalkalimicrobium aerophilum AL3	717772	>tr|W0DYD0|W0DYD0_9GAMM Trk system potassium uptake protein OS=Thioalkalimicrobium aerophilum AL3 GN=THIAE_09770 PE=3 SV=1MQNSMIIKILGLLLMVYSVTLVPPIIVALIYQDGAHWAFATALVLTLIAGLLLWYPNRHERRELKIRDGFIVVVMFWTALGLVGALPL VLEEEVPISITDAVFESFSGLTTTGATVLSGLDTMPHAILWYRQQLQWLGGMGIIVLAVAILPMLGIGGMQLYRAEMPGPTKDNKIAPRI SETAKTLWLIYVALTVACAAAYKLAGMNWFDAIGHSFSTVAIGGFSTHDASIGYFDSALIEAIAIFFMFLAGANFALHFRAFRTLEVRTYF TDPEFKTYTSVLLIGVLISTGYLYWQAVYPSWTEALRYGSFMTVSIATTTGFGNADFATWPGFLPVMLILMSFIGGSAGSTGGGIKVIR FLLLLKQGVREVQRLMHPNALMPVKLNGRAISERVMSSVWGFFALYVATFVVILLLLMAFGMDQVTAFSATAATLNNLGPGLGEVAAN FGQINDPQKWILTLSMLLGRLEIFTLLVILTRTFWRA

3.8E-86	299	15.5	4.9E-86	298.6	10.7	1.1	1	B1KCZ6_SHEWM	Trk system potassium uptake protein	Swoo_0024	Shewanella woodyi (strain ATCC 51908 / MS32)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella woodyi, Shewanella woodyi (strain ATCC 51908 / MS32)	392500	>tr|B1KCZ6|B1KCZ6_SHEWM Trk system potassium uptake protein OS=Shewanella woodyi (strain ATCC 51908 / MS32) GN=Swoo_0024 PE=3 SV=1 MQYRTIIRITGFLMGLFSLSLLPPALVAVIYKDGGGTAFIQAFFLSLFLGFLLWYPNRRHKKDLRTREGFLLVVLFWAVLGSIGAVP FIFTNQPDLSITDSFFESFSALTTTGATVIVGLDSLPKAILFYRHLLQWLGGMGIIVLAVAILPMLGIGGMQLYRAEMPGPVKDSKMTPRI AETAKALWYIYFALTIACAVAYWLAGMDVFDAICHSFSTIAIGGFSTHDASMGYFDSTAINMVCVVFLLIAALNFSLHFAAFTRRGINLKI YFKDAEFKALVIVQLVLTGICFGVLYHSGIYDSPEQTLDFALFQAVSISTTAGFGTESFHMWPLFLPMLLIFSSFIGGCGGSTAGGIKVIR MILLLKQGSRELKRLVHPRGMFSIRIGDKALPDRIIDAVWGFFSAYALVFVLCMLLLMAMGMDNITAFSATAACLNNLGPGLGEVASNY ASIGDGEKWVLLMAMLFGRLEVFTLLVLFTPTFWKN
4E-86	299	11.4	1.4E-85	297.1	7.9	1.6	1	R4V295_9GAMM	Trk system potassium uptake protein	SPISAL_00315	Spiribacter salinus M19-40	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Spiribacter, Spiribacter salinus, Spiribacter salinus M19-40	1260251	>tr|R4V295|R4V295_9GAMM Trk system potassium uptake protein OS=Spiribacter salinus M19-40 GN=SPISAL_00315 PE=3 SV=1 MHPDAVQRVLGVLLMVFSLTMLPPGLLSVAAADGAATAFFMTFAALLSLGALLWLPVRQSRRELRTRDGFFVVAMFWVVLSAA GALPLILQKVAPFSLVDALFESVSGLTTTGATAVIGIDQLPISLRYYRQQLQWLGGMGIIVLAVAILPMLGIGGMQLYRAELPGPVKDGK LTPRIAETAKALWYIYLGLTVVCAVAYWLAGMSVFDAIGHAFTTIATGGFSTHDASIGYFDSALIEMIAVVFMLMSALNYSLHFMAWRR MSTEPWRHDPELVTFLSAVAVVCVLAMGGLFIYQAAHDLPLDETWHHAIFQVVSFATTTGYTTASYYVWPAFLPVLLLFIAVVGGCAN STSGGLKVVRILLLWRQGGREVMRLIHPQAQIPIKIGNRPVNERVIDAVWGFFAAYVVLFVILMLSLLAMGLDQVTAFSAVASGLANLG PALGDVAANFASVGDGPKLVMCVAMILGRLEFLTLLVLFTPAFWRR
4.3E-86	299	0.5	3.4E-83	289.2	0.3	2	2	A0A0D2XTE5_FUSO4	Uncharacterized protein	FOXG_07247 FOXG_06683	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	574	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0D2XTE5|A0A0D2XTE5_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_07247 PE=4 SV=1 MSLLALPILAPYGNISVTDAYFFGASASTESGLNTVDVKDLKTYQQLYIYFIPIITNLGFINIGVVIVRLYWFKKHLKRRAPQLFSPR RRDASGENVEDGKIVEEKAQNDLPAVTAPSNNLEQHATTDTPVPRTTTITFDPSIDQRRDSATLYIPGPQDRDRDRITPVPTAASGEP SSSMRRRLPRRISTGDGLQMTATRSMDRVAGIASSLLMMGSETTRPRRQSSSSVSQQQPALNDRPFLSRQATIGRNSEFQNLTSHD RELLGGIEYRSLKLLLKIVTAYFFGVHLFGAICLLGWIQTANPKYREYLQSTGQDKNWWAFYSAQTMVDNLGFTLTPDSMISFRDAKW PMILMSFLAFAGNTLYPVFLRLIIWTMSKLLPKHSSTQEPLGFLLNYPRRCYTLLFPSKPTWILFGIIFSLNFIDVLLIIILDLDNPEVASLPL DSRIPAAIFQAASARHTGTATFNLANVNPGVQLSLLVMMYIAVFPIALSIRLSNTYEEKSLGIWEPEGSLNERNGKSYLMQHIKNQLGFD LWYIFLGTFCICVAEATRIADVKDPVGISSPWQVLFDSIS
4.7E-86	299	18.2	1.4E-84	293.8	12.6	2	1	Q21PV9_SACD2	Trk system potassium uptake protein	trkH Sde_0017	Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Saccharophagus, Saccharophagus degradans, Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024)	203122	>tr|Q21PV9|Q21PV9_SACD2 Trk system potassium uptake protein OS=Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024) GN=trkH PE=3 SV=1 MHYAIISKVLGILLMLFSLTMVPPIFVSLFYKDGAYLSFIMAFAITFSTGGLAWLPVYRVRQDLRTRDGFLITSLFWSVLGIFGSLPF ILAEATQLTAVDAVFESLSGLTTTGATVLTGLDFLPKSILYYRQQLQWLGGIGIIVIAVAVLPMLGIGGMQLYRAETPGPVKDSKLTPRIT ETAKALFFIYVSLTLACLFAYWAAGMSLFDAIGHAFATVAIGGFSTHDLSIGYFDSPLIMLICMVFMVLSGVNFALHFYAWQAQTIRHYL QDPEFKFYASMILLGVFITVSYLFGKGTYGLSESAIKGSFELISVLTTTGFGVADFSLWPTFLPFLIFMFAFMGGCAGSTGGGIKMMRV LLIMKQGVREIHRLIHPNAVIPIKIGTKSVSDRVVEAVWGFFAIYVIAYLTMTIVLLATDLDFVTAFTAVGACLNNLGPGLGSVASHYGDL NSAAKWVLCFAMLLGRLEVFTLLVLFTPMFWRR
4.9E-86	299	18.9	1E-85	297.6	13.1	1.4	1	K8WAC6_PRORE	Trk system potassium uptake protein	OOC_19262	Providencia rettgeri Dmel1	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia rettgeri, Providencia rettgeri Dmel1	1141663	>tr|K8WAC6|K8WAC6_PRORE Trk system potassium uptake protein OS=Providencia rettgeri Dmel1 GN=OOC_19262 PE=3 SV=1 MHFRAITRIVGLLVIIFSFTMVIPGIVALIYRDGAGRAFSQTFVTALLIGLFLWLPTRNSRHELKAKEGFLIVVLFWTVLGSVGALPFI FSERPNLSVTDAFFESFSGLTTTGATTLGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRI AETAKTLWLIYVLLTIACAVALWIAGMDVFDAISHSFSTIAIGGFSTHDASIGYFNSPAINTIIGIFLIISGCNFGLHFAVLTGRSLGIYWRDP EFRMFISFQFVLVVICTLVLMFHSVYSSFGQTLDQAFFQVVSMATTAGFTTDSFSGWPLFLPMLLLCAAFVGGCAGSTGGGLKVIRILL LFLQGSRELKRLVHPNAVYTIKLGQRALPERIIEAVWGFFSAYALVFVVSLLLIATGVDEFSAFSAIATTLNNLGPGLGTVADNFTTMN PTGKWILVVTMLFGRLEVFTLLVLLTPTFWRE
6E-86	298	13	9.5E-85	294.4	9	2	1	B8GU18_THISH	Trk system potassium uptake protein	Tgr7_0202	Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Thioalkalivibrio, Thioalkalivibrio sulfidiphilus, Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	396588	>tr|B8GU18|B8GU18_THISH Trk system potassium uptake protein OS=Thioalkalivibrio sulfidiphilus (strain HL-EbGR7) GN=Tgr7_0202 PE=3 SV=1 MQLTVIQRILGLLIMLFSVTMLPPAAVGFYYGEQSMWPFLEAFAILLLTGLIIWAPVYRVRRELRLRDGFVVVLMFWLVLGVFGAL PLYLDKALHISVTDAVFESMSGLTTTGATVITALDDLPRAILIYRQQLQWMGGMGIIVLAVAILPMLGVGGMQLYRAEMPGPVKDTKLT PRITETAKALWYLYLGFTVACALAYWAVGMEPFDAIAHSFSTVSLGGFSTHDASIGYYDSAAVEAVAITFILLGGVNFALHFLTWRGLS VRHYWQDAEFRTYVLIISTVAAVSVGYLYYTATTEGWSETLRQGIFQAVSIGTTTGFTTTDFYNWPGFLPVLLIFTSFIGACAASTGGG IKVIRFLLLFKQGQREVVRLVHPNAEIAVKVGRSALSDRVVEAVWGFFSAYVAVFAVIMLALMASGLDQVTAFSAVAASLNNLGPGLG DVGPHYADINDFAKWMLCIAMLMGRLEIFTVLVLLTPAFWRK
6.5E-86	298	15.3	9.4E-86	297.7	10.6	1.1	1	F9T296_9VIBR	Trk system potassium uptake protein	IX91_15315	Vibrio tubiashii ATCC 19109	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio tubiashii, Vibrio tubiashii ATCC 19109	1051646	>tr|F9T296|F9T296_9VIBR Trk system potassium uptake protein OS=Vibrio tubiashii ATCC 19109 GN=IX91_15315 PE=3 SV=1 MQFRSIIRIVGLLLALFSLSMLAPALVALIYRDGAGVPFVTTFFVLLFCGTVCWFPNRRHKHELKARDGFLIVVLFWTVLGSAGSL PFLIADNPNVSVTDAFFESFSALTTTGATVIVGLDDLPKAILFYRQFLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDTKMTPR IAETAKALWYIYLSLTIACAASFWLAGMTPFDAISHSFSTIAIGGFSTHDASMGHFDSYAINMITVVFLLISACNYSLHFAAFASGGVHPK YYWKDPEFRAFIFIQVLLFVVCFLVLLNHHSYNSVYDAFDQALFQTVSISTTAGFTTTGFAEWPLFLPVLLLFSSFIGGCAGSTGGGMK VIRILLLTLQGVRELKRLVHPRAVYTIKVGGSSLPQRVVDAVWGFFSAYALVFVVCMLGLIATGMDELSAFSAVAATLNNLGPGLGEVA LHFGDVNDKAKWVLIVSMLFGRLEIFTLLILLTPTFWRS
7E-86	298	20.2	3.7E-85	295.7	14	1.8	1	K4KNE5_SIMAS	Trk system potassium uptake protein	M5M_12400	Simiduia agarivorans (strain DSM 21679 / JCM 13881 / BCRC 17597 / SA1)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, Simiduia, Simiduia agarivorans, Simiduia agarivorans (strain DSM 21679 / JCM 13881 / BCRC 17597 / SA1)	1117647	>tr|K4KNE5|K4KNE5_SIMAS Trk system potassium uptake protein OS=Simiduia agarivorans (strain DSM 21679 / JCM 13881 / BCRC 17597 / SA1) GN=M5M_12400 PE=3 SV=1 MHFSVIFRVLGVLLMIFSLTLLPPIGISLWYADSHHYAFLAAFGITFATGLGMWLPVYRAKHDLQTRDGFLITALFWVVLGLFGSL PFVISAELDASFTDAMFESMSGLTTTGATVFTGLDFLPKSILYYRQQLQWLGGIGIIVIAVAVLPMLGIGGMQLYRAETPGPVKDNKLTP RITETAKALFIMYLGITFICALAYYLAGMSEFDAIGHAFSTVAIGGFSTHDASIGYFNSPLIMGICTFFMFFSGVNFALHYFGWREHSVSH YFKDPEFRFYGSWVLVGMAITILYLYYTGTYGFFDSVMHGSFEFVSVLTTTGFGTADFSAWPTFLPFMLILFAFMGGCGGSTAGGMK VMRVMLICKQGYREIKRLIHPSAIFPIKVGKKSVPDRVVEAVWGFFAVFIISFMVMFLLLLASGLDFTTSFSAVAACITNLGPGMGDVAA HYGNINDFSKWILCFAMLLGRLEVFTLLVLFSPMFWRR
8.9E-86	298	15.9	1.1E-85	297.4	11	1.1	1	D4ZDA4_SHEVD	Trk system potassium uptake protein	trkH-1 SVI_0055	Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella violacea, Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)	637905	>tr|D4ZDA4|D4ZDA4_SHEVD Trk system potassium uptake protein OS=Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12) GN=trkH-1 PE=3 SV=1 MQYRTIIRITGLLMGLFSLSLLPPALVAVIYKDGGGTAFIQAFVLSLFLGFILWYPNRRHKKDLRTREGFLLVVLFWGVLGSIGAVP FIFSSQPDLSITDSFFESFSALTTTGATVIVGLDYLPKAILFYRHLLQWLGGMGIIVLAVAILPVLGIGGMQLYRAEMPGPVKDSKMTPRI AETAKALWYIYFLLTVACAFSYWVAGMNVFDAICHSFSTIAIGGFSTYDASIGHFDSPAINMVCVVFLLIAALNFSLHFAAFTRRGINLRV YFKDAEFKVLIIVQLVLTGICFATLYHTGIYDSPEETFDYALFQAVSISTTAGFGTESFHMWPLFLPMLLIFSSFIGGCGGSTAGGIKVMR MILLLKQGSRELKRLVHPRGMFSIRIGNKALPDRVIDAVWGFFSAYALVFVICMLALLAMGMDNISAFSATAACLNNLGPGLGEVASNY ASINDGSKWILLLAMLFGRLEVFTLLVLFTPTFWRS

1.1E-85	298	0.3	1.5E-85	297	0.2	1.1	1	A0A066WV32_COLSU	Putative low-affinity potassium transport protein	CSUB01_07611	Colletotrichum sublineola (Sorghum anthracnose fungus)	630	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum sublineola (Sorghum anthracnose fungus)	1173701	>tr|A0A066WV32|A0A066WV32_COLSU Putative low-affinity potassium transport protein OS=Colletotrichum sublineola GN=CSUB01_07611 PE=4 SV=1MVVVARLYWFQQRLKTMAATERGNPDDLEANCPPESRDNKVIRDMRNPQTEHTHNVEANAEQDTPRTTYPNPTARSTTITFG DKVPHPRSHQTGETVLHVPGPRDRDDGKMAATVLVTSQLNVALAGHSMIEIDEAADNDDGQSTPCTSDRPKELAWLLMPEIDAIRPV ESSATGLSRRRPHNLEGPAMRAARSMEKVASSILVLGHGKSSERESHRLDLSTRRRTADLPQLSRQVTIGRNSQFFHLTERDRELLG GIEYRSLKLLLKIVSSYFLGLHLLGVICLLPWIMHAPYKYTAWLAENGQGRTWWAFYSAQTMVDNLGFTLTPDSMATFKDATWPMLV MTFLAFAGNTCYPVLLRLVIWAMSKVVNKKSATKEHLQFLLDHPRRCYTLLFPSRPTWILFGIVFVLNFIDVLLIIVLDLDNPAVNDLAMG PRILSALFQAASARHTGTATLNLSLVNPAVQFSLLCMMSNLGVFPIAISIRASNTYEERALGVYGASSSHLDENNGYSYVMAHIRNQLS FDLWYIFLGTFCICIAESQRIMDLNEPLDDKLLTLDINRTDPIGFPNRPRPRRRLQFFNGDSILTTRFPSLSSRGLRTLIPPGRTTPPMMQ TFAAAAEDDDDNDNLL
1.3E-85	297	18.9	2.9E-85	296.1	13.1	1.4	1	A0A060B7W7_9GAMM	Trk system potassium uptake protein	FF32_09220	Halomonas campaniensis	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas campaniensis	213554	>tr|A0A060B7W7|A0A060B7W7_9GAMM Trk system potassium uptake protein OS=Halomonas campaniensis GN=FF32_09220 PE=3 SV=1MSLRVILRILGLLLMLFSLTMLPPMLISLWFRDGVWHAFMSGIAISVITGLLLFLPNRRAHKELRIRDGFIIAAMFWTVLALFGSLPL MLFGEGSLGITDAVFESFSGLTTTGATVITGIDFLPESILYYRQQLQWLGGMGIVVLAVAILPTLGVGGMALYRTEIPGPLKDSKLTPRIT ETAKALWYIYATLTLACMVAYMLAGMSWFDALGHSFSTVAIGGFSTYDASIGYFDSAAIELICVGFMLISAFSFSLHFIAWREKRLLHYF QDPEARFLMIFLAGLTTITVITLWLTDTYDDFEGLRHALFEVVSVATTAGFAVADFSGWPGALPFLLFVAAFVGGCSGSTAGGMKVIRII LILKQGMREVMRLIHPNAVIAVKVGKVSVPDSIAQAVWGFFSAYVMLFFLMLVGVMATGVDQVTAWSTVGSALNNLGPALGEASSHY GDLPSLAKWILVLAMLLGRLEIFTVLVLFTPAFWRR
1.3E-85	297	21	3E-85	296	14.6	1.5	1	I1YJ42_METFJ	Trk system potassium uptake protein	Q7C_1794	Methylophaga frappieri (strain ATCC BAA-2434 / DSM 25690 / JAM7)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Piscirickettsiaceae, Methylophaga, Methylophaga frappieri (strain ATCC BAA-2434 / DSM 25690 / JAM7)	754477	>tr|I1YJ42|I1YJ42_METFJ Trk system potassium uptake protein OS=Methylophaga frappieri (strain ATCC BAA-2434 / DSM 25690 / JAM7) GN=Q7C_1794 PE=3 SV=1MQLLTIQRILGILLALFSLTMLPPIFVSWLFEDGEAQAFISALFLLLAFGLALWLPARKHRKELKIRDGFIVVVMFWLALGLSGSLPF FLSTNPLMSFTDAVFESMSGLTTTGSTVLTGLDELPQSILFYRQFLQWLGGMGIVVLAVAILPLLGVGGMQLYRAETPGPMKDAKLTP RITETAKALWYIYMSLTIACAIAYHWAGMTWFDAICHSFSTVAIGGFSTHDASIGHFNSGLIEMIAVLFMLISALNFSLHFLAWRGRSVK HYWQDSELRVFFGIMLVVSLVTFAYLMLTATVEGIGLTARQAIFQTVSIGTTAGFATADFAYWPGFLPILLLFCSYIGGCAFSTAGGMK VIRVMLLFKQGYREVLRLIHPNGVFAIRVNGKALPAKVVGAVWGFFALYVFCFTIMHLALMSTGLDVVTAFSAVTACLNNLGPGLGDV SANFGTINDTSKWILCVAMLLGRLEIFTLLVLLTPAFWRR
1.4E-85	297	5.7	4.3E-82	285.6	0.5	2.2	2	A2QAA9_ASPNC	Aspergillus niger contig An01c0330, genomic contig	An01g10810	Aspergillus niger (strain CBS 513.88 / FGSC A1513)	1025	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus niger, Aspergillus niger (strain CBS 513.88 / FGSC A1513)	425011	>tr|A2QAA9|A2QAA9_ASPNC Aspergillus niger contig An01c0330, genomic contig OS=Aspergillus niger (strain CBS 513.88 / FGSC A1513) GN=An01g10810 PE=4 SV=1MERVNPALLCLGEMESTEDHPQIPYSRREMIDCLGLEIYKTPEEWLRLTAFQPNKFALVSFPGLDWLSFNFQVQFAACDCPRLE DLNQYDCTNYRVITNVPGLYVTIDAYTYLDIQHFSMLRNLLAIPVWDRILTVVTPHFQGSFACGSVFLNMLFQSYVHVNSESSIQVLCK MPSAMSDQSTIIPANRSGYIHHKSPAGSTVRTTPTLYDIIPATESKEWVESSVKVNCVVPLAKIMNKETAEAQGNIGTRGNQAPRTDPE KSAHLEDRGRKSPTGNYEMKPNAVGAKIKSRPASHLTLSDLDWTAYATTDQKSKHELSYTSKNPSEIFAKPLWLALLSRSIIAMLPPFN FLTLHYVYFIATSLICSVIFWGSSTPRRSVSYTDSLFLCISAMTGAGLNTVDLSSLNSFQQSILFALLLLGHAILISITVLFVRMGAFQAKF KGISLERARKALQQQLVGQDTILEPIQESVASEEHYQLAKIDGATLDVKHAVTAGAAPADKCNDVRDDDQIRWVDDDQVTLSHMRAR QKHHHHHRVFPMVGVGARLDLNNHPRDAAPRMTQNDGDTDLPALKGLIKGTQKYFRSKGSIARNSQFHGLTPEERERLGGVEYKAV SLLLVIVALYWILFLICGIIGMGTWIAVNHPDIPRSNGLSPFWTGAFFAVSAFVNSGMSLLDANMTAFQTNAYPLLTMAFLILSGNTLYPC FLRFIIWAMRCLIPDKPSWATWKVTLDFILDHPRRVYTNLFPRRHTWYLLGTIIILNAIDWAGFEVLSIGNKEIESLPTGYRVLDGLFQAC AVRAGGFYVVTIADLRQGLLVLYGKHLFPQALIRIILTNTNVYEERSLGIYAHDNTDDETEEKASPNMLIQLVRHHLLGRQDASTPEASR SYFVHQQLRSQLSHDLWWIALAVFLIAIAESGNYSRMPVAYSTLNIIFEVVSAYGCVGISVGFPSSNASFCSSWHTISKLILAAVMLRGR HRGLPVAIDRAVMLPNESLEWAEEEDAAMRREQSRAWGSDKMPVGSV
1.6E-85	297	20.2	6.2E-85	295	14	1.7	1	Q1QTI9_CHRSD	Trk system potassium uptake protein	Csal_2873	Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Chromohalobacter, Chromohalobacter salexigens, Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)	290398	>tr|Q1QTI9|Q1QTI9_CHRSD Trk system potassium uptake protein OS=Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768) GN=Csal_2873 PE=3 SV=1MSLLVILRIVGLLLMLFSLTMVPPVAISLIFDDATWDAFVIGLGISFATGMALYWPTRHARRELRTRDGFLITVMFWSVLGLFGSLP LMLAEDPSLSLTDAVFESFSGLTTTGATVLTGIDLLPESIRFYRQQLQWLGGMGIVVLAVAILPTLGIGGMQLYRTEIPGPLKDSKLTPRI TETAKALWYIYAALTLACFLAYWLAGMSWFDAIGHSFSTVAIGGFSTHDASIGYFDSATIELICVFFMVISSLSFGLHFAVWREKRLRHY LVDPEFRFFIIFLTLLVTITIATLMLSGTYTDTLGLRHGLFEVVSVATTTGFGVADFTAWPGVLPFMLFIAAFVGACSGSAGGGMKVIRIL LILKQGLREIHRLIHPNAVFSVKVGKMRISSGVAEAVWGFFSAYLLLFVLMLMVLLATGLDQVTAWSAVGSALNNLGPGLGSVATHYG DMPALAKWTLVMAMMFGRLEIFTILVLFTPAFWRR
1.9E-85	297	9.1	6.7E-46	166.2	1.4	4	4	C4JEH1_UNCRE	Putative uncharacterized protein	UREG_00810	Uncinocarpus reesii (strain UAMH 1704)	627	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Onygenaceae, Uncinocarpus, Uncinocarpus reesii, Uncinocarpus reesii (strain UAMH 1704)	336963	>tr|C4JEH1|C4JEH1_UNCRE Putative uncharacterized protein OS=Uncinocarpus reesii (strain UAMH 1704) GN=UREG_00810 PE=4 SV=1MLSIVGTIILYPIKSMSGIDAFFQAVSGSTVTGLNTVDLKEMSLYQQITVWFLPMLGNMCFVNLVVVYVRLRWFEKKFNDIVQLSR LPSSERSRAHLLSVSSKADRTDGTTNTHNIRVLHPDPADEEANWATLRHRPQASANGESDSSTAKAPSPENVERSAQPGHITFSEDT FDKPRGRALRIPGPREFEKGHGVQEVDDEDDADMTKSINDASGAGPSDATRKLPTMERLLSRAASVEHAASSAFIIGGSSKARSRSR SRALSRTSSRTTIQALPYLSYNPTVGRNSKFLGLTDEQKEELGGIEYRSLRLLLKIAAGYYFFFHVLGAVCLVAWIWNSERKYRDYVRN DCAINPTWCFRESTFPMLWMTFLIYIGNTAYPCMLRLIIWIAFKLTPEGAAIKEPLNFLLDHPRRCYTVLFPSKVTWVLFGSLVVINGFD VILFLILDLHYPEVTVIKSGWHRFCAALFQTASARTTGTSSFAVAKVHPAAQFSLMVMMYISVFPIALSVRGTNTYEESSLGIFDDSEEL VEMKRTSYLGVHIKMQLAFDLCGNVGLSLGHPSINTALTGKFSTVGKLVICAMMIRGKHRGLPYEVDRAIILPGEKRLAEEDARLEAMS HGLSRRHTN
2.1E-85	297	18.1	3.6E-85	295.8	12.6	1.2	1	U4K866_9VIBR	Trk system potassium uptake protein trkH	trkH VIBNI_A0034	Vibrio nigripulchritudo	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio nigripulchritudo	28173	>tr|U4K866|U4K866_9VIBR Trk system potassium uptake protein trkH OS=Vibrio nigripulchritudo GN=trkH PE=4 SV=1MQFRSIIRIVGLLLALFSVSMLAPAFVALIYRDGAGVPFVTTFFVLLIAGGFFWFPNRHHRHELKARDGFLIVVLFWTVIGSAGALP FLISDTPDISVTDAFFESFSALTTTGATVLVGLDDLPKAILFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRI AETAKALWYIYLSLTIACAAAFWLAGMSLFDAISHSFSTIAIGGFSTHDASIGYFDSTAINMITVVFLLISACNYSLHFAAFASGGVHPKYY WKDPEFRAFFFIQGILFLICFLLLLKHHSYTSVFDAFDQALFQTVSISTTAGFTTTGFSEWPLFLPVLLLFSSFIGGCAGSTGGGMKVIRI LLLTLQGARELKRLVHPRAVYTIKVGGTALSQRVVDAVWGFFSAYALVFVVCMLALIATGMDELSAFSAVAATLNNLGPGLGDVALHF GDINDTAKWVLVVSMLFGRLEIFTLLILLTPTFWRS

2.4E-85	296	0.6	3.7E-83	289.1	0.1	2.1	2	A0A0J9VL89_FUSO4	Uncharacterized protein	FOXG_11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	647	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9VL89|A0A0J9VL89_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLV WFRRYLKNAAPALLSRRRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDI LSPTIKEEKVKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRR RSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIII GYYVFLHCLGAVCLIAWVQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLR LVIWATSKAVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHT GTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHK KIMDGNDPAFTMWPMLFEGVSA
2.4E-85	296	4.5	2.7E-84	292.8	3.1	1.9	1	W0E6Q9_MARPU	Trk system potassium uptake protein	MARPU_16000	Marichromatium purpuratum 984	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Marichromatium, Marichromatium purpuratum (Chromatium purpuratum), Marichromatium purpuratum 984	765910	>tr|W0E6Q9|W0E6Q9_MARPU Trk system potassium uptake protein OS=Marichromatium purpuratum 984 GN=MARPU_16000 PE=3 SV=1MRLPLIGAIVGVYALLFGLTLLAPIAVGLWYGEPQWRHFLWPMLGSIGLGALLWLGGRHQARTLGVADGYLVVALFWILLSLLG AWPLHLGFGLAPVDALFESTSGVTTTGATVISGLDTLPRALLFYRQQLQWFGGMGLIVLGLAVMPLLGIGGMQLYRAEAPGPLKEEKL TPRLTQTARTLWALYLGLTLACALAYWLAGMTPFDALCHSLSTVSTGGFSTHDASIGYFASPAVETVAVCFMLLAAINFAVHYAAWSS REPMRYLRDAETRAFLALVFGCVLLIGVVLRLEGGYEGLDESLRDALFEVVSVVTSTGFGTVDFAHWPDFLPILLIYISFIGGCGGSTA GGIKVLRVLLMVKQGLLEIRQQIHPHALLPLRLGGRSVDPRLARSVWGFFALYLTTFALLTLLMIHAGLAPLDAFSAVATSLNNLGPGLG EVATSFATVSDLGKLIAVGAMLLGRLEVLTILVILSPAFWRR
2.8E-85	296	11.9	5.5E-85	295.1	8.2	1.5	1	V4JLF6_9GAMM	Trk system potassium uptake protein	N838_08775	uncultured Thiohalocapsa sp. PB-PSB1	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiohalocapsa, environmental samples, uncultured Thiohalocapsa sp. PB-PSB1	1385625	>tr|V4JLF6|V4JLF6_9GAMM Trk system potassium uptake protein OS=uncultured Thiohalocapsa sp. PB-PSB1 GN=N838_08775 PE=3 SV=1MKRFIAVQTVLGLLLMVFSITMLPPALVALAYGDGSGMPFVYAFLVILGIGMLIWLPVAHRRQELRIRDGFLVVVLFWVALGLSGA LPFWISPEPDLSLTDSIFESLSGLTTTGATVILGIDELPHSMLWYRQQLQWFGGMGIIVLAVALPMLGVGGMQLYRAETPGPIKDTKL TPRITETAKALWYIYLGLTIACGLAYWAAGMNAFDAIGHAFSTVAIGGFSTHDASIGYYESRLIEMIAVVFMLLSGVNFALHFIVVRDKNP LVYVRDSEFRFYLFMMVLATAIVTVALFRTDTYISWGDSFIKGLFQVVSIGTTTGFTTAEFYYWPPFTGILLLFLAFVGGCAGSTGGGIK VIRFLLLIKQGMREIERLIHPNAQLPVRVGGKVVNHRIVDAVWGFFSLYVAAFTFMYLALAATGLDLLTAFSAVAACINNLGPGLSTVGA DYHDMHDAGIWILCFAMLLGRLEIFTLLVLLAPAFWKR
3E-85	296	19.6	4.5E-85	295.4	13.6	1.2	1	A0A0C5UZA8_9GAMM	Trk system potassium uptake protein	YC6258_00610	Gynuella sunshinyii YC6258	468	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, unclassified Oceanospirillales, Gynuella, Gynuella sunshinyii, Gynuella sunshinyii YC6258	1445510	>tr|A0A0C5UZA8|A0A0C5UZA8_9GAMM Trk system potassium uptake protein OS=Gynuella sunshinyii YC6258 GN=YC6258_00610 PE=3 SV=1MLFSLTMLPSAMVSLLYQDGAYETFIIAFGVVLVSGFLIWLPVMNYQGDLRTRDGFVITVVFWLVLGLAGSLPFYFAPSVKLDFT NAFFESFSGLTTTGATVITGLDDLPQSILFYRQQLQWLGGMGIIVLAVAILPLLGVGGMQLYRTETPGPVKDNKLTPRIKETAKALWYIY VTLTIACALAYFIAGMGVFDAITHAFSTIAIGGYSTHDASIAYFDSVAIETVAVIFMLIAAANFSIHFVAFRHRSIKIYFQEPEYRTFLYIFGV LLLIVVFTLWVTGTYPALSALRYGLFEVTSILTTTGFGAADFSSWPLFVPFMLFLSSFIGGCAGSTAGGMKVIRVMLITKQGLREVQRL MHPQGVFPLKVGKRTMSDNVIQSAWGFFSVYILMYGLIFMLLLATGLDFTTSWSAVGACMNNLGPGLNEIAQHYENINEPAKWILCFA MLLGRLEVFTLLVLFTPMFWRR
3.5E-85	296	19.9	6.8E-85	294.8	13.8	1.4	1	M1SMD9_MORMO	Trk system potassium uptake protein	MU9_1980	Morganella morganii subsp. morganii KT	488	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Morganella, Morganella morganii (Proteus morganii), Morganella morganii subsp. morganii, Morganella morganii subsp. morganii KT	1124991	>tr|M1SMD9|M1SMD9_MORMO Trk system potassium uptake protein OS=Morganella morganii subsp. morganii KT GN=MU9_1980 PE=3 SV=1MISTRTRVIIHLSSFLIVIYSLTLLLPMLVALIAQEQSFFAFAGSFLIFFPAGLVCWYRSKTTGLQLQTRDGFLVIAVFWLLFSVISAM PFWLDDHLNMAFEDALFEGVSGITTTGASVFHNVTDLPRSVLYYRAQLNFIGGLGVIVLAVAIFPLLGIGGMRLYQSEMPGPFKDEKLT PRLASSARNLWFTYLLLGFCCTVAFKLAGMTWFDALCHGLSTVSLGGFSTYSESIGYFNSSAIELVAGAFSLLSAVNFTLYFVALAKRS LKPLFSNTELRFYFAVAALIIGLVFFEVWRANMYSSAEESFVHAFFLTSSMLTDNGLATGDYAQWPSHIIVLLLFASFFGGCVGSTCGG IKAIRFLILSKQSWREVYSLIHPKAQTLIKVGDTVVQHRLINSVLSFFFLYVICTCFFIWCLNLMGYDLMTSFASVAACINNMGLGFGLTA PGFGEISPAAKYLLCFAMLLGRLEIYTLLVLLSVSFWRNWP
3.7E-85	296	23.9	4.8E-85	295.3	16.6	1.1	1	A1SRF0_PSYIN	Trk system potassium uptake protein	Ping_0197	Psychromonas ingrahamii (strain 37)	488	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Psychromonadaceae, Psychromonas, Psychromonas ingrahamii, Psychromonas ingrahamii (strain 37)	357804	>tr|A1SRF0|A1SRF0_PSYIN Trk system potassium uptake protein OS=Psychromonas ingrahamii (strain 37) GN=Ping_0197 PE=3 SV=1MAFRSIIRIVGMLVGLFSLTMLPPAFISTFYEGAAGEDGGNFLAAFVMTLFIALLLWIPNRHVKKELRVREGFLIVVLFWVTLGSVG AIPFMMSSSIEMDAASAFFESFSGLTTTGATVIEQLDTLPKSILFYRQMLQWFGGMGIIVLAVAVLPMLGIGGMQLYRAEAPGPVKDSK MTPRIAETAKALWNVYLFVTVACMLAFWLAGMSLFDAIGHSFSTVSIGGFSTYNESIGHFDSNLINLITVLFLLISGVNYALHFSAFSSRK FSFNIYRQDPELRAFIFIQVLLTTVCFIGLMGHEVYDSIENTFSQALFQAVSISTTAGFTTTSFHDWPAFFPILLIMSSFIGGCAGSTGGG MKVIRILLLNLQGIRELKRLVHPKAVFKIKLANNALPDRVIEAIWGFFSTYALVFVVCMLALLLTGMDELSSFSATAAMLNNLGPGLGAVA LHFNEVSAASKWIMILAMLFGRLEIFTLLVLFTPIFWKN
4.4E-85	295	12.6	6.2E-84	291.7	8.7	1.9	1	Q3JEH4_NITOC	Trk system potassium uptake protein	Noc_0242	Nitrosococcus oceani (strain ATCC 19707 / NCIMB 11848)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Nitrosococcus, Nitrosococcus oceani, Nitrosococcus oceani (strain ATCC 19707 / NCIMB 11848)	323261	>tr|Q3JEH4|Q3JEH4_NITOC Trk system potassium uptake protein OS=Nitrosococcus oceani (strain ATCC 19707 / NCIMB 11848) GN=Noc_0242 PE=3 SV=1MQLAVVQRILGLLLALFSTAMLPPVIVSLFYRDGAGAEFLIAFGLILGIGLLCWLPVRNYRQELRLRDGFVVVVMFWVVLSLSGAL PLFLTAEPRLSFTDAVFESVSGLTTTGATVITGLDNLPKSVLFYRQELQWLGGMGIVVLAVAILPMLGIGGMQLYRAEIPGPMKTTKLT PRIAETAKALWLIYLGLTIACATAYWIAGMTLFDAVGHSFSTIAIGGFSTHDASMGYFNSPLIEMIAVFFMLLAGVNFSLHFLAWRHRTV GHYWQDEEFRTYLSVLAGVAALTSSYLWITHSFDNPLLALQHGIFHTVSIGTTTGFTSSDYYSWPGFLPILLLMTSYIGGCAASTAGG MKVIRILLLYKQGVREIKRLIHPSAIIPKIGSKSLPDRIVEGVGGFMAVYVACFIVMYLLLLATGLDMITSFSAVTACLNNLGPGLGQVGA HYEVINAASKWVLCFAMLLGRLEIFTLLVILSPTFWRR
4.8E-85	295	17.3	1.1E-84	294.1	12	1.5	1	A0A0D8PSX1_9GAMM	Trk system potassium uptake protein	UB37_10005	Photobacterium iliopiscarium	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium iliopiscarium	56192	>tr|A0A0D8PSX1|A0A0D8PSX1_9GAMM Trk system potassium uptake protein OS=Photobacterium iliopiscarium GN=UB37_10005 PE=3 SV=1MQFRSIIRIVGLLLALFSVTMLIPALVALIYRDGAGFPFVVTFFLLLAGGSALWFPNRYHRRELKARDGFLIVVLFWAVIGSAGAVP FLLSKNPDLSVADSFFESFSALTTTGATVIVGLDHLPKAILFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAETPGPVKDSKMTPR IAETAKTLWYIYLALTIACTLAFWLAGMSGFDAISHSFSTIAIGGFSTHDASIGYFNSPTINMITVVFLLISACNFSLHFAAFGNGNINLKTY WRDPEFRAFFVVQLILFVICFGLLLKHHSYDHSFDAFDQALFQTVSISTTAGFTTTGFSDWPLFLPVLLLFSSFIGGCAGSTGGGMKVI RMLLLSLQGVRELKRLVHPRAVYTIKLGHKALPQRVVDAVWGFFSAYALVFVVCMLALIATGIDELTAFSAVAATLNNLGPGLGEVAVH FGQINDSAKWILIIAMLFGRLEVFTLLVLFTPTFWRN

5.3E-85	295	16.6	7.1E-85	294.8	11.5	1.1	1	A3Q8U7_SHELP	Trk system potassium uptake protein	Shew_0022	Shewanella loihica (strain ATCC BAA-1088 / PV-4)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella loihica, Shewanella loihica (strain ATCC BAA-1088 / PV-4)	323850	>tr|A3Q8U7|A3Q8U7_SHELP Trk system potassium uptake protein OS=Shewanella loihica (strain ATCC BAA-1088 / PV-4) GN=Shew_0022 PE=3 SV=1MQYRTIIRITGLLMGLFSLSLLPPALVAVIYKDGGGTAFLQAFFLSLLLGFVLWYPNRRHKKDLRTREGFMLVVLFWGVLGSIGAVPFIFSSQPDLSLTDSFFESFSALTTTGATVLVGLDSLPKAILFYRHLLQWLGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIAETAKALWYIYLALTIACAFAYWVAGMDVFDAICHSFSTIAIGGFSTHDASMGYFDSTAINMVCVVFLLIAALNFSLHFAAFTRRGINLKVYLRDAEFKALIVIQLALTLICFATLYHTGIYDSAEETFDFALFQAVSISTTAGFGTESFHMWPLFLPMLLIFSSFIGGCGGSTAGGIKVMRMILLLLQGSRELKRLVHPRGMFSIRINGKALPDRIIDAVWGFFSAYALVFVVCMLILMALGMDNITAFSATAACLNNLGPGLGEVASNYASIGDGEKWVLVVAMLFGRLEVFTLLVLFTPTFWKN
5.8E-85	295	1.1	5.8E-85	295.1	0.8	1.4	1	J4VWM2_BEAB2	Cation transporter	BBA_08177	Beauveria bassiana (strain ARSEF 2860) (White muscardine disease fungus) (Tritirachium shiotae)	600	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Cordycipitaceae, Beauveria, Beauveria bassiana (White muscardine disease fungus) (Tritirachium shiotae), Beauveria bassiana (strain ARSEF 2860) (White muscardine disease fungus) (Tritirachium shiotae)	655819	>tr|J4VWM2|J4VWM2_BEAB2 Cation transporter OS=Beauveria bassiana (strain ARSEF 2860) GN=BBA_08177 PE=4 SV=1MTEAGLNTVNLSTMTTWQQTMLFLLIVFGSTIWVSICTVLTRKHVFYRRFMRLEGLPRQHGKATAQESPRCAGSELPGSRQAPAPDTSDSAAVVAVQESSSPCDSVCALEQGPDRLDCDEQGLSSAKSKQMCGCEYRALELLSIIVPLYFLVWQLLGCISLGAWIHHHMPDTALTNGINPWWLGLFNGVSAFNNSGMSLLDANMMPFQESYFVLVTMGLMILAGNTAYPIFLRFIFWSGMKLLDLTTEATSFRSTRLAMKLLLKDPRRIYTNLFPSRLTWWLVFMLVCLNGIDWVLFEVLNLHNPAVQSIPVGPRVLVGLFQALAVRSGGFYVVPIAQISIAVQFLYVIMMYISVYPVVITIHQSNTYTGDSHHDMDDETHDASHSPRGGIISAASYPAEKRNLATAQETRSVSGVPPAQSFCHGPVNQSAATPTTAIDGRPISTRSTSHSESRHREKRPSLPPRPFSFRSMSPHGTRDGRMSFIHQQIHGQLGQDIRWLVLAVLIIVIIESGHFDADPINFSVFNVIFEVVSAYGTVGISVGTPSGAYSFAGTWYAGSKLVLCLVMLRGRHRVLPMALDRAIQLPDQYLSCRHDEVEEK
6.4E-85	295	18.5	1E-84	294.3	12.8	1.3	1	E0WQY3_9ENTR	Trk system potassium uptake protein	trkH REG_0340	Candidatus Regiella insecticola LSR1	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, ant, tsetse, mealybug, aphid, etc. endosymbionts, aphid secondary symbionts, Candidatus Regiella, Candidatus Regiella insecticola, Candidatus Regiella insecticola LSR1	663321	>tr|E0WQY3|E0WQY3_9ENTR Trk system potassium uptake protein OS=Candidatus Regiella insecticola LSR1 GN=trkH PE=3 SV=1MHFRAIARIVGFLVILFSVTMFIPGLVALIYHDGAGRAFGETFFVALIIGLLLWLPNKTQKHELKSREGFLIVILFWTVLGSVGALPFIFSERPNLSVSDAFFESFSALTTTGATTLAGLDSLPKAILFYRQMLQWLGGMGIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYLLLTILCAFTLWCAGMSVFDAISHSFSTIAIGGFSNHDASIGYFASPAINTIIAIFLLISACNFSLHFAALSGLNLKAYWRDLEFRVFIFIQLILVTICTAVLWQYNVYPSHSDTLNHAFFQVVSMATTAGFTTDTFAKWPSFLPMLLLSSAFIGGCAGSTGGGLKVIRIILLYLQGTRELKRLVHPNAVYTIKLGRRALPEGILEAVWGFFSAYALVFIISVLAIIATGVDEFSAFSAVTASLNNLGPGLGVVADNFISMNDTAKWILVITMLFGRLEIFTLLVLFTPTFWRE
7.3E-85	295	0.3	5.3E-81	282	0	2.1	2	D8QG86_SCHCM	Putative uncharacterized protein	SCHCODRAFT_258434	Schizophyllum commune (strain H4-8 / FGSC 9210) (Split gill fungus)	912	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Schizophyllaceae, Schizophyllum, Schizophyllum commune (Split gill fungus), Schizophyllum commune (strain H4-8 / FGSC 9210) (Split gill fungus)	578458	>tr|D8QG86|D8QG86_SCHCM Putative uncharacterized protein OS=Schizophyllum commune (strain H4-8 / FGSC 9210) GN=SCHCODRAFT_258434 PE=4 SV=1MSSPADVENGHGPDGQAGGDNPSPPPRTGLKAIWAEISDLNFFRVHLLAFTFIPLILSGIFYAAGPHDGSTTTTTSGDEPINLAYLDALFLCYSAMTVCGLATANLSALSKVQQVILYILMLCGNITTVSYCMLLVRMRYFRVKCEYVVKKELEEHRRLPMWMQRTKKGIIDQLSAPTTTEPTLSAQATALAPSTHATLIPSDGRATPKVGVQHPTPGPTPAGTLVERDRHRSGFLNDLLHADSDSDSDTAEEQFLSDAQILSSSPQSGNIDLPQLTPVASRASGVSLGHRSRAAKRKGTGVAFADAVERQQKMMERFPTRRGTTVLAPRGTMVYPPNLPQPTRKNTPARKNAVDMNGPPYADPLSTRYESPHKYTGLGGFPGPAALLAAAARAAAPGVTDKLKNALEVKTEHHTGHDSFLADLRGRLRVWRNGYFETDELTEDDVEKIGGAEYRALRLLSYLVPAYLIGFQAVSCLIFAPWLAATNAYADVFAAQAGGQVRPVTIGWFSVFQVMSSYTGGGMSLVDAGMVPFRNAWPMIVGMSLCILAGNHAMPILLRFTIWVLSKTAGDRSELAQATEFLLKYPRRCFIYLFPAPQTWFLVICLVVFSAAEWLMFPVLNSGLPFYTALPAAERAVSGLFQGLAARASGFPIVPMTDIAPALQFLYMVMMYIAVYPVALSIRSTNVYEERSLGVFEAPEEDEDDEPDVVDQDMRELAPRERVGRYVGWHLRRQVSVDIWWLVWGVFLVAVIERGHLIDPDKKWFDLFRVIFELVSAFGGIGLSLGFPSDNYAFVGAMRPLSKIVVIIIMVRGRHRGLPVAVDRAVLLPRELVTQSSVPATDGAGQEKPDGQPSQEKKSEESTTEGHSATIAGSATALGKGAPSAMSTEESDHAGKPDALVEAIPLRQIGSR
1.3E-84	294	1.5	3.5E-83	289.2	0.1	2.1	2	A0A0J9VKX0_FUSO4	Uncharacterized protein	FOXG_11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	629	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9VKX0|A0A0J9VKX0_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLVWFRRYLKNAAPALLSRRRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWVQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPAFTMWPMLFEGVSA
1.4E-84	294	19.6	2.7E-84	292.9	13.6	1.4	1	A0A0F5ZRY3_9GAMM	Trk system potassium uptake protein	RN22_20750	Grimontia sp. AD028	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Grimontia, Grimontia sp. AD028	1581149	>tr|A0A0F5ZRY3|A0A0F5ZRY3_9GAMM Trk system potassium uptake protein OS=Grimontia sp. AD028 GN=RN22_20750 PE=3 SV=1MQFRSIIRIVGLLLALFSITMLAPAVVAFIYRDGEGFPFVLTFFLLLAGGGLLWFPNRRFRHELKARDGFLIVVLFWTVIGSAGSIPFMLSEQPNMSVTDAFFESFSGLTTTGATVMVGLDNLPKAVLFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIAETAKALWYIYLALTVSCASAYWLAGMSVFDAISHSFSTVAIGGFSTHDASIGYFNSPAINFITVFFLFISACNFSLHFAAFASGKLHPGFYFKDPEFRAFIVIQLILLAIVFGMLINHGTYESEFEAFNQAIFQTVSISTTAGYTTTSFSEWPLFLPVLLLFSSFIGGCAGSTGGGMKVIRILLLSLQGSRELKRLVHPRAVYTIKVGNKALPQQVVDAVWGFFSAYALVFVICMLGLIATGIDELTAFSAVAATLNNLGPGLGEVAVHFGDINSGAKWVLIVSMLFGRLEVFTLLVLFTPTFWRS
1.6E-84	294	18	2E-84	293.3	12.5	1.1	1	Q08A36_SHEFN	Trk system potassium uptake protein	Sfri_0016	Shewanella frigidimarina (strain NCIMB 400)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella frigidimarina, Shewanella frigidimarina (strain NCIMB 400)	318167	>tr|Q08A36|Q08A36_SHEFN Trk system potassium uptake protein OS=Shewanella frigidimarina (strain NCIMB 400) GN=Sfri_0016 PE=3 SV=1MQYKTIIRITGLLMGLFSITMLPSALVAILYKDGGGTAFIQAFFVSIFLGFLLWYPNRHQKGDLRTREGFLIVVLFWTVLGSIGALPFIFSNNPDLSWTDSFFESFSALTTTGATVIVGLDDLPKSILFYRHLLQWMGGMGIIVLAVAILPLLGIGGMQLYKAEVPGPVKDTKVTPRIAETAKALWYIYFLLTTACALAFYFAGMDAFDAICHSFSTIAIGGFSTHDASIGYFQSPLINVICAFFLLIAAVNFSLHFAAFTRRGINVKVYLKDAEFKVLIAVQLVLTAICFATLYQSGIYDSPEKTLDYAFFQVVSISTTAGFGTESFHSWPLFLPILLIFSSFIGGCAGSTGGGMKVIRLILLVLQGSRELKRLVHPKAMYSIRIGSTALPDRIIDAVWGFFSAYALVFVVCMVILMAMDMDAITAFSATAASLNNLGPGLGDVASNYSSISDGAKWVLVMAMLFGRLEVFTLLVLFTPTFWKN

1.6E-84	294	17	2.9E-84	292.8	11.8	1.4	1	D3RV70_ALLVD	Trk system potassium uptake protein	Alvin_2080	Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Allochromatium, Allochromatium vinosum (Chromatium vinosum), Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	572477	>tr|D3RV70|D3RV70_ALLVD Trk system potassium uptake protein OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) GN=Alvin_2080 PE=3 SV=1MKFDAVQKVLGLLLTIFSFSMLPPVVVSLIYDEGGAGPFLAAFTLIFGLGLLIFLPVSRSHEVLRVRDGFLVVVLFWTVLGLAGALP FWLAPNPAVSATDAVFESISGLTTTGATVIIGLDHLPKSILFYRQQLQWLGGMGIIVLAVAVLPMLGVGGMQLFRAEMPGPMKDSKLT PRITETAKVLWYIYLWMTIACALAYWLAGMTVFDAIGHAFSTVAIGGFSTHDLSIGYFDSTAIELIAVIFMVLAGMSFTLHFMVVRRQDP RLYFQDSEFRLYLLVLLTVIAITTLVLYETQTYSSWWESFTKGLFQAVSIGTTTGFATAEFYAWSPFLQILLLLSSFIGACAGSTGGGIKV IRFLLLIKQGVREIGRLIHPNAQIPVRIGGKTINHRVVDAVWGFFSLYVASFILMYLMLAATGLDLVTAFSAVAACINNLGPGLATVGPHY ADLNDTAKWILCFAMLLGRLEIFTLLVLLSPAFWQR
1.8E-84	294	7.5	3.4E-82	285.9	0.1	2.1	2	Q2H7X2_CHAGB	Putative uncharacterized protein	CHGG_03682	Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	800	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Chaetomium, Chaetomium globosum (Soil fungus), Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	306901	>tr|Q2H7X2|Q2H7X2_CHAGB Putative uncharacterized protein OS=Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) GN=CHGG_03682 PE=4 SV=1MPLSVIKKPLDGFREWYSNSPVAEWVAKIRPYLPPINFVTLHYAYFIFSCLILALIFWGTQSSTSLPVSFLDSLFFVMSALTGTGLN PINISQLSIAQQVLLALAMMLGQPILISLWTVLFRRHVFEKRFRAIVKAERARKLKAGSTIWLYSGFSDLLALAKLRSLSKTESKDETANK LPGLGSRIQGSESGAQEQDVEAGLAPDTNVTMPKTPGAKGVAFLEPPPRGNSKKVTIPSDEDRTAEVRTFLQEKRKNVGRNGEFFN LTIKEREYLGGVEYRAVEVLVVTVAMYYVLWPLLGAIALGAWLAVNAPEVTAVNEQNAWWTGIFLSVSAFCSAGMSLLDAGMTAFQS GSYFVLIVGALLILAGNQASPIFLRFIIWVLSRTLRFSTKHQNYAVWKETFDFILQYPRRVYINMFPSRPTWMLTLSIGGFLAVDWIMFFL LNIGNEAIESIPPGPRVMDGFFQSTSLLSAGFAVVSASSVYFGLQVLWLVKMYASAYPTSITVRGSNVYEERSLGIYAGDDPEDSDDE DKEKKESNAPAAGGLFVNPGTTTGAQPPLTPMSATSNASRLSRLSQASRGGIDKIVNLGREGGAKLGRQLQRRMTEFQGVGVATAP LRRHKTSLPQPSQPTPHSSASSTTASVDSVDDSLPPKQDLVSHHVRSQLSHDVWWIALAFFLITIIETSHTLEDPAAYSLFNILFEIVSA YANNGISIGLPNASYSFSGGWKAGSKFVLVLVMLRGRHRDLPVALDRAVKLPSMDLDEQEEDDAEIRRTITRTPKLVQSPPLHSPGRI RPFAPM
1.8E-84	293	13.5	5.2E-84	291.9	9.3	1.6	1	D5C3K1_NITHN	Trk system potassium uptake protein	Nhal_3896	Nitrosococcus halophilus (strain Nc4)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Nitrosococcus, Nitrosococcus halophilus, Nitrosococcus halophilus (strain Nc4)	472759	>tr|D5C3K1|D5C3K1_NITHN Trk system potassium uptake protein OS=Nitrosococcus halophilus (strain Nc4) GN=Nhal_3896 PE=3 SV=1MQLVVVQRILGLLLTLFSTAMLPPVIVSLFYQDGAAEEFLSAFGLILSLGLLCWLPVRHYQRELRLRDGFVVVVMFWVVLSLSGA LPLFLTTEPRLSFTDAVFESVSGLTTTGATVITGLDSLPKSVLFYRQELQWLGGMGIVVLAVAILPMLGIGGMQLYRAETPGPMKTTKL TPRIAETAKALWLIYLGLTVTCAAAYWVAGMTLFDAIGHSFSTIAIGGFSTHDASIGYFNSPLIEMIAVFFMLLAGVNFSLHFLAWRHLTA RHYWEDEEFRAYLLVLTGVAVLTSAYLWITHRFDDPLLALQHGIFHAVSIGTTTGFTSSDYYSWPGFLPILLLMTSYIGGCAVSTGGG MKVIRVLLLYKQGAREIKRLIHPSAIVPIKIGNKSLPDRVVEGVAGFMAVYVACFSVMYLLLLSTGLDMITSFSAVTACLNNLGPGLGQV GAHYEGINATSKWILCFAMLLGRLEIFTLLVILSPTFWRR
2.3E-84	293	1.9	5.5E-81	282	0.4	2.1	2	T0JSH4_COLGC	Trk family potassium uptake protein	CGLO_14942	Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	602	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Cg-14) (Anthracnose fungus) (Glomerella cingulata)	1237896	>tr|T0JSH4|T0JSH4_COLGC Trk family potassium uptake protein OS=Colletotrichum gloeosporioides (strain Cg-14) GN=CGLO_14942 PE=4 SV=1MWKPKLNFISLHYTWILVCSLLSFPVLYPAGNLAAIDAFFFGASGSTESGLNTIDVKDLKTYQQVYIYVIPMITNLMFINIVVVVARL YWFQQRLKNIAKERTLSRSAEDLEAGPPDQQAEVRGRESALDETHAQRNAVQTGPSESKENEVLDTEFASGPRATTITFQKNLPNR GQSSADNAVLHVPGPRDRDDGQSMIEIRQDTESIDDIDAIRPVEPVASGLSRRRPHNMEGPAMRAARSMEKVASSVLVLGHSKSLDR ESRLSDLSTRPRPPRTADLPYLSRQVTVGRNSQFFHLTEQDRELLGGIEYRSLKLLLKIVFIICLLPWILHAPQKYKSWLLENGQGQVW WAFYSAQTMVDNLGFTLTPDSMSTFKDATWPILAMTFLAFAGNTIYPVLLRLVIWVMSRVVNKKSATKEHLEFLLDHPRRCYTLLFPS RPTWILFGIVFLLNFIDVLLIIVLDLDNPAVNDLAMGPRILSALFQAASSRHTGTSTLNLSLVNPAVQFSLLCMMYIAIFPIAISIRASNTYEE RALGVYEADSHLDENNGASYVMTHVRNQLSFDLWYIFLGTFCICIAESQRIMDLNEPVRTKLTPIHGSQC
2.3E-84	293	15.6	4.1E-84	292.3	10.8	1.3	1	A0A0C5W6C9_9GAMM	Trk system potassium uptake protein	H744_2c0337	Photobacterium gaetbulicola Gung47	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium gaetbulicola, Photobacterium gaetbulicola Gung47	658445	>tr|A0A0C5W6C9|A0A0C5W6C9_9GAMM Trk system potassium uptake protein OS=Photobacterium gaetbulicola Gung47 GN=H744_2c0337 PE=3 SV=1MQFRSIIRIVGLLLALFSVTMLAPALVALIYRDGAGLPFVVTFFLLFAGGALLWVPNRHYRRELKARDGFLIVVLFWTVIGSAGAVP FILAKTPDLSVTDSFFESFSALTTTGATVIVGLDHLPKAILFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIA ETAKALWYIYLALTISCALAFWLAGMTAFDAVAHSFSTVAIGGFSTHDASMGYFNSPTINMITVVFLLISACNFSLHFAAFANGGIHLRT YWRDPEFRAFFASQLILFLICFGMLLKHHSYDSYHDAFDQALFQTVSISTTAGFTTTGFSEWPLFLPVLLLFSSFVGGCAGSTGGGIKV IRMFLLLLQGVRELKRLVHPRAVYTIKVGNKALPQRVVDAVWGFFSAYALVFVICMLALIATGIDELTAFSAVAATLNNLGPGLGEVAVH FGEVNDPAKWVLVIAMLFGRLEVFTLLVLFTPTFWRS
2.7E-84	293	16.6	6.4E-84	291.6	11.5	1.5	1	A0A0D8MTX8_PHOLE	Trk system potassium uptake protein	UB34_12455	Photobacterium leiognathi	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium leiognathi	553611	>tr|A0A0D8MTX8|A0A0D8MTX8_PHOLE Trk system potassium uptake protein OS=Photobacterium leiognathi GN=UB34_12455 PE=3 SV=1MQFRSIIRIVGLLLALFSVTMLIPALVALIYRDGAGFPFVVTFFILIAGGALLWLPNRRHRHELKARDGFLIVVLFWVVIGSAGAIPFL LSKTPDLSVADSFFESFSALTTTGATVIVGLDHLPKAILFYRQLLQWFGGMGIIVLAVAILPVLGIGGMQLYRAEIPGPVKDSKMTPRIAE TAKTLWYIYLALTVSCAFAFWLAGMSGFDAISHSFSTIAIGGFSTHDASMGYFNSPTINMITVVFLLISACNFSLHFAAFGNGGVHLKTY WRDPEFRAFLGVQFILFVICFGLLIKHSPYDPYFTAFDQALFQTVSISTTAGFTTTGFSDWPLFLPVLLLFSSFIGGCAGSTGGGMKVIR ILLLSLQGVRELKRLVHPRAVYTIKLGNKALPQRVVDAVWGFFSAYALVFVICMLALIATGLDELTAFSAVAATLNNLGPGLGEVAVHFG EINDSAKWILIISMLFGRLEVFTLLVLFTPTFWRN
2.8E-84	293	6.5	2E-83	290	4.5	1.8	1	L0GW33_9GAMM	Trk system potassium uptake protein	Thimo_1240	Thioflavicoccus mobilis 8321	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thioflavicoccus, Thioflavicoccus mobilis, Thioflavicoccus mobilis 8321	765912	>tr|L0GW33|L0GW33_9GAMM Trk system potassium uptake protein OS=Thioflavicoccus mobilis 8321 GN=Thimo_1240 PE=3 SV=1MKLLAVQKVLGLLLVVFSATMLPPLAVSLLYRDGATLAFLWAFATILAVGLLSWAPVARHQRELRLRDGFLVVALFWTVLGLGG ALPLVFSSDPSLSITDAVFESMSGLTTTGATVITGLDDLAPSILYYRQQLQWLGGMGIVVLAVAVLPMLGVGGMQLYRAEIPGPMKDA KLTPRITETAKALWYIYLGLTVACALGYRLAGMSAFDAVGHAFSTVAIGGFSTHDASMGYFSSAAIEAVAVVFMLFSGANFALHFLAW RRRSPLVYWHDEEFRFYLGLMTLSAALVTTALAVSETYLDWGESLSKGVFQTVSIGTTAGFTTANYYTWPPFPAILLLLSFVGGCAA STGGGIKVIRLLLLIKQGIREVQRLIHPNAQIPVRMGNRSVTHRVVDAVWGFFSLYVASFVLMYLALTATGLDLMTAFSAVAACINNLGP GLADVGPHYQSLPDAAKWILCLAMLLGRLEIFTLLVLFAPSFWRN
3.7E-84	292	12.8	1.8E-83	290.1	8.9	1.8	1	U5T0S1_9GAMM	Trk system potassium uptake protein	SPICUR_00300	Spiribacter sp. UAH-SP71	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Spiribacter, Spiribacter sp. UAH-SP71	1335757	>tr|U5T0S1|U5T0S1_9GAMM Trk system potassium uptake protein OS=Spiribacter sp. UAH-SP71 GN=SPICUR_00300 PE=3 SV=1MHPDAVQRVLGVLLMVFSVTMLPPALVAVVAADGVAEAFLMTFVLLLVLGGLLWLPVRQSRRELRIRDGFFVVAMFWVVLGAA GSLPLVIQNAVPFGFVDALFESVSGLTTTGATVLTGIDSLPLSIRYYYRQQLQWLGGMGIIVLAVAILPMLGIGGMQLYRAELPGPVKDAK LTPRIAETAKALWIYIYLGLTVVCALAYWAAGMGAFDAVMHAFTTIATGGFSTHDASMGYFDSALIEMIAVVFMIISALNYSLHFMAWR WRSTEPWRSDPELVAFLTVLGIVIALVLGGLLIYQAAHSLLLDETWHHAIFQVVSFATTTGYTTASYYVWPAFLPVLLLFVAVVGGCAN STSGGLKVVRILLLWRQGGREILRLIHPQAQIPVKIGDRPVNERVIDAVWGFFAAYVLLFVLLMLVMLAMGLDQITAFSAVASGLANLG PALGDVAANFASVGAGPKLVMCVAMLMGRLEIFTLLVLFTPAFWRR

4.2E-84	292	0.8	5.2E-84	291.9	0.5	1	1	H1VIZ0_COLHI	Na+/K+ transporter	CH063_10820	Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)	387	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum higginsianum, Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)	759273	>tr|H1VIZ0|H1VIZ0_COLHI Na+/K+ transporter OS=Colletotrichum higginsianum (strain IMI 349063) GN=CH063_10820 PE=4 SV=1MPSVATSNGANPWWAGIFFAVSAFNNSGMSLLDANMVPFQQAYFVLITMGLLILAGNTAYPLFLRLIFWSALKVLRLATAEEAY VELKCTLEFILKYPRRVYTNLFPSRPTWWLCFMVVMTNGIDWMAFEVLNIGNPVIEAIPVGARVLDGLFQALAVRSGGFYVIPIASAYP GLQVLYVIMMYISVYPVVITMRHSNVYEERSLGIYADDEAHPSNAYPSDERKHSKSTGFLAQLLRDNLSFAGVGAAKPKSSADRFESR TSFVSQQIRGQLAHDLWLLTLAVLVIVTIETSHFLADPVHFSVFNVVFEVVSGYGCVGISVGLPKDAMSFAGGWHAGSKLVLCLVMLR GRHRGLPVALDRAVRLPGQRLLEDEEEDWRLRQVRTGR
4.3E-84	292	0.3	4.1E-78	272.5	0	2.1	2	C8VUH3_EMENI	Cation transporter, putative (Eurofung)	ANIA_10136	Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans), Emericella nidulans (Aspergillus nidulans), Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	671	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Emericella nidulans (Aspergillus nidulans), Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)	227321	>tr|C8VUH3|C8VUH3_EMENI Cation transporter, putative (Eurofung) OS=Emericella nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) GN=ANIA_10136 PE=4 SV=1MTRECFLSSPGIGGANCTVHKARRCLRLIASGVSTLLPPFNFLSLHYTYFIVVSLISSLIFWGASNPPRSVSYTDALFMCVSAMTG TGLNSVEASTLTTFQQVIMFVLLMLGHAILISITVLHVRKRAFQHKFKGISHALAQRTAQEAPAPNRNEDKSYPAADNVPMEPPTISSAE INVHFTNTGAQGVSHDQPRKAMVDQPSNLKSENERHRDNYQPINKAQLLQLGIWRGTQKYFESKGLISRNSQFHGLTLEERDRLLGV EYKAVSFLSVIVPLYWVLFLCCGILGMGIWLEVNKPQVPRDNGLSPFWTGAFFAVSAFVNSGMGILDANMTALQTDAYPLITMGLLILA GNTLYPCFLRLIIWSVRRMLPDQQAWKTWRSTLDFILDHPRRVYTNLFPARHTWYLLATVVIFNGIDWAGFEVLSIGNKEIEGLPTAYR IMDGLFQALAVRAGGFSVVTISDLRQGLLVLYVVLLVSAGPAVLIARRHTNVYEERSLGIYAEDETLYGHDKRPPNTVTNFLRRHLFLNK EGTRRHFLREQLKDQLSHDLWWIALAVFLISIMESSNYTKDPVGYSTFNILFEVISAYGCVGISTGYPGRDLSFCGVWHSLSKLILAAV ALRGRHRGLPVAIDNAIMLPSESNAQAWAEEENVVSGREHQQVGHLGPGIV
5.3E-84	292	16.6	9E-84	291.1	11.5	1.3	1	J7TWT8_MORMO	Trk system potassium uptake protein	MU9_774	Morganella morganii subsp. morganii KT	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Morganella, Morganella morganii (Proteus morganii), Morganella morganii subsp. morganii, Morganella morganii subsp. morganii KT	1124991	>tr|J7TWT8|J7TWT8_MORMO Trk system potassium uptake protein OS=Morganella morganii subsp. morganii KT GN=MU9_774 PE=3 SV=1MHFRAITRIVGLLVIIFSVTMIIPGIVALIYKDGAGKAFSQTFLAALIIGLLLWIPNRNKKSELKPKEGFLIVVLFWTVLGSVGALPFIFS ERPNLSVTDAFFESFSGLTTTGATTLVGLDTLPKAILFYRQMLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEMPGPLKDNKMRPRIAE TAKTLWLIYVFLTIVCAIALWFAGMDVFDAISHSFSTIAIGGFSTHDASIGYFNSPAINTIIAIFLLISGCNYGLHFAVLTGRSLGVYWRDLE FRMFISLQFVLVVICALVLWKFDVYATEGQTLNQSFFQVVSMATTAGFSTDSFYKWPLFLPMLLLCAAFVGGCAGSTGGGLKVIRIML LFLQGARELKRLVHPNAVYTIKLGRRALPERIIEAVWGFFSAYALVFVVSMLLIATGVDEFSAFSAIATTLNNLGPGLGTLGENFTTLNP GGKWILVVTMLFGRLEVFTLLVLLTPTFWRD
6.5E-84	292	15	1E-83	291	10.4	1.2	1	G4QEE9_GLANF	Trk system potassium uptake protein	trkH GNIT_0017	Glaciecola nitratireducens (strain JCM 12485 / KCTC 12276 / FR1064)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Glaciecola, Glaciecola nitratireducens, Glaciecola nitratireducens (strain JCM 12485 / KCTC 12276 / FR1064)	1085623	>tr|G4QEE9|G4QEE9_GLANF Trk system potassium uptake protein OS=Glaciecola nitratireducens (strain JCM 12485 / KCTC 12276 / FR1064) GN=trkH PE=3 SV=1MQYRAIIRILGLLVALFSVTMIPPALISLIYGDGSGLAFVLAFVLSILTGLAFWYPNRRSKVDLRAKEGFLIVVLFWTVLASFGALPF ALLEQPHMSITDAMFEAFSGLTTTGATVIEGIEYLPKAVQFYRQQLQWLGGMGIIVLAVAILPILGVGGMQLYRAETPGPVKDSKMTPR IADTAKHLWYIYLSLTIACSGAYWLAGMNLFDAVCHAFSTIAIGGFSTYDASLGYFNSVAVNIVCVVFLWIAALNFSLHYAAVSGRNIKN YFKDPECKAFFTIQLSLVTLCFLALVYHSVYETAEMALDQALIQAVSISTTAGFATTDFSAWPAFLPIVLIFSSFIGGCAGSTGGGLKVIR VFLLFLQGKREVDRLIHPKAVYAVKLGDRAMPERVVEAVWGFFSAYAVVFVVIMVALIATGMDDITAFSATAATLNNLGPGLGAVSGT YADVTDAGKWLLVVAMLFGRLEIFSLLVLFSPTFWRS
7.3E-84	291	0	8.3E-80	278.1	0	2.2	2	G2QGF2_THIHA	Uncharacterized protein	MYCTH_53804	Thielavia heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) (Myceliophthora thermophila)	801	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Myceliophthora, Thielavia heterothallica (Myceliophthora thermophila), Thielavia heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) (Myceliophthora thermophila)	573729	>tr|G2QGF2|G2QGF2_THIHA Uncharacterized protein OS=Thielavia heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) GN=MYCTH_53804 PE=4 SV=1MKWLGDFYERQWEGRWAERFARVRPYLPPINFITLHYAYFILSCLFFALVFWGSGSSSSVKIGFLDSLFLIMSALTSTGLNTQNL SQMSLGQQIVLFLAMLLGHPILVSLWTVLFRRHVFEKRFRAIVKRERERKLRAGSSIWLYSGFSDLLALARLKSLSKSKSKCDEGQQQ LPGLGSRIRAGQSSTSEVPGSESGRPRERDVEEGLAPIPENRLSRSPGARSVVFVEPPRPPPGKAAAQEINRDRTAEVRNFLQEKRK NVGRNGEFFNLTLKEREYLGGVEYRAIEVLVVTVALYYVLWQVLGALALGAWIAANAPEIPTANGQNAWWTGIFLAVSAFSNTGLSLL DAGMTAFQSGYYFVVLVGAVLMLVGSQASPIFLRFIIWVCSRLLRLATDSPNYEVWKETFEFILHYPRRVYINMFPARPTWMLGLWLG AFLIVDWIMFFLLNIGNKALDKIPPGPRVVDGLFQSVSILSTGFSIVSVSAVYFGLQVLWLIKMYASAYPTSITVRGSNVYEERSLGIYAG DEPEMPHDDKGMKEKEGQQPLSPTSVSSQASRLSRLSVASRGGIDKIVDIGREGGQFISRQLQRRMTGFQGVGVPPGPLPRRPNKR PKTGALASAQPTPYIQTSGGGGGSTKDAAGRGPDLMAHHVRSQLSHDVWWVALAFFLVTVMETSHTLADPAAFSLFNILFEVVSAY ANNGISTGLPAASYSFSGGWHAGSKLVLILVMLRGRHRDLPVALDRAVKLPSMDLDDKEEDDAEIRRFISRTAATPYMAGGEQSSPQ ARSPGRSVIRPFAPV
8.1E-84	291	0	1.1E-83	290.8	0	1.1	1	G2X359_VERDV	Low-affinity potassium transport protein	VDAG_04844	Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	610	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, mitosporic Plectosphaerellaceae, Verticillium, Verticillium dahliae (Verticillium wilt), Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) (Verticillium wilt)	498257	>tr|G2X359|G2X359_VERDV Low-affinity potassium transport protein OS=Verticillium dahliae (strain VdLs.17 / ATCC MYA-4575 / FGSC 10137) GN=VDAG_04844 PE=4 SV=1MAVINIIVVATRLYWFERRLRQVGTARHLPAQGHQHGSPPASAVEATSDPTCAANEEPQRSGNSVLSSFALDSAQIDTDPQED DAGGPAYKRRSVSDLPLGDEDGMPDNRSHIAFAPVLHHPRMDSTTLYIPPPNQRDQGRPFEAQGGAGETADEEDCRRSATAMTSK SDRESRWNRPNRLDLEKVASVERVASSLFVLGQTHSHTRERSHIHRTASRSAPLRTSSSDLPRLSSQVTVGRNSQFHGLSVEDRELL GGIEYRSLKLLLWICIGYFIGLHVLGVICLVPWILHAPSKYTDYLDEEGQNIVWWAFYSAQTMANNLGFTLTPDSMVQFRDATFPMLIM TFLAYAGYNFYPIFLRVVIWTIYKIVPRNSALREPLNFLLQHPRRCCMLLFPSRPTWILFGFLFALNFIDALLLIVLDLDNPSVTDLPLAQRI LAAVFQAASSRHTGTSTFNLADLNPAAQFSLLVMMYISVYPIALTIRASNTYEERSLGKYAPEQVDPDEEPTGGKYVMAHIRNQLSFDL WYVFLGIFLICIAESDKVRDTSQPLHDARDFVDNTANGRNSPCFPSSSKLHLHMATSGSVSAIQPSKLLSRGSYLYSASSLFVL
8.6E-84	291	21	1.3E-83	290.6	14.6	1.2	1	Q12TB1_SHEDO	Trk system potassium uptake protein	Sden_0018	Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella denitrificans, Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013)	318161	>tr|Q12TB1|Q12TB1_SHEDO Trk system potassium uptake protein OS=Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013) GN=Sden_0018 PE=3 SV=1MQYKTIIRITGLLMGLFSITMLPPALIAVFYGDGGGTAFIKAFVVSILLGLMLWYPNRHQKAELRTREGFLIVVLFWTVLGSIGALPF IFSKVPDLSWTDSFFESFSALTTTGATVIVGLDTLPKAVLFYRHLLQWMGGMGIIVLAVAILPLLGIGGMQLYKAEVPGPVKDSKMTPRI AETAKALWYIYLLLTVSCATAFYFAGMSVFDAICHSFSTIAIGGFSTHDASIGYFNSPMINTICAVFLLIAAVNFSLHFAAFSLRGINFKVY FKDTEFKALIAIQLILTAICFVTLYSTGVYDSPEQTLDYAFFQVVSISTTAGFGTESFHTWPLFLPILLIFSSFIGGCAGSTGGGMKVIRLIL LLLQGSRELKRLVHPKAMYSIRIAGSALPDRIIDAVWGFFSAYALVFVVCMLALMMMEMDAITAFSATAASLNNLGPGLGDVANNYASI SDGAKWVLVTAMLFGRLEVFTLLVLFTPTFWKN

8.6E-84	291	17.5	1.8E-83	290.2	12.1	1.4	1	M5DMI2_9GAMM	Trk system potassium uptake protein	TOL_0124	Thalassolituus oleivorans MIL-1	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Thalassolituus, Thalassolituus oleivorans, Thalassolituus oleivorans MIL-1	1298593	>tr|M5DMI2|M5DMI2_9GAMM Trk system potassium uptake protein OS=Thalassolituus oleivorans MIL-1 GN=TOL_0124 PE=3 SV=1MHLTVIARVLGIFLMLFSLTMLPPILVSMWYNDGATQAFSMAMGLIFGIGFLSWMPVRFVRQELRTRDGFLIAALFWFTLGLAGTLPFILAEDPGLSFADAFFESLSGWTTTGATVMTGLEYLPKSILWYRQQLQWLGGMGIIVLAVAILPMLGIGGMQLFRAEMPGPLKDSKLTPRITETAKALWYIYLSLTIACALAYWLAGMNTFDAIAHSFSTVGIGGFSTYDASMGHFDSPLIEMIAVFFMLVAALNFSLHFYAWRNRSITHYWRDSEVRFFTFIIIGGIIITITALWLTDTYGITESIRYGIFEMVSVATTAGFATADFSGWPVFLPVMLFMAAFIGGCAGSTGGGMKVIRVLLVYKQGVREIRRLIHPNAIIPVKLGRMPVSDRILESVWGFFALYVVTFMVMMLALMATGLDQVTAFSAVGSCLNNLGPGLGDVAVHYGGISDTAKWLLALTMLLGRLEIFTLLVLLSPTFWRS
9.4E-84	291	7.6	1.4E-83	290.5	5.3	1.2	1	A6UX77_PSEA7	Trk system potassium uptake protein	trkH2 PSPA7_0016	Pseudomonas aeruginosa (strain PA7)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	381754	>tr|A6UX77|A6UX77_PSEA7 Trk system potassium uptake protein OS=Pseudomonas aeruginosa (strain PA7) GN=trkH2 PE=3 SV=1MHYASIFRILGVLLMLFSSAQIPPLLVALFYAEPVWQPFLLAFVITLATGACIWWPVRGVQEELRIREGYLITALFWVVLGSFGAIPFMFSETPHMSLTDALFEAISGISTTGATVLTGLDRLPRAILYYRQQLQWFGGMGIVVLAVAIMPMLGIGGMQLYRAEMPGPLKEQKLSPRIADTAKTLWLIYCGLTLACALAYWAAGMSLFDAVGHSFSTIAIGGFSTHDASIGYFDSPLIEAICMFFLVVSGINFGLHFLAWRRRSLAHYLRDPECRAYLSILLAVFLVTALALVAQRHYEQPLQAIRYAAFMVVSIGTTTGFGLADFATWPTFLPHLLLYTTFIGACAGSTGGGMKVMRILLVYRQGMREFMRLLHPSGVFLVKLGRRPIPDRVVESVWGFCSIYLVTFVVLMLVLLALGVDLLTAFSSLSSCLNNLGPALGEAAAHYGGLPDSAKLVLAFAMMLGRLEVFSLLILFTPAFWRY
1.3E-83	291	19.2	3.3E-83	289.3	13.3	1.6	1	F2JUI4_MARM1	Trk system potassium uptake protein	Marme_0011	Marinomonas mediterranea (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Marinomonas, Marinomonas mediterranea, Marinomonas mediterranea (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1)	717774	>tr|F2JUI4|F2JUI4_MARM1 Trk system potassium uptake protein OS=Marinomonas mediterranea (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1) GN=Marme_0011 PE=3 SV=1MRIQVILRVIGILVMVFSLSLIPPIIVSLIYQDDTLGAFASALAINLLSGFLIWFPVRNQRADLKIRDGFVVTVLFWFVLGLSGSVPFLISTDPVLTFTDALFESISALTTTGATIITHIDGLPPSILFYRQQLQWLGGMGIIVLAVAIMPMLGIGGMQLYRAETPGPVKDSKLTPRIAETAKALWYIYASLTTVCAVGYWLAGMTLFDAICHSFSTVAIGGFSTHDASIGYYNSVAIEVVCSLFMFISAINFGLHFYAWRNQSVLHYFKDPEARFFIFILFCTVTLTTLGLTLTATYDWDLAFRYAVFESISIATTAGFGTSDFSAWPHFLPFLLIVTSFAGGCASSTGGGMKVMRILLILKQGVREIQRLVHPSAVIPIKVGGKAIPERVVSAVWGFFSAYLIVYVILMIGLMATGIDQVTAWSAVAATLNNLGPGLGDVSANFAGINDPAKWMLCFSMLLGRLEVFTLLVLFTPMFWQR
1.3E-83	291	19.5	4.8E-83	288.7	13.5	1.7	1	I1XEW5_METNJ	Trk system potassium uptake protein	Q7A_73	Methylophaga nitratireducenticrescens (strain ATCC BAA-2433 / DSM 25689 / JAM1)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Piscirickettsiaceae, Methylophaga, Methylophaga nitratireducenticrescens (strain ATCC BAA-2433 / DSM 25689 / JAM1)	754476	>tr|I1XEW5|I1XEW5_METNJ Trk system potassium uptake protein OS=Methylophaga nitratireducenticrescens (strain ATCC BAA-2433 / DSM 25689 / JAM1) GN=Q7A_73 PE=3 SV=1MQLMTIQRILGILLSLFSITMLPPVLVSWWFNDGAATAFLTAFVILVSTGLLLWLPARKHHKELKIRDGFIVVVMFWIALGFSGALPFYLTESPEMSITDAVFESMSGLTTTGATVLVGLDTLPEAVLFYRQFLQWLGGMGIVVLAVAILPLLGVGGMQLYRAETPGPMKDAKLTPRITETAKALWYIYLSLTIACTIAYYWAGMSWFDAIGHSFSTVAIGGFSTHDASMGFFNSATIEMIAVAFMLVSAMNFSLHFLAWRHRSLMHYLRDSELKVFLSIMFVISLVTASYLFFTGTFDDGWTAAHHGIFQAVSIGTTAGFTTTDYYLWPGFLPILLLMSSYIGGCAFSTGGGIKVIRVMLLFKQGYREVLRLIHPNAVFAIKVNGKALPPKVVGAVWGFFALYVFCFSIMHLLLMATGLDVVTSFSAVTACLNNLGPGLGDVGANFGQINAPSKWILCVAMLLGRLEIFTLLVVLTPAFWRR
1.7E-83	290	13.8	1.6E-82	287	9.6	1.9	1	Q2SQX5_HAHCH	Trk system potassium uptake protein	trkH HCH_00025	Hahella chejuensis (strain KCTC 2396)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Hahellaceae, Hahella, Hahella chejuensis, Hahella chejuensis (strain KCTC 2396)	349521	>tr|Q2SQX5|Q2SQX5_HAHCH Trk system potassium uptake protein OS=Hahella chejuensis (strain KCTC 2396) GN=trkH PE=3 SV=1MHYSAIAKILGVLLMLFSTTMIPPIVVSLIYEDGHMQPFLTAMCGIFLTGLMVWLPVFRQTSELRIRDGFVVTVLFWVVLSLSGAVPLYLSEHPHLSLVDAIFESVSGLTTTGATVMTGIDVLPKSILWYRQQLQWLGGMGIIVLAVAILPMLGIGGMQLYRAEAPGPVKDNKLTPRITETAKALWYIYVSLTAICALLYWWAGMDAFDAIGHSFATIAIGGFSTHDASIGYFNSPLIEFICIIFMFLAGINFAMHFFAWRRRSVLVYLKDPEFVFYSLILITVSVITVGVLIGTGTYDPFTAIIRGVFEVVSIATTTGFATADFAHWPHLLPFLLFVVAFIGGCAGSTGGGMKVIRVLLIFKQGMREVKRIVHPNAVIQVKLGRKPVPDRVLEAVWGFFSVYMFMFVFMLMGLLATGLDQVTAWSAVGACINNLGPGLGGVALHYGELNEPAKWILCFAMLLGRLEVFTLLILFTPAFWRR
1.7E-83	290	16.5	6.5E-83	288.3	11.4	1.7	1	F5Z9W4_ALTSS	Trk system potassium uptake protein	ambt_00075	Alteromonas sp. (strain SN2)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Alteromonas, Alteromonas sp. (strain SN2)	715451	>tr|F5Z9W4|F5Z9W4_ALTSS Trk system potassium uptake protein OS=Alteromonas sp. (strain SN2) GN=ambt_00075 PE=3 SV=1MHYRAIVRILGLLIALFSVTMIPPAVVSLIYQDGSGLPFTLAFFICVGGGMVLWYPNRQQKNDLRAREGFLIVALFWSVLASVGAIPLMLLEQPSMTVTDAFFESFSGLTTTGATVIEGIDFLPHSVQFYRQQLQWLGGMGIIVLAVAILPILGVGGMQLYRAETPGPVKDNKMTPRIADTAKHLWYIYLSITIACAAAYWLAGMDMFDAICHAFSTVAIGGFSTHDASLGYFNSPMVNVVCTVFLLIAALNFSLHYAAVSTRSVKGYFNDPEFKAFFFIQATLIMLCFLVLTLSGFYDSAETALDQAMIQAVSISTTAGFATTDFSIWPTFLPILLIFSSFIGGCASSTGGGLKVVRVCLLFLQGKREVDRLIHPKAVYSVKLGERAMPDKVVEAVWGFFSAYAVVFVVLMIGLIATGLDNLSAFTATAAMLNNLGPGLGSVASNYAGVTDAGKWILVVGMVFGRLEVFSLLVLFSPTFWRS
2.1E-83	290	14	4.1E-83	289	9.7	1.4	1	A0A0F4NSG1_PSEO7	Trk system potassium uptake protein	TW73_06395 TW75_18445	Pseudoalteromonas piscicida	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas piscicida	43662	>tr|A0A0F4NSG1|A0A0F4NSG1_PSEO7 Trk system potassium uptake protein OS=Pseudoalteromonas piscicida GN=TW73_06395 PE=3 SV=1MQFRTIIKILGQLVALFSITMVPPAIVSLIYKDGGGVPFVLAFIFSVLMGLFAYYPNRKENGDLKAREGFLIVVLFWLVLGSFASLPLIFLDKPNLSLADAVFEAFSGLTTTGATVLTGIEHLPKAVLFYRQQLQWLGGMGIIVLAVAVLPMLGVGGMQLYRAETPGPVKDSKMTPRIADTAKHLWYIYVSLTAACTLAYWIAGMNWFDAICHAFATIAIGGFSTYDASMGYFDNPFINVICVVFLLIAAINFSLHYAAVSSRNIKAYLRDPEFKVFLFIQLALVVICFAVLSSNNVYETGDETLDQAMFQAVSISTTAGFATDSFSTWPLFLPILLIFSSFIGGCAGSTGGGMKVVRVFLLYLQGIRELNRLVHPRAIYSIKLGRKALPDKVVEAVWGFFSAYALVFVIIMIALLGTGLDNITAFSATAACLNNLGPGLGDVAAHYGDISDTAKWILTLAMVFGRLEIFTLLVLFTPTFWRG
2.5E-83	290	16.4	2.5E-81	283.1	0.6	2	2	N1J620_BLUG1	Cation transporter	BGHDH14_bgh02018	Blumeria graminis f. sp. hordei (strain DH14) (Barley powdery mildew) (Oidium monilioides f. sp. hordei)	633	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Erysiphales (powdery mildews), Erysiphaceae, Blumeria, Blumeria graminis (Powdery mildew) (Oidium monilioides), Blumeria graminis f. sp. hordei (Barley powdery mildew) (Oidium monilioides f. sp. hordei), Blumeria graminis f. sp. hordei (strain DH14) (Barley powdery mildew) (Oidium monilioides f. sp. hordei)	546991	>tr|N1J620|N1J620_BLUG1 Cation transporter OS=Blumeria graminis f. sp. hordei (strain DH14) GN=BGHDH14_bgh02018 PE=4 SV=1MDRIPNSPLHQTPLKCFESLLANSSIAKFKRWCSTFPRPTFLVLHWVYFIVTCFISSILFWSINSSNISYVNSIFMVVAAMTQAGLNTVNLAALNLFQQVLLLVLMIAGNHILVSIIVIHVRKRAFEARFKEEEEEDTQRSQFTLKASPPSSVFSHKIQNATSRSSIAAQSFISTDMTIYNRQQYKPTQIDRNSQFHSLTVEERKRVRCVEYQAVKLLGYIVPAYYIIWQVVGCLALGFYISANKPSIAAEIQSNSWWVAIYLGVAAFNNAGMSLLDGSVAPLQSSTFSLVVLSLLMLAGNTAYPIFLRWLLRALRIIPDNEKYSDWTETLRFILRFPRRVYTNLFPSEQTWWLLALLIFFNAFDWTAFEILNHYSAALRSLPVGSLALDGLFQTIAIRSSGYTVIPIASLFVGLQSLYVLMMYISAFPVTITMRSSNVYEERSLGIYTRDVPKTSDPEKSENCQSFKAFPNRHLDRFYFVQEQIRRQLGHDLWFLVIGMMIITCFESSNYERDPLTFALFNIIFEIISAYGGVGFSVGLPDQAYSFCGAWHPFSQLILCAMMMRGRHRGLPFDIDKAIQLPGEKSEIAEEQDHNIRIVSWMTDRIEYSENVKTERFSQIGPTPPINARLKI

3.6E-83	289	19.3	7.8E-83	288	13.4	1.5	1	A3N2N8_ACTP2	Trk system potassium uptake protein	trkH APL_1590	Actinobacillus pleuropneumoniae serotype 5b (strain L20)	492	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Actinobacillus, Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae), Actinobacillus pleuropneumoniae serovar 5, Actinobacillus pleuropneumoniae serotype 5b (strain L20)	416269	>tr|A3N2N8|A3N2N8_ACTP2 Trk system potassium uptake protein OS=Actinobacillus pleuropneumoniae serotype 5b (strain L20) GN=trkH PE=3 SV=1MQFLSILRIVGILVMSFSFTMLLPAFVALIYGDGGGREFLQSFLLTFSVGTLLWWFSRNQKNELRSREGFLIVVLFWVVLGSLGA VPFIILEHPDLNFSESIFESFSGLTTTGATVITGLDDLPKAILFYRQFLQWLGGMGIIVLAIAIIPLIGLGKLYRAEMPGPLKDQKMRPRIAEI SKLLWQIYLSLTVLCALAFKIAGMSWFDAICHSFATISIGGFSTHDASIGYFDSIVINSITAVFLLISSINFGLHFALIDQLKDKNNKQTGNIF KRLYWKDYEFRSFAVIQLSLFLICFAILSIYNYFDNAEITFQHALFQSVSISTTAGFTTNDFSQWPSFLPILLVMASFIGGCAGSTGGGLK VIRVMLLYLQANREIHRFVHPNSVKPIKLGAHIFSERIEEGIWAFFSAYIFVFVMCWFGTIAFGMETFDAFNAVVASLNNLGPALGNVSS NFTQVPDGAKWVLTIAMVCGRLEVFTLLVILSPVFWKD
3.6E-83	289	2.4	4.9E-81	282.1	0.2	2.1	2	C6HRS4_AJECH	Potassium uptake transporter	HCDG_08659	Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	596	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	544712	>tr|C6HRS4|C6HRS4_AJECH Potassium uptake transporter OS=Ajellomyces capsulatus (strain H143) GN=HCDG_08659 PE=4 SV=1MWKPPLNFITIHYAYIVTLSISSLVVLYPYGNLKAIDAYFFGASSCTESGLNTYDVKDLKTYQQLFIYVIPIISHHAFINIAVVLVRLH WFRKRLDEIGNMAHYPPTQVRHRHDVEAKAYKPLENGKKYTSNDQHITDATALNVISTGEHTNETDKPQAQTAEPTGRSISFAADVR GYDKSKALYVPPPQERDRGRPMVEIDEIFSDDDEITKTNDSNVRGSLPARRKIMGSSRITSTTTLERVASSIFVLEGRPSTRQKQPPLQ HSLSEHLHLPLSSHAALGPNSQFRNLTAEDRETLGGIEHRSLKLLLKIVTVYFFGLHLFGAVCLLGWILHSDPKYRKYLKECAQSPVW WAFYSSQTMISNLGFTLTPDSMISFRDAEWPMILMSFLAYVGNTFYPCFLRFIIWTMSLIVPKTSPLKEQLNFLLKHPRRCYTHLFPSG TTWALFAVLFILNFVDIILMITLDLHNPAVNDLPWGKRILASLFQAASTRHTGTASFNLANVNPAVQVSILVMMYIGIFPIALSTRASNTYE QRALGIYPQDRELDEYNGKAYILAHIKNQLTFDLWYIFLGFFCICASESKKIMDPNEPVRVV
3.6E-83	289	14.9	1E-82	287.6	10.4	1.6	1	Q160A1_PSEA6	Trk system potassium uptake protein	Patl_0016	Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas atlantica (Alteromonas atlantica), Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087)	342610	>tr|Q160A1|Q160A1_PSEA6 Trk system potassium uptake protein OS=Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087) GN=Patl_0016 PE=3 SV=1MQYRTIIRILGLLVALFSVTMIPPAIISLYFKDGSGLPFFLAFLLCLGTGLMFWYPNRLHRRDLRAKEGFLIVVLFWTVLASFGALPL LLLEQPEMSVSDAFFEAFSGLTTTGATVIQGIDYLPKAVQFYRQQLQWLGGMGIIVLAVAILPILGVGGMQLYRAETPGPVKDSKMTP RIADTAKHLWYIYLTLTICCGVAYWFAGMNWFDALCHAFSTVAIGGFSNYDASIGYFDSPWINIVCVIFLWIAALNFALHYAAASGRTL MGYFYDPELRAFFLIQFVLVAVYFFVLMKFSWFDGAGIAFDQALIQSVSFSTTAGFATTDFSHWPAFLPIMLIFSSFIGGCAGSTGGGL KVVRVLLLFLQGKREVDRLIHPKAVYTVKLGDRALPDRVVEAVWGFFSAYAMIFVIIMVCLIATGMDDVSAFTATAATLNNLGPGLGTV SGSFADVSDTGKWLLILAMLFGRLEVFSLLVLFSPTFWRS
4.2E-83	289	15.1	1E-82	287.7	10.5	1.5	1	A0A0F4PW86_9GAMM	Potassium transporter	TW72_10965	Pseudoalteromonas ruthenica	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas ruthenica	151081	>tr|A0A0F4PW86|A0A0F4PW86_9GAMM Potassium transporter OS=Pseudoalteromonas ruthenica GN=TW72_10965 PE=4 SV=1MQYRTIIKILGQLVALFSITMVPPALVSLIYKDGGGLPFILAFVFSVIAGLIAYYPNRNEHGDLKAREGFLIVVLFWLVLGSFASLPLI FLDAPKLSMADAVFEAFSGLTTTGATVLTGIEYLPKSVLFYRQQLQWLGGMGIIVLAVAVLPMLGVGGMQLYRAETPGPVKDSKMTP RIADTAKHLWYIYVSLTLTCTLAYWVAGMNWFDAICHAFSTIAIGGFSTYDASMGHFDSPVINLICVVFLLIAAINFSLHYAAVASRSGKV YLRDPEFKAFFLIQVALIIICFAVLSSNNIYANGDETLDQAMFQAVSISTTAGFATDNFSAWPLFLPMLLIFSSFIGGCAGSTGGGMKVV RVFLLLYLQGIRELNRLVHPRAIYSIKLGRKALPDKVVEAVWGFFSAYALVFVIIMISLMGTGLDNITAFSATAACLNNLGPGLGEVAAHY GDISDSAKWILTLAMVFGRLEIFTLLVLFTPTFWRG
5.8E-83	289	9.4	1.1E-82	287.6	6.5	1.3	1	D3SDF7_THISK	Trk system potassium uptake protein	TK90_2266	Thioalkalivibrio sp. (strain K90mix)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Thioalkalivibrio, Thioalkalivibrio sp. (strain K90mix)	396595	>tr|D3SDF7|D3SDF7_THISK Trk system potassium uptake protein OS=Thioalkalivibrio sp. (strain K90mix) GN=TK90_2266 PE=3 SV=1MLHLASTARLLGVLLTLFSLTMLPPAAIGFLYGEATAWVFLQAFALLLLIGGILWGSLYKARCDLQVRDGFILVVLFWLGLGIAGA APLVLDPNLPVSFTDAVFESMSGLTTTGATVLTGLDDLPRAILWYRQQLQWMGGMGIIVLAVAILPLLGVGGMQLFKAETPGPIRDNK LTPRIAETARNLWYIYLGLTVACALAYWAAGMEAFDAVAHSFTTVAIGGFSTYDASIGHFNSVAIETVAIAFMILGGMNFALHFLVLHRA TWKPYQRDEELRTYLLLLGSAAVIVVSYMLWSGFTDQAGDALRRGVFHVVSIATTTGYATDAFYLWPGFLPVLLIFLSFIGGCTGSTG GGMKVVRVLLLVKQGLREIKRLIHPHARIAVKVNGKEAPDRVVQAVWGFLAAYVMVFVVMMLALMASGLDQVTSFSAVAATLNNLGP GLGEVGPNFQSINDFSKWVLVLAMLMGRLEIFTVLVLLSPAFWRR
6.3E-83	288	15.9	2.5E-82	286.4	11	1.7	1	Q31J91_THICR	Trk system potassium uptake protein	Tcr_0186	Thiomicrospira crunogena (strain XCL-2)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Piscirickettsiaceae, Thiomicrospira, Thiomicrospira crunogena, Thiomicrospira crunogena (strain XCL-2)	317025	>tr|Q31J91|Q31J91_THICR Trk system potassium uptake protein OS=Thiomicrospira crunogena (strain XCL-2) GN=Tcr_0186 PE=3 SV=1MHSKIILKVLGILLMVFSLTLIPPFIIALIYQDGGMSDFGFSAIGLFITGFLLWFPSRKSHHDLKIRDGFLIVVMFWTVLGFAGAVPM YFASTIYISLTDAIFESFSGLTTTGATVINGLDALPHSLLWYRQQLQWLGGMGIIVLAVAILPMLGIGGMQLYRAETPGPIKDNKLAPRIS ETAKALWYIYLGLTIACALGYWLAGMDWFDAFAHSFSTVAIGGFSTHDASIAHFDDVHIEIIAMIFMFLAAINFALHFTAFRNLSTRPYTL DPEFKVFSALILVGIAISSFYLYYQDVYLTWQDALRYGAFQTISFASTTGFANADFSLWPIFIPFMLIMMSFIGGSAGSTAGGMKVIRFIL LAKQGSREIRRLLHPNALMPVKLHGKPIPDKVITSVWGFFSLYVVSFVGIMLLLMALGLDQTTAFSTVAATINNLGPALGQAAANYQHL SDPVKWVLTFTMLLGRLEIFTLLVLFTSSFWRK
6.9E-83	288	21.3	1.2E-82	287.4	14.8	1.3	1	Q7VK99_HAEDU	Trk system potassium uptake protein	trkH HD_2028	Haemophilus ducreyi (strain 35000HP / ATCC 700724)	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Haemophilus, Haemophilus ducreyi, Haemophilus ducreyi (strain 35000HP / ATCC 700724)	233412	>tr|Q7VK99|Q7VK99_HAEDU Trk system potassium uptake protein OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=trkH PE=3 SV=1MQLLTIIRIIGILVMSFSITMLLPAFIALIYGDGGGREFVRSFLLTFSVGAFLWWFCREHKYALRSREGFLIVVLFWVVLGLLGAVPF IILDNPDLSLSESIFESFSGLTTTGATVITDLDSLPKAILFYRQFLQWLGGMGMIVLAVAIIPLFGISSVQLYRAESSNPLRDKSLPRITEVA KILWIIYLGLTLCCAGAYYLLGMNLFDAVSHSFSTVANGGMSTHNDGLAYFNSNKIYLVTALFMLIGGCNFGLHISLIYQYERRYSIVKHY WHNPEFRFFISQLIFIALFSFGLYLAYNYSFNDAISKGAIQLTSMSMTSGYTIFDLNTLPPVLGLLLVFSAILGGCSGSTSGGLKAIRVLV LWLLLKKELNMLIHPNLQKTIKIGDQVLPISTQERIWAFLIASIFVFLCFVFAAILCGMGIGDAVGAVLATLTNAGPGLGMVSGNFSGVSD SAKYIFSLAMICGRLEIFSLLIIFTPYFWKD
1.1E-82	288	23.9	5E-82	285.4	16.6	1.8	1	W0BBD7_9GAMM	Trk system potassium uptake protein	Loa_00428	Legionella oakridgensis ATCC 33761 = DSM 21215	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella oakridgensis, Legionella oakridgensis ATCC 33761 = DSM 21215	1268635	>tr|W0BBD7|W0BBD7_9GAMM Trk system potassium uptake protein OS=Legionella oakridgensis ATCC 33761 = DSM 21215 GN=Loa_00428 PE=3 SV=1MQIRTILRLIGLLLMMFSLSMLTPLPFNFIFHEHFWVPFIAAFLCTASTGASLWLMFHKHRQELKIRDGFLIVVLFWFVLCFFASLP FLFALHTPSMTDALFESVSGFTTTGATIITNIEALPHALLYYRQQLQFLGGMGIIVLAVAILPMLGVGGMQLYRAETPGPMKETKLTPRIA QTAKALWFIYFLLTLLCMACYSLAGMDWFDALGESFATVSTGGFSMHDASFSYYQSNTIELIACFFMLLGGTNFALHFIALKKRTLKHY WQDEEFRCYIRVLFIASFIVVLGLVCYGFFHANHHALIKSLFNVISLATTTGFISAPFGTWPTFIPILILFLAIIGGCAASTSGGIKMLRALLL YKQSKREMSRLLHPHGVIPIKFGNHTLAEPVLQSMWGFISVFIALFLTLMILLLALGNDFITTFSAITATLANAGAGIGTISITFADLNLPSK WVLMFAMIAGRLEIFSLLILFSRQFWQK

1.2E-82	288	1.9	1.4E-82	287.2	1.3	1	1	Q0UEL9_PHANO	Putative uncharacterized protein	SNOG_09795	Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	412	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae, Parastagonospora, Phaeosphaeria nodorum (Glume blotch fungus) (Septoria nodorum), Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	321614	>tr|Q0UEL9|Q0UEL9_PHANO Putative uncharacterized protein OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) GN=SNOG_09795 PE=4 SV=2MELSEHDRLELGGVEYRALQALLFILVGYQIFWYTMGTIFLVPYAYRSSTKAILRDAQPGGVNPGWWAFFATVTEFANGGLNILNANFIPFSGKPFILLVAGSLAFLGQTQFPIFLRLTIWLMKKMSPKGSRFQNTLDFLLQHPRRETWYLLFIQISIDITAWLCFEILNIGIPDVESIPTGTRILDGLFQATGLRTSGAYIISFSSLAPACLVAYLIIMYISSYPLVLTLRKTNTYEERSIGLQEHDSSAAGIASHLQKQLAYDIWFQFFAFFLICIIERGHIVRGDPGFSEFSVLFEVTSAYGTVGLSTGVPGKDYSLCGDFASLSKVVLLFVMVRGRHRGLPLAIDRSILLPGEELMQRMDAEYSERGVYSSGEIEELRDDIEQSGRRVPGTKGKQDPERTRSDREHSR
1.2E-82	287	5.9	2.2E-82	286.6	4.1	1.4	1	J4GKB9_FIBRA	Uncharacterized protein	FIBRA_01473	Fibroporia radiculosa (strain TFFH 294) (Brown rot fungus) (Antrodia radiculosa)	2042	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Polyporaceae (bracket fungi), Fibroporia, Fibroporia radiculosa, Fibroporia radiculosa (strain TFFH 294) (Brown rot fungus) (Antrodia radiculosa)	599839	>tr|J4GKB9|J4GKB9_FIBRA Uncharacterized protein OS=Fibroporia radiculosa (strain TFFH 294) GN=FIBRA_01473 PE=4 SV=1MDVSPIVLPLAFPSGGLTSSNDDVGKHLISWSCSSSSPTRLVAWGYSSNASAFPSIPESIGHYQGVAIGCEDGSIYIFHPLTFPD RRKRSSIDSKSAETHGSSRPTSPLRYSGLNRPHSHSRSGSPSSTKSGLSPFHVTRSRVVSCISTEQVEAPKNYVDFEDEPDRLKGML KGRSAKEKSFGELLTIGGERTSQTTSGRNPAALSSTSSVRSSVSTPPSPTLAPVSAIEATGPVTSLSLKCHVMPQFGGVMHSVAALLD YQIGRYIISLQRTGEITILSSVDGTCVASAHASDEGASPPSSSRRISVIPTIWQWKSLHLASIRESNILLLCASSDSSSSANQMLDVPTGD SEAETRLVAFELQAGTQIDSSQMRLLRIGDWYMDGPAEAMVFHEEADASLALFHISSTHHLMRRSLTLAIPGSPADLEKIKSSSSTALPI PNPFKALKALSREEQGSDDGVESTYTLRLSDASDLGIIQIHGSVTGVRSMFFGDTLRIACWSDTELTTFDVCDQSLKFLFTHLFAEICG LNWTDVDSFIVMLPEGLKTYRIVAVDENTDDVSPGASRNVIQRTRPVIVRSIELSSHDCCPLLFGDHVFLTGTKQEKRYISHIPLDVLDE QVHPRTLWKMREYHYAAPHITCMLPIDLDLIIVGLSDGRLRRSSFAQLSGKSVTPTSLESDVPLQGFITSLHIVEDERTREKFIVGGADD GSIAIWSLQQVYATFSLQLHARWIVFTTPLAQVIQISGDHVGRLKGCSLCISQDGTIAIITVDGYQFIILVPASAAPLSRIHVGDDNILLLYS DGRARLWDSKTMEFRRSMNADKADELLKQDGWNGWSAGPTTSPSKAILSIMGSTVGPDSEAFIRACIASGPVASSADRSHTDHLRS MLSVLLTFGLSGQIDIMCREKLKVDTAYGLVGYASQLTACLFTRLDPLDAWTVSSEVSASRSLALVAVLQALIHREGLEDNSDVDTVMT FYVTSLPEVVGPAYKSPSLSYLAKCWLQSTVPEIRAAARLLFEVGVMRLSNNDTAQIVEYWQHNLPSTRSHAEPESLSDSMALLICGFI AVEKYSLLSTSVLIEISKSIASYLHDEESPYRFLAIDLCSRGFPVWQQYVDAVEMLRALFILATTTRKEAISLHNLGLQARSAVLYIASTNT PLFMTTLTIDILHPRSVQHRKSIMQLVIFLIRKKPLVLYSNLPRLVEAVVKSLDPNSTHNRDAVLDSATDILGHVVQTFPTVDFHMPTQRL AVGTSEGAVVMYDLKTATRLYVLEGHKKRTAGLSFSPDGRRLVTVSLEESAVLVWKVGSSFTSFFTPGAPPRQGHNGSEPYKTLNF NVGEEARMTLAATLDNIRFEWPADRSKVVRRYFLNHLEHIVTVSLKGKRTHDESAITGDPVASLRVVVRDVLLHKTRHNPVEEHSTKDN GAVSALSKPKRGKLHPDMVRRVDIDPHPVDPVGKSIFREVREDIGPQACSSSVPFPCVSGGRMSPCSHRSPSPSVGEPDEFGGFPG PPRIVSHVLKATFPGLHRRLKRSFTMPRTETLIPQVNRAELGSQPPSNLPNSKHVSYLPFKAIVSRNSAFSQLSTEHLEELGGIEYRALT ALLWIVPLYYFGILTISFIVIAPYMSLPRWAPILVPPEQHRVINPVWFSAFQVVGAWANTGMSLVDQNMIPFREAYPMIIFLVICVLAGNS AFPVFLRFMIWVLSKICPVDSRINETLQFLLDHPRRCFIYLFPSSQTWILFTIQFSIDLIAFVAELVLNINNPEIDSIPTGVRVINALLAAAAV RSSGFQSIAVSSLAPAVQVLDVILMYITIYPIALSVRSTNVYEERALGIYKHRDREDEYILDEAHWNAGQESRVAIWGRYLLLRHARKQLS FDMWWLALSLFLLCIIERTPLAATYNAVWFNIWSLIFELVSAYGTVGLSLGIPYANYSFSGALHTLSKLILCAVMIRGRHRGLPVALDRA VLLPREFARKSSTVTETHRDENVCGTSEKARDDSQQDVPQLKDRTSTLSFAEDPKRGLGKGTHSADRISEVEWEDGS
1.5E-82	287	9.9	2.3E-82	286.5	6.8	1.2	1	A0A0C5VI29_9GAMM	Trk system potassium uptake protein	YC6258_00978	Gynuella sunshinyii YC6258	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, unclassified Oceanospirillales, Gynuella, Gynuella sunshinyii, Gynuella sunshinyii YC6258	1445510	>tr|A0A0C5VI29|A0A0C5VI29_9GAMM Trk system potassium uptake protein OS=Gynuella sunshinyii YC6258 GN=YC6258_00978 PE=3 SV=1MQNSSRLITILRICSFLVLLYSLSMPLPVFVGLLFGEHHLHGFLITFAFAFIAGLLGWQLTGRDEMNLKTRDGFLVAVLFWVIFSAI STMPLYLDSRLGLSLTDAIFEGVSGITTTGASVLDDIDHLPKSILFYRAQLNFLGGLGIIVLAIAVMPFLDIGGAKLYQSEMPGPMKEEKF TPRLTDTARDLWMIYAGLAACGMVAYRLAGMNWFDAVCHSLSTVSLGGFSTHADSLGYYQNPAIELVGGTYSILAALNFSLYFLALHR RSLRPIFHNSEARFFMLIISLVITLVCLELARTQTFALPQAFVHGFFQTASIMTDNGLGAAHYPDWPAHIVILLLGASFFGGCVGSTAGGI KAMRFLLLYRLSSQEIKQLIHPDAVFRTKVGRHSVSDRVIRSVWALFFLYIFFSCAFVWGLMIIGHDFATAFGTVAACINNMGVGYGDT AAGFGPLKEPGKWLMCVAMIFGRLEIFPILIVFSRTFWRF
1.7E-82	287	17.7	3.1E-82	286.1	12.3	1.4	1	R4I0B3_9ENTR	Trk system potassium uptake protein	trkH SCc_012	Serratia symbiotica str. 'Cinara cedri'	522	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia symbiotica, Serratia symbiotica str. 'Cinara cedri'	568817	>tr|R4I0B3|R4I0B3_9ENTR Trk system potassium uptake protein OS=Serratia symbiotica str. 'Cinara cedri' GN=trkH PE=3 SV=1MTINLYCLAINYVCLVAVIFNNTYCAIITLNLITKDRAEMHFRAIIRIVGLLVILFSGTMFIPGFVALIYKDGAGRAFSQTFFVAIIIGLIL WYPNRNKKYELQPREGFLIVVLFWTVLGSLGALPFLFSAQPNLSLTDAFFESFSGLTTTGATMLVGLDSLPKAILFYRQMLQWMGGM GIIVLAVAILPILGVGGMQLYRAEIPGPLKDNKMRPRIAETAKTLWLIYVLLTIACTLALWVAGMPIFDAISHSFATAIAIGGFSTHDASIGYY ASPTINTIIAIFLLISGCNYGLHFALLSGCSLRVYGKDPEFRIFILVQLTLVVVCILVLWEHSIYATGIETLNQAFFQVVSMETTAGFTTDSIA KWPLFLPMLLLCSSFIGGCASSTGGGMKVIRILLLYLQGARELKRLVHPNAIYTIKLGDHVLPERILDAVWGFFSAYALVFIVSMLAIIATG VDNFSSFVAVTASLNNLGSGLGVMAENCTTMPSVAKWILVVTMLFGRLEVFTLLVLFTPTFWRS
1.9E-82	287	14	3.7E-82	285.8	9.7	1.4	1	W0E273_MARPU	Trk system potassium uptake protein	MARPU_04170	Marichromatium purpuratum 984	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Marichromatium, Marichromatium purpuratum (Chromatium purpuratum), Marichromatium purpuratum 984	765910	>tr|W0E273|W0E273_MARPU Trk system potassium uptake protein OS=Marichromatium purpuratum 984 GN=MARPU_04170 PE=3 SV=1MKFAAVQKVLGLLLAVFSFAMLPPVVVELIYADGEAWPFLVAFAILLSAGLLIFLPVMRYQAVLRLRDGFLVVVLFWTTLGLAGAL PFLLAPDPELSPTDAVFESISGLTTTGATVIVGLDALPKSILFYRQQLQWLGGMGIIVLAVAVLPMLGIGGMQLYRAEMPGPMKDSKLT PRITETAKALWYIYLWMTVACALAYWGAGMTLFDAIGHAFSTVAIGGFSTHDLSMGHFDSTLIEMIAVVFMLLAGMNFALHFVAVHRH SLGVYLHDSEWRFYLLIMVTVTAIATIALYRTDTFITWDDAFTKGLFQAVSIGTTTGFATAEFYFWPPFLQILLLFTSFVGGCAGSTGGG IKVIRFLLLIKQGVREIGRLIHPNAQIPVRIGGKSIDHRVVDAVWGFFSLYVACFVLMYLMLAATGLDLLTSFSAVAACINNLGPGLAMVG PHFADIYDPAKWILCFAMLLGRLEIFTLLVLLTPTFWQR
2.3E-82	287	19.4	3.4E-82	285.9	13.4	1.2	1	A0A0F4R6Y3_9GAMM	Trk system potassium uptake protein	TW85_02155	Marinomonas sp. S3726	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Marinomonas, Marinomonas sp. S3726	579484	>tr|A0A0F4R6Y3|A0A0F4R6Y3_9GAMM Trk system potassium uptake protein OS=Marinomonas sp. S3726 GN=TW85_02155 PE=3 SV=1MHIKVIFRVIGILVMVFSLTLIPPLIVSLIYQDGDTHAFLYALLINLIGGFCMWLPFKGNRKELRIRDGFIITVLFWSVLGLFGAVPFML VDSQALSFTDALFESISGLTTTGATILTGIDDMPHALLFYRQQLQWLGGMGIIVLAVAIMPMLGVGGMQLYRAETPGPVKDSKLTPRIA ETAKALWYIYASLTIACALGFWAAGMSLFDAICHSFSTVAIGGFSTHDASIGYFDSPMIEAIAVIFMIISALNFGLHFYAWRSRSIMHYFK DSEVKFFGFILLCTITITTLVLAMTSSYEWSTAFRYAMFESISIATTTGFGTEDFSTWPNTLPFLLIVTSFAGGCASSTGGGMKVIRILLIL KQGFREIQRLIHPNAIIPVKLGGKAIHERVISAVWGFFSAYLLVYVILMIGLMATGLDQLTAWSAVAATLNNLGPGLGEVAANFGSISDP AKWMLCFSMLLGRLEVFTLLVLFTPMFWQR

2.5E-82	286	21.5	1E-48	175.5	5.7	2	2	K0C6M2_CYCSP	Trk system potassium uptake protein	Q91_21112	Cycloclasticus sp. (strain P1)	479	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Piscirickettsiaceae, Cycloclasticus, Cycloclasticus sp. (strain P1)	385025	>tr|K0C6M2|K0C6M2_CYCSP Trk system potassium uptake protein OS=Cycloclasticus sp. (strain P1) GN=Q91_21112 PE=3 SV=1MHYNVIRRVSGLLLGLFSITMLPPIAVSFIYDEQNHQPFLIGFFTIFLTGFVLWLSAKNAKGDLRTRDGFVIATLFWVSLGLSGAIPLYFSSLPSLSLTDSIFESISGLTTTGATVITGLDTLPKSILFYRQQLQWFGGMGIVVLAVAVLPMLGIGGMQLYKTEMPGPVKDAKLTPRITETAKALWEIYLGLTIACTLAYWIGGMTFFDALTHSFSTVSIGGFSTHDLSFAFFDSTALNYICIVFMLVAGINFALHFRAAKSLSLKVYTHNNEFQTYLSILVVHTLLISGVLLFLGHVDIIEQTLFQVVSFATTTGFTSSNHANWPLFIPVLLLFMSFYGGCGGSTAGGIKVIRILILLKQLGKEITHLIHPHADMPIKLDQRVVSRPVINAVWSFFSAYILSFGLLMILMMMTGLDQITAFSAVAATLNNLGPGLGDISSSYATLPDTSKWIACFSMLLGRLEIFTLLVLFSPVFWRD	
2.8E-82	286	14.3	1.2E-81	284.1	9.9	1.7	1	W0TMB1_9GAMM	Trk system potassium uptake protein	TBH_C1842	Thiolapillus brandeum	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, Thiolapillus, Thiolapillus brandeum	1076588	>tr|W0TMB1|W0TMB1_9GAMM Trk system potassium uptake protein OS=Thiolapillus brandeum GN=TBH_C1842 PE=3 SV=1MQLLIVSRTSGLLASMFSLSLAVPVLVGLWYGEPVMRDFLLPLMVTLGAGLLLWLPGRKKQSRISRKDGFLIVTLFWGLLSFMGAWPLFLSLDLDFIDALFESASAITTTGATVITGLDDLPRSVLLYRQQLQWMGGMGLIVLGIAVLPMLGIGGMQLYRAEAPGPMKEEKMTPRLASTARALWLIYLSLTAACAFAYWAFGMEPFDAIAHSLSTVSTGGFSTHDASLSWFHSSQIEFVSVVFMLLASLNFGVHYLAIYHKAPRQYWEDVEARSFLILVLALVILVGLMLRLEGGYHELPPSLRDATFEVVSVITSTGFGTVDFTQWPDFLPVLLIFISFIGGCGGSTAGGMKVMRVLMLFKQGMREIRKLIHPNAILPVRLGHHVVDQRIMNAVWGFFAAYTVVFVVLMLLMIHAGLDQVSAFSAVATCMNNLGPGLGVVASNFQDVSDLGKWISILAMLLGRLEIFTILILLTPSFWKD	
3.5E-82	286	6.1	3.3E-80	279.4	1	2.2	2	Q0UGI6_PHANO	Putative uncharacterized protein	SNOG_09128	Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	582	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae, Parastagonospora, Phaeosphaeria nodorum (Glume blotch fungus) (Septoria nodorum), Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	321614	>tr|Q0UGI6|Q0UGI6_PHANO Putative uncharacterized protein OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) GN=SNOG_09128 PE=4 SV=2MWKPPINFITLHYAYIISFGILALVILYPEKNLRTVDAYFFGVSASTESGLNPVDLKALKTYQQVFLYIVPMITNIGFVNVIVVVVRLRWFRQRFKAVTARKDDAVQAGSVTRDMEKGPTLTTPAVLSREEEQPKSDTTRITFAPVMQRGRTGEHALYIPGPRERENDEDVDRISIARTESNSIMRRKKFDTRKMSKATSMETAVSSIFVLGSTARGQSQDRSRKSFDRAKSMERTKSMDRTKSIDIATLTPDELGGIEYRALRVLLKVAVGYFVGLHLLGVICLVPWIHLASPKYREYLASTGQNETWWAIYSAQTMVDNLGLTLTPDSMISFRDATWPMLVMSFLAFAGNTFYPCFLRLLIWTIYKLSAIDSSLRESTRFLLDHPRRCYTLLFPGTATWILAAILITLNFLDTLLIIVLDLDNPEVNVLPVGSRILAAIFQAASARHTGTATFNLANVNPAVQFSLLVMMYISIYPIAISIRMSSDYEDGSVGLYEVEESLDEQTGGKKYLVNHMRNQLSFDLWYIFLGVFCICCAESERIMSREDYVSLKRDVEGGFWANDWIGVLGFLGLLRGRECVW	
4.4E-82	286	4.7	8.6E-73	254.9	0.1	3	2	K9GAG3_PEND2	Potassium transporter, putative	PDIG_06730	Penicillium digitatum (strain PHI26 / CECT 20796) (Green mold)	668	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium digitatum (Green mold), Penicillium digitatum (strain PHI26 / CECT 20796) (Green mold)	1170229	>tr|K9GAG3|K9GAG3_PEND2 Potassium transporter, putative OS=Penicillium digitatum (strain PHI26 / CECT 20796) GN=PDIG_06730 PE=4 SV=1MHAPLIFRKWRKYIGNAMMAVLPPLNFLTLHYLYFIATCMIASIIFYLTSTPWRSVAYVDSIFLCVSAMTGAGLNTVDLSTLNSFQQAVLFILILGHAILISLTVLLVRKRAFEAKFKGVSNERERERSSCNPLEVELQARGREPAQGSTGTDIPGESNGHSGKPHPKTSVLAQVKSGEPSSRDEQPWMEDDQKTIGGTPRHHHHRVFPMAGIGARPDLHNHPRDAVPNVPLVVEDSVSGFKGILRGTQKYMASKGLVSRNSQFHDLTPAERDELGGVEYKAVSFLSVVVFLYFILFIIFGMVGVGGWLEVNDPAVTRTNGLSPFWTGAFFAVSAFVNSGMSLLDANMTALQLNAYPLLTMGFLILAGNTLFPCFLRFIIWTMRIMLPDRPRWQSWRITLDFILKHPRRVYTNLFPARHTWYLLGTIVILNGIDWASFELLSIGNKDIESLPTEYRVLDGLFQAIVLMMYVSAYPVTLTMRNTNVYEERSLGIYAHDESPDSPANTSRSNVVMDLIRHHLGRPGLSETSRGYFVHQQIRSQLSHDLWWIALAIFFIAIRESDHYESQPVSFSTFNIIFEVVSAYGCVGVSLGFPGKNYSFCGAWHTVSKLILAAVALRGRHRGLPVAIDKAIMLPSESLAWAEEEDAAMRRDRSRVWAQEHGPVGSV	
5.6E-82	285	20.8	8.5E-82	284.6	14.4	1.3	1	C5BKP6_TERTT	Trk system potassium uptake protein	TERTU_0033	Teredinibacter turnerae (strain ATCC 39867 / T7901)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadales genera incertae sedis, Teredinibacter, Teredinibacter turnerae, Teredinibacter turnerae (strain ATCC 39867 / T7901)	377629	>tr|C5BKP6|C5BKP6_TERTT Trk system potassium uptake protein OS=Teredinibacter turnerae (strain ATCC 39867 / T7901) GN=TERTU_0033 PE=3 SV=1MHFAIIAKVLGILLMLFSLTLTPPILVSLYYGEQAHISFLLAFAITFSTGLFTWLPVHNVQSDLSTRDGFLITSLFWTVLALFGALPFIIAHSTQLSVTDAVFESLSGLTTTGATVLTGLDYLPRSILFYRQQLQWLGGIGIIVIAVAILPMLGIGGMQLYRAETPGPVKDSKLTPRITETAKALFFMYVALTAACAFSYWLAGMPPFEAVAHSFATVAIGGFSTHDLSMGYYDSAPILIVSSLFMVLSGINFALHFVAWQSRGISHYLTDPEFRFYLTMILIGIVITVSYLASTGIYPTEKSILYGIFELISILTTTGFAVVDFTLWPTFLPYLIFMFAFMGGCAGSTGGGLKMIRVVLIMKQGLREIIHRLIHPNAVIPIKLGRKTISDRVVEAVWGFFAVYVVSFLVMVIALLGLELDFVTAFTAVGACLNNLGPGLGAVAAHYGDIGDTAKWILCFAMLLGRLEVFTLLVLFTPMFWKR	
5.7E-82	285	12.5	9.3E-82	284.5	8.7	1.3	1	A0A0F4QP82_9GAMM	Trk system potassium uptake protein	TW77_09565	Pseudoalteromonas rubra	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas rubra	43658	>tr|A0A0F4QP82|A0A0F4QP82_9GAMM Trk system potassium uptake protein OS=Pseudoalteromonas rubra GN=TW77_09565 PE=3 SV=1MQFRTIIKILGQLVALFSLTMVPPALVSLIYKDGGGVPFVLAFIFSVLIGLMAYYPNRKEQGDLKAREGFLIVVLFWLVLGAFAAVPLIFLSEPNLSFADAVFEAFSGLTTTGATVLTGIEYLPKSVLFYRQQLQWLGGMGIIVLAVAVLPMLGVGGMQLYRAETPGPVKDSKMTPRIADTAKHLWYIYVTLTLACTLAYAWAGMSWFDAICHAFATIAIGGFSTYDASIGYFDSPMINAICVFFLLIAAANFSLHYAAVAGRNIKVYFRDPELKVFLFIQLALVVLCFAVLSSKQVYSNGDETLDHALFQAVSISTTAGFATDSFAAWPLFLPILLIFSSFIGGCAGSTGGGMKVVRVFLLLYLQGIRELNRLVHPRAIYSIKLGRKALPDKVVEAVWGFFSAYALVFVIIMIALLGTGLDNITAFSATAACLNNLGPGLGDVAAHYGDIPDSAKWILTIAMVFGRLEIFTLLVLFTPTFWRG	
7.4E-82	285	15.5	1.4E-81	283.9	10.7	1.3	1	F2G1R9_ALTMD	Trk system potassium uptake protein	MADE_1000085	Alteromonas macleodii (strain DSM 17117 / Deep ecotype)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Alteromonas, Alteromonas macleodii (Pseudoalteromonas macleodii), Alteromonas macleodii (strain DSM 17117 / Deep ecotype)	314275	>tr|F2G1R9|F2G1R9_ALTMD Trk system potassium uptake protein OS=Alteromonas macleodii (strain DSM 17117 / Deep ecotype) GN=MADE_1000085 PE=3 SV=1MHYRAIIRILGLLIALFSVTMIPPAIVSLIYQDGSGLPFTLAFILCVIGGMALWYPNRLEKSDLRAREGFLIVALFWSVLASVGAIPLILLEQPSMTVTDAFFESFSGLTTTGATVIEGIDFLPHSVQFYRQQLQWLGGMGIIVLAVAILPLGVGGMQLYRAETPGPVKDNKMTPRIADTAKHLWYIYLSITIACAGAYWLAGMNVFDSICHAFSTVAIGGFSNHDASLGYFNSPMVNVVCTVFLLIAALNFSLHYAAVSSRSVKGYFKDPEFKAFFIIQASLIGICFLVLTLSGYYTSAEQALDQAMIQAVSISTTAGFATTDFSIWPTFLPIMLIFSSFIGGCASSTGGGLKVVRVCLLFLQGKREVDRLIHPKAVYSVKFGDRAMPDRVVEAVWGFFSAYAVVFVVLMIGLIATGLDNLSAFTATAAMLNNLGPGLGSVAANYADVTDAGKWILVTGMVFGRLEVFSLLVLFSPTFWRS	
1.5E-81	284	15.7	2.7E-81	283	10.9	1.3	1	Q3IJ19_PSEHT	Trk system potassium uptake protein	trkH PSHAa0015	Pseudoalteromonas haloplanktis (strain TAC 125)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas haloplanktis (Alteromonas haloplanktis), Pseudoalteromonas haloplanktis (strain TAC 125)	326442	>tr|Q3IJ19|Q3IJ19_PSEHT Trk system potassium uptake protein OS=Pseudoalteromonas haloplanktis (strain TAC 125) GN=trkH PE=3 SV=1MQFRTIIKILGQLVALFSITMVPPAIVSLIYKDGGGVPFVLAFIFSVTIGLMAYYPNRHEDGDLKAREGFLIVVLFWLVLGAFASLPLIFLQEPNLSLADAVFEAFSGLTTTGATVLTGIEYLPKSVLFYRQQLQWFGGMGIIVLAVAILPMLGVGGMQLYRAEIPGPVKDSKMTPRIADTAKHLWYIYVSITLACTLAYWIAGMDWFDAISHAFSTVAIGGFSTYDASMGHFDSPVINFICVFFLIIAAINFSLHYAAVASRNISVYIRDPEFKVFLCIQLALVVICFTVLSSHEVYANGDETLDQALFHAVSISSTAGFATDNFSAWPLFLPILLIFSSFIGGCAGSTGGGMKVVRVFLLLYLQGVRELNRLVHPRAIYSIKLGSKALPDKVVEAVWGFFSAYALVFIIIMLALMGTGMDNITAFSATAACLNNLGPGLGDVASHYGSISDGAKWLLTIAMVFGRLEIFTLLVLFTPTFWRG	

1.8E-81	284	23.7	6.7E-81	281.7	16.4	1.8	1	Q0VTE5_ALCBS	Trk system potassium uptake protein	trkH ABO_0127	Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Alcanivorax, Alcanivorax borkumensis, Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2)	393595	>tr|Q0VTE5|Q0VTE5_ALCBS Trk system potassium uptake protein OS=Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2) GN=trkH PE=3 SV=1MHFALISKILGLLLVVFSFTMMPPVAVSYWYQEGSETPFLISFVITLALGLSLWLPFFRNKSELQTRDGFLVVTLFWSVLGVIGALPLIISDDVPVGFTDAVFESISGLTTTGATILSGIDFLPKSILYYRQQLQWLGGMGVVVLAVAILPMLGIGGMQLYKAEIPGPMKDTKLTPRIAETAKALWFIYLFITIACAVLYWAFGMTVFDAICHSFSTVATGGFSTHDASMAYWDNALIDWTATIFILIGGLNFALHFAVWRGRSLLAYLRDPEFRFFIGLFLIYTAIITVGLLFFHYDFTVDDALRHSAFQVASFSTGTGLTSTNAAAFPGFIPFLLVFTSFIGGCAGSTGGGMKAVRAALVYHHSIRELRRLIYPNGVFALRFGRQTIPDRVLQAVWGFVGVYIAISVIFTLLFTMTGMDLTTAVSAVAASLNNLGVGIGQVGGGFANITDSAKWMMTVLMVAGRLEIFTLLVLFTPMFWKQ
2E-81	283	13.1	4.2E-81	282.3	9.1	1.4	1	A0A0F6A8F0_9GAMM	Trk system potassium uptake protein	N479_02085	Pseudoalteromonas luteoviolacea S4054	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas luteoviolacea, Pseudoalteromonas luteoviolacea S4054	1129367	>tr|A0A0F6A8F0|A0A0F6A8F0_9GAMM Trk system potassium uptake protein OS=Pseudoalteromonas luteoviolacea S4054 GN=N479_02085 PE=3 SV=1MQFRTIIKILGQLVALFSLTMVPPALVSLIYKDGGGVPFVLAFIFSVLIGLMAYYPNRKERGELKAREGFLIVVLFWLVLGSFASVPLIFLDEPNLSFADAVFEAFSGLTTTGATVLTGIEYLPKSVLFYRQQLQWLGGMGIIVLAVAVLPMLGVGGMQLYRAETPGPVKDSKMTPRIADTAKHLWYIYVALTAACTLAYKFAGMGWFDAICHAFATIAIGGFSTYDASIGHFDSPMINFICVVFLLIAAVNFSLHYAAVASRSVRAYLRDPEFKVFLFIQLALVVICFAVLSSNEVYGDGDETLDHALFQAVSISTTAGFATDSFSAWPLFLPILLIFSSFIGGCAGSTGGGMKVVRVFLLYLQGIRELNRLVHPRAIYSIKLGRKALPDKVVEAVWGFFSAYALVFVIIMIALLGTGLDNITAFSATAACLNNLGPGLGDVAAHYGDITDTAKWILTLAMVFGRLEIFTLLVLFTPTFWRG
3.2E-81	283	0.8	3.2E-81	282.7	0.5	1.6	1	B6HHW1_PENCW	Pc21g23090 protein	Pc21g23090 PCH_Pc21g23090	Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)	654	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium chrysogenum complex, Penicillium rubens, Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)	500485	>tr|B6HHW1|B6HHW1_PENCW Pc21g23090 protein OS=Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) GN=Pc21g23090 PE=4 SV=1MALCPPLNFLTLHYFYFIATSIIASIIFYLTSTSWRSVAYVDSIFIFQQAVLFTLLILGHAVLISLTVLLVRKRAFEAKFKGVSDERERERSTRHHSEVELQTRDQVPANESTGTDLPGESTEGQGCKPRPKTHLLVQVTPGESSSRNEQPWVEDDQITIGGTPRHHHHRVFPMAGIGARPDLNNHPRDAVPNVPLVAKDSVSGFKGILRGTQKYMASKGLVSRNSQFHDLTPAERDELGGVEYKAVSFLSVIVFLYFILFTVFGMIGVGGWLEANDPAVTRANGLSPFWTGAFFAVSAFVNSGMSLLDTNMTALQLRAYPLLTMGLLILAGNTLFPCFLRFIIWTMRAMLPDRPKWQSWRITLDFILEHPRRVYTNLFPARHTWYLLGTIIILNGIDWAAFELLSIGNEDIESLPTEYRVLDGLFQALGLSTATASYSTQANELSRVKRVSWFSMYVSAYPVTLTMRNTNVYEERSLGIYAHDETPDSPANTSRSNVAMDLIRHHLGRPGLSETSRGYFVHQQLRSQLSHDLWWIALAVFFIAIAESDHYESQPVAFSTFNIIFEVVSAYGCVGVSLGFPGKNYSFCGAWHTISKLILAAVALRGRHRGLPVAIDKAIMLPSESLAWAEEEDAAMRRDRSRAWAQERGPVGSV
6.1E-81	282	0.6	1E-78	274.5	0.1	2.1	2	A0A0J9VM35_FUSO4	Uncharacterized protein	FOXG_11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	668	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9VM35|A0A0J9VM35_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIIVVVVRLVWFRRYLKNAAPALLSRRRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWVQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPVSMAPQGIGYNTHHNRHLQCGQCCLRAFQHTVMSA
6.3E-81	282	0.6	1E-78	274.4	0.1	2.1	2	A0A0J9VME1_FUSO4	Uncharacterized protein	FOXG_11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	674	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9VME1|A0A0J9VME1_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIIVVVVRLVWFRRYLKNAAPALLSRRRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAWVQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPVSMAPQGIGYNTHHNRHLQCGQCCLRAFQHSKDDTLHHQQN
7.7E-81	282	4.6	1.6E-64	227.6	0.1	2	2	A0A060S9Q0_PYCCI	Uncharacterized protein	BN946_scf184829.g55	Pycnoporus cinnabarinus (Cinnabar-red polypore) (Trametes cinnabarina)	658	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Trametes, Pycnoporus cinnabarinus (Cinnabar-red polypore) (Trametes cinnabarina)	5643	>tr|A0A060S9Q0|A0A060S9Q0_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184829.g55 PE=4 SV=1MRDRLAKIVSGVGPSTHHRHVEDGVEKGGRHHSAHGIHASDGIGAALAGGAATGLGLGIALGTGDSPEPKQPKGGYTLEDPSQPEQTGTPWSDSVSELRVVVDSPMRASPSDELTMNVDANERGILADAHSFTSSPRSGAMPLQSPTSQHSNRVHFPAFFPGLYARLERLMLRERSTSKEIKWLSDSLKDLVIGRNSEFYIEELTDEQLEELGGIEYRALRLLSYIVILQYFIGTQMISFILIAPWLSTTHTYDGVFASQPRLVNKSWFTVFQIVGAYTGGGMSLVDAGMVPFQTAYLMIFAMIFVILAGNHGMVSAPLVCVTAFVDHYDLFPSRRIAHILHSHADTQVYVDNRWISWVYTKFVKPNTPKDAALDFLLDHPRRCFLYLFPSHVTWYLTATLITFTIIELVCFIVLDIGLQVTDSLSPGTRVVAGLFQSFAVRASGFSIVSIASLAPSFQFLCVIMMYIAIYPVALSIRSTNVYEEKSLGVFEASPEDEDEEPNLDERQPRHERIGKYFSWHLRRQLAFDIWWLVFAIFAVCIIERTKIMDDENAPWFNVFRIVFELVSAFGGIGLTLGIPTQNYSFSGAFGPVSKIVVIIIMVRGRHRGLPVAIDRAILLPEDLKPNKNGPQADQNGVVPAVGPQVVNTSEKEMSHAA
1.2E-80	281	15.8	2.1E-80	280	10.9	1.3	1	TRKH_HALED	Trk system potassium uptake protein TrkH	trkH HELO_1371	Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9)	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas elongata, Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9)	768066	>sp|E1V0S5|TRKH_HALED Trk system potassium uptake protein TrkH OS=Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9) GN=trkH PE=1 SV=1MSLRMILRILGLLLMMFSLTMVPPILISLLFADGMWQAFVVALGITVGTGALMYLPNRHARKELRTRDGFLIAALFWSVLGLFGSLPLMLTGAAALSPTDAVFESFSGLTTTGATVITGIDLLPEAILYYRQQLQWLGGMGIVVLAVAILPTLGVGGMALYRTEIPGPLKDSKLTPRITETAKALWYIYATLTVTCALAYMAAGMNWFDALGHSFSTVAIGGFSTHDASIGYFDSAAIELICSAFLLISAFSFSLHFVAWRERRLTHYFQDPEARFLMLFLAGLIIITSVSLWLTSDYETLQGLRHAVFEVVSIATTAGFSVADFSTWPGALPFLLFVAAFVGGCSGSTGGGMKVIRIILILKQGMREVMRLIHPSAVIAVKIGKKVSVPDGIAQAVWGFFSAYVLLFFLMLVGVMATGVDQVTAWSTVGATLNNLGPALGEASAHYGDLPSLAKWILVVAMLLGRLEIFTVVVLFTPAFWRK

1.5E-80	281	10.3	2.2E-80	279.9	7.2	1.2	1	L0DVA2_THIND	Trk system potassium uptake protein	trkH [H] TVNIR_1873	Thioalkalivibrio nitratireducens (strain DSM 14787 / UNIQEM 213 / ALEN2)	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Thioalkalivibrio, Thioalkalivibrio nitratireducens, Thioalkalivibrio nitratireducens (strain DSM 14787 / UNIQEM 213 / ALEN2)	1255043	>tr|L0DVA2|L0DVA2_THIND Trk system potassium uptake protein OS=Thioalkalivibrio nitratireducens (strain DSM 14787 / UNIQEM 213 / ALEN2) GN=trkH [H] PE=3 SV=1MRMIQLATTLRLLGILVTLFSLTMLPPALIGWIYGEASLWVFLHAFFILLAAGLLIWVPFFWSRGDLHVRDGFVVVVMFWLVLGIF GALPLHLDPALHISLTDAVFESMSGLTTTGATIVVGLDDLPRALLWYRQQLQWLGGMGIIVLAVAILPLLGIGGMQLFRAEMPGPLKDN KLTPRIAETARNLWFIYLGLTVARALAYWAAGMEAFDAVTHSFSTVAIGGFSTYDASIGHFDSALIESVAVVFMLLGGMNFALHFLAVR RQGLAPYARDEEVRFLYLLLAAGAAIAVGYLLYAGVVADAPEALRQGIFHAVSIGTTTGYATTEFHLWPGFLPVMLVLFSFVGGCTAST GGGMKVIRVLLLAKQGLREIQRLIHPHAHIAVKVNERVMPDRVVEAVWGFMAAYILVFALMTLVLMASGLDQVTSFSAVAATLNNLGP GLGDVGANYAGISDFSKWVLVFSMLLGRLEIFTVLVLLSPAFWRR
1.8E-80	280	6.1	1.7E-53	191.2	0	3.1	3	D8QA14_SCHCM	Putative uncharacterized protein	SCHCODRAFT_77793	Schizophyllum commune (strain H4-8 / FGSC 9210) (Split gill fungus)	837	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Schizophyllaceae, Schizophyllum, Schizophyllum commune (Split gill fungus), Schizophyllum commune (strain H4-8 / FGSC 9210) (Split gill fungus)	578458	>tr|D8QA14|D8QA14_SCHCM Putative uncharacterized protein OS=Schizophyllum commune (strain H4-8 / FGSC 9210) GN=SCHCODRAFT_77793 PE=4 SV=1MFPWPEGGLFRSIRKHLNFYRVHLLCFTFVPLILSGILYACNGRYPISYVDCLFVCVSAATVCGLATIDLSTLTPLQQVIVFVQMCL GSPVFVSWLILLIRRHYFGKKFQNVINAARKNGDLTDEEAQTQPVLARLRTWLSARAQNAVREGGSRATSKSSDTNNKGGIVRKLKP EMIRRMDNAPQLVNPSGWISDAVPVKKVPTTVQAPPASADSSASPQQRASSTSPDAPIRDAAARQGATSATTRPTSEPHEHSFTIPA YSDHRVRADADYPSPRKIDCAGPRMHPSLATNMTGAGQSFRPSTKHNNFGGFPMPHHIIQRIVHALFPKLHHKIARTVTIPVTTTITSL RGEGLEGARPVPYISFDAVVGRNSAFHLLTKEQLEELGGVEYRAVNALLWIVALYHICVQVLGYVLIAPYISMSKWDADFEEPNLHRPL AAPWFALFQTVSSYTNTGMSLVDQSMIPFQTAYLMIFVMAFLILAGNTAFLTQLRSFTDWFFFMVLDIGNAAIEAIPLGTRFCIGLLQAIA VRAAGFSTVALSVLAPAVKILYIIMMYVSVCECPPLLSVRATNVYEEQSLGIFEDDDLEDDEENELANMGGSRVTAWSRYLVMHARKQ LAFDMWWLGLATFLICIIERAPIDDDATYLWFNEFTILFELVSAYGTVGLSLGLPTANYSFAGALRPLSKLILCAVMLRGRHRGLPVAIDR AVMLPNEFKIRDQVEDARSMRRTFTRQSQFGSQMPRTQTYQSGWQSQMPRTQTYQSGWQTQSQYQGEGHLEGIMKLPTANDET SWRRRNAHGTESDEEVVGDGGGKEESGDDTLTEKGSRRTNESDKV
2.7E-80	280	28.5	5.5E-80	278.6	19.8	1.5	1	A0A0F2P4V9_9GAMM	Trk system potassium uptake protein	VR73_02585	Gammaproteobacteria bacterium BRH_c0	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, unclassified Gammaproteobacteria (miscellaneous), Gammaproteobacteria bacterium BRH_c0	1629722	>tr|A0A0F2P4V9|A0A0F2P4V9_9GAMM Trk system potassium uptake protein OS=Gammaproteobacteria bacterium BRH_c0 GN=VR73_02585 PE=3 SV=1MHPNIVSRILGLFLMVFSVTLLIPIVVAVIYQEHTSQAFFLAFAITFSLGLVMWLPFSRATVELRTRDGFIITVLFWVVLGLTGTLPL MLVDEVHLSFSDAIFESVSAITTSGGTVITGLDFLPKSILYYRQQLHFLGGIGIVVIAVAIMPMLGIGGMQLYKAENVGPSKETKMTPRIA ETAKALFIIYVFLNAVCTLAYWAAGMTFFDALTHSFSTIATGGFANYDASLGYYDSNLIIAIGIFFMTVSAMSFGLHYYAWVRGTVFHYW RNPEAKTFLLTLLGCSVVVCAYLYFTGMYSAEKSLYHGTFQLVSIMTSTGFTTDNFSAWPTFLPFFLLVMSFFGGCVGSTTGGVKMG RMLIMTKQVMREIGRLVHPSGVFSMKIRNWAVPTRVTDAVWAFFGVYLAVFYMIVLVLMASGLDYVTAWSATAASLNNMGPGLGAV SAHFGDINNFAKWVLSVAMILGRLEIFTVLVLFSPMFWRR
3.2E-80	279	1.4	9.4E-79	274.6	0.1	2.1	2	A0A0J9WR37_FUSO4	Uncharacterized protein	FOXG_11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	650	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0J9WR37|A0A0J9WR37_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLVWFRRYLKNAAPALLSR RRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHE TRITFDPSTDHHPRHEQQESTLYIPGPRARDQGLPFVELNTERRFSRDTRDEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERV ATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIGYYVFLHCLGAVCLIAW VQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQ EPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQM ALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPVSMAPQGIG YNTHHNRHLQCGQCCLRAFQHTVMSA
4E-80	279	23.2	3.1E-79	276.2	16.1	1.9	1	A0A0F6TSN4_9GAMM	Trk system potassium uptake protein	TQ33_2255	Kangiella geojedonensis	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Kangiella, Kangiella geojedonensis	914150	>tr|A0A0F6TSN4|A0A0F6TSN4_9GAMM Trk system potassium uptake protein OS=Kangiella geojedonensis GN=TQ33_2255 PE=3 SV=1MQFATITRILGLLIMVFSLTMIPPSIVALIYQDGGGSAFVLTFFLTIIFGFIIYFPKRRAKSELKVRDGFLVVVLFWTVLSLMGSVPFL LMNTIEMSLADSVFEAFSGLTTTGATVISGLDTLPHSILYYRQQLQWLGGMGIIVLAVAILPMLGIGGMQLYRAETPGPMKDNKLTPRIA GTAKALWYIYLGLTIACGVSYWLAGMTPFDALAHSFSTVAIGGFSPHDASIGYFDSASIELIASLFMLLSGVNFSLHFMVVRRLSLTPYF KDPEFRSYLVMLVSITLICLTVLLAYNRFDFSEGLVKSIFHTVSIATTTGFASSDFSAWPSFLPVLLILTSFAGACAASTGGGIKIIRIVLLF KQGFREIKRLVHPTGVFLIKLGKTSVSDRVVQAVWGFFATYVMLFLILMILLMANGIDQITAFSAVAACLNNLGPGLGEVAVNYSGLND FTKYILSFAMLLGRLEIFTLLVLFTPYFWRR
4.1E-80	279	7.6	7.8E-80	278.1	2.3	2	2	A0A0B1PC27_UNCNE	Putative cation transporter	EV44_g5860	Uncinula necator (Grape powdery mildew)	531	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Erysiphales (powdery mildews), Erysiphaceae, Erysiphe, Uncinula necator (Grape powdery mildew)	52586	>tr|A0A0B1PC27|A0A0B1PC27_UNCNE Putative cation transporter OS=Uncinula necator GN=EV44_g5860 PE=4 SV=1MVIGAMTQAGLNTVDMSDLNLFQQCLTVVLSMIGNPIVVSIIVVLVRKRAFEKGLKKRRKEEKKRDHTSLTTSIASSIIANLDDYSE SRVLNSFVSGVKNIIELIMKSTRHRENQYVDRNAQFHSLSLEEREYVQCVEYRAVKLLGYMITAYYFIWQFFGCLVLGIYLSLNYTEEIS REGFNPWWLGASLAIGAFNNSGISLLDTSVIPFRDSSFVLLNMSLLMLAGNTAFPIFLRWILSQILNLIPDNEKCEDLRETLRFILKFPRR VYTNLFSSDQTWCLLALLIFFNAFDWTAFEVFNLYSPDLQTMPTKPLIDGLFQTVSMRSSGFIVIPISSLFIGLQTLYILMMYISAFPITIT MRSSNVYEERSLGIYAQELYSSDLPINDESTSGLPIRRRDRFYFVQEQVRRQLSHDLWFLVIGAVMIISTESSNFNRDPQTFSIFNMIFE IVSAYGCVGFSVGLPDKTYSFSGAWHKLSRLILCAIMLRGRHRGLPVDIDKAIQLPGQEMDFAEEQDHRFRAISKMTGHL
5.3E-80	279	21.3	1E-79	277.8	14.8	1.4	1	J3TXC9_9ENTR	Trk system potassium uptake protein	A359_04220	secondary endosymbiont of Ctenarytaina eucalypti	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, ant, tsetse, mealybug, aphid, etc. endosymbionts, aphid secondary symbionts, secondary endosymbiont of Ctenarytaina eucalypti	1199245	>tr|J3TXC9|J3TXC9_9ENTR Trk system potassium uptake protein OS=secondary endosymbiont of Ctenarytaina eucalypti GN=A359_04220 PE=3 SV=1MHFRTITRIVGLLVILFSVTMIIPGLVALIYRDGAGSAFAKTFFFAQTIGLVLWLPNRCQKSKLKSREGFFIVVLFWTVLGSVGALPF LFSAHPNVSVTNAFFESFSGLTTTGATVLVELDTLPHAILFYRQMLQWFGGMGIIVLAVAILPMLGVGGMQLYRAEMPSPLKENRIRPR IAETAKTLWLLYLALTIACALALWVAGMPAFDAIGHSFSTIAIGGFSTHDASIGYYCSPLINTIVAVFLLISGCNYGLHFAALSSHTLQVYW RDTEFRMFIAVHLTLVAVCILILWRYNVYDSSMQTLNQAFFQVVSIATTAGFTTDSIAHWPLFLPILLLFSAFIGGCAGSAGGGLKVVRIL LLYLQGSRELKRLVHPNAVYIIKLGHQALPERMLDAVWGFFSAYVLVFFLSMLAVIATSVDNFSAFSAVAATLNNLGLGLGVVADNFTP MNTMAKWILILTMLFGRLEVFTLLLLFTPTFWRE
6.4E-80	278	21.2	5.7E-79	275.3	14.7	1.9	1	A0A098GEC4_TATMI	Trk system potassium uptake protein	trkH LMI_0484	Tatlockia micdadei (Legionella micdadei)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Tatlockia, Tatlockia micdadei (Legionella micdadei)	451	>tr|A0A098GEC4|A0A098GEC4_TATMI Trk system potassium uptake protein OS=Tatlockia micdadei GN=trkH PE=3 SV=1MQIKTILRLLGLLLMMFSLMLTPLIINFIFRENFWLPFVVAFICTFCTGFLLWLCCRTQHHELKIREGFIIVVLFWFVLCLFASLPFIF VLHHQNQGMTDAFFETVSGLTTTGASVIEHLQGLPQAILFYRQQLQFLGGMGIVVLAVAILPMLGVGGMQLFRAETPGPMKDSKLTP RIAHTAKAMWYIYLLLTITCMFCYWIAGMDWFDALGESFATVSTGGFSMHDNSFAHYESDVIELIACFFMLLGGTNFALHFVAFQKKS LSHYWHDEEFRNYIFFLISATVLVGISLVVYGFFRANHHAFIKSLFNVISMATTTGFISAQFSQWPTYIPLLITLLALIGGCAGSTSGGLKV IRALLIYKQSKREIVRLIHPNAIIPIKFGNHSLAEPILQSMWGFLSVFIALFFILVLLFMALGNDFVTSFSASTASLSNSGAGIGNIHETCAHL NQPSKWVMIFAMLAGRLEIFSLLILFSPYFWQK

8E-80	278	20.4	1.6E-79	277.1	14.1	1.4	1	K0C9L3_ALCDB	Trk system potassium uptake protein	trkH B5T_00113	Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoraceae, Alcanivorax, Alcanivorax dieselolei, Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	930169	>tr|K0C9L3|K0C9L3_ALCDB Trk system potassium uptake protein OS=Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5) GN=trkH PE=3 SV=1MHFALISKVLGLLLVVFSFTMMPPVAVSYFYQDGSEGPFLASFVISLLLGLVLWLPFFRHRAELQTRDGFLVVTLFWSVLGVIGG LPFLISADTPVGFTDAVFESVSGLTTTGASVLSGLDTLPKSILYYRQQLQWFGGMGVIVLAVAILPMLGIGGMQLYKAEIPGPMKDAKL TPRIAETAKALWYLYLFITVACASAYWLAGMSLFDAITHSFSTVATGGFSTHDQSMAYWDSAAIDWITTVFIIIGGTNFALHFAAIRGLS PLTFVRDPEFRFYIGMVFLYILLVTLGLLAFNVFQGADETLRHAAFQVASFSTGTGYTSTNAAAWPGFVPFLLVFTSFLGASAGSTGG GMKSVRGALVFHHSIRELRRLIYPNGAFALRFGRHTVNDRVLQAVWGFVGVYITIAVVFTLLFTVTGLDLTTAVSCVAASLNNLGVGIG GVASGFADISPAAKWMMTLLMLLGRLEIFTLLVLFTPLFWKQ
1.2E-79	278	27.8	5.2E-79	275.4	19.3	1.8	1	A0A0A7S467_9GAMM	Trk system potassium uptake protein	FPB0191_00215	Frischella perrara	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Orbales, Orbaceae, Frischella, Frischella perrara	1267021	>tr|A0A0A7S467|A0A0A7S467_9GAMM Trk system potassium uptake protein OS=Frischella perrara GN=FPB0191_00215 PE=3 SV=1MMHWRSIIRIVGLLISLLSVFMLIPALIAVIYRDGGGTIFVQSFLVAFTLGIILWMPNRKNKQELNIREGFIIVVLFWVVLGTIGAFPFI FDKHLNLNLTSAFFESFSGLTTTGATSIIHLDTLPKALLFYRQLLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEIPGPQKDSKVQPRIAQ TAKTLWSIYIFLTVICAVCLWLAGMNGFDAITHSFSTISMGGFSTHDASLAYFNNPIINYTISFFIILSGCNFALHFNAFNQFSIKTYFKDQ EFRTFIFILVTLVIISVITIYIKEKVNFPITLDKIILQVVSTATTTGFSVDSAYQWPALLSILLLCASFIGGCAGSIGGGMKVVRVLLLFMQGS RELKRLIHPNAIYTLKLNRRVLPERIIESVWGFFSAYALVFLVSFFLVMANGLTAMDAFYIVASSLNNLGIGIDAASDTFNHVGEIVQWIMI IDMLFGRLEIFTLLIIFTPAFWKS
1.2E-79	278	16.9	2.7E-79	276.4	11.7	1.4	1	M4RF04_9ALTE	Trk system potassium uptake protein	trkH C427_0014	Paraglaciecola psychrophila 170	463	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Paraglaciecola, Paraglaciecola psychrophila, Paraglaciecola psychrophila 170	1129794	>tr|M4RF04|M4RF04_9ALTE Trk system potassium uptake protein OS=Paraglaciecola psychrophila 170 GN=trkH PE=3 SV=1MIPPAIVSVIYEDGSGLPFLLAFLLCLITGLAIWYPNRSYKNDLRAKEGFLIVVLFWTVLASFGALPFLLLEQPQMSTTDAFFESFS GLTTTGATVIEGIDYLPKAIQFYRQQLQWLGGMGIIVLAVAILPILGVGGMQLYRAETPGPVKDSKMTPRIADTAKHLWYIYLSLTIFCTL AFWVVGMNWFDAICHAFSTIAIGGFSNYDASLGHFNSVGVNIVCVIFLWIAALNFALHYAAASGRSLKGYFRDPELKVFFVIQVSLVLIC FIVLMQFSWYSDAGIAFDQALIQSVSVSTTAGFTTTDFSNWPVFLPIMLIFSSFIGGCAGSTGGGLKVIRVFLLYLQGKREVDRLIHPKA VYSVKLGERALPDRVVEAVWGFFSAYAMIFVIIMVGLIATGMDDVTAFSATAATLNNLGPGLGEVAATYADVSDSGKWLLIIAMLFGRL EVFSLLVLFSPTFWRS
3E-79	276	46.9	3E-79	276.2	32.5	1.6	1	Q73QY1_TREDE	Potassium uptake protein, TrkH family	TDE_0312	Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222)	574	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema denticola, Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222)	243275	>tr|Q73QY1|Q73QY1_TREDE Potassium uptake protein, TrkH family OS=Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222) GN=TDE_0312 PE=4 SV=1MRKRDYFVVMAFALSLILLFLQQFYPKNTPASIIHAIDILILLFVISETFFAVRQEKYIRKYFQNNLPNFLAMVIFASIFITFKIQIGFKNI SEELSIVFDIFKNIFLFGKIIRLISKRAGLTAKIISNPARTLIISFFMVIIIGSFLLMLPAASAKGSPLNFLTALFTSASAVCVTGLSVIDVSSELT IVGKFILIVLIQVGGLGIMVFSFFGMLAFRKKMTVSEKLTISYMVSEDDMSNLFKTLRVIVLSTFFIEALSAVFLFIGFSRILGFNLKTLGFA LFHAISAFCNAGFALFSNNLESFTSDIIISLTIGFTIILGGISFAVIYDVLAKVKTDIKNTFLKKKKTDYLISVNTKMILSLTVFILFISFAFFYLL EHRNTMKEMSLGTQYLASLFQAITLRTAGFSTVSFLNLTNATLLFMIFIMFMGGAAGSTAGGIKLNTIAVVFAFFKSFLKNQKTVVIKNV SVPEEQVKKAFLIFGFGLAAISVGIFLLTITESLPFLALLFETVSAFATVGLSTGITAALSPAGKIVIIILMFIGRVGPLTFLTAAGKKQKNDDI EYPYGNIAIG
3.6E-79	276	10.1	2.8E-77	269.7	1.8	2	2	L2G0T0_COLGN	Cation transporter	CGGC5_7685	Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	576	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata), Colletotrichum gloeosporioides (strain Nara gc5) (Anthracnose fungus) (Glomerella cingulata)	1213859	>tr|L2G0T0|L2G0T0_COLGN Cation transporter OS=Colletotrichum gloeosporioides (strain Nara gc5) GN=CGGC5_7685 PE=4 SV=1MCRHLEAPQEAAAAXXXPPLNFITLHYAYFIGTSLLASAIFYASSNPRGSISYVDALFLVVSAITEAGLNTVNLSQMTVWQQVML WLLIIVGSTIWVSIWTVLARKHVFEKRFREIVEAERERDQMREGEGCLPISHGPGKKAAEASGAGAVGEGVSTRVRAVDNHVTWEAE NITRRSTASVSSKTKPSRPWLSILSASKEGRNAQFHSLTAAERSRLGGHEYRALRLLSVVVPLYSILWQVLGSVALGAWIANNMPTTA TSNGANPWWAGIFFAISAFNNSGMSLLDANVVPFQQAYFVLITMGLLILAGNTAYPLFLRLIFWAALKVLRLTTAEGRHGELKSTLEFIL KYPRRVYTNLFPSRPTWWLFFMVVLINGIDWVAFEVLNIGNPVIEAIPVGARVLDGLFQALAVRSGGFYLIPISSAYPGLQVLYVIMMYI SVYPVVITMRHSNVYEERSLGIYADDEEQHSNPFLPSEKKHHTAGSNIVADFFRQNLSFAGVGAARPAAGPHGYESRTSFVSQQIRG QLAHDLWLLTLAVLLIVIIETSHFLEDPVHFSVFNVVFEVVSAGTSTI
1.3E-78	274	22.3	2.5E-78	273.2	15.4	1.4	1	A0A0B4XEN0_9GAMM	Trk system potassium uptake protein	S7S_00125	Alcanivorax pacificus W11-5	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoraceae, Alcanivorax, Alcanivorax pacificus, Alcanivorax pacificus W11-5	391936	>tr|A0A0B4XEN0|A0A0B4XEN0_9GAMM Trk system potassium uptake protein OS=Alcanivorax pacificus W11-5 GN=S7S_00125 PE=3 SV=1MHFALITKILGILLMVFSFTMAPPVAIAYWYNDGSEMAFLAAFAVIFLLGLGMWLPVWRHRAELQTRDGFLVVTLFWTVLGVIGG IPFLFNPALDISITDAVFESVSGLTTTGATVLSGLDALPKSLLFYRQQLQWLGGMGIIVLAIAILPMLGVGGMQLYKAETPGPMKEAKLT PRIAETAKALWFLYVAFTILCAVLYRAAGMDWFDAVAHSFSTISTGGFSTHDASMAHFDSPTIDMIASLFILIGAMSFTLHFAAFRSRSL RAYVLDPEFRFFIGLLTIYITMVAVGLWVYDHYHHNAGTTLRHAIFQVMSFSTGTGLTSTNMAAWPTYVLYFLVLTSFIGGCAGSTGG GMKVIRSALVFHHSLRELRRLIYPSGVFAVGFGNRSTDDRVLQAVWGFVGVYIMLAVIFTMIFIMTGLDPGTALATSAASLNNVGQGIA GVASGFGDITDFAKWMMCFAMLLGRLEVFTMLVLFMPLFWRQ
1.5E-78	274	0.1	2E-74	260.3	0	2.1	2	G4MU45_MAGO7	Uncharacterized protein	MGG_07233	Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	642	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Magnaporthe, Magnaporthe oryzae (Rice blast fungus) (Pyricularia oryzae), Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	242507	>tr|G4MU45|G4MU45_MAGO7 Uncharacterized protein OS=Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) GN=MGG_07233 PE=4 SV=1MSRDEHYAKKASTLAAGRGRLRRLLPSITFVAVHYGYFVGVCIVSSLVLWASSGPDASSSSSDGAAAGRHGRVGYVDSLFLVV SAMTETGLNTVNLSELNTWQQTILFLLIVCGGSVWVSIWTVLARKWAFERRFDELVAAECAAAGVSPSPPGLLRRIASRLHTVSSGVE PGSLGRLDDAEGFGGVVLAGPSYSITRDTALSKSTSLTRRRRAGQGEAIAQMRADILRGVVDRQMRGGGGNRHVAKLTSEERCRLG GVEYRAIRLLAVVVPLYSALWQVLGCLALAAWIQVNLPHPPVSNGLSPIWLGIFNGASAFNNSGMSLLDANMVPFNQAYFVLATMGA MILAGNTAYPVFLRLVLWAALGLLRLASSDAVLPDLKTALAYALKHPRRVHPHLYPPRQTWWLAGSVVVLNAVMWVAFELLNLGNPIV ESLPGAARVVDGLFQAIATRSGGFMVVPMAQVYIGMQVLYAIMMYIPVHPVSIKKSIVYRARRDVVLGIHSESEKTPPPTLGLEQEDAH GESTRAFLSRQLKASRVGRHDAWVLVAAVLVITTIETGHFLGDPVTWSVWNVLFEVVSAYGCVGVSTGVPFDSFSFSGGWNAPSKL VLCLVMLKGRHRGLPESVYPAVVLPGEEEDVEGVE
2E-78	274	34.2	3.1E-78	272.9	23.7	1.2	1	A0A0A0WZH9_9SPIO	Potassium transporter	JO41_00910	Treponema sp. OMZ 838	578	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema sp. OMZ 838	1539298	>tr|A0A0A0WZH9|A0A0A0WZH9_9SPIO Potassium transporter OS=Treponema sp. OMZ 838 GN=JO41_00910 PE=4 SV=1MNTIVTKLRANLSGVAFILSLALLFLQQFYASLAATIVIHTLDAVILLLIIAETFLPMRHEKYFQQYFQKHAALCVSTVLFCAAFIFFKI KIGFIPSSPELILMFALIKNIFLFGKIIKNTADTAGGTERVMLNPAGTLLVSFFMVIITGTFLLMLPAATPGTDHLDFLTALFTATSAVCVTG LSIINVATELTTVGKVILILLIQIGGLGIMVFSFFGMLAFRRKLSIAEKLTVSYMVSEDDMSGLFKALRVIVGSTFLVEAISAGFLYLGFSRT MGVSVETLGFAAFHAVSAFCNAGFALFPNNLESFTGDPIISLTISFTIILGGIGFAVMYDTVRKIKTETQNVFKKKKTTFFLPLNTQIVLVM TAGALFISFAAFYLLEHTHAMKDFSLHEQYLGAFFQAVTLRTAGFSTVSFASLTNATLLMMIFVMFVGGASGSTAGGIKLNTVAVVFAF FRSFLKNDRTVIIKKMSIPDEQVKKAFLILGFGLTIVSAAIFVLTVTESLPFLPMAFETVSAFATVGLSTGITAQFSIAGKLILIFLMFIGRGG PLTILTAAGKKEGSDTVEYPYGAISIG

1.9E-77	270	17.5	6.9E-77	268.4	12.1	1.7	1	S6BV75_9GAMM	Trk system potassium uptake protein	EBS_0116	endosymbiont of unidentified scaly snail isolate Monju	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, unclassified Gammaproteobacteria (miscellaneous), endosymbiont of unidentified scaly snail isolate Monju	1248727	>tr|S6BV75|S6BV75_9GAMM Trk system potassium uptake protein OS=endosymbiont of unidentified scaly snail isolate Monju GN=EBS_0116 PE=3 SV=1MHIRTIARIIGFFALGFGLILLAPLAVAALYGEDEIGHFLEAIGASLGTGLAFLLAGGRARHDLNNRDGFLVVALFWAGVGSLASLPFVLSAHLGPVDALFEAVSAFTTTGATVISGLDDLPHSLLFYRQLLQWLGGMGMIVLAIAVLPMLGIGGMQLYKAEAPGPFKEEKLTPRLNQTARYLWGFYVGMTGACALAYWLAGMSGFDAVSHAFSTVSTGGFSTHDASLGFFDNPLIEGIAILFMTLGAINFSVHYLAWRQRSLLTYLGNVEVRTFLLIILAVVLVIGGFLHFAGTYPDYNSALRNSIFEVVSVITSTGFGTVDFSHWPSFVPVLLIFISFIGGCGGSTAGGMKVMRIVLLTHQGWREVRRLIHPRAQLPIHVGNQVVSVQTVQAVWGFMAAYVVSFVILMLLMMATGLDQVSAFSAIAATMNNLGPGLGEVATSFSSVSEPGKLIAVFAMLLGRLEIFTILVLMTPEFWRA
5.5E-77	269	11.4	2E-76	266.9	7.9	1.7	1	D3RUV0_ALLVD	Trk system potassium uptake protein	Alvin_0027	Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Allochromatium, Allochromatium vinosum (Chromatium vinosum), Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	572477	>tr|D3RUV0|D3RUV0_ALLVD Trk system potassium uptake protein OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) GN=Alvin_0027 PE=3 SV=1MHWRAIIRLFGLLLMLYSLSFLPSLAVALVYQDGQWSVFLESLAATLSAGLLLWLPNSHRESELSVRDGFLIVALFWALLGVFGALPFILGLHLSLTDAVFESISGFTTTGATVIAGLDRLPPSILYHRQQIQWLGGMGVIVLAVAVLPLLGVGGMQLYRAEASGVAKHEKPTPRIGETARVLWSLYFGLTAACALAFWLAGMTLFDAVGHAFATVATGGFSTHDASLGHYDSPLIEAIAIVFMLAGAVNFAIHFVAWRDLDVRAYLNDPETRVFGLTILGGSLFIAASLYWAQAYADVGSSLRHGTFQVVSIMTSTGFGTATFGDWPLHIPLVLVILSFTGGCGGSTAGGLKVLRVMLLVKLGVRQLFQAHPRAVLEVKIGRRVIKEDVLLSVWGFYVLYIATCLLLTVAMMAAGLDLESAFGAVFTTVNLCGPGLGEVAVTFATVDPVVKWLGVFGMLAGRLEIFTLLILFMPAFWRQ
1.2E-76	268	23.6	5.1E-76	265.6	16.3	1.7	1	X2H404_9GAMM	Trk system potassium uptake protein	GAPWK_2557	Gilliamella apicola	461	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Orbales, Orbaceae, Gilliamella, Gilliamella apicola	1196095	>tr|X2H404|X2H404_9GAMM Trk system potassium uptake protein OS=Gilliamella apicola GN=GAPWK_2557 PE=3 SV=1MLLPALIALIYRDGAGAIFVRSFFAALILGCLLWLPNRHQRHELSTREGFFIVVLFWVVLGTIGAFPFIFDTHINLNLTTAFFESFSSLTTTGATTIVHLDHLPKALLFYRQLLQWLGGMGIIVLAVAILPLLGVGGMQLYRAEIPGPQKDSKMRPRIAETAKTLWSIYILLTTLCAISLWAAGMNIFDAVSHSFSTISMGGFSTHDDNLAYFNSATINYIITIFLILSGCNFALHFAALNGLSIKVYWRDQEFRTFIFILLILVICACGVYFYQVKHKLSIDKIILQVVSVAATAGFTVDDINTWPSLLPLFLLCASFIGGCAGSTGGGLKVVRVLLLFMQGSRELKRLIHPNAIYTLKLNNRVVPERIIEAVWGFFSAYALVFLVSLFIIMATGVAASDSFYIVASSLNNLGVGLGSVSDNFASVSDMVKWVMIVDMLFGRLEIFTLLVLFTPTFWRN
2.5E-76	267	6.9	7.7E-57	202.3	1.2	2.1	2	K5XCV0_AGABU	Uncharacterized protein	AGABI1DRAFT_127160	Agaricus bisporus var. burnettii (strain JB137-S8 / ATCC MYA-4627 / FGSC 10392) (White button mushroom)	733	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Agaricaceae, Agaricus, Agaricus bisporus (White button mushroom), Agaricus bisporus var. burnettii, Agaricus bisporus var. burnettii (strain JB137-S8 / ATCC MYA-4627 / FGSC 10392) (White button mushroom)	597362	>tr|K5XCV0|K5XCV0_AGABU Uncharacterized protein OS=Agaricus bisporus var. burnettii (strain JB137-S8 / ATCC MYA-4627 / FGSC 10392) GN=AGABI1DRAFT_127160 PE=4 SV=1MTKFQQFLLFAQLNIGNNVFISWFVVFFRRQYFKKELRHILMAAERKASLRSPVRANTKHRSWSRRMFSVFRPKLSVVLEENVERKTDRDVEGRLRTDMIRRIDDAPKPVNPSGRVVEKVSPRRTSPNDASDEIFEFVNPDQTPRSLSLVESLASGVANDGLTDTTASNTPSEPPAGGASRVTRPFPHHQTIEFAPTPHRPKENEIQSVTADPSSSNLRSIHRPSLGRQNTLNSMQTTPSRGAGESSDSRSRGFGGFPMPFSLLNSIVSKAFPKFKRRLSRTVTMPATTSLVTTHSAQRAPPNAKAVPYISFNTTVGRNSNFDNLTNQQLEELGGLEYRALNVLLWMIGAYYIGFQVLGVVITLPYMYQQRWRTAFDPPTNERHVTPGWFTVYQISSSLTNTGNSLVDQSVIPFQDAYLLVIVQWFLILVGNTVYTWFLLAVTALFTSLEWFFFLLLDIGNAAIEAIPLNIRFSSSGLFQAVAVRAAGFTIFSLANVSPAVQVLYLVMMYITIFPITLSVRATNVYEERTLGLYKEDGEPEYSFDATGSNRVKIWGRYLAMHARKQLAFDIWWLTIAVFLICIIERHNITNPDRPWFNVFAIIFEVVSAYGPVGLSLGVGYDNFSLSGAFSTLSKLIVCVTMLRGRHRNLPFALDRSIMLPKEFKQTNEGDTTNDNTAQRSFGAGTGSLYSRDDNNVNVDAQLHKRVPRRESMTSSSTSESSAQNANMGNTAEV
4.6E-76	266	21.2	1.3E-75	264.2	14.7	1.6	1	A4A938_9GAMM	Trk system potassium uptake protein	KT71_04705	Congregibacter litoralis KT71	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, OMG group, OM60 clade, Congregibacter, Congregibacter litoralis, Congregibacter litoralis KT71	314285	>tr|A4A938|A4A938_9GAMM Trk system potassium uptake protein OS=Congregibacter litoralis KT71 GN=KT71_04705 PE=3 SV=1MHFSVSLRILGLLLALFSVTMLPPLLIAVLNDDDTVTGFISAFSITLLSGATLWLPLRGVKRDLQIRDGFLVTALFWTVLGLFGALPFGLTASLNMSVTDAIFESVSGLTTTGATVLTGLDNMPASILLYRQMLQWLGGIGIIVVAVAVLPMLGIGGMQLYRAETPGPSKDSKLTPRITETAKALFTVYLALTVLCAGAYGLAGMSGFDAVCHAFATVAIGGFSTHDASMGYFESDAIYLISSLFMLISALNIGLHFTAFRRRSVLGYWEDSEARFFLSAMAVCVAITCAYLVFSQTLDLEESVVHGLFQAVSITTTTGFATQNFAVWPGFLPMMLLMFSFMGGCVGSTGGGIKAMRLMLIYKQGIRELKQLVHPHAIIPLKVGNRRVEATVVSAVWSFFAVYTFAFIVIMLVLMATGLDFMTAFSAVAAALNNLGPGLGSVAANYGEVSDFAKSVLCFAMLLGRLEVFTLLVLFTPMFWRN
1.4E-75	264	34.2	1.8E-75	263.7	23.7	1	1	Q7NAZ5_MYCGA	Cation transport protein	trkG MGA_0171	Mycoplasma gallisepticum (strain R(low / passage 15 / clone 2))	588	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma gallisepticum, Mycoplasma gallisepticum str. R, Mycoplasma gallisepticum (strain R(low / passage 15 / clone 2))	710127	>tr|Q7NAZ5|Q7NAZ5_MYCGA Cation transport protein OS=Mycoplasma gallisepticum (strain R(low / passage 15 / clone 2)) GN=trkG PE=4 SV=2MLKINGKNRKNSLSKRNKIIKWLKIIFTGETISQKIAHFYIYFILIGSILLYLPISLKYSDTYEKATNVTFQGLAAEPIIEKAKYSFIDSFFIATSAFSDTGLSTLVVRETYTIFGQIILAILIEVGGVGFVVFWYLIWRIFAKIFKDQSSLEKTLLLQSERGGEKLSTTSKTIMVAVTAVMIFQIIYAIFYSLYFYFVPSFEQQNIIDLQNSDVNGLLIDFKASQITVDNPYRKFFTYHNAGSAIWAGIFHSVSSINNAGFDIFGPFSLSSFRNDHHIVLLFITATQFFIGGIGYYPTIFDIYEKIRYKRLYKNRVKYKFSIFTKLSLITSAILLMLPIVIVAPVEVLSKNGSFNVTSQIFEQSLKNNLKFEPSLNIQTPEQLYQTIYGKNSKLDYVLNLWFMIFSSRSAGFSTISMYNLTDVSKLIFSLLMFIGAAPSSTAGGVRTTTFALVMVAIFQKFKGYKQVRLFKRSIPSETINSAYLITLLSAIFLIVAAVGTKITFDFVLPDVRFSIMDVFFEYSSGYGTVGLSVGITSYLTSINLVPLVLLIALMIIGQLGVSTSILAWVKSDAIKWNYSYVDEDVKIG
3.2E-74	260	14.9	6.7E-74	258.6	10.3	1.4	1	L0GW58_9GAMM	Trk system potassium uptake protein	Thimo_1265	Thioflavicoccus mobilis 8321	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thioflavicoccus, Thioflavicoccus mobilis, Thioflavicoccus mobilis 8321	765912	>tr|L0GW58|L0GW58_9GAMM Trk system potassium uptake protein OS=Thioflavicoccus mobilis 8321 GN=Thimo_1265 PE=3 SV=1MNWRGVIRLIGILLTLYALSFIPPLLLALAYQDGEAPHFLAAWIISTAIGLAIWLPVRAERSALGYRDGFLVVALFWAVLGVVGSIPFIVGLHLGVTDAIFESVSGFTTTGATVIAGIDDLPPSILYHRQQIQWLGGMGVVILAVAILPLLGVGGMQLYRAEASGITKDEKLTPRITKTAQVLWSIYFALTLACTLAYWAAGMNLFDAVGHAFSTVSTAGFSTHDASIGYFDSLEIELICVVFMTLGGVNFAIHFVVWHRRNPLLYLRDPEVRTYLLILLGAILFIAISLLWFGTYTGVGEALRRSLFEVVSVITTTGFSTADFATWPRHIPLVLVMLAYVGGCAGSTAGGLKVVRVMLLAKMGVRQMFVLSHPRAMAPLKLGRRGVPEDAAYSIWGYYVLYLSTALVLTVAMMAAGLDLESAFGAVSATLNLLGPGLGDVATTFAAMSPLVKWLAIFGMLVGRLEVFTLLILFTFAFWRQ
3.3E-74	260	21.5	5.8E-74	258.8	14.9	1.4	1	A0A0A8UPP9_LEGHA	Trk system potassium uptake protein	trkH LHA_0388	Legionella hackeliae	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella hackeliae	449	>tr|A0A0A8UPP9|A0A0A8UPP9_LEGHA Trk system potassium uptake protein OS=Legionella hackeliae GN=trkH PE=3 SV=1MQIKTILRLLGLLLMMFSVSMLTPLIINFIFHEQFWLPFVAAFACTFTTGAFLWLSFRKQHHELKIRDGFLIVVLFWFVLCLYASLPFIFAIKHHNHSITDAFFESVSGFTTTGASIIRHIEGLPHAVLFYRQQLQFLGGMGIVVLAVAILPMLGVGGMQLFRAETPGPMKDSKLTPRIAQTAKALWSLYLLLTLFCWLSYWVAGMDWFDALGESFATVSTGGFSMHDTSFAFYQSDTIELIACFFMLLGATNFALHFLALKKRTLFPYWHDEELRFYLLFLFGASILISISLVFYGFFDANPHALIKSLFNVISLATTTGFMSAPFSTWPTYVPVFLMILALVGGCAASTSGGVKVIRALLIYKQSKREIVRLLHPHALIPIKFGKHSLPEPILESMWGFLSVFIALFLSLMILFMAFGNDFITSFSAITASLANAGAGLGTISENFADLNQPSKWLLIFSMLAGRLEIFSLLILFSPHFWQK

3.6E-74	259	8.8	2E-73	257	1.2	2.1	2	M7T3N4_EUTLA	Putative low-affinity potassium transport protein	UCREL1_1798	Eutypa lata (strain UCR-EL1) (Grapevine dieback disease fungus) (Eutypa armeniacae)	630	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomycete, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Xylariomycetidae, Xylariales, Diatrypaceae, Eutypa, Eutypa lata, Eutypa lata (strain UCR-EL1) (Grapevine dieback disease fungus) (Eutypa armeniacae)	1287681	>tr|M7T3N4|M7T3N4_EUTLA Putative low-affinity potassium transport protein OS=Eutypa lata (strain UCR-EL1) GN=UCREL1_1798 PE=4 SV=1MKDPREVALAIFQWIRPSFLSRDPHFNFITVHYFWIIGWAILGSILIYSTARGELAYIDALFFATGANTQAGLNTVDTNLLNLFAQIIIYIMAMLSSPITIHGISKSRSKAKPTAADVEKGVNGRHITVMYNTAKASRMTNDGTLLDGELMNGTVEPNQTPNETQSTDDADPNGSDHPARHGPPQIKFSDQVKRSNALDDDGDENVPLPQRRSDAEHIAILERQRKGNKSVLRIPGPRDVERGVRPEEFEEDEETQAEDVQAAAHTVSPLKFRKNRVQGEKLQTAETSTSTNTHRANPLQRIKTALTQILVLLNGLDLLLFIILDLNSEVVEQLPLNIRFLDGWFQATSTRTAGFSCVNLANLHPAIQVSYMVMMYISVFPIAISIRSTNVYEEKSLGVYKPVEEVDDENPSGMAYLGSHLRRQLSFDLWYVFIGFFILSISEGSRLASGDISMFAVLFEIVSAYGTVGLSLGYATVNTSLCSQFTVVGKLVIIAMMIRGRHRGLPYGLDRAVLLPSEHLNRKEAEEAELRLQRRDSAVTTGRAASLARGRSHSVDRRHVLTNLLHPGPVFPVSMAKSGAKSEHTLNFGYSETLKKYKTNQEEEEEANQIHLSTPPRPQRRATTQPVYEH	
4.9E-74	259	0	2.8E-38	141.1	0	3.1	3	Q2GMG5_CHAGB	Peptidyl-prolyl cis-trans isomerase	CHGG_10839	Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	890	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomycete, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Chaetomium, Chaetomium globosum (Soil fungus), Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)	306901	>tr|Q2GMG5|Q2GMG5_CHAGB Peptidyl-prolyl cis-trans isomerase OS=Chaetomium globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) GN=CHGG_10839 PE=4 SV=1MQHLLLSLSLLASAAVGALASDDLKIDVTLPVECERKTQKGDTINVHYRGTLQSNGEKFDASYDRGTPFSFRLGSGMVIKGWDEGLLDMCIGEKRTLTIGPSYGYGDRNIGPIPAGSTLIFETEMMGIEGVPQPESIVTKSATDSPASSASEKVAEKVASAESIDGYLTFMRWLLFSHPDHRSRATFLCQTADLEQKPLLADAPLGCGTDQKTWCRGVESTTARMHKRSRCLRMRSWLPPMNFITIHYAYFIIGCLVSSLIFWGSSNPARSISYTDSLFLVVSAMTESGLNTVNLSLMTTWQQVLLFLLIIFGSSIWVSIWTVVARKHVFEQRFHDIVLAERTRRANQPGSAGSPPRLDRFLSCRRASTTTLPPVRTETAPDVPAGGDVAALAVDAKAPRGKSPSPDRIAFANTPNPIDAVSTAAQHYSRENQATRRNHGREGGSTVDQKDNEFSMHQLLAGKSGGRNSQFHGLTTEERERLGGCEYQALRVLSVIVPVYFILWQLLGCLALGAWINHNLPGPPLENGIKPWWLGIFNGVSAFNNSGMSLLDANMIPFQNSTFVLLTMGLLILAGNTAYPVFLRLIVWSLRRLLILLLTREDDYTRLKDTLKFILRYPRRVVTNLFAARPTWWLVFMLILLNSIDWVGFELLNLRNPAIQQIPPSSRILDGLFQALVVITMRHSNVYEERSLGIYTEDEAPTEDPEKATADSIHSRRRHRGNSNSSVSAALGRVISHAFTLHGVGARAPPPPKQGPESHINFITQQIHGQLAHDIWWLVLAILVIVTINTDRFLADPVRFSVFNVIFEVVSAYGCVGISVGAPGADYSFSGAWHPASKLVLCAVMLRGRHRGLPVALDRAVRLPREELHREEEEDQCIRRSMTTRRISVEV	
5.2E-74	259	18.1	3E-73	256.4	12.5	1.8	1	A0A0F4Q8Z5_9GAMM	Potassium transporter (Fragment)	TW86_22600	Halomonas sp. S2151	440	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas sp. S2151	579478	>tr|A0A0F4Q8Z5|A0A0F4Q8Z5_9GAMM Potassium transporter (Fragment) OS=Halomonas sp. S2151 GN=TW86_22600 PE=4 SV=1MSLRMILRILGLLLMMFSLTMVPPIAISLLFGDGTWDAFLIAIAITVLTGALMFLPNRRARRELRTRDGFLIAAMFWTVLGLFGSLPLMLTGSTALSFTDAVFESFSGLTTTGATVITGIDFLPEAILYYRQQLQWLGGMGIVVLAVAILPTLGVGGMALYRTEIPGPLKDSKLTPRITETAKALWYIYATLTVVCMLAYMAAGMDWFDALGHSFSTVAIGGFSTHDASIGYFDSAVIEAICIVFMLISALSFSLHFLAWRERRIGHYWEDSEARFLLLYLTGLASITVVVLWLTGTEETTVGLRHGIFEVVSVATTAGFSVADFSAWPGALPLLLFIAAFVGASSGSTGGGMKVIRIILIIKQGMREIMRLIHPNAVIAVKIGKVSVPDGIAQAVWGFFSAYVLLFFLMLVGVMATGVDQVTAWSTVGSALNNLGPALG	
5.5E-74	259	14.1	1.4E-73	257.5	9.7	1.5	1	Q0AAX9_ALKEH	Trk system potassium uptake protein	Mlg_0654	Alkalilimnicola ehrlichii (strain ATCC BAA-1101 / DSM 17681 / MLHE-1)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Alkalilimnicola, Alkalilimnicola ehrlichii, Alkalilimnicola ehrlichii (strain ATCC BAA-1101 / DSM 17681 / MLHE-1)	187272	>tr|Q0AAX9|Q0AAX9_ALKEH Trk system potassium uptake protein OS=Alkalilimnicola ehrlichii (strain ATCC BAA-1101 / DSM 17681 / MLHE-1) GN=Mlg_0654 PE=3 SV=1MHWRTILRITSLLVVIFSFNFIPPLGVSLFYGDGQWGTFGLSWLIVAVLGVLFWLPVRADRKDLMVRDGFLVVALFWSVLGLVGSLPFMFGLGMTPTDAVFESISGFTTTGATVIVGLDDLPRSILYYRQQLQWLGGMGVVVLAVAILPMLGIGGMQLYRAEVSRVTADEKLTPRLMHTARALWAIYLTLTVACALAYWLAGMTPFDAIGHAYSTVATAGYSTHDASIGYFNSVTIELIAVVFMLLGGMNFALHFLVWRSRDPRVYLRTPEARFFLGLFLAATVVIASALVFMSTYESVWDAVRYALFQTASVLTTSGFSTAVFAEWPLYIPLVLASLSFIGGCAGSTAGGMKVIRIMLLFKQGAREVNATIHPHGVYRVKLGDRAVPEQVVQAVWGFYTVYILAALVLTGLNMAMGLDMESAFGATIASLNLLGPGLGEVATTFALQPDPIKWMASFAMLLGRLEVFTLLILFTFAFWRN	
1.4E-73	258	16.5	6.1E-72	252.1	4.1	2.2	2	G4NGE5_MAGO7	Potassium transporter 1	MGG_04338	Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	825	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomycete, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Magnaporthe, Magnaporthe oryzae (Rice blast fungus) (Pyricularia oryzae), Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)	242507	>tr|G4NGE5|G4NGE5_MAGO7 Potassium transporter 1 OS=Magnaporthe oryzae (strain 70-15 / ATCC MYA-4617 / FGSC 8958) GN=MGG_04338 PE=4 SV=1MGEGSGSDGFFNRLQLQDRWAGIYRTIKPYLPPINFITVHHAYFIFVGLIISAIFFALADREEFKTLSFVDSWFLIMSAFTGSGLNTVNLSELVVAQQAILFVMMVIGSPVLVSLFTIWFRFRIFEKRFDRIVEAERERRRRKRATGAMLGMAGAMAGLPVMSTFGAGPRTKPQSPEERAKNDAFELSKPKSPRPGDVERLQAESPKLSPTTNPNTMAMHPQVAAMHTNFQENDAASLPPSPRPAPPSGQSYRHRQPLSPLGRPATATAKNGTTEAGGETGFDFRTFVHKHKHSIGRNGQFFDLDDDQREYLGGVEYRALKLLFVIVAIYFVVLQILGAITLGAWLAVHGRAATAVNAQDPWWSGIFLAISSFNNCGLTLLDAGLTAFVDDAFVLTVVTLLSFAGNAAFPAFIRGTIFLARLFFKHIIARHGPASDEYGEWEEAFDFILKYPRRLFMLMFPSKANLAFVSFFSTVVVVNWIGLLLVLGLGNSVLEAFPLAKRVGVALFQATTTPSGGFAVFSISGLWFDAQVLLLIVMYLAAYPEIIVMRNSNVYEERSLGLYSTAEAAKQDEEEDAADEAAAAGMTFIVPQLSTNSMSHASGISAKHGIATTTVKTLAQVGRRGTAFVGKQLQQRMSDFQGVGIDNAAARRRSQAAASLPVIVGIKRSKTIDFEPPPAAAAASDGSVSLVSQHLRGQLAHDVWSIALALFLITIIETSHSIFDPRTFSVFNFLFEIVSGYTNIGISVGLPDQSYSFSGGWYTGSKVVMVFMMIRGRHRGLPVALDHSVKLPGWDDVAREEQDAEIRRSLSVARASMENNGQQVLY	
3E-73	256	9.3	4.3E-39	143.8	0	3	3	Q2UQW8_ASPOR	Na+/K+ transporter	AO090005001071	Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	646	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomycete, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus oryzae (Yellow koji mold), Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	510516	>tr|Q2UQW8|Q2UQW8_ASPOR Na+/K+ transporter OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=AO090005001071 PE=4 SV=1MVTSRGWLRPLGRIIMAVVPPFNFITLHYAYFIVTSLVCSVIFWGASNPLRSVSYADALFMCVSAITGAGLNTVDLSSLNTFQQAILFALLMLGHAILISITVLFVRKRAFESKFKGISNRLAQYRESRPTSDLNVPLDEADFKVVNVQPSNMNAGHGDKAPGMTEVSPVENSTDLTSDDHIHWAEDDQITIGARRRSHHQSHRVFPMVGVGARPDLNNHPKDAIPNLPREESDILRLKGIIQGTQKYFASRGFISRNSQFYGLTPDERERLGGVEYKAVSFLAVIVAVYWLMFLIIGMIGVGGWLEANHPDISRENGLSPFWTGAFFAVSAFVNSGMSLLDANMTALQKNVYPLLTMGLLILAGNTLYYPCLFRFIIWSMRCMIPDQPAWKTWEVTLDFILDHPRRVYTNLFPRRHTWYLLGTIIVLNAIDWAGFEILAIGNQEIEQLPPGYRVLDGLFQALERSLGIYAHDDPESESEGQAKPGLFMSLVRHHLLGRQDVPSAEVSRSYFVHQQLRSQLSHDIWWIALAVLFISIAESPNFNRDPVSYSTFNIIFEVVSAYGCVGVSVGIPGRNSSFCSGWHTISKLILAAVALRGRHRGLPVAIDQAVMLPNDSLAWAEEEDAALRREKTRAWGVDKMPVGAV	
3.4E-73	256	18.4	4.8E-72	252.5	12.7	2	1	R4W8X9_9EURY	Potassium transport system protein trkH1	L593_05400	Salinarchaeum sp. Harcht-Bsk1	516	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Salinarchaeum, Salinarchaeum sp. Harcht-Bsk1	1333523	>tr|R4W8X9|R4W8X9_9EURY Potassium transport system protein trkH1 OS=Salinarchaeum sp. Harcht-Bsk1 GN=L593_05400 PE=4 SV=1MSGAAATIGRDVGRILEALGGLMIVSVLVTLAWGEYFALPALLVSAVVPLGIGRFLYRRYRSADAPGRLHGMIVAAAGWLFVGLFGSLPFLLVAWSVELGVPIVSTPQQTATLAAFTNPLNAIFESMSGFTGTGLTMTDDESALPRTLQWWRTFSEWVGGVGIVILTTAILSRPGSGSLTLYESEARSEKIHPSVVSTVRTIWWIFILFTFGAILTLWLAGMPIWGAINHAMTGLSTGGFSITDNSIATYDSVAIDFALIPIMLLGSIAFPVHYLILQGDLRNFYSDLQTRWVFLYMSTGSALLWGLLYFAGPYETPFAALRYGLFQFVSAATCTGFQTAVDATNVAIGRWPSYAQLTVTFGMFVGGAAGSTVGGIKIIRGLTLAKGIRYQISEVFYPESAVRRLVINGRRLNDEASSREFMEAAIVFVLWVTFLVVGTFVLLLALPADDYTLPNVFFEVASAQGNVGLSSGITGPDSLPTIGKVTFLFHMWIGRLEIIPVLVMLRTVFQRGGLYA	

4.8E-73	256	2.5	1E-53	192	0	2	2	A0A060SIZ0_PYCCI	Uncharacterized protein	BN946_scf184970.g46	Pycnoporus cinnabarinus (Cinnabar-red polypore) (Trametes cinnabarina)	553	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Trametes, Pycnoporus cinnabarinus (Cinnabar-red polypore) (Trametes cinnabarina)	5643	>tr|A0A060SIZ0|A0A060SIZ0_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184970.g46 PE=4 SV=1MERDHAAVDDESTPPALRHIRETLARLKKEKGIGGSRGRSSSRGSTSRRSSQHLEIRAGLRADMTLVPRAAPDEIRQNEGRVK RVPYLSFSATVKRNSSFYGLTADNIEELGGVEYRALCSLSWIIPVYYFGLLGVSFIVTAPYMTLPKWQVNFHPPLQHKDINAIWFSAFQI MGAWANTGMSLVDQNMVPFQTAYPMVIFIIICVLAGNTALPIFGSQVRRFTLSLSAVIADTDPNTSGTNLFFYLILDIGNPATESLPFGV KFIDAILDAAACRNAGYQPIPISSLMPAVQVLSVIMMYIAIFPIAMSVRATNVYEEKSLLIYESESEEDELNDDTHWNTPSESRVAIWGRY LLRHTRRQLSFDMWWLAVSLFLLCIIERSNLTDPAKLSYFSIFALLFELVSAYGTVGLSLGIPGANYSLSGGMHTLSKLVICAVMLRGRH RGLPVALDRAVLMPSEFLVIKSENQREGANDEKEARGSPQSPRFPQTLHNPDELAAQMRLRTRTISLVVEERRDTTTKDTKYPAWSP DRVPEESRDTSVDEVGRSDHHA
7.4E-73	255	6	2.2E-71	250.3	4.2	2	1	T2GDU9_DESGI	Trk system potassium uptake protein	DGI_2568	Desulfovibrio gigas DSM 1382 = ATCC 19364	483	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio gigas, Desulfovibrio gigas DSM 1382 = ATCC 19364	1121448	>tr|T2GDU9|T2GDU9_DESGI Trk system potassium uptake protein OS=Desulfovibrio gigas DSM 1382 = ATCC 19364 GN=DGI_2568 PE=3 SV=1MRLGRTLFVVGAIVCCVGFSMAFPLLWGLMRGDAGALPMLQAMLTTLLCGGALLLGFRRSSQDSPLGHRDGMAIVSLGWVAA GVCGALPYLFGGVCGTVTDAVFESVSGFTTTGASILTDIEAVPESLLLWRSLTHWLGGMGIIVLSLAILPFLGVGGMQLYKAEAPGPTP DKLKPRIKDTAAILWKVYVGMSALECVLLLLGGMSLFDSLCHTFGTMATGGFSTRNSSVAAYDNAYIYWVITAFMFLAGMNFSLHYRL LSGHAKDIWKDGELRFYATVVLGSTVLIAWNIWGRHYDDAAEALTQSAFQVSSIITTTGFATADFEQWPAFSQMLLVLLMFVGGCAG STGGGMKVVRILLMLKHCSMELIRLVHPRAVRHVKLGGRNVPPEVLSGVWGFFGLYLFCYVATSLALSAMDLDIVTSFTATLACISNIG PGLGTVGPAENFFHLPAAAKVLLTWCMLLGRLELYTVFILFVPEFWRK
1.2E-72	254	18.4	2.7E-72	253.3	12.8	1.4	1	L0JLX0_NATP1	Cation transporter (Trk-type K+ transport system, membrane component)	Natpe_1693 C488_14010	Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	516	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema pellirubrum, Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	797303	>tr|L0JLX0|L0JLX0_NATP1 Cation transporter OS=Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786) GN=Natpe_1693 PE=4 SV=1MKGAARTIGRDLGRIFQALAGLLFVSILVALIWGEYYAIPALVVAGLVPFVVGYILTSRFRDAARPGKLHGMIIAALGWFCVAIFGS LPFLLIAWTVELAPPILGEPSQTSTLAAFTNPINAVFESMSGFTGTGLTMTDNEEVLPRTLQWWRTFIEWIGGVGVIVLTTAILARPGSG SLTLYESEARSERIHPSIVSTVQTIWWIFILFTFVSILLLWVVGMPLWGAINHGMTGLATGGFSITDNSIATYDSVAIDFALLPVMLLGSIA FPVHYLILQGDLRNLYSDLQTRWVFIYMGIGTVLLTVLVYVSDTYDSLFTAFRYGSFQFVSAATCAGFQTAADTTNVALGRWSAQAQL TVVFGMVVGGAAGSTVGGIKLIRALTLLKGIRFRIADVFYPETAVRRLKINGRRLNEQEMRQEFEEAAIIAALWFLFLGLGTFALLIMLPQ GEYTLENVIFEVASAQGNVGLSAGITGPESLPTLGKVMFLFNMWIGRLEIIPVLVTLRAVFDRGGLYR
1.6E-72	254	12.9	2.3E-72	253.5	9	1.2	1	B8FH02_DESAA	Trk system potassium uptake protein	Dalk_0381	Desulfatibacillum alkenivorans (strain AK-01)	482	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfatibacillum, Desulfatibacillum alkenivorans, Desulfatibacillum alkenivorans (strain AK-01)	439235	>tr|B8FH02|B8FH02_DESAA Trk system potassium uptake protein OS=Desulfatibacillum alkenivorans (strain AK-01) GN=Dalk_0381 PE=3 SV=1MRWGHTFSVVGILLVFCGLAMALPMLVGLYYQDQSIIPLAKGMGITLLVGAMVYLAAPTKKQETLSHREGMAIVALGWAAVGVA GALPFYFSTSFLGFTDAVFESVSGFTTTGSSVLSDIEGVSKGLLMWRSMIQWLGGMGIIVLSVAILPFLGVGGMQLYKAEVPTPVPDK LKPRIRDTAVILWQVYALFTVLEAVLLFVGGMSVFDAVCHAFTTMPTGGFSTLNTSVGQYHSPYFEWVIIFFMIVAGINFSLHFQLLRG KPMALWKDPECRFFLGLVLVLVAVITLDIHGKVFSSLNESIRASAFQVSSIITTTGYATADYELWPALSQLLIMFCMVVGASAGSTGGGI KCLRVMLLFKYCYRELFRMIHPRAVIPVKLGGRVVPEEVLHSVCAFFVLYMGLFAISALGLAAMGVDLVTSMAAVAATIGNIGPGIGGV GPMDNFANIPLAGKWLLVWCMLLGRLEIYTVIILFVPEFWRK
1.9E-72	254	29.3	6E-72	252.1	20.3	1.7	1	Q8D379_WIGBR	Trk system potassium uptake protein	trkH	Wigglesworthia glossinidia brevipalpis	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Wigglesworthia, Wigglesworthia glossinidia, Wigglesworthia glossinidia brevipalpis	36870	>tr|Q8D379|Q8D379_WIGBR Trk system potassium uptake protein OS=Wigglesworthia glossinidia brevipalpis GN=trkH PE=3 SV=1MHFRTICRIVGLLLIFSVTMIVPSLVSIIYKEDTGIAFIKTFICAQIIGFLFWAPNFKEKNELQTREGFLIVVLFWIVLGSVGALPFLFL KYPNLSITNAFFESFSGLTTTGATILFNLDKLPQSILFYRQMLQWFGGMGIIVLALAILPILGTGGMQLYKAEMPGPLKDNKMQPRIAET AKILWLIYVALTFLCALSLWFAGLPIIEAIGHSFSTVSIGGFSTHDENIGFYKNTNVEIIISIFLIISGCNYSLHFFAFSKKKINIYYKDMEFRIF FLIQITLIISFLTLLKFSDDSTFNLDLFNKVFFQVISISTTAGFTSDKISNWPTYLPILLIISSCIGSCSGSTGGGIKVIRIILLYLHWSTELKKII HPNAIYSIKINDYAISEKIIKNILCFILSYILILIISTLILISTGIDYFSSFSSVAATLNNVGIGFGVVENNFFNLNDFSKWILILTMLFGRLEIFTLLI ILTPTFWRE
2.2E-72	254	13	3.9E-72	252.7	9	1.4	1	C7LRM5_DESBD	Trk system potassium uptake protein	Dbac_2454	Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) (Desulfovibrio baculatus)	481	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfomicrobiaceae, Desulfomicrobium, Desulfomicrobium baculatum (Desulfovibrio baculatus), Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) (Desulfovibrio baculatus)	525897	>tr|C7LRM5|C7LRM5_DESBD Trk system potassium uptake protein OS=Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) GN=Dbac_2454 PE=3 SV=1MRWTIALHVTGLILLCVGLCMFLPLVCGWYYGDTSVAPLFLSLCVTVLAGVFLMFSFQRPKPMVINHREGMVIVSLGWAACAFF GALPFALGGFPTFTDAFFESVSGFTTTGASILTNIEALPKGLLFWRSLTHWLGGMGIIVLTIAILPFLGVGGMQLYKAEVPGPVADKLQP RIKDTAMSLWKVYVLFTVAQVLLLMFGGMDLFESICHAFGTMATGGFSTRNASIAAYDSAYIDGVITFFMLVAGVNFALHFQLFRGRPL AVWRDPEFRFFAILTLLLTAVVTFSIQSSSYSSWPDALRFGSFQVASILTTTGYATADYELWLPLPQGVLLLCMFIGGCAGSTAGGIKC MRIMLLFKHAYRELFRLVHPRAVLPLKFGPKLVKEEVLTSIWGFFILFIVLFVLSGLALTAMGVDVLTAFAAVVACIGNIGPGLGEVGPVD NYAAIPTLGKWVLSFCMLLGRLEIYTVLVLFVPEFWRK
3.2E-72	253	25.2	3.8E-72	252.8	17.5	1	1	K8GG23_9CYAN	Potassium uptake protein, TrkH family	OsccyDRAFT_4571	Oscillatoriales cyanobacterium JSC-12	448	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, unclassified Oscillatoriales, Oscillatoriales cyanobacterium JSC-12	864702	>tr|K8GG23|K8GG23_9CYAN Potassium uptake protein, TrkH family OS=Oscillatoriales cyanobacterium JSC-12 GN=OsccyDRAFT_4571 PE=4 SV=1MTVSRTICLGFLAVIAAGTLLLSMPFSTATGTFSWDNIIVGLFTATSAVCVTGHIVVDTATYFSTWGHIFIIALIQIGGLGYMTANTF LLLLLGRKMGLRQKVAMQQALDRSELNGVSMLMRSIIATTLIFEITGALLLLIAFMPKHGLDSSLWLAVFHSVSAWNNAGFSLFSDNLM SYRASPLVNLIIPGLVIFGGIGYEVIFEMYLWLNERILRKPRQIILSLNFKVAVSTTLILLTVGTIAFLFVEARNSATLATLSLPERLMAAWF QSVTCRTAGFNTIDVGKMSAAGLFISIGLMFIGGSPGGTAGGIKTTTLRILTSCTKAILRGREEVHLYERQIPLPLILKAVGVVVGSLATAI LGTILISLSDPEFDFIQILFETVSAFGTVGLSTGITLNADFSVFAKLVLVAMMYVGRVGVLLLMAAVIGDPKPSFVRYPEENLLVG
3.3E-72	253	15.8	7.6E-71	248.5	10.9	2.1	1	R4W6R7_9EURY	Cation transporter	L593_12715	Salinarchaeum sp. Harcht-Bsk1	511	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Salinarchaeum, Salinarchaeum sp. Harcht-Bsk1	1333523	>tr|R4W6R7|R4W6R7_9EURY Cation transporter OS=Salinarchaeum sp. Harcht-Bsk1 GN=L593_12715 PE=4 SV=1MRESLATIGRDLGRILQVLSVLVAGTAPIAVIWREFYVLPAVAASCLLPLAVGTGLARTFADANDPGKRHAMVIAAAGWFLVALL GALPFYLIAWTVALDPPMLAAPAGSETLAAFRNPLNALFESMSGFTGTGLTMTQREPALPATLQWWRSTTEWIGGVGVIVLTTAVLA RPGSGSLTLYESEARSRKIHPSVVSTVRTIWWIFILLFTVSAIVLLWTAGMPLWEAINHGMTGISTGGFSVTDASIGSYDSAVIDLTLVPI MIAGSIAFPIHYLMFQGELRNVYRDPQTRWLLGLYAAGTIFLTALLLDGGPYDGLRETARFGLFQFVSALSCTGFQTAGSLGTEWSPA SQLTVAGAMTIGGAAGSTVGGIKIIRLIMLVQGTRHRIAGIWIPSTAVRRLSIGDRRLRETETAREIEEAAIVSFLWVVFLGIGIYVLLLTVD GGQFTLENVVFEVASAQGNVGLSSGITGPGMPTPAKLVFLLNMWIGRLEIIPVLVFLRGMFSWGGLYE

3.5E-72	253	13.2	4.7E-71	249.2	9.2	2	1	F7PQE0_9EURY	Cation transporter (TRK potassium uptake system protein) (EC 4.1.2.13)	trkH1 HLRTI_001862 HTIA_1133	Halorhabdus tiamatea SARL4B	513	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halorhabdus, Halorhabdus tiamatea, Halorhabdus tiamatea SARL4B	1033806	>tr|F7PQE0|F7PQE0_9EURY Cation transporter OS=Halorhabdus tiamatea SARL4B GN=trkH1 PE=4 SV=1MNRTTATIGRDVGRILEALGGLMAVSVVVPLVWGEWFGVLAFGVAGIVPFAVGYGLHHRFRDADSPSRLHGMIVAATGWLFV GVFGSVPFLLVAWGVHLGLPTGLEGTPTLAAFRDPLNAIFESMSGFTGTGLTMTDNEEVLPRTLQWWRTFSEWIGGVGVIVLTTAILS RPGSGSLTLYKSEARSEKIHPSIVSTVRTIWWIFILFTFVSILALFAAGMPLWDAINHAMTGLATGGFSITDNSIATYDSAVIDGVLIPIMLL GSIAFPVHYLILQGDIRNLYEDLQTRWVFIYMSLGSALLGAFLYVGPYDTPLSALRYSGFQFVSAATCTGFQTAVDTTNVALGSWPAQ AQLLVAFGMFVGGAAGSTVGGIKLIRGLTLIKGIRYKIGDVFYPDSAVRRLDIDGRRLTEEEVNREFVEAAIIAVLWTTFLVVGTFLLLVV LPAEEFSLSNAFFEVASAQGNVGLSSGITGPESLPTLGKISFLGHMWIGRLEIIPVLVALRTLLRRGGMYQ
3.5E-72	253	15.1	5.4E-72	252.3	10.4	1.2	1	A0A0F2QZ28_9DELT	Trk system potassium uptake protein	VR64_13470	Desulfatitalea sp. BRH_c12	483	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfatitalea, Desulfatitalea sp. BRH_c12	1629708	>tr|A0A0F2QZ28|A0A0F2QZ28_9DELT Trk system potassium uptake protein OS=Desulfatitalea sp. BRH_c12 GN=VR64_13470 PE=3 SV=1MRWRYILYIVGTLVLFLGFSMLLPLAFGLYYGDRSVPPLIKSIGLTVSAGALLFMSFRKRREENIRQREGMAIVAVGWTAVGLFG ALPFYLASDSWYFVDAFFESVSGLTTTGATILTDIEVLPKGLLMWRSFIQWLGGMGIIVLSIAILPFIGVGGMQLYKAEVPSPVPDKLKP RIRDTAVILWKVYALFSVIEIALLMLGGMTFFDAVCHAFTTMPTGGFSTHNDSITHFGSLYVDVVIIFFMIMAGINFSLHYQMLRGRPLAF WKDGECRFFLAIVGAFVLLVTLDIVRHDVYVSLGESLRYGAFQVVSMITTTGYATADYEQWPAMSQVILFTCMFLGASAGSTGGGMK CLRILICFKYCYRELFLLLHPRAVTSIKIGGKTVSDDVMRSVLGFLALYVGLFIITAIVLGGLGVDFVTAFSAVAATIGNVGPGFGSIGPVE NYAHIPYAAKWVLIWCMLLGRLEIFTVLIFIVPEFWRK
3.7E-72	253	17.1	1.1E-71	251.3	11.9	1.6	1	I7BU20_NATSJ	Cation transporter	NJ7G_1108	Natrinema sp. (strain J7-2)	516	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema sp. (strain J7-2)	406552	>tr|I7BU20|I7BU20_NATSJ Cation transporter OS=Natrinema sp. (strain J7-2) GN=NJ7G_1108 PE=4 SV=1MNEATKTIGRDLGRIFQALAGLLFVSVLIPLIWGEYYAIPALVVSGLLPLGIGYLLTSRFREATKPGKLHGMIIAALGWFCVAIFGSL PFFLIAWTVELAPPILGEPSQTETLAAFTEPLNALFESMSGFTGTGLTMTDNEEVLPRTLQWWRSFIEWIGGVGVIVLTTAILARPGSG SLTLYESEARSERIHPSIVSTVQTIWWIFILFTFVSILLLWVVKMPLWGAINHAMTGLSTGGFSITDNSIATYDSAAIDFALLPIMLLGSIAF PVHYLILQGDLRNLYADLQTRWVFIYMSAGTALLTALVYMGDTYDSLFTAFRYGSFQFVSAATCAGFQTAVDATNVALGRWSAQAQL TVTFGMIVGGAAGSTVGGIKLIRVLTLLKGIRFRISDVFYPETAVRRLKINGRRLDEQEVRQEFEEAAIIGFLWFVFLGIGMFVLLLVLPE GEYTLENVIFEVASAQGNVGLSAGITGPESLPTLGKLMFLFNMWIGRLEIIPVLVTLRAVFSRGGFYQ
4.6E-72	253	19.2	7.3E-71	248.6	13.3	2	1	I3R0Q0_HALMT	Potassium transport system protein trkH1 (Potassium transporter Trk)	trkH1 HFX_0068 BM92_08950 C439_10055	Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (Halobacterium mediterranei)	516	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Haloferax, Haloferax mediterranei (Halobacterium mediterranei), Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (Halobacterium mediterranei)	523841	>tr|I3R0Q0|I3R0Q0_HALMT Potassium transport system protein trkH1 OS=Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) GN=trkH1 PE=4 SV=1MNGSVATVGRDLGRILEALGGLMLVSLVVPVIWGEYYALPALLISAIIPLGIGRLLYRRFRNAEDPGRLHGMVVAALGWFSVGVF GSLPFLLIAWSIHLGVPGFTTPDQTATLAAFTEPLNAIFESMSGFTGTGLTMTDNEEVLPRTLQWWRTFSEWVGGVGVIVLTTAVLSR PGSGSLTLYESEARSEKIHPSIVSTVRTIWWIFTLFTFVSILALWLAGMPIWGAINHAMTGLSTGGFSITDNSIATYDSAVIDFVLVPIMLL GSIAFPVHYLILQGDLRNFYSDLQTRWVFIYMSIGSALLWSFLYFGGPYETPFDALRYGLFQFVSAATCTGFQTAVDATNVALGRWPA YAQLTVTFGMVFGGAAGSTVGGIKLIRGLTLVKGIRYQIADVFYPQTAIRRLGINGRRLNDEEASREFMEAAIIVVLWITFLVVGTFVLLL TLPSAEYSLANVVFEVASAQGNVGLSSGITGPESLPPVGKVVFLFHMWIGRLEIIPVLVTLRTIFHRGGLYS
6.6E-72	252	12.8	5.2E-71	249	8.9	2	1	L0JFP3_NATP1	Trk-type K+ transport system, membrane component	Natpe_0187	Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	513	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema pellirubrum, Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	797303	>tr|L0JFP3|L0JFP3_NATP1 Trk-type K+ transport system, membrane component OS=Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786) GN=Natpe_0187 PE=4 SV=1MRTTVAPIGRDLGWMLRVFGGLVLVSILVPLVWGEYYAIPGLVVSGVIPVTIGWVLSTVFADAAPPDKLHGMMIAAIGWLAIAAF GSLPFLTTAWIVTLAPAGLETPPPESVDALTSPLNALFESMSGFTGTGLTMITDEGSLPRTLQWWRSIIEWVGGVGVIVLTTAILARPG SGSLTVYEGEARSQKIHPSIVSTVRTIWWIFLLFTSIAILSLWLAGMPPWQAINHGMTGISTGGFSVIDGSIGAYDSVVIEVVLLPIMIAG GIAFPIHYLVLQGDLRGLYTDVQTRWLAAVLLLGSAALWLSVSTAYDSVTDALRYGVFQFVSAVTAAGFQTATDPTPLSLGDWPTSAL LTLVFAMVVGAAAGSTAGGIKLIRLIMLVKGIRFRVSYVFYPDSTVHRFRIDDRVLDEEDGPREFGEAAIIALLWFVFLAVSVFVLLATLP SGAYPLEQILFEIASAQGNVGLSTGITGPHSLPTAGKVAFILNMWIGRLEIIPILVTLRALFWRGGIYE
1E-71	251	25.1	2.5E-43	157.7	4.3	2	2	G0J6C3_CYCMS	Cation transporter	Cycma_3909	Cyclobacterium marinum (strain ATCC 25205 / DSM 745) (Flectobacillus marinus)	473	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cyclobacteriaceae, Cyclobacterium, Cyclobacterium marinum, Cyclobacterium marinum (strain ATCC 25205 / DSM 745) (Flectobacillus marinus)	880070	>tr|G0J6C3|G0J6C3_CYCMS Cation transporter OS=Cyclobacterium marinum (strain ATCC 25205 / DSM 745) GN=Cycma_3909 PE=4 SV=1MGGLMMLLGVLMFPSVAFSYYYQSGDQITLIGSALICLTIGGTFFFSFAKQDQNIRKREGYMIVALSWIIMSVFGMMPYLLSGTIP NYSDAIFETVSGFTTTGASILTDIERLPEGILLWRSMTQWIGGLGIIVLTVAIFPLLGIGGIELFVAESPGPTSDKVHPRIRETAKRLWLIYF GLTLLLVVIYYLEGMSFFDAMNHSLTTMSTGGFSTKNNSMAFFDSPVIQYTAVFFMFLAGTNFTLIYFAFKGHFKRIWASDEFRAYFIS VCFLVIGIFGAVYFLANENIEKSFRDVLFQVVSLITTTGYVTADYTGYSNGLTIIFFMMLFMGACAGSTSGGIKFIRHLTFVKNSTLEFKRI VHPRAVVPLKINGERVTGKVITHIMNFLLLYLMIFVLGSIVMSIAGYDLITSFGAVATSMGNVGPGIGRVGPVDNFAFFSPFAKLFLSFLM LLGRLELFTILVLFTPYFWRAN
1.1E-71	251	14.1	2.9E-71	249.9	2	2.2	2	Q0U2P7_PHANO	Putative uncharacterized protein	SNOG_13917	Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	775	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Pleosporomycetidae, Pleosporales, Pleosporineae, Phaeosphaeriaceae, Parastagonospora, Phaeosphaeria nodorum (Glume blotch fungus) (Septoria nodorum), Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)	321614	>tr|Q0U2P7|Q0U2P7_PHANO Putative uncharacterized protein OS=Phaeosphaeria nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) GN=SNOG_13917 PE=4 SV=2MARLKERWGSFETNHAKMRTIIETVKPYVPPINFITLHYAYFISMTLLGSLIFWGASHPARSIGWWDSMFMVMSAMTATGLNTV NVSQLTVFQQVELVVLMMMGSQVLVSYFTVAFRKHMFEKRFEDVVKMEKEKRQARKGDIGAVVGMTGAMFGMPVMGSFGKGRKG MPPRNKAMVTAMTIPEAEETEMPPGTPVGQTQTRPSLSERERSAPQHVGFLDPIREREPHKRPMSATTGHSIYNVQSHQTMSERRR SLGEKSTLNDGFNVQSFVKEQKRSIGRNGQFFNLSSDQREYLGGVEYRALKFLFIFVPAYFILWQLFGAIALGAYMSVYEKEACAVNA QNPWWAGIFLAISAYSNAGFTLLDAGFIPFQSSYYILCVVTLLSLAGPAAFPVFVRFLVWSMSTLLDLFSKDKEYGIWKEGFDFILKFPR RVYTSMFPARDTWLFIATFGSFVAVDWVLILVLGIGNPTMEAIPLGRRIFISLFEGFSIPSGGYAIVSPSAMYFDVQVLWLVIFYTAAYPH IITMRKTNVYEERSLGIYEGDEAEPEQLHSASSSLFDVDAAMPSLPSSVPQPEKSSLAPIKSLGKVGVRGTAFVGRQLQRRMTAFNGV GVAHAPATTTPAPLKRSVTMDFNRATSVHSLTQHPPTNPPSLISQQVRGQLSHDVWWIAFALFLITLIETHHSIGDPRTYSVFTILFEIV SGYTTIGISIGLPDQAYSFSGGMFTGSKIVMILVMLRGRHRGLPVALDRAVRLPGKKLGEIEEEDAEIRSMFSQ

1.5E-71	251	17.1	7.9E-37	136.3	0.7	2	2	K4LYP1_THEPS	Trk system potassium uptake protein TrkH	trkH Tph_c28840	Thermacetogenium phaeum (strain ATCC BAA-254 / DSM 12270 / PB)	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Thermacetogenium, Thermacetogenium phaeum, Thermacetogenium phaeum (strain ATCC BAA-254 / DSM 12270 / PB)	1089553	>tr|K4LYP1|K4LYP1_THEPS Trk system potassium uptake protein TrkH OS=Thermacetogenium phaeum (strain ATCC BAA-254 / DSM 12270 / PB) GN=trkH PE=4 SV=1MNIHLVAHLLGRSLVFLGLTMVFPLFWAVYYQGPDRAALLSSALITLASGVAVALLVPPRGDIRYREGFAIVTFGWLLVSLYGALPYLLCGVCSGFPDAFFESMSGFTTTGASILTDVEAVPKGILFWRSLTQWLGGMGIIVFLVAFLSHVGVGANQLFRAEVPGPVADKIKPRISEAAKILWLIYLFLTVLETALLWFFGMPLFDALCHAFTTISTGGYSPRNASIGYYDSAAIQWVITIFMFLSGTNFALYYQALRGRSLKAFWRSDEFRCYFSVVLLATLITAVSIRSLFPGGEPLVRAAAFQVFSVITTTGFTTADFSLWSPVAQAVLVSLMFIGGCSGSTAGSVKIGRVLILLRQGMLELKRLIHPRAVLSLKIDGKNISKDLAVNSLEFFFLYLAIAGVATIIMAATGLDLVSAFTSVAATLGNVGPGLGAVGPAGNYAAVSAFGKVFLSILMLLGRLEIFTVLVLLSPGFWKR	
1.6E-71	251	16.7	8.7E-71	248.3	11.6	1.8	1	D2RT83_HALTV	Cation transporter	Htur_2080	Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (Halococcus turkmenicus)	516	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Haloterrigena, Haloterrigena turkmenica, Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (Halococcus turkmenicus)	543526	>tr|D2RT83|D2RT83_HALTV Cation transporter OS=Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) GN=Htur_2080 PE=4 SV=1MNEALETIGRDLGRMFEALAGLLFVSLLVPLVWGEYWAIPALAVSGLVPFAIGYSLTSRFREATRPGKLHGMIIAAVGWLCVAIFGSLPFLLIAWTVELGVPLLETPSRTSTLAAFTDPLNALFESMSGFTGTGLTMTDNEEVLPRTLQWWRSFIEWVGGVGVIVLTTAVLSRPGSGSLTLYESEARSERIHPSIVSTVQTIWWIFLLFTFVSILLLWAVGMPLWGAINHGMTGLATGGFSITDNSIATYDSAAIDFALLPVMLLGSIAFPVHYLILQGDLRNFYTDLQTRWVFIYMGIGTIVLSGIIYATETYDTLFSAFRYGSFQFVSAATCAGFQTAVDTTNVALGRWPAQAQLTVVFGMIVGGAAGSTAGGIKLVRSLTLLKGIRFRISEVFYPDSAVRRLKINGRRLNEQEVRQEFEEAAIIGFLWFVFLAIGTFVLLLILPQGEYALENVIFEVASAQGNVGLSAGITGPESLPTPGKIMFLFNMWIGRLEIIPVLVTLRTIFDRGGLYR	
2.8E-71	250	15.4	1.6E-70	247.4	10.7	1.9	1	I7BGI2_NATSJ	Cation transporter	NJ7G_0078	Natrinema sp. (strain J7-2)	510	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema sp. (strain J7-2)	406552	>tr|I7BGI2|I7BGI2_NATSJ Cation transporter OS=Natrinema sp. (strain J7-2) GN=NJ7G_0078 PE=4 SV=1MAPIGRDLGWMLRVLGGLVLSILVPLAWGEYYAIPGLVVSGVIPVTIGWVLSTAFADAAPPDKLHGMMIAAIGWLAIAAFGSLPFLTTAWVVTAAPAGLETPPPTESIDALASPLNALFESMSGFTGTGLTMTTDESTLPRTLQWWRSIIEWVGGVGVIVLTTAILARPGSGSLTVYESEARSQKIHPSIVSTVRTIWWLFLLFTSIAILSLWLAGMPPWHAINHGMTGISTGGFSIIDGSIGAYDSVVIEAVLLPIMIAGGIAFPIHYLVLQGDLRGLYTDAQTRWVLAAVLLLGSAALWLSVSTVYDSVTEALRYGVFQFVSAVTAAGFQTATDPTPLSLGGWPTSALLMLVFAMVVGAAAGSTAGGIKLIRLIMLVKGIRFRVSYVFYPDSTVHRFRIDDRVLDEKDGPREFGEAAIIALLWFVFLAVSVFVLLATLPSGAYSLEQILFEIASAQGNIGLSTGITGPHSLPTAGKVAFILNMWVGRLEIIPILVTLRALFWRGGIYE	
3.4E-71	250	16.6	6E-71	248.8	11.5	1.3	1	A4CPH3_ROBBH	Trk system K+ uptake protein TrkH	RB2501_02680	Robiginitalea biformata (strain ATCC BAA-864 / HTCC2501 / KCTC 12146)	496	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Robiginitalea, Robiginitalea biformata, Robiginitalea biformata (strain ATCC BAA-864 / HTCC2501 / KCTC 12146)	313596	>tr|A4CPH3|A4CPH3_ROBBH Trk system K+ uptake protein TrkH OS=Robiginitalea biformata (strain ATCC BAA-864 / HTCC2501 / KCTC 12146) GN=RB2501_02680 PE=4 SV=1MSLNTRIILHLMGLLLLFNGGFMLLAALVSGIYQDGVTYQISLAAITTLFAGTVAMYFTRGHKKEVKRKEGYIIVTFGWIVMSVSGVLPYLFSGAIPDVTNAFFETISGYTTTGASILDDIERLPEGILFWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPTGDKLHPRITDTAKRLWLIYVGYTLAETLLLRLAGMSFFDAINHALATLSTGGFSTKNASIAYWNSQPLIQYIIIVFMFLAGSNFVLSYFAFKGRVQKVLRDEEFKVFGLMVVVFAIMAALVIYFRADVPESEYHPMVWGAGESAFRHGLFQVVAVVTTTGFVTADFTNWTPFLTVFFFGLMFAGGSAGSTAGGIKIMRHLIILIKNGLLEFKRTLHPSAIIPVRYNDKTVTEHIVYNIIAFFVLYMLLFIIGALVLSLLGLDFVSAIGGAASSLGNVGPAFGSLHPLSNFNGLPALGKWWCGFLMLAGRLELFTVLILLTPYFWKRT	
3.5E-71	250	16.6	3.2E-70	246.5	11.5	1.9	1	W0JWW1_9EURY	Potassium transporter Trk	HALLA_00080	Halostagnicola larsenii XH-48	445	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halostagnicola, Halostagnicola larsenii, Halostagnicola larsenii XH-48	797299	>tr|W0JWW1|W0JWW1_9EURY Potassium transporter Trk OS=Halostagnicola larsenii XH-48 GN=HALLA_00080 PE=4 SV=1MIIAAMGWFCVALFGSLPFFLISWTAELAPAALGIPAQTSTLAAFTDPLNAVFESMSGFTGTGLTMTDNEEVLPRTLQWWRSFTEWVGGVGVIVLTTAILARPGSGSLTLYESEARSERIHPSIVSTVQTIWWIFLLFTFVSILLLWAVGMPIWGAINHGMTGLSTGGFSITDNSIATYDSAAIDFALLPVMLLGSIAFPVHYLILQGDLRNFYTDLQTRWVFIYMGIGTIVLSGIIYATETYDTLFSAFRYGSFQFVSAATCAGFQTAVDTTNVALGRWPAQAQLTVVFGMIVGGAAGSTAGGIKLVRSLTLLKGIRFRISEVFYPDSAVRRLKINGRRLNEQEVRQEFEEAAIIGFLWFVFLAIGTFVLLLILPQGEYALENVIFEVASAQGNVGLSAGITGPESLPTPGKIMFLFNMWIGRLEIIPVLVTLRTIFDRGGLYR	
4.5E-71	249	2.7	3.8E-65	229.7	1.7	3	2	A0A0D2XRH7_FUSO4	Uncharacterized protein	FOXG_06579	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	546	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0D2XRH7|A0A0D2XRH7_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_06579 PE=4 SV=1MSLLALPILAPYGNISVTDAYFFGASASTESGLNTVDVKDLKTYQQLYIYFIPIITNLGFINIGVVIVRLYWFKKHLKRRAPQLFSPRRRDASGENVEDGKIVEEKAQNDLPAVTAPSNNLEQHATTDTPVPRTTTITFDPSIDQRRDSATLYIPGPQDRDRDRITPVPTAASGEPSSSMRRRLPRRISTGDGLQMTATRSMDRVAGIASSLLMMGSETTRPRRQSSSSVSQQQPALNDRPFLSRQATIGRNSEFQNLTSHDRELLGGIEYERSLKLLLKIVTGLECVLTIAFRAFYSAQTMVDNLGFTLTPDSMISFRDAKWPMILMSFLAFAGNTLYPVFLRLIIWTMSKLLPKHSSTQEPLGFLLNYPRRCYTLLFPSKPTWILFGIIFSLNFIDVLLIIILDLDNPEVASLPLDSRIPAAIFQAASARHTGTATFNLANVNPGVQLSLLVMMYIAVFPIALSIRLSNTYEEKSLGIWEPEGSLNERNGKSYLMQHIKNQLGFDLWYIFLGTFCICVAEATRIADVKDPVGISSPWQVLFDSIS	
6.6E-71	249	0.6	2.1E-56	200.8	0	2	2	V2XSR0_MONRO	Potassium transporter	Moror_8536	Moniliophthora roreri (strain MCA 2997) (Cocoa frosty pod rot fungus) (Crinipellis roreri)	499	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Marasmiaceae, mitosporic Marasmiaceae, Moniliophthora, Moniliophthora roreri, Moniliophthora roreri (strain MCA 2997) (Cocoa frosty pod rot fungus) (Crinipellis roreri)	1381753	>tr|V2XSR0|V2XSR0_MONRO Potassium transporter OS=Moniliophthora roreri (strain MCA 2997) GN=Moror_8536 PE=4 SV=1MGSTRNANQHKYQGLGGFPGPIELAQMAAKRFAPKTYRKMERKLTMPYTTTLEKNRTPWLNFDLIVGRNSDFHTETLTDAQLEKIGGTEYIALRYLSYLVPAYFVGTQLISYLLFGPWISVIHRYDSIFEAQPRLVQKPWFALFQVMGAYTGGGLSLVDQGMLPFQQAYLMIISMMFVILAGNHALRTAYLFAVPYVGGPSLSTRCELAHPRNSWVGSRIARAEGTEAEEAFSFLLDHPRSFPSHQTWFLVICLVIFSAVEWILFEVLNIGLEAYESLTIGPRIICGLFQGLAARASGFSIVPLASLAPALQFLYVVMMYIAIAISIRSTNTYEEQSLGVFEQPPEDEDEEPQAQDLKDLAVGQRVHRYLGWHLKKQMSVDIWWLVWGVFIVTIIERNNLLDPDKKWFDLFRVLFELVSAFGGIGLSLGVPYDNFSFVGAMRPLSKLVVIVIMVRGRHRGLPVAVDRAVMLPHELMQQRERRAKEERARTAGQMQNGFPA	
6.7E-71	249	9.8	2.1E-69	243.8	6.8	2	1	F3YU46_DESAF	Trk system potassium uptake protein	Desaf_0295	Desulfovibrio africanus str. Walvis Bay	484	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio africanus, Desulfovibrio africanus str. Walvis Bay	690850	>tr|F3YU46|F3YU46_DESAF Trk system potassium uptake protein OS=Desulfovibrio africanus str. Walvis Bay GN=Desaf_0295 PE=3 SV=1MRWDFIFFVTGALMACVGLSMLPALGFSLYYGEGGLMPLALSAGLTCMAGATLLLAFRERSRRAPLSHREGMAITALAWIAAGLCGALPFYFAGTFGNFTDCLFESLSGFTTTGASVLTDIEVQPRGLLFWRSLTHWLGGMGIIVLSLAILPFLGIGGMQLYKAEVPGPTPDKLRPRVKDTAAVLWKVYLLLTAAQTVLLMLGGMDFFDSLCHTFGTVATGGFSTKNASIGYYQSAYIELVITVFMLLAGVNFTLHYLALKGRLSDVWRNPELKFYLAIFLAFFAIITVSLTLSGGQDNLPRAALDSAFQTASILTTTGYATANFEVWPALTQAILLLCMFIGGSAGSTAGGMKCMRILLLRQSYQEIIRLIHPRAVVHVKFGGRVVPGDVMGGVWGFSVLWLGLLFLSVFLVAASGVDLMTSFTSVLACIGNIGPGLGSVGPAENYAHLPTFAKWVLLWCMLLGRLEIYTVIVLFVPEFYRK	
6.8E-71	249	26	2.4E-70	246.9	18	1.7	1	Q0W135_METAR	Putative K(+) uptake system, membrane component	RRC145	Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	485	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanocellales, Methanocellaceae, Methanocella, Methanocella arvoryzae, Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	351160	>tr|Q0W135|Q0W135_METAR Putative K(+) uptake system, membrane component OS=Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50) GN=RRC145 PE=4 SV=1MGFVQDIQIILNNLKGLFLIIGIVMLAMAIFSWRVGDAPAFYGFMSGAVLGIGMGLVIRMLIPGNINPELKHAMIIAALAYLIVPAISMIPFMTVANMSPLDAFFESISGWTGTGYSMLSSPEKASPMVQFWRSVNQWIGGLGVIVLMVTILIRPGTSTYMFYQSEAHKDKIHPSIRSTIKTIWILYIVLSVCGFLLLYAAGMPIWDATNTAMTAIGTGGFSVYGESIAAYDNIFIELAILPIIIAGAIPFVVIYRMFRKGPGSLLKNIQVRTFFIVIAIGSVVLTIQNFFFYNDIVMSLRYSVFQFISAITSAGFQTADLSGWTTPALLIMSVAMVIGGCAGSTASGIKIARAIFLGDQVKLWFAKVLRSKNAIAVVKIGNRRVTEDLVAAELTEATFISFLWVVGILLSVFIMANIVGPSYDLGHIVFEVSSAIGNVGITCGIVNPDLSVLGKIVIIFDMWIGRLEIIPVLLLARYLLKGLKF	

7.7E-71	249	15.8	2.1E-70	247.1	11	1.6	1	I7BTT8_NATSJ	Cation transporter	NJ7G_1023	Natrinema sp. (strain J7-2)	516	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema sp. (strain J7-2)	406552	>tr|I7BTT8|I7BTT8_NATSJ Cation transporter OS=Natrinema sp. (strain J7-2) GN=NJ7G_1023 PE=4 SV=1MSEAMKTIGRDLGRMLEALSGLLFVSLLVPLVWGEYWTIPALIVSGLLPLALGYALTSQFREATQPGKLHGMIIAATGWLLVAVF GSLPFLLIAWTAELAPPILGEPSQTETLAAFTEPLNALFESMSGFTGTGLTMTDNEEVLPRTLQWWRSFIEWIGGVGVIVLTTAVLARP GSGSLTLYESEARSERIIHPSIVSTVQTIWWIFILFTFVSILLLWIVGMPLWGAINHAMTGLSTGGFAIKDHSIATYDSAAIDFALLPIMILGS IAFPVHYLILQGDLRNLYADLQTRWVFIYMSLGTLALTALVYVGDTYDSLFTAFRYSSFQFVSAATCAGFQTAVDATNVALGQWPAQA QLTVIFGMVVGGAAGSTVGGIKLIRALTLLKGIRFRIADIFYPQTAVRRLGINGRRLNDQEMRQEFEEAAIIGLLWFVFLGLGLFVLLLVL PQGEYVLENVLFEVASAQGNVGLSAGITGPDSLPSVGKLMLLFNMWIGRLEIIPVLVTLRTIFSRGGLYQ
8.4E-71	248	28.8	1.4E-70	247.6	20	1.2	1	A1AW29_RUTMC	Trk system potassium uptake protein	Rmag_0364	Ruthia magnifica subsp. Calyptogena magnifica	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, sulfur-oxidizing symbionts, Candidatus Ruthia, Candidatus Ruthia magnifica, Ruthia magnifica subsp. Calyptogena magnifica	413404	>tr|A1AW29|A1AW29_RUTMC Trk system potassium uptake protein OS=Ruthia magnifica subsp. Calyptogena magnifica GN=Rmag_0364 PE=3 SV=1MQFSIVFKTIGLLLMVFSLTQLPPIVVDFIYAQNEALSFMVAFSLTLLSGFVLWFPFRNSTKNFRIREGALVVVSFWFVLSLFATTP FLLSVSLDMSFSDAFFESMSGLTTTGATVLSGLDDLPKALLYYRQQLQWLGGMGIIVLAVAILPMLGVGSMELYHAELSGISKERLTPK LTQTAKALWKIYISFTVVCALGYYFAGMNAFDAIGHSYATVAIGGFSTHDASIGYFNSYAIEMVAMIFMLLAGINFSLHFLVWRKNNLFF YLKDSEFKAYLLILSASILLVSSYLFDKGYYQTIEESIRYGIFQSISIITTTGFSGTNFSLWPFVLPVFLIFASFIGACVGSTGGGIKVVRILL MFKLAMKEIKKFIHPNAQINIKLNQKSVPENTLISVWGFFSLYVIVFVMLMLMLMFTGLDQVSAFSATAASINNLGPGLGDVADNYGNIN DTAKWILSFSMLLGRLEILTLMALLHKSFWRF
8.6E-71	248	6.4	2.9E-68	240	0.6	2.2	2	J3NUY6_GAGT3	Potassium transporter 1 (Uncharacterized protein)	GGTG_05095 GGTG_05095	Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	828	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Gaeumannomyces, Gaeumannomyces graminis, Gaeumannomyces graminis var. tritici, Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	644352	>tr|J3NUY6|J3NUY6_GAGT3 Potassium transporter 1 OS=Gaeumannomyces graminis var. tritici (strain R3-111a-1) GN=GGTG_05095 PE=4 SV=1MGIASTNNGASNSLQARLVAAWHSLRDAWARVYPGIKPYLPPVNFITIHYSYFVFFGLVMSAVFFALSDREEFTTLSFIDSWFLI MSSFTGSGLNTINLSDLVTGQQAILFLMMILGSPILVAESTILVRLYHFSKRFEHVENFEREKRRRKRATGAMIGMAGAMAGLPVMSSF GAHQADASEHSRRAKLDAFELSKPNKHASDRRSSHFEDSDATPAAQPASTTTPTATHPHAAVLQNVLDGNNGNNGNPLSPGGRGD HTAPSHAHFRHRNHRPPQLARAATARVGGGAGGFGGAHHGFDFRHFVKEHKSSIGRNGQFFDLDEDQREYLGGVEYRSLKLLFVIN AVYFFLWQALGAIALGAWMATYSREICAVNNQDPWWTGVFLAVSAFNNAGMTLLDAGIAAFNRDPFVLTIVTILSLAGNAAFPAFVRG TVYVCRLGFKYGIARYGPTGHDYGAWEEAFDFILKYPRRLFMLMFPSRQNLVFIGFFFSTLVLINWVGLVVLNIGNSLFDDTPNPARTGI MLFQAIATPSSGLAVFSISGLWFGLLVLLLVTMYLAAYPEIIVMRNSNVYEERSLGLYSVDEAQKQDEEEDAAEAAAEMTVIAPLLSPTS VAASHTTAISRSMQPIKSLAAVGRRGTAFVGKQIQRRMNDFQGVGIDTSSRRDYVPIPGLKRSEEIDFDDPAPVAAPEGGISLVSQHL RGQLSHDMWSIALALFLVALIETAHSIADPQGYSIFNFLFEIVSGYTNIGISVGLTGKSFSFCGGWFAGSKVVMVLMMIRGRHRGLPVA LDHSVKLPGWDDAAREDQDAEIRRTISRARTSVDAHRVP
1.2E-70	248	20.3	1.8E-70	247.2	14	1.2	1	G2PL56_MURRD	Cation transporter	Murru_2046	Muricauda ruestringensis (strain DSM 13258 / LMG 19739 / B1)	496	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Muricauda, Muricauda ruestringensis, Muricauda ruestringensis (strain DSM 13258 / LMG 19739 / B1)	886377	>tr|G2PL56|G2PL56_MURRD Cation transporter OS=Muricauda ruestringensis (strain DSM 13258 / LMG 19739 / B1) GN=Murru_2046 PE=4 SV=1MKLNTRIIIHILGLLLLCNGSFMLLAAIASGIYKDGATMEIMLAAIVTMLFGMMAMFYTRGHKKEVKKREGYIVVTFGWIVMSISGM LPYLFSGAIPSITDAFFETMSGYTTTGASILDNIEALPKGILLWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPGGDKLHPRIT DTAKRLWLIYFGYTVLETLLLKFAGMSFFDAINHALATMSTGGFSTKNASLAFWNDQPLIQYIVILFMFLAGSNFVLSYFALTGKVQRIL RDEEFKYYLGFVVIFTIVVALGIYFRADVPVSDFHPMVLGEVESTIRHGLFQVVAVITTTGFVSADFTSWTPFLTVFFFGLMFLGGSAG STAGGIKVMRHLLIIKNGILEFKRTLHPNAIIPVRYNQKTVTEHIVYNVIAFFVLYMLLFIIGSLVLGLLGLDFVSAVGGSASSLGNVGPALG SLNPVSNYNSLPAAGKWWCSFLMLLGRLELFTVLILLTPYFWKKT
1.3E-70	248	22.7	2.7E-69	243.4	15.8	2.2	1	D3PEH5_DEFDS	K+ transport (Trk) system, membrane component	DEFDS_1538	Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1)	483	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Deferribacter, Deferribacter desulfuricans, Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1)	639282	>tr|D3PEH5|D3PEH5_DEFDS K+ transport (Trk) system, membrane component OS=Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1) GN=DEFDS_1538 PE=4 SV=1MHLKTVINIIAILLVIVALFMIFPALWALYYGEKSCFVVFLKVIISVIISCGIVFFATKKNKENNLSTRDGFLLVSLSWVLASLIGALPFY LSGSIPSFTDAFFETMSGFTTTGASILTNIEALPKSMLFWRSLTHWLGGMGIVVLTVAILPLLGIGGLQLIKAEAPGPTVDKITPRIGETA KYLWLIYVGFSVLETILLLFGGMNLFDALTHTFGTMATGGFSTKNTSVAHFNSAYIDYVITIFMILAGINFTLHYKLITGNFKDLIKDSELKA YLTIFAVSTLLLTYDLTKNHFDNFWHGLRYGSFQAATILTTTGYATFDYEKWPAMSRTVLFLLMFIGGCSGSTGGGIKVIRIFTLFKQALI EMRYLIRPKGIFTLRLSGNVVKKDIVYAISGFFFLYIAIVLTVALLVSLEDVDILTSVSSALATVGNIGPGFGRIGPTENYAFYSDFSKWVL SFAMMIGRLEIYTVLVIFTPYFWKK
1.5E-70	248	30.9	2.3E-70	246.9	21.4	1.2	1	D4G8W3_RIEPU	Trk system potassium uptake protein	RIEPE_0539	Riesia pediculicola (strain USDA)	488	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Candidatus Riesia, Candidatus Riesia pediculicola, Riesia pediculicola (strain USDA)	515618	>tr|D4G8W3|D4G8W3_RIEPU Trk system potassium uptake protein OS=Riesia pediculicola (strain USDA) GN=RIEPE_0539 PE=3 SV=1MDFKNIIRIIGLLFVMFSITMVIPGLVSLFYQDKTERSFIHTFLVTLLVGLILWVPNKNRNRELSQKEGFLVVSLFWVVLGSLGSLPF IFLDQPNISVTDAFFESFSGLTTTGATNLIQLNDLPKSILFYRQMLQWLGGMGIIVLAIAIFPLFGISGGFQLYKAEISGPIKENKIHPRASK TAKTLWSIYILLTIICTILLWIAGMDFFDAISHSFSIISLGGFSTHDENIGYFKNIWINDIVLFFLLVSSCNFNLHFLVLSGKSLKIYWNDLEFK TFIFFQVLLVVVVLIVSLYHSSGNKSILTIIHQSFFQVISSSTTAGFSIDNIETLPLFLQMLLLFSTFIGGCSGSVGGGLKVIRILLLFFQVST ELKRLVHPNAIYTIKINYNNHRVLSEKNIDTIWGFFSSYVLIFISSLLLLISTGVDEFSAFSSIVATLNNFGPALGDFSENFINMNFAGKWILI FTMLFGRLEIFTLLILFTPIFWKK
1.9E-70	247	25.5	1.2E-69	244.6	17.7	1.8	1	D0KVR6_HALNC	Trk system potassium uptake protein	Hneap_2078	Halothiobacillus neapolitanus (strain ATCC 23641 / c2) (Thiobacillus neapolitanus)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Halothiobacillaceae, Halothiobacillus, Halothiobacillus neapolitanus (Thiobacillus neapolitanus), Halothiobacillus neapolitanus (strain ATCC 23641 / c2) (Thiobacillus neapolitanus)	555778	>tr|D0KVR6|D0KVR6_HALNC Trk system potassium uptake protein OS=Halothiobacillus neapolitanus (strain ATCC 23641 / c2) GN=Hneap_2078 PE=3 SV=1MQFIVVLRVLGLLLMVFGLTFIPPWLVGSMMGDTDLRPFEYSFLITFVLGLLIWIPLRNHRRELKLRDGLLIVVLFWVVLGVIGAFP IYFQPMLHINFIQAVFESVSGITTTGATVLVGLDQLPRSLLFYRQQLQWLGGLGIIVLVVAFLPLLGVGGMQLYKAEISGPMKDNRLSGR ISETAKLLWLVYAGLTLLCAFLFKLEGMSWFDAVGHAFATLATGGFSTHDASFGYFNSPTMEMTAVVFMLLGATPMALHYLALREFSL RAYLLSSEFKFFMLLVIVLYVLMVVTMLFDMPRIGWLHDFRWALFNLVSFITTTGFSVTDHTTWPYFLPVLLITTALIGGCAGSTSGGLK NVRLLLLTRQGLNEIRRLVHPHAEFVVKMGGRAIEPSVISAVWAFFSAYVFVFVLIFFAMMMTGLDMVSAYGAAIATLTSLGPGLGTVA SNFASVGNGTLIVSIVAMILGRLEIFTVLVLFLPMFWRR
2.2E-70	247	12.6	1.4E-69	244.3	8.7	1.9	1	C8X4N0_DESRD	Trk system potassium uptake protein	Dret_1969	Desulfohalobium retbaense (strain DSM 5692)	482	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfohalobiaceae, Desulfohalobium, Desulfohalobium retbaense, Desulfohalobium retbaense (strain DSM 5692)	485915	>tr|C8X4N0|C8X4N0_DESRD Trk system potassium uptake protein OS=Desulfohalobium retbaense (strain DSM 5692) GN=Dret_1969 PE=3 SV=1MRWGYTLQVVGLVILFTGLSMLVPLGFGLYYSDGSVLPLLESIALTCSVGLGMYLALRQYQVKVMTHREGMAVVALGWAAAGI FGGMPYFFADIFPSFIDCIFESMSGFTTTGASVLSDIEALPEGILMWRSLTHWLGGMGIIVLSLAILPFLGVGGMQLYKAEVPGPTPDKL RPRIKDTAKLLWQVYALFSFLEFILLLGGGMDVFDSLCHTFGTMATGGFSTKNTSIAAFDSVYIDTVIIVFMFIAGTNFALHLQLLRGKPL ALWRDPEFRFFFLLICVCTLLSTVFVYGDIYASWGLSLRHAAFQVISIVTTTGYATADYELWAPLPQALLVFCMFVGGCAGSTGGGIKG MRVILLVKQSYRELIRLIHPRAVVPVKLGGRSVPEGILGGVWGFFILFLMLFLLSALALAAMGVDIMTSFAAVVACIGNIGPGLGDVGPT DNYASLPLAAKSILSFCMLLGRLEIYTVIILLVPEFWRK

5.2E-70	246	23.7	9.5E-68	238.3	16.4	2	1	D3S16_FERPA	Potassium uptake protein, TrkH family	Ferp_0113	Ferroglobus placidus (strain DSM 10642 / AEDII12DO)	476	cellular organisms, Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales, Archaeoglobaceae, Ferroglobus, Ferroglobus placidus, Ferroglobus placidus (strain DSM 10642 / AEDII12DO)	589924	>tr|D3S165|D3S165_FERPA Potassium uptake protein, TrkH family OS=Ferroglobus placidus (strain DSM 10642 / AEDII12DO) GN=Ferp_0113 PE=4 SV=1MNRKAVLNVLGRILLYFSLVFIIPVAVAFYYEESTKPFLISMAASFFLGFLFYFVSRKAEIEIRYKEGYAIVGLGWLLVSMIGAVPYLFVGLDYFDAFFEAMSGFTTTGATVFDSVEDLPKSILIWRSLTQWLGGMGIIVLFVAILPSLAKSGYALLQAEVPGIKLTRLKPRLRDTAITLYLIYLFFTLLEAAILKFLGVSLFDAINHAFTTLSTGGFSTHTESIAYYNNPAIEATIFVFMIIGGTNFALFYYIFNRNFKILEDAEFKAYILILLTASAILTVINFEELNLQALRLYSFFQAASVMTTTGYTTADFDQWNDAAKILLLMLMFVGGSSGSTGGGIKVIRIYLLSTYSLLQIMKSAEPRTVRVVKYGEEIVEKEAFSAITSFFSLYIMIFAISSFLISLFGYDLLTSISAVAACINNVGPGMGLVGASESYSALHDLAKLILSIDMWVGRLEVFTVLALFIPSFWREKW
7.5E-70	245	2.3	4.2E-67	236.2	0.8	2.9	2	A0A0D2Y5N4_FUSO4	Uncharacterized protein	FOXG_11590	Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	600	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. lycopersici, Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) (Fusarium vascular wilt of tomato)	426428	>tr|A0A0D2Y5N4|A0A0D2Y5N4_FUSO4 Uncharacterized protein OS=Fusarium oxysporum f. sp. lycopersici (strain 4287 / CBS 123668 / FGSC 9935 / NRRL 34936) GN=FOXG_11590 PE=4 SV=1MWRPNLNFVKIHYIYIICMGLSSFLFIYPEGKLSAIDAYFFGVSASTVTGLTTVDVPVLKTYQQLFLYFVPLVCNIVTINIIVVVVRLVWFRRYLKNAAPALLSRRRPVDLDPKEDPENAADNPLSEVLDKRPGLARSVTERVHKNVAEQDALPPIEARSRTDPAPDHPHQRPVDILSPTIKEEKVKEGDQHETRITFDPSTDHHPRHEQQESTLYIPGPRARDQEDVIEPISRTQSTPVGTLRRRRSAGLSLAQVRSVERVATVASSLFVIGNPAQAPKERPLARAPTLAVGDFPRLSREVTIGRNSIFHNLSSKDREELGGIEYKSLKLLLKIIIAWVQHAPNKYVEYIDKCGQNRIWWAVYSAQTMITNLGFTLTPDSMISFNDAPAPLLIMSALALAGHTFYPVLLRLVIWATSKAVSKQSSLQEPLHFLLNHPRRCYTLLFPSGPTWALFGILALLNLVDVLFIILLDLDNSTVTVLPGWQRFCAAVFQAVSSRHTGTASFNLANVNPAVQMALLIMMYISVYPISIVVRSSNTYEERSLGIYEHSLQYDEEDGGSYFVTHLRNQLSFDLWYICLGLLCISIAEHKKIMDGNDPL
8.2E-70	245	4.1	2.3E-69	243.6	2.9	1.6	1	I3R3G3_HALMT	Potassium transporter TrkH (Trk-type potassium transport system, permease protein TrkH)	trkH HFX_1057 BM92_03920 C439_05195	Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (Halobacterium mediterranei)	534	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Haloferax, Haloferax mediterranei (Halobacterium mediterranei), Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) (Halobacterium mediterranei)	523841	>tr|I3R3G3|I3R3G3_HALMT Potassium transporter TrkH OS=Haloferax mediterranei (strain ATCC 33500 / DSM 1411 / JCM 8866 / NBRC 14739 / NCIMB 2177 / R-4) GN=trkH PE=4 SV=1MKLRVDYRASLRLVGTVLKYLTVPLLFPLVVALYYGESVLPFVVTMAVTVLIGTGLERLAEEPDIGAREGFLMVAMTWLAVAFVGAIPYLIEAHGIPFIAQPIHPESTLGNPANALFETMSGFTTTGATVLGDISFDSHTRGIMMWRQLTQWLGGMGIVVLAVAILPELSVGGAQLMDAEAPGPGIEKLTPRIAETARALWGAYLGLTVLEIVLLHGLNVTGHAPGMGVYNAIAHGLTTTMPTGGFSPEAKSIEAFSAAAQWVIIPFMVAAGTNFALFWHVLTGEPKRLVRDTEFKSYLGIMGVISAILAGVLFFGDGLMSVAPAGETYDQVYLEGIRTAIIGNVEPAIRQSVFQVVSIVTTTGYASMDFNAWSAPTQYGLLFAMFIGGSGGSTGGAIKIVRWYVILKSLRRELFTTAHPEAVRPVRLAGRTVDERAIRGIYAFTLLYLVLFFVSTGLLHLDAARAGFDVSILETMSAVAATLGNVGPGFGVVGPMGSYLDFSNSSKLYMVLLMWVGRLEILPVLVIFTPEYWRR
1E-69	245	34.5	1.4E-69	244.4	23.9	1.1	1	R5QN02_9FIRM	Potassium uptake protein	BN550_01176	Coprobacillus sp. CAG:235	467	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:235	1262854	>tr|R5QN02|R5QN02_9FIRM Potassium uptake protein OS=Coprobacillus sp. CAG:235 GN=BN550_01176 PE=4 SV=1MQRKTLHKQYKKLGISAVRRIGFSFFAVILIGSILLSLPMSHTIHSTSSYLDHLFVATSATCVTGLVTHVTASEYTLFGQIVIILLIQIGGLGFLTLMSMFFVLLKRKLTYANKIVMQEALNRNSLNETGIYIKRRVIKYTVCFELIGAICLAFVFIPQFGILKGIYYSLFHAISAFCNAGFDILGNNSMVPYVGNVWINLVICGLIIAGGLGFVVWIDLRLSLIHYREHFKYFKMKRYLESLSLHTKIALISTFVLIFGGMTVIFILEFQNPLTLKSLPFSQKILASFFQSVTLRTAGFATVDMASLHQATKFFMSIIMFIGGSPAGTAGGVKTVTFVIGLLYVRALMRGDENIHVFKRTIDDQIVKRALTIMLISFAIALTGLFILSISEQADFIDLLFEVFSAFATVGLTAGLTPTLTFVGKIVIIILMYIGRIGPITMVLIFVRKYNAKKGKDVNYIKEHILIG
1.1E-69	245	19.5	1.4E-69	244.3	13.5	1.1	1	E6X6K5_CELAD	Cation transporter	Celal_2250	Cellulophaga algicola (strain DSM 14237 / IC166 / ACAM 630)	496	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Cellulophaga, Cellulophaga algicola, Cellulophaga algicola (strain DSM 14237 / IC166 / ACAM 630)	688270	>tr|E6X6K5|E6X6K5_CELAD Cation transporter OS=Cellulophaga algicola (strain DSM 14237 / IC166 / ACAM 630) GN=Celal_2250 PE=4 SV=1MSLNYRIIFHLMGLLLLCNGGFMIIAAIFSGIYNDGATLDITLAAIVTMIIGTLSMFLTRGHKKEVKKKEGYIIVTGGWLVMSLSGVLPYLFSGAIPDFTNAFFETISGYTTTGASILDDIEALPEGILFWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPSSDKLHPRITDTAKRLWLIYFGYTVAETILLKLAGMSFFDAINHSLATLSTGGFSTKNLSTAYWNDQPLIQYIIILFMFLAGSNFVLSYYAFKGKVQKILFDEEFKFYTIFVVGFTIVSALVVYFKANVAVSEYHPMIWGEAESAFRHSLFQVLSVITTTGFVTADFTNWTHFLTIFYFGLFFLGGCAGSTSGGIKVMRHLLIIKNGLLEFKRTLHSNAVIPVRYNNKTVREHIVYNIIAFFVLYMLMFIIGSLVLGALGLDFESAIGGAASSLGNVGPGLGSLNPLSNFNGLPALGKWWCGFLMLLGRLELFTVLILFTPYFWKKI
1.4E-69	244	20.8	1.9E-69	243.9	14.4	1.2	1	Q9HQ81_HALSA	TRK potassium uptake system protein	trkH1 VNG_1284G	Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	537	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halobacterium, Halobacterium salinarum (Halobacterium halobium), Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	64091	>tr|Q9HQ81|Q9HQ81_HALSA TRK potassium uptake system protein OS=Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) GN=trkH1 PE=4 SV=1MVDRLGTIARDLGRMLEALAGLIFVSVLVPLVWGEFWVVPAMVVSGLIPLVVGLTLRRTFEHAADPGRLHGMMIAASGWFLVAAFGSVPFLLAAWTAQLDPGMLDVPARFTVPGTRTFSTLAAFQNPLNGFFESMSGFTGTGLTMADNEAALPHTLQWWRSFIEWVGGVGVIVLTTAILARPGSGSLTLYESEARSEKIHPSIVSTVRTIWWIFLLFTFFSILLLWIAGMPMWDAINHAMTGLATGGFSITDNSIATYGSAAIDFALIPVMVLGSIAFPIHYLVLQGDLRNLYTDLQTRWVFGFFALGTALLTAVLLQQGYYVTESVAVAGVVLHGSAATLFQTVRYALFQFVSAASCTGFQTAGALGSGWTAPAQLTVAFGMVVGAAAGSTVGGIKLIRLLTLVKGILFRIRGVFYPSDAVRTFRLDGRALSDTEAAQEFEEAAIITFLWLVFLGVAAFVFMLAIPMGPDAYTVENVLFEVASAQGNVGLSSGITGPGMPTVTKAMFLFNMWIGRLEIIPVLVLLRGLFSTLEVYD
2E-69	244	28.5	2.7E-69	243.4	19.8	1	1	D5X803_THEPJ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	TherJR_1874	Thermincola potens (strain JR)	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Thermincola, Thermincola potens, Thermincola potens (strain JR)	635013	>tr|D5X803|D5X803_THEPJ Potassium uptake protein, TrkH family OS=Thermincola potens (strain JR) GN=TherJR_1874 PE=4 SV=1MDLNKPKIKLSPPQVLVIGFATVILMGAILLSLPAAAADGKPTPFLDALFTATSAVCVTGLVVVDTGTHYSIFGQLVIMFLIQIGGLGFMTTATLFALLMGKRIKLKERLIMQEALNQLTMEGVVRLTKYILIMTFCFEGFGAIVLGLRFMQDMSPAKAFYYGLFHAVSAFNNAGFDLFGEFRSLTSFADDVVVNLMIAALIIFGGLGFTVLVDMFTRRRWKKFSLHTKLVLTMTTLLLALGTVSVFALEYSNDHTLGQLNMGGKLLASFFQSVTPRTAGFNTLNIAELRNATQFLLVILMFIGASPGSTGGGIKTSTLGTLFVAVWSMIRGDSDVVIFERRIPKDQVYKSLTVMFAALTLVIGVSMLLSITEKAQFLAVLFETTSAFGTVGLSMGITPELSTIGRIVIILTMFMGRVGPLTLAFAIAKKNRRTAFRYAEEKVMVG

2.7E-69	243	23.8	8.8E-67	235.1	16.5	2.1	1	I0AHB7_IGNAJ	TRK system potassium uptake protein TrkH	trkH IALB_0662	Ignavibacterium album (strain DSM 19864 / JCM 16511 / NBRC 101810 / Mat9-16)	462	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Ignavibacteriae, Ignavibacteria, Ignavibacteriales, Ignavibacteriaceae, Ignavibacterium, Ignavibacterium album, Ignavibacterium album (strain DSM 19864 / JCM 16511 / NBRC 101810 / Mat9-16)	945713	>tr|I0AHB7|I0AHB7_IGNAJ TRK system potassium uptake protein TrkH OS=Ignavibacterium album (strain DSM 19864 / JCM 16511 / NBRC 101810 / Mat9-16) GN=trkH PE=4 SV=1MISGIPFSLYYDDNDVIVLLLTGMSTSLLGALVWFFTRDADKSDIGKREGYLIVTSGWIIMSLFGAIPFVIHGSIPSYVDAFFEVMSGFTTTGATILTDIESLPHGLLFWRSITQWIGGMGIIVLSLAILPLLGIGGMQLYAAEVPGITKDKFHPRVKETAKRLWGIYVIFTALETILLMIAGMTFFDAINHSFTTLATGGFSTKNSSTAYYSSPFIQYIFIVFMFLAGTNFTLHYFALHRNFSFLKTNDEFKAYSIFIIISSVLIMIIHHPHLNLSLEEKFRQSLFHVVSLVTTTGYVSSDYENWAIFSRMIFFVLLFIGGCAGSTGGSIKIVRHYLLFKNGFLELKRLIHPRAVIPVRVNGKAILPEIISNVQAFFILYILIFVLSSIILSISGLDFLTSIGASATCLGNVGPGIGTVGPVANFSHLPDLAKIILSFLMLVGRLELFTVLVIFSPSFWKK	
2.7E-69	243	19.5	6.4E-69	242.1	13.5	1.5	1	R4KIP9_9FIRM	Potassium uptake protein, TrkH family	Desgi_3751	Desulfotomaculum gibsoniae DSM 7213	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum gibsoniae, Desulfotomaculum gibsoniae DSM 7213	767817	>tr|R4KIP9|R4KIP9_9FIRM Potassium uptake protein, TrkH family OS=Desulfotomaculum gibsoniae DSM 7213 GN=Desgi_3751 PE=4 SV=1MNRSLILRTLGLVLLGEAGAMLPSLGIALYLKESAYFAFGISILVLALIGLILSRNRITTNDVGYREGFIIATASWLLLALFGTLPFMICEAIPGFIDAFFETMSGFTTTGATVIIDVESLPKSILFWRSITHWLGGMGIIVLTLALIPSLKIAGMKLFRAEVTGPAKSKVLPRVAQTSRELYKVYIMITVIEIAALKVAGLNWFDSFNHSFSSVATGGFSNYNESVGALNNAAAEYIIIFFMLICGMNFALHYHALRGNFRPLWKDTETRLYLGITITAWLFISINLMIAMDYQTETALRQSAFQTVSILTTTGFATTDYNLWPTFSQGVIFLLMFIGGCAGSTGGGIKNVRYLILVKAASRQISKLIHPKAVIPIRVGRDVVPDELVESVQSFFFLYFGLLLVCTLMITAMGIDLLSAITAVAATLGNIGPGFGIVGPASNYAAIPPAGKLLLTICMLVGRLEIYTVLVFFSARLWRS	
3.9E-69	243	21.3	9.6E-69	241.6	14.8	1.5	1	A0A0E3X1I5_METMT	Potassium uptake protein TrkH	MCMEM_1217	Methanococcoides methylutens MM1	478	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanococcoides, Methanococcoides methylutens, Methanococcoides methylutens MM1	1434104	>tr|A0A0E3X1I5|A0A0E3X1I5_METMT Potassium uptake protein TrkH OS=Methanococcoides methylutens MM1 GN=MCMEM_1217 PE=4 SV=1MRYDVVLGVLGSILWLLAGVLVIPLIVAVYYGETLFTFGLPLLITVLAAFVFSLFFTKVEEEWNMKEGFFIVASGWLIAAVIYSIPYILEGVPVLNALFESMSGVTATGATALTDIESHSRSLLFWRSMTQWLGGMGIIMLFIAILPKLGIAGRQMFRAEVPGLHEEQLRPRIRETAKILWLVYIMLSLAEIIVLDLAGLSLYDSVTHTFTSISCSGFSPYSDSIAAFNDPVVEAIFIVFMFLGGANFALHYKTVFSDRKSLIRDEEFKFYFLLIGIATLVLAYMLFSTRVYPLGEAFRYSSFQVISILTTTGYATADFNLWPDSSRFILFLLMFIGGCAGSTSGGVKVVRVLLLIKYAQNVLFKVLHPKAIRHIRFNGKTVPEDVIHSIVSFMVIYFMIFVASSTMLSLMGMDFVTSLSASIATLGNVGPGLGLVGPMESFDNIPALGKLLLTANMWIGRLEVFTVMVILTPAFWRK	
4E-69	243	6.6	9E-69	241.6	4.6	1.4	1	E1QEJ5_DESB2	Trk system potassium uptake protein	Deba_0609	Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	484	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfarculales, Desulfarculaceae, Desulfarculus, Desulfarculus baarsii (Desulfovibrio baarsii), Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	644282	>tr|E1QEJ5|E1QEJ5_DESB2 Trk system potassium uptake protein OS=Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14) GN=Deba_0609 PE=3 SV=1MNVAFAISLVGLICLGVGLCMLLPLAVALIHAEPGWLAFLGGSFVCCLLGGVLFWSFRDRRVKELNHREGMAVVGLSWLAAGVLGGLPLLLSGDFKSWADAVFESVSGFTTTGASVLTNVEAAQKCVLFWRALTHWLGGMGFIVLGVAVLPFLGVGGMQLYKAEAPSPTPDRLVPRIADTAKALWWIYVLLTAAEALLLLGGMDLFDSLCHAMATMATGGFSTKNLSVGHWPSPFIQWVVTIFMILAGINFTLHFQLFSQRRWDAFWRDEECRFYLALTVGAALIITICLWLAQGLDTASALRLAFFQTATILTTTGFATADYTLWPPLALAVLTMLLFIGGSAGSTGGGPKVMRVLVVLKQSLAEFGRLIHPRMVNPVKLGRRTVDKQVVAAIWAFMGLYLACFALTTLGLAALGLDGQTAFSAAIACLGNIGPGLGPIVGPVGNYASLPEAGKWLLSAAMLVGRLEVYTVLVLFIPGLWRD	
4.8E-69	243	22.7	9.1E-68	238.3	15.8	2	1	W0E7Y9_9FIRM	Membrane protein	DESME_07795	Desulfitobacterium metallireducens DSM 15288	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium metallireducens, Desulfitobacterium metallireducens DSM 15288	871968	>tr|W0E7Y9|W0E7Y9_9FIRM Membrane protein OS=Desulfitobacterium metallireducens DSM 15288 GN=DESME_07795 PE=4 SV=1MNIRLVLGILGKLLSAYSFAMFIPLMIALILNESSLMAFIISILITGLTGVFLVYRCKLSNLKFGAREGFAIVAATWILTSLFGALPYWFSHAAPTYIDAVFETVSGLTTTGASVINDVEALPQSLLFWRSLTHWIGGMGIIVFFITLLPRTGVGAVTLFNAEVPGPTNERIQPRIRDTATALWKIYTVFTAILTFLLWGAGMTFFDAINHAFATMATGGFSTKNTSVMYYDSLSIELILTLFFMILAGGNFGIYLMAWRKKNFKPFRNNEFSIYLLIILGATLLIAGSLWYSGGKPIDYALRHALFQVASIITTTGFASDDFDRWTAITKLILFLLMFIGGSSGSTSGGIKVSRIILLTKSTWAELKRAIHPRAVLSIKLDGKAIEPNTIVMVSIFFFLYIVTFAAASMIITGTGLEPFDAMSAVAATLGNVGPGFGVVGPTKTFANVSLLGKSVLTFCMLLGRLEFFTLLILLRPEFWRTKKNW	
5.1E-69	243	30.2	6.4E-69	242.1	21	1	1	R7GM20_9FIRM	Ktr system potassium uptake protein B	BN591_00065	Catenibacterium sp. CAG:290	467	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Catenibacterium, environmental samples, Catenibacterium sp. CAG:290	1262767	>tr|R7GM20|R7GM20_9FIRM Ktr system potassium uptake protein B OS=Catenibacterium sp. CAG:290 GN=BN591_00065 PE=4 SV=1MKDIVLTRRKHSGRLSAPKKVSLSFLAVIIIGAIVLSLPFSNKKEAASFLDNLFIATSAVCVTGLSPLTVVDQYNLFGQTVLIILVQIGGLGFLTFLYLFLFLARQRITLSRKLVFTEALNQNSLSMLPRLLKTIFIYTVSIETIGLIFFSMFFIPRLGALKGLYYGIWHSISAFCNAGFDLCGSTSLVAYNTNPIINFIVPFEIIMGGLGFIVVLDIHDKYIKEKRRSSSFSWRHLFGSFALHTKIVLMMTVSLIVIGTLLFFIMEFNNPATIGKMNLVDKLVVSFFQSVTTRTAGFSTVDMYSLNRITKILMCSLMFIGGSPASTAGGIKTVTFALVLLLMRTTYRGIEETTVFQRRIKKRTLVRAFSIFFLGLMLCIISSSIMLITEPKQDYLNILMEVFSAFGTVGLSASVTPALSIVGKCVDIILMYAGRIGPISLMILFTKRSHDKNTKEFKYPDEDVLVG	
5.6E-69	242	16.3	2.9E-67	236.7	11.3	2	1	K9RDU2_9CYAN	Trk-type K+ transport system, membrane component	Riv7116_2750	Rivularia sp. PCC 7116	498	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Rivularia, Rivularia sp. PCC 7116	373994	>tr|K9RDU2|K9RDU2_9CYAN Trk-type K+ transport system, membrane component OS=Rivularia sp. PCC 7116 GN=Riv7116_2750 PE=4 SV=1MNSYTKTILRDIGLFLHVPAIMAFFSIPVCLLWGEFYAILPFIICGIIPLIIGQLLYRLFSRGAEETKIRHAMITAALCWLIVPIIGAIPFLMVASNLAAASETSQTILNFQNPWNALFEAFSGFTSTGLSVALRASQLPRSLQWWRSFMEWIGGVGVIVLVISLLETTTDAYQLYSSEGREKRIASNVQATARRIWWIYLIYTIASIFIFRIAGMPWWDALNHGMAGMSTGGFSVRDDSIGSYSSIIQMAVIPTMIIGAVSFPVHYRLLTKGRFSALWSDNQHQALWLLLASGIAFLGLINYSFFGSPLWLHTVFQWASAFGTCGFNTIDLYDWSNSAKLLLTLAMIVGGTAGSTVGGFKLNRLVFLSKGAVWRLRRISLKSDESMSYRLDGEVLNETEATRKIEAAAVLGFLWIVILIIGVFILLQLALPDYSLSDVLFESASALGSVGITSPELPWLGKLTLIIFMWMGRLEIIPVLILFSEVGKKIRGKS	
7.4E-69	242	25	5.1E-68	239.2	17.3	1.9	1	L0K8X4_HALHC	Potassium uptake protein, TrkH family	Halha_1525	Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Halobacteroides, Halobacteroides halobius, Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	748449	>tr|L0K8X4|L0K8X4_HALHC Potassium uptake protein, TrkH family OS=Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1) GN=Halha_1525 PE=4 SV=1MRLRMVLGMIGILLVFVGASMLLPILVSLYYREIDGIAFIVSMGFTIICGQLLRKFATEKEGIRHREGFAIVTLGWLIIPIFGALPLMLAGTFDSFVNAFFESVSGFTTTGATVIMSLESLSHTILFWRSLMHWLGGMGIIVMSIVILPELAGSMQLFKAEVPGPVHDRLKPRIRETAKTIWVIYIILTCLQTIILYFNDIPLFDAVIHSFGTISTGGFSSRTLSVRAYDSVVIDAIMSFFMFLGGINLTLHYQCLKGNIKSLFKDKEFRFYALIVASSIILITINLRFQVYNSFTEALRYASFQVTSIISTAGFATVDYDIWPPFSRGILLILMFIGGCAGSTAGGIKVIRIYALMKKGFQELHKLIHPRAVTSLKIGNRAVSDEVSTSILGFFFLYIIVFVISTVTLTSFGIDLVSSISAVAATLGNIGPGLGLIGPLNTYVPLPITGKLLLSFCMILGRLEIYTVLVLFLLSGFWRK	

8.2E-69	242	23.7	4.6E-41	150.2	5	2	2	I3Z8B1_BELBD	Trk type K+ transport system, membrane component	Belba_2949	Belliella baltica (strain DSM 15883 / CIP 108006 / LMG 21964 / BA134)	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cyclobacteriaceae, Belliella, Belliella baltica, Belliella baltica (strain DSM 15883 / CIP 108006 / LMG 21964 / BA134)	866536	>tr|I3Z8B1|I3Z8B1_BELBD Trk-type K+ transport system, membrane component OS=Belliella baltica (strain DSM 15883 / CIP 108006 / LMG 21964 / BA134) GN=Belba_2949 PE=4 SV=1MIHFKAIGKILGALLMLLALLMLPGVGFSFYFESNDEVALLASAFISLSVGATLYFSFSKQDQNIRKREGYLIVSLSWLFMSIFGMLPYILSGSISSIPDAIFETVSGLTTTGATILNDIEATPKGILFWRSMTQWIGGLGIIVLTVAILPLLGIGGIELFVAESPGPTSDKLHPRIRETAKRLWFVYMGLTVLVGILYYVGGMTVFDAINHALTTIATGGFSTKNASMAFYDSAFIQYVAIIFMFLAGTNFTIIYFGLIGKFDRVFRSDEFKTYTLTIIFLAICFAFPIYHYSDQEFEKSFRDGLFQIVSLITTTGYITADYTAYHDGLTLIFFMMLFLGGSAGSTSGGIKFVRHLTFVKNTWLEFKRIVHPRAVVPLKINGDRVTGKIITHIMNFLLIYLMIFVIGSIILTLMGYDILTSFGAVATSLGNVGPGIGSVGPVDNFAFFGPGAKIFLSFLMLLGRLELFTILIVFTPFFWRAN
8.9E-69	242	21	1.3E-68	241.2	14.6	1.1	1	F6B406_DESCC	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Desca_1200	Desulfotomaculum carboxydivorans (strain DSM 14880 / VKM B-2319 / CO-1-SRB)	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum carboxydivorans, Desulfotomaculum carboxydivorans (strain DSM 14880 / VKM B-2319 / CO-1-SRB)	868595	>tr|F6B406|F6B406_DESCC Potassium uptake protein, TrkH family OS=Desulfotomaculum carboxydivorans (strain DSM 14880 / VKM B-2319 / CO-1-SRB) GN=Desca_1200 PE=4 SV=1MAGNNGFLSDPPKVLVAGFATVILIGALLLTLPVSSANGQPTGFLTALFTSTSAVCVTGLVVVDTGTYWSTFGHLVIITLIQVGGLGFMTMAVLFWLLMGRRVTFRERLLIQESLNVIDLSGLIKLAKRVLILTFTIELAIATVLALRWIPEFGLAKGVWFGLFHAISGFNNAGFDLFGEFRSLTQYVSDPVVNLAITTDIILGGIGFTVMSDLLRWKERKRLTLHTKLTLLVTVILLLVGTLVIFFLELNNTLAPLSLSGKLWASWFQSVTPRTAGYNTLDIGALRPATLFFMVILMFIGASPGSTGGGIKTTTFGMLGLAVFSMARGKEDPEIFNRRIIPKDQIYKGLAIIFLAMSWIVIAVLILDITEREDFLKILFEVVSAYGTVGLTAGLTPHLSSVGQVIIIFTMFLGRLGPLTVAFALAAKQRQRKQTVRYAEERVIIG
1.4E-68	241	24.2	2E-67	237.2	16.8	2	1	Q24WP9_DESHY	Putative uncharacterized protein	DSY1754	Desulfitobacterium hafniense (strain Y51)	495	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium hafniense (Desulfitobacterium frappieri), Desulfitobacterium hafniense (strain Y51)	138119	>tr|Q24WP9|Q24WP9_DESHY Putative uncharacterized protein OS=Desulfitobacterium hafniense (strain Y51) GN=DSY1754 PE=4 SV=1MRINWRVNKMNLPVILGLLGKLLVIYAGAMCIPLTLAVVLGEWSVYSFLLSIIIIGIPGFFLMRRFKLTEMKFGVREAFAAVTGAWLLASFTGALPYWFADVVPTYIDALFETVSGLTTTGASVISDVEALPQSILLWRSLTHWVGGLGIIVLFIVLLPKTGMGSVLLFNAEVPGPTNDRVMPRIRDTAAALWKIYLIFTAICAVLLWMAGMSFLDALNHAFATIATGGFSTKNTSIMYYNSLTIEMIVAFFMIFSGANFVIYLTVWRKKTMKAFRNTELMVYLLIIIAATLLIAGSLWSNAGNSPGYAFRHALFQVASIMTTTGYASVDFDQWPSMTKIILFLLMFIGGSAGSTSGGMKVSRIILLVKATWAELKRGIHPRVVSSIKLDDKVIDTENLSRVGIFFFLYIVTFTGASIIVAASTGLSPFEAMSAVAATLGNVGPGFGTVGPTTTFAGISLLGKIVLTVCMLLGRLEFFTLLIIFRPEFWGKGKVW
2.5E-68	240	25.5	1.2E-67	238	17.7	1.9	1	B5YIV8_THEYD	Trk system potassium uptake protein TrkH	THEYE_A2045	Thermodesulfovibrio yellowstonii (strain ATCC 51303 / DSM 11347 / YP87)	481	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Thermodesulfovibrio, Thermodesulfovibrio yellowstonii, Thermodesulfovibrio yellowstonii (strain ATCC 51303 / DSM 11347 / YP87)	289376	>tr|B5YIV8|B5YIV8_THEYD Trk system potassium uptake protein TrkH OS=Thermodesulfovibrio yellowstonii (strain ATCC 51303 / DSM 11347 / YP87) GN=THEYE_A2045 PE=4 SV=1MNYKTVINIIGIILIILSIFMIIPILVSIINHSSDIPALGLSCFLTFFCGTVMLALTKQYRHEELMYREAFMTVTLTWIAVAFFGCLPYIFTGSVSSFTDAFFEAMSGFTTTGASIFADVESLPAGLLFWRSMTQWIGGMGIIVFVLAVLPLMGIGGMQLFKAEVPEISVDKLRPRIIDTAKSLWFIYIGITAIIIILYFIAGMDIYDAVCHAFTTISTGGFSTKNASIAHFKSPMLEYISSFGMFLGGINFALYFYLLLKGRVRRFLKNAEFRFYFCIISITVVLLTVDLLFYYHSFSEAFRYALFQVISIMTTTGYATADYLKWSSFSQLVLLIIMFFGGMIGSTGGGIKQVRVYLMIKQIYREFYQLIHPRAVLALKLDDKFLTKEILGSIWGFVFLAIFVCALASIGMTATGLDMVTSVSTVVSSMNNVGPALGEAGPAGNYFSIPPLGKWILILCMLAGRLEYYTVLILLTPAFWKR
2.5E-68	240	15.4	1.7E-67	237.4	10.7	2	1	D8J3P4_HALJB	Cation transporter	HacjB3_09840 C497_12836	Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	508	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halalkalicoccus, Halalkalicoccus jeotgali, Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	795797	>tr|D8J3P4|D8J3P4_HALJB Cation transporter OS=Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3) GN=HacjB3_09840 PE=4 SV=1MGGTPATVGRDLGRVLLAFSGLVFVSVAVSLVWGEYYAIPGLLVSGAIPLSLGWALSRRYADAREPGKFHGMVIAASGWLLIALFGSLPFLAVAWTVTLAPDRFGTPEMTSTLRAFRSPLNALFESMSGFTGTGLTMADRESVLPRTLQWWRSFSEWVGGVGIVILTTAILTRAGSGSLTLYESEARSERIHPSIVSTVRTIWWIFLLFTFLSISALWLAGMPLWHAINHAMTGLSTGGFSVTDASIATYDSASIDAALLPVMVAGSIAFPVHYLVLRGDLAAIRGDVQTRWLLVGFSALALLLSALLYVEGTYETASEALRFGAFQFVSAATCTGFQTANDLGTGWSPLAQLTVAAGMVVGGAAGSTAGGIKLIRAITLVRGARWRIAGVFEPSSAVRRLRIGDRSLSETQASKELEEAAIVFVLWLLFLAVGVAVLLATLPTDVRAEYVLFEVMSAQSTVGLSAGITGPEMPTAAKLVFLLNMWVGRLEIIPVLVLFRGALLRAGLYR
2.6E-68	240	14.6	2.2E-67	237.1	10.1	2	1	F8D7L4_HALXS	Cation transporter	Halxa_1869	Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6)	515	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halopiger, Halopiger xanaduensis, Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6)	797210	>tr|F8D7L4|F8D7L4_HALXS Cation transporter OS=Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6) GN=Halxa_1869 PE=4 SV=1MRVEFRTVCRDVGRILQIVSLMMFVSTGIAILYDEFYAIPPLVVAGLVVFGAGAGLARQFSDAPEPNKLHGMLIAAAAWAAVGVLGGLPFLLIAWTIAIDPFFPAWANAPALNETTAAFRDPLNGIFESLSGFTSTGLTMARTEEQLPATLLWWRSFTEWIGGVGVIVLTVAILARPGSGSLTLYESEARSTKIHPSIVSTVREIWKIYVILTVGGIALLFVAGMPLWGAINHAMTGIATGGFSIHADSIGHYDSAAIEYAVIPIMVAGSIAFPVHYLLFKGELENFYKDLQTRWVFIWFTVGSLALTGTLYLRGTYDTLEESFRHGLFQFVSGTSNAGFGTTAIGNGAEQIWTADATLIVCAGMLTGAAAGSTVGGIKLIRAITLVRGARWRIAGVFEPSSAVRRLRIGDRSLSETQASKELEEAAIVFVLWLLFLAVGVAVLLATLPTDVRAEYVLFEVMSAQSTVGLSAGITGPEMPTAAKLVFLLNMWVGRLEIIPVLVLFRGALLRAGLYR
2.7E-68	240	18.8	1E-67	238.2	13	1.7	1	R7LGL0_9BACT	Potassium uptake protein TrkH family	BN805_00526	Prevotella sp. CAG:891	502	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:891	1262937	>tr|R7LGL0|R7LGL0_9BACT Potassium uptake protein TrkH family OS=Prevotella sp. CAG:891 GN=BN805_00526 PE=4 SV=1MEEWYQSNKVSFQRNRDCMVNYRHVSYALGVLVLVEAGLFALCAAISFYYQEEEYIHFLQTLLINVVLGGLMLLVGKRNEVSINRRDGYCIVCLSWLLFSALGMLPFLFSGHITSVADAFFETMSGFTTTGATILDHIESLPHGLLFWRSLTQWIGGLGIVLFTIALLPLFSGSSQQLFLSEATGVTHDKIHPKIKVMARWLWIIYIGLTATETLLLVGGNMDWFDAICHAFSTTATGGFSTKQASVAYWNSPYIEYVISVFMILSGVNFSLYYVAAMRGNFRNLWKDEELRWFLKSVGILTLLITAALFLNDYYNLETSFRKALFQVATAHTSCGFATDDYNLWPPFTWMLLIFAMISGGCTGSTSGGVKNMRLLIMARNIRNQFKQMLHPRAVLPVRVNGICVPVQTSATVYTFFVTYLICIFVGWILLMGCGVGLTESMSTVISAIGNVGPGLGAFGPAFSWAALPDAAKWILSALMLIGRLEIFGILLLFYRGYWKEK
4.3E-68	239	9.4	6.4E-68	238.9	6.5	1.1	1	L0JIZ2_NATP1	Trk type K+ transport system, membrane component	Natpe_0632	Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	541	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema pellirubrum, Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	797303	>tr|L0JIZ2|L0JIZ2_NATP1 Trk type K+ transport system, membrane component OS=Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786) GN=Natpe_0632 PE=4 SV=1MSHSTVGRSGFVAASKTVSRDIGSLQVLIGGLMSVPLLVSLFYQEWYSAVAFLIAGMITALSGATVYKICEDAPEPKRHHAMIVAALGWFVTAAFGALPFIVAAHITPPAVLESFVPAGESYSSSLRYFRNPLHAFFESMSGYTTTGLTMSIHEPSVGHGFLWYRSQMQWIGGAGMIVLSAILRQPHGVAGISLYQSEGRNEKLRPSIAGTARAIWKIYVGVTALVAVYLAAATFLIAPNYGIENTIFDAINHAMTGQSTGGFSTLDDSIAGYDSYAMELVHIPAMITGAISIPVYYGVLSERDVREFTRDPQVRGLCAMFIVGVVGLTAFLARWVGVPYTGDPIAYLSNVVTSQALRDGLFQFISAQTTTGWQTSAIGDWNGGAVMVILVGAMLFGGSAGATVGGIKIIRGHIIARGIRWEISRVFLPKHAIDDLRIGQRRVTADEANDEIRAAMTFAFIYLIVLAVSLFVLLAVLPSDFTLADGIFEVATAQGTVGLSSGITGPDMPVIAELLFIGQMWMGRLEIIPVLVLLNSLFRR

4.5E-68	239	19.8	1E-67	238.2	13.7	1.4	1	A0A0E3X222_METMT	Potassium uptake protein TrkH	MCMEM_1756	Methanococcoides methylutens MM1	478	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanococcoides, Methanococcoides methylutens, Methanococcoides methylutens MM1	1434104	>tr|A0A0E3X222|A0A0E3X222_METMT Potassium uptake protein TrkH OS=Methanococcoides methylutens MM1 GN=MCMEM_1756 PE=4 SV=1MRFGIVFSVMGLLLRFLGPMMLVPLGVALYYGESPFPFAVAFSVTTIVGSALSFRYSSDDREWEKREGFAIVAFGWFAAALFGSIPYMFDGVTPLNALFESMSGFTTTGATVFVDIETHSKSLLFWRSMTQWLGGMGIIMLFIAILPKLGVAGRQMFRAEAPGPKEDQLRPRIQETAKILWTVYVSISVVELLLLLSAGMSFYDACTHTFTTMACGGFSPYADSVAAFDSPLIEGIITLFMFIAGANFALHYKTLYSDKKSLLKDNEFKFYLIVGLATILLTLVLWRDTPDSIPTSFRYAIFQVISILTTTGYATTDFNLWTDSGKVVLLAMMFIGGCAGSTAGGIKVVRLILLKYARNELFKAIHPKAVRPIKFNGKSVPNDIMHAIISFVVIYFLIFLISSAVLSIFGMDLTSSVTASIATLGNIGPGFNVVGPMANFSTVPAIGKIVLIANMWIGRLEVFTVIVMLTPEFWKR
4.6E-68	239	19.4	7.2E-68	238.7	13.5	1.2	1	A4ATI5_MARSH	Putative potassium uptake protein	FB2170_16761	Maribacter sp. (strain HTCC2170 / KCCM 42371)	496	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Maribacter, Maribacter sp. (strain HTCC2170 / KCCM 42371)	313603	>tr|A4ATI5|A4ATI5_MARSH Putative potassium uptake protein OS=Maribacter sp. (strain HTCC2170 / KCCM 42371) GN=FB2170_16761 PE=4 SV=1MDLNSKIIFHLMGLLLLFNGLFMLIAAVVSGVYDDGATLDITIASITSMFIGLSSMYFTREHKKEVKRKEGYIIVAFGWIIMSLSGMLPYLFSGAIPNVTNAFFETISGYTTTGATILDDIESLPEGILLWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPSADKLHPRITDTAKRLWYIYVGYTIAETLLLKLAGMSFFDAVNHSLATLSTGGFSTKNASLAYWNDQPLIQYIVIFFMFLAGSNFVLSYFAFKGKVQKVIKDEEFKFYLGFVVLFTVVVALVIYFDANVPVSDYHPMVNGAEESSFRHALFQVVAVVTTTGFVTADFSSWTPFLTVFFFGLFFLGGSAGSTAGGIKVSRHVLLFKNGLLEFKRTLHTNAVIPVRYNNKTVKEHIVYNIIAFFVLYMLSFIIGSMVLSFLGLDFESAIGGAASSLGNVGPALGSLNPLSNFNDIPMLGKWWCGFLMLLGRLELFTVLIILTPYFWKDI
4.7E-68	239	0	5.8E-68	239	0	1	1	N1RBY1_FUSC4	Low-affinity potassium transport protein	FOC4_g10010474	Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	336	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. cubense, Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	1229665	>tr|N1RBY1|N1RBY1_FUSC4 Low-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 4) GN=FOC4_g10010474 PE=4 SV=1MNSFNTSECMQLVSPSLNSGPVAELPVHTRIADGLFQAASTRTAGFSCFSLSDLHPAIPVLYMIMMYISIFPIAISIRRTNVYEEKSLGVYHNKKDEDEEESASALNYVGTHLRRQLSFDLWYVFVGFFLLAISEGESLKAKDFNLFDVLFEVISAYGTVGLSMGVPNVNASLCSQFTVVGKLIIVAMQIRGRHRGLPYGLDRAVLLPSEARFQKEAEENQPILVRTRTNASMGTTSGMEPPISPGLPGRRGSMGRIRERANSRIISQFLYPGPVIPSNEIHGHKRATSNNSNNLRDFPRFNTEPVFEEEKDDVPPLRTIESHSGGPRRAETNPMP
5.6E-68	239	19.3	9.5E-68	238.3	13.4	1.3	1	A0A0D2WTN7_CAPO3	Uncharacterized protein	CAOG_006299	Capsaspora owczarzaki (strain ATCC 30864)	645	cellular organisms, Eukaryota, Opisthokonta, Opisthokonta incertae sedis, Ichthyosporea, Capsaspora, Capsaspora owczarzaki, Capsaspora owczarzaki (strain ATCC 30864)	595528	>tr|A0A0D2WTN7|A0A0D2WTN7_CAPO3 Uncharacterized protein OS=Capsaspora owczarzaki (strain ATCC 30864) GN=CAOG_006299 PE=4 SV=1MEMSNMRRSRRGSRTDSVKHRSSPSVVSVFWHRITKPITESHAWLNFCFYLSIIWAQIRRHLNYYRIHFLYIFLVALLGGIAVYLSELYASSGTISFVDAIFMSTSAVTQTGLSSVDVAELHQGTQAVLIIVMMFGGSMIMTVAPVIMRKFYFRKQLRRHHIESYRKDLAEYNALNALLRIVPILWGTCLISFYLMLYIYCIANDGAIQVMEANNQTTAWFALFQTVSAFHNCGLSTISTNIVPFRFQYFPLLLISLMTVTGNVAFPFIMRIIVVARYWLSKNPTTRATYKFLLDHPRRCFTHLFPRAQNRWLLLVFVVLTVVQWSALMGYEWTESLFAEFNAGEKIVNSFFQAAVTRSAGFNSIDLGQLQPGLLVLFLAMMYISVSPIAVAVRNSGLDGTVSSSRKTVLDRNVMGDVEERAGRSSSNTITSQAKRVMTQDSIFLFLAYLIVSIETDHLEEDVSFTLFKILFDIISGYGTVGLSLGYPGVPFAFCGVWWHPVSKLVLLLVMILGRQRNLPDSIDKAVQVPKRLFSAVSSRHNSEDEDMENSTAETSGDRSRQHATPDADSGAGVDGGQIVPIPHLAHAHSQDGMLAITIDNNPDVLRAVLWKSCKSRTARAMQTRKLQAPAREQRLESLRVDND
6.4E-68	239	19.2	1.9E-35	131.7	3.8	2.2	2	N0BF99_9EURY	Potassium uptake protein, TrkH family	Asulf_01727	Archaeoglobus sulfaticallidus PM70-1	475	cellular organisms, Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales, Archaeoglobaceae, Archaeoglobus, Archaeoglobus sulfaticallidus, Archaeoglobus sulfaticallidus PM70-1	387631	>tr|N0BF99|N0BF99_9EURY Potassium uptake protein, TrkH family OS=Archaeoglobus sulfaticallidus PM70-1 GN=Asulf_01727 PE=4 SV=1MNYLLVINFLGRIMLYFTALFSLPLITAFIFKESFYPFLVAIAVNLIISLILYSVKPKSEVFRYKEGFAIVGLGWFLISLIGAIPYCMIGTGFIDAIFESMSGFTTTGATIFDRIEVLPKSILLWRSLTEWVGGMGIIVLFVAVFPSIAKKGYALFQAEVPGITVSKVTPRLKDTALRLWEIYLLFTVLEVALLYLAGLNLFDAINHSFTTMSTGGFSTHTESIAYYRSPLIETIITIFMIVAGVNFSLHYYWLKGDARILRDPEFKAYISLLAIAIACLTILNSKGDLIESFRYSAFNAVSLMTTTGYASYDFDRWMDSSKLIILTLMFIGGCSGSTAGGIKVIRIYLLEKYSIHQILKEADPRTARVIKMNDRILKKEIIDDITAFFVLYVLIFAVSSVVISLFGMDLLSAVSAVVATMSNVGPGLGAVGATESYSALHPVVKLILFFNMWAGRLELFTVLSLFIPSFWKERW
6.8E-68	239	21.3	1.9E-66	234	14.8	2	1	X5DXY9_9BACT	Potassium transporter	FH5T_12140	Draconibacterium orientale	461	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prolixibacteraceae, Draconibacterium, Draconibacterium orientale	1168034	>tr|X5DXY9|X5DXY9_9BACT Potassium transporter OS=Draconibacterium orientale GN=FH5T_12140 PE=4 SV=1MGIALLVALIYGESDISAFLISGGINLVIGGLIVAATSKAKKDIGKREGFIIVSMVWIVFSFFGSLPYVISGSIPGFTDAFFETMSGFTTTGSSILNDIEALPHGILFWRSITQWLGGMGIIVLSLAILPVFGIGGMQLFMAEVPGPTPDKISPRIKQTAKTLWVIYLTFTVAETLLLWVGGMTFFDSICHSFTTMATGGFSTKQASIAHWPSPFIQYVIIVFMFLAGTNFTLSYFAIKGKFSVAFKDEEFKYYSFFTLGFTALIFIGLLISTEFGVEKAFRDSLFQVITIITTTGYATADYLTWPPVLTMLIFLLFFFGGSAGSTGGGIKIMRIVVLLKNGYYELKRLVHPNAVIPVRFNKHSVDAKIVTNVLAFFIIYFVIFAISTVIFTLIEPDMESSMGAVATCLGNIGPGLGTVGPAENFYHIKPIGKWFLSFLMLLGRLELFTVLVLFSPSFWKG
7.8E-68	239	4.9	2.2E-67	237.1	3.4	1.6	1	D0MG77_RHOM4	Potassium uptake protein, TrkH family	Rmar_0735	Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) (Rhodothermus obamensis)	494	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidetes Order II. Incertae sedis, Rhodothermaceae, Rhodothermus, Rhodothermus marinus (Rhodothermus obamensis), Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) (Rhodothermus obamensis)	518766	>tr|D0MG77|D0MG77_RHOM4 Potassium uptake protein, TrkH family OS=Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) GN=Rmar_0735 PE=4 SV=1MVLNLRALAATLGALLGFLAVALLLPAGIALLYEEAAWKPFVLAALLAGVVGGGLWVLGGRRPHEPGIREGFAIVALAWLVLSLFGALPFVLGDVLSYTDAFFETMSGFTTTGATILGGERTPEIEALPRAYLFWRSLAHWLGGMGIIVLTLAILPILGVGGMQLYKAEVPGPTADKLTPRVVRETARRLWLIYVGITALEVLLLLPAMDWFDAVNHAFATMATGGFSTKNSSVGQFGSAYVEWVITVFMLLAGANFALHYRLLHGQWRPVWRDTELRVYLSIVAVATVLITLGIWAPLHAEGDYQTYAELADALRHGAFQTVSIITTTGFGTADYEQWSPLAVGVLFLLFFVGGMAGSTGGGIKVVRHVLLFKNSFRELKQLVHPRAIVPVRLNGRMVSDEILRNVLSFFVLYFGLLGMGTLALSAMEVDLLSAFGAVLSCLGNIGPAFGTMGPAENYAHLPALAKWILALLMMIGRLEIFTVLILLTRTFWRR
8.2E-68	239	5.2	1.4E-67	237.7	3.6	1.2	1	D4GVN5_HALVD	Trk system potassium uptake protein TrkH	trkH2 HVO_1057	Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) (Halobacterium volcanii)	534	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Haloferax, Haloferax volcanii (Halobacterium volcanii), Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) (Halobacterium volcanii)	309800	>tr|D4GVN5|D4GVN5_HALVD Trk system potassium uptake protein TrkH OS=Haloferax volcanii (strain ATCC 29605 / DSM 3757 / JCM 8879 / NBRC 14742 / NCIMB 2012 / VKM B-1768 / DS2) GN=trkH2 PE=4 SV=1MKLRVDYRASLRVGTVLKYLAVPLCFPLVVALYYGESVLPFVVTMAVTVLVGTGLERLADDPDIGAREGFLMVALTWLAVTIVGAIPFLIEAHGIPFVASPIHPESTLGNPVNALFETMSGFTTTGATVLGDISFDSHTRGIMMWRQLTQWLGGMGIVVLAVAILPELSVGGAQLMDAEAPGPGIEKLTPRIAETARALWGAYLGLTVLEIVLLYGLNVTGHAQNMGVYNAIAHGLTTMPTGGFSPEARSIEAFSAAAQWVVIPFMVAAGTNFALFWHVLTGDPKRLFRDTEFKSYLGVIGVVSAILAGILFLGDGLMSVAPAGETYDQLYLEGIRTAIIGNVEPAVRQSVFQVVSIVTTTGYASIDFNAWSAPAQYVLLFAMFIGGSGGSTGGAVKIVRWYVIVKSLRRELFTTAHPEAVRPVRLAGRAVDERAIRGIYAFTLLYLVLFFVSTGLLHLDAARIGFDVSILETMSAVAATLGNVGPGFGVVGPMGSYLDFSNGSKLYMVLLMWVGRLEILPVLVIFTPEYWRR

8.7E-68	238	35.8	1.3E-67	237.8	24.8	1.2	1	K4KYD4_9FIRM	Potassium uptake protein, integral membrane component, KtrB	ktrB DCF50_p76	Dehalobacter sp. CF	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Dehalobacter, Dehalobacter sp. CF	1131462	>tr|K4KYD4|K4KYD4_9FIRM Potassium uptake protein, integral membrane component, KtrB OS=Dehalobacter sp. CF GN=ktrB PE=4 SV=1MNDIFKIDINTPTTQGKKKLSPPQILAIGFISVILVGTLLLSLSIATVNGKGLPFIDALFTATSAVCVTGLVVVDTGSVFSVFGQIVILLIQIGGLGFMTFATFFAILLGKKINLQERMILQEAYNQSSLEGIVRLAKYIFLAAFLIEAIGIIILTIRWSFDFNVGKAFYYALFHTVSAFNNAGFDLFGNSLMRFQRDIVINLTVMVLIVLGGIGFSVISDVYFQRGRKMSLHSWIVIRTTGLLIAIGAILFLLEFNNPDTLGNLGYQGKILSSLFQSVTPRTAGFNTIDISALQDTTILLMIVFMFIGASPGSTGGGIKTTTFVAIMLSIFSIFRNKSQVTIHGRSIPKEVIQKAVAIMTLAIIWIILVTGLLSITEEADLITLLFETVSAFGTVGLSLGITSDLTLFGKILIILTMFVGRVGLLTIAFSIGKGNNPGNQAKYPESKIMIG
1E-67	238	23.6	2.7E-66	233.5	16.4	2	1	L0G334_ECHVK	Trk-type K+ transport system, membrane component	Echvi_3017	Echinicola vietnamensis (strain DSM 17526 / LMG 23754 / KMM 6221)	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cyclobacteriaceae, Echinicola, Echinicola vietnamensis, Echinicola vietnamensis (strain DSM 17526 / LMG 23754 / KMM 6221)	926556	>tr|L0G334|L0G334_ECHVK Trk-type K+ transport system, membrane component OS=Echinicola vietnamensis (strain DSM 17526 / LMG 23754 / KMM 6221) GN=Echvi_3017 PE=4 SV=1MIHYKAIAKVMGGLLMLLGLLMLPGIAFSFYYKSGDHMPLIYSAFVSMAIGGLLFFSFSKEDQNIRKREGYLIVALSWIFMSIFGMLPYLVSGTLTNLSDAVFETVSGLTTTGASVLNDIEALPKGILFWRSMTQWIGGLGIIVLTVAIFPLLGIGGIELFVAESPGPTSDKLHPRIRETAKRLWYVYVGLTILCAGLYYIGGMDFYDAVNHSLTTLATGGFSTKNASMAYFDVPFIQYVAILFMFLAGTNFTVIYFGIMGKFDRVWKSDEFKAYVLVVALIIVGLTVPVFLASGFGFEKAFRDTAFQVVSLITTTGFVTADYTSFGHGLTILFLLLFVGGCAGSTAGGIKFIRHLTTFFKNTLLEFKRIVHPRAIVTLKINNERVTGKIITHIMIFLLIYLMVFVVGSVLLSIVGYDMLTSFGAVATCLGNVGPAIGNVVGPLDNFSFFDPFTKVFLSAIMLLGRLELFTILVLFTPYFWRAN
1.1E-67	238	22.8	4.3E-66	232.8	15.8	2.2	1	D4H731_DENA2	Potassium uptake protein, TrkH family	Dacet_2985	Denitrovibrio acetiphilus (strain DSM 12809 / N2460)	483	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Denitrovibrio, Denitrovibrio acetiphilus, Denitrovibrio acetiphilus (strain DSM 12809 / N2460)	522772	>tr|D4H731|D4H731_DENA2 Potassium uptake protein, TrkH family OS=Denitrovibrio acetiphilus (strain DSM 12809 / N2460) GN=Dacet_2985 PE=4 SV=1MHYKLIIKTIAILQLVIAFFHLVCAGVAMYYGETEALISFAVSISLLVGIGGFFMLFYKNTIPDNISTKDGFLLVALSWLAASIGGSLPFYISGAIPSYTDAFFETISGFSTTGASILTNIEGLPLSILFWRSLTHWLGGMGIVVLAVAILPLLGIGGMQLIKAEAPGPTVDKITPRIAETAKYLWYIYVGFTAAETVLLMLGGMNLFDALTHTFGTVATGGFSTKNISVSHFDSAYIDWVITIFMILAGVNFTLHFRLLTGRFKSVTKDSELKAYLAIIALTTIIITFSLNGTVYTSLADSLRFAAFQVATFITTTGFATANYEQWPYLAQIILFMLMFVGGCSGSTGGGIKVIRLVTLLKQGINEMKYLVHPRGVFLIRLSGQTVKKDIVYAVSGFFFLYIFLLLVVTMIVATSGVDVLTSFTTSLATVGNIGPGFGMVGPADNYAFYPDYVKWTLSAAMIIGRLEIYTILVLFTPTFWRR
1.1E-67	238	19.6	4.3E-67	236.1	13.6	1.7	1	F4AYJ8_DOKS4	Cation transporter	Krodi_0479	Dokdonia sp. (strain 4H-3-7-5) (Krokinobacter sp. (strain 4H-3-7-5))	498	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Dokdonia, Dokdonia sp. (strain 4H-3-7-5) (Krokinobacter sp. (strain 4H-3-7-5))	983548	>tr|F4AYJ8|F4AYJ8_DOKS4 Cation transporter OS=Dokdonia sp. (strain 4H-3-7-5) GN=Krodi_0479 PE=4 SV=1MPKLNYKIIFHLMGVLLLINGGFMLISALVSFITKDGVMLEVSAAALITALVGTLLMFITRGHEKELKKREGYIIVTFGWLFMSLSGMLPYLFSGTIPGVANAFFETISGYTTTGATILSEIETLPKSILFWRSMTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPSADKLHPRITDTAKRLWLIYVSFTVIETILLKLAGMSFFDAINHALSTLSTGGFSTKNASVAYWNDKPLIQYIIIFFMLLAGTNFVLSYFAFKGKIQKILRDEEFRLYMAFVFGFGIIASLVIYFNVDLGISSIDHPMVWGKAEASVRHALFQVLAVITTTGFITADYTMWTPFLTVIFFGLMFLGGSAGSTSGGIKVVRHLLTIRNALVEFKRTLHPNAILPVRYNTKSVDRSIIFNILAFFILYMLSWIIGASVLASMGLDFRTALGGAASALGNVGPAFGGLGPVDNYGWLPLAGKWWMAFLMLIGRLELFTVLILLTPFFWRNR
1.3E-67	238	12.4	2.2E-66	233.8	8.6	2	1	C1D7N7_LARHH	Trk system potassium uptake protein	LHK_01488	Laribacter hongkongensis (strain HLHK9)	484	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Laribacter, Laribacter hongkongensis, Laribacter hongkongensis (strain HLHK9)	557598	>tr|C1D7N7|C1D7N7_LARHH Trk system potassium uptake protein OS=Laribacter hongkongensis (strain HLHK9) GN=LHK_01488 PE=3 SV=1MHKLLPILHVLSKLIMLFAGLYVVPAVVSIIYQDGTLDEFLVSMFVGMALGLLLWAVTRRYEAELKPRDGFMLVSFLWIGFAATATTPFLLHFPDLGFTSAFFEAMSGLTTTGATVLSGLDHLPPAINFWRHFLNWLGGMGIIVLAVAVLPLLGIGGMQLYKAETPGPMKDSKLSPRITHTAKNLWFAYALLTAACVVALRLAGMDWFDAVCHAFAALSLGGFSTHDASVGYFNSVPIEVVLSFFMLLAAMNFATHFLAIRDRNIRHYIRDSEAKSMLALIAISILAVSGYLTWMGIYDFVDALRHVSFNLISIATDSGFASTDFSVWPVAAPLWMLLLSCITACAGSTGGGIKMGRTLVLAKQSNGEMVKLLHPNAVVPVKIRDRVIPSNVVQSVLAFIFVYAASIVLFTFVLMVSGLDFLSSFTAVIACINNAGPGLGVVGPAENYSVLSNFQIWVCSLVMLLGRLEIFTLLILLSPAFWRK
1.7E-67	238	17	1.1E-65	231.5	11.8	2.1	1	H6L3T7_SAPGL	Trk system potassium uptake protein	trkH SGRA_0027	Saprospira grandis (strain Lewin)	500	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Saprospiraceae, Saprospira, Saprospira grandis, Saprospira grandis (strain Lewin)	984262	>tr|H6L3T7|H6L3T7_SAPGL Trk system potassium uptake protein OS=Saprospira grandis (strain Lewin) GN=trkH PE=4 SV=1MPKNRFHLKVILNVLGSMLFFNGLFMLACLPIALIYQAEGGGMMEMAGFWEFLIPGLGSILFGLGSWFATRKHSGNLSKRDGYLIVSLGWLLMSVVGALPYYLFGGVEFPDFACALFESVSGFTTTGASVINDIEAMPRSILFWRSLTHWIGGMGIIVLTIAILPLLGIGGMQLFVAEAPGPTADKLHPRITETAKRLWVIYVMLTVVETILLLFCGLDLYHAVNHAFATVSTGGFSTQNASLAAYGPAVHYVVIVFMFLSGMNFSLTYWGLKGQLHRIWRNEEFRAYLFSVLIITAIATALVFSYDPQKLNVSLEEAFRDALFQVIAVITTTGFVTEDFTAWGPFLKVVFFLMMFMGASAGSTSGGVKIVRHILILKNGILEFKRQLHPHAILPLRYNKKAVEGKIAYNVLAFFLVYMALYCFGCLIMAAWGFDFETVLGSVATSLGNVGPGLGQVNPVSNFAFFNQGQKFFLSFLMLLGRLELFTVLIVLTPFFWKKY
1.7E-67	237	14.4	1.1E-66	234.7	9.9	2	1	Q30ZS0_DESAG	Trk system potassium uptake protein	Dde_2029	Desulfovibrio alaskensis (strain G20) (Desulfovibrio desulfuricans (strain G20))	481	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio alaskensis, Desulfovibrio alaskensis (strain G20) (Desulfovibrio desulfuricans (strain G20))	207559	>tr|Q30ZS0|Q30ZS0_DESAG Trk system potassium uptake protein OS=Desulfovibrio alaskensis (strain G20) GN=Dde_2029 PE=3 SV=1MRIGYTLYVIGALLCSVGLTMIFPLMFGVYYQDESILPLLYSMGITVIAGGCLIAVFRERTKTLLNHREGMAIVALGWIGAGIAGALPFWFGGMLGFTDALFESVSGFTTTGSTVLTDIEIVPRGLLMWRSLTHWLGGMGIIVLSLAILPFLGVGGMQLYKAEVPGPVPDKLKPRIKDTAMALWKVYLLFSVLQAVLLYFGGMDVFDSICHTFGTMATGGFSTKNASVGHYDSGYLQTVIIIFMFIAGVNFSLHFRLLLGEPGAFLKDAEFRFYTVVVLVSTAVVALAVYGTEYDSFLEALRHAAFQVVSICTTTGFATADYEQWAPVTMAVLLFLTFLGGCAGSTGGGIKCMRVLLLLKQAYHEIFRLIHPHSVSYVKLGNRIVRAEVLSGVLGFFVLYIGLFVLSSTLIAAMGVDVLTAFSATAACIGNIGPGLGSVGPAENFAHLPQAAKWVLTLCMLLGRLEIYTVFILFVPEFWRK

1.7E-67	237	7.7	2.3E-67	237	5.3	1.1	1	E4NQC9_HALBP	Trk-type K+ transport system, membrane component (Trk-type k+ transporter, membrane component)	Hbor_22410C499_17234	Halogeometricum borinquense (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3)	534	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Halogeometricum, Halogeometricum borinquense, Halogeometricum borinquense (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3)	469382	>tr|E4NQC9|E4NQC9_HALBP Trk-type K+ transport system, membrane component OS=Halogeometricum borinquense (strain ATCC 700274 / DSM 11551 / JCM 10706 / PR3) GN=Hbor_22410 PE=4 SV=1MKLRVDYRASLSLVGTVLKYLAVPLFVPLLVALYYDETVIPFVVTIAVTVVLGTALERLEPDPDIRAREGFLMVAATWFAVTVVGAIPYLVEALGLPPVVPAIHPDSTLANPANALFESMSGFTTTGATVLGDISFQTHTRGIMMWRQLTQWLGGMGIVVLAVAILPELSVGGAQLMDAEAPGPGIEKLTPRIAQTARALWGAYLGFTVLEATLLFGLGVLQIDPNMTLYNAVAHALTTMPTGGFSPEAKSIEAFSAAAQWIIIPFMVAAGTNFALFWHALTGDPRHIFEDSEFRFYIGVIATITAVLSVLLFTGAGFVQAVPTQSTFSAMDLGQYVGDIAGQIEPSVRQAVFQVVSIVTTTGYASMDFNAWSPVAQYILLFAMFIGGSAGSTGGAVKIVRWYVILKSIRRELFTTAHPDAVRPVRLGGRALDERAIRGIYAFTLLYLVIFFVASGLLFIDASRYGQSLSVLETMSAVAATLGNVGPGFGTVGPMGSYLAFSDAGKLFMVVLMWIGRLEILPVLVLLTPEYWRR	
2.3E-67	237	21	3.2E-67	236.5	14.6	1.1	1	A0A0D5YUZ5_9FLAO	Potassium transporter	VC82_2129	Muricauda lutaonensis	496	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Muricauda, Muricauda lutaonensis	516051	>tr|A0A0D5YUZ5|A0A0D5YUZ5_9FLAO Potassium transporter OS=Muricauda lutaonensis GN=VC82_2129 PE=4 SV=1MWLNFRIIVHIMGLLLLCNGSFMLLAALVSGIYQDGATLDIMLAAIVTLFVGVMAMFYTRGRKKEVKRKEGYIIVTFGWIIMSLSGVLPYLFTGSIPSLTNAFFETISGYTTTGASILNDIESLPKGILFWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPGGDKLHPRITDTAKRLWLIYVGYTIAETLLLKLAGMSFFDAINHSLSTLSTGGFSTKNLSVAYWNDQPLIQYIIMLFMFLAGTNFVISYFAFTGKVQRIIKDEEFKFYSLFIAIFAIVAAVVVYLQADVPVSDYHPKVLGDFESSIRHGLFQVLAVITTTGFVTADFTNWTPFLTVFFFGLMFLGGSAGSTSGGIKVMRHLLLIIKNGILEFKRTLHTNAIIPVRYNNKTVSEHVVYNIIAFFVLYMLLFIIGALVLGFLGLDFESALGGAASSLGNVGPALGDLNPVVNFSSLPAFGKWWCAFLMLLGRLELFTVLIVLTPVFWKST	
2.4E-67	237	13.5	3.4E-67	236.5	9.4	1.1	1	D8JCT2_HALJB	Cation transporter	HacjB3_17423HacjB3_19423C497_00320	Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	524	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halalkalicoccus, Halalkalicoccus jeotgali, Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	795797	>tr|D8JCT2|D8JCT2_HALJB Cation transporter OS=Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3) GN=HacjB3_17423 PE=4 SV=1MIRDIGALQVLIGGLMLVPLIVSLLYQEWYSALAFLIAAGVTAIAGGAMYKLCEDAPEPQRHHAMIVAALGWLATAAFGAIPFVIAAYITPSAVLESFVPAGASYQSSLLNFQNPLHAFFESMSGYTTTGLTMSVHEPSVGHGFLWYRSQMQWVGGAGMIVLSLAILRQPHGIAGISLYQSEGRSEKLRPSIAGTARAIWKIYVGITALVAVYLAVATFIVLPGYGIEQTIFDALNHAMTGQSTGGFSTLDNSIAGYNSYAMDIVHIPAMITGAISIPVYYAAASERDIREFTRDPQVRALFGLFIVGVVGLTAFLARWVGVPYNGDPLGYVGRVATSQAFREGLFQFISAQTTTGWQTSAIGDWNNGAVMFIVFGAMLLGGSAGATVGGIKILRGYIVARGISWEVSRVVFLPDHAIDDLRIGQRIFKADEANDEIRAAGTMAAAYLIVLALSLFVLLAVLPSEFTLADAIFEVATAQGTVGLSSGITGPGMPVIAEILFIIQMWMGRLEIIPVLVLITSLFRR	
2.9E-67	237	25.1	4.2E-67	236.1	17.4	1.1	1	F6DNY5_DESRL	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Desru_2471	Desulfotomaculum ruminis (strain ATCC 23193 / DSM 2154 / NCIB 8452 / DL)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum ruminis, Desulfotomaculum ruminis (strain ATCC 23193 / DSM 2154 / NCIB 8452 / DL)	696281	>tr|F6DNY5|F6DNY5_DESRL Potassium uptake protein, TrkH family OS=Desulfotomaculum ruminis (strain ATCC 23193 / DSM 2154 / NCIB 8452 / DL) GN=Desru_2471 PE=4 SV=1MQIITGFFRHPPRVLVAGFALVILTGALLLSLPLASASGQPTDFLTALFTATSAVCVTGLVVVDTGTYWSSFGHLVIIALIQVGGLGFVVMAVLFWLLMGRRVTFRERLLIQESLNVIDLSGLVRLVKKIILLTFSIQAVIALLLMLRWVPELGLGKGIWFGLFHGISAFNNAGFDLFGQFRSLTGYVNDPIVNIAIGVAIILGSIGFTVIFDLLNFRKRRRLSLHTKFTLVMTALLLLVGVGIIFLLELNNTLASLSPGGKLLASWFQSVSPRTAGYNTLDIAALRPATLFFLIIMMFIGGSPGSTAGGIKTTTFGMLGLTVLSLARGKEDAELFGRRIPKDQIYKGLGILLIAISWIVFATLLSISEKADFLVVMFEVVSAYGTAGLSAGLTPELSPFGQVIIIFTMFLGRLGPLTITFALAARQLRKQHLRYPEERIIIG	
2.9E-67	237	22.2	7.2E-65	228.8	15.4	2	1	Q24WQ0_DESHY	Putative uncharacterized protein	DSY1753	Desulfitobacterium hafniense (strain Y51)	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium hafniense (Desulfitobacterium frappieri), Desulfitobacterium hafniense (strain Y51)	138119	>tr|Q24WQ0|Q24WQ0_DESHY Putative uncharacterized protein OS=Desulfitobacterium hafniense (strain Y51) GN=DSY1753 PE=4 SV=1MNYSLVQGIVGRLLMGYALTMFVPLVLAAFKNEDSTWAFLLTLLITACLGAAMVYFRKPTQEKMSIRESFVIVGGAWLLTSLLGALPFWISDSVPTYIDALFESVSGLTTTGSSVIDDVEALPLSILLWRSITHWLGGIGIIVLFIILLPSTGFGAVHLFNAEVPGPLGKRTMPRIRDTAITIWKIYAFFTVILVALLMLAGMSLFDAINHGFSTISAGGFSTKNTSMMYYNSLGIELVVILFIIIAGGNFRIYLEAWTKKSFKPFKNTEFITYLSIIMFSTLLIVGGLWLTHDKPPDYAVRHALFQVVSLVTGTGFASTDYNQWPAITKLTLLALMFVGGCAGSTTGGMKVSRIMLLSKHVWAVLTRGLHPRAVSSIKLDGRAVDAVAVNMVSVFFFLYVGIFALATIVMAGTGLEPFDAMSAVAASLGNVGPGFGLVGPTTTYSGITLFGKFILSLCMLLGRLELFTLLIILLRPEFWRTKGGW	
3E-67	237	37.4	8.5E-67	235.1	25.9	1.6	1	F2LXZ2_HIPMA	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Hipma_0280	Hippea maritima (strain ATCC 700847 / DSM 10411 / MH2)	440	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfurellales, Desulfurellaceae, Hippea, Hippea maritima, Hippea maritima (strain ATCC 700847 / DSM 10411 / MH2)	760142	>tr|F2LXZ2|F2LXZ2_HIPMA Potassium uptake protein, TrkH family OS=Hippea maritima (strain ATCC 700847 / DSM 10411 / MH2) GN=Hipma_0280 PE=4 SV=1MTITKNPLKAIVLGFFAVIVLGCVLLLLPFSSKNGTSLVDALFTSTSAVCVTGLITLPMSHFTLFGQIVILALIQVGGFGYMSMTSFVMIAFKRKLTYKDKLLLKEALNYPEMHSITSFFKRIMFFGIFCELVGAIILMFAFAPKMGLEKGLYYAVFHSISAFNNAGFSLFADSLVGYKYNVVVNFTIMSLIVLGGIGFIVIDELFLYKKGKISYLSLHTKAVLSFTAALIIGGALLIFLLERNGILAHHSFLKDALVSFFQSITTRTAGFNTIDLSYMHNSTIFLFVILMFIGASPGGTGGGIKTTTFAVVLKAIYSYIRGEKDVNAFKRRVSDEVVYKSFVVLSLSFIVVSLSSFILSDIENVNFLKVLFESVSAISTVGLSIGNTNVSLSGSFDDLGKLIIIVLMFVGRVGLFSFSVALFRRKSTKHYRLAEGRIFV	
3.7E-67	236	19.4	7.2E-67	235.4	13.4	1.4	1	F6GCR7_LACS5	Cation transporter	Lacal_0520	Lacinutrix sp. (strain 5H-3-7-4)	501	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Lacinutrix, Lacinutrix sp. (strain 5H-3-7-4)	983544	>tr|F6GCR7|F6GCR7_LACS5 Cation transporter OS=Lacinutrix sp. (strain 5H-3-7-4) GN=Lacal_0520 PE=4 SV=1MRKSLKLNYKIIFHFFGLLFLFNGGFMLLSTLVSLIYKDGVTIELLISGVVTMLIGVVSMVYTRNHKKEMNKREGYIVVAFGWIVMTLSGSIPYVLTESIPSFTDAFFETMSGFTTTGASILDDIEAVPEGVLFWRSLTHWIGGMGIIVLAVAILPLLGIGGMQLFAAEAPGPSADKLHPRITDTAKRLWLIYFGYTAAETILLKAAGMSFFDAINHSLSTLSTGGFSTKNASVAYWNDKPLIQYIIILFMFLAGTNFVLSYFAFKGRVQKVFKDEEFKLYFRFIVIFTAIAAILIYCNADVSKSSINHPMVFGEGESAIRHSLFQVLAIVTTTGFVSADYTLWTPFLTVFFFGLMFLGGSAGSTSGGIKVVRHLITIKNGFLEFKRALHPNAILPVRYNKRSVSGDIVFNILGFFILYLLAFIVGALGFSMMQIDFTSAIGLAASSLGNVGPALGDFGPVDNYNALPAIGKWWSSFLMLIGRLELFTVLILLTPFFWRNR	

3.8E-67	236	27.7	7.6E-66	232	19.2	2	1	Q65FR3_BACLD	K+ transporter integral membrane subunit	ktrB	BL02516	Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	439	cellular organisms, Bacteria, Firmicutes, Bacili, Bacillales, Bacillaceae, Bacillus, Bacillus subtilis group, Bacillus licheniformis, Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	279010	>tr|Q65FR3|Q65FR3_BACLD K+ transporter integral membrane subunit OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) GN=ktrB PE=4 SV=1MKFKQIQLSPSQLLVLVFLFFIILGTLLLKLPAATPKPIGWIDTLFTSTSAMTVTGLAVVDTGTDYTMFGQLIILVLIQLGGLGIMSFAVLIFIMLGKKIGLKERLLIQQSLNQTSLGGIIKLIKSLFIYSFAIEMLAMLILAVKWIPEYGLARGIYYSLFHAVSSFNNAGFSIWPDSLMRYEGDPLVNLVISFLFIVGGIGFTVLSDLWHKRSFKKLSLHSKLMIYGTFIVNLAAMILIFLLEYQNQKTLGMLPLAEKLWGAYFQAVTPRTAGFNTTDIGSLRESTITLLLLMFVGAGSASTGGGIKLTTFLVILLSVITFLKGKKHISIAKKTLKDQLILRSLAISTISVLLILTAIFILNMTEPIPFLAILFEVVSAFGTVGLSMGITADLSPIGKMLIVFIMFLGKLGPLTLAFSLARPEKENIRYSSEDILTG
4.2E-67	236	32.6	5.8E-67	235.7	22.6	1.1	1	D1AKW7_SEBTE	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Sterm_0248	Sebaldella termitidis (strain ATCC 33386 / NCTC 11300)	451	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Leptotrichiaceae, Sebaldella, Sebaldella termitidis, Sebaldella termitidis (strain ATCC 33386 / NCTC 11300)	526218	>tr|D1AKW7|D1AKW7_SEBTE Potassium uptake protein, TrkH family OS=Sebaldella termitidis (strain ATCC 33386 / NCTC 11300) GN=Sterm_0248 PE=4 SV=1MSRKKSISPYWILLDSFLIIIFIGTVLLTLPISSATGERVPVIDSLFTTTSAVAVTGLVVNDVSTTFSLFGKTVIIILIQLGGLGIMTFSSIIVLLISKKISYRTKKIVQEDLNYNTLFDIQKYIKNVVKTVLFIEFLGAFCLFFTFIKKYSFWKAVYYSVFHSVSAFCNAGFSLFSDNLGGYRSNISVNIVICSLIVLGGIGFAALNNIHLYIKKKIKRDKNKIRLNLTTKMAVLMSAILIAAGILVTFVIEANNPATLQNFSMHDKILASLFQSVTTRTAGFQTMDLANMRIATLISYIFFMYIGASPGSTGGGIKTTTIGVIILGVYSTLTNREDIEIKKKKIAWDVFNKATSIVFISLTYIIICIVFFLSLLEKNKGFLELVFETVSAFGTVGLSLNITPDLGSISKLLIALTMFIGRVGPLTVAMALSAHSKRRGAYKYPVEDVQVG
4.5E-67	236	28.4	7.3E-67	235.3	19.7	1.2	1	A0A0F2QXP4_9DELT	ATPase	VR64_12790	Desulfatitalea sp. BRH_c12	456	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfatitalea, Desulfatitalea sp. BRH_c12	1629708	>tr|A0A0F2QXP4|A0A0F2QXP4_9DELT ATPase OS=Desulfatitalea sp. BRH_c12 GN=VR64_12790 PE=4 SV=1MAIRSGILKMHPATLVLASFILVILTGMMLLMLPIATTSGAIRWIDALFTATSAVCVTGLTVVDTGNYFSTFGQCVILVLIQIGGLGLMTISVALFRWVGRSISIRQRMAMQDLFAHTPRGDILGLVKSIFLFMFIAEAIGAVLLTIHWTGELGFSQALYAGVFHSISAFCNAGFSLYSSSLMNYSDSILLTGTISGLIVIGGLGFPVLYDLQCWMRLRKKMRCRLSVQTRTVLLTTVILIFGGAIVFALLERHSLANAPSIMHRIMVPLFQSITCRTAGFNTVDISALREATLAMMMFLMFFGASPGSCGGGVKTTTLALLTAFTISRIRKRRRVNLYRKTIPVETVTRSLSLILVAIGILCVVLFLLLAGDPVTGQESAREGHTFLAYLFEAVSAFGTVGLSMGITPDLNTLGKYWIILLMLVGRVGVLTFSYIVVGTGTAEGVEHAEENIMIG
6.1E-67	236	12.1	3.8E-43	157.1	0.1	2.1	2	G0A5X6_METMM	Trk system potassium uptake protein	Metme_0814	Methylomonas methanica (strain MC09)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomonas, Methylomonas methanica, Methylomonas methanica (strain MC09)	857087	>tr|G0A5X6|G0A5X6_METMM Trk system potassium uptake protein OS=Methylomonas methanica (strain MC09) GN=Metme_0814 PE=3 SV=1MQRFCTFAFVLGLILMVFGLTYCLPIVTAWLYQDGMEVYFMDGMSLNIGIGGALALTTQRFRGELKNRDGYLLVAFFWVLMASAATLPLKWGIPGLSFTDAFFETTSGFTTTGATVLVGLDHLAPSLNLWRHELNWIGGLGIIVLAVAVLPLLGIGGMQLYKAEIAGPVKDGKITPRITETARLLWLVYLGITMICALCLKLAGMSWFDAVCHAFATALGGFSTHDASIGFFDSVAIELVLTVFMLISAINFTTHYTALSERRLPPYLTDPETMPMLGLVAVSILLCTGYLEYFDIYPDFFVNLRHVTFNLVSLATDCGFASVDYGQWPMFVPLWMLFLSCITACTGSTGGGIKMFRALLLTKQAGREIFRMIHPRAINPIRIGEMTIANKIIFSVLAFVFFYFISVLSLTFILIFSGLDPISAFSAIIACINNAGPGLQQVGPATNYASLTDFQTWICSLAMLLGRLEVFTLIVILTPTFWRT
6.4E-67	236	26.9	3.6E-65	229.8	18.6	2	1	A0A0F2Q7R2_9CLOT	Potassium transporter	VR72_05895	Clostridiaceae bacterium BRH_c20a	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, unclassified Clostridiaceae, Clostridiaceae bacterium BRH_c20a	1629719	>tr|A0A0F2Q7R2|A0A0F2Q7R2_9CLOT Potassium transporter OS=Clostridiaceae bacterium BRH_c20a GN=VR72_05895 PE=4 SV=1MNFRVIFSTLGIILMIIGISMLLPLAWSVYYASNDLLAFIISSVITFLVGLFLFKGIKKPGEIRYKEGFAIVSLSWVLASIFGALPYLISGTFTNIADAIFETMSGFTTTGASVLTDIEVLPHGILFWRSLTHWLGGMGIVVLFVAVLSSIGVGGMQMFRAESPGPVAERIKPRISETAKILWFTYVIFTIIEIILLWIFGMNLFDAMCHTFGTLATGGFSTKNLSIGYYNSTIQWIIIIFMFLSGANFALYYSFLHNKTPKVFWKSDEFRLYSYIILSSITIITIILATNSYMPLDEAITAAAFQVVSIITTTGYATYDFDQWPLLAKSILFTLMFVGGCAGSTGGSIKVGRILILIKQAALELKKAIHPRMIIQLKIREKVIPENIVINILQFFFIYMMIFMLSSIIMTGFGLDILSAMTSVAATLGNVGPGLGLVGPAQNYNFVPSLGKLFLSFLMLLGRLELYTVLVIFSPHFWKK
7.3E-67	235	27.6	2.4E-66	233.6	19.1	1.6	1	F2JI29_CELLD	Cation transporter	Clole_0220	Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Cellulosilyticum, Cellulosilyticum lentocellum, Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	642492	>tr|F2JI29|F2JI29_CELLD Cation transporter OS=Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) GN=Clole_0220 PE=4 SV=1MNLKIVLRSLGILLICEAIALLPPTLVAFLYQDGDLPAFLITISIVLAVGATLSFIKPTSKNIYARDGFAIVAMGWLLMSFFGAFPFYISGAFPSFIDSFFESSSGLTTTGSSILTAIEGLPHGVLFWRSFTHWIGGMGILVLTIAILPSLGTGSMQIMKAESPGPIVGRIVPKLGKTAKILYSIYLGITLVEVLLLCLAGMNVFDAFIHALGTVGTGGFSNMNASVGYYNSALIDWIITIFMIVCGVNFSLYYLIFKGNIKTFFKNNELRVYLCILLGAILLITVDLLARHTYGSFGEALRFSSFQAASVMTTTGYATADFNEWSMFSKMILLILMFIGGCAGSTAGGLKVSRAIICFKSIKHSLKQIIHPNGYYSVRMDGKKIDDKTVLSVLNYFFIYMIIFTIGIIISLDGFDFTTTLTSVITTLNNIGPGLGLVGPTGNFSAFSDVSKLVFSILMIIGRLEIYPILLLLTPDLWKKN
8.1E-67	235	17.2	2.2E-66	233.8	11.9	1.6	1	I3YSR6_AEQSU	Trk-type K+ transport system, membrane component	Aeqsu_0522	Aequorivita sublithincola (strain DSM 14238 / LMG 21431 / ACAM 643 / 9-3)	501	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Aequorivita, Aequorivita sublithincola, Aequorivita sublithincola (strain DSM 14238 / LMG 21431 / ACAM 643 / 9-3)	746697	>tr|I3YSR6|I3YSR6_AEQSU Trk-type K+ transport system, membrane component OS=Aequorivita sublithincola (strain DSM 14238 / LMG 21431 / ACAM 643 / 9-3) GN=Aeqsu_0522 PE=4 SV=1MSSLTKLNYKIISHLMGLLLMVNGGFMLLSSVVSWYYKDGVLAQMLMAGAVAVGVGGIVMVSTKNHRKEIQKREGYIIVAFGWIFMALIGTLPYIFTGAIPSFTNAFFETMSGYTTTGASILTDIESIPKGVLFWRSITHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPGGDKLHPRITDTAKRLWLIYVGYTLAETILLKIAGMSFFDAINHSLATLSTGGFSTKNASVAYWNDNPMVQYIIIVFMFLAGSNFVLSYFAFKRKFQKILHDEEFKMYSILIVGLTIVGALLIYFQADVSLSSIAHPMVWGPFESAVRHSLFQVLTIITTTGFVSADYTLWTPFLTIFFFGMMFLGGCAGSTAGGIKIMRHLIMIKNGVLEFKRTLHPHAILPVRYNQKAVPQPIVFNILGFFILYMLSFIIGTLVFSWLGLDFKTALGGAASTLGNVGPALGDLGPVDNYAYLPDAAKWWSSFLMLIGRLELFTVLILLTPFFWRNR
9.2E-67	235	22.9	2.9E-65	230.1	15.9	2	1	Q12WE9_METBU	K+ transporter TrkH	Mbur_1309	Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M)	479	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanococcoides, Methanococcoides burtonii, Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M)	259564	>tr|Q12WE9|Q12WE9_METBU K+ transporter TrkH OS=Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M) GN=Mbur_1309 PE=4 SV=1MINYRVVFSVLGSLLCFLGPLMLIPLVVALYYGESPYPFAVSFAVTTVIGSLLSFKFISSEDEWEKREGFAIVAFGWFAAALFGSIPYMFDGVTPLNALFESMSGFTTTGATIFVDIESHSRSLLFWRSMTQWIGGMGIIMLFIAILPKLGVAGRQMFRAEAPGPQEDQLKPRIRETAKILWAVYVSISVLELILLLAAGMSFYDASTHTFTTMACGGFSTYADSVAAFNSPLIEGIITLFMFIAGANFALHYKTLYSDKKSLLKDNEFKFYFAIVAISTILLTGILLRDSYDTIPTAFRYAVFQVLSILTTTGYATADFNLWSDSGKVILLAIMFIGGCAGSTAGGIKVVRVLILLKYARRELFKAIHPKAIRPVKFNGKSVPGDVMHAIISFVVIYFLIFLFSSSILAILGMDLTSSITASIATLGNIGPGFNVVGPMANFSTVPVLGKLILIANMWIGRLEVFTVIVMLTPEFWKR

9.8E-67	235	27.9	1.9E-64	227.4	19.3	2	1	L0KZX3_METHD	Trk-type K+ transport system, membrane component	Metho_2064	Methanomethylovorans hollandica (strain DSM 15978 / NBRC 107637 / DMS1)	477	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanomethylovorans, Methanomethylovorans hollandica, Methanomethylovorans hollandica (strain DSM 15978 / NBRC 107637 / DMS1)	867904	>tr|L0KZX3|L0KZX3_METHD Trk-type K+ transport system, membrane component OS=Methanomethylovorans hollandica (strain DSM 15978 / NBRC 107637 / DMS1) GN=Metho_2064 PE=4 SV=1MNSAVVLSVLGTLLRFQGIIMIIPLLVAVYYNESTMPFIVGIVLTEIAGTFLWLRYKSDAEWKHREAFATVAFGWLTVTIFGTIPFIISGISPINALFESMAGFTATGATILDNIESHSKSILFWRSMIQWIGGMGIIVLFIAILPKLNIGSRHLFRAEVPGLKEEKIKPRIRETAKILWMVYLLISSLQIAMLYLAGMSIYDAIVHTFTTIGSAGFSPYGESIVAFNSPLIEAIITLFMFIAGVNFVLLYRTFYIDHTSIFRDEEFKFYTAIILTATAVLILTLRYGIAADPFTCLRYALFQVVSIITTTGFASVDFNLWPDSSRIVLVFMMFIGGCAGSTSGGPTVVRVLLLLKYANGELFKFIHPRAVKPIKFNGKVVPAEIIHQVISFMVIYFLIFVTSTFLISLMNVDIVTAFTASIATLGNVGPGLNLVGPMSSYNCMPSIAKLIMIMNMWIGRLEVFTVMVLFTPEFWKK
1E-66	235	37.1	1.4E-66	234.4	25.7	1.1	1	Q6KHL8_MYCMO	Potassium uptake protein B	ktrB MMOB4260	Mycoplasma mobile (strain ATCC 43663 / 163K / NCTC 11711)	527	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma mobile, Mycoplasma mobile (strain ATCC 43663 / 163K / NCTC 11711)	267748	>tr|Q6KHL8|Q6KHL8_MYCMO Potassium uptake protein B OS=Mycoplasma mobile (strain ATCC 43663 / 163K / NCTC 11711) GN=ktrB PE=4 SV=1MFQRAYFKNKLRSNFRFSRFNRTNNKKISNGFFHFFRNLSTPKRIFLTYFLITIITSLLLWGKFSHNQGANVSYIDALFTSASAFSDTGLTVSPTALTYNIFGQTIIAIVILLGGFGFFALKAYFINLFVTNLQGKNYSMKLVERNVLSAERGSSVVGETRKIVLSSIWILAIIMIIGAIVLSFYFYFVPGNFIGNTNADPLGDISLSIRYGFFHSISAINNAGFDIIGANSIAPYFKNYTIQIIFLILFIIGGMGYPVIFDVYTKLKYKIVPKHRLNKERHRFSLFTKISVTTYLIVAFIGLLLVFIFEIFSSSPETIWGIQEINGQPISQGDKIMAIIFNTMSTRNAGFSSFDLNKLTTNSILVFSIMMFIGSAPASTAGGIRTITLAVIILSIIARATGRSSVRVFKRRLPFETSSGASTVLAVSTILCTIGIFGVLTSFSTGLSNTTNGPRNVINAIFEVTSAFGTTGLSLGITSSLNIFSKILLIFIMFIGQLGISSTILVAGNKKSKSYAYEYISEDVTIG
1.3E-66	235	29.5	1.9E-66	234	20.5	1.1	1	I5AYQ8_9DELT	Potassium uptake protein, TrkH family	DespoDRAFT_00341	Desulfobacter postgatei 2ac9	453	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfobacter, Desulfobacter postgatei, Desulfobacter postgatei 2ac9	879212	>tr|I5AYQ8|I5AYQ8_9DELT Potassium uptake protein, TrkH family OS=Desulfobacter postgatei 2ac9 GN=DespoDRAFT_00341 PE=4 SV=1MTLRRKLLKLHPAALILISFLALILIGTLLLSLPVSSKSAPLQVIDALFTSTSAVCVTGLAVVDTGTRFTLFGQIIILVLIQMGGLGVMTLSVLLFRIIGRKTFYHQRMAVQDMFLHTPQDDIFKIVKNIIYMTFCIETAGAVLLAIYWSRTMPVHEAVYTALFHAISAFCNAGFSLFPDSLSTFGDSYLLNFTICMLIVTGGIGFSVLYEFKNWIKLRKKKRFRFSVQTRIVLLTTAILIVGGTVWLFILERQGILDGKSPAYQFLVALFQSITCRTAGFNTVDISALNEATIAMMLVLMFFGASPGSCGGGVKTTTLALLTATTITRIKRMQRVNLFKKSIPDETVRRASTLIIVSVGIIGMVLFMILSEGAITGRSLGGEFLPYLFEVVSAFGTVGLSLGVTADLSVWGKFWIVITMIIGRVGILTFSYIIIGTNPTNGFERAEENMMIG
1.5E-66	234	22	1E-63	225	15.3	2.1	1	F2LTJ4_HIPMA	Trk system potassium uptake protein	Hipma_0342	Hippea maritima (strain ATCC 700847 / DSM 10411 / MH2)	478	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfurellales, Desulfurellaceae, Hippea, Hippea maritima, Hippea maritima (strain ATCC 700847 / DSM 10411 / MH2)	760142	>tr|F2LTJ4|F2LTJ4_HIPMA Trk system potassium uptake protein OS=Hippea maritima (strain ATCC 700847 / DSM 10411 / MH2) GN=Hipma_0342 PE=3 SV=1MKLKLIGRFISILLIITTLFLCVPLVFSIYYKDGASLGFLITITLNASFGSAGLLLTKNPPKSLSRKEGFILVVLSWVVISVFGSIPYVIIGNLSFTDAFFETMSGFTTTGASILKNIEAMPKSLLFWRSLTHWLGGMGIVVLAVAILPMLGIGGIKLIKAEAPGPSIEKISPRITETAKYLWFAYILLSAFETVLLLVGGMDLFDALTHTFGTMATGGFSPKNSSVAYFHSAYIDWVITIFMFIAGANFSIHFKVLTGKFSSLKDEEFLAYSAIVIIAVLLVSLDNLAIYKDFLNSLRFSAFQVVSIVTTTGYATADYEKWHSLSKVILFTFMFVGGCAGSTGGSIKVIRIYTLLKQAVNELKYNIHPKGVFTLTINKQTIRKNIVYSIAGFFFLYIATFFVVALVVSAFGVDLLTSLSASAATLGNIGPGFGGVGPTDNYAWLPSPAKWVLSFAMLSGRLEIYTVFVLFTPAFWKK
1.9E-66	234	14.7	9.1E-34	126.2	1.9	2.1	2	I0I8B5_CALAS	Trk system potassium uptake protein TrkH	trkH CLDAP_34630	Caldilinea aerophila (strain DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1)	460	cellular organisms, Bacteria, Chloroflexi, Caldilineae, Caldilineales, Caldilineaceae, Caldilinea, Caldilinea aerophila, Caldilinea aerophila (strain DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1)	926550	>tr|I0I8B5|I0I8B5_CALAS Trk system potassium uptake protein TrkH OS=Caldilinea aerophila (strain DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1) GN=trkH PE=4 SV=1MLTPIPFSLYYRSDDLLAFLTSALVTMGAGLTVIRHTDIERDVRVREGFAIVTFGWFLAAAFGALPFVISGAIPSYTDAFFETMSGFTTTGASILTDIEALPRGVLFWRSFTHWLGGMGIILLSLAILPFLGIGGMQLFKAEVPGPVADKLAPRVTQTAKILWAVYIVLSGLQTTLLMLGGMDLFDALCHTFGTMATGGFSTRNASIAAFPSPYIQWVIIVFMFLAGVNFALHYRVLQRGLNSYRYDREFGVYTTFIVVASLLIFAFAMAQEGQFNEKAVRDVVFQVVSIQTTTGYVTVDYEKWPFAAQMVLFLLMFVGGSAGSTGGGMKVLRIYLLIKFVFAELARLIHPHAIVPVRMRGQTIPREVMTNVLGFAVLYIVIFFLGSLLVAAAGYDMPTSFGAVIATLSNVGPGLGDVGAVDNYSAFHPAVKWLLAFFMLLGRLELYTVMILFAPAYWRR
2E-66	234	22.7	3.9E-66	232.9	15.7	1.3	1	A0LYD0_GRAFK	Trk system potassium uptake protein	trkH GFO_0390	Gramella forsetii (strain KT0803)	498	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Gramella, Gramella forsetii, Gramella forsetii (strain KT0803)	411154	>tr|A0LYD0|A0LYD0_GRAFK Trk system potassium uptake protein OS=Gramella forsetii (strain KT0803) GN=trkH PE=4 SV=1MPRLNYKIILHVMGLLLLCNGGFMLLATLVSWFYRDGVTLEISTAALITLFIGTLLMFTTRGHSKEVKKREGYIIVTFGWIFMALSGSLPYLISESIPGFTNAFFETMSGYTTTGASILNDIEAIPKGILFWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFTAESPGPSADKLKPRITDTAKRLWLIYVSYTVAETILLWAAGMTFFDAINHAFSTLSTGGFSTKNASLAYWNDNPLIQYIIILFMLLAGSNFVLSYFAFKGRISKVLHDDEFKWYIYFIAGFTAISALIVYFQADVSISSIDHPMVWGAGESAFRHSLFQVLTVITTTGFVSADYTMWTPFLTILYFGLFFLGGSAGSTAGGVKVVRMHIIMIKNGIIEFKRTLHPNAILPVRFNGKSISKEIVFNILGFFILYMLSFIIGAVVLASLGLDFETAIGGAASSLGNIGPAFGGLSPVNNFDMLPDFGKWWTAFLMLIGRLELFTVLIILTPFFWRNR
2.2E-66	234	29.2	3E-66	233.3	20.3	1	1	K9SRI6_9SYNE	Potassium uptake protein, TrkH family	Syn7502_00216	Synechococcus sp. PCC 7502	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. PCC 7502	1173263	>tr|K9SRI6|K9SRI6_9SYNE Potassium uptake protein, TrkH family OS=Synechococcus sp. PCC 7502 GN=Syn7502_00216 PE=4 SV=1MTPARTICLGFVAVILAGAILLMLPISTSDSNWGNFITALFMSTSAVCVTGLAVVDPGTFYNFTGQAVLLLLCQIGGLGYMTATTFLLLLIGRKFSLREKVTLQQSLDISGIRSGVPLVKSIIVTTILLEVIGVFLMTPEFEKSFDLGRSLWCATFHSVSAFNNAGFSLFPNNLINYVHSPIINFTVTGLIILGGIGYQVILEVYLWLRMKIRRSQDRFSFSLNFKVATSTTVVLLLLGTLGILLTELNNPKTIGEFSATEKLMVAWFQSVTARTAGFNTIDYSGMTLAGLFVTIILMFIGASPSGTGGGIKTTTLRVLTNCTHAALQGEDDVHLYNRQISSVLILKAVGVIIGSMLTVMVSTTLLLVTEPKIDFVKILFESVSAFGTVGLSTGITAQVSALGQIVLILTMYTGRVGVLLLIGAIFGDSRRKLVKYPEETLLVG
2.6E-66	234	20	4.6E-66	232.7	13.8	1.3	1	Q1MQ98_LAWIP	Trk system potassium uptake protein	trkH LI0775	Lawsonia intracellularis (strain PHE/MN1-00)	488	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Lawsonia, Lawsonia intracellularis, Lawsonia intracellularis (strain PHE/MN1-00)	363253	>tr|Q1MQ98|Q1MQ98_LAWIP Trk system potassium uptake protein OS=Lawsonia intracellularis (strain PHE/MN1-00) GN=trkH PE=3 SV=1MQLRSVFFIIGVLLICIGTSIIFPLLTSIYYNDGVAKDLALSLSVVIISGFLLAFICHQNNPIILSNQEGFAVVGLCWIIASIAGSLPYVYIGIPFTDAVFETASGFTTTGATILTDIEAIPKSILLWRSLTHWLGGMGIILLSLAVLPLLGVGGMQLYKAEVPGPSPDKLTPHMQDTAMLLWKVYGIMTLFQIILLYLAGMDLFDAINQTFSTVSTGGFSTKNNSIAAFPTPVIQWIIILFMFASGINFTLHYKLLLGLLPHYTHDTEFNLYTLLLIIGAITIGVLLIFYHIYPSNTLSQIEQIVRASVFQLVSICTTTGFITEDYSKWPQLAQGILLFFMFMGACAGSTAGGLKTMRIIVIAKVAYQEIFRLLHPHSIRFAKLGDKTIQKDVLSGIIGFLILYLFILLINTLALMALNYDLITSFSATLTCLSNVGPGLGSVGPVDNFHHLDNIAKWFLIFCMLLGRLEIYAILILFIPEFWKALK

2.6E-66	234	15.5	1.1E-64	228.2	10.8	2	1	D9SIC1_GALCS	Trk system potassium uptake protein	Galf_0133	Gallionella capsiferriformans (strain ES-2) (Gallionella ferruginea capsiferriformans (strain ES-2))	486	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Gallionellales, Gallionellaceae, Gallionella, Gallionella capsiferriformans, Gallionella capsiferriformans (strain ES-2) (Gallionella ferruginea capsiferriformans (strain ES-2))	395494	>tr|D9SIC1|D9SIC1_GALCS Trk system potassium uptake protein OS=Gallionella capsiferriformans (strain ES-2) GN=Galf_0133 PE=3 SV=1MQRTLTVIHALGLMLAVFSFAYLMPLLTALLYGHEEVFQDFLLAMIWTLATGVLMWMLTRRYKGELSIRHGYLLVVAMWTAMPAVATLPLLLLPELSFTDAYFETMSGLTTTGATVLVGLDTLPPALNIWRHELNWLGGMGIIVLAVAILPLLGIGGRQLFKAETPGPMKDSALTPRITETARNLWLVYLGITIACIASLKLAGMNWLDAVCHSFSAMGLGGFSTHDASVGYFNSPLIEFVLMVFMLIAVMNFAVHFLALRERTLSVYRTDPEAIPTLILILGSCVGIAFCLWIWEIYPTYWIALRHASFNLISIATSSGYASVDYAQWPIFAPLWMMFLTATVASSGSTGGGIKMIRTLVLLKQAGREFVKLLHPAAINPMKIGGQVIPNGVVFSVLGFIFLYFMSIMTLTFALLLSGMDFISAFTAILASINNCGPGLGSVGPASNYAGLTDFQTWVCTAAMLIGRLEIFTVLILFTPHFWRR
2.6E-66	234	31.9	2.9E-64	226.8	22.2	2.1	1	C9A6R0_ENTCA	TrkH family potassium uptake protein	ECBG_00440	Enterococcus casseliflavus EC20	456	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus casseliflavus (Enterococcus flavescens), Enterococcus casseliflavus EC20	565655	>tr|C9A6R0|C9A6R0_ENTCA TrkH family potassium uptake protein OS=Enterococcus casseliflavus EC20 GN=ECBG_00440 PE=4 SV=2MKKRNRLKKKLASQRFLIPQIVTLVFVLLILAGTGLLMLPAVTQSGEGTNFLDALFTATSAVCVTGLSTLTVADHYNLWGQGILLMLIEIGGIGFMSIPVFFYILARKRVHLSTRMILRESLNLDRMSGEIHLAWYLIRIAFLIQVSGIILLAFAFVPRFGWEQGLWYSVFHAISAFCNAGFDLFGNSMVGFQNDPFVLGVISFLIIAGGLGFLVWFDLLHTASKKRSLHSRLAWIAMIVLVVFGTAGFFLTEANSQLITGDSVIERFFQYLFLAVTPRTAGFFSIDYGQMSQAGLMLTMILMYIGGTSGSTAGGLKTTTFAVLIIKIRSLLKGRSRAEVFGRTIKESAVSRAFTLFFLTLTLCFVAIFLLSITESMPQTPNFGLPTIAFEVFSAFGTVGLTMGLTPYLSVFGKLLIIFLMFIGRVGIMTVAFSLMKKANKQEAGYKYPDETVMIG
2.6E-66	234	31.9	2.9E-64	226.8	22.2	2.1	1	K7WNK2_9NOST	Potassium uptake protein TrkH	trkH ANA_C20680	Anabaena sp. 90	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena sp. 90	46234	>tr|K7WNK2|K7WNK2_9NOST Potassium uptake protein TrkH OS=Anabaena sp. 90 GN=trkH PE=4 SV=1MTVARTICLGFVAVILLGAILLTMPFSTGNGNWNDPIVALFTSTSAVCVTGLAVVDTGTDFSFLGQLFIALLAQIGGLGYMTTTTFLMLLIGRKFDLRQKVAIQQALDRPGMSGSSQIIRSIIATTLLFELTGVFLLMIVFVPEKGWQEGTWLAIFHSVSAWNNAGFSLFKDNLIGYQSSPLVIITIGCLIIFGGIGYQVILDMYLWLRDRIVKKTSCLVFSLDFKVATSTTLILLVLGTIAILFVEIRNDSVFGQLSLSDKILAAWFQSVSTRTAGFNSIDIGKMTNAGLFIMIALMFIGASPGGTGGGIKTTTLRVLTSCTNAILQGKEEVLLYNRKIAISLILKAVGVVFGSLATVIVATVLISITDPKLAFIQILFEVVSAFGTVGLSTGITGTVSIAAKLILILTMYIGRVGVLLLMSSILGDPRPSRIHYPEENLLVG
3E-66	233	19.8	5E-66	232.6	13.8	1.2	1	G0L1Z0_ZOBGA	Trk system potassium uptake protein trkH	trkH zobellia_758	Zobellia galactanivorans (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Zobellia, Zobellia galactanivorans (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij)	63186	>tr|G0L1Z0|G0L1Z0_ZOBGA Trk system potassium uptake protein trkH OS=Zobellia galactanivorans (strain DSM 12802 / CIP 106680 / NCIMB 13871 / Dsij) GN=trkH PE=4 SV=1MGLLLLCNGGFMLLATLVSGIYDDGATLSIALAAITTMFIGIFAMFYTKGHKKEVKRKEGYIIVTFGWLVMSFSGMLPYLFSGAIPSVTNAFFETVSGYTTTGASILDDIEVLPKGLLFWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPSADKLHPRITDTAKRLWLIYVGYTLAETLLLKLAGMSFFDAINHSLATLSTGGFSTKNLSVAYWNDQPMIQYIIIVFMFLAGSNFVLSYFAFKGKVQRVLRDEEFRYYGGFVVIFTLVSALVVYFHAEVPLTEYHPMVLGQAESAFRHTLFQVISVITTTGFVSADFTSWTPFMTVFFFGLMFLGGSAGSTSGGIKVMRHILIIKNGLLEFKRTLHPNAIIPVRYNNKTVKEKIVYNIIAFFVLYMLLFIIGALVLGAMGIDFVTAIGGSASSLGNVGPAFGGLYPLSNFNGLPDAGKWWCGFLMLAGRLELFTVLILLTPYFWKRT
3.3E-66	233	28.5	1.9E-63	224.1	19.7	2.2	1	E4TIZ4_CALNY	Potassium uptake protein, TrkH family	Calni_1218	Calditerrivibrio nitroreducens (strain DSM 19672 / NBRC 101217 / Yu37-1)	483	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Calditerrivibrio, Calditerrivibrio nitroreducens, Calditerrivibrio nitroreducens (strain DSM 19672 / NBRC 101217 / Yu37-1)	768670	>tr|E4TIZ4|E4TIZ4_CALNY Potassium uptake protein, TrkH family OS=Calditerrivibrio nitroreducens (strain DSM 19672 / NBRC 101217 / Yu37-1) GN=Calni_1218 PE=4 SV=1MRFKFIFKVFGYLVLIVSLFMIFPIIVAYIYKEVFVAKVFFFTMIFNLCVSFILIFLFRKVKKNYLSSADGMFLVSIGWIVISLVSALPYTLSGVVNSFTDAFFESISGYTTTGATIFTAVEHLPKSILFWRSLTHWLGGMGIVVLTVAILPLLGIGGMQLIKAEAPGPSVDKISPRITTTAKYLWFIYIALTLAEVLLLMVGGMNFFDALNHSFATLATGGFSVKNESFLSYKNPYYEWVVAIFMILAGMNFTLHYKLFLGRFEILKKDSEWKFYVALIGLYTFIIGVDLYNSLGLSFHDSIRSAFFQVATIITTTGFASADYEKWSAFSQVLLFALMFVGGCSGSTGGGIKVIRVLTLLKQAINEMKLVVHPRGVFVLKINGESVRKNTVYAISGFFFLYMLTNLFIIIISISGVDLTTAVTASLACVGNIGPGFGAVGPMDNYSSFSDFTKWTLSFGMLLGRLEIYTFLIIITPYYWKK
4.1E-66	233	15.8	1.3E-64	227.9	10.9	2	1	I0I4C3_CALAS	Trk system potassium uptake protein TrkH	trkH CLDAP_20710	Caldilinea aerophila (strain DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1)	458	cellular organisms, Bacteria, Chloroflexi, Caldilineae, Caldilineales, Caldilineaceae, Caldilinea, Caldilinea aerophila, Caldilinea aerophila (strain DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1)	926550	>tr|I0I4C3|I0I4C3_CALAS Trk system potassium uptake protein TrkH OS=Caldilinea aerophila (strain DSM 14535 / JCM 11387 / NBRC 104270 / STL-6-O1) GN=trkH PE=4 SV=1MTATPWSFYYGEKDWLYLLLSAGAAAVTGVCLLCFTDLSEEIRIREGFAVVSFAWLLFSFFGALPFWLSGAVPSFTDAMFETLSGFTTTGASILTDIEALPHGLLFWRSMTHWIGGMGIIVLSLAVLPIIGIGGMQLYRAEVAGPTTDKLAPRITQTAKILWGVYAALTFLQTALLMFGGMSLFDALCTAFGTIASGGFSPRNTSISYYNSAFINWVTVFFMMMAGINFALHYRFATGNLRTYWRDREFHVFIASLTVASLLVLWNVWNSYQDKWRALEDSIFSVVSLHTSTGFALADYEAWPPGAQFVLLVVMIIGGSAGSTSGGLKVVRVYLLLKYIAALFTRLLHPQALVPTRIHGIAVSREIMGDVLGYIGIYFIAIIVGSYCLTATGVDWVSGLSAVVSCLGGVGPGMEAVGPFDNYAWLSPFAKWVLMACMLLGRLEFFSLLILFSPAYWRR
4.6E-66	233	13	9.2E-33	122.9	0.8	2.1	2	D1B6Q7_THEAS	Cation transporter	Taci_1468	Thermanaerovibrio acidaminovorans (strain ATCC 49978 / DSM 6589 / Su883) (Selenomonas acidaminovorans)	483	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Thermanaerovibrio, Thermanaerovibrio acidaminovorans, Thermanaerovibrio acidaminovorans (strain ATCC 49978 / DSM 6589 / Su883) (Selenomonas acidaminovorans)	525903	>tr|D1B6Q7|D1B6Q7_THEAS Cation transporter OS=Thermanaerovibrio acidaminovorans (strain ATCC 49978 / DSM 6589 / Su883) GN=Taci_1468 PE=4 SV=1MRPRLVARVLSLMGGIVSLSMLWPLLWALYDGSRDRWPFVASIGIGLGVSGVLYLWGRGCQYRELGIKDGFAVVSLSWILASGIGALPFLLSGTVPTFADAFFEAISGFTTTGASVISDIEANPRGILFWRNLTHWLGGMGIIVLSLAILPFLGVGGMQLYKAEVPGPIKEKMTPRIQQTALYLWGVYVLLSGLQLLFLMAGGMGLFEALTHTFGTMATGGFSPLNKSIGQYDSAYFDWVITVFMFLAGVNFALHYRILTGRWSVMLRDEEFKLYGGITLVSALVVSGVLLLRGVYGSPLDALRFGTFQVVSIMTTTGYVTADFDLWPSSIRFLLLLLMFVGGCAGSTGGGMKNLRILVLARHVRAGLYSILHPNAVVHVRVGGKVVGKDVIASVTSFFVLYMGLFMLGTLAMAAMDLDIITAMSSVAATLGNIGPGLGGVGPMRNYAEIPQLGKWVLSLLMLMGRLELYTVMLLFFPETWRR
4.9E-66	233	30.8	8.1E-66	231.9	21.3	1.3	1	R5QCW2_9FIRM	Uncharacterized protein	BN550_01781	Coprobacillus sp. CAG:235	441	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:235	1262854	>tr|R5QCW2|R5QCW2_9FIRM Uncharacterized protein OS=Coprobacillus sp. CAG:235 GN=BN550_01781 PE=4 SV=1MIKRRTNVEIIALGFAIVILVGTFLLLLPVSSDHTDFLDALFTATSATCVTGLVVYDTATHWTLFGQIVILLLIQIGGLGFITIGVFLATYLKKKISLRQRGLIEESVNSLKLAGGVKLVKHIIKGTFLFEGIGAIILSLVFIEDFGLLKGVYLGIFHAISAFCNAGFDLLGTIEPYGSLTPYASNIIVNITIMALIIIGGLGFIVWQDIYEKGFKFKKYLLQTKIVLIMTIILIVGGAVLFYLFECQNSLSSLSQEEMILASFFQSVTCRTAGFNTVDVSHLKPSTSLLMMFLMFVGGSPGSTAGGIKTTTFAVLTIFVYATMTNKSEANAFNRRFDSKTIKKACSVFLINLIFIFISAIALFDMQPQLPMQDVFFEIFSALGTVGISTGITRQLTMLSKIVIILLMYCGRVGSLTLALSLSRKKKISNCKNPVEKIAIG
6E-66	232	0.3	6.9E-62	218.9	0	2.1	2	Q7S450_NEUCR	Potassium transporter	NCU02456	Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987)	656	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Sordariaceae, Neurospora, Neurospora crassa, Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987)	367110	>tr|Q7S450|Q7S450_NEUCR Potassium transporter OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A / CBS 708.71 / DSM 1257 / FGSC 987) GN=NCU02456 PE=4 SV=2MESTHSRLRTMLPPINFISIHYAYFIIVCLFASLIFWGSSNPAHSISYADSLFLVVSAMTETGLNTVNLSEMTTWQQILLFLLIFGSAIWVSIWTVVARKHAFEKRFEDVVRAERLRRANRSSSVNLSRLRFMRFQGRRSLNVISPPAMTETLDLVSISTPSPGKSNNPILDVHAHHTHYTGTAKLSDKNTPQRSSTPAHIAFAETPHSSPENHPPTGFSTAAQHGYLVSQNNTARRIAPQRQEHLETEGDAKGDFSVRSLFARAAGRNAQFHGLSREERRVLGGCEYRALRVLAVIVPLYFFLWQFIGCMALGAWINRHRPEPPLRNGVNPWWLGIFNGASAFNNSGMSLLDLNMIPFQDSYYVLVTMGLLILAGNTAYPIFLRLILWGILQILDVATMETELRELKETLQFILDYPRRVYTNLFPQRQTWWLVFMVILVNSVDWVAFELLNMGNPAVESLPKGSRVVDGLFQAVAVRSGGFYVIAIPSLYIGVQVLYTIMMYISCFPVVITLRHTNVYEERSLGIYSGDPISPDIESGLHGRSGVTSLARHISHSGTSAIGQAFRHTLTWHGVGVRTPLTNSAADSRISFISVSYVDLIHSTKDCPHNDLPNSNKSRDNWRTICGGWRLRSLSSLRLRQATFWPIRPLSACST

6E-66	232	21.3	2.5E-65	230.3	14.8	1.7	1	D5E8M7_METMS	Potassium uptake protein, TrkH family	Mmah_2022	Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP)	478	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanohalophilus, Methanohalophilus mahii, Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP)	547558	>tr|D5E8M7|D5E8M7_METMS Potassium uptake protein, TrkH family OS=Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP) GN=Mmah_2022 PE=4 SV=1MKFKIVIGVLGTLLWLLGLLMLIPLFVGMYYGESPQTFAIAFTITTMAGTIFAFRIEPSKEDWDLKEGFMIVAFGWLAAAMFGAIPFILEGMTPINAFFESMSGFTTTGATVMVDIESHSRGLLFWRSMTQWLGGMGIIMLFIAILPKLGIAGRQMFRAEVPGPQEDKLRPRIRETAKILWMVYVAISVVECVALYLAGLNLYDAVTHTFTTMACGGFSPYADSIAAFNSPVVEGIICFFMFVAGANFALHYRMFYVDKNSLVRDDEFKFYTLIVAIATLSLTLLLFKDHIYGLDTSFRYSVFQVLSILTTTGYATVDFNQWADSGRMLLFIVMFFGGCAGSTGGGIKIVRTLLLLRYANRELFKAIHPKAVRIIRFNGKAVPDDVMQSIISFVIIYFILFFISSGLLSMMGMDVFSSLSASIATLGNIGPAFNLFGPMANYNLLPFLGKLLLVLNMWIGRLEVFTVMVMLTSAFWKK	
6.4E-66	232	13.2	8.4E-38	139.5	0.2	2.1	2	D5CQE5_SIDLE	Trk system potassium uptake protein	Slit_2941	Sideroxydans lithotrophicus (strain ES-1)	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Gallionellales, Gallionellaceae, Sideroxydans, Sideroxydans lithotrophicus, Sideroxydans lithotrophicus (strain ES-1)	580332	>tr|D5CQE5|D5CQE5_SIDLE Trk system potassium uptake protein OS=Sideroxydans lithotrophicus (strain ES-1) GN=Slit_2941 PE=3 SV=1MGRALTVLNALGLMLVVFSFSYVLPILTSLAYDDGTEIDFLLAMLWTAGTGVLLWLLTRRYKGELSIRHGYLLVVAMWTAMPAVATFPLLLVINGLPFTQAYFETMSGITTTGATVLSGLDNMPPAINLWRHELNWLGGMGIIVLAVAVLPLLGIGGRQLFKAETPGPMKDSALTPRITETARNLWLVYAGITLACILSLKLAGMNWLDAICHAFAAMGLGGFSTHDASVGYFNSPAIEFVLIIFMLLAAMNFATHFLAWRGRSLKIYLHDAEAVATVSLILGSCLGVGLFLWWQGTYPNFWTALRYASFNLVSMATDCGFANADFNKWPTFAPMWMLFLSCVAVSSGSTGGGIKMIRTLVLVKQAGREFLLLLHPAAVNPMKIGGHVVANHIVFAVLGFIFLYFVSIATLTFALLISGLDFVSSFSAVIACINNAGPGLGIVGPASTYAVLTNFQLWVCTLAMLIGRLEIFTILILFTPAFWRR	
6.8E-66	232	33	8.9E-66	231.8	22.9	1	1	D9RXT2_THEOJ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Toce_1401	Thermosediminibacter oceani (strain ATCC BAA-1034 / DSM 16646 / JW/IW-1228P)	439	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family III. Incertae Sedis, Thermosediminibacter, Thermosediminibacter oceani, Thermosediminibacter oceani (strain ATCC BAA-1034 / DSM 16646 / JW/IW-1228P)	555079	>tr|D9RXT2|D9RXT2_THEOJ Potassium uptake protein, TrkH family OS=Thermosediminibacter oceani (strain ATCC BAA-1034 / DSM 16646 / JW/IW-1228P) GN=Toce_1401 PE=4 SV=1MKLRPAQILVLGFATVILVGTVLLSLPVASRNGETVGFLNALFTATSAVCVTGLVVVDTYTQYSLFGQIVIMLLIQIGGLGFMTMTTLIFLILGKRITLRRERLVMQEALNQLTLAGVVKLTRYIIFTTLIFEAVGALLLSLRFSRIYGVPRGIYYGIFHGVSAFNNAGFDLIGDFKSLTPFVEDPLVNIVIMALIIFGGLGFSVIYDVFTTRNIYKLSLHSKVVLTMTGLLLVVGFLVIYALEHTNPKTLGSLSPAGKILAAAFQSVTPRTAGFNTISLSDMSLAAKYFTIFLMFIGASPGSTGGGVKTSTFALVLMMIYSVITSKENVEIYKRRIPMDNLFKAVVIMLIALLLVLTVSFLLTITERADFMSILFETVSAFGTVGLTLGITPHLSDAGKVLIILTMFSGRVGPLTIALALASKKKTAIMKYPEERILVG	
7.3E-66	232	25.7	2.3E-65	230.4	17.8	1.6	1	R7LFR5_9BACT	Trk system K+ uptake protein TrkH	BN805_01474	Prevotella sp. CAG:891	486	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:891	1262937	>tr|R7LFR5|R7LFR5_9BACT Trk system K+ uptake protein TrkH OS=Prevotella sp. CAG:891 GN=BN805_01474 PE=4 SV=1MLHIPIIYKVLGTLLYLLALLMSICFGMSYWFNEGSTHLAFGIPMLIAFVAGALLQYFGRHAENCMGRRDGFLIVSLTWIVFSVIGMLPLIISGCQPRVSAAFFETMSGFTTTGATALDNIDSLPYSILTWRSMTHWIGGMGIVFFTIAVLPNMGDGGTKLFSAESTGLKIGKLHPRISTTARWMWSLYLLLTLTCTAAYYWGGMSLFDAVNHGLSTIGTGGFSTHQDSIAFFKSNRIQWIATLFMFIASINCTLLYLFFVKRRFKDVWHDGELRCFLVIFFTAALSITGILYFVEGIDIMSSLRIAFFNTVSLQSTTGFSDEDFMIWHPTIWLILSFISIIGACAGSTSGGLKCIRVLMVWKLTKTEFRQMLHPHAVLPVRINNTQITAQMGRTVVFAFFVVYFILIMVACFFMVAMGHTLLDSFGLAISSFSNIGPSIGHQVGPLGSWSCLNDATLWINSFLMLAGRLEIFSLLLPFTPAFWRDE	
7.5E-66	232	8.1	1.1E-65	231.5	5.6	1.1	1	S6D870_9EURY	TRK potassium uptake system protein (EC 4.1.2.13)	trkH2 HLRTI_001867 HTIA_1128	Halorhabdus tiamatea SARL4B	548	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halorhabdus, Halorhabdus tiamatea, Halorhabdus tiamatea SARL4B	1033806	>tr|S6D870|S6D870_9EURY TRK potassium uptake system protein OS=Halorhabdus tiamatea SARL4B GN=trkH2 PE=4 SV=1MSDSPASFRSRIDRLSAPTAAKTVLRDIGALQVLIGLLMLIPFVVSLLYGEWYSAVSFLIGSGVTALVGGVTYKLCEDAPEPKRHHAMIVAALGWLVTAAFGAVPFIVAAYITPEGVLNSFIPAGADYARSSLLNFRDPLHAFFESVSGYTTTGLTMSVHEPSIGHGFLWYRSQMQWIGGAGMIVLSLAILRQPHGTAGISLYRSEGRDEKLRPSIAGTAKAIWKIYLGVTALLAVYLAAATFLVQPGYGIENTIFDALNHAMTGQSTGGFSTLDNSIAGYGSYAMELVHIPAMITGAIAIPVYYGAISERDIREFTRDPQVRLLFGMFVVGVIGLTAFLARWVGVPYHGDPIGYVGRVATSKAFRDGLFQFISAQSTTGWQTSAIGDWVPGGVMFIVFGAMLLGGSAGATVGGIKILRGYILARGIGWEVSRSFLPEHAIEDLRIGDRIFTAEEANDEIRAAATLAVAYLVVLGLSLFVLLAVLPSEFTLADAIFEVATAQGTVGLSSGITGPGMPAVAAEILFIVQMWMGRLEIIPILVLISSLFRR	
8.3E-66	232	21.4	3.1E-65	230	14.8	1.7	1	D5BHB1_ZUNPS	Trk system potassium uptake protein	ZPR_0938	Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87)	486	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Zunongwangia, Zunongwangia profunda, Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87)	655815	>tr|D5BHB1|D5BHB1_ZUNPS TRK system potassium uptake protein OS=Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87) GN=ZPR_0938 PE=4 SV=1MGLLLICNGGFMLLSVLISFIYKDGVTLGMSAAALVTLLIGTLLMFTTRGHRKELKVREGYIIVSFGWIFMALSGSLPYVMTKAIPDFTNAFFETMSGYTTTGASILNDIESIPKGVLFWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAESPGPSADKLKPRITDTAKRLWLIYVSYTAAETLLLMLAGMDFFDAINHAFSTLSTGGFSTKNASMAYWNDNPMIQYIIILFMFLAGSNFVMSYFAFKGRVQRVLQDDEFKWYFYFVAAFTIISSLIVYFQADVSLSSIDHPMIWGEGESAFRHSLFQVLTVITTTGFVSADFTMWTPFLTIFYFGMFFLGGCAGSTAGGVKVMRHIIMIRNGLIEFKRTLHPNAILPVRFNKKSINSGIVFNIQGFFILYMLSFIIGAVVLAALGLDFETAIGGAASSLGNIGPAFGALSPVNNFDLLPDFGKWWCSFLMLIGRLELFTVLIILTPFFWRNR	
8.6E-66	232	19.5	4.4E-65	229.5	13.5	1.8	1	K4M9I2_9EURY	K+ transporter Trk	Mpsy_0704	Methanolobus psychrophilus R15	472	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanolobus, Methanolobus psychrophilus, Methanolobus psychrophilus R15	1094980	>tr|K4M9I2|K4M9I2_9EURY K+ transporter Trk OS=Methanolobus psychrophilus R15 GN=Mpsy_0704 PE=4 SV=1MGVLGSILWLLAGFMLIPLLVAVYYREPLHTFVIPLLLILIFAVLLKSFVKKESGEWNLKEGFLIVASAWLLAAVFYSIPYMLEGVPPINALFESMSGVTATGATALTEIESHSKSLLFLRSMTQWLGGMGIIMLFVAILPKLGVAGRQIFRAEVPVLQEDKLHPRIRGTAKNLWFIYILLSLIEFIVLSIAGLSPYDAITHTFTSISCSGFSPYSDSIAAFNDPLVEIIIMCFMFLGGANFALHYRTIFSDRKSLINDQEFRFYFFIIATATLLLAFNLFRTEIYSLTDAFRYSSFHVISILTTTGYATADFNLWPDSSRFILFLLMFIGGCAGSTSGGLKVVRLLLLLKHTEKVLFRTIHPKAVTPIRLNDKIVPEDVMHSIVSFMVIYIMIFFTSSALLSFMGMDFVTALSASIATLGNVGPGLGLVGPMESFDAIPDMGKLILTLANMWIGRLEVFTVIVLLTPAFWKK	
8.8E-66	232	27.9	1.4E-65	231.2	19.3	1.3	1	W8TJ23_EUBAC	Ktr system potassium uptake protein B	ktrB EAL2_c08870	Eubacterium acidaminophilum DSM 3953	451	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium acidaminophilum, Eubacterium acidaminophilum DSM 3953	1286171	>tr|W8TJ23|W8TJ23_EUBAC Ktr system potassium uptake protein B OS=Eubacterium acidaminophilum DSM 3953 GN=ktrB PE=4 SV=1MASIIKKREKKAKALSPAQIVVVGFAITILLGAMLLNFPFASKSGKSIGFVNALFTATSATCVTGLVVVDTGTYWTNFGKVVIIGLIQVGGLGFMSLATLFSMLLGKKISLRERLIIQESLNQNDLAGLIRLTRHILFGTFIIEGAGALLASVFIPENGIAKGLAYGAFHSISAFCNAGFDLTGNGRSLVPYVDNVTVNLTICSLVILIGGLGFTVIADVLQKGKAQRLALHSKIVLTMTSILLAAGFVLFFVFESGNPSTLGGLSAKGRVLAALFQSVSPRTAGFNTIDLAAMTDSSKLLTIILMFIGGSPASTAGGIKTSTFALLVIAIITLIKGREHVEIYRRNISYSAVTKSLAVFGLAMTLVVTVTMILNITEKFDFLDILFEAVSAFGTVGLTLGITSGLTVIGKLVLIFTMFAGRVGALTILIALASREKKTLIKYPEGKVIVG	

1.1E-65	232	19.4	1.7E-65	230.9	13.5	1.2	1	F0RB77_CELLC	Cation transporter	Celly_0644	Cellulophaga lytica (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy I20)	496	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Cellulophaga, Cellulophaga lytica (Cytophaga lytica), Cellulophaga lytica (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy I20)	867900	>tr|F0RB77|F0RB77_CELLC Cation transporter OS=Cellulophaga lytica (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy I20) GN=Celly_0644 PE=4 SV=1MTLNYKIIVHIMGLLLLCNGGFMGLSAGISAIYKDGATLEIAMAALVTLAAGAMAMLSTKGHKKEVKRKEGYLIVTFGWIVMSISGVLPYLFTDSIPSFTNAFFETVSGYTTTGATILNDIEILPEGVLFWRSLTHWIGGMGIIVLAIAILPILGIGGMQLFSAESPGPSADKLHPRITDTAKRLWYIYVGYTVAETILLQLAGMSFFDAINHSLATLSTGGFSTKNASLAYWNNDPLIQYIVILFMFLAGSNFVLSYFAFKGKIQKMLKDEEFKFYTGFVVFFTLIAAVTVYLKAEVPVSDYHPMVLGEAESAFRHTLFQIISVITTTGFVTADFTSWTPFLTVFFFGLMFLGGCAGSTAGGIKVMRHLLIIKNGLLEFKRTLHVNAIIPVRYNNKMVPEKIVYNIIAFLVLYMLLFIIGALVLSFLGLDFISAIGGAATSLGNVGPGLGSLNPLANFDSLPALGKWWTAFLMLAGRLELFTVLIILTPYFWKRI	
1.1E-65	232	28.1	9.2E-42	152.6	4.1	2	2	A6VZP5_MARMS	Trk system potassium uptake protein	Mmwyl1_3013	Marinomonas sp. (strain MWYL1)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Marinomonas, Marinomonas sp. (strain MWYL1)	400668	>tr|A6VZP5|A6VZP5_MARMS Trk system potassium uptake protein OS=Marinomonas sp. (strain MWYL1) GN=Mmwyl1_3013 PE=3 SV=1MIRPLLIMRLLTMPCLWMSVVQFVFGELSFMLFKDDVGRAFATPALITFTISLVLLLGFKKYPLPSVNTREAMLFATLTWLAVGVLGAIPIISVTHISFTDGVFESISALTTTGATVLSGLDEMPPTFLMYRQFLQWMGGLGVVIFVVAILPMLNIGGMRLLKAETPGPIKDDKLSPRVSSTTHYLWMVYLAITGLCALSYYFAGMSAFDAIGHSFTTVSTGGFSTHDASMGYFKSPLILWICNLFMVLGAVNFALHYRIYIARSIRLYWKDEETRGFLKIITFVALLLALFLFQTGSEDGLWVSITQSFFHVISFITSTGFAATDFGAWPAVTSIVLIFVGYIGGCAGSTAGGNKVIRNIISLKSILELKRLVHPNGVFAMKFQGRTISADVRHSVMGFMCLAAMVTVFFTILLMMTGMSFMASLSATAACLNVLGPGFAELGSNFSPLSDTGTWLMSFAMILGRLEYFTVLVLFFPVMWRH	
1.2E-65	231	23.3	1.8E-65	230.8	16.1	1.2	1	G2DLL0_9NEIS	Trk system potassium uptake protein	l11_12830	Neisseria weaveri LMG 5135	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Neisseria, Neisseria weaveri, Neisseria weaveri LMG 5135	1051985	>tr|G2DLL0|G2DLL0_9NEIS Trk system potassium uptake protein OS=Neisseria weaveri LMG 5135 GN=l11_12830 PE=3 SV=1MYKVIPIIHVLSKLGVLFSFMLIVPTFVSYLFLDDAFSAFGQTALITITSSSLVWLLTRKYNRELRSRDGFTLVFMLWIGFAAIAAMPFYLYFPNISYTDAFFEAMSGLTTTGATVMTSLDTLAPSVNFWRHMLNWLGGMGIIVLAVAILPMLGIGGTQLFKAEIPGIDKDSKMAPRISQVAKKLWLFYFICTVLIGLALHWAGMSWFDAVCHAMSAFSLGGFSTHDNSIAYFNSVAVEVVLMIATILGAISFASHFTVLKARSVKPYWRDEECRIMLVTLFASIVAASLYLWHKQYYTSLYDSFRFVSFNFVSIGLANGYANADFAKWPLLTSLWMFFLANVLASSGSVGGGIKNVRAIVLFKFSLREMLLLLHPKAVRTVKVNGRSIPERMALTVLAFIFVYFFTVVLFTFLMMATGLDFVSALTAVIACITNAGPGLGAVGPAGNYAGLNDFQKWLCTGTMLLGRLEIFTVFILFTPAYWKK	
1.3E-65	231	32.2	1.8E-65	230.8	22.3	1.1	1	E5BEA1_9FUSO	Potassium uptake protein, TrkH family	FSBG_00874	Fusobacterium gonidiaformans 3-1-5R	444	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Fusobacterium, Fusobacterium gonidiaformans, Fusobacterium gonidiaformans 3-1-5R	469605	>tr|E5BEA1|E5BEA1_9FUSO Potassium uptake protein, TrkH family OS=Fusobacterium gonidiaformans 3-1-5R GN=FSBG_00874 PE=4 SV=1MKRDKKQMSPSRKLILGFLLVIIVGVFLLMLPFSLKEGKSLSPLEALFTVVSAVCVTGLSVVDVAEVFSPVGDAILIAFIQIGGLGVMTFSSIVFLLAGQKMTLYTRILLKEERNANSVGEILNFVRLMLLTVFIIESIGAVILMHEFRKIMPYEQAVYYGIFHSISAFCNAGFSLFSNNLENFRGNPVISLTISYLIILGGMGFAIINSFIMMIRKGVSRFTLTSKLAIQISMILTFGGAILFFLLEFSNSATLFPLPWSEKIIASIFQSVTLRTAGFNTIPLANLRSATVFMACIWMLIGASPGSTGGGIKTTTLGVILFYVIGIIRGKEHVEIFNRRLDWDVMNKALALLVVSLSYIALVILLLLVIEPFSMEKIVFEVVSAFGTVGLTMGITPYLTVTSKLIIIVTMFIGRLGPMTIALALGEKKKKARVQYPKEDILIG	
1.5E-65	231	15.7	2.6E-64	226.9	10.9	2.1	1	Q2LX96_SYNAS	Trk system potassium uptake protein	SYN_02617	Syntrophus aciditrophicus (strain SB)	495	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Syntrophus, Syntrophus aciditrophicus, Syntrophus aciditrophicus (strain SB)	56780	>tr|Q2LX96|Q2LX96_SYNAS Trk system potassium uptake protein OS=Syntrophus aciditrophicus (strain SB) GN=SYN_02617 PE=3 SV=1MKTGTVLHILGGLLLFLSAALLIPTPFSYYYQDGQIASFLWSALITALAGFLLRSLFVPEGDLGFRDGFAIVTLGWLGAAFFGALPFHFSGEFSGFLDCFFESMSGFTTTGSSVLEKVEVLAPSTHFWRTFIQWLGGMGIIVLSLAILPVLGIGGMQLFQAEVPGPTKDRLSPRIRDTARILWAVYLLLTLFETGLLMAGGLSAFDALCHSFATLATGGFSLYTPSIGKFNSLWVECVVAFFMFAAGVNFTLHYYVMQGRGSAYWKSDEFRFYLFLTLLATALLTVFNFAGKAYGSLGESLRYSLFQVCSIMTTTGFATADFDQWPYVSRFLLVCLMFFGGCAGSTAGGIKHVRVLLLWRHFRLQVFQLLHPKAVKAVKLDGTKVAPAVMQAVLGFFFLYIGVFASASMAVCAQGVDLITAVSAVATTLNNIGPGLGGVGPMANFGNLPDFSKLVLSVCMLVGRLELFTVMVLLFPSFWKETRKPLWFWQRKKLK	
1.7E-65	231	0.3	2.1E-65	230.5	0.2	1	1	G2YXQ6_BOTF4	Uncharacterized protein	BofuT4_P145730.1	Botryotinia fuckeliana (strain T4) (Noble rot fungus) (Botrytis cinerea)	382	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Sclerotiniaceae, Botrytis, Botryotinia fuckeliana (Noble rot fungus) (Botrytis cinerea), Botryotinia fuckeliana (strain T4) (Noble rot fungus) (Botrytis cinerea)	999810	>tr|G2YXQ6|G2YXQ6_BOTF4 Uncharacterized protein OS=Botryotinia fuckeliana (strain T4) GN=BofuT4_P145730.1 PE=4 SV=1MGLLILAGNTAYPLFLRLILYTLLKLLDTFPNVLSPFQHHKPTLLFILRYPRRVYTNLFPSRPTWWLLFMVITLNSIDWVAFELLNIGNSATQVIEPRYRVLDGLFQAIAVRSGGFYVISIPSLRIGLQFLYVIMMYISVYPVVITMRHSNVYEERSLGIYRGDVETDSHTSRWGRGMKRIRKSISGRDIGIPHTASSNSNITSTSPPDETTGTQFIHHQLRSQLSHDLWWLTLATFLIVCIESSSFEKDPITYSVFNVIFEVVSAYGCVGISTGLPDQDYSFSGGLRTASKVVLVAVMVRGRHRGLPRALDRAVRLPGWEGEGLGGEGGGEREEEEAVIGECGEGGKERDGGKGKERERSEEGRGLRKRRFSRGVGGTEEV	
1.9E-65	231	19.9	1.5E-64	227.8	13.8	1.8	1	Q5JGD2_THEKO	Trk-type pottasium transport system, membrane component	TK1182	Thermococcus kodakarensis (strain ATCC BAA-918 / JCM 12380 / KOD1) (Pyrococcus kodakaraensis (strain KOD1))	492	cellular organisms, Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae, Thermococcus, Thermococcus kodakarensis, Thermococcus kodakarensis (strain ATCC BAA-918 / JCM 12380 / KOD1) (Pyrococcus kodakaraensis (strain KOD1))	69014	>tr|Q5JGD2|Q5JGD2_THEKO Trk-type pottasium transport system, membrane component OS=Thermococcus kodakarensis (strain ATCC BAA-918 / JCM 12380 / KOD1) GN=TK1182 PE=4 SV=1MLDFRKHINVSDDFFVVRNLTGSILEGVGVAYLVPALLVWVYPEEIKYVPYFALPGMASILFGAWLSRHSSKIEDVNLRQAMVAAAFTWLLASLVSVVPFVKIAHMPLLDSYFECMSAWTGTGLTMMSNLQSYPKMLLFWRAWMQWLGGIGIVLVALTVLIRPGVAAARLYRAEARSERILPNLVNTAKVIFEIYLVLTLVGVYLYYINGMGLFDALTHSMTGLGTGGMSTHDESIGFFHSPAINAVTIFLMIMGAVNFTVHYRVFKDRSLKPFFADIQVRYMFFFLIPAVSLIAYGLVQVGDSLAQALQDAVFHAVSAISCTGFQISDLSKYPEVGKFLLAVLMVIGGGAGSTAGGIKLIRITLMYESLKWTIESAILPKGAVIKRKVGNYVFSEEDIQEVMSFTMTYVAFLLAGVLYTMLRVHANLADALFEVASAQGNVGLSVGITSPAMPADLKFVYILLMWIGRLEIFSTLVFIISVFFLLPRGLRR	
2.2E-65	231	26.8	1.9E-64	227.4	18.6	1.9	1	C4II90_CLOBU	Putative Trk system potassium uptake protein TrkH	CLP_2125	Clostridium butyricum E4 str. BoNT E BL5262	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	632245	>tr|C4II90|C4II90_CLOBU Putative Trk system potassium uptake protein TrkH OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_2125 PE=4 SV=1MNYKAVLSILGNVVKYMVALLFVPLLIALYYGEGDAKSFLLTIFIGAPIGFILSNIKAEKKAIYAKEGFLIVGFAWIISAIGALPFVISGAIPGFIDAFFETVSGFTTTGATILTAIEGLPKGILFWRSFTHWIGGMGFLIFMLALIPSLGSNSIHLLKAESPGPSPGKIVPKIKETAKILYLIYFALTLIEGILLMCAGMNLYDAVIHAMGTAGTGGFSNMNASIAAFNSPAIEWIITIFMLIFGINFALYFQILKGNFKGFFKNEELRYYLLLIILSAFILITVNIISLNGGDIILSVRQSAFQVSSIVTSTGFATVDFNFWPTLSKLIIVMLMFVGAMAGSTGGGIKTVRIVIMLKAIKREINKIIHPKRVNSVKIDGKTVDEDIIHGVFLFIGAYIIISLIAIFISFDNFDVVTTVTSVITTMSNIGPGLEVVGPAGNFAAFSPLSKLVLSFCMLAGRLEIYPMLIMFSPSIWRKNH	
2.2E-65	231	26.7	2.8E-65	230.1	18.5	1	1	R5QV48_9FIRM	TrkH family potassium uptake protein	BN521_01316	Coprobacillus sp. CAG:183	467	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:183	1262853	>tr|R5QV48|R5QV48_9FIRM TrkH family potassium uptake protein OS=Coprobacillus sp. CAG:183 GN=BN521_01316 PE=4 SV=1MKVSTLKMHHEHHPMRPTRQIAISFLAVILIGSVLLMLPICNNTTPTAYLNNLFIATSATCVTGLVPVVTSEQFNILGQIVIIILIQIGGLGFLTFLNLLLIMVKKKISLTNKLVLQEALNQPSLNDLPKFVKNVIKYTFIVEGLGAIILAFVFIPDFGIVKGIYYSIFHSISAFCNAGFDVLGANSLIGYQNNLIINLVIPGLIIMGGLGFVVWFDVAHCIKKEYGKRSKFSKKHLFKSFSLHTKLVIIATVVLLLAGAVLFYLCEFNNIKTIGGLPLFDQIQISFFQSATLRTAGFASVDMASLHPSTKLMMCVLMFIGGSPAGTAGGIKTVTFAIGVLEVYNIYHGRKEVTAFSRRIPKRLIVRSFAIISMALAIVFLSIFALSITEQAPFIDICFEVVSAGATVGLSASLTPYLSVFGKIVIIMLMYIGRIGPITMMISFARKSYMQASKKEVRYPDGNILLG	

2.4E-65	230	32.3	3.8E-65	229.7	22.4	1.2	1	A0Z9Y1_NODSP	Potassium uptake protein, integral membrane component, KtrB	NSP_7190	Nodularia spumigena CCY9414	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nodularia, Nodularia spumigena, Nodularia spumigena CCY9414	313624	>tr|A0Z9Y1|A0Z9Y1_NODSP Potassium uptake protein, integral membrane component, KtrB OS=Nodularia spumigena CCY9414 GN=NSP_7190 PE=4 SV=1MTVSRTVCLGFLAVITVGTILLMMPFSTSSGNWNDPIVALFTATSAVCVTGLAVVDTGTDFSFWGQLCILLLAQIGGLGYMTTTTFLIMLVGRKFNLRHKLAIQQTLDRPGMQGSAQVIRSIIATTMIFEITGILLLLPAFVPDFGWNEGLWLAIFHSISAWNNAGFSLFSDSLVGYQSSGLVVFTITMLIIFGGIGYQVILEVYLWVRDRLLKKTTNLVFSLDFKVASSTTLILLFIGTIAFFLIETKNRETFGSLNLPTQLLAAWFQSVTTRTAGFNSIDVSQMTTAGLFITIAFMFIGASPSGTGGGIKTTTVRVLTSCTKSILQGKEEVLLYERKIAISLILKAVAVLVGSVAMVLFSTILISLTDPELNFIQLLFEVVSAFATVGLSTGITSSVSVPAKLILIVTMYVGRVGVLLLMAAVLGDPRPSRVHYPEESLLVG
2.4E-65	230	27.9	4E-64	226.3	19.3	2	1	R6BNM3_9FIRM	Potassium uptake protein TrkH family	BN708_00393	Firmicutes bacterium CAG:56	434	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:56	1263031	>tr|R6BNM3|R6BNM3_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:56 GN=BN708_00393 PE=4 SV=1MTSFQIIILGFMGVILAGSLLLMLPWASRSGRWSSFSDTLFTATSAVCVTGLVVQDTATYWSEFGQVIILLLIQIGGLGVVTVAVSIATIAGRKIGLMQRSTMQEAIAAPKMGGIVRMTTFILKTSFLIELIGAVLLFPVFYREFGLGKGIWYAVFHAISAFCNAGFDLMGVKGKFSSLTSFAANPVVNLVIMTLIVVGGIGFFTWLDIKENKWHIKKYRLQSKVVLGVSAFLILIPAIMFFFLEFQHMPLGERIWSSFFQSVTTRTAGFNTADLDKMTDSGKMGMVLLMVIGGSPGSTAGGMKTTTAAVLFAMAISVFRKNEQAHLYNRRIAEETQRNAATIFVLYMMLFTGSAMVISYVEKVPLVTAFFETGSAIGTVGLSLGLTPTLGLASRLVLICLMFFGRVGGLTLIFATVSGKRTEYKYPQEKITVG
2.9E-65	230	24.6	8.5E-65	228.5	17	1.6	1	G7WAC7_DESOD	Trk-type K+ transport system, membrane component	Desor_0793	Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus orientis, Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	768706	>tr|G7WAC7|G7WAC7_DESOD Trk-type K+ transport system, membrane component OS=Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) GN=Desor_0793 PE=4 SV=1MNYSFVANILGRLMIAYTGFMGIPFVVAVIYQEESMFSFALSLIVSVFTGLVLKTFGQKEGRMGVREGFVVVAGAWLLTALIGALPYALSGAVPTYLDGVFEAVSGFTTTGASVIDAVESLPKSVLLWRSLTHWLGGMGIIVLFIVFLPNMTGAVHLFNAEVPGPTSERVLPRIRDNALKLWQIYFGFTVVQIILLIIVGMNWFDAVNHSFATMATGGFSTKNTSIAYYDNVGIELIIIIFMIIAGGNFGLYFQAWRSGFMKIIKDLEFQFYLLIIAVSTLIIAFSLWRSMGVEGGNSLRQALFQVVSIMTTTGFASADFDKWPAVCKIVLLCLMFIGGSAGSTAGGIKVSRIILLFKHSWAELRRAIHPKAVINVRFAKRTVDPVMLNTISVFFFLFLSIFAFASFLLAATGLEPLDAMSAVVVTLGNVGPGFGVVGPTTTFSSINAFGECVLIICMLLGRLELFTLLVLVQPEFWRSRKGW
3.4E-65	230	13.8	1.2E-40	148.9	0.4	2.1	2	I3YBW1_THIV6	Trk system potassium uptake protein	Thivi_2541	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiocystis, Thiocystis violascens, Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	765911	>tr|I3YBW1|I3YBW1_THIV6 Trk system potassium uptake protein OS=Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) GN=Thivi_2541 PE=3 SV=1MRSLLSVANVLGRLLMIFGIAYLMPIVCAVVYRDGTLLTFVVSLGACLIAGGALTLSTRGYQAELKARDGFILVALAWTLTAAIATVPLILHEQLSFTDAFFETMSGMTTTGATVMVGLDTVAPTINLWRHELNWLGGMGIIVLAVAILPMLGVGGMQLFRAEVPGPKIDARLTARIADTAAVLWSVYFVITLACALSLRLAGMGWFDAICHAFSALSLGGFSTRDASVGAFDSPLIEGVLIFFMVVAALNFATHFTVWRERSFRPYWRDAEVKGVLSVLLVSCLGCAVYLWLGEVYASFWTALRHVSFNLVSIATDCGFVSTDYALWPTFVPFWMLFLSALTASSGSTGGGIKIMIRTLILVRQSSRELTRLLHPALAAPVTVGGMAVPNRVVVAILGFIFLYFMSIVAMTFLLIFGGLDFISAFSAVIACINNMGPGLGQVGPAANYAGLTDYDLWVLSFTMLLGRLEVFSLLILLLTPMFWRK
3.4E-65	230	14.8	3.2E-64	226.7	10.3	2	1	F8A9R9_THEID	Cation transporter	Thein_1981	Thermodesulfatator indicus (strain DSM 15286 / JCM 11887 / CIR29812)	487	cellular organisms, Bacteria, Thermodesulfobacteria, Thermodesulfobacteria, Thermodesulfobacteriales, Thermodesulfobacteriaceae, Thermodesulfatator, Thermodesulfatator indicus, Thermodesulfatator indicus (strain DSM 15286 / JCM 11887 / CIR29812)	667014	>tr|F8A9R9|F8A9R9_THEID Cation transporter OS=Thermodesulfatator indicus (strain DSM 15286 / JCM 11887 / CIR29812) GN=Thein_1981 PE=4 SV=1MRTGAFLYILGWFLIFFSVTFFFPGLISLIYHEPVWPFIYAEAITLVTGVLLVLLVKPEREIGYREGFAVVVFSWLAAGVFGALPFVFSGHLGLIDALFESISGFTTTGSTVFESLEELPRGLHFWRALSQWLGGMGIIVLSLAILPLLGIGGMQLYQAEMPGLTKDKLAPRIQDTARILWGVYSFFTVFEVLLLLAGGLDLYEALCHAFTTMATGGFSTRTASVAAFDSAYLDYVITFFMFVAGMNFSLHYRFLKGDLGAYFKSEEFRFYLLIGMAAVFICMFFNYIYGTYSDPSLNFRYSLFQVVWSVMTTTGYGTADFDLWHPACRYLLLILMFFGGMAGSTGGGVKQIRFLILFKFIRFQFRKLIHPKAVEIIRYEDKKIAESIIQAILGFMALYGLFFVVASLLVCAQGIDLITATSAVAATLNNIGPGLAKVGPTQNFGWMPDFSKLVLTFCMLAGRLELYTVAILFSRSYWRGARKPTWRF
3.7E-65	230	18.7	1.3E-64	228	13	1.7	1	M1WQG9_DESPC	Trk system potassium uptake protein	trkH BN4_10459	Desulfovibrio piezophilus (strain DSM 21447 / JCM 15486 / C1TLV30)	487	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio piezophilus, Desulfovibrio piezophilus (strain DSM 21447 / JCM 15486 / C1TLV30)	1322246	>tr|M1WQG9|M1WQG9_DESPC Trk system potassium uptake protein OS=Desulfovibrio piezophilus (strain DSM 21447 / JCM 15486 / C1TLV30) GN=trkH PE=3 SV=1MRWRYVLHIIGALVACIGMTMFFPLLWGLYYADGTAGPLAESMAITLLCGVILFAIFRDPEASKASSVMTHREGMAIVALGWFVAGAFGGLPFYLSGTFHSIVDCIFESLSGFSTTGSSVLTDIEAIPRGILFWRSLTHWLGGMGIIVLSLAILPFLGVGGMQLYKAEVPGPVPDKLKPRIKDTAVTLWKVYVFFSVVETVLLMFGGMDFFDALCHTFGTMATGGFSTKNTSVAAFNSAYIDYVITIFMFIAGINFTLHYMLMKWRPMSMLKDPEFRVFSCMVILFTGVVAVACYSAGNYETVSDSIRYTSFQVASILTTTGFATADYELWPGITQAILLFCMFVGGCAGSTGGGMKVMRIMLLIKHSYKELFRLIHPRSVNRVKLGQTVVQDDVLSGVWGFFILWIGLFFLAAFIIAGTGVDVVTSFAASLACIGNIGPGIGGVGPTENFAWLPDTAKWVLTFCMVLGRLEIYTVVILFVPEFWRK
3.9E-65	230	26.8	2.1E-63	224	18.6	2	1	D9QQS7_ACEAZ	Cation transporter	Acear_1355	Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Acetohalobium, Acetohalobium arabaticum, Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	574087	>tr|D9QQS7|D9QQS7_ACEAZ Cation transporter OS=Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288) GN=Acear_1355 PE=4 SV=1MRLKIIFNILGKLLIFVGLAMLLPLAVALFYKEVDGLSFLVSMGLTISVGKIMQKFSYSQQEIRHREGFAIVTLGWILISLFGAIPFMLSGVFDNFVNAFFESVSGFTTTGATVILSLESLSHSILFWRSLSHWLGGMGIIVMSIAILPELAGSMQLFKAEAPGPVNDRLRPRIKETAKTLWVIYILLTILQMILLFFNDMSFFDAVLHSFGTMSTGGFSSRTLSVKAYDSLIIEGIMVFFMFLAGTNFTLHYQALRGNIKALFNNKEFRFYLFLVTTAILLITVNLRLQVYKGWLQSIRYAAFQTLSIISTAGFATVDYDIWPPFARGILLVLMFIGGCAGSTAGGIKIIRIYALMKKGFQELYKLIHPRAVTSLKIGNRAVSEEVSTSILGFFFLYIIVFVVAAITLTSFGIDLISSISAVAATLGNIGPGLGLIGPLNTYVPLPIVGKLLLSFCMLLGRLEIYTVLVFMLAGFWRR
4.1E-65	230	14.1	3.5E-64	226.5	9.8	2	1	G7V6W6_THELD	Potassium uptake protein, TrkH family	Tlie_1429	Thermovirga lienii (strain ATCC BAA-1197 / DSM 17291 / Cas60314)	483	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Thermovirga, Thermovirga lienii, Thermovirga lienii (strain ATCC BAA-1197 / DSM 17291 / Cas60314)	580340	>tr|G7V6W6|G7V6W6_THELD Potassium uptake protein, TrkH family OS=Thermovirga lienii (strain ATCC BAA-1197 / DSM 17291 / Cas60314) GN=Tlie_1429 PE=4 SV=1MRFMVVLKVLGVLSAIISAFMIWPLGWAIIDGSSDVLPFVKSVTIGLLTSLAFLFLSRKSKIQDIEAREAFVIVSLSWIVASAIGGLPYLFNGTVKTFTDAFFEAMSGFTTTGASVLTDIQSNPRGILFWRDLTHWLGGMGIIVLSLAVLPFLGVGGMQLYKAEVPGPVPEKLTPRIQQTALLLWGVYVFLSALEVALLLGGGMNLFESLTHTFGTMATGGFSPLNGSIGQYNNPYFDWVITIFMFLAGANFALHYMMLRGDLKAWWKDEEFRFYTIVIFLGIATATSFLYFSETYGSLLESLRYAAFQVVSIVTTTGYVTADYEKWPFYVQYMLLFLMFVGGCAGSTGGGIKNLRIMLLLRHVKNELRRLLHPSAVLHVRTAGQVVERDVIGSVTAFFILYIGLFAVAALFMSALGVDVLTSIASVAATIGNIGPGLGTVGPAENYAHIPLAGKWVLSFCMLLGRLEIYTVMILFLPETWRR

4.2E-65	230	22	2.1E-63	224	15.3	2.1	1	A0A0F7DBW8_9EURY	Potassium uptake protein, TrkH family	GAH_00854	Geoglobus ahangari	477	cellular organisms, Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales, Archaeoglobaceae, Geoglobus, Geoglobus ahangari	113653	>tr|A0A0F7DBW8|A0A0F7DBW8_9EURY Potassium uptake protein, TrkH family OS=Geoglobus ahangari GN=GAH_00854 PE=4 SV=1MNTRLVVNYLSQIVLYFSLVFTIPLAAAIRYHEDVYAFAIPMAVCAFLGSIVYVISKPESDVAKYKEGYAIVGIGWLLIAIAGSIPYVYYSISPVDAFFEAMSGFTTTGATIIDRIEDLPKSLLLWRSLTQWLGGMGIVVLFVAIFPTLAKKSETLLQAEVPGLKVEKIKPRLKDTALRLYATYMLLTVLEIVLLYILGMSLYDAVNHTFTTLSTGGFSTHTESIAYFNSPAIEFVIFIFMILGGMNFVLIYLLLKGQTKFLRDTEFRFYMAILLAGAIMTAINLERFELGESLRYSFFQVASIMTTTGYTTFDFDTWSDSARLLLLMLMFVGGSTGSTGGGIKVVRIYLLTVYSLGQILKSAEPRTARIVRLNDEVVDKETLHNITAFFTLYVLIFVLSTFLVSLTGLDMISSISAVSATINNVGPGLGAVGAAESYSSLSATAKLILAFNMWIGRLELFTVLSLFIPSFWRERW
4.3E-65	230	17	5.5E-64	225.9	11.8	2	1	I3Y577_THIV6	Trk system potassium uptake protein	Thivi_0056	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiocystis, Thiocystis violascens, Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	765911	>tr|I3Y577|I3Y577_THIV6 Trk system potassium uptake protein OS=Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) GN=Thivi_0056 PE=3 SV=1MRALLSVLNVLGHLLMVFSVTYLLPIVCAILYRDGTLLTFVISLAACVAVGGALTLATRRYRRELKARDGFILVTLSWTLISAIATVPLMLHEQLSFTDAFFETMSGLTTTGATVMVGLDTVAPSINLWRHAINWLGGMGIIVLAVAILPMLGVGGMQLFRAEVPGPIKDAKLTARIADTAAVLWVIYLVLTLACILGLWLVGMSWFDAICHAFAALSLGGFSTRDASVGAFDSPAIEAVLIGFMVLAALNFATHFTVWRERSPRAYWRDAEARGVVIVLLASSLGCAFYLWWGEVYQDFLTALRHVSFNLVSIATDCGFVSTDYALWPTFVPFWMLFLSAITASSGSTGGGIKMIRTLILVRQSSRELTRLLHPALAAPVTVGGMAVPNRVVVAILGFIFLYFMSIVAMTFLLIFGGLDFISAFTAVIACINNAGPGLGVVGPATNYGGLTDFETWVLSVTMLLGRLEVFSLLILFTPQFWRK
4.8E-65	229	7.9	1.9E-63	224.1	5.4	2	1	F8D974_HALXS	Cation transporter	Halxa_1049	Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6)	514	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halopiger, Halopiger xanaduensis, Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6)	797210	>tr|F8D974|F8D974_HALXS Cation transporter OS=Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6) GN=Halxa_1049 PE=4 SV=1MRYTLRVDWRSGLSLVGTILAFLSLAYVVPIVTALLYGGDDLWLFVVTMAATAGFGLALRRLEPEPDPGAREAFMVVALTWLFAAVFGAVPFVLAGNGTVAHPVNALFESMSGFTTTGATVMGDISFETHSRAMLMWRQLTQWVGGMGIIVLAVAILSQMAVGGAQLMEAETPGPGVSKLTPHIAETARVLWIAYVGFTVLYITLLYAAHLAGYAPSMDAYNAVAHGLTTLPTGGFSPEARSIEAFSPVVQWLVVPFMFIAGVNFVLWWHVVSGDPRTMLRDNEFRLYLGAVTVLSIVGTAMLFYSTLEGPDGQIGGNLERSARYATFQIASLVNSTGYANIDFAQWNGPTKGLLLFAMFIGGSTGSTGGGIKVLRWLVILKTFRREIFTTIHPEAVRPVRMNGRILDEDAVRGIYSFSLLFLVFFVGIALLAVDAARVGLYADPDFEVIDIVGASIATLGNIGPGLGTVTGPMGGYNDFPLSSKGLMIVYMWIGRLEIFPVLVLLTRAYWQS
5E-65	229	8.5	9.7E-65	228.4	5.9	1.4	1	Q3IM29_NATPD	Trk-type transport system (Probable substrate potassium)	trkH3 NP_6112A	Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) (Halobacterium pharaonis)	551	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Natronomonas, Natronomonas pharaonis (Natronobacterium pharaonis), Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) (Halobacterium pharaonis)	348780	>tr|Q3IM29|Q3IM29_NATPD Trk-type transport system (Probable substrate potassium) OS=Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) GN=trkH3 PE=4 SV=1MGTFSTVARDVGRILQVVSLMLVVSAVVAVVTSEFFAVPAFLVSAGIMAAIGTGLAQRYADAPSSGKLEAMVTAASAWGVLTILGGLPFIFIAWTIYLDPLPAWANTPEMISDTTDVFRHPLNGFFESISGFTSTGLTMAVVEDDLPRSLHWWRSFTEWIGGVGVIVLTVAILARPGSGSLTLFESEARKKKSKVLPSVVSTVKEIWIKYLGLTVASILLLLFAGPVWAAATGQASFVEELLAVLGNGDPAVGMPLWPAINHGMTGIATGGFSVHAASIGEYGPIIQYAVIPIMVAGSIAFPVHYLILKGEIKNFYADLQTRWVFGWFAIGSVLLTTVLLLGGDASGQFDTFEETFRAAFFQFVSAASNTGFGTAAIGGGTERAMSAGATFLLCLGMLTGAAAGSTVGGLKLIRVLTLIKGTIWQVRDIFAPDHAVRQLQMGKRTLSEEQVQAEYTEAAVVFVLWVLCLIVGVAVLLWTLSPDHPAEYVIFDVMSAQSNVGLDAGITGPDMPDAAKVMLIFNMWIGRLEIIPVAVLLGAILQQLNLYRTDG
5.1E-65	229	27	1E-64	228.3	18.2	1.8	1	J7IMQ9_DESMD	Potassium uptake protein, TrkH family	Desmer_0813	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	768704	>tr|J7IMQ9|J7IMQ9_DESMD Potassium uptake protein, TrkH family OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=Desmer_0813 PE=4 SV=1MNYSLVENILGRLMISFSGFMVIPFLVALIWQEGSVLAFVLSIIITLVMGLILLAYGKKDGRMGVREGFVIVAGAWLLTSLTGALPYALSGAVPTYLDGLFESVSGLTTTGASVIDNVEILPKSILLWRSLTHWLGGMGIIVLFIVFLPNMTGAVHLFNAEVTGPTSERVLPRIRDNALKLWQIYFGLTVAQIFLLIIVGMNWFDAINHSFATMATGGFSTKNTSIAYYYDNLWIELIIIVFMIIAGVNFSLYYQAWRSGLNKIFKDIEFQFYLLIIIVSTLLIALSLWWTMGIDGGNSLRQALFQVASIITTTGFATANFDQWPSATKIILLCLMFIGGSAGSTAGGMKVSRIVLLFKLGWVELRRAIHPKAVINVRFAKKTVDPVIFNTVAVFFFLFLSIFAVATLLLAAIGLEPLDAMSAVVATLGNVGPGFGVIGPTTTFSSINAFGESVLILCMLLGRLELFTLLVLVQPEFWRSRKGW
5.7E-65	229	25.2	1.8E-64	227.4	17.4	1.8	1	C7RFB2_ANAPD	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Apre_0121	Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) (Peptostreptococcus prevotii) (Peptococcus prevotii)	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptoniphilaceae, Anaerococcus, Anaerococcus prevotii, Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) (Peptostreptococcus prevotii) (Peptococcus prevotii)	525919	>tr|C7RFB2|C7RFB2_ANAPD Potassium uptake protein, TrkH family OS=Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) GN=Apre_0121 PE=4 SV=1MEKNILKRTFDKATENPAFVLSMGFLILISLGGLILSTPYVTQNGKSTGLIDSFFVAASASCVTGLTTVNTGLYWNTLGHVVIIILIQIGGLGIMTLASLIPLILRKKIGIKSRQILKEQLNVESMEGLVRLFRYVLAFTLIVEALGALFLSIRFIPTYGWGKGIWYSVFHSISAFCNAGFDIMGDSIYPLRKDLLVNTTLMVLIVIGGLGFMVTSEFFYRRKFKQVSTHSKLVLIINAVLILFGALGFLLLESIQKGVLIGEGLKGSIIESFFQSVSARTAGFYSVNLSNIKDSTSLLLIGLMFIGGSPGSTAGGIKTTTFGVLVLATYSIIKRQKEPVVFNKHIGDETIKKALSIFMISLALVLMVTFIITITDDFDLIDTLYEVVSALATVGASRGITANLSRIAKVLIGLCMYLGRIGPMTMALAFGLKPDEKLIRYPECFISIG
5.8E-65	229	19.5	9.6E-64	225.1	13.5	1.9	1	F6CQH6_DESK7	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Desku_0642	Desulfotomaculum kuznetsovii (strain DSM 6115 / VKM B-1805 / 17)	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum kuznetsovii, Desulfotomaculum kuznetsovii (strain DSM 6115 / VKM B-1805 / 17)	760568	>tr|F6CQH6|F6CQH6_DESK7 Potassium uptake protein, TrkH family OS=Desulfotomaculum kuznetsovii (strain DSM 6115 / VKM B-1805 / 17) GN=Desku_0642 PE=4 SV=1MGIRRKMVRVDTKKGFPLKLSPPQVLVLGFATLILVGALVLMLPVSSRSGQVTDFLTALFTATSAVCVTGLVVVDTGTYWSTFGQAVILALIQIGGLGFMSMATFFFILMGRRIGLKERLIIQESLNQLRVAGVVRLVRAVLLFTVLTEGFFAVILSLRFYFDYGFPRCLWLGLFHAVSAFNNAGFDLLGGFRSLTGYVSDPVVNLSVTTLIILGGLGFATVMELYNYPRTRRLSVHSKLVLRVTGGLILCGTLLFGLLEWGHILRDLPLSGKIFASYFQAVTPRTAGFNTVDIGHLNAATQFLIIILMFIGASPGSTGGGIKTTTFALLGITLWSLSEGKEDVEVFRRRIPPWQVYKALSVALWAILLIIMITLLLSITESSNFLAILFETVSAFGTVGLSMGLTPELTPLGRVAIIFTMFAGRLGPLTLAYAFAQRRRKTTIRYPEEKIMVG
6.3E-65	229	16.8	1.9E-64	227.4	11.6	1.7	1	A9A0A1_DESOH	Trk system potassium uptake protein	Dole_3217	Desulfococcus oleovorans (strain DSM 6200 / Hxd3)	482	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfococcus, Desulfococcus oleovorans, Desulfococcus oleovorans (strain DSM 6200 / Hxd3)	96561	>tr|A9A0A1|A9A0A1_DESOH Trk system potassium uptake protein OS=Desulfococcus oleovorans (strain DSM 6200 / Hxd3) GN=Dole_3217 PE=3 SV=1MSWPRIFYITGYLLVWIGLCMVLPLGVSLYFGEAGVWPFVYAMAVTVSCGLLLIAGFRAGRGEMISHREGMAIVAFCWAGAGFFGALPFYFGNAIPSFTNALFESISGFTTTGASVLSNIEGLERGFLFWRSMIQWLGGMGIIVLSVAILPFLGVGGMQLYKAEVPSPVVDKLQPRIRDTAKTLWRVYLLISVAQVFLLKVGGMSLFDAVCHAFTTMPTGGFSTQNLSIAAYNSAYLDWVVALFMLLAGVNFSLHYQMLRGNTLAFWKNPECRFFLVLVLCLTAVVSLDLHGRAYETIGQSLRYGAFQVVSIITTTGFATADYETWPALSQLILFICMFVGASAGSTGGGMKCIRIMLCVKYCYRELFSMVHPKAVTHVKIGGKTVPDEVMRSVLGFLCLYVLIFIACSFLLAAMGVDAVTSAAAVAASIGNIGPGFGAVGPLDNYANIPVMGKWLLMWCMLLGRLEIYTILILLVPEFWRK

7E-65	229	18.2	8.4E-64	225.3	12.6	2	1	W8VX51_9FLAO	Potassium uptake protein TrkH	NMS_1308	Nonlabens marinus S1-08	489	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteraceae, Nonlabens, Nonlabens marinus, Nonlabens marinus S1-08	1454201	>tr|W8VX51|W8VX51_9FLAO Potassium uptake protein TrkH OS=Nonlabens marinus S1-08 GN=NMS_1308 PE=4 SV=1MYIMGLLLVFNGGFMSISALVSAIYREDEASDLLGASLVAIGLGAVLMILTRDHVKELAKKEGYLIVTLGWLIMAFAGTMPYLFTGAITNYTDAFFETMSGFTTTGASIMNDIEIMPKGVLFWRSMTHWIGGMGIIVLAVAILPLLGIGGMQLFAAEAPGPSADKLHPRITDTAKRLWLIYVGFTGVQTILLKVAGMGWFDAVNHAMSTLSTGGFSTKNASIAYWNDNPYIQWIIVFFMFVAGMNFVLSYFGFKGQFRKIFMDTEFKWYTSFVVGFSIIGAILIYLQADVSVSSIPHPMVWGEAESAVRHSFFQVLAVITTTGFVSADYTMWTPFLTIMFFGLFFLGGSAGSTSGGIKVMRHIILIRNGILEFKRTLHPNAILPVRYNSRALPNGIVFNILGFFILYMLAFIIGSVGLAALGLDFDTAIGGALSSLGNVGPAFGDLSPVNNFAGLPDLGKWWCAFLMLIGRLELFTVLILLTPFFWRNR
7.8E-65	229	0.4	4.7E-46	166.7	0	3.1	3	B0D780_LACBS	Predicted protein	LACBIDRAFT_326076	Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) (Bicoloured deceiver) (Laccaria laccata var. bicolor)	756	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Tricholomataceae, Laccaria, Laccaria bicolor (Bicoloured deceiver) (Laccaria laccata var. bicolor), Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) (Bicoloured deceiver) (Laccaria laccata var. bicolor)	486041	>tr|B0D780|B0D780_LACBS Predicted protein OS=Laccaria bicolor (strain S238N-H82 / ATCC MYA-4686) GN=LACBIDRAFT_326076 PE=4 SV=1MTIYVHRKSGDDRVWRAGSASPPDGRNFHIPDVLKNRSTSWTKAVWIFWLRRTRLLDHLLEQVTFFRVHPFAFTFIPLIFSGIFYASNGRYHVSYVDALFLCYSAMTVTGLSTVDLSTTTGWQQAILYFLMTIVGTTRFFRTHCEYVAEQRRSRRGKRRSIFPTISSPIAAFKQRQPVPVQTLDEERSIPQFDFTGPTPGATLNNGQGNVLPPINEQPEEPILSDVRTFSSSPRQASILLPSPIDERRRSETSVFATATGVSPQVVTYHPMVLREGRRAPSRGDTRRTSNGPGSPMNQTKYRGLGGFPGPLELADKVIKFAAPATHRRLERKLTMPTITTLEEKSVPWLEFDGLVVGRNSNFHTESLTDNQLEEIGGAEYRALRLLSYLVPSYFVGVQLLTLMIFGPWLCATKTYNNVFESQPQLVPKAWFSLFQIMGAYTGGGLSLVDAGMVPFEKAYPMIFALGFSILAGNHALVRFVYEYNDPILFVRSLLSCCLCTNSTSEAFASSFPDKSQLDIGLPAYDSIPVGPRVIAGLFQGLAVRASGFSIVPIASLAPSLQFLYVVMMYIAVYPDIAFPECLKRNHRYEEQSLGVFERPPDQEDEEPNDLGKLETRRERVGRYVGWHLRRQMSIDIWWLVWGVFLVAIIERNNLLDESKKWFDIFRILFELVSAFGGIGLSLGFPDDNFAFSGTLRPLSKLVVIVIMLRGRHRGLPVAVDRAVLLPDELVVHHGHDEYGDEKAITSNPSIPTRPGN
9.2E-65	228	17	9.9E-34	126.1	5.5	2	2	R5T5E2_9CLOT	Cation transporter	BN544_03181	Clostridium hathewayi CAG:224	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	1263067	>tr|R5T5E2|R5T5E2_9CLOT Cation transporter OS=Clostridium hathewayi CAG:224 GN=BN544_03181 PE=4 SV=1MNKKIIFYLLGWIMNMEAIFMLLPCAVAVIYRESSGIWFLAVMAVCGSAGLFLTRRKPDNMVFFAKEGFVSVALSWIVLSFFGSLPFYLSREIPRFEDAMFEVISGFTTTGASILPDVESLSHCMLIWRSFTHWIGGMGVLVFILAVLPLAGGYNMYLMKAESPGPSVGKLVPKVKSTAKILYGIYFFMTVVEILLLAGGMPLFDSLATGFGTAGTGGFGIKNSSIAYYDSYYLQGVITVFMILFGINFNVVYYLFLVHHPKDALRCEEARVVLGIIGVTVLLITLNIRGSFTSLFAAFHHAAFQVASIITTTGFSTVDFDKWPEFSKGLLVVLMFIGACAGSTGGGIKVSRVIILLKTVKKELFSLLHPRSVKVLKIEGKPVEHQVIRSINTFLVAYLVIFIFSTILVSLDNFDFTTNFTAVAATFNNIGPGLGAVGPTGNFSGFSALSKWVMMFDMLAGRLEVFPMLFLFAPSTWKK
9.6E-65	228	20	6.5E-64	225.6	13.9	1.9	1	L7WA23_NONDD	Trk system potassium K+ uptake protein	trkHDDD_1852	Nonlabens dokdonensis (strain DSM 17205 / KCTC 12402 / DSW-6) (Donghaeana dokdonensis)	498	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Nonlabens, Nonlabens dokdonensis, Nonlabens dokdonensis (strain DSM 17205 / KCTC 12402 / DSW-6) (Donghaeana dokdonensis)	592029	>tr|L7WA23|L7WA23_NONDD Trk system potassium K+ uptake protein OS=Nonlabens dokdonensis (strain DSM 17205 / KCTC 12402 / DSW-6) GN=trkH PE=4 SV=1MTKLNYKIIVFIMGLLLVFNGGFMSLSAIVSAIYGESEGLQILAAAGVAISLGGVVMYFTRDHVKELSKKEGYLIVTLGWLIMAFAGTMPYAFTGAISNYTDAFFETMSGFTTTGASIMNDIEIMPKGILFWRSLTHWIGGMGIIVLAVAILPLLGIGGMQLFAAEAPGPSNDKLHPRITDTAKRLWLIYVGFTGLETVLLKIAGMGWFDAVNHALSTLSTGGFSTKNASTAFWNDNPAIQWIIVIFMFIAGTNFVLSYFAFKGRFSKILKDTEFKWYASFVFGFSIIGGVLIYLQADPAVSSINHPMVLGEFESAFRHSTFQVLAVITTTGFVTADYTMWTPFLTIMFFGLFFIGGSAGSTSGGVKVMRHIILIRNGIMEFKRTLHPNAILPVRYNGRALQSGIVFNVLGFFILYMLSFIIGATVLAALGLDFETAIGGALSSLGNVGPAFGNLSPVDNFAGLPPLGKWWCSFLMLIGRLELFTVLILLTPFFWRNR
9.7E-65	228	6.6	5.2E-64	226	4.6	1.9	1	C4K9E6_THASP	Trk system potassium uptake protein	Tmz1t_4081	Thauera sp. (strain MZ1T)	491	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Thauera, Thauera sp. (strain MZ1T)	85643	>tr|C4K9E6|C4K9E6_THASP Trk system potassium uptake protein OS=Thauera sp. (strain MZ1T) GN=Tmz1t_4081 PE=3 SV=1MSSDARARAYYPALNALGLIIMIFGLLMGFPLVVSAVLGDGATLAYDQGLFVTFVAGLLLWAATRSKRRDLRVHDGFLLVAATWVVLPLFGALPLLAYIPDLGFTDAYFEAVSGLTATGATVLTGLEHLPISINLWRTFMHWVGGMGVIVLVVAILPLLGIGGRQLYKAEVPTPMKDSSLTPRIAETAKGLWLTYVLLTIACGFSLWWAGLAPWDAVIHAFSVAGLGGFSNRDASLGHFDSVGVELVTAGFALLAGLNYATHYLALVRRSSAPYRRDPEIPFYFGVLALSTLMLTAYLLAQGIFTDFGEALRYVAFHVVSISTSLGLATIHDVTLWPMFAQIWILFLGSFVACSGSTGGGIKMMRAMILYKQVIREIVRSLHPNAVRPVRMGRNPVPEHILHAVLGFSFMYMVSIVSLTLVLSAAGLELVTAFSAVVACLNNTGPGLGLVGPASNYQGLDDLHKWVLCFAMILGRLEIFTFLVVLTPTFWRR
1.2E-64	228	20.5	8.9E-64	225.2	14.2	1.9	1	A0A024FH14_9FLAO	Potassium uptake protein TrkH	WPG_1996	Winogradskyella sp. PG-2	497	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Winogradskyella, Winogradskyella sp. PG-2	754409	>tr|A0A024FH14|A0A024FH14_9FLAO Potassium uptake protein TrkH OS=Winogradskyella sp. PG-2 GN=WPG_1996 PE=4 SV=1MKLNYKIIFHFFGLLLLFNGGFMMIATLISLIYKDGVTFELLLSGLATLLIGTFAMIGTKNHRKEMNKREGYIVVAFGWIVMSLSGTLPYLVTEAIPSFTNAFFETMSGYTTTGASILNDIEVVPKGVLFWRSTTHWIGGMGIIVLAIAILPLLGVGGMQLFAAEAPGPSDKLHPRITDTAKRLWLIYVGYTAAETILLQVAGMSFFDAINHALSTLSTGGFSTKNASIAHWNDNPAIQYIIMFFMFLAGTNFVLSYFLFKGKVVNIIKDEEFKLYFKFIAAFTIIAALLIYFRADVSQSSIDHPMIFGEGESAIRHGLFQVLAIVTTTGFVTADYTMWTPFLTVFFFGLMFLGGSAGSTSGGVKVVRQLILIKNGFLEFKRALHPNAILPVRYNTKSVSKDIVFNILGFFILYMLSFIVGALVFSMFQMDFISAVGLSASSLGNVGPALGDFGPVNNYSALPPLGKWWASFLMLIGRLELFTVLILLTPFFWRNR
1.2E-64	228	11.8	1.9E-44	161.4	1	2.1	2	G0A3F0_METMM	Trk system potassium uptake protein	Metme_1833	Methylomonas methanica (strain MC09)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomonas, Methylomonas methanica, Methylomonas methanica (strain MC09)	857087	>tr|G0A3F0|G0A3F0_METMM Trk system potassium uptake protein OS=Methylomonas methanica (strain MC09) GN=Metme_1833 PE=3 SV=1MQRFCTLAFVLGLILMIFGLTYALPIATSIYFDDGMTEHFLRGMSLNIGVGGLLASVTMQFRGDVKTRDGYLLVAFFWLLMASAATLPLMWGIPGLSFTDAFFETMSGFTTTGATVLTGLDSLAPSLNLWRHELNWIGGLGIIVLAVAILPLLGVGGMQLYKAEIPGPVKDSKLTPRITETARLLWMVYVAYTLLCIVSLKLAGMSWFDAVCHAFSTLSLGGFSTHDASIGYFDSPAIELIITVFMMLSGMNFATHYTALHNISVKPYSLDPEAIPMLGIIATTILLCSFYIWHFDIYPDFLSGLRYISFNTVSLATGTGYSSTNYEVWPAFIPWLILFLSGVTPCTGSTGGGIKLFRALLLWKQAGRELFSLLHPHAVNPIRIGHTPIANKIIFAVLAFIFLYFISIVLMTFTLMFTGMDPVSAFSAVMACINNTGPGLNTVGPAANYAHLNDFQTWLCAITMLLGRLEVFTLVVLFTPTFWRK
1.3E-64	228	19.3	1.6E-63	224.3	13.4	2.1	1	Q12X31_METBU	K+ transporter	Mbur_1063	Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M)	478	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanococcoides, Methanococcoides burtonii, Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M)	259564	>tr|Q12X31|Q12X31_METBU K+ transporter OS=Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M) GN=Mbur_1063 PE=4 SV=1MRYNVVLGVLGSILWLLAGFMFIPLFVAIYYGEPVQTFGIPLAITVLVASIFSFFFKRRDEEWDLKEGFFIVAMGWLIAAVFYSFPYMLEGVPPINALFESMSGVTATGATALTEIESHTKSLLFWRSMTQWLGGMGIIMLFIAILPKLGIAGRQMFRAEVPGLQEEQLRPRIRETAKILWLVYIILSVVELTILLIAGLSFFDAITHTFTSISCSGFSPYSDSIAAFSDPLVEGIIMVFMFLGGANFALHYKTIYSDKKSLIKDQEFKFYLSIIVIGTLVLAYVLFRTEVYSLPDAFRYSSFHVISILTTTGYATVDFNIWPDSSRFILFILMFIGGCAGSTSGGLKVVRFLLLLKYTQKVLFKVIHPKAIVPIRFNNKTVPEDIIHSIVSFMIIYFLIFFASSTLLALMGMDFVTSLSASIATLGNVGPGLGLVGPMANFDAIPDPGKLILIANMWIGRLEVFTVIVLLTPAFWKR

1.6E-64	228	20	9E-64	225.2	13.8	1.8	1	F2KRK7_ARCVS	Potassium uptake protein, TrkH family	Arcve_0754	Archaeoglobus veneficus (strain DSM 11195 / SNP6)	475	cellular organisms, Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales, Archaeoglobaceae, Archaeoglobus, Archaeoglobus veneficus, Archaeoglobus veneficus (strain DSM 11195 / SNP6)	693661	>tr|F2KRK7|F2KRK7_ARCVS Potassium uptake protein, TrkH family OS=Archaeoglobus veneficus (strain DSM 11195 / SNP6) GN=Arcve_0754 PE=4 SV=1MNVRLVLNFLGRILIYFSLIMLLPLAIAYYYGEPVKPFIAAQAAAIATGVVFMLLKPESELLRYKEGMAIVGLGWLSVSIVGSIPLLFHTHPVNAFFETMSGFTTTGATIFDRVEDLPKSILFWRSLTQWLGGMGIIVLFVAVFPAMARKGEKLFQAEYPGVNLGKLKPRVEDTAIILYSIYLFYTVLEAMILYFLGLSPFDAITHAFTTLSTGGFSTHTESIAYFSSPAIEAVISLFMFLGGTNFALHYFLLTGKRLPFRDPEFRIYAAIIAISAAMLAVVNLQKFDLLESIRYSVFQTVSIVTTTGYTTSDFDTWSDAAKMVILILMFVGGCSGSTAGGMKVIRLYLLLEYAILQVLKAAERPRIVRIVRYGEQVINKEALDAIAAFFILYILVFVFSSLTLALSGLDIITSISSVAACLGNIGPAMGLAGAAAESYAALPYHVKLVLAVDMWVGRLEMFTVISLFIPQFWMRKW
1.7E-64	228	32.2	2.8E-64	226.9	22.3	1.2	1	E1WYT9_HALMS	Cation transport protein	BMS_2962	Halobacteriovorax marinus (strain ATCC BAA-682 / DSM 15412 / SJ) (Bacteriovorax marinus)	575	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Bdellovibrionales, Halobacteriovoraceae, Halobacteriovorax, Halobacteriovorax marinus, Halobacteriovorax marinus (strain ATCC BAA-682 / DSM 15412 / SJ) (Bacteriovorax marinus)	862908	>tr|E1WYT9|E1WYT9_HALMS Cation transport protein OS=Halobacteriovorax marinus (strain ATCC BAA-682 / DSM 15412 / SJ) GN=BMS_2962 PE=4 SV=1MGKISQKLPFLLEFIFNGLFIFLYSLRSIKKLPENWSPEFIDSVIQNCAYIVPVILLINVVNNFKNSKGLEDFLRRYIFSMVVFVPLLITWGDVEFAFWLASAHLLSSILALYDDVNDVKVQRGRQEQNLFQGLRLRPAQMVLFSFIGVIFLGTFLLMLPVSSADGNSISFVDGLFMATSATCVTGLSTLSVQDNLSVFGQVVLLVLIQIGGLSIMTLYSSMAILLGRSMRMKDRIIMQDLLDVSSLEELFAMIINIIKYTFLIELWGGIVLTIAFTFEGFEFGKAIYYGFFHSISAFCNAGFSLFNNSLESYAASPLINGTIAILIILGGLGFIVLKELAEVITKGKKLVRLGLHSKIVLVTTIVLTVAGTLFIFFGEFLNSLDSYTLWEKMQISFFQSVTLRTAGFNTIPLTNLHKYTIYMMTLFMFIGGSPGSTAGGVKTTTLAILFYSIKSTLKGDKKVTVLDRKIPAPVVVRATALMFISILITSSFILILMKLEPEQSFLPIFFEVISASGTVGLTLGITPYLSMVGKIAVSLLMLIGRIGPLTLILAIGQRNRDKGKFDYPDGRIMIG
1.7E-64	228	22.5	1.1E-63	224.9	15.6	1.9	1	A6L6S8_BACV8	Trk system K+ uptake protein TrkH	BVU_3781	Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	502	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides vulgatus, Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	435590	>tr|A6L6S8|A6L6S8_BACV8 Trk system K+ uptake protein TrkH OS=Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154) GN=BVU_3781 PE=4 SV=1MGEFYNPDKLYKGGSRNNSLINKKMIFRVLGVLLFIESAMFLLCAAVSLCYGEQDYQYFLYTILLNTLVGGVLLICSRGAENRLTRRDGYCIVTFTWFLFTLFGMLPFYFSGGIPSVTDAFFETMSGFTTTGATILDDIESLSHGLLFWRSLTQWIGGLGIVFFTIAVLPIFGGGTIQLFSAEAIGVTHDKTHPRIDVMAKWLWMIYAILTIAETVLLMIGGMSFFDAVCHSFSTTATGGYSTKQASVAYWNSPFIEYVIAIFMILSGINFSLYFMCLKGKGKRLFQDDEFRWFMKSVSILTLVITFALVFQNHYDWEKAFRRALFQVATAHTSCGFATDDYNLWPSFTWMLLIFAMLSGGCTGSTSGGIKNMRLMILARNIKNEFKRMLHPRAVLPVRVNRQVISPSIIASVNTFFVFYLFCILAGWILLMFFGVGIIEAMSTVISSLGNVGPGLGAFGPAFSWAALPDAAKWILSFLMLIGRLELFAVLLLFYSGFWERR
2E-64	227	8	7.9E-62	218.7	5.6	2	1	D2RT85_HALTV	Cation transporter	Htur_2082	Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (Halococcus turkmenicus)	514	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Haloterrigena, Haloterrigena turkmenica, Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (Halococcus turkmenicus)	543526	>tr|D2RT85|D2RT85_HALTV Cation transporter OS=Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) GN=Htur_2082 PE=4 SV=1MNIRVDWQASLALTGTVLKYLALTLFVPLVVAVVYQEDIFVFVATIGIVVAIGYGLERLDPDPDSDLGPREALLLVAISWLVVAVVGAIPYLIAGYGTESALRHPVNALFESMSGFTTTGATVMAAISVEQHSHALMMWRQLTQWLGGMGIIVLMIAILPELAVNGAQLIRSEAPGPELQKLTPKIAETARILWLVYFGFTILLIGLLYGLHLVGLAPNMHFYNAVAHGFTTLPTGGFSPEADSVAAFSAVVQWIIIPFMAVAGTNFALFWYVLDGEPRRLFQNTEFRAYAGAIAVVTAIVAALLYSGSAPALGELGGATEGYGESALRHAAFQTVSLLNSTGYATSDFAQWDPIAQTVLLIAMFIGGCAGSTGGGVKIIRWLVVLKGAVRREVMRTLHPRSVGVVKLEGKRVDNATLNGVSAYFPIYFAFIAGIFLILSLEPNFNIESNLSATVSCFNNIGPGLGLVGPVQSYTGYSNLSKFVLSMAMLLGRLEIFPLWFALSPSTWSKK
2E-64	227	13.4	2.7E-32	121.3	1.5	2.1	2	R6IZD2_9CLOT	Uncharacterized protein	BN539_01704	Clostridium sp. CAG:217	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:217	1262779	>tr|R6IZD2|R6IZD2_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:217 GN=BN539_01704 PE=4 SV=1MNRKMVFYMIGKIVQAEAAMLLLPLVVALLYKETPLPFLITIGIALVLGIALSLIFKPKDRVIYAKEGFVIVAFAWIALSLIGCIPFVLSGALPNFFDAFFETVSGFTTTGASVMADVESMPHGVLMWRSFTHWVGGMGVLVFIMAIIPSVTDRSIHILRAEMPGPIVGKLVPRAKQTARILYLIYVFLTAAEVILLVCGKMPLFDALVHSFGTAGTGGFGIKADSIGSYSYTYCQVVITIFMLVFGVNFNLYFLALLRNFRSLFKSQELWCYLGIFGVATALITANIYNLYHSVGKALQLSTFQAASILTTTGFSTADFDQWPDLSRSILFLLMFVGGCAGSTAGGLKVSRVMLLFKLIRRELRHMLHPRSVGVVKLEGKRVDNATLNGVSAYFPIYFAFIAGIFLILSLEPNFNIESNLSATVSCFNNIGPGLGLVGPVQSYTGYSNLSKFVLSMAMLLGRLEIFPLWFALSPSTWSKK
2E-64	227	22.8	4.3E-62	219.6	15.8	2	1	A6TWB9_ALKMQ	Potassium uptake protein, TrkH family	Amet_4415	Alkaliphilus metalliredigens (strain QYMF)	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus metalliredigens, Alkaliphilus metalliredigens (strain QYMF)	293826	>tr|A6TWB9|A6TWB9_ALKMQ Potassium uptake protein, TrkH family OS=Alkaliphilus metalliredigens (strain QYMF) GN=Amet_4415 PE=4 SV=1MNYGIVLKVLGSLLLFEAGFLLFPLGISMYYRESDTLAFVYSIIALLGVGVPMVKFSHSSRRIKAKEALTIVVGGWVLVSFFGSLPFVLSGSIPSFIDAFFETVSGLTTTGATIIDDIEVLPRGILFWRSLTHWLGGMGILVLTLAILPVIGVGGFQIFKAESPGPVSDKLVPKMKDTAKILYTVYLGITILQTVLLYVGGMSLYEALVHTFGTLGTGGFSTRNSSIGAFNSYYIQIIIAIFMIASGINFSLYYDLYKGRWKEVVKNSELKLYLSIIVVAIILITINLNGRIYTSLNETFRYALFQVSSIITTTGYGTADFDQWPTFSKGILFMLMFVGGCAGSTGGSIKVIRLLVLFKLVRREISKILHPRAFIPVKINNKSISPDVTASVASFFFLYMLIFVAGTLLISLEGIGLISAASSVAATLGNIGPGFELVGPAQTYSQFSVPSKLLFSLLMLFGRLELFTVFILLMPTFWRDR
2.2E-64	227	20.6	1.9E-63	224.1	14.3	1.9	1	D6Z710_DESAT	Trk system potassium uptake protein	DaAHT2_2332	Desulfurivibrio alkaliphilus (strain DSM 19089 / UNIQEM U267 / AHT2)	500	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfurivibrio, Desulfurivibrio alkaliphilus, Desulfurivibrio alkaliphilus (strain DSM 19089 / UNIQEM U267 / AHT2)	589865	>tr|D6Z710|D6Z710_DESAT Trk system potassium uptake protein OS=Desulfurivibrio alkaliphilus (strain DSM 19089 / UNIQEM U267 / AHT2) GN=DaAHT2_2332 PE=3 SV=1MHTGGVLNILGKLLLLISLFLLTPIPVSAYYDDGLMDIFLLCAAIGAGAGAALILLFKPIKELSLRDGFAVVTVCWLGMALLGSLPYQLSAQVPSFIDALFESMSGFTTTGSTILTDIEALAPSLLFWRATTQWLGGMGIIVLSLAILPLLGIGGMQLFQAEMTGPTKDRLTPRIQDTARILWTVYLLFTILLIALLLLGGLSFYDAVTQAFCTISTAGFSPYNDSVGHFNSLYVEVVVIIFMFIGGINFAMHHHVLRGRLSTYWHSEEFRLFLGLAVGATLLITFFNYHFNLYENLAGSLRYASFQTVSILTTSGFGTADFTLWPSSSQLILVGLMLVGGMAGSTAGSIKTVRFLLFFKYVRLQLRSLIHPQTVSIIKLGGHRVPREVMTAVLGFFALYFMIFLIATLVVTALGVDLVTGTTAVIATLNNIGPGLHLVGPAHGFAELPALAKVVLTFCMLAGRLELYTVIVLLTPAFWRTARRPEIRLFSRKQAAGTGS
2.2E-64	227	30.7	3.3E-64	226.6	21.3	1.1	1	C7LVC3_DESBD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Dbac_0338	Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) (Desulfovibrio baculatus)	456	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfomicrobiaceae, Desulfomicrobium, Desulfomicrobium baculatum (Desulfovibrio baculatus), Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) (Desulfovibrio baculatus)	525897	>tr|C7LVC3|C7LVC3_DESBD H(+)-transporting two-sector ATPase OS=Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) GN=Dbac_0338 PE=4 SV=1MTFQSKVLKMHPATLVLASFLLVISAGTILLMLPVSTHDGHIPFIDALFTATSAVCVTGLVVVDTGSYYTLFGQCVILALIQIGGLGLMTISVALFQWLGRSVSFRHRMAMQDLFAHTPREDIFVLVKSIILFTLAAESVGAIFLTLHWMNEYSIKEALYMGLFHSVSAFCNAGFALFSDSMVRYSDSIILNSTICFLIVLGGIGFPVLYDIQIWSAGRKGARGRLSIQSKTVLLTTVVLILFGAIMFAFLEQSGENLQTSLVHRILSPLFQSITCRTAGFNTVDIGSLKDATLTMMIFLMFFGASPGSCGGGVKTTTLALLLAFTIGRIKKRRRVNMFKKSIPNETVTRSVSLVLVSLVVIGVALFLLLIGDAVGGHETGGSNGAFLSYLFETVSAFGTVGLSMGITADLTTWGKIIIILMMVVGRVGVLTFSYIIVGSVATKGFEYSEENLMIG

2.2E-64	227	30.3	3.2E-64	226.6	21	1.1	1	A6TNP5_ALKMQ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Amet_1636	Alkaliphilus metalliredigens (strain QYMF)	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus metalliredigens, Alkaliphilus metalliredigens (strain QYMF)	293826	>tr|A6TNP5|A6TNP5_ALKMQ Potassium uptake protein, TrkH family OS=Alkaliphilus metalliredigens (strain QYMF) GN=Amet_1636 PE=4 SV=1MKDKIGHPKIDPTQVLVMGFASVIMIGALLLNLPIAAQDGRSIGFLNALFTSTSAVCVTGLVVVDTGTYWTIFGKTIILILIQIGGLGFMTMATMFAILLGKKISLKERLIIQESLNQNTLTGLVRFTKYIILGTFAIEAIGAFFLAFRFVPELGWAKGIAYSIFHSISAFCNAGFDIIGNGVGLTPYVNDPIVNVTLWAMVILGGIGFSVMVDVVNQRKFKKFTLHTKMVLIITGALLGLGFVGFLILEWNNPETLGSLNFGGKLMAAFFQSMTTRTAGFNTIASDQMTNASKFLSILWMYIGGSPASTAGGIKTATLGVLVFTVISVVKGREETELYGRRIPRTIVNRALTVASIGLVLIVFVTMILSITETGFSFMDILFETTSAFGTVGLSLGVTPELSVIGRIVIIFMMFAGRVGPLTLAVAVAEKRHKANIRYPEEKILVG
2.2E-64	227	23.5	6.9E-64	225.5	16.3	1.7	1	R6MV97_9BACE	Potassium uptake protein TrkH family	BN659_00681	Bacteroides sp. CAG:443	501	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:443	1262739	>tr|R6MV97|R6MV97_9BACE Potassium uptake protein TrkH family OS=Bacteroides sp. CAG:443 GN=BN659_00681 PE=4 SV=1MQDIIANNEYLNGNRTNSLINRKMIFRILGILLFIEGVMFLVCAGGSLCYKEHSYIYFIYSTLITAVAGAVLVFLGRKAENKLSRRDGYCIVAFTWLLFTVFGMLPFYLSGEIPSVSDAFFETMSGFTTTGATILDDIESLSYGMLFWRSFSQWIGGLGIVFFTIAVLPIFGVGNQVLFSAEATGVTHDKIHPKISIMAKWLWTVYLLLTVTETILLMLGGMNLFDAVCHAFSTTATGGYSTKQDSVAYWHSPFIEYVIAIFMVLSGINFSLYFMCLKGKFLHLFKDDESRWFLMSVGIVTLLITIPLVTQNHYGWEEAFRKAFFQVASIHTSCGFATDDYNGWPPFTWMLLIYTMMAGGCTGSTGGGIKNMRLVILFRNMKNEFSRLIHPRAVLPVKVNQQTISFSTISTVNTFVLLYLITLFIGWIVLMFLGLGLTESLGLSVSSLGNVGPGLGAYGPAFSWSALPDLAKWVLSFMMLIGRLELFGILLMFSPGFWHKR
2.5E-64	227	27.7	3.6E-64	226.5	19.2	1.2	1	L0KD20_HALHC	Potassium uptake protein, TrkH family	Halha_2091	Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Halobacteroides, Halobacteroides halobius, Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	748449	>tr|L0KD20|L0KD20_HALHC Potassium uptake protein, TrkH family OS=Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1) GN=Halha_2091 PE=4 SV=1MKKFFNLYNLSSAQILSLGYSTVILLGALLLTLPIATTNGQGMNFLDAVFTATSATAVTGLIVENTASFFTTFGQVVIMCLIQIGGLGIMSMSTLFVFLVGKRVTLKHRLMIQDDLDQFELSGILQLVKYVIAVTFTIEGTGALLLFTRFIQDMPLGKAIYFAIFHSVSAFNNAGFDIFGNSLENFTGDITVNLTITSLIILGGIGFAVIAEIYDGKKFKNFSLQTKLVLSVTAILIVVGMIGAFILEHSNPATLGKLPLGDKLLASYFLSVTPRTAGFNTVPTGALRSSTIFFVIILMFIGASPGSTGGGIKTTTFGALLAVLYSRVTGKDDIEVYKRRLDKEVIFDALSICLIALTIVALVTTILTITEKAPFLDLLFETVSAFGTVGLSTGVTGNLSVIGRVVLIILTMFAGRVGPLTLAVAVAEKRHKANIRYPEEKILVG
2.6E-64	227	25.8	5.5E-64	225.9	17.9	1.5	1	T2KIE6_9FLAO	TrkH system potassium uptake protein	BN863_4840	Formosa agariphila KMM 3901	455	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Formosa, Formosa agariphila, Formosa agariphila KMM 3901	1347342	>tr|T2KIE6|T2KIE6_9FLAO TrkH system potassium uptake protein OS=Formosa agariphila KMM 3901 GN=BN863_4840 PE=4 SV=1MAGMIPIMIGAVVMLATKDHTKEMNKREGYVVVTFGWLVMTLSGTLPYILTQSIPNFTDAFFETMSGFTTTGSSIIHDIEIIPHGVLFWRSLTHWIGGMGIIVLAVAILPLLGIGGMQLFAAEAPGPSGDKLHPRITDTAKRLWLIYFGYTLAETLLLWLAGMTFFDAINHAMATLSTGGFSTKNASVAYWNNHQPIIQYIIIFFMFLAGANFVLSYFAFKGKIQKIFKDEEFKLYSWFIAIFTAIVALIIYFRADLSMSTITHPMVWGQAESAFRHGLFQVLSIITTTGFVSADYTLWTHFLVVFFFGLMFLGGSAGSTAGGVKVVVRHLIMIKNGFMEFKRSLHPNAILPVRYNTKAVSGDIVFNVLAFFILYMLSFIIGALVFSMLGINFESAVGLSASSLGNVGPALGNFGPVTNYAALPAFGKWWCSFLMLIGRLELFTVLVLLTPFFWRNR
2.7E-64	227	7.8	7.1E-64	225.5	5.4	1.5	1	L0ADF0_NATGS	Cation transporter (Trk-type K+ transport system, membrane component)	Natgr_0197 C490_12130	Natronobacterium gregoryi (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2)	514	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natronobacterium, Natronobacterium gregoryi, Natronobacterium gregoryi (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2)	797304	>tr|L0ADF0|L0ADF0_NATGS Cation transporter OS=Natronobacterium gregoryi (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2) GN=Natgr_0197 PE=4 SV=1MTRTRLHVDLRAGLSLVGTILAFLSFAFLVPILVALVYGGEDLWVFVASMAVTAGLGLALRKLDPEPGAREAFLVVALTWLFAAMVGALPYVLAGNGTVAHPVNALFESMSGFTTTGATVMGDISFDTHSRAMLLWRQLTQWLGGMGIIVLAVAILSQMAVGGAQLMQAETPGPGVSKLTPHIAETARVLWIAYIALTVVFIALLYGVHLLGYAPNMDLYNAIAHGFTTLPTGGFSPEARSIEVFSPVVQWLVIPFMFAAGVNFVLWWHVISGDARTLLRDNEFRLYLGATAVLAVLTTAVLFVSALETPETGQISGNLERSARYATFQIASLINSTGYANMDFDAWNGSAKALLLFAMFVGGSTGSTGGGIKILRWLVILKSLRREVFTTIHPEAVRPVRMNGRALDEEAVRGIYAFTLLYVVIFFAGVALFAADASRVGLYADPEFGLLDVISASIATLGNIGPGLGTMTGPMGGYLDFPDSSKLLMTLYMWIGRLEIFPVLVLLTKAYWTD
2.8E-64	227	6.8	6.8E-64	225.6	4.7	1.5	1	Q18JJ2_HALWD	Trk-type transport system (Probable substrate potassium)	trkH HQ_1686A	Haloquadratum walsbyi (strain DSM 16790 / HBSQ001)	534	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Haloquadratum, Haloquadratum walsbyi, Haloquadratum walsbyi (strain DSM 16790 / HBSQ001)	362976	>tr|Q18JJ2|Q18JJ2_HALWD Trk-type transport system (Probable substrate potassium) OS=Haloquadratum walsbyi (strain DSM 16790 / HBSQ001) GN=trkH PE=4 SV=1MSVRVEYKASISLVGSVLKYLTVPLVIPLVVAFWYGESIVPFIATMILTGTVGVILDRIDPSPDIRPREGLLMVALTWIAVTIVGAVPYLVEAHGVPFITPAIHPGSTLANPMNALFESMSGFTTTGATVLGDISFSSHTRSIMLWRQLTQWLGGMGIVVLAVAILPELSVGGAQLMETEAPGPGIEKLTPRIAETARALWVAYLGLTVIQAGLLYGLFITGIDPQMTLYNAVSHALTTMPTGGFSPEARSVEAFSAAAQWIIIPFMIAAGTNFALFWRAATGDPRRLFDDSEFKFYLGVLAALTAVLTGILFSAQSLIITPPAGGTVDAAYLESLRSAVPGQFEPALRDALFQIVIVTTTGYANVDFNAWRTPAQYLLLFAMFIGGSAGSTGGGIKIVRWYIILKTVRRELFTTAHPEAIRPVRLGGKPLDERAIRGIYAFTLLYVVIFFAGVALFAADASRVGLYADPEFGLLDVISASIATLGNIGPGLGTMTGPMGGYLDFPDSSKLLMTLYMWIGRLEIFPVLVLLTKAYWTD
2.9E-64	227	23.2	7.8E-64	225.4	16.1	1.6	1	D5E8T4_METMS	Potassium uptake protein, TrkH family	Mmah_0056	Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP)	481	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanohalophilus, Methanohalophilus mahii, Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP)	547558	>tr|D5E8T4|D5E8T4_METMS Potassium uptake protein, TrkH family OS=Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP) GN=Mmah_0056 PE=4 SV=1MSGLRINIVLGAIGSILWIIGGLMIIPFMVAVYYGESLFPFSLSLTITLLIAFIFSLMLTEERGEWNMREGFMIVALGWLTAAIFSSMPYIFEGTPPINALFEAMSGVTATGATALADIESYSKSLLFWRAMTQWVGGMGIILLFIVVLPKLGVAGRQMFRAEVPGLKEEQLRPRIRETATLLWFVYVGLSIVEFILLYFAGLNAYDAITHTFTSISCAGFSTYSDSIAAFNNTTVEGIFLIFMILGGANIALHYKTIFSDKTSLIKDEEFKFYLLIIALTLVLAYTLTRGEVYAIADSFRYSLFHVVSILTTTGYATTDFNMWPDSSSRFILFLLMFIGGCAGSTSGGIKVVRVLLLMKYADNVLFRTIHTKAIRPIRFNHRRIPEEIMHAIVSFLIIYFMIFIASATLLSLMGVDFVTTLSASIATLGNVGPGLGLVGPMANYGTLPDLGMLVLTANMWIGRLEVFTVMVLLTPAFWRH
3.4E-64	227	19.3	2.8E-63	223.6	13.4	2	1	H1XS24_9BACT	Potassium uptake protein, TrkH family	Calab_2910	Caldithrix abyssi DSM 13497	480	cellular organisms, Bacteria, unclassified Bacteria, Caldithrix, Caldithrix abyssi, Caldithrix abyssi DSM 13497	880073	>tr|H1XS24|H1XS24_9BACT Potassium uptake protein, TrkH family OS=Caldithrix abyssi DSM 13497 GN=Calab_2910 PE=4 SV=1MIHYRSIFHVLSALLLFMIVVLIIPLLISFNFAEPDEIAFLQTMGVLLIVALPLFLLTRGEVTLDIKDGFLIVTLGWTLYALFGALPFYFSGFIPSYTDAFFETMSGFTTTGASILTDIEALPEGLLFWRSLTHWLGGMGIILLSLAILPLLGIGGMQLFKAEVPGPTPDRLTPRIKHTAELLWVVYVAISVIEAVALKLAGMNWFDAWCHTFGTMATGGFSTKNASVGAFNSGLIDYIIIIVFMIIAGTNFSLHYRAFKGKFFSYFKDPETLTFMAIILAATVFIAIDILSILGYEQFSFRHVLFQVVSIITTTGYGTSDYEQWPILSKVVLIILMYFGGCAGSTGGGMKIIRSIILFKFAINQVKQLLHPNAVFVVRVGKRSVPQEIVTNIAGFTLLYILLSIIGVLFMSGLGLNWETCIGSVAATINNIGPGFGSVGPTENYAHLPLIGKWFLSFLMLAGRLEIYTVLVLFVPIFWKR

3.4E-64	227	22.7	1.1E-63	224.9	15.7	1.6	1	Q465Z6_METBF	Trk system potassium uptake protein	Mbar_A3423	Methanosarcina barkeri (strain Fusaro / DSM 804)	476	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina barkeri, Methanosarcina barkeri (strain Fusaro / DSM 804)	269797	>tr|Q465Z6|Q465Z6_METBF Trk system potassium uptake protein OS=Methanosarcina barkeri (strain Fusaro / DSM 804) GN=Mbar_A3423 PE=4 SV=1MNFRVVLYVLGGLLRLLGLIMIVPLGVAYYYGESLTPFLVSILITTLTGFLLLSYKTEEEWMRKEGFAIVALGWLAAAVFGAIPFMLDGISPLNAVFESMSGFTTTGSTILTDIESHPKGILFWRGMIQWLGGMGIIVLFIAILPKLGVAGRQLFRAEAPGPTEDKLKPRIKETARILWVVYFAISFLQVIVLLLAGVSLYDAVNHTFTTMACGGFSNYSLSVEAFNSPLIEFIITFFMFVAGANFALHYRAIYIDKKFLLKDDEFRFYTGLVLSATGLLAILLWRDMGTGIFNSFRFAIFQIVSIITTTGFATADFNLWSDSAKMVLILVMFIGGCAGSTGGGMKVVRILILLRYSRAELFKVIHPRAIRAVKFNNKNVSDEIVNSIVSFVVIYLLVFLLSTLILSVLGMDIITSFTASIATLGNIGPGLNVVGPMSSFDSVPALGKLVLIANMWIGRLEVYTVILLFTPEFWSK
3.6E-64	227	23.9	5.2E-64	225.9	16.6	1.1	1	B8HR41_CYAP4	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cyan7425_5257	Cyanothece sp. (strain PCC 7425 / ATCC 29141)	443	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7425 / ATCC 29141)	395961	>tr|B8HR41|B8HR41_CYAP4 Potassium uptake protein, TrkH family OS=Cyanothece sp. (strain PCC 7425 / ATCC 29141) GN=Cyan7425_5257 PE=4 SV=1MTVSRTICLGFIAVILMGAFLLLLPVSTASGNWNDPIVALFTATSAVCVTGHIVVDTATYFSTIGQATIAALVQIGGLGYMTATTFLLLVIGRKFNLREKVALQQALDRQGMQGVAQVVRSIIATTALFELTGIFLLLLVFVPDHGWGRGLWLSIFHSVSAWNNAGFSLFSDNLVGYQSSILINLVIPGLIILGGIGYEVIFEFYLWLRSSLSPKPEVMIFSLNFKVATSTTLVLLVGGTITLFCTELRNPATSGLSLDTQFLLAWFQSVVTARTAGFNTVDIGKMTNAALFVLIALMFVGGSPGGTAGGIKTTTFRVLTRITRSILQGKEEVLLYERKVPDSLILKAVGVTVGSIAAVIIATFGISITDPEVDFIRILFEVVSAFGTVGLSTGITAALSAPAKLILIAMMYVGRVGVLLLMSALVGDPRPSAIHYPEENLLVG
3.7E-64	226	27.6	7.5E-64	225.4	19.1	1.4	1	A0A0F2JIZ3_9FIRM	Potassium uptake protein, integral membrane component, KtrB	UF75_0349	Desulfosporosinus sp. I2	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	1617025	>tr|A0A0F2JIZ3|A0A0F2JIZ3_9FIRM Potassium uptake protein, integral membrane component, KtrB OS=Desulfosporosinus sp. I2 GN=UF75_0349 PE=4 SV=1MNALGKIMTPSRVLVFGFAGFILFGALLLTLPQATQDGLGLPFLNAAFTATSAVCVTGLVVVDTASTFTLFGQWVILFLIQVGGLGFMTFATLFAMLLGRKITLKERLLLQEALNQVSVEGIVRLTKSILKISFAIEAMGALILTLRWYSDFGWSKALYYGVFHSISAFNNAGFDLFGNFSSLTAFVGDPIVNITIMLLIICGGLGFIVLADLLGPRKRFRLHTKIVLQVSVALILLGAVFILIMEFTNPKTLAPLPFGTKVLAAFFQSVSPRTAGFNTINLAGMRDTTLLSMIVLMFIGASPGGTGGGIKTTTFISIVLSVLSTYRSDPHVVLEGRTLPKDVIQKAWAITTSAAILIFLILSILSYTENSDLLTVLFEVTSAFGTVGLSLGITPTLSSVGKMAIILTMFIGRVGPLTLAFVLSQKKAKQVAHVKYPDERILIG
3.8E-64	226	33.6	7.1E-63	222.2	23.3	2	1	T0VMF4_9ENTE	Potassium uptake protein, integral membranecomponent, KtrB	HSIEG1_779	Enterococcus sp. HSIEG1	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	1316414	>tr|T0VMF4|T0VMF4_9ENTE Potassium uptake protein, integralmembranecomponent, KtrB OS=Enterococcus sp. HSIEG1 GN=HSIEG1_779 PE=4 SV=1MKKRMSKKISAPQLVTLVFMMLILMGTGLLMLPVVTNDGQGVPFLDALFTATSAICVTGLSTFSISEQYNMGGQAILLILIEIGGIGFMSIPVFFYILAKKRVNLSTRMILRESLNLDRMSGEFQLAWYIIRIAFLIQFLGICLLALSFVPRFGWQQGLWFSIFHAISSFCNAGFDLFGNSLVSFQSDPFVLGVISLLIIAGGLGFLVWFDLLATSKRRSLHSRIALLAMIVLLILGTVGFYVTEYHSSIVSGDSIVSRFFQLFFLAVTPRTAGFYSIDYGQMSQAGLMLTMILMYIGGTSGSTAGGLKTTTVSVLIIKIRSLLKGRKRAEVFGRTIKEAAVSRAFTLFFLTLSLCFIAIFLSITESMPGNSQFGLEYIAFEVFSAFGTVGLTMGLTPYLSVFGKLLIILLMFIGRVGIMTVAFSLMTKANRREAGYKFPDETVMIG
3.8E-64	226	11.9	4.1E-63	223	8.2	1.9	1	R5DCS0_9FIRM	Putative Trk system potassium uptake protein TrkH	BN795_01596	Firmicutes bacterium CAG:83	481	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:83	1262992	>tr|R5DCS0|R5DCS0_9FIRM Putative Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:83 GN=BN795_01596 PE=4 SV=1MNFRLILNIMGYTLWVEAGCLLLPLLVSVGYGEACWEPFLWTLGLCSLCGLILTHIPARKNRLQGRDGYAVVAMAWVVLCLFGAVPYVLSGAVPHYADALFETASGLTTTGATILTDVEAMPRGILFWRALTQWMGGMGVLVLFLALMPWTGAGGVHLMRAESPGPIKSKLLPHVNDTAKVLYGIYIGLTTAEIVALCLAGMDLYDAVVHSFATISTGGFSTRNASIAAFGSPAITWIVAIFMFLSGINFSLIFISLRGHIREALHSEELRLYTLLTLGSIGLIAASLMVQQSVPLGRALKDSVFNAVSTVTTTGFATADFAQWPVFGQMLLVILMFTGACAGSTSGGIKVSRILLLGKLLHREIKKILHPKHISVITVDGQLVEDRVVSSAAAYMVAYMILLLGGATLLAWDNLGFTESFTAVLTCLGNVGPGLGRLGPAGNFSPFSGFSKVVVMSLLMLLGRLELMPILVMLSPRMWRER
3.8E-64	226	32.1	9.6E-63	221.8	17.1	2.9	1	A3HRV3_9BACT	Trk system potassium uptake protein TrkH	ALPR1_10160	Algoriphagus machipongonensis	482	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cyclobacteriaceae, Algoriphagus, Algoriphagus machipongonensis	388413	>tr|A3HRV3|A3HRV3_9BACT Trk system potassium uptake protein TrkH OS=Algoriphagus machipongonensis GN=ALPR1_10160 PE=4 SV=1MIHFKEIGKIMGALLVLIAIMMLPGIGFSIHFEEDPWPILSSAVITLIIGTTLFFSFSKQDQNIRKREGYLIVTLSWIFMAGFGMLPFILSHEIISFSDALFETTSGITTTGASILNDIEAMPKGLLFWRSMLQWIGGLGIIVLTVAIFPLLGIGGIELFVAESPGPTSDKVHPRISETAKRLWYVYVGLTFAATILYWVGGMTFYDAINHALTTLATGGFSTKNASMAHFDSAFIQYTAIVFMFLAGTNFTVIYFGLVGQFRKVLKSDEFKAYACVVLGITVVLFFPIYAQIGTDAELAFRNSMFQVVSLITTTGFVSDDYTQYGQGVTFICFILLFVGASAGSTAGGIKFVRHLTFFKNSYLEFKRLVHPRAIVPLMINGDRVTGRIITHIMNFLLLYLLIFVFGAFVLSIMGYDLPTSLGAVATCLGNVGPAIGDVGPVDNFSFFSPGAKIFLSFIMLLGRLELFTILILFTPFFWRAN
4.2E-64	226	9.4	3.5E-63	223.2	6.5	1.9	1	R4VYY9_9EURY	Cation transporter	L593_12705	Salinarchaeum sp. Harcht-Bsk1	502	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Salinarchaeum, Salinarchaeum sp. Harcht-Bsk1	1333523	>tr|R4VYY9|R4VYY9_9EURY Cation transporter OS=Salinarchaeum sp. Harcht-Bsk1 GN=L593_12705 PE=4 SV=1MALTGTVCKYLAITMVVPLLTAIVYGGDLLVFVGTMTLTVGIGLLLERIEPQPDLGAREATLLVTIVWFVVAVVGAIPFVLAGWGTESTLAHPVNALFESMSGFTTTGATVMGDISFDQHSRALLMWRQLMQWLGGMGIIVLMVAILPELAINGSQLLQAEAPGPELQKLTPKIAETARVLWLVYFGFTIVYVALLYSLHLLGFAPDMTFYMALSHGFTTLPTGGFSPEADSIAAFSAAVQWVVIPFMVVAGTNFALFWATIGRNRRALVEDTEFRAYAGAIAVFSALASATLYLGTAPPLGALGGVTEGIAGDALRHGTFQIASLLTSTGYATSDFASWGPAGQMTLLIAMFVGGSAGSTGGGIKVIRWVIALRAVRRELVTSAHPDAVQPVRLRGRVVDEDAVRGVLVFTFLYIFVFGIATLLLTLDAARIGYELNGYEAISASLATLGNIGPGFGSLGPFGSYLEFPWTSKLLMVFLMWFGRLEIIPVLLVFSGSFWNR
4.4E-64	226	22.1	5.9E-62	219.2	15.3	2	1	F6B787_DESCC	Potassium uptake protein, TrkH family	Desca_0444	Desulfotomaculum carboxydivorans (strain DSM 14880 / VKM B-2319 / CO-1-SRB)	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum carboxydivorans, Desulfotomaculum carboxydivorans (strain DSM 14880 / VKM B-2319 / CO-1-SRB)	868595	>tr|F6B787|F6B787_DESCC Potassium uptake protein, TrkH family OS=Desulfotomaculum carboxydivorans (strain DSM 14880 / VKM B-2319 / CO-1-SRB) GN=Desca_0444 PE=4 SV=1MHINLVLKTLGLVLLFEAAAMVPSLFVGLFFHESNPQPFLISITAAGLVGLGLYLVPIKNKNVGYREGFAIATFGWLLLAIFGAIPFVLSGALPSYVDALFETMSGFTTTGSSVLTNIEILPKSVLFWRSMTHWLGGMGIIVLTLALIPSLNIGGMQMFKAEVPGPTKSKVLPRVAQTSRQLYKVYVIITVTQIILLKLAGLSWFDAAIHSFGTVATGGFSNYNASVGHFQSVSVEIIIIFFMIISGMNFSLHYYAMRGNLAPLWKDRESKLYLGVIVVSIALIIIDLMNNMDYAATKALREASFQVTSIITTTGFATADFEKWPPLSKFILLILMFFGGCAGSTGGGLKAGRILILFKSVSCQLTRLIHPQAVLRVRIGRDVVNHEVVESVYNFFTLYILIFAAGALILTGLGLDILSAASASITALGNVGPGLNLVGPMSNFSGVPDLGKLTLTLLMLIGRLEIYTVLVVFSVRFWR

4.5E-64	226	28.3	2.2E-62	220.6	9	3	2	A0A0D2WXT2_CAPO3	Uncharacterized protein	CAOG_010143	Capsaspora owczarzaki (strain ATCC 30864)	2589	cellular organisms, Eukaryota, Opisthokonta, Opisthokonta incertae sedis, Ichthyosporea, Capsaspora, Capsaspora owczarzaki, Capsaspora owczarzaki (strain ATCC 30864)	595528	>tr|A0A0D2WXT2|A0A0D2WXT2_CAPO3 Uncharacterized protein OS=Capsaspora owczarzaki (strain ATCC 30864) GN=CAOG_010143 PE=4 SV=1MSHSSHSNPPAESAYLREGQKPELLSFPSDDSSQPHRASLDQQHHHPQHQHQLQEGEEEQDHHENNSNNIFPLPASSHAHYP TTIAPLSTSTATAAAAAAAAAAAATTSTAAAASLGAGLGGDGAMLSECSTATPPTPATAIPTASDAANPLPSSSSSSSSSTSSTSTSPS SSSSSPAPGSAPVDRTALSSSSSAAAAPPAPLSSDIASIAPLAHHHHDYQHHHHPSTGRSAVDPSLNQSPQQQQKPASLENRFDQVS AATAQLAQLATTTTTTTTTTMTASNDAGNAVNWPSLESGSATTAAGGGVNESSPRANGRSMEQANTNTTTATAIATTTADKHSASTE ITHLASTGHRDEAEQEQVDHAANGHHASRDKTTTSTTTTPPTATTTTTTTTLAYAAADAYQADPITASQSLDLVSSSTALLLAPAEKDA QGIFLPEQQQQQQQQQQQQQQQQQQQQQQQQQQQHPDMLESPAAASFDHRPPELQRTDPLQRTHSLSSFDSGQSNRQQSGGGGSRRD SPAPSRSSQHLPPRGSRGLRQRRRQSKRHSIHRQSTNSLAISMSENPSTETDSSNRSLFGGRSRLGLWLQIQLRPVMRPLSRTWRR MWRSPFGLWLIIKWSMFWSFVSPHINFYRVHWLYMFCLSLFGGVILYGIQLNSAQPIDFVDALLTAASCMGQAGLSSYDISYSPLASQ IVMALIIIAASPCLLTIVPVIMRRIYFRRQLVKYGLSRFRSDLAEYMALKQLLKIVPIYWISCHVVGFIGLFIFMSTDSGAIEVMTVNNQSTV WFSAFATISAFQNNGFGLLSANFVPIAPFKFPLVWLGLIIICGNTGFPLLLRLIVVGRYYLAKGTKKEPTYKFLLDHPRRCFTHLFPRAQY RWLLLVFILLFLVHFVAMLAFEWNEISFATFDVGDRITNSFFQVFNARTCGMNSLDLSILEPGLLVLFVIMMYISSTPITVALRNSELDER TSGKKATTVTERDVSGGLWSAATENSTANTINHQVKRVMTQDSIFLAVCIFVIVTIETSHMESDPLNYTFFKILFEVISAYGNVGLTLGT RGSNVPFCGSWYTGSKLVLVLVLLVGRHRGLPNSIDKAVQVPRKIFSTMPSRHASDDEDSADGVSYTSRRSRRGRSSSTGVVRLSN VSNIAAPSVGGDLGDGVVALSMDNRANPDPSHAQDSDTASEVSGSASSYSSRGSSDGRRGRRRRHGRRSSRHSRSTYSRGSRRR SRSSRSGSSSFSGSSSRSQSPMRSRPSQSLGGPTDFELVELSHSGGIAAAEQSHQPLPAAAISVSNDVTLIAADESVSSVPLQRNYWD VTAEQLVGRANSTPLLIGNSAALTAVAAKSAHEEGTFANSTSAGGAEVSAPATAAAAAAATTPAPAAAAPPVPGSTVLKSGNLLANLS FLSLTSVEKWASHAASVSSTATPNSVFPQPVLQQRAIESVASSSLPPDSEQPTAASSVQHLSPAVSSVDVRVAKSLTDSAPATNVVS SELASTTPTTTTTLAAETRGGVAGPLQQLASSGAAVAANVDPAKLATAVTSTASSTTGTPPQVGMLGRSASNSLVHPPPLNLNDSLN HSNPSSVAQTPASSRPISPPATADAIHSSPSQVHLQLLIAQQHAARAFQQGSGGAGEPTASGPSSSGLRSNPLSFLLQTGPDGSLMF PTVVMTEQQLQRLQQQQQQQQQQQQQQQQQQQQQQPSDSAHGPSVVVGTRGLGHLSRAASDLGVLPLGSRSPGGQPGATSGLALGTF LPRSPLDQPHQLDLRYSGHNSPAAVPSPSAPLRSGELSSAPSITGLDEPLHIGFISLAQLGPAGVNIAQELAHLAAKPVSAQSPSHQPS GSPFGMPSQPSQLSLQQHGGQSQSHAHAHSHSHSHSQPSSQPHSQRVTRANSPENESDRHHHSGHHHHSRHGHHHHHRDHGS SHHSSDTTGDGHARSAVHSPDHQSSSSAIDSSSSSTHHHHSHGHHHHRSHSRHHGSHHDDHHHSPSHHDDRPHSSHHDSRHHSSS SSSSAHHEDRHHPSSHRDDRHHSSLRDDERHSRSSPHQDHHHSSSSAGGGHHEGPSHRSSSASSSHHHGSHHHHHHSSSSSSHG NHHSHGSSSQSSSHHHASRRRRVRHVSIGEPSTDESDESDENDLLTYGVVPDSHDADMVILGATPARKVFVAQSSSSSESDSETSP SASRPKSPKTVEPAPPVVRVPATGGSTTAPSGPSKSAATFRRIFSNGGLLSLGSSSRNSLARGSTDPESAVPSPSSAPSLAAVALAAL AAHRETKKSHDLSPSSTTPDIAPSASVSSMSPSNAASLHDLSAQDSPLSRDSSGRSDTLPQQQQQQQQQQQQQQQQQQQQQQQQQR DASSPSGGMEGAGSRHRSQQEFAAESSNVPRVPSHLSFVRQSSGHGSSHLSSHHHSSHHGSHHHHGHHGHHHHHETVVHFDLSP TATLQQTGDHHPIKTPASMNAQPLKSALASSNRSKLGLNVRSQSMNSQFSMESAHSSASPGHLPPFSVASTTSPASTPLSTHPEHSP SWPVISKVHHGLSPPASLPITTAAMASSEPLAPVVESALAPPSHTVVEPPAPEATLTSPKRILFFQGHDDDDDDASMA
4.7E-64	226	28.8	1.1E-63	224.8	19.9	1.5	1	F0LKU2_THEBM	Potassium uptake TrkH-like protein	TERMP_00694	Thermococcus barophilus (strain DSM 11836 / MP)	494	cellular organisms, Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae, Thermococcus, Thermococcus barophilus, Thermococcus barophilus (strain DSM 11836 / MP)	391623	>tr|F0LKU2|F0LKU2_THEBM Potassium uptake TrkH-like protein OS=Thermococcus barophilus (strain DSM 11836 / MP) GN=TERMP_00694 PE=4 SV=1MLGVRRYINLTEDLFVVKNLIGALLQGIGLAYLIPPLIVWFYPNEIVYVYYFVIPGVISILLGAWLGRHVKMIEDVNLRQAMISAAFV WLFASFISVVPFMKIAHMSFIDSYFESMSAWTGTGLTMMSNLESYPHILLFWRSWMQWLGGIGIVLVALTILIRPGVAAARLYKAEART ERILPNLANTSKIIFQIYAILTLLGIYLYYINGMPMFDAVIHSMTGLGTGGMSSHDLSIGYFNSLSIEAVTIFLMIMGAVNFTVHYKMFKNRS IRHFFEDIQVRYMFIFLIPTIVLIGYSLITWNHMQIAKAFRESVFHAVSAITCTGFSIDDLSKYPELAKLLIGFLMVVGGGAGSTAGGIKLIRI TLTYESLKWTIQQAILPKGAVIKRKVGNYIFSEDEIQEVFSFTMTYFAFLLIGTVWVMARLGVSIANAFFEVASAQGNVGLSVGITSPAL PLDIKILLILHMWIGRLEIFSTLVFIVSALMLIPRVVERE
4.9E-64	226	17.2	9.6E-64	225.1	11.9	1.4	1	I4BWK2_ANAMD	Potassium uptake protein, TrkH family	Anamo_1034	Anaerobaculum mobile (strain ATCC BAA-54 / DSM 13181 / NGA)	483	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Anaerobaculum, Anaerobaculum mobile, Anaerobaculum mobile (strain ATCC BAA-54 / DSM 13181 / NGA)	891968	>tr|I4BWK2|I4BWK2_ANAMD Potassium uptake protein, TrkH family OS=Anaerobaculum mobile (strain ATCC BAA-54 / DSM 13181 / NGA) GN=Anamo_1034 PE=4 SV=1MRFKIILRVLGLIVEVVSFFMLWPLVWAVLDRSHDVGAIFTSMIIGIALGVVLLLYGGNNASEDMRPKEALVTVGLSWLVVSAIGA LPFWLSGSAPSFTDAFFESVSGFTTTGASILTNIEANPRGILFWRSLTHWLGGMGIIVLGLAILPFLGVGGRQLFHAEVPGPVPEKLTP RIHHTALLLWGVYVFLTILETLFLYFGGLSVFDALTHTFGTVATGGFSPLNGSVGQYNSVYVDVVITVFMFISGANFALHYRMLKKDFT AWWKDEEFRFYLYIVLGSIATISLVLLKDHIYSSISDALRYVSFQVVSIMTTTGFVTADFEQWPAYAQLLLILLMLIGGCAGSTGGGMKV VRLLILLKHLSIELKTMLHPRAHYAMRLNNNTVEKEIALSISAFFVLYFAVFVVSFLLLSLMGMDFISSVAAVAATLGNVGPGLGAVGPM DNYSALAAPAKWILSFCMLFGRLELYPMIALFLPDSWKR
5.2E-64	226	18.5	7.8E-63	222.1	12.8	2	1	Q0AYH5_SYNWW	K+ transporter trk	Swol_0913	Syntrophomonas wolfei subsp. wolfei (strain DSM 2245B / Goettingen)	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Syntrophomonadaceae, Syntrophomonas, Syntrophomonas wolfei, Syntrophomonas wolfei subsp. wolfei, Syntrophomonas wolfei subsp. wolfei (strain DSM 2245B / Goettingen)	335541	>tr|Q0AYH5|Q0AYH5_SYNWW K+ transporter trk OS=Syntrophomonas wolfei subsp. wolfei (strain DSM 2245B / Goettingen) GN=Swol_0913 PE=4 SV=1MIRTRVILGYLGRIILIIGISMLSSVLCSLYYRESIIIPFSLAAGVTIVTGLLLVFSAEKQAIHYKEGFVIVSLGWLLASLFGSLPYIFTGC LPSFADAFFETVSGFTTTGASVISNVEATPKGLLFWRSLTQWLGGMGIIGLFVAIISGMGAQANHLFKAEVPGPVANKISPRVRETAKK LWITYIVLSVCCTVLLYLFGMNIFDSLCHTFATMATGGFSTRNASVGYYNSPLIQWTLTLFMFIAGVNFTLHYLGFKQRNLQVYLKNRE FLFYTAIVVVASLLVTLSLSLGGSELSTEGKLRAAFFQVVTIVTTTGYSSVDFELWPNMALGIIFLMMFVGGCAGSTGGNIKPGRYLILL HRSIIEIKRIIHPKAVISLRFNDRIISDSLLINVLQFFFLYIMFLALGTIGLSCLDVDLITSLTAAASCLGNIGPGLGQVGPMDNYSFIADSGKY LLSLLMLIGRLEIYPLLLLFLPDFWRE
6E-64	226	23.8	5.6E-63	222.5	16.5	1.9	1	R6RLG4_9CLOT	Potassium uptake protein TrkH family	BN719_02216	Clostridium sp. CAG:58	455	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	1262824	>tr|R6RLG4|R6RLG4_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:58 GN=BN719_02216 PE=4 SV=1MWQNLKWEINAKFKEKIHRHVSSFQVIILGFMLVILLGSLCLTLPLATRDGQGASFLDALFTSTSAVCVTGLVLHDTASYWSVFG QAVILFLIQIGGMGVVTVSVAVAIFSGRKISLMQRSTMRESISAPQVGGIVRMTEFILKTVFLVELLGAVAMAPVFVRDFGFLKGVWYA MFHSISAFCNAGFDLIGIRSPFSSLTTYASQPVINLTIMALIIVGGIGFLTWEDVKRNRLHFSRYRMQSKVILVTTAVLIAAPAAWFFFFEF SELPLGTRLLSSLFQSVTPRTAGFNTADLTKMTEAGQMLMIVLMLIGGSPGSTAGGMKTTTIAVIFSSARAVFRQKERAHFFQRRIPEE AIRNAGAILLMYLGLFLAGGMFISYEEGIPLLDALFETASAIGTVGLSLGVTPELGRISQLILIGLMFFGRVGGLTIIYAAVSSRCVSGSAF PQERITVG
6.1E-64	226	14.3	2.3E-33	124.9	0.6	2	2	I7BJ56_NATSJ	Cation transporter	NJ7G_1105	Natrinema sp. (strain J7-2)	514	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema sp. (strain J7-2)	406552	>tr|I7BJ56|I7BJ56_NATSJ Cation transporter OS=Natrinema sp. (strain J7-2) GN=NJ7G_1105 PE=4 SV=1MRVRTDWRASVALVGTVLKYLSVPLVFPLVVALIYAEPVVPFLATIALTIAVGHGLEQLCPDPDLQVREAMLFVAISWLAVAMIGA VPYVIAGWGTESTLAHPVNALFESMSGFTTTGATVLGRISVDDHSHAIMMWRQLTQWLGGMGIIVLMVAILPELAVSGAQLVESEAP GPQLQKLTPRIAETARILWLVYFAFTVVYIAILYGFNLAGMADEMTLYNAIAHGFTTLPTGGFSPEADSVAAFSAIVQWTAIPFMIIAGTN FALFWHVFSGDGHRFVRNSEFRAYIGAIAGLTVLLAGILYTGAAPPLGDLGGVTAGVFENSLRQSAFQIVSLLTSTGYATSDFVDWSS TGKIVLLFAMLVGGCAGSTGGGVKVVRWLIVFKVLRRELFTASHPEVVRPIRLGGNIVDEDAIRGVLGFSFMYLIIFALATLVIALDVSRV AAIEEFTALEAFSASLATIGNIGPGFGFLGPFGNYNAFPIPSKLLMVFLMWIGRLEIIPVLVMFTGGFWTR

6.3E-64	226	31.7	8.5E-64	225.2	22	1.1	1	O67474_AQUAE	K+ transport protein homolog	trk1 aq_1504	Aquifex aeolicus (strain VF5)	443	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Aquificaceae, Aquifex, Aquifex aeolicus, Aquifex aeolicus (strain VF5)	224324	>tr|O67474|O67474_AQUAE K+ transport protein homolog OS=Aquifex aeolicus (strain VF5) GN=trk1 PE=4 SV=1MVKKLNPSRTLLFSFSLLILVGALLLYLPISTTRPISFLDALFTATSAVTVTGLAVLDTYSDFTLFGKLVILFLIQVGGLGYMTLSTFFLVLLGRRIGLKERLILAESLEYPSMHGLIRFLKRVFSFVFITELTGAILLSIYFSLKGVEDPVFNGIFHSVSAFNNAGFSTFKNGLLDFRGDLFVNLVISFLIILGGIGFFVVNDIYLWYTKKVPRLSVHTKLVMITSVLLILLGTVGLIFTEFGNYKGLWQYDWYERILSSYFMSVSSRTAGFSTVDLIDMSESSQFLLMILMFIGASPGGTGGGIKTTTFVVILIAVYSFVRGREQSVIFERSVPESTIKKALVILSLSIFFINFVNLMLDKFENKDFLYTMFEVVSAFSTVGLSIGNPEGLSFCADFSPLGKIVIIITMLVGRLGILGFALALTGRSEVQRIKYPEARILV
6.4E-64	226	34.9	6.4E-64	225.6	24.2	1.4	1	R4U4U9_9MOLU	Potassium uptake protein KtrB	ktrB SSYRP_v1c09180	Spiroplasma syrphidicola EA-1	522	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma syrphidicola, Spiroplasma syrphidicola EA-1	1276229	>tr|R4U4U9|R4U4U9_9MOLU Potassium uptake protein KtrB OS=Spiroplasma syrphidicola EA-1 GN=ktrB PE=4 SV=1MQIYQQFFKNIFKRKHEPSKGKGEDTAAPITRSRFHFLPFSKVAGKLFLIYVLVVFITGFLLSVPGIVVGNRIVYDPWGEIIGEYNFQWNFLVGLFTASSAFSDTGLSIANAAADYTFFGQFIIIVLIQIGGFGVLTFKVMLLVLLGRRISIKDRQLVQGERGSSNFGQTMDLIKNSFIFLVIIEFIAAVLLFFNFYFSPGSTAGEHMIDNVTYHDFWNSLWSGVFHSVSAINNAGFDIIGNSSLMPYNGNYFMQFIFLFEFVIGGLGFPTFYDLKRKIIAWKNKENVKFSLFTKINFITYVLISFVGVFGVWLIEFVNINAPGESILAQASSNWNGFMNVFFNTMSTRNAGFSTVDMTKFLPGSRAIMSMMMFIGSAPSSTAGGIRTTTFAIIILAIWSVIRNNDSVNVFKRKIPNETVKRALVVTVISGMLVGLAVTIICAENPHLNFLNVLFTICSAFGTVGLSAFSFTEMYGLGVFSTLVLILLMFIGQLGVSSTLLVSVRGTGKKEYSYVEENIVIG
6.5E-64	226	19.6	9E-64	225.2	13.6	1.1	1	M5A0L3_9ACTN	Ktr system potassium uptake protein KtrB	ktrB YM304_20740	Ilumatobacter coccineus YM16-304	462	cellular organisms, Bacteria, Actinobacteria, Acidimicrobiia, Acidimicrobiales, Acidimicrobiaceae, Ilumatobacter, Ilumatobacter coccineus, Ilumatobacter coccineus YM16-304	1313172	>tr|M5A0L3|M5A0L3_9ACTN Ktr system potassium uptake protein KtrB OS=Ilumatobacter coccineus YM16-304 GN=ktrB PE=4 SV=1MIDRRGGERSGVRRVVARRSRSLATPTRLITLSFAGAIALGTLLLALPVSHGDRRIGVLDALFTATSAVCVTGLAVVDTGTAFSGFGQFVILLLFQLGGLGLLTIGTLLALATGRRLGVGDRLKVQEQVTGSDAGGIVALVRSIAVVVALAEITGALLLYSRFASTEGIGTGAWHAVFHSVSAFNNAGFSLNSDSLMGYVDDPIVNVTVMLLIVVGGLGFMVITNLYRWSQRSSPRVRLTLHTRMVVSMTAFLTAAGASLILITEWNNDDTLGALGAPGRVLAGIFQSVTPRTAGFNTVDYGDLTTAGLLVTMLLMFIGGNPGSTAGGIKTITFYVVVLSIWSTLRGRADTTVFHRRIAQETVARAAAIAGGAAIVGGAAVTMLAMLEPDIALQSLLFETISALGTVGLSVGITAELGDSARLIVIMLMFVGRIGLLTFALALVSRERPTTMRHPVEDVVVG
6.7E-64	226	33.4	9.5E-64	225.1	23.1	1.1	1	K8E6P8_CARML	Ktr system potassium uptake protein B	ktrB BN424_3134	Carnobacterium maltaromaticum LMA28	434	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium maltaromaticum (Carnobacterium piscicola), Carnobacterium maltaromaticum LMA28	1234679	>tr|K8E6P8|K8E6P8_CARML Ktr system potassium uptake protein B OS=Carnobacterium maltaromaticum LMA28 GN=ktrB PE=4 SV=2MALGFLSTIFIGGILLSLPFASQSNQATNLLDAFFTATSAVCVTGLTTLNTAVHWSLAGKLIIMLLIEIGGLGFMSFTIIILLASRKKINFRTRIIMKEALNTNQLSGGVNFIIYILKFSVGLQLLAACLLSIDFIPRYGLAKGAFFSLFHSVSAFCNAGFDLFGNSLESFQKNPLVLGVLSFLIIAGGLGFIVWRDLLTYRKNKRLSFHSKLTLRVTFILLIGGFLFFLLTEQNLSHLKDLTFGERLMNTFFLTVTPRTAGFNSVSFSGLSQASILLSCFLMYIGGSSGSTAGGIKTTTLGILVLMHAYSVFKGEERTQFSGRSINPTLINRAFVLLFITMTVITTAIITLSITETIPPDFGIEYIVFEVFSAFGTVGVTLGLTPQLTAIGKIIIMALMFTGRIGMFTFLLSIIKRTNQANTKIKYPEENVIIG
6.9E-64	226	35.4	1.3E-63	224.6	24.5	1.3	1	F0SYQ7_SYNGF	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Sgly_0493	Syntrophobotulus glycolicus (strain DSM 8271 / FlGlyR)	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Syntrophobotulus, Syntrophobotulus glycolicus, Syntrophobotulus glycolicus (strain DSM 8271 / FlGlyR)	645991	>tr|F0SYQ7|F0SYQ7_SYNGF Potassium uptake protein, TrkH family OS=Syntrophobotulus glycolicus (strain DSM 8271 / FlGlyR) GN=Sgly_0493 PE=4 SV=1MSEIFKITDRSAATPKKQGRSPAQILALGFLSVILIGTFLLTLPVSTADHLGLTFLDALFTSTSAVCVTGLAVVDTSAVFSVFGQIVLMVLMQIGGLGFMTIASFFAILLGRKINLKERMILQEAYNQSSLEGIVKLAKYVFLFAFILEGIAVIILFLRWSSYMSFGKALYFSLFHAISAFNNAGFDLLGNSLMDFHHDIVINLTIMTLIIIGGLGFAVISEIYSKRFRKISLHSWLVLRTTGILILAGAIIFFLLEFNNTNTLGNLSIQDKLLSSLFQSVTPRSAGFSTVDISSLGDTAKLLLIVLMFIGTSPGSTGGGIKTTTFVAILSIFCTLKNKRQITIRGRALAKETTEKAVALAALAIMWIILVTGLLTLTERSDFLPLLFETVSAFSTVGLSLGITANLSDIGKLLLILTMFIGRVGFLTLAFAIGKRRVAGNQAKYPETKIMVG
7E-64	226	25.5	2.9E-63	223.5	17.7	1.7	1	A0A0F2SD02_9FIRM	Membrane protein	VR66_11595	Peptococcaceae bacterium BRH_c23	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c23	1629714	>tr|A0A0F2SD02|A0A0F2SD02_9FIRM Membrane protein OS=Peptococcaceae bacterium BRH_c23 GN=VR66_11595 PE=4 SV=1MNYSLVEDILGRLMVAYAAFMGAPLLVSLIWQEKSMLAFLISIVVTLILGISLVAHGQKDGRMGLREGFVIVASAWLLTGITGALPYALSGAVPTYLDGLFETVSGLTTTGASVIDNVEILPKSILLWRSMTQWLGGMGIIVLFIVFLPNMTGTVHLFNAEVPGPISERVLPRIRDNALKLWQIYLGFTVLQIILLILVGMTWFDAINHSFTTMATGGFSTKGASIMYYDNWGIELIIIIFMIIAGGNFGLYYLAWRSGVKKILKDVEFQFYLLIIAVSTLTITLSLWWTMGTGVSNSLRQALFQVASIMTTTGYASADFNQWPSVSKFILLCLMFIGGSAGSTAGGIKVSRIILLFKLGWAELKRAIHPKAVINVRFAKRSVDPLVLNTVAVFFFLFLSIFAFATLLITATGLEPFDAMSAVAATLGNVGPGFGVVGPMTTFSSINAFGESVLILCMLLGRLELFTLLVLIQPEFWRSRKGW
8.5E-64	225	9.2	2.7E-30	114.7	2.3	2	2	R5RVY6_9FIRM	Trk system potassium uptake protein TrkH	BN483_00615	Firmicutes bacterium CAG:129	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:129	1263003	>tr|R5RVY6|R5RVY6_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:129 GN=BN483_00615 PE=4 SV=1MNKKLIFKILGIILGIEGVSLLIPFVIALVCRENTAVFGITALLCLAVGLPLSRLHTAKSRLQNRDGYVAVALGWIVLSAFGALPYALSGCCGYVDALFETVSGFTTTGASIFGAPASLPRGIQLWRALTQWLGGMGVLVLLLALMPKLGEGSVNLMKAESPGPISSKLLPRTNDTAKMLYSIYILLTAAETLALRAARIPWFDAVTTALTTISTGGFSVRNESIAYYQSSAVNWIIVVFMFVSSVNFTLLFLAGTRRWREVLRSDELRVYSGIVFGSSALIALDLVLKTGRSVGSAIEHAAFQVTTLISTTGYCTEDFDLWPQFSRLVLLVVMFAGGCAGSTAGGIKVSRIVLLFKGLKRDLRRILHTREVRPITLDGQRVEEDTISSVSLFFFAYMIILFFSALIVSLDELDFTSAFTASLTCISNVGPGLGLVGPTCNFGFLSPLSKLVLSFTMLLGRLEIMPLLVLFLPSVWRKK
8.7E-64	225	12.5	2.2E-63	223.9	8.7	1.5	1	L0IEN5_HALRX	Trk-type K+ transport system, membrane component	Halru_2094	Halovivax ruber (strain DSM 18193 / JCM 13892 / XH-70)	519	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halovivax, Halovivax ruber, Halovivax ruber (strain DSM 18193 / JCM 13892 / XH-70)	797302	>tr|L0IEN5|L0IEN5_HALRX Trk-type K+ transport system, membrane component OS=Halovivax ruber (strain DSM 18193 / JCM 13892 / XH-70) GN=Halru_2094 PE=4 SV=1MVFGRFTMGRGHLRVDVRAGLSLVGTLTAALSVAHIVPIIVSLAYGGEDLWVFVATFVLTAAVGLSLRQLDPHPEPGAREAFMVVALTWLFAAVFGAVPYVLAGNGAIAQPVNAFFESMSGFTTTGATVMDNISLDHHSHAILMWRQLTQWLGGMGIIVLAVAILSEMAVGGAQLMRAETPGPGVSKLTPHIEQTARVLWLAYVFFTALFIVLLYALHLAGFAENMTLYNAFAHGFSTLPTGGFSPEARSIQAFSPAVQWLFVPFIFVAGVNFVLWWHVLTGDPRSLVRDAEFRLYLGAVTVLSAVGAVVLFTSSLETVDAGVVGGQLERSLRYAVFQIVSLVNSTGFANMDFYEWSGPAKAILLFAMFVGGSTGSTGGGIKILRWLVILKTLRRELFTTVHPDAVRPVRMNGRVLNEEAVRGIYAFTLLYVVLFFVGIGLLAADAARVGADLTLLDILSASIASLGNIGPGLGEVTGPMGGYGSFPTTSKLLMILYMWIGRLEIFPVLVLLTKAYWRS
9.1E-64	225	23.6	3.4E-35	130.9	5.3	2.1	2	B4S373_PROA2	Cation transporter	Paes_0107	Prosthecochloris aestuarii (strain DSM 271 / SK 413)	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae, Prosthecochloris, Prosthecochloris aestuarii, Prosthecochloris aestuarii (strain DSM 271 / SK 413)	290512	>tr|B4S373|B4S373_PROA2 Cation transporter OS=Prosthecochloris aestuarii (strain DSM 271 / SK 413) GN=Paes_0107 PE=4 SV=1MNFPAIANVLGTLLMFIGSTMLIPLACALIYNEGDALSFMLAMMITIGLAFPLWWFFRRQRNLTIRDGFFIVSVGWILVSAVSSLPFMIHGSIPSFTDAFFEMMSGYTTTGATILNDVEALPHGLLFWRSMTHLIGGMGFIMVTIIILPLGIGGMQLYKAEADPGQVITGEKFLPRVKEAAIWLWAIYLALILIQSLLMWVAGMPLFDSLCHAFGTVSTSGYSTKNSSIGYFNNAWIDWITTIFMLLGGMTFMLHYQIIKRDWEPVKQNTEFRWYGGFVLFFCLVTTLLLFASPQYDNIFDSARFATFQIVSILTTTGFTTTDYEVWPQAAQMFILIVCFIGACAGSTTSGIKIVHYEIISKYLYATGKKLMQPMAVVPVRINGRIAEQPVITLAVSYFIINIFMVFIGAAVLTICDDMDLFSSMTAVIATLFNIGPGFGDVGPTHTFAHISEIGKWFLSFNMLTGRLEMFSVLVMFYPSFWKG

9.4E-64	225	11	9.4E-64	225.1	7.6	1.8	1	N6YS45_9RHOO	Trk system potassium uptake protein	B447_02266	Thauera sp. 27	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Thauera, Thauera sp. 27	305700	>tr|N6YS45|N6YS45_9RHOO Trk system potassium uptake protein OS=Thauera sp. 27 GN=B447_02266 PE=3 SV=1MRAYHPALNALGLIIMIFGLLMGFPLTVSAVLEDGATLAYDQGIFVTFVSGLLLWAATRSRRRDLRVHDGFLLVAASWVVLPVFG ALPLVAYIPELRFTDGYFEAVSGLTATGATVLTGLDDLPISINLWRTFMHWIGGMGVIVLVVAILPLLGIGGRQLYKAEVPTPMKDASLT PRIAETAKGLWITYVLLTVACGFALWWAGLEGWDAVIHAFTIAGLGGFSSKDASLGHFANLNVEIVTIVFAVLAGLNYATHYMALIRRS YKPYLRDPEIPFYFAVLAGSIVLLTVYLMQHGAHDDAATALRYVAFHVVSISTSLGLATYDYTLWPMFAQIWILFLGSFIACSGSTGGGI KMMRAMILYKQVFREIVRSLHPQAVRPVRLGTKPVPETILHAVLGFSFMYMVSIVSLTLILSATGLELITAFSAVVACLNNTGPGLGLVG PASNYQGLEDIHKWVLSFTMILGRLEIFTFLVVLTPTFWRR
9.8E-64	225	31	3E-62	220.1	21.4	2.1	1	U5L4T7_9BACI	Ktr system potassium transporter B	N288_01210	Bacillus infantis NRRL B-14911	439	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus infantis, Bacillus infantis NRRL B-14911	1367477	>tr|U5L4T7|U5L4T7_9BACI Ktr system potassium transporter B OS=Bacillus infantis NRRL B-14911 GN=N288_01210 PE=4 SV=1MKRKYLNITPPQLLTLIFLFFILLGAALLKLPFSTVHGVSWIDALFTATSAMTVTGLTVADTASTYTLFGQIVIMCLIQLGGLGIMSFA VLIYLMLGRKIGFKERLVLQQALNQTSVGGVIRLVRYLFIFSFTIEAIAVFFLCLRWVPLYGWQDGFYYSLFHSVSAFNNAGFQLWPDG LSRFVGDPVINIVISMLFIIGGLGFTVLADLWKSKQFKRLSLHSKMMIVGTFAVNIVSMAVIFYLEYNNPQTLAHLTSWEKLWASYFQAV SPRTAGFNSVDIGGLEDATVLYMLLLMFVGAGSASTGGGIKLTTFIIIIMAVITFIRGKKDIVIFRRTISVNYLTKALAISMISILFVFIAIFVLSI TEDLPFIKIIFEVVSAFGTVGLSMGITADLSEIGKEIIIFIMFLGKLGPLTLAFSFAKQKPEKIRYPGEDVLLG
9.9E-64	225	26.3	1.3E-63	224.6	18.2	1	1	K9XM98_9CHRO	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Glo7428_4761	Gloeocapsa sp. PCC 7428	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	1173026	>tr|K9XM98|K9XM98_9CHRO Potassium uptake protein, TrkH family OS=Gloeocapsa sp. PCC 7428 GN=Glo7428_4761 PE=4 SV=1MTVSRSICFGFLAVIAVGTLLLMMPFSTSSGTWNDPIVALFTATSAVCVTGLGVVDTGTYFSFWGQFFLAALVQIGGLGYMTAN TFLLLLLGRRFSLKDKIAIQQSLDRPGIHGSTQILRSIIALTAVMEITGVLLLLPTFNADYRFNQALWLAIFHSINSWNNAGFSLFSDSYIRY QFYLPLIIPVSLLIILGGIGYPVIFEVYLWMRDRFLRKPYRTVFSLNFKVATSTTLALLVMGTIAFLFIELRNPDTFGNISFGNQLVLAWFQ SVTTRTAGFNTIDIGRMTTAGLFLTIALMFIGASPGGTGGGIKTTTARVLANCTKAILQGKEEVEMYQRQVPISLILKAIGVVVGSTITVIL ATILISITDPTVNFIQILFEVVSAFATVGLSTGITASVSGAGKLILIATMYVGRVGILLLMAALLGDPRPRAIHYPEENLLVG
1E-63	225	22.6	6E-63	222.4	15.7	1.8	1	A0A0C5W8V6_9FLAO	Potassium transporter	AW14_08170	Siansivirga zeaxanthinifaciens CC-SAMT-1	498	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Siansivirga, Siansivirga zeaxanthinifaciens, Siansivirga zeaxanthinifaciens CC-SAMT-1	1454006	>tr|A0A0C5W8V6|A0A0C5W8V6_9FLAO Potassium transporter OS=Siansivirga zeaxanthinifaciens CC-SAMT-1 GN=AW14_08170 PE=4 SV=1MLKLNYKIICHFLGLLLLFNGGFMLLSALVSLIYKDGVTFQIFMAGVLTLCSGVIAMFLTRYHRKEMNKREGYIVVTFGWIIMSLSG TLPYVLSGGIPNFTNAFFETMSGYTTTGASILNDIEALPKGVLFWRSTTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPSADKLHPR ITDTAKRLWLIYFGYTAAETLFLKLAGMSFFDAINHSMATLSTGGFSTKNASLAYWNNQPVIQYIVILFMFLAGANFVLSYFAFKGKIQKI IHDEEFKLYFKFIGIFTIIATLLIYFGADVSISTIHHPMVWGEFESAFRHALFQVLSVITTTGFVSADYTLWTPFLVVFFFGLMFLGGSAGS TSGGVKVVRHLILIKNGFLEFKRTLHPNAILPVRYNQRAIPETIVFNVLGFFILYMLSFIIGALVFSMFGLDFTSSVGLSASSLGNVGPAFG NFGPVSNYAALPHLGQWWASFLMLIGRLELFTVLILLTPFFWRNR
1E-63	225	10.2	1.4E-62	221.3	7.1	1.9	1	D3SZE9_NATMM	Cation transporter	Nmag_0698 C500_16030	Natrialba magadii (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) (Natronobacterium magadii)	505	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrialba, Natrialba magadii, Natrialba magadii (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) (Natronobacterium magadii)	547559	>tr|D3SZE9|D3SZE9_NATMM Cation transporter OS=Natrialba magadii (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) GN=Nmag_0698 PE=4 SV=1MRRLHVDLRAGLALVGTLLALLSIAFVVPIVTALLYGGEDLWVFVVSMVATAGFGLLLRRLDPNPTPGAREAFFVVAFTWLFASIF GALPYILAGTGAIAHPINALFESMSGFTTTGATVMETISVEEHSHAIMLWRQLTQWLGGMGIIVLAVAILSQLAVGGAQLMEAETPGPG VSKLTPHIAETARVLWLAYIGFTLLYIALLYGLHLTGYAPEMDAYNAIAHGFTTLPTGGFSPEADSMAAFSPAVQWLVIPFMFIAGVNFV LWWHMLAGDHTALINDTEFRFYLGVVTGMTLLLTAVLAVTASDVGPDPGLESSLRHAAFQIVSLTNSTGYASVDFDAWSGPAQALLL FVMFLGGSTGSTGGGIKMLRWLVILKSLRREVFTSIHPEAVRPVRMNGKVLNEEAIRGIYAFTLLYVAIFLVGIVLLAVDTARVGYDIGTI DLVSASIATLGNIGPGFGVVGPMAGYGDFPETSKLLMILYMWIGRLELFPVLVLLTRAYWRS
1E-63	225	20	1.1E-61	218.2	13.8	2.1	1	B7KLB8_CYAP7	Cation transporter	PCC7424_4119	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	511	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	65393	>tr|B7KLB8|B7KLB8_CYAP7 Cation transporter OS=Cyanothece sp. (strain PCC 7424) GN=PCC7424_4119 PE=4 SV=1MNPLIKTVLRDLGLLLLVPGGMAIISIPVCLFWGEYYAIIPFLTCAIASWGIGYLLYRCFAGAKSSRTTEAMITAAIGWGIIPLFAAIP FVLVANTLATRPLTPLTILEFQHPINAIFEAFSGMTSTGLTMALHESKLPHSLQWWRSFMEWVGGVGIVLVVSLLDTNTDPYQLYSAE GRSKTINLTVRSTVRRIWWIYLLYTIAGVFWLKIVGMPWWDALNHGMTAISTGGFTITDDSIDAYAPLIQWAIIPIMIAGAISFPVHYRLL YKRRISALWGNAQHRALWVLLVIGALGLVLVNYRFKDDWLWRDSVFQWVSALGTCGFSTVTFTRWSETAKLLLSLAMIIGGTSGSTV GGIKLNRLVFLIKAVLWRFQRIVLRPHQLMRYKLNDEVVTEVEAIRRVEGAAVIFILWLTMLFVGVLILSEIVLPRYVLSDVIFEAASALGS VGLSTGITHPNLPFIGKLTLIIFMWMGRLEIIPVLLLFSFSTQHFVNLLSRFNIRAFFSKKSL
1.1E-63	225	21.3	5.3E-63	222.6	14.7	1.8	1	A0A0F3ILS1_9GAMM	Trk system potassium uptake protein	VZ94_10750	Methylococcaceae bacterium Sn10-6	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, unclassified Methylococcaceae, Methylococcaceae bacterium Sn10-6	1632867	>tr|A0A0F3ILS1|A0A0F3ILS1_9GAMM Trk system potassium uptake protein OS=Methylococcaceae bacterium Sn10-6 GN=VZ94_10750 PE=3 SV=1MNVIATIIHILGVVTMGSSGLMATCLLTSLIAQDGAQTAFLLATALTLLVGAIMFFPTISTPKIVSRQAGFLLVSITWSLLPVFCTLPL LFYMPKLSFLDAYFEVVSGLTTTGATILSGLDHLPMSINLWRHELNWIAGMGIIIFAVAILPILGVGGMQLYIAETPGSVKESELPPRIAQT AKALWLVYAGISVLCIAILKLAGMSWFDAICHAFAAMSLGGFSTHDNSVGYFNSVPIEVVLTIFQLVAAINFATHFIAIKKRSYRPYVEDM EARAFLALVLTSCLMTAAVLYRDGTYDNYFTALRHATFNLVTIATDCGFASQDFNQWPIFVPMWMLFLSCLSASSGSTGGGIRMIRTII LMKQARLELFKFIHPNSVRPLRIGDAIINNKIVTSVTGFIFLYFISIVILVFLLLFSGLDFVSALSAIIACFNNAGPGLNQVGPATNYASLSDF QTIVCTFAMLLGRVQIFSIVILFVPEFWKK
1.1E-63	225	17.2	9.4E-63	221.8	11.9	1.9	1	Q8TQQ7_METAC	Sodium transport protein	trkH MA_1483	Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A)	476	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina acetivorans, Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A)	188937	>tr|Q8TQQ7|Q8TQQ7_METAC Sodium transport protein OS=Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A) GN=trkH PE=4 SV=1MNIKIVFYVLGGLLRLLGLLMIVPLGVAYYYGESLTPFLVSIVITVLTGLILLSYKTDEDWMRKEGFAIVALGWLAVAVFGAIPFMLD GISPLNSLFEAMSAFTTTGSTILTDIESHPKGILFWRSMMQWLGGMGIIVLFIAVLPKFGVAGRQLFRAEAPGPTEDKLKPRIRETAKIL WMVYFVISFAEVVALLLAGLSLYDAITHTFTTMACGGFSPYGTSIEAFRSPLVEYIITFFMFVSGANFALHYRAIYVDKDFLLKDDEFRFY TALTLAATGLLTLLLYRDINTGFFDSFRLAIFQVVSIMTTTGFATADFNFWSDSAKMVLLLIMFVGGCAGSTGGGIKVVRILMLLRHGRV ELFKSLHPRAIRGVKFNNKNVPDEVINSIFSFVVIYLFIFMSSALILAVLGMDIITSTTASIATLGNIGPGLNVVGPMGTFDPIPPLGKLILIA NMWIGRLEVYTVIVLFTPEFWNK
1.3E-63	225	13.9	2.8E-62	220.2	9.6	2	1	E6VYG9_DESAO	Trk system potassium uptake protein	Daes_1720	Desulfovibrio aespoeensis (strain ATCC 700646 / DSM 10631 / Aspo-2)	485	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio aespoeensis, Desulfovibrio aespoeensis (strain ATCC 700646 / DSM 10631 / Aspo-2)	643562	>tr|E6VYG9|E6VYG9_DESAO Trk system potassium uptake protein OS=Desulfovibrio aespoeensis (strain ATCC 700646 / DSM 10631 / Aspo-2) GN=Daes_1720 PE=3 SV=1MRWRYVLHVIGALVACIGLTMILPLAWGVYYDDGSAWPLAESLGITVASGAFVFFAFRDPAASRAAMSHREGMAIVALGWFAA GVFGGLPFYLGGTFESVADCVFESLSGFTTTGSTVLADIEAVPRGILFWRSLTHWLGGMGIIVLSAILPFLGVGGMQLYRAEVPGPS PDKLKPRIKDTAMTLWKVYLVFSVAETILLMFGGMDLFEALCHTFGTMATGGFSTRNASVAAFDSVYIDTVITVFMLIAGVNFSLHYLLL KWHPSALIRNPEFRVFAGMVLFFVIIVTVAVLVGGNYDSGGDAVRYAAFQVASIITTTGFATADYELWPGLAQAVLLFCMFVGGCAGS TAGGMKVMRVMLLLKHSYKELFRLIHPRAVSRVKMGRVVVQDDVMSGVWGFFILWLGLFVLAALVVAASGVDVVTSFASALACIGNI GPGIGGVGPMDNYAWLPDTAKWALTFCMVLGRLEIYTVIVLFVPEFWRK

1.4E-63	225	38.5	1.1E-62	221.5	26.7	1.8	1	G4L881_TETHN	Ktr system potassium uptake protein KtrB	ktrB TEH_14280	Tetragenococcus halophilus (strain DSM 20338 / JCM 20259 / NCIMB 9735 / NBRC 12172) (Pediococcus halophilus)	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Tetragenococcus, Tetragenococcus halophilus (Pediococcus halophilus), Tetragenococcus halophilus (strain DSM 20338 / JCM 20259 / NCIMB 9735 / NBRC 12172) (Pediococcus halophilus)	945021	>tr|G4L881|G4L881_TETHN Ktr system potassium uptake protein KtrB OS=Tetragenococcus halophilus (strain DSM 20338 / JCM 20259 / NCIMB 9735 / NBRC 12172) GN=ktrB PE=4 SV=1MSYLDRDVFFKAPQQILLGFAGIILAGTFILMLPFVTRSGHSTNFLDALFTATSAVCVTGLTTVSTIGHWNMFGQAVILLMIEIGGLGFMSLPFLYFTLTKRKINLSMRMILKDTLNTFDISGTVSLMLAIFRIAFIIQFLGFLLLSVDFIPRFGWEKGLWYSFFHAVSSFCNAGFDLFDNSLISFQNDPWILMVISFLIIAGGLGFIVWQDLLKNKTLRKLRLHSQITLKVTGLLLVLSSIFFFFTNTVGSNPLSRLSNVFFLAVTPRTAGFFSIDYATMSHAGLVLTMILMFIGGSSGSTAGGFKTTTLGIILIKLYSVIRGRSKAQYKGRTIKENTISQAFMLFFIFLIMIISSTMILSVTETIPNVDQLGLEYIVFEVISAMGTVGLSLGILSAHLTWIGKLVLIFLMFIGRVGILTMIFSTINQTHKRETNYKYPEENVIIG
1.5E-63	225	24	7.5E-63	222.1	16.7	1.8	1	D6DEW0_CLOSC	Potassium uptake protein, TrkH family	CLS_04080	[Clostridium] cf. saccharolyticum K10	448	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, [Clostridium] cf. saccharolyticum K10	717608	>tr|D6DEW0|D6DEW0_CLOSC Potassium uptake protein, TrkH family OS=[Clostridium] cf. saccharolyticum K10 GN=CLS_04080 PE=4 SV=1MLSNKVWALTPAKIILGGFFLIILCGGILLSLPISSRSGEMTPFIDAVFTATSATCVTGLVVHDTSTYWSVFGQAVILLLIQIGGMGVVTLAIAITILSGRKIGLKQRFVMQESISAPQVGGIVRMTRFIVKCTILFELLGALVMAVQFCPQFGIVRGIWYSVFHSISAFCNAGFDLMGGTSGPYSSLTSYRTNPFITIPVMALIVIGGIGFFVWDDIYKHRQSYKFYRLQTKIVLTTTFLLILIPAVLFFLFEFTPQRWEGYTLADRIYSSIFQSVTPRTAGFNTVPLDQLSTQSQLATIILMIIGGSPGSTAGGIKTTTFALAVLCILSVFQNQEDIHCYKRRVPYDILRNAIAILVLYLFLFLSASFLITRADGVSMMESSFEAASAIATVGLSLGITEDLGIFSKIILILLMYLGRVGGLTMLYALTNHRKFPVHLPQERITVG
1.5E-63	224	11	1.6E-62	221	7.6	1.9	1	L0JJX7_NATP1	Cation transporter (Trk-type K+ transport system, membrane component)	Natpe_1690 C488_13995	Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	514	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema pellirubrum, Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	797303	>tr|L0JJX7|L0JJX7_NATP1 Cation transporter OS=Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786) GN=Natpe_1690 PE=4 SV=1MRLRTDWRASVALVGTVLKYLSVPLVIPLVVALIYRDPVVPFVATIALTIAVGEGLERLSPEPDLDIREAMLFVAISWLAVAIVGAVPYVIAGWGTESTLAHPVNALFESMSGFTTTGATVLGEISLERHSHAIMMWRQLTQWLGGMGIIVLMVAILPEVAVSGAQLVESEAPGPELQKLTPRIAETARILWLVYFAFTVVYIAILYGLHLAGMAPNMGLYNAIAHGFTTLPTGGFSPEADSVAAFSAAVQWTAVPFMIIAGTNFALFWHVFSGEGHRFVRNSEFRAYITAIAGLTALLAGMLYVGTEGVFENSLRQSAFQISSLLTSTGYATSDFVDWSSTGKIVLLFAMLVGGCAGSTGGGVKVVRWLIIFKVLRRELFTASHPEVVRPIRLGGNVVDEDAIRGVLGFTFMYLIIFAGATLLIALDVSRASAIANFSPLEAFSASLATIGNIGPGFGHLGPFGSYLDFPVPSKLLMIFLMWIGRLEIIPVLVLFTGGFWTR
1.5E-63	224	24.2	5E-63	222.7	16.7	1.7	1	H8GLG8_METAL	Trk system potassium uptake protein	Metal_1550	Methylomicrobium album BG8	494	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomicrobium, Methylomicrobium album (Methylobacter albus), Methylomicrobium album BG8	686340	>tr|H8GLG8|H8GLG8_METAL Trk system potassium uptake protein OS=Methylomicrobium album BG8 GN=Metal_1550 PE=4 SV=1MAEASYRTDNPMILTIFHIFGLVTMGFSGLMATSLMTSYFADDGATQAFFRGTGITLLSGAALFFPTLRVPKKVSRQTGFLLVAITWSATPVFCTLPLLYYFPGMSFIDAYFEVVSALTTTGSSVMSGLDQLPVSINLWRHELSWIAGLGIIIFAVAILPILGIGGMQLYIAETPGSVKESDLPPRIAQTAKALWMVYAGISVVCIIALKLAGMNWFDAICHAFSAMSLGGMSTHDQSVGYFNSLPIEIVLTVFQLIAAVNFATHFIAIRKLSLKPYAVDMEARSFLVLMLGSCVMTATILWQEGSYPDFWIAFRHATFNLVTIATTCGFATQDFNQWPIFVPMWMLFLSCISASSGSTGGGIRMIRTIILLKQARLELFKFIHPHAIRPLKIGEQIIKNSIVTSVTGFIFLYFMCIVILVFTLLFSGMDFISALSAVISSINNAGPGLNQVGPATTYASLTDFQTAVCTFAMLLGRVQIFSIIILFLPEFWKK
1.6E-63	224	23.2	2.8E-36	134.5	1.3	2	2	G8R0D2_OWEHD	Trk-type K+ transport system, membrane component	Oweho_0576	Owenweeksia hongkongensis (strain DSM 17368 / JCM 12287 / NRRL B-23963)	472	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Cryomorphaceae, Owenweeksia, Owenweeksia hongkongensis, Owenweeksia hongkongensis (strain DSM 17368 / JCM 12287 / NRRL B-23963)	926562	>tr|G8R0D2|G8R0D2_OWEHD Trk-type K+ transport system, membrane component OS=Owenweeksia hongkongensis (strain DSM 17368 / JCM 12287 / NRRL B-23963) GN=Oweho_0576 PE=4 SV=1MGTLLILVSGMMAISIFVALYYHEAWLNLLIASSVTAAAGIALRLMRDDKNRDVRKRDGFLIVSMGWLLMSLFGSLPFVIGGAIPDFVDAFFETVSGFTTTGATILTDIEAMPKALLFWRSMTHWLGGMGIIVLTIAILPLLGVGGMQLFVAESPGVTPDKMHPRITETAKRLWIIYFALTAIEAVMLWIAGMGLFDAVNHAMATMATGGFSTKNASIAFYDSPAIHYIITLFMFLAGVNFTMLYFGFTGKVGRIFKNEEFRVYALNMLIMSIIVSFGLAVYGDYGVEEAIRSGFFQVASIITTTGFITDNYLLWPNFLIMIIFVLFFSGGSTGSTSGGLKTMRVIVMIKNSLLELRRQIHPTAVIPVRFNGKAVPQNITNTIAAFVLIYLIIFFGGTLVMSMIGLDFMSAVGSVAASLGNIGPGLGSVGPVDNFAHIVPEGKLFLSFLMLMGRLELFTILILFMPYFWRNR
1.7E-63	224	30.8	2.5E-63	223.7	21.3	1.1	1	Q8YW14_NOSS1	All1802 protein	all1802	Nostoc sp. (strain PCC 7120 / UTEX 2576)	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	103690	>tr|Q8YW14|Q8YW14_NOSS1 All1802 protein OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=all1802 PE=4 SV=1MTVSRTVCLGFIAVIVVGTILLMMPFSTSNGNWNDPIVAIFTSTSAVCVTGLAVVDTGTYFSFWGQFFIALLAQIGGLGYMTTTTFLILLIGRKFDLRQKIAIQQALDRPGMSGSTQVIRSIIATTLIFEITGVFLLLPAFVPDYGWNQGLWLAIFHSVNAWNNAGFSLFKDNLISYQSSSLVVFTITGLIIFGGIGYQVILETYIWLRDRILKKKETLVFSLDFKVATSTTLILLFLGTIAFFCIEVRNPQTFGSLNLRDQFLVAWFQSVTPRTAGFNTIDIGKMTTAGLFITIALMFIGASPGGTGGGMKTTTLRVLTSCTKTILQGKEEVLLYERKIAVALILKAVGVLVGSIATVILATILISLTDPKLDFIQILFEVVSAFATVGLSTGITASVSPAAKLVLIITMYVGRVGVLLLMSAILGDPRPTRIHYPEENLLVG
1.7E-63	224	24.4	8.5E-63	221.9	16.9	1.9	1	D1YVZ8_METPS	Trk system potassium uptake protein	MCP_0548	Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE)	485	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanocellales, Methanocellaceae, Methanocella, Methanocella paludicola, Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE)	304371	>tr|D1YVZ8|D1YVZ8_METPS Trk system potassium uptake protein OS=Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE) GN=MCP_0548 PE=4 SV=1MLSGGDLKIILSNLKGLFIIIGAIMLAMATISALTGRPGTADGFFYGAVIGIGAGLALNTIYPKSGEPELRHAMVIAAIAYIIVPAISALPFMVTGHMSPIDAFFESISGWTSTGFTMITGPEQADPIILLWRSVTQWFAGLGVILLMVTILIRPGTSTFMLYQSEGRRDKILPSIRSTLKVIWVLYLALTIVSFVLLLVAGMPVWPAVNTALVAISTGGFSIDSDSIAAFHSIPIELALLPIMIAGALPFAVVYRAIGKGVLSLFRDPQVKVFLIIIVIGALLLSLENFYYYNDILASIRYSVFQFITAITGTGLQSADVSQWSQSALFLISIAMIIGGCAGSTASGIKVARVIFIWNEIKLWLARMFQSKNSIVAIKISGKRVTEDTIDQEMAEASLISFLWIFSIVISMFLLSHIAGAQYNLIDILFDVCSAQGNVGVSCGVINPEMPAIGKVLVILNMWIGRLEIIPVMVLVRYAIKGFRI
1.7E-63	224	23.9	4.4E-63	222.9	16.5	1.5	1	G7W7P7_DESOD	Potassium uptake protein, TrkH family	Desor_0408	Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus orientis, Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	768706	>tr|G7W7P7|G7W7P7_DESOD Potassium uptake protein, TrkH family OS=Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) GN=Desor_0408 PE=4 SV=1MNALGKIMSPSRVLVSGFASLILLGGILLTLPQATQDGLGLPFMNAIFTATSAVCVTGLVVVDTGTTFTPFGQGVILVLIQVGGLGFMTFATLFAMILGKRITLKERLLLQEALNQVSIEGVVRLAKSVLQISFAIEGVGALILALRWHSDFGWSKALYYGVFHSVSAFNNAGFDLFGNFSSLTAFVGDPIINITIMVLIVLGGLGFIVLAELLEHKKKFRLHTKIVLKVSGFLILFGAGLILIMEYSNPKTLGPLPFGTKVMAALFQSVSPRTAGFNTIDLSGMYNTTLLSMIVLMFIGASPGSTGGGIKTTTFIAIVLSVLRTYRSDPHVVIEGRTLPKDVIQKAWAITTSASCLIFIIISVLSLTENTDLLTVLFEVTSAFGTVGLSLGLTPYLSGLGKIAIIITMFIGRVGPLTLAFVLSRKKSKQSLHVKYPDERIMIG

1.9E-63	224	14.4	4.4E-38	140.4	0.4	2.1	2	A0A0E9M653_9PROT	Trk system potassium uptake protein	trkH OYT1_01326	Ferriphaselus amnicola	486	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Gallionellales, Gallionellaceae, Ferriphaselus, Ferriphaselus amnicola	1188319	>tr|A0A0E9M653|A0A0E9M653_9PROT Trk system potassium uptake protein OS=Ferriphaselus amnicola GN=trkH PE=3 SV=1MKRALTVIHALGLLLVVFSLTYLLPLATAFIYGDSAMMTDFALAIMWTAMAGALMWLATRRFKGELSIRHGYLLVATMWAAMPA FATIPLLMLLPGLSFTDAYFETMSGMTTTGATVLVGLDNLPPAINLWRHELNWIGGLGIIVLAVAVLPLLGVGGRQLFKAETPGPMKDS ALTPRIADTARNLWVVYVGITLACVGLLKWAGMSWLDAVCHSFSAMGLGGFSTHDASIGWFDSPLIEFILIVFMLIAVLNFATHFLAWH GRTFKVYLRDAEAVGSLVLILTSCLGIAIFLWWQGVYPEFGVALRHATFNLVSIATSSGYASVDYAQWPMFAPMWWMMFLTAIAASSG STGGGIKMMRTLVLVKQAGREFLNLLHPAVVNPMKIGGQVVPNSIVFSVLGFIFLYFMTLATLTFILLISGLDFISSLTAVLASVNNCGPG LGVVGPASNYQGLSDFQTWVCTFGMLIGRLEIFTLLILFTPAFWRR
2E-63	224	24.5	1.6E-62	221.1	17	1.9	1	H3ZNU8_THELN	Potassium transporter	OCC_11657	Thermococcus litoralis (strain ATCC 51850 / DSM 5473 / JCM 8560 / NS-C)	494	cellular organisms, Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae, Thermococcus, Thermococcus litoralis, Thermococcus litoralis (strain ATCC 51850 / DSM 5473 / JCM 8560 / NS-C)	523849	>tr|H3ZNU8|H3ZNU8_THELN Potassium transporter OS=Thermococcus litoralis (strain ATCC 51850 / DSM 5473 / JCM 8560 / NS-C) GN=OCC_11657 PE=4 SV=1MLELRKYINITDDIFVIRNLIGALLQGIGVAYLIPVLITWIYREEMQYVYYFVIPGLACILFGAWLARHSEHIEDVNLRQAMISAAFVW LFASFVSVVPFMRIAGMGFVDSYFESMSAWTGTGLTMMRNLESYPHIILFWRAWMQWLGGIGIVLVALTILIRPGVAAARLYRAEARS ERILPNLANTSKIIFRIYAVLTVVGVYLYYINGMGLFDAVIHSMTGLGTGGMSSHDLSIGFFNSLSIEAVTIFLMIMGATNFTVHYKMFKEK SLVPFFRDIQVKYMFFFLTPVIALIGYGLMVYNGLTIGESFREAVFHAVSAITCTGFSISDLSQYPELAKLLIGFLMVVGGGAGSTAGGIK LIRITLTFQSLKWTIQQAILPKGAVIKRKIGDYIFTEEDMQEVLGFTMTYIAFLLIGTVWVMLRVGASLADAFFEVASAQGNVGLSVGITS PGLPLDVKVLLILHMWIGRLEIFSTLVFIFGVLLMVPRIVERE
2.1E-63	224	34.4	8.7E-63	221.9	23.8	1.7	1	KTRB_BACSU	Ktr system potassium uptake protein B (K(+)-uptake protein KtrB)	ktrB yubG BSU31100	Bacillus subtilis (strain 168)	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus subtilis group, Bacillus subtilis, Bacillus subtilis subsp. subtilis, Bacillus subtilis (strain 168)	224308	>sp|O32081|KTRB_BACSU Ktr system potassium uptake protein B OS=Bacillus subtilis (strain 168) GN=ktrB PE=1 SV=1MTLQKDKVIKWVRFTPPQVLAIGFFLTIIIGAVLLMLPISTTKPLSWIDALFTAASATTVTGLAVVDTGTQFTVFGQTVIMGLIQIGG LGFMTFAVLIVMILGKKIGLKERMLVQEALNQPTIGGVIGLVKVLFLFSISIELIAALILSIRLVPQYGWSSGLFASLFHAISAFNNAGFSLW PDNLMSYVGDPTVNLVITFLFITGGIGFTVLFDVMKNRRFKTFSLHTKLMLTGTLMLNAIAMLTVFILEYSNPGTLGHLHIVDKLWASYF QAVTPRTAGFNSLDFGSMREGTIVFTLLLMFIGAGSASTASGIKLTTFIVILTSVIAYLRGKKETVIFRRSIKYPIIIKALAVSVTSLFIVFLGI FALTITEQAPFLQIVFETFSAFGTVGLTMGLTPELTTAGKCIIIVIMFIGRIGPLTFVFSFAKTEQSNIRYPDGEVFTG
2.2E-63	224	26.2	7.4E-63	222.1	18.1	1.6	1	E7GJB0_CLOSY	Potassium uptake protein KtrB	HMPREF9474_01003	[Clostridium] symbiosum WAL-14163	448	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	742740	>tr|E7GJB0|E7GJB0_CLOSY Potassium uptake protein KtrB OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_01003 PE=4 SV=1MIGKQVWSLTPAKIILGGFFLIIITGAVLLTLPFASKTGEATPFIDAVFTATSATCVTGLIVHDTYTYWSVFGQAVIIILIQIGGMGVVT LAIAITILSGKKIGLKQRYVMQESISAPQVGGIVRMTSFIVKGTIFFEAAGAVIMAFQFCPQMGLIKGIWFSVFHSISAFCNAGFDLMGGT SGPTTSITSYTGNPLINIPIMLLIIIGGIGFFVWDDVKTHKLQHKYYHLQTKIVLTTTFCLIMFPALFLFLFEFSRDCWDGLSLQERFMASL FQSVTTRTAGFNSVDLNQLSEAAQLLVVILMIIGGSPGSTAGGIKTTTFALAILCLRSAFQNQESIQCYKRRIPYDILRNAIAILALYISLML TATFLITWLDDVNLMEAAFETSSAVATVGLSLGITGDLSTFSKIILILLMYFGRVGGLTMLYALTNRKKLPVLLPQERITVG
2.5E-63	224	16.8	2.2E-62	220.6	11.7	1.9	1	R5SLI2_9CLOT	Trk system potassium uptake protein TrkH	BN771_00503	Clostridium sp. CAG:75	506	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:75	1262836	>tr|R5SLI2|R5SLI2_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:75 GN=BN771_00503 PE=4 SV=1MNYSAVKYILSYVLMIEGALLLFPFIVGVLYMEQKSVWYLLVAVICIVLGVLGTRHKPKNTMFYFKEGCLATAASWITLSIFGSLPLI LTGEYPSYVDALFEIVSGFTTTGATVLSDVECLCHATLFWRAFTHWIGGMGVLVFLLMIIPMSGGSNMNLMRAESPGPSVGKLVPHLK STAQILYVIYFGMTVVQVILLLLGGMSLFEAITTSFSVAGTGGFGIKNDSIASYSPYLQWVITIFMLLFGVNFNAYYLLLLRKWKNALKME EVRYYFLIIAVAIGIIFCNILQMVGNAADALRQASFQVASIITTTGYSTVDFNLWPQSSRTIMVLLMFIGACAGSTGGGMKVSRIVILFKTV GKELHSYIHPKSIQKVKFEKKPVEHEVLRATNVYFITYIIVFAVSTFLISFEEKDLVTTFTSVATTLNNVGPGLEKVGPIENFGAFTPFSKC VFMFDMIAGRLELFPLLILFHPALWKDTLFHRSKDKKSSRRVTAPAKAAKKKANK
2.6E-63	224	32.2	3.4E-63	223.2	22.3	1	1	V9W6X8_9BACL	Ktr system potassium uptake protein B	ktrB1 ERIC2_c10110	Paenibacillus larvae subsp. larvae DSM 25430	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus larvae, Paenibacillus larvae subsp. larvae, Paenibacillus larvae subsp. larvae DSM 25430	697284	>tr|V9W6X8|V9W6X8_9BACL Ktr system potassium uptake protein B OS=Paenibacillus larvae subsp. larvae DSM 25430 GN=ktrB1 PE=4 SV=1MRLRFKRAYLSPQQFLVVGFALIITIGTILLALPDASAKGISIGFLNALFTAASATCVTGLVVLDTGTHFSTFGQVVILMLFQLGGIG FMTTTTWIATVLRKKVTLRERLILKESMNQNKVEGIVRLIRKVVMYSVCIELTAALLFAFRWSLEMPFSKALYYGFFHAISFFNNAGFDL FGEFQSLTPYVNDVFMNVLSVFLILLGGIGFIVMSDLIEYPKTRRLSLHSKVVLATSGILLFLGTVVILICEFTNSRTLGSLDGGNRILASFF QSASLRSSGTSTLDITEMRQATQFFMVVMMFIGAAPGSTGGGIKVTTFAILVVSVITMLRGKEDVVLFRHRLSKNQIYKAITVTLISLMLI VASTMILSTTEGKDFLVILFEVVSAFGTVGFSMGLSQDLSLFGKILFVVLMFAGRLGPVTLAYAIQSKKRKDLYRYPEGKIIIG
2.9E-63	224	14.2	1.2E-62	221.5	9.9	1.7	1	D8JCS9_HALJB	Potassium transport system protein trkH3	HacjB3_17408 HacjB3_19408 C497_00335	Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	496	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halalkalicoccus, Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	795797	>tr|D8JCS9|D8JCS9_HALJB Potassium transport system protein trkH3 OS=Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3) GN=HacjB3_17408 PE=4 SV=1MSAVSIIVAVVNGEFYATPAFAVTAVTLGGFGTGLVRWYRDADPPEKRDAMVTAATAWAVIGFLGGLPFLLVAWTIQIDPFPVW MNTPPMDDTTVIFLNPLDAVFESMSGFTGTGLTMAAVEDKLPRSIHWWRSFIEWVGGVGVIVLTVAILHRGGGSSGSYTLYESEARS EKIHPSIVTTVQEIWKIFVGLTIGSIILFLLVGMPLWDAINHGMTGIATGGFSVHGASIGHYDSPLIEYAVVPVMFAGSIAFPIHYLIFKGEL RNFYADLQTRWVFIWFTAGSLALAAILYANGQYDTLEHTFRASVFQFVSAVSNTGFGTETIGGGTDRVWDTGATLFMCLGMLTGGA AGSTTSGLKIIRMVTLFKGTAWQIRDVFEPSSAIRYLKIGDRRLSEEQAQREYTEATVVFILWILFLIIGVAVLLRVLSPGHPLEYVIFDVM SAQSNVGLDSGITGPTMPDTAKAMLIINMWVGRLEIIPVAVLLGSIFQRLNLYR
3E-63	223	7.7	1.1E-39	145.7	0	2	2	G8QHR3_DECSP	Trk system potassium uptake protein	Dsui_0807	Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azospira, Azospira oryzae, Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	640081	>tr|G8QHR3|G8QHR3_DECSP Trk system potassium uptake protein OS=Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) GN=Dsui_0807 PE=3 SV=1MRRFYPVFHILGLIVLIFGLTMLAPLAVSAYAQDGATAAYDEAIVVTMGVGLLLWVCTRRYRQDLRVRDGFLLVALTWTILPLFAS LPLLLFLPDISFTDAYFEAASGLSATGATVMSGLDSLPLSINFWRTFLHWLGGMGVIVLAVAILPLLGIGGRALFKAELPGPMKDSSLTP RIAETAKGLWGVYLLFTVLCALALWWAGMEGWDALMHAFSILGLGGFSTRDASLGYYNSLTIELVAMGFALLSGINYATHFLALRGW SLKPYQRDFELPFYLGVLAVSAVGLALYLMPYGLYDSFGTALRYTAFHVISLATSLGFATTDYTMWPMFAQLWVLFLCSFVACGGST GGGIKMMRAVILYKQVFRELVRAMHPTAVHPVRIQGVIVPDPVLHAVLAFSFIYMVTIVSLTLLLSASDLPIVTAFSAVVACLNNAGPGL DAVGPAANYSVLSDFQTWVCSFAMLLGRLEIFTLLVVLTPAFWRK

3.1E-63	223	18.8	7.2E-63	222.2	13	1.5	1	Q5FA04_NEIG1	Trk system potassium uptake protein	NGO_0230	Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090)	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Neisseria, Neisseria gonorrhoeae, Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090)	242231	>tr|Q5FA04|Q5FA04_NEIG1 Trk system potassium uptake protein OS=Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090) GN=NGO_0230 PE=3 SV=1MHKILPIAHVLSRLGMLFSFILLIPAALSYAFSDGAYTAFATTATVTLSGSCIVRLATLRFRRELRPRDGFTLVLMLWLAFAAMAAM PMYLYFPNMGFTDAFFESMSGLTTTGATVIPHVDGLAPSVNFWRHMLNWLGGMGIIVLAVAILPMLGVGGTQLFKAEIPGIDKESKMS PRISQVAKKLWFGYTLITILAAACLHFAGMGWFDAVCHALATLSLGGFSTHDASIGYYNSPLIEAVIIVFTIFGGINFASHFAALNSRSLK TYWKDEECRTMLLLLSGSILASALYLWHTGHYAGFGESLRYTAFNFVSIGLANGLSNTDFAQWPLLISLWMFFLANILASSGSTGGGI KTIRALVLFKFSLREMMVLLHPKAVRTVKISGKAIPDRLALTVMSFIFIYFMTVVLFSFLLMASGMEFTTAFTAVIACITNAGPGLGEVGP AGNYAGLDVMQKWICVTAMLLGRLEIFTVFILFTPAYWKK
3.2E-63	223	43.4	3.6E-62	219.9	30.1	2.1	1	F9VJE6_ARTSS	TrkH family potassium uptake protein	SFBM_0475	Arthromitus sp. (strain SFB-mouse-Japan)	448	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Candidatus Arthromitus, Candidatus Arthromitus sp. SFB-mouse, Arthromitus sp. (strain SFB-mouse-Japan)	1029718	>tr|F9VJE6|F9VJE6_ARTSS TrkH family potassium uptake protein OS=Arthromitus sp. (strain SFB-mouse-Japan) GN=SFBM_0475 PE=4 SV=1MKNFKKLYPVQILALFFIVVIIIGSFLLTMPISSSSGVMTNYLDALFTATSATSVTGLVTLDTGTYWSPFGTTVILMLIQIGGLGIMSF TTFGVLKYGNKISLYTSLLMKEALNVDEFQGMSRMIRYVIIFVVAVELLGMIFLSFVFVPKYGLFHGLYVSLFTSISAFCNAGFDIFGNFS SLTSYYSSAYVLIICMALIILGGIGFSVITEFIIYRYTKKISVTTKVVLVTTFFLVLIGAALYFIFEYDNPLTFQNMSLGNKVLNSIFSSVSPRT AGFNSIDLSGIRSGTVFLTCILMLIGGSPGSTAGGIKTTTFGVIILSIYHYIRNKNRTIVLGKEIPAKTINKAFIVSFVALFFISTFVILISMTNK DASFRSIVFEVFSAFNTVGLSLGLTSELNGLGKILIILAMYLGRVGTLTLIFAFTNKHDNSKKSSSIKYPEVKITVG
3.4E-63	223	11.8	2E-31	118.4	0.4	2	2	Q5V404_HALMA	Potassium uptake protein TrkH	trkH2 rrnAC0757	Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) (Halobacterium marismortui)	511	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Haloarcula, Haloarcula marismortui, Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) (Halobacterium marismortui)	272569	>tr|Q5V404|Q5V404_HALMA Potassium uptake protein TrkH OS=Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) GN=trkH2 PE=4 SV=1MSVRVDWRQSVALTGTVTKYLAVAMLVPLGISFVYGEDTVVFLISIAIAIVVGLALEQVSDSHELGPREALLFVGLSWGAVAVIGA IPYVIAGYGTESALGEPVNALFESMSGFTTTGATATDEISFARHSHALLMWRQLTQWLGGMGIIVLMVAILPEAAVNGAQLIESEAPGP ELQKLTPKIAETARLLWLFYLGFTVLYILILLGLHYTGYAPNMDAYNAVAHGFTTLPTGGFSPQAESIAYFSPAVQWAVIPFMLIAGMNF ALFYLLLQDEYAAFLQDRELQAYLGANAGVAVILWGLLFTGSAPPLELGGITQGALENSLRQATFQVASLLNSTGYATSNFAEWGNTA QGVLLFAMFIGGSAGSTGGGVKIVRWLVVLKSIRRQLFTTAHPSAVRPVRLGGQVIDEDVINAIYGFTLLYLLTFGIATVFLLLDAGRVG LELTVFEAISASLATIGNIGPGFGFLGPFGTYELFPETSKLLMIFLMWIGRLEIIPVFVLFTGAFWNE
3.7E-63	223	2.5	4.6E-63	222.8	1.7	1	1	Q2UUQ8_ASPOR	Trk-type K+ transport systems	AO090009000216	Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	254	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus oryzae (Yellow koji mold), Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	510516	>tr|Q2UUQ8|Q2UUQ8_ASPOR Trk-type K+ transport systems OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=AO090009000216 PE=4 SV=1MGQFQASLAVRAFYAAQTMANNLGFTLTPDSMVSFQDATFPMLIMTFLAYAGNNLYPVFLRLIIWTTYRCTPKNSSLREPLDYLL KYPRRCYTLLFRSKPTWVLFGIIFVLNFVDVLLIVVLDLHNPAVNTLPGGPRVLAAIFQAASARHTGTSSFNLADVNPAVQFSLLVMMYI SVFPIAISMRASNTYEERSLGLFSSDGEVVDESNTTNYVLSHVRNQLSFDLWYIFLGIFCICVAESNRIMNPSEPVRSS
3.8E-63	223	36.7	4.9E-63	222.7	25.4	1	1	A0A097SS92_9MOLU	Cation transport protein	trkG MGM1_0670	Candidatus Mycoplasma girerdii	529	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Candidatus Mycoplasma girerdii	1318617	>tr|A0A097SS92|A0A097SS92_9MOLU Cation transport protein OS=Candidatus Mycoplasma girerdii GN=trkG PE=4 SV=1MSTNSKKKWDRKRITKTIKTILLGKNLLQVFLRIYVLTVILGAVLLYSGWTHKAWSLENTTPYTFWDALFVSCSAFTNTGLTAIDIA AFYNFFGQFIIFVLIGLGGIGIISLFFIIWNWFKKSNEIKIDHLILLQSERGNNKYSSSYKSIRFCVIFIVLTEIIFGLLMSFWLCFVKAYVPML LPNTGSPSLTYDDKNHLINTYHNYLDALWAGMFTSVSAMNNAGFDIFETYSSIAMFRNDWGIVFQMMIVILIIIGGVGYPLIFDIYESRRI KHLGLSYRYSLFTKVGLSSYFIVLFIGLAISYGFEFGAATSKSLIGVETIHHEWGNAKTFNQIFAIFFNTVSTRSAGFSSFDQNLLTEGSKI NYSIMMFIGANPSSTGGGIRTTTFAIMFISIWHLIRGYRNVSLFKKTIPSRTVRNSFIITFVAFLLVLISSVIIFYSTTNNKGVLISNDPNFNF TMVLYEVTSAFGTVGLTTGITNDAGTTAKIVLIINMFIGQLGVSTALLVWFKKMSKSKDILYPSEDVKIG
3.8E-63	223	13.1	6.1E-63	222.4	9.1	1.3	1	C6BV64_DESAD	Trk system potassium uptake protein	Desal_1979	Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763)	484	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio salexigens, Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763)	526222	>tr|C6BV64|C6BV64_DESAD Trk system potassium uptake protein OS=Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763) GN=Desal_1979 PE=3 SV=1MRWKIVLHIIGALTLCVGLTMLFPLGFSLYYQDAGILPLLKSFGLTCFSGLALFLIFRDREEAKGLSHREGMAIVALGWVFAGFFG SLPFYFGDVFTSYVDCFFESLSGFTTTGASVMMDIEKNAKGILFWRSLTHWLGGMGIIVLSLAILPFLGVGGMQLYKAEVPGPVPDKL KPRIKDTALVLWKVYVLFSAIEAVLLMLGGMDLFDSLCHTFGTLATGGFSTKNSSVAYFQSAYIDYVITFFMLVAAVNFSLHYQMIKGR PLLLWKDPEFRFFGVVTLIIVGIITISVYSATNYDSIADSFRYTSFQVASIISTTGYATADYEIWPAVAQGLLLFCMFLGGCAGSTSGGMK HLRIMLLLKQAYQEVFRIIHPRSVNRVKLGKTVVKPETMNDILGFFVLWLLLFVICGLIVAATGVDVVSSFAASLACIGNIGPGIGSVGPT ENYAHIPELGKWALIFCMLLGRLEIYTVIVLCVPEFWRK
4E-63	223	21.3	1.6E-62	221.1	14.8	1.8	1	A0A0F2PIU2_9FIRM	Potassium transporter	VR67_05005	Peptococcaceae bacterium BRH_c8a	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c8a	1629715	>tr|A0A0F2PIU2|A0A0F2PIU2_9FIRM Potassium transporter OS=Peptococcaceae bacterium BRH_c8a GN=VR67_05005 PE=4 SV=1MNKALVLRSLGLVLLCEAVAMLPSLGIALYLHENAYRAFIISVIVIGLIGVALIRIKVQSNDVGYREGFVIATAGWLFMALFGTLPFIL SGAIPGLVNAFFETMSGFTTTGASVLTNVEILPQSILFWRSITHWLGGMGVIVLTLALIPSLKIAGMKLFRAEVPGPTKNKVLPRVAQTS RELYKLYIIITVAEIVALKIAGLSWFDSIIQTFGTVATGGFSNYNASVGAFANPVVHYIIIFFMLICGMNFALHFLALRGDFRSYLKDPETRL YMFITTGACLLITANLIASLGYNAEEAFRQSAFQTVSILTTTGYATADYIQWPFLSQAVIFLLMFIGGCAGSTSGGMKNVRYLILFKTASR QIARLIHPKAVIPVRLGRNVIPEELVGSVQTFFFLYFAILLGCTLVIASMGFDLLSALTAVAASLGNIGPGFGAVGPMSNFAAIPDLGKILL ALCMLVGRLEIYTVLVVLSVRFWRTC
4.1E-63	223	33.7	5.4E-63	222.6	23.4	1.1	1	R5XLB7_9CLOT	Potassium uptake protein TrkH family	BN716_00030	Clostridium sp. CAG:571	469	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:571	1262822	>tr|R5XLB7|R5XLB7_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:571 GN=BN716_00030 PE=4 SV=1MERRKKTKLTATQSLVLGVVVVIFIGAIILKLPISNNEGRSIKFLDSLFVSTSCVCVTGLTTVVPSEQFSKFGQIVLMCLIEIGGLGF MSFIALILMFMGRKINLSDRMLIKESLNQNNVGGLIKLIKKIFLYTITFQIVGMLLLSIRFIPKYGVGEGLFYSAFHSISAFCNAGIDIIGRNSF SDYQYDILINVTLMLLIIIGGLGFTVWDDIFNTVKERINKNSGIWRNLTIHTKIVLITTITLLISGTILTFTFEKNNVHIMKSDSVSQKILKSAFY STTLRTAGITTTNPDKLTTATKFISVIYMFIGGSPASTTGGIKNVTFAIIILMVISFIKGNDSTIVFKREIPFKIIKRAIAVVTISICIVATAIILLTV TEQLYLEQNYNMISENIDFIGIIYEAFSAFGTVGISLGVTRKLSLFGKIIIMILMFIGRLGPITLSFALFSKYNKKRKSSIKYPQCDLLVG
4.1E-63	223	17.8	2.2E-32	121.6	4.3	2	2	L0KUQ8_METHD	Trk-type K+ transport system, membrane component	Metho_0946	Methanomethylovorans hollandica (strain DSM 15978 / NBRC 107637 / DMS1)	477	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanomethylovorans, Methanomethylovorans hollandica, Methanomethylovorans hollandica (strain DSM 15978 / NBRC 107637 / DMS1)	867904	>tr|L0KUQ8|L0KUQ8_METHD Trk-type K+ transport system, membrane component OS=Methanomethylovorans hollandica (strain DSM 15978 / NBRC 107637 / DMS1) GN=Metho_0946 PE=4 SV=1MNQKVILSVLGTLLRFLGMMMIVPLLVAFYYHESPLPFLIGIGLTEITGIYLWSSYKSDDDWKLREAFAIVAFSWLAAMFFGAIPFI VEGISPLNAFFETMSGFTTTGSSILDNIESHSKSILFWRSMIIWVGGMGIIVLFVAILPKLAIAGRQLVRAEAPGPTEDKIKPRIRDTAKIL WMVYVVLSALEVAALHLAGMSTYDAVTHMFASMGTGGFSPYGRGIEAFNSPLIEAILILFMFIAGANFALLYRTLYVNHKIIFKDEEFKF YTAVVVVATAVLILALRRDIGADPFTCLRYALFQVVSLLTTTGFANTDFNLWPDSSRIVLLLVMFIGGCAGSTAGGPKAIRILLLLKYARW ELFRSVHPKAVKPIKFNGKTVPENTMQEIISFVVIYFLVFIASTFCISIMGVDILTSITASITTLGNIGPGFNLVGPMASFNGMPALAKVIMIA NMWIGRLEVFTVIVMFTPEFWKK

4.1E-63	223	25.3	5.5E-63	222.6	17.5	1	1	Q2RHN3_MOOTA	K+ transporter Trk	Moth_1755	Moorella thermoacetica (strain ATCC 39073)	443	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Moorella group, Moorella, Moorella thermoacetica (Clostridium thermoaceticum), Moorella thermoacetica (strain ATCC 39073)	264732	>tr|Q2RHN3|Q2RHN3_MOOTA K+ transporter Trk OS=Moorella thermoacetica (strain ATCC 39073) GN=Moth_1755 PE=4 SV=1MREWPFRLRPPQIMVLGFGLVIATGTLLLSLPVASQTGHPVAVIDALFTATSATAVTGLNTVDTQTTYSLFGELVILALIQTGGLG FMTLSTLVALLIGKRITLRRERLVMQEAMNQLTVEGVVRLSKYVLVFTLLAEGLGAVILSMRFSRQMPLGQAIYFGIFHSVSAFCNAGFDL FSKSLVDYRGDWVVNLVITGLIITGGIGFSVVADIYTKRSWQRLSLHSKIVIRTTLWLILAGTLIILALEYTNAKSLAPLPLSEKVLAAYFQA VTPRTAGFNTLSIADLRPVTLLFIIILMFIGASPGSTGGGIKTSTFAAIAAAVWTIIRGNVDIEVFGRRLPRDTVLKALAIVAVSMLLVVTVT GILLITEGAELETVLFEVTSAFGTVGLSMGLTPRLTVIGKLLISATMFTGRVGPLTLAFAIAQRLGRQGVKHYPEERIIVG
4.5E-63	223	36.3	2E-62	220.7	25.1	1.8	1	B9E873_MACCJ	K+ transporter integral membrane subunit homolog	MCCL_1684	Macrococcus caseolyticus (strain JCSC5402)	438	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Macrococcus, Macrococcus caseolyticus, Macrococcus caseolyticus (strain JCSC5402)	458233	>tr|B9E873|B9E873_MACCJ K+ transporter integral membrane subunit homolog OS=Macrococcus caseolyticus (strain JCSC5402) GN=MCCL_1684 PE=4 SV=1MKKKKSNPYLVIISSFFIFLAIGTMLLALPIAQRQPTSFIDCLFIATSAFTVTGLATIDITANFNTFGHIIIMILVQAGGLGIITLAMIVFIM LGRKVGLKSRSLATEALNQQNLGGILRLVLKLLLISLLFESIGAVLLALEWVPLLGIKRGLFNSFFTAVSAFNNAGFALHSDNLVQYQTN PLTNFIITTLIILGGLGFTVILDLYQKKKFSHLRLHTKIMIFGTIIIINTFATLSIYLLEMMNNLKTLGGHNTFDQFQMAYFQAITTRTAGFNTIDI GALQTPTILLMMLFMFIGGGSTSTAGGIKLTTAVVIFFGTSIYIKQREQISLFKRAIDTKNLFKSFAIVVLSSTFIFIITLALVIAEPDLPFLAV MFEVISAFGTVGLTMGITAKLSVIGKLLIILMMMIGKIGVLTIVLTFSKPQKALYTYPKEDVLTG
5.2E-63	223	0.3	5.2E-63	222.7	0.2	2.2	2	A0A0C4EFL4_MAGP6	Potassium transporter 1 (Uncharacterized protein)	MAPG_11565	Magnaporthiopsis poae (strain ATCC 64411 / 73-15) (Kentucky bluegrass fungus) (Magnaporthe poae)	685	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Magnaporthiopsis, Magnaporthiopsis poae (Kentucky bluegrass fungus) (Magnaporthe poae), Magnaporthiopsis poae (strain ATCC 64411 / 73-15) (Kentucky bluegrass fungus) (Magnaporthe poae)	644358	>tr|A0A0C4EFL4|A0A0C4EFL4_MAGP6 Potassium transporter 1 OS=Magnaporthiopsis poae (strain ATCC 64411 / 73-15) GN=MAPG_11565 PE=4 SV=1MGIASADDDGADNSSSSFSARLAAAWRPLRDGWAHVYPVIKPYLPPLNFITIHYSYFVFFGLIMSAIFFALADRADFTTLSFVDS WFLITSSFTGSGLNTVNLSELVTGQQPPPLSRATTGGLFNHHHQSPRPPPLSRATTGRLGAGLGGGLAGAYPGFDFKHFVKEHKNSI GRNGQFFDLDEDQREYLGGVEYRSLKLLLVINAAYFVLWQGLGAIALGAWMAAYSRDICAVNRQDPWWTGVFLAVSSFNNAGMILL DAGIGAFNRDPFVLTIVTILSLAGNAAYPAFVRGTVYVSRLGFKYGIARYGPAGHDYGVWEEAFDFILKYPRRLFMLMFPSRQNLVFV GFFSTLVAVNWVGLLVLNIGNPLFDDTPYPGRAGIMLFQAVAAMASGLGIFNISGLWFGLLVLLVVTMYLSAYPEIIVMRNSNVYEERS LGLYSTAEAQKQDEEEDAAAEMTVIAPLLSPSSAAGSHTSALSRSLQPIKSLATVGRRGTAFVGKQIQRRMQDFQGVGIDTTRRDYVS IPVPGIKRTPVMQFDGPPPVAAPEGGVSLVSQHLRGQLSHDMWSIALALFLISLIETAHSIDDPRGYSVLNFLFEIVSGYTNIGISVGLTG KSFSFCGGWFTGSKIVMILMMIRGRHRGLPVALDHSVKLPGWDDAAREEQDAEIRRTISRARAGVDALHVP
5.4E-63	223	31.3	6.7E-63	222.3	21.7	1	1	R7GD23_9FIRM	Potassium uptake protein TrkH family	BN631_00467	Eubacterium dolichum CAG:375	463	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium dolichum CAG:375	1263076	>tr|R7GD23|R7GD23_9FIRM Potassium uptake protein TrkH family OS=Eubacterium dolichum CAG:375 GN=BN631_00467 PE=4 SV=1MVEFIHSMLNFKKMSPAQKIAASFLLVILCGTLLLMLPISNVDGNFMNPIDALFSATSACVTGLSTINVSEQLNLFGQIVLMLLIQI GGLGLMTFMAVFLLIIKSRLSLNEKIVMKEMLNQEHVFNMKKFIVDILYYTLFFETIGAILLSIPMIEQYGLFDGSFKAIFLAVSAFCNAGFD TLGSTSLQAYADQPLICFTIMALIVLGGLGFAVWFDVRDKLVSLVKGKLAWKKFRRSLSLHTKLVLFVTFLLIVSGALFIVVFEYNNSATL GNMPFPQKIMCGLFESISLRTAGFTSINYGALQSQTSLIMMVLMFIGGCPGGTAGGIKTTTFFIIVIYIIGMLKGSKQTVVFRRAIEESIVIR AMGIFFLNLVVLFVGVLLLCIIQSQDFLSIAFECVSALATVGSSLGLTGDLEALGKLVIICMMYIGRIGISTLVLSMMRQRSFDENKISLPK GNIIVG
5.4E-63	223	32.3	7.3E-63	222.2	22.4	1.1	1	C6CZQ3_PAESJ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Pjdr2_4814	Paenibacillus sp. (strain JDR-2)	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. (strain JDR-2)	324057	>tr|C6CZQ3|C6CZQ3_PAESJ Potassium uptake protein, TrkH family OS=Paenibacillus sp. (strain JDR-2) GN=Pjdr2_4814 PE=4 SV=1MAKYFNILRWSPPRILVFGFAMIIVIGAVLLSMPIASSDGSRLPFIDALFTATSATCVTGLVVVDTGTYFSTFGKIVILSLIQIGGLGF MTMSTLIALVLRKRISLKERLILQEAMNQTSMEGIVRLIRRVIFYSLTIELVGAALFAIRFAFDMPFGRAAWFGLFHSISFFNNAGFDIFGH FRSLTMYVGDPLVNIVSMLLIIFGGLGFVVMADLLDFRKNKRLSLHSKVVLSTTGILIAAGALVIFIFEFSNSNTLGSLHWGEKILAAFFQS VTPRTAGANTLDYTQLRQATVFFTVILMFIGASPGSTGGGIKTTTFTTMVGAVIAMIRGRDDIVLFHYRLGKDRIFKALTITMLSLTLVIFV TMLLSTTEDQQFLKILFETTSAFGTVGLTIGITPELTFFGKMVIALTMFAGRLGPLTLAYALGPKTERELYRYPEGKITIG
5.6E-63	223	21	5.7E-61	215.9	14.5	2.1	1	Q5LH46_BACFN	Putative potassium uptake protein	BF9343_0759	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides fragilis, Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	272559	>tr|Q5LH46|Q5LH46_BACFN Putative potassium uptake protein OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) GN=BF9343_0759 PE=4 SV=1MINSKMIYRITGFLLLIETGLLLCCAGVSLIYREDDLSSFLLSAGLTTLVAILLLALGKGAEKQLNRRDGYVIVSVAWVVFSLFGMLP FYLSHYIPSITNAFFETMSGFSSTGATILDDIEALPHGLLFWRSMTQWIGGLGIVFFTIAVLPIFGVSGVQLFAAEASGPTYDKVHPRIGV TAKWIWTIYAGLTAIEVILLLFGGMGLFDSICHSFATTGTGGYSTKQDSIAYYNSPYIEYVIGVFMFLSGINFTLLLLLFTGKLKKVSQNAE LKWYVMSVILFTAFIAAVLYRTTPMGAEESFRKAFFQVASLHTSTGFVTADYMQWVPVLWGTLTVIMLIGACAGSTTGGMKCIRMVIL AKVSRNEFKHIVHPNAVLPVRVNKQVISPAILSTVLAFSFIYAVIIIVSVLLMLAMGVGFTESIGTVISSIGNMGPGLGSCGPAYSWDGLP DLAKWLLSFLMLLGRLELFTVLLLFSSDFWKRN
6.3E-63	222	35.2	8.1E-63	222	24.4	1.1	1	A5N021_CLOK5	Predicted transport protein	CKL_2455	Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium kluyveri, Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	431943	>tr|A5N021|A5N021_CLOK5 Predicted transport protein OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=CKL_2455 PE=4 SV=1MKLKSKPLFKINEIQILILGFLLIIIVGAILLWLPISSENHTYTNFIDSLFVATSATCVTGLITVDTGTHWNYFGKTVILALIQIGGLGFM AFSTLIALILGRKITLKERLLIHESLNSFNIQGLVKMSKYILLFTLVETVGAVVLSSQFIPQFGVYRGLFYSIFHSVSAFCNAGIDLIGEGR SLMPYYNNFTIIFTISVLIIIGGLGFYVWQEIYNLSFKYTKRLSLNSKVCITMAVVLLASGTILFFLFEFNNPATMKYMTSGDKLLSSFFASV SVRTAGFNSISISDMNESSKFLTIVFMFIGGAPGSTAGGIKTTTFAALIIMTAVSVIKGRQETEIYKRTIKKDLVYKAIVIFIVYIILIFISALILGV TEKDESLETIIFECISAIGTSGLSFGTTPDLSIIGKIVIIISMFFGRLGGLTIILSMINRKIPKSIKYPEDKILIG
6.5E-63	222	18.5	2.1E-33	125	3	2.1	2	F4LU04_TEPAE	Trk system potassium uptake protein TrkH	trkH TEPIRE1_0363	Tepidanaerobacter acetatoxydans (strain DSM 21804 / JCM 16047 / Re1)	497	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Tepidanaerobacter, Tepidanaerobacter acetatoxydans, Tepidanaerobacter acetatoxydans (strain DSM 21804 / JCM 16047 / Re1)	1209989	>tr|F4LU04|F4LU04_TEPAE Trk system potassium uptake protein TrkH OS=Tepidanaerobacter acetatoxydans (strain DSM 21804 / JCM 16047 / Re1) GN=trkH PE=4 SV=1MNLNTVRYILGTLLIVLGISMVPSLGWSIYYGDSDINAFLFSIVAAIIVGVLLRVKTYLRKDLGLREGFLIVTLGWILAGIFGALPFVF YGAVDTFIDGFFEAISGFTTTGATVINNVEALPHGILFWRSFTHWLGGMGIIVLFLAILPGVGAGGFHMFRAEVPGPSVSKLSSKIANTA KILWRIYMGLTILQTILLMVAGLDLFDSLTHTFGTVATGGFSTRALSVGAFKNPAAEIIIIFMAMSGVNFSLYYYLLKRQWDRVFGDEEL KFYLGVIIVTTLLIAWNIRGLIPLKTDLFRTSAFQVVSIMTTTGYATANFDLWPAFSKMLLLLLMFFGGCAGSTGGAIKQIRMLILFKYCRR ELTHTLHPKAVVPVKIGGKPIPDDVLRNILAFSYIYIALFVLGSLFIAMLGEDMITSVSSVAATLGNIGPGLGSVGPESTFSEIPQIGKLVLS FLMLMGRLEIFTVMLCFTPSFWQGVTIFGKPKDYSLRKDHSI

6.7E-63	222	20.4	5.3E-38	140.2	4	2	2	F4LMU5_TREBD	Cation transporter	Trebr_2428	Treponema brennaborense (strain DSM 12168 / CIP 105900 / DD5/3)	473	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema brennaborense, Treponema brennaborense (strain DSM 12168 / CIP 105900 / DD5/3)	906968	>tr|F4LMU5|F4LMU5_TREBD Cation transporter OS=Treponema brennaborense (strain DSM 12168 / CIP 105900 / DD5/3) GN=Trebr_2428 PE=4 SV=1MIFLLLAIISVTFILPIGTAAYYGETEVIPAFAFPGAVCIAAAAVFFIAGRKQRVSLTARDAFIVVAASWVFASILGAVPFVLSGTIPRIADAVFESVSGFTTTGATILSDIESLPVSVNLWRCQMHWLGGMGIVALTVALLPLLGVGGFQLIKAETTGPEKGKVTPKIATTAKILWFIYAGFTVIQTVLLKLAGMTWTDALAHTFSTLGTGGFSTKNQSIAYYQSASVEWICTIFMILAGVNFSLYYYAILGKFDDIRHNSELKAYLAIIGVSTAAITPFILAGSDSVGDAVRTAAFQVASIISTTGYSSADFNLWLPGAQLVIVLLMFIGGCSGSTGGGVKVVRWVILSKQMSNEVRKMLHPHGVFSIRLNGRSGRKDVVFSVAAFLFLYLLLVFITAYIAALDGTDVLSAVTASLAMVGNIGPGLGKVGPVANYGFFADGVKWWFSFAMIAGRLELYTMLIFFMPSFWKK
6.8E-63	222	15.5	1.8E-62	220.8	10.8	1.6	1	F0JEV9_DESDE	Trk system potassium uptake protein	DND132_0377	Desulfovibrio desulfuricans ND132	485	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio desulfuricans, Desulfovibrio desulfuricans ND132	641491	>tr|F0JEV9|F0JEV9_DESDE Trk system potassium uptake protein OS=Desulfovibrio desulfuricans ND132 GN=DND132_0377 PE=3 SV=1MRWRYVLHVIGALVACVGLTMVLPLAWGLYYHDGTAAPLAMSMGITVALGGIAFLVFRDRSHKASIMTHREGMAIVALGWFAAGAFGGLPFYLGGTFGSVVDCVFESLSGFSTTGSSVLADIEAVPRGLLFWRSLTHWLGGMGIIVLSLAILPFLGVGGMQLYKAEVPGPSPDKLKPRIKDTAMTLWKVYVLFSALETVLLMFGGMDLFEALCHTFGTMATGGFSTRNASVAGFDSAYIDYVITVFMLIAGVNFSLHYLVLKWKPSAMLKDPEFRVFAGMVLVFVVILTITVYVAGNYDNLADSVRYTSFQVASILTTTGFATADYELWPGLAQAILLFCMFVGGCAGSTGGGMKVMRIMLLFKQSYQELFRLIHPRSVSHVKMGRTVVKDDVISGVWGFAFLWVGLLVLAAFVVAATGVDVVTSFAASLACIGNIGPGIGGVGPTDNFAWMPDAAKWVLTFCMVLGRLEIYTVIILFVPEFWRK
7.4E-63	222	24.4	8.9E-62	218.6	16.9	1.9	1	L0F913_DESDL	Trk-type K+ transport system, membrane component	Desdi_1998	Desulfitobacterium dichloroeliminans (strain LMG P-21439 / DCA1)	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium dichloroeliminans, Desulfitobacterium dichloroeliminans (strain LMG P-21439 / DCA1)	871963	>tr|L0F913|L0F913_DESDL Trk-type K+ transport system, membrane component OS=Desulfitobacterium dichloroeliminans (strain LMG P-21439 / DCA1) GN=Desdi_1998 PE=4 SV=1MNIPVILGLLGRLLVVYACTMSIPLILALALEEVSRMAFLLSMFLTLITGIVFAWQAKLTDMKIGVREAFATVVGAWILAALFGALPFQFADVVPTYVDAVFETVSGLTTTGASVIPEVESLPQSILLWRSLTQWLGGMGIIVLFIVLLPKTDLGTVLLFNAEVPGPTHDRVMPRIRDTAITLWKIYLIFTAVCTILLWAAGMTFLDAVNNSFATIASGGFSTKNMGIMFYDSLAIEMIISFFMIIAGANFVIFLMVWQKKNFKPLRNVELIIYLLIFVSTLVIAASLWSNVGESPLYALRHALFQVASIMTTTGFASANFDQWPSIAKIILFLLMFIGGSAGSTSGGIKVSRILLLAKTAWAELKRGIHPRAVSGIKLDGKVIGTETLNQVGIFFFLYIVTFAGASILIAGIGLKPFDAMSAVAATLGNVGPGFGFVGPTTTFAGLNLFGKVVLTFCMLLGRLEFFTLLIIFRREFWRRQKTW
7.5E-63	222	28.8	8.8E-63	221.9	19.9	1	1	K9SYA5_9CYAN	Potassium uptake protein, TrkH family	Ple7327_0133	Pleurocapsa sp. PCC 7327	444	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Pleurocapsa, Pleurocapsa minor, Pleurocapsa sp. PCC 7327	118163	>tr|K9SYA5|K9SYA5_9CYAN Potassium uptake protein, TrkH family OS=Pleurocapsa sp. PCC 7327 GN=Ple7327_0133 PE=4 SV=1MTISRTICLGFLAVITVGTLLLIFPFSTSDGSWNNPIVALFTATSAVCVTGLAVVDTGTYFSFWGQLILLLAQVGGLGYMTITTFLMLLIGRKFDLQQRFAIQESFDRPFILGSQNLIRSIIATTLIFEITGIFLMLYPFSRDYGLEQGLWLSIFHSVSAWNNAGFSLFKDSLIGYRSSPIINLTITGLIIFGGIGYQVIIELYSWLTEKCQRKKARFVFSLNLKVVVSTTIILLGLGTITIFFAELRNDGTFVDLNLQEKLLAAWFQSVTSRTAGFNTLDIGKMTVEGLFITMILMFIGASPSGTGGGIKTTTLRVISSCTRSVLRGDEEVILYQRKVPYPLILKAIAVVFGSVMTIFIATLIISYIENNLNALAILFEVISAFATVGLSMGITASLSPLSQLVIVAVMYIGRVGIIILIAAIIGDPRPSVIQYPEENLLVG
7.7E-63	222	28.9	1.4E-61	217.9	20	1.9	1	B0USD8_HISS2	Potassium uptake protein, TrkH family (EC 3.6.3.14)	HSM_0699	Histophilus somni (strain 2336) (Haemophilus somnus)	439	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Histophilus, Histophilus somni (Haemophilus somnus), Histophilus somni (strain 2336) (Haemophilus somnus)	228400	>tr|B0USD8|B0USD8_HISS2 Potassium uptake protein, TrkH family OS=Histophilus somni (strain 2336) GN=HSM_0699 PE=4 SV=1MKFEHINTKPPYVLAGGFLFIILIGTLLLELPFAHHKSISWLHALFTSTSAVTVTGLSVEDTANFTLFGQVVLMCLIQIGGLGFMTFAIYIARRMGARIGLFGNAIAQEALGDVPFNLLLHTAKNVLKFALTFELIAMIILTVHFYGDVSFFQALYQSLFYSISAFNNAGFALSSESLMPYVDDIVVNIVITVLIIIGGLGFVVLMDIKNQRQYKKFSLNTKVVLWATCILNIVSFLIFYILERQNPLTFGPLSETGKLFAAWFQAITPRTAGFNTVDTAGLTDASSLLTMFLMFIGGGSLSTASGIKIGTFCIIVVATFAYLHKESHVNLFKHNLPDELIKKSFALFFTSLSCIGISSFLLLAVEPQFHFLDVLFEVVSALGTVGLSRGITAELSPFGESILIILMFIGRVGLLTMIYLIMQPHSSKIKYPKEYIQIG
7.8E-63	222	22.2	2.3E-61	217.2	15.4	2	1	A0A0F2PKD9_9FIRM	Potassium transporter	VR67_02160	Peptococcaceae bacterium BRH_c8a	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c8a	1629715	>tr|A0A0F2PKD9|A0A0F2PKD9_9FIRM Potassium transporter OS=Peptococcaceae bacterium BRH_c8a GN=VR67_02160 PE=4 SV=1MNKALILRTLGLVLLCEAVAMLPSLGIAIFLREDAMRAFVISISVIGLIGAALGRIKVHSNVVGYREGFVIATASWLFMAMFGSLPFLLSGAIPSFVNAFFETMSGFTTTGATILSDIEKLPQSILFWRSLTQWLGGMGVIVLTLALIPSLKLAGMKLFRAEIPGPAKSKVLPRVTQTARELYKLYIIFTVLEIVALKIAGLSWFDSFIQTFSTVATGGYSNYNASIGAFANPAVHYIIIFFMLICGMNFALHFHALQGNFRPMWRDPETRLYLSLVVLACILVGANLIAYNGYGLEEAFRMSSFQVVSIITTTGFTTTDFNHWPLLSQGILFVLMFIGGCAGSTSGGIKNVRYLILFKTASRQIAKLIHPKAVIPVRLGREVIPEELVESVQSFFFIYFALLLVSILIIASMGVDLFSAIAAVVATLGNVGPAFGAVGPAYNYDFIPVAGKLLLSLCMLVGRLEIYTVLVVLSVRFWRA
8.2E-63	222	9.3	6.8E-62	219	6.4	1.9	1	C7P4G8_HALMD	Cation transporter	Hmuk_1876	Halomicrobium mukohataei (strain ATCC 700874 / DSM 12286 / JCM 9738 / NCIMB 13541) (Haloarcula mukohataei)	520	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halomicrobium, Halomicrobium mukohataei, Halomicrobium mukohataei (strain ATCC 700874 / DSM 12286 / JCM 9738 / NCIMB 13541) (Haloarcula mukohataei)	485914	>tr|C7P4G8|C7P4G8_HALMD Cation transporter OS=Halomicrobium mukohataei (strain ATCC 700874 / DSM 12286 / JCM 9738 / NCIMB 13541) GN=Hmuk_1876 PE=4 SV=1MSWGVDWRASTSLVGTVVKYLSLTMLVPLVVAVVYGEDIAVFVVSIAATAVLGLALEQLDPEPDVGPREALVLVSFAWLAAAAVGTIPYLIAGNGIPFVMAPSAPASTLANPVNALFESTSGFTTTGATVLGEISTDRHSHAVMMWRQLTQWLGGMGIIVLMIAILPELAVNGAQLMQSEAPGPELQKLTPKIVETARALWLIYFGFTVLYVAVMYGLQFVGLAENMTLYNAVAHGFSTMPTGGFSPEAASIAAFKPIVQWVAIPFMVAAGINFALFWHVVRGEFRSLLEDTEFRAYAGATAVLIAVLSALLFRGAAPPLELGGTTAGATENALRQAAFQIASLLNSTGFATDSDFAQWDDHTKIFLLFTMFIGGSAGSTGGGVKVVRWLVVFKAVRRELFTTANPNTVRPVRLAGQVVDEDAIRGIMGFTLLYLVLFGISAVFLGLDSARVGYDLTVLESVSASLAALGNIGPGFGRLGPFGSYLDLPDTSKLLMVFLMWIGRLEIVPVLALFVDRLDRS

9.2E-63	222	15.9	1.1E-62	221.5	11	1.2	1	A0A088QIC6_9CORY	Cation transport family protein	DR71_738	Corynebacterium sp. ATCC 6931	476	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium sp. ATCC 6931	1487956	>tr|A0A088QIC6|A0A088QIC6_9CORY Cation transport family protein OS=Corynebacterium sp. ATCC 6931 GN=DR71_738 PE=4 SV=1MVITLSRQATKTRRGVRPTTLVVWCYVALITAGTVLLMLPISAVNSHPTGQCAPSPGDMCLPTALSDALFTATSATSLTGLITVDTATHWSTFGKVVIMLLIQLGGLGFMTLASLFGLFVAGRLGLNRRAGARVEGRGMDMGEISWVVRAAVSFTLLVEFVVAVALTLRFHSGYGYGWGKAAWEGLFHAISSFNNAGFALYTDNVIGFYSDAWVLLPLAFALIVGGLGFPVLLEAWRHGKAWLSVCTRGQLPKRWSLTTRFTIKGTILLIALGTLMVAFGEWSNAMSGFTAGEKILNSFFAGVSPRTAGFNALDYAEFHPSTLLGTDFLMFIGGGTGGTAGGVKITTSAVILAAVLAEIRGDTSVSVARRRLNPKVLRQALVVVLAFGIGQVFLAVIAVSFLAPQFSTDQILFEVISAFATVGLSTGITADLPVAAQAIFIVLMFTGRVGPIALATALAARPRQRVYEYPEERPFIG
9.7E-63	222	32.3	1.3E-62	221.3	22.4	1.1	1	Q10XV4_TRIEI	Potassium uptake protein, TrkH family	Tery_3883	Trichodesmium erythraeum (strain IMS101)	443	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Trichodesmium, Trichodesmium erythraeum, Trichodesmium erythraeum (strain IMS101)	203124	>tr|Q10XV4|Q10XV4_TRIEI Potassium uptake protein, TrkH family OS=Trichodesmium erythraeum (strain IMS101) GN=Tery_3883 PE=4 SV=1MTVARRICQGFVIVITIGSILLMLPISMSNGNWSHPVTALFTATSAVCVTGLSVVNVGEYYSFWGQLFLLLLVQIGALGYMTATTVLLLLLGHKFGLRQKVAVQQSLEQVGLAGVEGLIKSILATTIVFELTGILLLLLVFVPIYGFQEGLWYSIFHSVNSFNNAGFSLYSDSFVQFVKSPLLNFVITGLIIFGGLGYQVIMEMYSWVKDRCQGKQAFHSFSLHFKVVTSTTIFLLIVGLIAFFIAEFHNPNTLENLNLGEKLIAAWFQSVTTRTAGFHTIDIDNFTDAGLFLTIALMFIGASPGSTGGGIKTTTFTILFNSTKAALQGRDEVLCYQRKIPMIVIIKAIGIVFASSLLVVFATTVIAFTDRQLELTEIFFEVVSAFATVGLSKGVTSNFTIPGQLVLITMYIGRVGVLLLVSTVFAQQKPSAVEYPEENLFV
9.7E-63	222	27.2	2.3E-62	220.5	18.9	1.5	1	Q8TZW9_PYRFU	Trk system potassium uptake protein	PF1856	Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1)	505	cellular organisms, Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae, Pyrococcus, Pyrococcus furiosus, Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1)	186497	>tr|Q8TZW9|Q8TZW9_PYRFU Trk system potassium uptake protein OS=Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1) GN=PF1856 PE=4 SV=1MFLFLTCKIGNRMVKLRTFINISEDLFVIRNLIGAILQGIGLAYLVPVLLAWFYPEEIPLVIYFAIPGFSCIILGWVLSKHMEKIEDVNLRQAMMASAFIWLFASLVSVIPFMGIAKMRFVDSYFETMSAWTGTGLTMMSNLESYPKILLFWRAWMQWLGGIGIVLVALTVLIRPGVAAARLYKAEARSERILPNFVNTAKIIVQIYAVLTLLGIYLYYSNGMSLFDATIHSMTGLGTGGMSSHDLSIGYFNSLAIETVTVFLMIMGATNFTVHYRMFKNRSLKEFFRDIQVRYMLYFITLIVALMTYSLVFFGHLTPIRALRESIFHAVSAITCTGFGISNLAEYPEIDKILLAILMVIGGSAGSTSGGIKLIRIVLMYQSLKWTIEQAILPKGAVIRKRVNGYEFTEEEIQEVLGFTMTYIAFLLLGTLYIMLRLGVRFADALFEVASAIGNVGLSVGITSPLLPLDIKILLTILMWVGRLEIFSTIVFIVGLAMIFSRRSKE
9.8E-63	222	0.1	1.3E-62	221.3	0.1	1	1	E2LVF7_MONPE	Uncharacterized protein (Fragment)	MPER_11175	Moniliophthora perniciosa (strain FA553 / isolate CP02) (Witches'-broom disease fungus) (Marasmius perniciosus)	278	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Marasmiaceae, mitosporic Marasmiaceae, Moniliophthora, Moniliophthora perniciosa (Witches'-broom disease fungus) (Marasmius perniciosus), Moniliophthora perniciosa (strain FA553 / isolate CP02) (Witches'-broom disease fungus) (Marasmius perniciosus)	554373	>tr|E2LVF7|E2LVF7_MONPE Uncharacterized protein (Fragment) OS=Moniliophthora perniciosa (strain FA553 / isolate CP02) GN=MPER_11175 PE=4 SV=1DISAIYDLTDWFFFLVLDIGTAEYESIPVGIRLIVGLLQATAVRAAGFGIVPLAALAPAVKILYVIMMYISVYPIAMSVRSTNVYEEQSLGVYRGEESDDEEKFQAAGPRVTVWSQYLTMHARKQLAFDMWWLCLGLFLVCIIERSNLEDENNATWFNIFNIIFEIVSAYGTVGLSLGAPMVNYSFSGTLRPLSKLIFCVVMLRGRHRGLPVAIDRAVMLPQEIRKHDEVEARSMSMGDRDDFFAGSSTIRNSDFPNGGHVMGEKQPSIVEEARSNID
9.8E-63	222	21.8	7.3E-61	215.6	15.1	2.1	1	Q5NEJ1_FRATT	Trk system potassium uptake protein	trkH FTT_1638	Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Francisellaceae, Francisella, Francisella tularensis, Francisella tularensis subsp. tularensis, Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4)	177416	>tr|Q5NEJ1|Q5NEJ1_FRATT Trk system potassium uptake protein OS=Francisella tularensis subsp. tularensis (strain SCHU S4 / Schu 4) GN=trkH PE=3 SV=1MMLSQKPKIIGIFLMFLSLTMLSPLLVDYIYDEDNAYPFVLSFTVTFLCGFLLWFISRKSNKKLSNRDGFLIVTLVWIFVTVFGAIPYMSFPGLNLSFTNAVFESVSGFTTTGGTVIEGLDKLPHSILFYRQQTEFFGGMGIIVLSVAILPLLGVGGMQLYKAEVSGQWKDDKIAPKISSTAKALWMVYLLLTFLCFISYLLVGVEPFDAICYTFSTVSTGGFAPSDASMTDKPLGMLIVCAIFLFLGATSFKAHYIALSKFKISHYFRNIEFKAYFYFLFFTSFIVCITIIAHTNDLSNIFSIVTNSIFQVISISSSAGFVSDNNYYLWPSFLPIMLMFIAIIGGCGGSTAGGLKMIRAILFKEKAILEAKRVIHPQGVFTVKLGDIHISEQALNRVSGFISVYIIIFAGGWLALLGCGLDIPTAFSTIATTLSNVGPGLGDIGSNFKNLPKEALWICNFAMIAGRLEIFTILVLFMPDFWRK
1E-62	222	32.5	1.4E-62	221.2	22.5	1	1	K9Q2B0_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Lepto7376_3664	Leptolyngbya sp. PCC 7376	445	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Leptolyngbya, Leptolyngbya sp. PCC 7376	111781	>tr|K9Q2B0|K9Q2B0_9CYAN Potassium uptake protein, TrkH family OS=Leptolyngbya sp. PCC 7376 GN=Lepto7376_3664 PE=4 SV=1MTIARTICLGFLGAILLGTLLLMLPLSMASGSWNDPLVALFTSTSAVCVTGLSVVVDTGTAFSTFGQCVILFLIQIGGLGYMTLSTFLMLLIGRRFDLAQKFAIKESFDQPYNQGTRTLIRSIIATTLIGELTGIFLLYIRFSQDFGAASGLWMSIFHSISAWNNAGFSLFSDSLVGYHNSWIINLVIPALVIFGGIGYEVIIEFYLWLQHRRKGKLRRFNFSLNFIVVTRTTLWLLGIGTIAFLFVEWNNLSTLAPMASFSDKAIAAWFQSMTTRTAGFNSIDIGNMTTAGLFITMGLMFIGASPSGTGGGVKTTTMSILANCTLSVLRGHNTVTIHQREISQTIIFKAIAVVFGSATVITLVTAIISVSNPNLELIDVLFEVISAFATVGLSTGITASLSGIGKIAIIGTMYCGRVGVLLLMSAILGEATPQRISYPEENLLVG
1E-62	222	33.3	2.1E-61	217.4	23.1	2	1	E3DNB5_HALPG	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Hprae_1406	Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL)	441	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium praevalens, Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL)	572479	>tr|E3DNB5|E3DNB5_HALPG Potassium uptake protein, TrkH family OS=Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL) GN=Hprae_1406 PE=4 SV=1MMNISKKNLTPAQYLVSGYFVVIILGALLLMLPIATTDGQGLRAIDAVFTATSATCVTGLIVVVNTKEAFTTFGSTVIMFLIQIGGLGIMSMSTLFAFIIGKKISLKERLIIQEDLNQYQISGMVRLVQYLLGFTFAIEGSAAVILFFRFLKDYPTGKSIYLAIFHSVSAFNNAGFDLFGNSLENFTGDLTINLVIMALIILGGIGFGVMVEAYNRIKFKKSTLQTKIVLIVTLSLLIFGFIVFFILEYDNTLAGLPLLDKTLGAMFLSVTPRTAGFNTVATGALKQSSLFIIIILMFIGASPGSTGGGIKTTTFGVMLATLKNMIIGKEDVEVYNRRFKKKIIYEAFVITMLAAGLVILVTTILLIVEDFQFIDILFETVSAFGTVGLSTGITGQLSDISRVLITITMFAGRVGPLTLALAFGERVRKGNYHYPTEKVMVG
1.1E-62	222	25.7	2.2E-61	217.3	17.8	2.1	1	A0A0A8E919_9GAMM	Trk system potassium uptake protein	SD28_02720	Francisella guangzhouensis	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Francisellaceae, Francisella, Francisella guangzhouensis	594679	>tr|A0A0A8E919|A0A0A8E919_9GAMM Trk system potassium uptake protein OS=Francisella guangzhouensis GN=SD28_02720 PE=3 SV=1MRLSQKPRVIGIFLMFLSVTMLSPIIVDYIYSEHNSFPFLISFIITFSAGFILWLIGKNSSKKLSNRDGFIIVALVWLIVTVFGAIPYMTFPGLGLSFSHAVFESTSGFTTTGGTVISGLDNLPHSILFYRQQTQFFGGMGIIVLSVAILPLLGVGGMQLYKAEIAGQWKDEKLTPKISSTAKALWMVYLLFTFLCFISYIIVGMDPFDAICYTFSTISTGGFTPTDASMTDKSTAVLIICGIFLFLGATSFKAHYIALSKLKFKHYFKNIEFKAYCYFLFFCSLIIAITMIAYTDDLSKIPRIITDSIFQVIAISSSAGFVSDNNFYLWPSFLPIMLMFMAIIGGCGGSTAGGLKMIRAILFKEKAMLEAKRVIHPQGIFTVKLGDVHISEQALNRVSGYISVYIIVFAVAWLALLGCGLDVTTAFSTTATTLSNVGPGLGEIGSNFKNLPTQALWICNFTMIAGRLEIFTILVLFMPEFWRK

1.1E-62	222	34.7	1.5E-62	221.1	24.1	1.1	1	D9SM21_CLOC7	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Clocel_2009	Clostridium cellulovorans (strain ATCC 35296 / DSM 3052 / OCM 3 / 743B)	455	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium cellulovorans, Clostridium cellulovorans (strain ATCC 35296 / DSM 3052 / OCM 3 / 743B)	573061	>tr|D9SM21|D9SM21_CLOC7 Potassium uptake protein, TrkH family OS=Clostridium cellulovorans (strain ATCC 35296 / DSM 3052 / OCM 3 / 743B) GN=Clocel_2009 PE=4 SV=1MDLLKRKKVVMTPVQILSLGFALTILTGAVILTLPISSVNGTATNFIDSLFTATSAVCVTGLTTLDTASHWSYFGKTIIMFLIETGGLGFMSFTTLYALIIGRRISMRERMIMKEALNAESMAGIVRLVKYVIIFTVSVQIIGALLLMTQFIPDYGVGEGIYFGIFHSVSAFCNAGFDLTGASLIPYNNNPVVILTISALIIIGGLGFAIWMEIYNFKTMKKLSLHAKFAIAVTLILLILGMIMMYIFDFAINQAYKDMSLPTKILNAFFASVTPRTAGFFSVPTVTMSHAAIAITIILMFIGGSPGSTAGGLKTTTIGLLVMTVISMLRGREDTEIFKKRINKMQVYKAFTILFIAFGVIFIGTLLLSIAEGEKVVGGITMNLEHYLYEIVSAYGTVGLTLNLTPTLTAPGKIIVMFAMYIGRVVGILTFIFSMLRRNKKDDYGLKYPEDKIVIG
1.2E-62	222	19.9	2.3E-62	220.5	13.8	1.4	1	Q5QZN3_IDILO	K+ transport system, membrane component	trkG IL1658	Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	393	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Idiomarinaceae, Idiomarina, Idiomarina loihiensis, Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	283942	>tr|Q5QZN3|Q5QZN3_IDILO K+ transport system, membrane component OS=Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) GN=trkG PE=4 SV=1MSVTGVSFTDAVFESVSAMTTTGATILTGLDEMPKSFLLYRQFLQWMGGLGIVIFVVAILPMLNVGGMRLLKAETPGPIKNEKLAPRVASTSRYLWLVYLCLTIGCAGSYWLAGMSPFDAIAHSLTTVSTGGFSPYDASMGHFQQPIILIVADVFMILGAISFALHHKLFTARAISGYWKDEETRWFLIALAVFSVILTALAFNAQTHHSFGESLNQAVFHVVSFMTSTGYGADDLSAWPAATAGFLVAASYLGGCAGSTAGGNKFVRNVITLRILKHQMLQAIHPRAILKVVYQGKAVTNDVIQAVMSFMLMVAISSMVLTLILMLTGLDFFSAFTAVSACLNVLGPGFGEVSSNFIPVSDTGTWVLTLAMILGRLEYFTLLTLLLPQFWRD
1.2E-62	221	22.8	3E-62	220.2	15.8	1.5	1	Q5L3I3_GEOKA	K+ uptake transporter (Trk family)	GK0212	Geobacillus kaustophilus (strain HTA426)	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Geobacillus, Geobacillus kaustophilus, Geobacillus kaustophilus (strain HTA426)	235909	>tr|Q5L3I3|Q5L3I3_GEOKA K+ uptake transporter (Trk family) OS=Geobacillus kaustophilus (strain HTA426) GN=GK0212 PE=4 SV=1MNTNRKFFDPPKVLVSGFALIILVGAFLLMLPTATVDGKGLPFLDALFTATSATCVTGLVVVDTGTTFTLFGQLVILALIQVGGLGFMTFATLFAFLLGKRISLKERLLLQEALNQLSIEGIVRLVKRILVFTVVIEGIGGLLLAIRFSFDMPFWKAVYFGFFHAISNFNNAGFDLMGEFRSLTGYVDDPVVSLVVPILIILGGIGFIVMNEVYEYRQTSRLSLHTKVVAITTAWLLVASMALILLLEWNNPKTMGPLSLSGKFLSAFYQAVTPRTAGSNTLNIPDLTQPTLFLIVFLMFVGASPGSTGGGIKTTTFTTLLGAVWSQIRGKEDVILFRKRIVYDTVYKSLTVTMSGLFIVMFVTMVLTITESGKDFLMILFEATSAFGTVGLSMGLTPELSPLGKAVIILTMFAGRVGPLTIAYAVTLRRQPDPFRYPKGKIMIG
1.4E-62	221	19.3	1.9E-62	220.8	13.4	1.1	1	D0MCT6_RHOM4	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Rmar_0138	Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) (Rhodothermus obamensis)	474	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidetes Order II. Incertae sedis, Rhodothermaceae, Rhodothermus, Rhodothermus marinus (Rhodothermus obamensis), Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) (Rhodothermus obamensis)	518766	>tr|D0MCT6|D0MCT6_RHOM4 Potassium uptake protein, TrkH family OS=Rhodothermus marinus (strain ATCC 43812 / DSM 4252 / R-10) GN=Rmar_0138 PE=4 SV=1MLGLKWSARRSSALLVKQPRRESFWRRLSPPQLFVGSFLLLILLGTLGLKTLPGLYTGAPLSWLDALFTATSAVCVTGLIVVDTATYFTVWGQAFILLLIQLGGLGIITFTTVLIVALGRRLSLRQQALAASAVEAAPHVDYRQLARDVVRFTFLIEAAGALLLYLGFLPELGWRGAFWPAVFHAISAFCNAGFSTFSDSLVGFRTNPVVLPVIMVLIVVGGLGFLTLEELYLWRRSIRERRRFRLSLHSRLVLTTTVLLLGVGWVFFVFFEWKATLAALPLAKLLNGLFMSVTARTAGFNTIDYGAATEQTNFLTILLMFVGGSPGSMAGGIKTTTIALLVLLAISRLRRGQEVPSCWSRSVPHEVVQRAVGLFVVAVAVLMLGSFVLTATEIEHGVTAPGSFLKYLFEAYSAFGTVGLSMGVTPSLSTTGRWIIILLMFIGRVGPLTFAAALTIRRHRTRQFRYAYEDVVVG
1.4E-62	221	24.6	5.2E-62	219.3	17.1	1.8	1	A0A0A7GFJ3_9EURY	Potassium uptake protein TrkH	GACE_1782	Geoglobus acetivorans	477	cellular organisms, Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales, Archaeoglobaceae, Geoglobus, Geoglobus acetivorans	565033	>tr|A0A0A7GFJ3|A0A0A7GFJ3_9EURY Potassium uptake protein TrkH OS=Geoglobus acetivorans GN=GACE_1782 PE=4 SV=1MNTKLVVNYLGQISIYYSFIFILPLISAHIYGEDLSAFIIPMVISMALGIVFYVSSRPESEYAKYKEGYAIVGLGWLITVLVGSIPYIYYGVGFIDAFFETMSGFTTTGATIFDRVENLPRSLLLWRSLTQWLGGMGIVVLFVAIFPALSKKGETLLQAEVPGLKIEKIRPRMRDTALRLYATYMILTVLEIVFLKLLGVSFFDAVNHTFTTLSTGGFSTHTESVAYFNSPAIEFIIFVFMVLGGSNFVLIYLLLTGKPKFLRDVEFRFYIFILILSGIILTAMNLSSYDLLESIRYSFFQVASIMTTTGYTATVDFNTWPTFSKAILVALMFIGGCAGSTAGGIKVARVVILQKVSVSEMRRMLHPNAVPAIQFEGKPLNERSIRGVHLFLAVYLMVFVASCLLVSLEQLDLVTTFTAVAACINNVGPGLEIVGPMGNFSSFSPWSKLLLSFDMLVGRLEIFPMLLLFAPSIWKRRLPSRRLVD
1.4E-62	221	15.1	7.6E-60	212.2	10.4	2	1	U2QKJ7_9FIRM	Potassium uptake protein, TrkH family	HMPREF1546_04078	Oscillibacter sp. KLE 1745	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	1226323	>tr|U2QKJ7|U2QKJ7_9FIRM Potassium uptake protein, TrkH family OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_04078 PE=4 SV=1MIGFAIGRILLVEAALLLLPMAVALGYGESPVPYLLPAALLVLCGGLLSFKKPRQASLFARDGLAVVALAWIAVSLFGALPFYISGSIESFVDCFFETVSGFTTTGATILTEVESLNRGILFWRSFTHWVGGMGVLVFVMAILPMGGDGHGMHMLRAEMPGPAVGKLVSRMSDTAKILYGIYLVMTVIEIVLLLAGGMPLFDACIHSFGSAGTGGFSSRNLSVGAYNNPYFEIVIGIFMLLFGINFNLYYFLLVRRFRDVFRSEELWAYVLIVATAVAAITLDIVHMYESVGTSLRHAFFQVSSIITTTGYATVDFNTWPTFSKAILVALMFIGGCAGSTAGGIKVARVVILQKVSVSEMRRMLHPNAVPAIQFEGKPLNERSIRGVHLFLAVYLMVFVASCLLVSLEQLDLVTTFTAVAACINNVGPGLEIVGPMGNFSSFSPWSKLLLSFDMLVGRLEIFPMLLLFAPSIWKRRLPSRRLVD
1.5E-62	221	24.6	1.6E-32	122	4.9	2.1	2	B3EK02_CHLPB	Cation transporter	Cphamn1_0087	Chlorobium phaeobacteroides (strain BS1)	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae, Chlorobium/Pelodictyon group, Chlorobium, Chlorobium phaeobacteroides, Chlorobium phaeobacteroides (strain BS1)	331678	>tr|B3EK02|B3EK02_CHLPB Cation transporter OS=Chlorobium phaeobacteroides (strain BS1) GN=Cphamn1_0087 PE=4 SV=1MNFPAISHVLGALLMFIGSTMLLPLACALIYNDGDALSLLISMGVTVSIGFPFWWSFRKYRDLTLKDGLFIVTFGWILVSSVSALPFMLHGTIPSFTDAFFEMMSGYTTTGATILDDIESVPHGLLFWRSTTHLIGGMGFIMVTIIILPLLGIGGMQLYKAEADPGQVITGEKFLPRVKQTAVWLWGIYLALILIQSLLLWIGGMPVFDSLCHAFGTVSTSGYSTKNSSIGYYDSAWIDWITIIFMFLGGMAFMMHYHILKKDWEPVRNNTEIRWYIGFVVFISLLATLILWATGSYSGFFDSIRHATFQVVSILTTTGFTTADYELWPQSAQMLLMIACFIGACAGSTTSGIKVVHYEIICKYLYANGRKFLQPLAVVPIKINQKNVASSVVTLAVSYFILNIFMIFVGSAIMTLIDDMDFFSSMSAVISALFNIGPAFGEVGPTHTFSHVSTAGKWFLSFNMLTGRLEMFTVMVMFYPSFWKK
1.5E-62	221	15.2	2.6E-62	220.3	10.5	1.3	1	X4RAL2_9ACTO	ATPase	CQ11_07330	Trueperella pyogenes	478	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Trueperella, Trueperella pyogenes	1661	>tr|X4RAL2|X4RAL2_9ACTO ATPase OS=Trueperella pyogenes GN=CQ11_07330 PE=4 SV=1MRTVIRINISSPAIDVCYITKINSAYRRAQDYAVFVHKSRHLRPASAVAFSFLGLIMIGTIALASPWASARYVAPLDALFTATSAVCLTGLITVDTATAWSPFGQVVIMILIQLGGLGIMTVTCLLSILLGARLGLRRRLSAQAEGRGDLGNVRWIVQATILFTLVIETVVFLVLLLRFHFGHGYGWARAAWEALFHAISSFNNAGFALYSDNLMSFATDAWVLLPLAFGLIVGGLGFPVLLETYRRLRTPRVLRRRWSLTARFTLTGTLVLAAVGTALMLTEWNGALAGIDAPNRLLNAFFAGVSPRTAGFNAIDYADARPQTLLAIDILMFIGGGSGGTAGGIKITTLAVLLATIRAEIKGRRTVSAYGRSISRRVIGQALAVTVAALALVVAATFMIITLAPQFSTDHILFEATSAFGTVGLSTGITPNLPRSAQLILVVLMFAGRVGPLALATTLAGRSTNRLYKYPEERPAIG
1.6E-62	221	27.2	1.4E-61	217.9	18.9	1.9	1	A0A0D5NQI4_9BACL	Ktr system potassium transporter B	VN24_25170	Paenibacillus beijingensis	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus beijingensis	1126833	>tr|A0A0D5NQI4|A0A0D5NQI4_9BACL Ktr system potassium transporter B OS=Paenibacillus beijingensis GN=VN24_25170 PE=4 SV=1MLGVQKYKKWNHLKLSPPQTLAIGFVITIMFGTFLLMLPISTHPEHRLAFMDALFEATSAVCVTGLVVVDTGTTFTVFGQVVLMVLITIGGLGFMTFGILIALLLGKKIGLSERLLIQSATNQFSLSGLVKLVKIILTATFFIEGAGALLLAVAWSNEMGWPKALYYGLFHSISAFNNAGFGLEFDNLSKWVGNPAINLIIASLFILGGIGFTVIMDVTHKKFNFRKWSLHTKLALISTLIINIVATILIFGIESRNPDTLGQLSIGDQILASFFHATTPRTAGFNTLDLTQLKNDSILLTMALMFIGGATGGTAGGIKITTFLLLLVVWAFITRKDGINVFKRRISNELVFRALSISMIGVIIIFSAVFLLELTEKDISLMNLAFEAVSAFGTVGLSLGATPELSSFGKLIIILLMFVGRLGPLTLAFALTKKQSQANFKYPEEKILIG

1.6E-62	221	24.4	2.2E-62	220.6	16.9	1.1	1	A0A073CG52_PLAAG	Trk system potassium uptake protein TrkH (EC 3.6.3.14)	A19Y_2155	Planktothrix agardhii NIVA-CYA 126/8	422	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Planktothrix, Planktothrix agardhii (Oscillatoria agardhii), Planktothrix agardhii NIVA-CYA 126/8	388467	>tr|A0A073CG52|A0A073CG52_PLAAG Trk system potassium uptake protein TrkH OS=Planktothrix agardhii NIVA-CYA 126/8 GN=A19Y_2155 PE=4 SV=1MLPFSLSARTWGNPLTALFTSTSAVCVTGLSVVDVGKFYSFWGQFIIVLLVQVGGLGYMTVTTFLLLLLGRKFRLKDKLALQQSLDASGIAGAVPLLKSIVATTALFEITGIFLLLFVFVPDLGWSQGLWFALFHSVNAFNNAGFGLLSDSFVRYVNSPVLNFIITFLIIWGGMGYQVIQELYLWIGNRLSKYPLRRDFSVHFRVVTSTTIFLLILGTALLFFTEHHNPGTLAPLNFPDQVMAAWFQSVTTRTAGFNTINNGELTVAGLFISIILMFIGASPGGTGGGIKTTTLRILANSTRSALQGREEVICYKRQIPLPLILKAIGVLFGSFMVICISAILISLSQPNIDFDSILFEVVSAFATVGLSTGITASLTPLSQLIIITTMYVGRVGVILLMSAILGDPKPTSIDYPEQNLLVG
1.7E-62	221	30.3	2E-62	220.7	21	1	1	A0A0F2JAP1_9FIRM	Potassium uptake protein, integral membrane component, KtrB	UF75_4161	Desulfosporosinus sp. I2	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	1617025	>tr|A0A0F2JAP1|A0A0F2JAP1_9FIRM Potassium uptake protein, integral membrane component, KtrB OS=Desulfosporosinus sp. I2 GN=UF75_4161 PE=4 SV=1MNILGKVLTPSRILVVGFALTILLGTLLLTSPHATKNGLGLSFLNAAFTSTSAVCVTGLVVVDTGTTFTLFGQWVILGLIQVGGIGFMTFATMFAILMGKRITFKERLLLQEALNQVSVEGVVRLAKSVFQISFVIELIGAIILTLRWSSDFGWGKAAYFGIFHSVSAFNNAGFDIMGEFSSLTAYVGDPIINITIMLLIICGGLGFIVLADLKANLKAKRGKRKFRLHTKIVLKVSGALILFGMLIILIVEFTNPKTLGPLPLGTKIMAAAFFQSVTTRTAGFNTLNFADMHETTLLSMIVLMFIGASPSSTGGGIKTTTFMTIVLSVLSTYRSEPNIILNGRTIPRDNIQKAWAITTTAVFLIFFIVSILSLTERIDLLPVLFEATSAFGTVGLSLGLTPTLTVVGKMAIILTMFIGRVGPLTLAFVLAQKKSNQAHFKYPDERILIG
1.8E-62	221	19.4	5.5E-37	136.8	3.4	2.1	2	F8F4H3_TRECH	Potassium uptake protein, TrkH family	Spica_2516	Treponema caldarium (strain ATCC 51460 / DSM 7334 / H1) (Spirochaeta caldaria)	481	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema caldarium, Treponema caldarium (strain ATCC 51460 / DSM 7334 / H1) (Spirochaeta caldaria)	744872	>tr|F8F4H3|F8F4H3_TRECH Potassium uptake protein, TrkH family OS=Treponema caldarium (strain ATCC 51460 / DSM 7334 / H1) GN=Spica_2516 PE=4 SV=1MRRRILIRVLALLLGIIALSMIPSLLIALVDRETQSIRAFLYPLVVCTSGALLALGLGKSSNIAFNAGDGFLLVSLAWFLTSILGSIPFVITGVTSNPVDALFESVSGFTTTGATIFKDLEKLPRSILLWRAMTHWLGGMGIVVLTVALVPLLGVGGFQLLKAETPGPEKDKITPKITATAKILWFIYIGLTALEVLLLMMGGMNWFDAVTHAFATMATGGFGTKNISIAYYNSAWIDWVCTIFMILAGMNFSLYYRILQGKFQDLLKNTELKVYLSIVIITSVLVALVVLPQYGTLAGALRFSSFQVASIITTTGFATADFDLWPSFAKAVLFLLMFIGGCSGSTGGGIKVVRHVVLFKQAGNEIRRLLHPRGVFSIQLNGRVGRKDVVYGVAGFVFLYLTLVLLVTLVVSSAGADLISAFSSALVTIGNIGPGFGLIGPSQNYSNFPNYVKLVWSFAMIAGRLELWTVIILFTPEFWRR
1.9E-62	221	29	2.8E-62	220.3	20.1	1.1	1	R5YS12_9CLOT	Uncharacterized protein	BN681_00514	Clostridium sp. CAG:492	474	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:492	1262813	>tr|R5YS12|R5YS12_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:492 GN=BN681_00514 PE=4 SV=1MEKSRRIKLTAPQILVLGVIASIFGIAILLKLPISNVSGKHIKFVDSLFTATSAVCVTGLNTIIPAEQFTIFGKVVLMCLIEIGGIGFMSFIALLLLMRKKIGLSERNLIKESLNQNYNKGIIKLIKKIFIYLGVIEIIGAIFLSIRFIPQYGTKMGIFYSIFLSISAVCNAGFDIMGSNSLINYQYDWLVSISIMVLIIVGGLGFTVWDDIIDAIKKICAKKIPARKFGREISTHTRIVLITTFILLVSGALFTFILEKDNVQIMKDDNIAQKILKSSFYSTTLRTAGFESIDSTELTTATKFISLIYMFIGGSAGSTAGGIKTTTFAIIILMVISYLKGNENTIINKRKVPQRLLKRAIVVMFVSVFIIIVSIVGLSITEDIKAEHTLPEAETSVRDVSFLDIFYEVFSAFGTVGLTLGITPKLSVAGKIIIMFVMFIGRLGPITISYAVLKKDKRNKGIKYPECDDLIVG
1.9E-62	221	23.9	4.3E-61	216.3	16.5	2	1	A0A0C5VQA2_9GAMM	Trk system potassium uptake protein	YC6258_00414	Gynuella sunshinyii YC6258	482	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, unclassified Oceanospirillales, Gynuella, Gynuella sunshinyii, Gynuella sunshinyii YC6258	1445510	>tr|A0A0C5VQA2|A0A0C5VQA2_9GAMM Trk system potassium uptake protein OS=Gynuella sunshinyii YC6258 GN=YC6258_00414 PE=3 SV=1MNLPALFKLSLFPVMAFGLVDLVFSFLSMLVFRDDVYRYFYETGVAFFAVSVFLAILLKFEITRIRLQEAILFVTLAWISAGFLASVPFILISGLTLTDAVFESLSALTTTGATVMSGLDAMPKTLLLYRQTLQWFGGLGIIILMVAIMPMLNIGGMKMYKAETPGPMKDDKLVPRVSKSSRYLWGVYLTITVLCTVSYYLAGMNWFDAVSHAFSTVSTGGFSPHDASMKYFDSVAVEMVSNVFMIAGALNFGVHFIAYKSRDIKTYWRDEETVLFLGIIALATLLAAIYLTLNQSQYTFWMALRSSLFQVISFITSTGFASDNFTDWPIFCAVILVIVGYVGGCAGSTAGGNKVIRTLLVLKTNHRNIKQLIHPKALFTIKSNGRVIGEDILDSVRAFMFFSFLVSLIFILLLMANGLDLWTSITAVAACVNVLGPAFGELGSNFQPLNDFSTWLMSLAMVMGRLEYFTVLLLFSVRFWRA
2E-62	221	22.5	4.5E-61	216.3	15.6	2	1	R7DKA6_9PORP	TrkH family potassium uptake protein	BN686_00650	Tannerella sp. CAG:51	488	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:51	1262979	>tr|R7DKA6|R7DKA6_9PORP TrkH family potassium uptake protein OS=Tannerella sp. CAG:51 GN=BN686_00650 PE=4 SV=1MSEINFRIVARVIGILLCFEALFMLLPLSVAIYYNESDIYAFLLTIGITAVVGLCSTFIFKRHSKQMGKREGFLIVSTSWVFFSLFGMLPFLIHGDIDNITDAFFETMSGCTTTGATILDDIESLPHGILFWRSLMQWLGGMGIILFTLAVLPMLNSGGGIQLFNAEVPGITHDKLRPRISETAKRLWIVYLSITVLLIVLLVLGPMNFFDAVCHALTTTATGGYSTKQNSIAYWDSAYIEYVIIIFMLISGINFSLVYHAALGDYKKLLQDEETKWFLFVVLLATAAIAAGLFISGQIYGNAEKTIRTALFQVSTCITTTGFATADFAKWGPFFNVVIFCIMFFGACAGSTSGGAKTIRMVVVLKNTANEFYRHLHPNAVVPVRINRRVISYDLVSKILAFLFVYVLIMAISALILSSLGLTFEESFGCTLSCLSNVGPGFGRMSSDFSFEIIPTFGKWVLSFDMLIGRLELFTVLILFSPYFWKKS
2.3E-62	221	8.1	8E-30	113.2	0.2	2	2	B9LN40_HALLT	Cation transporter	Hlac_1184	Halorubrum lacusprofundi (strain ATCC 49239 / DSM 5036 / JCM 8891 / ACAM 34)	512	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Halorubrum, Halorubrum lacusprofundi, Halorubrum lacusprofundi (strain ATCC 49239 / DSM 5036 / JCM 8891 / ACAM 34)	416348	>tr|B9LN40|B9LN40_HALLT Cation transporter OS=Halorubrum lacusprofundi (strain ATCC 49239 / DSM 5036 / JCM 8891 / ACAM 34) GN=Hlac_1184 PE=4 SV=1MTRTIDPRAVFSYTGTIVKILSASMAVPLVVGLIYGEDALAFAVSMIIAVAIGAGMERLHDDPDLGPRDALAVVSLAWFAAAVVGAIPYIIAGYGTASALGHPMNALFESMSGFTTTGATVTTEISFEQHSHAVLMWRQLTQWLGGMGIIVLMVAILPQLAVNGAELMKSEAPGPGLQKLTPRIAQTARALWIIYAGFTAALIAILFGLGLTPLAPEMNLYNAIAHGFSTLPTGGFSPQAESIAAFSPVVQWVFVPFMVIAGVNFALFWFVLRDDPMRMYKNTEFRMYLGLVTGLTAVLAAGLFYGGAPATAIGGATEGVGENALRQGAFQIASLMNSTGFATADFAEWDTQTKFFLLFVMFIGGSAGSTGGGIKVIRWLIVAKALYRELYTTANPEVVRPVRLGGEVVDEDVIRGIFVFTLLYFLLFALSAVFIEIDTSRVAGVSLTGTQALAASLATIGNIGPGFGPLGPFGTYELLPNTTKLLMIGLMWIGRLEIVPVLALFVAGFDDR
2.4E-62	220	26.1	9.6E-62	218.5	18.1	1.7	1	R6A6W7_9BACT	Trk system K+ uptake protein TrkH	BN693_01850	Prevotella sp. CAG:5226	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:5226	1262930	>tr|R6A6W7|R6A6W7_9BACT Trk system K+ uptake protein TrkH OS=Prevotella sp. CAG:5226 GN=BN693_01850 PE=4 SV=1MLNIPIIYKALGTLLLEALLLGLCFGMGFYFGEVNHLTFGLPSALAAVIGALLLYFGRHAENRMGRRDGFLIVSLTWVVFSLVGMLPFIVSGYQPRVAAAFFETMSGFTTTGATAFTDIDVLPHSILLWRSITHWIGGMGIVFFTIAVLPNMGGGDVKLFSAEATGLKIGKLHPRISTTARWLWSIYSLLTITCMAAYFFGGMGLFDALCHSLSTIGTGGFSTHTASIAWFQSPRLQWIVTLFMFLASVNSTLLLYLFFIKRRVRDVLHDDELRCFLVIFFVAAFSIMGILMYADHMDFATALRSAFFNTASLQSTTGFSDEDFMKWHPTIWLILSLISIIGACAGSTSGGLKSVRVLMVWRLTKAEFKKMLHPHAVLPVRINNTVITSQTARTVFVFFVVYFMLIMLSTFAMVAMGLSLLDAFGLAISSFSNVGPSIGHLIGPLGSWGVLNDAILWINSFLMLAGRLEIFSLLLPLTPAFWRDE

2.5E-62	220	22.7	4.5E-62	219.6	15.7	1.3	1	Q7M8V2_WOLSU	PUTATIVE K+ UPTAKE PROTEIN	KTRB WS1379	Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W) (Vibrio succinogenes)	442	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Wolinella, Wolinella succinogenes, Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W) (Vibrio succinogenes)	273121	>tr|Q7M8V2|Q7M8V2_WOLSU PUTATIVE K+ UPTAKE PROTEIN OS=Wolinella succinogenes (strain ATCC 29543 / DSM 1740 / LMG 7466 / NCTC 11488 / FDC 602W) GN=KTRB PE=4 SV=1MDIRSVRILLLSYMLIALLGALLLSLPPMQRAPLPFVDLLFTSTSAVCVTGLIVQNTASDFTFWGQLVILLLIQVGGFGYMTLATLLY LVLRRRLGFREKQVLKETLDYPTMDGLIRFMRRIVFFVLYIELVGALLLFGRFSLDKEMEEALWLAIFHAVSAFNNAGFSLFESNLMEYR GDVAINLIITSLIIIGGLGYFVLLELREHHKKRFFHLSLHTKVVVTMTAALLVFAALVVLILEWNNPRTLGELPVWERFMAAYFASVNFRTA GFNTLDIGGFRDATMFFSSVFMSIGGAPGGTAGGIKVTTVAVLLLYGWASLRQGEPVIFKRKVADEVVQKSFVILLGAAIYIILSAMALS MIEEGVSFLPLLLEVSSAFGTVGLSAGDGGVLSLSANFDTFGKFFMIVLMLLGRVGVLAFTIVFFGASSPRRVQYPEGRIIL
2.6E-62	220	22.5	5.3E-62	219.3	15.7	1.5	1	A0A0E3NV32_9EURY	Potassium uptake protein TrkH	MSMTP_0953	Methanosarcina sp. MTP4	476	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina sp. MTP4	1434100	>tr|A0A0E3NV32|A0A0E3NV32_9EURY Potassium uptake protein TrkH OS=Methanosarcina sp. MTP4 GN=MSMTP_0953 PE=4 SV=1MNFKIVFYVLGGLLRLLGILMIIPLAVAYYYDESLVPFLIAILITAVTGLFLLTYKTEGEWLRKEGFAIVGLGWLAAAIFGAIPFVLDGI SPLNALFESMSAFTTTGSTILVDIESHSRSILFWRSMMQWLGGMGIIVLFIAILPKLGVAGRQLFRAEAPGPTEDKLKPRIRETAKILWM VYMVISVLEVVALLLAGMSLYDSVTHTFTTMACGGFSPYGTSIEAFNSPLVEFIITFFMFVAGANFALHYRAIYVDKNFLFKDDEFRFYT ALTLGATGLLTLLLWRDLGTGLVDSFRFAIFQVVSIMTTTGFATTDFNLWPESGKMILLMVMFVGGCAGSTGGGIKVVRILMLLRHGR AELFKTMHPRAVRGIKFNNKTVPEEVVNSIVSFVVIYLLVFFSGALILSVLGMDIMTSVTASIATLGNIGPGLSIVGPMGTFDSIPAVGKLV LIANMWIGRLEVYTVILLFTPEFWNK
2.7E-62	220	20.5	3.4E-62	220	14.2	1.1	1	L0A0I6_DEIPD	Potassium uptake protein, TrkH family	Deipe_0952	Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	453	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus peraridilitoris, Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	937777	>tr|L0A0I6|L0A0I6_DEIPD Potassium uptake protein, TrkH family OS=Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200) GN=Deipe_0952 PE=4 SV=1MKAVMLRRRFFRKLSPPQLIALSFALISLLGGVLLSMPATHAPGVRLTFLQALFMATSAVCVTGLVVVPTGETFNLLGQIILLLLMQ IGGLGIVTFGTLFALLAGRRIGFGDRVRLAEQTGAFDVGSVARLIRLIVLYTLAFEALGALVLYSRFGPLEGWGTGAYYAIFYSVSAFNN GGFTLYSDSLERFAGDPVISLTVATLVILGGLGFLVVVNLAAWRASGRSNVLLTYSKIVLLMTAILLPLGMLGFAALEWTNPQSLGTLPL WEKLIVSFFESTTPRSSGFNTVDYSLLRPATLMFTIILMFIGASPGSTGGGIKVTTLFVLILASWSMIRGRGEPQAFQRRIDTETIVRALV VTVLSLALVNGALVLMVLANPKLPFLNLLFETVSAFGTVGLSMGTTAQLSEWGQGIVIALMYLGRVGPLTFAVAFSTHGRHRLVSYPA EKNILIG
2.7E-62	220	23	4E-62	219.7	16	1.1	1	U3GWV8_9CORY	Uncharacterized protein	CARG_08520	Corynebacterium argentoratense DSM 44202	450	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium argentoratense, Corynebacterium argentoratense DSM 44202	1348662	>tr|U3GWV8|U3GWV8_9CORY Uncharacterized protein OS=Corynebacterium argentoratense DSM 44202 GN=CARG_08520 PE=4 SV=1MKDSHSFSPAQLVAGSFALLVLVGTTLLLLPMSRADGSADFVTALFTATSAVCLTGLIVVDTATYWSHFGQAVIMMLIQLGGLGI MTLATIASWVIAGQIGVKSRLNASAEGRGGNQLGDVKTLLVATLSFTAAVEGVIATFLIAKFHFSYGYDWGSAIWQGTFHSISAFNNG GFSLESNNLVLFVNDIGLLFPIACAIMIGGVGYPVLLELTLRLRRRTQGFKHLPRLSLTTQFVVAGSLILWSVGALGVAVLEWNGALSGL SILGKISNAIFQSVSTRSAGFNAIDVGAFHPSTLILSDIMMFIGGGSGGTAGGVKITTVAVLLAVMVSEIRGDEYTLLSERRIPNRTMRQA LAVFVLAGSIVVVAIGLVQLLAPEFSTHQLVFEVISAFATVGLSTGITGSLPVSAKLLITVLMYSGRIGPITLVAAMAARSQRRQYSYPVE RPLIG
2.7E-62	220	28.5	6.5E-62	219	19.7	1.5	1	Q3ABT0_CARHZ	Potassium uptake protein KtrB	ktrB CHY_1575	Carboxydothermus hydrogenoformans (strain ATCC BAA-161 / DSM 6008 / Z-2901)	451	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Carboxydothermus, Carboxydothermus hydrogenoformans, Carboxydothermus hydrogenoformans (strain ATCC BAA-161 / DSM 6008 / Z-2901)	246194	>tr|Q3ABT0|Q3ABT0_CARHZ Potassium uptake protein KtrB OS=Carboxydothermus hydrogenoformans (strain ATCC BAA-161 / DSM 6008 / Z-2901) GN=ktrB PE=4 SV=1MAINTKKEINFFRRLTPSQILVLGFAGVILLGTVLLMLPISTKDGTVTPFLDALFTATSAVCVTGLVVVDTGTYWSLFGQIVILLLIQV GGLGFMTIATLFAILLGRRINLRERIVIQEALNQASLEGIIKLTKQVILFTFSFEGVFAVILGLRFSLDYGFIKGMWFGVFHAVSAFNNAGF DLIGNFKSLTPYVGDVIVNLSIAILIIAGGIGFYVISELFNLRKKGRLSLHSKITLMTTGLLLLVGTLVIFVMEYNNDKTLGALPFGEKILAAF FQAVTPRTAGFNTVDIAALHPATQYFIIILMFIGASPGSTGGGVKTTTFAVLTLAVINIILGRDEILVYNRRLPREQIFKAIAIVMISLSLINIV TFILTFTEGHNILMNMFETVSAFGTVGLSMGLTPKLSELGRILIILMMFFGRVGPLTITYALAQRRKKALFTLPEEKVMVG
2.7E-62	220	33	4.4E-61	216.3	22.9	1.9	1	B8CXA1_HALOH	Potassium uptake protein, TrkH family	Hore_11700	Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562)	441	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halothermothrix, Halothermothrix orenii, Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562)	373903	>tr|B8CXA1|B8CXA1_HALOH Potassium uptake protein, TrkH family OS=Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562) GN=Hore_11700 PE=4 SV=1MISIFKNLSPGQILVIGYSTVILVGTILLLLPVSTVEGQTTNFLEALFTATSATAVTGLIVVNTAEHWTGFGQTVIMLLIQVGGLGFM TTTTLLFLILRRKVLLQERLIVMEEINYNKLSGVIRLTRYIILLTFITEITGTLLLYLYFKGLMPDNRAWFYALFHSISAFNNAGFDLFGNSLE NFTGSLYINLIITFLFIFGGLGFLVISEIYNKRQYKKLSLHSKMVISMTLFLIISGTLALFILEFNNPATLGNYTPGIKLLASYFQAVTPRTAGF NTIPINQFRDVSLFIMIVLMFIGASPGSTGGGVKTTTAGTLLVVVYNMARGKEDIEIFRRRIKKKDIYKTLSVVVISLLIIVVVTIVLSITEEFA FIQIVFEVFSAFGTVGLTTGITPQLSNTGRLFIIITMFIGRVGPFTIAMALGRKRIKAIRYPQEDILIG
3.2E-62	220	31.4	4.5E-62	219.5	21.7	1.1	1	I0GIC0_CALEA	Kti system potassium uptake protein KtrB	ktrB CSE_03810	Caldisericum exile (strain DSM 21853 / NBRC 104410 / AZM16c01)	451	cellular organisms, Bacteria, Caldiserica, Caldisericia, Caldisericales, Caldisericaceae, Caldisericum, Caldisericum exile, Caldisericum exile (strain DSM 21853 / NBRC 104410 / AZM16c01)	511051	>tr|I0GIC0|I0GIC0_CALEA Kti system potassium uptake protein KtrB OS=Caldisericum exile (strain DSM 21853 / NBRC 104410 / AZM16c01) GN=ktrB PE=4 SV=1MKKFKLTPVQFVLASFAGVILTGAVLLMLPFSSRSYTFTDPITALFTATSATCVTGLVVVDTYNYWSFFGQLIILLLIQVGGLGYMT IATFVLIGLRRRVALRERVVVLKEGLNVPHLRKIILFAEVVFYTVIIMEGLGAIFLFIRFARMFPLYRAIWASIFHSVSAFCNAGFDVMGDFV SLTPFVNDPIVNITVMLLIVVGGIGFLTIRELIELSLARLRGDNVKKLSLHTKIVIRTTGILIVFSALLFLIEYRNPNTLAKLPFYGKVLASFFQ SITPRTAGFNTVDIASLNQPTLLLLIILMFIGGSPGGTAGGIKTTTFTVLVFLIINAYRERAPIVVSGRTLPLKTIRKAIFIFGFALTLILISTFLI LVNQGREFSFLQVLFEVTSAFGTVGLTTGITSHLSIFSRLIIILTMFIGRVGPLTIMVSFSVRKTRAMPQFPEEDIAVG
3.3E-62	220	30.9	1.3E-61	218	21.2	1.8	1	E6W6Z7_DESIS	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Selin_0319	Desulfurispirillum indicum (strain ATCC BAA-1389 / S5)	620	cellular organisms, Bacteria, Chrysiogenetes, Chrysiogenetes, Chrysiogenales, Chrysiogenaceae, Desulfurispirillum, Desulfurispirillum indicum, Desulfurispirillum indicum (strain ATCC BAA-1389 / S5)	653733	>tr|E6W6Z7|E6W6Z7_DESIS H(+)-transporting two-sector ATPase OS=Desulfurispirillum indicum (strain ATCC BAA-1389 / S5) GN=Selin_0319 PE=4 SV=1MSQLPYHWRRRIARLDLAWKKHYRRARLTYQFFQDDLYDFSQRAHPVLKALSIVLGVLVFGSLLIPLAMDSSRQSPVAMLVEQT LLVAFGLHFFTRLLLTPRKKELLRKRWAEGTGATLACAMGLDLLLADGRHLVSALQGIGVYGSDTLMLLAIQIYLVTLVTIKIIQAIPETIA NSDNPAKLILSSFLGVILVGTLLLMLPASTHDRSGLELINALFMSTSAVCVTGLIVVDTATHLSRFGQSVILILIQLGGIGVITFATYLALYLS GGIGVSERSLLRGVVQQDDVRAVSRTLKRIVLFTLGFEGIGAAVYFFSWKEFIPDMGERLFFAVFHTVSAFCNAGFSVFSNSLADPSN AVSLPINIVTMSLIIVGGLGFTTVSELVQKYFGAPATRHRCLSVHSLIVLRMTAGLIVAGTLLVLAIEWHGVLAGYSTSEKFLLSLFQSVT SRTAGFNTLDTGALSAATSLIIMLLMIIGASPSSTAGGLKTTTVYVLFASMIATIQGKDRVEIASRTLPQSVIFRAISATFLAFLILSVCTIILT ITEDFPFLDILFEQISAFMTVGLSRGITADLTNIGKLVLVFSMFLGRVGLLTFAVAFAVRSDNRTYSYPEEVVLVN

3.3E-62	220	18.6	5.8E-62	219.2	12.9	1.3	1	Q4W573_NEIMB	Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (EC 3.6.1.41)	NMB0661	Neisseria meningitidis serogroup B (strain MC58)	766	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Neisseria, Neisseria meningitidis, Neisseria meningitidis serogroup B, Neisseria meningitidis serogroup B (strain MC58)	122586	>tr|Q4W573|Q4W573_NEIMB Bis(5'-nucleosyl)-tetraphosphatase, symmetrical OS=Neisseria meningitidis serogroup B (strain MC58) GN=NMB0661 PE=4 SV=1MAHYAIGDIQGCFDELTALLGKIGFNHGTDTLWLTGDIVNRGPKSLETLQFCIRHENSVQIVLGNHDLHLLAVGCGEGAPKRSDT IEPILKHPDGKKMLDWLRAQPLLIREGSRVMVHAGILPQWRITKAESLAREAEAELRGKKYVKFFSKMYGNKPAAWDEGLKGYARLR FIVNAFTRMRALTFKNELDFDYKSTVKKMPPYLRPWFKAPDRQNLDAHHLRTLVLAGLHECRQRHLAGHRRAVGRTADRRQPRNGR NYPSPSRRRHRLEKLRKITDRPTMHKILPIAHVLSRLGMLFSFILLIPAALSYAFSDGAYTAFATTATVTLSGSCIVRLATLRFRRELRPR DGFTLVLMLWLAFAAMAAMPMYLYFPNMGFTDAFFESMSGLTTTGATVIPHVDGLAPSVNFWRHMLNWLGGMGIIVLAVAILPMLGV GGTQLFKAEIPGIDKESKMSPRISQVAKKLWFGYTLITILAAACLHFAGMGWFDAVCHAMATLSLGGFSTHDASIAYYNSPLIEAVIIVF TIVGGINFANHFAALNSRSLKTYWKDEECRTMLLLLSGSILAAALYLWHTGYYAGFTESLRYTAFNFVSIGLANGLANTDFAQWPLLISL WMFFLANILANSGSTGGGIKTIRALVLFKFSLREMMVLLHPKAVRTVKISGKAIPDRLALTVMSFIFIYFMTVVLFSFLLMASGMEFTTAF TAVIACITNAGPGLGEVGPAGNYAGLDVMQKWICVTAMLLGRLEIFTVFILFTPAYWKK
3.7E-62	220	22.5	7.8E-61	215.5	15.6	2	1	R6SBQ0_9BACE	Potassium uptake protein TrkH family	BN612_00840	Bacteroides coprophilus CAG:333	501	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides coprophilus CAG:333	1263041	>tr|R6SBQ0|R6SBQ0_9BACE Potassium uptake protein TrkH family OS=Bacteroides coprophilus CAG:333 GN=BN612_00840 PE=4 SV=1MEDFVSINVNTGRSRTNSLINRKMIFRILGILLFMEAAMFLVCASVSWYYREKEYIYFIYSILINVGVGGVLLLLGRNAPNMVTRRD GYYIVAFTWLLFTAFGMLPFYLSGEIPSITDAFFETMSGFTTTGATILDDIEALPYGMLFWRSFTQWIGGLGIVFFTIAVLPIFGVGNQVL FSAEATGVTHDKIHPKISVMAKWIWTVYLILTLTLIVLLVWGGMSVFDAVCHSFATTATGGYSTKQDSIAYWNSPFIEYVTAIFMILSGV NFSLYFMCLKGKCKQLFRDDEFKYYLMSIGGVTLLITISLVLQNHYGMEVAFRKALFQVASIHTSCGFATDDYVKWAPFTWMLLIYTML AGGCTGSTGGGIKNMRLLIVIRNIKNEFNRLMHPRAILSVKVNRQAVSPATISTVSTFILFYLICIFVSWTVLMFLGIGLTESFSLVVSSLG NVGPGLGAFGPAFSWSALPDVAKWLVSFLMLIGRLELFGILLMFAPSFWEKR
3.7E-62	220	25.5	4.9E-60	212.8	17.1	2.2	1	F5YC76_TREAZ	Trk system potassium uptake protein TrkH	TREAZ_0496	Treponema azotonutricium (strain ATCC BAA-888 / DSM 13862 / ZAS-9)	483	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema azotonutricium, Treponema azotonutricium (strain ATCC BAA-888 / DSM 13862 / ZAS-9)	545695	>tr|F5YC76|F5YC76_TREAZ Trk system potassium uptake protein TrkH OS=Treponema azotonutricium (strain ATCC BAA-888 / DSM 13862 / ZAS-9) GN=TREAZ_0496 PE=4 SV=1MLRWPIIRLIIMFSGIFSLAMLFPLVIAIIFQEEVMVFSFGITIIVIFVISLPVFIFSKKQKTNFMAHEGIFLVCIAWITASLLGAVPYYLS GFMPHYSNAVFESVSGFTTTGATIIPDLEILPRSFHLWRGMTHWLGGMGIVVLTVALVPFLGAGGFSLVNAETTGPMKEKFTPKITMT AKILWIIYLGLTIIMTVLLMLGGMNWFDAIIHAFSTLGTGGFSTKNAGIAAWNSPYIEWVCIIFMLIAGFNFTLIYRFLQGKFSEITKNSEAK AYAMIVIIATTVVAIQIMPRIGSLEKSLRFAFFDIISIMSTTGFMIDDHNQWPPLAQFVVFMLMFIGGCSGSTAGGVKVIRYVIIFKQTKNE MFRHLVPKGVFSIHLDGKIGRKDIVYSVSSFFYLYAIMVVLGTLLVSSAGVSLYDSLNAALITVGNIGLGFGKLISGAIFYEVPEYVVKWGL SALMIIGRLEIYTFILLFYPGFWKKSF
3.9E-62	220	30.8	5E-62	219.4	21.3	1.1	1	A0A075R2J9_BRELA	Ktr system potassium uptake protein B	ktrB_1 BRLA_c010980	Brevibacillus laterosporus LMG 15441	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus laterosporus (Bacillus laterosporus), Brevibacillus laterosporus LMG 15441	1042163	>tr|A0A075R2J9|A0A075R2J9_BRELA Ktr system potassium uptake protein B OS=Brevibacillus laterosporus LMG 15441 GN=ktrB_1 PE=4 SV=1MLVKLIKKFHLSPPKVLVLGFALIIAIGAILLTLPIATNDGQGLSLINAVFTSTSATCVTGLVVTDTGTTFTLFGQLVILALIQVGGLGF MTLATFFALLMGKKISLQQRLLLQESLNQISIEGVVRLAKMLLIFTGLIELTGGILLTLRFAFDMPFAKALYYGMFHSISNFNNAGFDLMG EFSSLTKYVSDPIVNITVCLLIILGGIGFIVMAEVYGYRDTKRLSLHTKVVLTTTAILIVLGTLAIFILEFTNSKTLQPLSPVGKFFGALYQSV TARTAGSNTISIGDMHQSSLFFMIVLMFIGASPGSTGGGIKTTTFATLLGAVWAQIKGREDVIFYRQRILPHMIYKSLTVTMTALFIVIIVS MILTITEPGKDFLMILFESVSAFATVGLSMGLTPDLSDIGKIVISLTMFAGRVGPLTIAFALAQRNRKEYFRYPKGKIMIG
4E-62	220	19.5	1.6E-61	217.7	13.5	1.8	1	Q72F05_DESVH	Potassium uptake protein, TrkH family	DVU_0413	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	445	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	882	>tr|Q72F05|Q72F05_DESVH Potassium uptake protein, TrkH family OS=Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303) GN=DVU_0413 PE=4 SV=1MAYHKHFGPLALPVLSFAAVILAGAVLLTLEACGTGKAVSFVDALFTATSAVCVTGLAVVDTGTTYSTMGQMVILALIQLGGLGIT TYSSLIFFLWRRRVSITDRLAVGQALLHDPSFHLGTFLQRVVVVVLCIEFSGAAALFIFGEGRIDVYAAIFHAISAFCNAGFGLMPDNLVS FRDNVGVNATIMLLIIFGGLGFSVLDECLSALRDRSVRLSRHSRLVLRTSALLIVGGAAAIWCIEAWRSGNGMSRADLVLPALFQSVSA RTAGFNTIDLGAVTHTTLLVIIFLMFVGGSPGSCAGGIKTTTFRVLAGFVTAQFKGRRQIILMDRAVDRATIEKALTLFLFATLTVVGGVTI LTLTTDAVVDPSAPRFDFIDLLFETVSAFGTVGLSTGVTPHLTTGGKLCITLIMFVGRLGPLWLLTTLQSLQTEPKYRWPEMDMPIG
4.1E-62	220	19	1.7E-61	217.7	13.2	1.8	1	A0A0E3S1W0_9EURY	Potassium uptake protein TrkH	MSLAZ_1438	Methanosarcina lacustris Z-7289	476	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina lacustris, Methanosarcina lacustris Z-7289	1434111	>tr|A0A0E3S1W0|A0A0E3S1W0_9EURY Potassium uptake protein TrkH OS=Methanosarcina lacustris Z-7289 GN=MSLAZ_1438 PE=4 SV=1MNIKIVFYVLGGLLRLLGLLMVIPLGVAYYYGESLTPFLVSIVITVITGLILLSYKTDEDWMRKEGFAIVALGWLAAAVFGAIPFMLN GISPLNSLFESMSAFTTTGSTILTDIEIHPKGILFWRCMMQWLGGMGIIVLFIAILPKLGVAGRQLFRAEAPGPTEDKLKPRIRGTAKILW MVYFVISFAQVVALMLAGLSLYDAITHTFTTMACGGFSPYGASVEAFHSPLVEFIITFFMFVAGANFALHYRAIYVDKDFLLKDDEFRFY TALTLAATGLLTLLLYRDLGTGLFDSFRLSIFQVVSIMTTTGFATTDFNLWSESGKMVLLLVMFIGGCAGSTGGGIKVVRVLMLLRHGR VELFKSLHPRAIRSVKFNNKTVPDEVINSIFSFVVIYLLVFISSALILSVLGMDIITSITASIATLGNIGPGLNVVGPMGTFDPIPPLGKLILIAN MWIGRLEVYTVIVLFTPEFWNK
4.2E-62	220	29.8	5.5E-62	219.3	20.7	1	1	K9V142_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cal6303_2076	Calothrix sp. PCC 6303	451	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix parietina, Calothrix sp. PCC 6303	1170562	>tr|K9V142|K9V142_9CYAN Potassium uptake protein, TrkH family OS=Calothrix sp. PCC 6303 GN=Cal6303_2076 PE=4 SV=1MSVSRTICLGFLAVILFGSICLMMPFSTSSGTWNDPIVALFTSTSAVCVTGLSVVDPGTYFSFWGQFFIALLAQIGGLGYMTTTTF LIMLIGKRFDLRQKIAIQQALDRPGISGSNQILRSIIATTLIFEITGVFLLLPAFVPQYGWNQGLWLAVFHSINSWNNAGFSLFKDNLVGY QSSPLVVFTVTGLIIFGGIGYQVILEAFVWLRERLASRKLRIGQRSENRLFSLDFKVATSTTLILLVLGTIAFVAVEFRNSGTLKNLSFGD QLLSAWFQSVTARTAGFNTIDIGKMTNAGLFITIALMFIGACPGGTGGGIKTTTIRVLTSCTKSILQGKEEVLLYKRKIALSLILKAVGVFIA SIATVIASTTLIALTDPELNFIQILFEVVSAFGTVGLSTGITGSVTIAAKLILIVTMYIGRVVGILLLMSAILGDPRQTRIHYPEENLLVG
4.6E-62	220	26.1	7.1E-61	215.6	18.1	1.9	1	J7ITR0_DESMD	Potassium uptake protein, TrkH family	Desmer_0444	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	768704	>tr|J7ITR0|J7ITR0_DESMD Potassium uptake protein, TrkH family OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=Desmer_0444 PE=4 SV=1MNALGKFMSPSRVLVFGFALLILFGALLLTLPQATQDGLGLPFLNAAFTATSAVCVTGLVVVDTGTTFSIFGQWIILFLIQVGGLG FMTFATLFAMILGKRITLKERLLLQEALNQFSVEGIVRLTKSVLQISFAIEAIGAVILTLRWHSDYGWSKALYYGVFHSISAFNNAGIDLFG NFSSLTAFVGDPIVNITIMLLIICGGLGFIVLAEILQHRKKFRLHTKIVLQVSGALILLGAVFIFIMEYSNPMTLGPLPLGTKVLAAFFQSVSP RTAGFNTINLAGMYDTTLLSVIVLMFIGASPGGTGGGIKTTTFISIVLSVLSTYRSDPHVVLEGRTLPRDVIQKAWAITTTAVILVFVILSIL SYTENSDLLTVLFEVTSAFGTVGLSLGITPTLSSVGKVAIILTMFIGRVGPLTLAFVLSQKKNQQAGHVKYPDERILIG

4.7E-62	220	32.7	1.7E-61	217.7	22.7	1.7	1	G7WAF6_DESOD	Potassium uptake protein, TrkH family	Desor_0824	Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus orientis, Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	768706	>tr|G7WAF6|G7WAF6_DESOD Potassium uptake protein, TrkH family OS=Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) GN=Desor_0824 PE=4 SV=1MNALSKFLTPSRVLVVGFAVLVLLGTLLLTLPQATTDGLGLSFLNALFTATSAVCVTGLVVVDTGTGLTLFGQSVILFLIQVGGIGFMTFATMFAILMGKKITFKERLLLQEALNQVSVEGVVRLAKSVFFISFMIELIGAVILSVRWSFDFGWSKAIYFGFFHSISAFNNAGFDIMGNFSSLTGYVGDPIINLTIMVLIICGGLGFIVLADIKSNRKKKFRLHTKIVLTVSGGLIVLGAVLIFVIEYSNPKTLGTLPLGTKVMAAFFQSVTARTAGFNTINLNDMYETSLLSMMVLMFIGASPGSTGGGIKTTTFVSIILSVLSTYRNESRIVLEGRTIPKDNIQKAWAITTTASLLIFFIVSILSLTERVDLMTVLFEVTSAFGTVGLSLGLTPALSVAGKAAIIITMFTGRVGPLTLAFVLAQKRKNQGQIKYPEERILIG
5.2E-62	219	31.6	6.9E-62	219	21.9	1	1	H6NED7_9BACL	Potassium uptake protein, TrkH family	PM3016_1148	Paenibacillus mucilaginosus 3016	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus mucilaginosus, Paenibacillus mucilaginosus 3016	1116391	>tr|H6NED7|H6NED7_9BACL Potassium uptake protein, TrkH family OS=Paenibacillus mucilaginosus 3016 GN=PM3016_1148 PE=4 SV=1MKPAAKKFELKPPQILVLGFAAIILGSILLSLPVASASGQPTPFLDALFTATSATCVTGLVVVDTGTHWSVFGQIVIILLIQVGGLGFMTMATLFAFVLKKRISLKERLILQEAMNQGSMEGIVRLIRKVIRYSLTIEAIAAVIFSIRWSFDLGVSRGIYYGIFHAISFFNNAGFDLFGSVTGKFSSLTAYADDWVINLVSMMLIILGGLGFVVISDLIEFKTVKKLSLHSKVVLSATGILIGVGTIVIFVFELTNMKTLGPLSWSGKFLASLFQSVSPRTAGANSVDIAGLRQATQFFIILMFIGASPGSTGGGIKTTTFTTLVGAIVAMIRGKEDIVLFHYRLGKDRILKAITLTMIALFLVIFVTMLLSTTEDHSFLMILFEVTSAFGTVGLSMGLTPDLTEFGKVMIALTMFAGRLGPLTLAYALGPKAEKELYRYPEGKITIG
5.2E-62	219	25.7	6.7E-62	219	17.8	1	1	D3EHH8_GEOS4	Potassium uptake protein, TrkH family (EC 3.6.3.14)	GYMC10_5442	Geobacillus sp. (strain Y412MC10)	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Geobacillus sp. (strain Y412MC10)	481743	>tr|D3EHH8|D3EHH8_GEOS4 Potassium uptake protein, TrkH family OS=Geobacillus sp. (strain Y412MC10) GN=GYMC10_5442 PE=4 SV=1MNAKLNWLTLSPPQILVLGFAAIIFIGTGLLMLPISTTTGEPLGFTDALFTSTSATCVTGLVVVDTGTTFSSFGEVVIMLLIQIGGLGFMTMATLFALVLKRRISLKDRLILQEAMNQSSMEGIVRLIRRVLLYSLVIEACGAVLLSVRWAFDMPLGRAIYYGVFHAVTMFNNAGFDLFGDFRSLTGYVYDPVVNFVVMFLIVSGGIGFIVLSDLIDYRKQRRLSLHSKVVLTMTAALLAVGFIVILIFEFTNPRTLGSLNWGGKFFGALFQSVTPRTAGANTIDITGLRQATQFFIVILMFIGASPGSTGGGIKTTTFTIMVGAVIAMMRGREDIVMFRYRLAQERVLKALTIALLALLLVLTVSMILSTTEEGDFLEILFETTSAFGTVGLSMGLTPDLTVFGKILISLTMFAGRLGPLTLAYALGPKKGKELYRHPEGKMIIG
6E-62	219	6.8	1.1E-35	132.6	0.4	3	3	N4UPA9_FUSC1	High-affinity potassium transport protein	FOC1_g10002144	Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	513	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. sp. cubense, Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)	1229664	>tr|N4UPA9|N4UPA9_FUSC1 High-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 1) GN=FOC1_g10002144 PE=4 SV=1MLRPPINFLTLHYAYITLMGLIALPILYPYGNMPAIDAWFFGASASTESGLNTIDVKDLKTYQQLYIYFIPILTNLGFINIVVVVVRLFWFKRHLKRLTPQNLDNSPGLRDVDIESARHESKVPADTTENSAEVTNEPNGKAKATDDHIEEDATIANEDRRVARTMTITFDPSTEKHKEDAALYIPGPRARDRGYPIAPRSHEAARHPDDSDDDDAIKPVPNEILNNGSSSMRRRRRFSSDDGLEITVSRSMDRVAGVAASFLALGSQTAPQPRVISSDSNRQPAINDVPFLSRQATLGRNSQFKNLTSHDREILGGIEYRSLKLLLKIVVVYFFGLHIFGAVCLVGWIHTADKQYADILQSSGQDKTWWGIYSAQTMVDNLGFTLTPDSMISFRTAKWPMILMSFLAFAGNTLYPVFLRLGIVVMSKLVPKTSPTQESLAFSVFSVLFEVTSAYGNVGLSLGYPTVSTSLCGMFGTFGKAVICLMMIRGRHRGLPYALDRAIMLPTGQIIEN
6E-62	219	27.3	9.2E-62	218.5	18.9	1.2	1	B8HNU9_CYAP4	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cyan7425_3208	Cyanothece sp. (strain PCC 7425 / ATCC 29141)	443	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7425 / ATCC 29141)	395961	>tr|B8HNU9|B8HNU9_CYAP4 Potassium uptake protein, TrkH family OS=Cyanothece sp. (strain PCC 7425 / ATCC 29141) GN=Cyan7425_3208 PE=4 SV=1MTVSRTICLGFIAVILIGTILLLLPFSTASGNWNDLIVALFTATSAVCVTGHIVVDTGSYFSPLGQFIILALIQIGGLGYMTATTFLLILIGRRFNLREKVALQQALDRQGIQGAAQMVKSIIATTLLFEISGIFLLFLAFVPDYGWGRGLWLSIFHSISAWNNAGFSLFSDNFVGYQSSLLINLVIPALIIVGGIGYEVIFEFYLWLRSLLSRRPEVMLFSLNFKVVTSTTLVLLLGGTITLFYTELHSPATNRLSLDIQLLVAWFQSVVARTAGFNTIDIGKMTNAALFCMIGLMFVGGSPGGTAGGLKTTTFRVLTIMKAVAVTVGSIATVIIGTFGIAITDPDLNFIQILFEVVSAFATVGLSTGITATLSVPAKLVLIAMMYVGRVGVLLLMSAIVGDPRPSAIHYPEENLLVG
6.2E-62	219	19	6.2E-62	219.1	13.2	1.9	1	D0LVM2_HALO1	Trk system potassium uptake protein	Hoch_5095	Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2)	491	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Nannocystineae, Kofleriaceae, Haliangium, Haliangium ochraceum, Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2)	502025	>tr|D0LVM2|D0LVM2_HALO1 Trk system potassium uptake protein OS=Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2) GN=Hoch_5095 PE=3 SV=1MRAGVLQRITSRLLGFAVFSLVVPMLVGLLAGDGVWWAFAIPAVFGAMASYGFARLPAAREASTSTLRRREGFVAVCLGWSVLVLLAAVAFSLTGAFPGFAEAFFESMSGFTTTGASVITNIEGLPASVLFMRSFSHWIGGMGIIVLSVAILPELGVGGMQLFSAESSGIESDKLAPRIAATSRRLWSIYVAITAVQALLLVGGMSFFDAINHAMSTIGTGGFSTKNSSVASFDSLYAEMVILVFMFISGISFTLQFRAVLDLRAGRLPSKLLGSPEVRLYTFVTLGATAVVTLSLLFGNIYETVGESLRYASFQVVSIITTTGFGTADFALWPPATQLLLVILMLIGGCAGSTAGGIKVIRFQVLYKQAKNEFKHILHPNAVLPVRVNKQVISPSIQSTVLAFTFLYAVIVIISVLVMMGLGVGFLESIGTVSSIGNMGPGLGTCGPAFSWSELPDAAKWLLSFLMLLGRLELFTVLLLFTSGFWKKN
6.3E-62	219	27.4	5.5E-61	216	19	1.9	1	D6D185_9BACE	Trk-type K+ transport systems, membrane components	BXY_31800	Bacteroides xylanisolvens XB1A	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides xylanisolvens, Bacteroides xylanisolvens XB1A	657309	>tr|D6D185|D6D185_9BACE Trk-type K+ transport systems, membrane components OS=Bacteroides xylanisolvens XB1A GN=BXY_31800 PE=4 SV=1MINSKMIFRILGFLLLIETAMLLCCGGVSLFYKENDLQSFLISSAVTACIGVLLLAIGKDAVNSLNRRDGYVIVSAAWVTFSLFGMLPYYIGGYIPSVTDAFFETMSGFSSTGATILNNIESMPHGILFWRAMTQWIGGLGIVFFTIAVLPIFGVGGIQVFAAEASGPTHDKVHPRIGITAKWIWGIYAGMTGTLIVLLVLGGMSVFDSICHAFTTTSTGGFSTKQASIEYYHSPYIDYVISTFMFLSGINFTLLLLMFNGKIKKFIHDAELKFYFLCVSFFTIFIAVWLHQTSSISIEEAFRKSLFQVISLQTSTGFATADYMLWPSILWGCLVIVMIIGACAGSTTGGIKCIRMVILLQVAKNEFKHILHPNAVLPVRVNKQVISPSIQSTVLAFTFLYAVIVIISVLVMMGLGVGFLESIGTVISSIGNMGPGLGTCGPAFSWSELPDAAKWLLSFLMLLGRLELFTVLLLFTSGFWKKN
6.9E-62	219	1	1.4E-37	138.8	0	2.1	2	Q3SMR7_THIDA	Trk system potassium uptake protein	Tbd_0021	Thiobacillus denitrificans (strain ATCC 25259)	488	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Hydrogenophilales, Hydrogenophilaceae, Thiobacillus, Thiobacillus denitrificans, Thiobacillus denitrificans (strain ATCC 25259)	292415	>tr|Q3SMR7|Q3SMR7_THIDA Trk system potassium uptake protein OS=Thiobacillus denitrificans (strain ATCC 25259) GN=Tbd_0021 PE=3 SV=1MLLFSRLVPVLHVLGLVVLIFSFTMLVPLVTAVFGADAAQHAFDEAFLITLGFGVALWAAGRRWKRELKPRDGFLLVILVWTGLPAFATLPLLIYAPQMSFTDAYFEMISALTTTGATVMSGLDTLPPSLNLWRHLLQWLGGMGIIVLAVAILPLLGVGGRQLMKAELPGPIKDSKLTPRIADTAKLLWAVYAVLTGLCASALKLAGMSWFDAVCHAFAALSLGGFSTHDASVGHFDSPLIEGVLIVFMLAAAVNFVTHFLAFRHRSLVPYRRDPEAFGVLGLVIGSILVVAGYIWHAGAYPDYLTALRHVAFNLVSLATDCGFASTDYGVWPMFAPMWMLFLSCVTASSGSTGGGLKMLRAVLMFRQGMRELERQLHPAARLPIKIGGHPVSNQIVFAVQAFVMMYVATVIAMTLVLLASGLDFVSAFSGVVACLNNAGPGLAELGPAGNYAGLDDYQTWALALTMLLGRLELFTVFVLLTRRFWRT

6.9E-62	219	37.1	6.5E-61	215.7	25.7	1.9	1	E3PXU4_CLOSD	Potassium transporter ATPase	ktrB CLOST_1139	Clostridium sticklandii (strain ATCC 12662 / DSM 519 / JCM 1433 / NCIB 10654)	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptoclostridium, Clostridium sticklandii, Clostridium sticklandii (strain ATCC 12662 / DSM 519 / JCM 1433 / NCIB 10654)	499177	>tr|E3PXU4|E3PXU4_CLOSD Potassium transporter ATPase OS=Clostridium sticklandii (strain ATCC 12662 / DSM 519 / JCM 1433 / NCIB 10654) GN=ktrB PE=4 SV=1MIRIPKDKHKYEFSASQIIVIGFAIVILIGGILLNLPMASINNENVGFLNSIFTATSAVCVTGLVVVDTGTYWTTFGKIVIMLLIQIGGLGFMSVATLGAMLLGKKISLRERLIIKESLNQSTLSGVVKLTRQMLYGTFFIEFIGALMLSLKFVPIYGFKKGIFYSVFHSVSAFCNAGFDLIGGGRSLIPFVDSGVVNITIMLLIILGGLGFTVIFDVVAKRSFRKLNLHSKIVITLSFVLIAISFVLFFIMESSNPDTMENLSIKGKVLASLFQSVTPRTAGFNTINLGGMENSSKLLTIILMFIGGSPASTAGGIKTSTLAILILAVRTLIVGKENVEIFGRRISYRAVNKSLAVVFIGIFVVISGTMILSLTEPAQDFLTIMFETVSAFGTVGLSLGMTSSLSNIGKILVIFTMFIGRVGSLTILLALASNEKKSLYNYPEEKVIVG
7.5E-62	219	25.5	3.3E-60	213.4	17.7	2	1	R5KIX5_9CLOT	Potassium uptake protein TrkH family	BN753_00422	Clostridium sp. CAG:678	469	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:678	1262831	>tr|R5KIX5|R5KIX5_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:678 GN=BN753_00422 PE=4 SV=1MERKTPAESHLYGVDQVSNDIPKQKKFHLTTFQIIILGFAGVILLGSLLLCLPISTRSGEWASYLDALFTATTSVCVTGLVTQDTGTYWSLFGQIIILILIQIGGMGVMTVAIMLGLMARRRRFSLMQRNTMQEAIGGPSLGNIIKLTKFIVSVTAATEIAGAVCMFPVFIQEFGVLKSIWYSVFHSVSAFCNAGIDLMGAKEQFSSLTSYYGNPVINLVICFLIVFGGIGFLTWDDMHRYGIKFKKYRLQSKIALVTTAFLIIVPAVFFYCFEFSRPVWNDLSAGDKVLASLFQSVTPRTAGFNTVDLNAMTEVSQTLMIILMLIGGSPGSTAGGMKTTTFAVVISSMLSVFKRKSDAEAFRRRINLASVRNASAVMAMYLVLFLLGGMAIAQIEGLPMLDCFYETASAIGTVGLTLGITPDLTAMSKIILILLMYFGRVGGLTLIFAAVNNNSKKYVKFPQENVNVG
7.7E-62	219	19.7	6.8E-61	215.7	13.6	1.9	1	F7XPL7_METZD	Cation transporter	Mzhil_1613	Methanosalsum zhilinae (strain DSM 4017 / NBRC 107636 / OCM 62 / WeN5) (Methanohalophilus zhilinae)	478	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosalsum, Methanosalsum zhilinae, Methanosalsum zhilinae (strain DSM 4017 / NBRC 107636 / OCM 62 / WeN5) (Methanohalophilus zhilinae)	679901	>tr|F7XPL7|F7XPL7_METZD Cation transporter OS=Methanosalsum zhilinae (strain DSM 4017 / NBRC 107636 / OCM 62 / WeN5) GN=Mzhil_1613 PE=4 SV=1MDFRVVLNVMGRLLGYMGFFMIIPLVLAIHYQEPLEPFLVAIVLTSGTGLFLFLKFRSAEEWHIRESFAIVALTWLSAAVFGTIPYILSGISPVDALFESMSGITATGASILTEIEQYPKSLLFWRNMTQWLGGMGIILLFIAILPKLGVGGRELFKAELPGPGEDKIKPRIRDTARVFWMIYIVFSVVLVGLLMLAGLSPYDSVTHMFTTIACAGFSPYSESIGAFQNPLAEWIIIVFMFIGGVHFALYYRTVFVNSKSLVRDEEFRFYAFILLAATVLLTVLLWRDFGGSLTDSLRYAAFQSISITTTTGYASMDFNQWSDSARMVLLVLMFFGGSAGSTAGGIKMVRILLLLSKYARRELFKTIHPRAVKPLRFNEATVTENVIQSIMAFIVIYFLIFVIGSILMALMGLDILSAISASVATLGNVGPGLGMVGPMEGYGSVPSAGKLILTLNMWIGRLEIFTVLVLLTPEFWKNR
8.5E-62	219	9.8	2.2E-61	217.3	6.8	1.5	1	D2RZ31_HALTV	Cation transporter	Htur_3134	Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (Halococcus turkmenicus)	510	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Haloterrigena, Haloterrigena turkmenica, Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) (Halococcus turkmenicus)	543526	>tr|D2RZ31|D2RZ31_HALTV Cation transporter OS=Haloterrigena turkmenica (strain ATCC 51198 / DSM 5511 / NCIMB 13204 / VKM B-1734) GN=Htur_3134 PE=4 SV=1MDLHVDYRISLSLVGTVLKYTTVPLFLPLAIAVIYGESVLPFVVTIVVALAVGIGLEELHPEPELGRREGFLFVSLTWLAVPLVGMLPYLVAGQGTIASPVNALFESMSGFTTTGSTVLGEISVERHSRSILMWRQLTQWLGGMGIIVLMVAILPKLSVGGAQLMEEEAPGFSFERLTPGIRETARALWRIYIGFTLLAFGLYYALHLVGLAPNMDLYNAVAHALTTMPTGGFSPEARSVEAFSPFIQWAVMPFMLIAGTNFALFWHAFNGRSDRLFENAEFRSYVGTVGFVGAILTAFLVTGLGLAETPEFVGTIPGNLEASARHALFQSLAFITTTGYASMDFNTWSEPTQTVLLFAMFLGGSVGSAAGSIKIVRWYVIQRVVRRELLTDVHPNAVIPIRVSDEVLDEETIYGLLAFTLLFLVLFAVSTLLIYFDTHRIEADLTALEAMSATIATLGNVGPGFGIVGPMNSFLPFTDAAKLYMVFLMWIGRLEILTVLVVLTPSYWWD
8.6E-62	219	27.6	8.5E-60	212	19.1	2.1	1	R7FW79_9FIRM	Potassium uptake protein TrkH family	BN651_01982	Dorea longicatena CAG:42	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea longicatena CAG:42	1263074	>tr|R7FW79|R7FW79_9FIRM Potassium uptake protein TrkH family OS=Dorea longicatena CAG:42 GN=BN651_01982 PE=4 SV=1MQQTNRSRHRHITSFQVISLGFLSVILLGSLLLMLPIATKSGQCTSFLDALFTATSAVCVTGLVVNDTATYWSLFGQGVILLLIQIGGMGIITIAIAIAVVSGRKIGLMQRSTMQEAISAPTVGGIVRRTQFIIRTTILIEIIGAVLLAPVFCRDFGFWKGIWYALFHSISAFCNAGFDLIGIRTPFSSLTSYSVQPIVNLVIMMLIIAGGIGFLTWEDIKNHKWHFKKYRMQSKVIFMVTGILIFLPALYFFYFEFSNVPLTERVWVSLFQSVTPRTAGFNTADLTLLSEVGQMLIIMLMLIGGSPGSTAGGMKTTTLAVLVSSALSVFRKKEHTNFFGRQIPDDTIRNAATIFLMYIVLFLVGGMVISRTEDIPLMTALFETASAIGTVGLSLGITPDLGLVSHIILICLMFFGRVGGLTLIFATISEKKPNGSKYPQEKITVG
9.5E-62	219	34.9	1.3E-61	218	24.2	1.1	1	A8MI81_ALKOO	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Clos_1975	Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus oremlandii, Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	350688	>tr|A8MI81|A8MI81_ALKOO Potassium uptake protein, TrkH family OS=Alkaliphilus oremlandii (strain OhILAs) GN=Clos_1975 PE=4 SV=1MEGNKKYVKLNPTQVLVIGFAALILMGGLLLNLPIASESGESVGFINAVFTATSAVCVTGLSVVDTGTYWTTFGKIVIITLIQIGGLGFMSVATMFAVILGKKISLKERLIIQEALNQYSLSGLVRFTKYVLIVTFTVEGIGALFLSFRFIPQFGWMKGIAYSIFHAISAFCNAGFDLIGNGRNLMPYVSDPLVSLTVAFLIIIGGIGFSVIADVITNKKLKRVSLHTKMVLLITAILLLVGTVGFALIEWKNVNTLGSLSPSSRWMASFFQSVTVRTAGFNTIDLVSMKDASHLLSIILMFIGGSPAGTAGGIKTTTLGVILFTVICVIRGKEETEIFKRRISWELVNRALTIAIIGVTLIVSVTMILTITDSEFSFIALLYETVSAFATVGLTLNITPQLSIIGKILMISMMFAGRVGILTIAFALARRQHSNKGNIKYPEGKILVG
9.6E-62	219	31.4	1.3E-61	218	21.7	1.1	1	K9Q9L0_9NOSO	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Nos7107_1173	Nostoc sp. PCC 7107	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	317936	>tr|K9Q9L0|K9Q9L0_9NOSO Potassium uptake protein, TrkH family OS=Nostoc sp. PCC 7107 GN=Nos7107_1173 PE=4 SV=1MTVSRTICLGFLAVIAVGTMLLMLPISTSDGSWNNLVVALFTSTSAVCVTGLSVVDPGTYFSFWGQLFIVLLAQIGGLGYMTTTTFLILLIGRRFDMRQKMAIQQALDRPGMQGSAQVIRSIIATTLIFEITGVFLLLPAFVPKYGWSQGLWLAIFHSVNAWNNAGFSLFKDSLIGYQTSGLVVFTVTTLIIFGGIGYQVILEMYLWLRDRLLKKNTCVVFSLDFKVATSTTIILLVVGTIAFFCIEFRNPETFGDLNIGGQFLVAWFQSVTPRTAGFNTIDISKMTTAGLFITIALMFIGASPGGTGGGMKTTTLRVLTSCTKAILQGKEDVLLYDRKIAINLILKAVGVLVGSVATVVLATILISLTDPKLDFIQILFEIVSAFATVGLSTGITSSVSTAAKLILILTMYIGRVGVLLLMSAVLGDPRPTRIHYPEENLLVG
1E-61	218	10	7.4E-60	212.2	7	2.1	1	E3HLN8_ACHXA	Trk system potassium uptake protein	trkH AXYL_06080	Achromobacter xylosoxidans (strain A8)	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Achromobacter, Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans), Achromobacter xylosoxidans (strain A8)	762376	>tr|E3HLN8|E3HLN8_ACHXA Trk system potassium uptake protein OS=Achromobacter xylosoxidans (strain A8) GN=trkH PE=3 SV=1MKRVLGTLYILGLTMVMFALTMLIPLTVAYVGGDAAREAFLDGFLLSVGIGGGLAAVTRRARCELRARDGFVLVSAVWAGLPLLAAIPLLLYFHGAGLPLSFTGAYFEAMSGLTTTGATVLTNLDTLPASINLWRATLIWIGGMGILVLAVAILPLLGVGGHQVVRAETPGPMKDERLTPRIASTAKALYAVYFVFSILCFLAYRAVGLSWFEAWCHMATTMGLGGFSTWDDGFAHFDSVAVEMVAMVFMLIAGINFATHFNAFRQRSGRAYLRCPEAIPYLVVVLGVGLVISVFLFLKGVYDDPLQALRYGMFNTISMATTTGYANTDFAQWPLFAPLTMLLLSGFATSAGSTGGGIKMIRAILLVKQARNELVTMLHPHAVSPVRINGRAVETRTMSSVLAFMLFYGLSIAVFTSLLLLSGLDPITAFSAVFASVNNTGPGLGPVGPMGNFAVLSDFQIWVCTFAMLIGRLELLTVLVLFTPIFWRK

1.1E-61	218	37.6	1.4E-61	217.9	26.1	1.1	1	E3H6H8_ILYPC	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Ilyop_0603	Ilyobacter polytropus (strain DSM 2926 / CuHBu1)	445	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Ilyobacter, Ilyobacter polytropus, Ilyobacter polytropus (strain DSM 2926 / CuHBu1)	572544	>tr|E3H6H8|E3H6H8_ILYPC Potassium uptake protein, TrkH family OS=Ilyobacter polytropus (strain DSM 2926 / CuHBu1) GN=Ilyop_0603 PE=4 SV=1MIGFALKKMPPSRILLLVFVVAIFVGSFLLLLPAAVTPGNKIGYLTSIFTVTSAVCVTGLTVVDVSKVFSPFGQSVILFFIQLGGLGIMTFSSILFMMIGKRITYHEMKILKEDLNAENTGEIVQLVKRLVMIVFTIEIIGTIFLTLEFLKEMPFKKALLFGIFHSISAFCNAGFSLFTTGLEGYSGSVIINLTIALLIILGGIGFAVISSFISYYKTKKKRFNLSSKMVLRISTILTLGGMVLFFALEYRNPLTIGKMNFFHKIMASFFQSVTTRTAGFNTVPIGSLTPGTIFLFCVLMFIGASPGSTGGGIKTTTFGVIMVYVVGIVRGQEDIEISNRRITWQILNRALAILVISVAYVSTIILIMLMTDHLGFSETIFEVISAFGTVGLSMGVTADMNEFSRILIIITMLIGRVGPLTFALALGEQSKKKERKYPKENILIG
1.1E-61	218	26	1.3E-61	218	18	1.1	1	Q8DM21_THEEB	Na+-transporting ATP synthase	tll0303	Thermosynechococcus elongatus (strain BP-1)	454	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Thermosynechococcus, Thermosynechococcus elongatus, Thermosynechococcus elongatus (strain BP-1)	197221	>tr|Q8DM21|Q8DM21_THEEB Na(+)-transporting ATP synthase OS=Thermosynechococcus elongatus (strain BP-1) GN=tll0303 PE=4 SV=1MLTVPRTICLGFLAVIMVGTCLLWLPWSTSNGHWNPFVIALFTATSAVCVTGHIIVDTATHFSPFGQLVILLLIQVGGLGYMTATTFLIILLGRKFNLRQKIALQQALDRRGIEGARQLVRSILGLTFLFELTGTFLLWLIFRQDFRDPQALWLAVFHSISAWNNAGFSLFSNSLMGYQTSVPLNLVISLLIIFGGIGYEVIFEFYLWLREHLRYWGKPAYLIRKASQMTFSLNFKIVTSTTATLLILGTVMLFLTEMRSPARFGLFSWDQKLLLAWFQSVTARTAGFNTVNIGEFNNSGLFIMIALMFIGGSPGGTAGGIKTTTLRILAGITKSALQGKEVVLLYRRQVPPSLIMKAVAVAFGSMFTVLVSTTLIAIADPEENFINILFETVSAFATVGLSTGITSDLSIFSKLVLIVTMYAGRVGILLLMAAIIGDPQPSNVQYPEENLLVG
1.1E-61	218	27.7	2.2E-60	214	19.2	2	1	C4ID03_CLOBU	KtrB	CLP_3230	Clostridium butyricum E4 str. BoNT E BL5262	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	632245	>tr|C4ID03|C4ID03_CLOBU KtrB OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_3230 PE=4 SV=1MHKLKKPNFTYSQISAISFMSIILIGALLLTLPISSRSGEATPFIDALFTSASATCVTGLVVYDTYTHFSLFGQIVILSLIQIGGLGFMIIATLFSLMLKRKIGLKERGMLQESVSTVHIGGIVRLTKHILFGTVIFEAIGAVILALRFYPDMGLKQGIYNGIFHSISAFCNAGFDLMGRFEPSSSLTLYRGDIVVNLVIMTLIVVGGVGFLVWEDIFTNKLKFCKYRLHTKIVLVVTATLIIVPAIIFYSIERTKSFADMGTTESWLASFFQSVTPRTAGFNTANIAELSEGSILLTIILMVIGGSPGSTAGGVKTTTSFAVIILSLIASIRHTEDINVFNRRLERDVIKKAYDVITIYFMCCALAVLLICALQPFGLKEVFFEVVSALSTVGMSTGITPDLNSLSKFIITLLMFFGRVGSLSVALVFSEKKEYIPIRKPVEKISIG
1.1E-61	218	21.9	2.3E-60	213.9	15.2	2	1	Q5LB99_BACFN	Putative K(+) transport-related membrane protein	BF9343_2842	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	477	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides fragilis, Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	272559	>tr|Q5LB99|Q5LB99_BACFN Putative K(+) transport-related membrane protein OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) GN=BF9343_2842 PE=4 SV=1MIGRVLGVLLFIEAGMFVLCSGISVVYGESDYKYFLYTAGINLLSGALLMFYGRGAENRLSRRDGYCIVTLSWVFFTLFGMLPFYLSGSIDSLTNAFFETMSGFTTTGATILDDIESLSHGMLFWRSLTQWIGGLGIVFFTIAVLPAFTSGGVQLFSAESTGVTHDRTHPKINVMAKWLWTVYLILTLAETILLMLGGMSLFDAVCQSFATTATGGYSTKQASISYWNSPFIEYVVAIFMLLSGVNFALFLMCLRGKVSRLLRDEELRWFLGSVAILTFLITFALVFQNHYDWETAFRKSLFQVATAHTSCGFATDDYNLWPAFTWLLLLIAMLSGGCTGSTSGGIKNMRLLIARSIRNEFKHLLHSNAVLPVRVNKQSVSPSIVSTVGMFFAFYLIIVILGWAVLLFLGVGFSESIGTVISSIGNVGPGLGSCGPAYSWNGLPDAAKWVLSFLMLIGRLELFSVLLLFYPGFWKS
1.4E-61	218	25.9	7E-60	212.3	17.9	2	1	K4L8P0_9FIRM	Potassium uptake protein TrkH	DCF50_p2831	Dehalobacter sp. CF	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Dehalobacter, Dehalobacter sp. CF	1131462	>tr|K4L8P0|K4L8P0_9FIRM Potassium uptake protein TrkH OS=Dehalobacter sp. CF GN=DCF50_p2831 PE=4 SV=1MNFTLLENILGRFLIAYSFAMVVPIAVALFFQEKVGWAFLISFCVTVIVGTVMRLHGKVEGKISVREGFAVVGGAWIFASLFGALPFIISGVVPTYIDALFEVVSGLTTTGSSVLSNLEVLPRSILFWRSLTHWMGGMGIIVMFIVLLPNLGIGAVHIFNSEVPGPISEKIVPRIKDTALILWGIYAGLTVATIVLLLFAGMSLFDAVNHAFATVATGGFSTRSASIAAYNSFPIELVLTIFMFIAGSNFSLFVQAWRKRSLRPLKDTELKYYFLIVVVSTLIITGSLVIQQGWGSLAALRHSVFQVVTLMTTTGFASTDFDQWSGLAKLILFFLMFIGASAGSTAGGLKVSRVILLVKMGLAQLRQAIHPRLVVNIVVQDKVIDTTVLSNVGRFFFVYFLTFAIGSILLAGTGLEPFDAMSAVIANLSNVGPGFGVVGPMFTYAPIEPFGKIVLTACMLLGRLELFTLLVFLTPEFWKSKKSW
1.5E-61	218	20.2	2.2E-61	217.3	14	1.1	1	K4IDG6_PSYTT	Potassium uptake protein TrkH	P700755_000078	Psychroflexus torquis (strain ATCC 700755 / ACAM 623)	486	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Psychroflexus, Psychroflexus torquis, Psychroflexus torquis (strain ATCC 700755 / ACAM 623)	313595	>tr|K4IDG6|K4IDG6_PSYTT Potassium uptake protein TrkH OS=Psychroflexus torquis (strain ATCC 700755 / ACAM 623) GN=P700755_000078 PE=4 SV=1MGVLLVFNGGFMLIPAIYSWLSQESVAFSIAVSAIISIFIGLLAMFFTKNHDKDISQREGYLIVTLGWLFMVLSGMLPYALSGEIKGIENIFFETMSGYTTTGASIINDIEALPEGILLWRSLTHWIGGMGIIVLAVAILPLFGIGGMQLFSAESPGPSADKVKPKIADTAKRLWLIYFGYTLSETILLKVAGMTWFDACNHALSTLSTGGFSTKNANLAYWNDNPSIQYIVIFFMFLAGTNFVVSYYAFKGKMANVLHNEEFKWYFLFIIGATAITSLSIYYFSDPSLASIEYPMVFGEAESAIRHGLFQVLAIITTTGFVSADYTLWTPLLTVLFFGLFFLGGSAGSTSGGIKVIRHLIMIKNGFQEFRRILHPNAILPVRYKGSSVDQKIVYNILGFFILYSLSFIIGAAVFAGTGLDFETALGASASSLGNVGPAFGELSPVDNYVSLSVFGKFWSSFLMLLGRLELFTVLILFTPYFWKNT
1.5E-61	218	35.5	4.4E-61	216.3	24.6	1.6	1	A0A0F2PNK6_9FIRM	ATP synthase subunit J	VR69_15845	Peptococcaceae bacterium BRH_c4b	443	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c4b	1629717	>tr|A0A0F2PNK6|A0A0F2PNK6_9FIRM ATP synthase subunit J OS=Peptococcaceae bacterium BRH_c4b GN=VR69_15845 PE=4 SV=1MKNKINFTPPQLLVMGFALTILLGAAFLSMPFSSASGQYTEFTTALFTSTSAVCVTGLVVVDTGTYWSHAGQFIILLLIQIGGLGFMTMATFIYLLMGKKIGLRNRLILQESLNQNSLQGIVRLSKYVLITTFLLEMFFAAILSVRWGMDMGYPRAIWFGIFHSISAFNNAGFDLFGGFRSITGYVGDTVVNLSIATLIILGGIGFSVIIDLLNYRKRKALFTHTKLALCTTAVLLAAGTLLIFLFELDNMLRGLCPWGKFLASFFQSVTSRTAGYNTLDIAHLHSYTQFLIVILMFIGASPGSTGGGIKTTTFSLLALAVLSLVRGKVFTQVFKRTITQDQVIKALAVLMLAIILVVTVSIALMVVENQENFLLVLFETVSAFGTVGLSMGLTPELSHAGRLLIIMTMFLGRVGTITAVFALTQRTRKTQRIKYPEDKILIG
1.5E-61	218	16	1E-30	116.1	2.4	2.1	2	R6D210_9FIRM	Trk system potassium uptake protein TrkH	BN516_00429	Firmicutes bacterium CAG:176	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:176	1263007	>tr|R6D210|R6D210_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:176 GN=BN516_00429 PE=4 SV=1MNFRLLSHTMGYILWVEAGFLLLPALTACIYAETCWQQFLLTALLCATAGTVLHLVPVKKTQMHSRDGFAAVALSWVLLALFGALPYVFTGAMTSYIDALFETVSGLTTTGSSTFTAVSHLPRSVLLWRSLTQWMGGMGVLVLFLALTPRMGEGAVFLMRAESPGPIKSKLVPKVGGTAKILYLIYVVLTLCEVLALRLAGESWFSAVCHSFTTMATGGFSIYDTSLAGASKAVMWIVTVFSFLAGVNFSLMFLAVRGKLKEVLRSEELRIYVGIVAAATLLLCINLRVQAGVPFRDSITDAAFQTVTIITTTGFATVDFSLWPTFCRMALVMLMFTGACAGSTSGGIKISRVAILCKSLKRELKRLAHPHHVSVLKVDGQAVEERVVSSAGAFIAAYLLVLLAGALVVSWDNYGFQESFAASLTCISNVGPGLGILGPMENFSILSPLSKLVLSLEMLMGRLELMPLLALFLGSTWRD
1.7E-61	218	10	7.1E-61	215.6	6.9	1.8	1	E3CYJ7_9ACT	Cation transporter	Apau_0293	Aminomonas paucivorans DSM 12260	483	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Aminomonas, Aminomonas paucivorans, Aminomonas paucivorans DSM 12260	584708	>tr|E3CYJ7|E3CYJ7_9ACT Cation transporter OS=Aminomonas paucivorans DSM 12260 GN=Apau_0293 PE=4 SV=1MRFPVVAKFLGLLTGVVTLWMLWPLGWALWDHTSDRDALALSMMSGFAASGALFFLGRRGQSSDMGLREAFAAVTLSWIAASAVGALPFWFAHAVPTYTDAFFETMSGFTTTGSSVLTDIEVVPRGLLFWRSLTHWLGGMGIIVLTLAVMPVLGMGGGQLFRAEVPGPVPEKLTPRVQQTALLLWGVYVFLSLAQTALMMAGGMNLFDALTHMFGTMATGGFSTYNSSVGHFSSPYLQWVIILFMFLAGANFTLHYLALTGHPGAFLKDPEFRFYALITLGCVVLTVSFLAGGGLYPHLEERVRAAAFQVVSILTTTGFATANYENWPYAAQFLLLLLMFVGGCAGSTGGAMKNVRLLVLCRHVGHELFLLLHPRAVVPIRLGHQALPPRLVSAIGAFFSLYIGALALCTLGVCALGVDILTALSGAAATLGNIGPGLGNVGPAENYAALPGGAKWIYSLAMLMGRLELFTVAVLLHPACWRK

1.8E-61	218	8.4	6.5E-38	139.9	0	2.1	2	A9IFL2_BORPD	Trk system potassium uptake protein	trkH Bpet4706	Bordetella petrii (strain ATCC BAA-461 / DSM 12804 / CCUG 43448)	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella petrii, Bordetella petrii (strain ATCC BAA-461 / DSM 12804 / CCUG 43448)	340100	>tr|A9IFL2|A9IFL2_BORPD Trk system potassium uptake protein OS=Bordetella petrii (strain ATCC BAA-461 / DSM 12804 / CCUG 43448) GN=trkH PE=3 SV=1MRRLLATFYVAGLTMVVFALTMLLPLLVAYVGDDAGFTAFLDGFLLAFGGGAAVWLSTRRGRCELHARDGFLLVSVVWVSLPLLAAIPLLIYFNRAGIPLSFTDAYFEAMSGLTTTGATILVHLDQLPASINLWRATLVWIGGLGILVLAVAILPLLGVGGHQVVRAETPGPMKDERLTPRIASTAKALYAVYFGLSLLCLVAYRGVGLSWFDAWCHTATTMGLGGFSTRDEGFAYFNSVSVEVVAMIFMTLAGINFATHFSALRQGRLRAYLVCPQTIPYLVIMLGAGLVISGYLYLRGVYADPLQALRFGMFNTISVATTTGYANVDYAAWPLVAPLSMLLLSGFVTSAGSTGGGIKMVRAVLLVKQARNELVTMLHPHAVSPIRMGGRLVDQRVMASVLAFMVVYGLSIGVLTSLMLVSGLEPVTAFSAVIASINNTGPGLGPVGPMGNFAVLTDFQTWVCTFAMLIGRLELLTVMVLFTPMFWRK
1.9E-61	218	22.6	4.4E-60	213	15.7	2	1	O29419_ARCFU	TRK potassium uptake system protein (TrkH)	AF_0839	Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126)	478	cellular organisms, Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales, Archaeoglobaceae, Archaeoglobus, Archaeoglobus fulgidus, Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126)	224325	>tr|O29419|O29419_ARCFU TRK potassium uptake system protein (TrkH) OS=Archaeoglobus fulgidus (strain ATCC 49558 / VC-16 / DSM 4304 / JCM 9628 / NBRC 100126) GN=AF_0839 PE=4 SV=1MNLRLTASILGKLLMLFSFSFILPLIAAHVFEEPYHPFLIPAALSLLVGAVLGYGIKTESEFDSLRHKESFAIVALIWLFMSIFGSIPYIIFGISPVDAFFESMSGFTTTGASVLTPEELPKSLLLWRSLTQWIGGMGIIVLFLAIFPNVAKRSTVLFQAEYPGVSLSKLKPRIRDTALSLYKVYLLLTIAEVALLYALGLSLFDAINHTFTTLSTGGYSTHSESIAFFKDVRVEAVVAFFAFLGGANFALIYFLLSGKPVIFRNTEFRAYVCFLALASVVIAAVNLDRYSIFESLRYSIFQAVSIMTTTGFTTADFDAWSDSAKLILVVLMFIGGSSGSTGGGIKVIRIYLLIKYAVHQILRAAEPRTVRAVKFEGRAIKKEILDDIAAFFVLYILIFAVSSILVSLSGYDIVTSISATAATLGNVGPGLGLAGAAENYASFPSLTKILLAVNMWIGRLEIFTVVVSLFIPTFWRERW
2.1E-61	217	11.2	1.3E-60	214.8	7.8	1.9	1	A7H955_ANADF	Cation transporter	Anae109_1042	Anaeromyxobacter sp. (strain Fw109-5)	533	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Anaeromyxobacteraceae, Anaeromyxobacter, Anaeromyxobacter sp. (strain Fw109-5)	404589	>tr|A7H955|A7H955_ANADF Cation transporter OS=Anaeromyxobacter sp. (strain Fw109-5) GN=Anae109_1042 PE=4 SV=1MHLHSPLNAEGERRRSALRIVGRDVGALQVLLSVGMLLSLLVSLLYGEVHSALSFLGAAAVTAAFGALAHRAGRDADEPKRRHAMIIAGGGWFVSAVFGALPFLFAAYWTPPEVAQGFVPAGESYGSSLAYFRNPLHALFESMSAYTTTGLTMAVHEPSIGHGLLFYRSLAQWIGGAGVIVLSLAIIPRPHVVGELELYQSEAAGTKLRPSILGTARAIWKVYSVVTLLVAVYLFAATLIVLPGYGVGPSLFDAVNHAMTAQSTGGFSTLDDSIAGYRSYAMDLVHVPPMVLGAISLPLYYAFLRARSLRVFWRDAQFRTMILVFGITIPAQVLLLVGAEAVADPFREGLFQVVSAVSTTGWQTSNIGAWDDAAVMLLAWGTMITGGAAGATVGGIKLIRAYLLLGAARWRIRKVFLPGDAVIPFRLGDRNLPSEAMQREVTDASVFTFLYLLVLGVATILVSHYVGGDFSLADVIFECVSAQSTVGLSSGITDPGMPIVVEIVFIFQMWVGRLEIFPVLVLLSALLSWMLRR
2.2E-61	217	10.4	3.9E-61	216.5	7.2	1.4	1	B1XWX4_LEPCP	Trk system potassium uptake protein	Lcho_4071	Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) (Leptothrix discophora (strain SP-6))	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Leptothrix, Leptothrix cholodnii, Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) (Leptothrix discophora (strain SP-6))	395495	>tr|B1XWX4|B1XWX4_LEPCP Trk system potassium uptake protein OS=Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) GN=Lcho_4071 PE=3 SV=1MRKLLGVLPVLGVVLVVFCLTMLVPLAFSWVQDDGAQFDHLRAIASTLACGIVLRLLGHRYQRELQPRDGFVLVALVWTVLPAFGALPLWLAIDGLSPTDAYFEAVSGLTTTGATVLTGLERLPVSINVWRCLMVLIGGMGIVVLAVAVLPLLGVGGAQLFKAESAGPMKDEKLTPRIAETARGLWSVYFVFAVACCLAYRWAGMGWTDAFMHMCSTMGLGGFAAYDASFGAFDSPRIEAVAIVFMLLAGINFALYFMAFKRRSLRGLWRNIEVRGYVILMFGAVMLIAAFLATHQVYPTFGESLRHAAFSVVSVATTTGFATVDYALWPAFAPVLMLLLCGFATCAGSTGGGIKLIRALLLMKQAQRELIRIVHPRAVVPVTLGGQVVPQQVLISVIAYMLAYGAVTLIASLMLLFTGLDMVSAVTAVIACINNTGPGLGQVGPSGNYQGLSDVQTWICSATMLLGRLELLSLLVLFTPTFWRA
2.2E-61	217	37.1	9.1E-60	212	25.7	2	1	D5DKK8_BACMD	Potassium transporter ATPase	ktrB BMD_3894	Bacillus megaterium (strain DSM 319)	439	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus megaterium, Bacillus megaterium (strain DSM 319)	592022	>tr|D5DKK8|D5DKK8_BACMD Potassium transporter ATPase OS=Bacillus megaterium (strain DSM 319) GN=ktrB PE=4 SV=1MKKQIIKLTPPQLLVSIFGGGIIIGALLLMMPVSTTEPIRWVDALFTSTSAMTVTGLAVVDTGTRFTVIGQIIIMLLIQIGGLGIMSFAVLIFMMLGKKIGFKERMLVQQALNQTSVGGVVLLVKRLFIFSFLIEFVALIFLAIRWVPEFGWSKGLFFSLFHSISAFNNAGFGLLSDNLVQYVGDPIINITISFLFIIGGLGFTVLADMWVKKSYRKLTLHSKIMIISTFAINVTAMLFIFFLEYSNSHTLGNLSLGDKVWASYFQAVTTRTAGFNTIDLAYLHDATVFLMVLLMFIGAGSASTGGGIKLTTFVVIVFSVWAFLRSREDIVLLKRRLLPLHVFKALAITMISIMFVFGAIFLLNISENLPFVKIMFEVVSAFGTVGLSMGATPELSYFGRVIIIFIMFLGKVGPLTLAFSLSKQKREAVRYPNEDIMLG
2.2E-61	217	27.8	1.1E-60	215	19.2	1.7	1	L0KAD9_HALHC	Potassium uptake protein, TrkH family	Halha_2089	Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	441	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Halobacteroides, Halobacteroides halobius, Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	748449	>tr|L0KAD9|L0KAD9_HALHC Potassium uptake protein, TrkH family OS=Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1) GN=Halha_2089 PE=4 SV=1MKKINELSSAQILSMGYAIIMFGGGLLLTLPIATTDGQGMNFLDALFTATSAAAVTGLIVENTVAYFSFFGELVIMCLIQIGGLGLMIMSTLLALLIGKKVTLKHRLMILDDLDQFQLSGVLQLVKYVVAVTFTIEGLGALILSIRLAQDMPVGKAVYYGIFHSISAFNNAGFDLFGNSLLNFTSDLTVNLTITSLIILGGIGFAVIAEVYSKKKFKRFSLQTKMVLSITLVLIMLSFIIFFILEYSNPQTMGKLSLKGKLLASYFLAVTPRTAGFATVSMGVLRDSSIFLVILLMFIGASPGSTGGGVKTTTLGAIGAVLYSRATGRDDVEIYKRRLNREIVLDALTVVALGLVHVATITIILTITEEAPFLDLLFETVSAFATVGLSTGITAGLSEIGKVLIIITMYLGRIGPVTLAVAIAEKRHKANIRYPEEDIMIG
2.2E-61	217	35.1	2.7E-61	217	24.3	1	1	K9Z1T2_CYAAP	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cyan10605_0990	Cyanobacterium aponinum (strain PCC 10605)	445	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobacterium, Cyanobacterium aponinum, Cyanobacterium aponinum (strain PCC 10605)	755178	>tr|K9Z1T2|K9Z1T2_CYAAP Potassium uptake protein, TrkH family OS=Cyanobacterium aponinum (strain PCC 10605) GN=Cyan10605_0990 PE=4 SV=1MTIARTICLGFIAVISVGTILLMMPFAVETGNWGSFITALFTSTSAVCVTGLIVVDTGTYFSFWGELIILCLIQIGGLGYMTTSTFLILLIGKKFDFRQKIAISESFDRPFLQGSRNLVISIFVTTFILEIIATIVLYSIFSQDYGWKQGLWLAIFHSVSAWNNAGFSLFPDSLIQYQSSIPINIVITALIILGGIGYQVIIEVFLWFLDFFKQKVHPHYEFSLNFKVVTRTTLILLLILGTVGFFITELHNNNTLAELPFKDKIITAWFQSVTTRTAGFNSIDIGAMTKAGLFITIGLMFIGASPGSTGGGVKTTTLSILYNSTKAVLRGQEQVVMHKREVPVSLILKAMAVVFGSGVTVVCITFFISLLHSDFEFQSIFFEVVSAFATVGLSTGITSSLSVLAKLAIVFTMYLGRVGVLLFMAAIVGDPQPSRIEYPEENLLVG
2.3E-61	217	33.4	3.1E-61	216.8	23.2	1.1	1	Q5HQE1_STAEQ	Sodium transport family protein	SERP0612	Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus epidermidis, Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	176279	>tr|Q5HQE1|Q5HQE1_STAEQ Sodium transport family protein OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) GN=SERP0612 PE=4 SV=1MSVLSQLLKKSSPQQGIILYYLFAIVVAFLLLNLPYVHKQGVEVNPIDTLFVAVSGISVTGLSPITIVDTYSTFGQIIILILNIGGIGVMAIGTMLWVVLGKHIGIRERQLIMLDNNRDTMSGTVKLILEIVRTIFIIEFIGALLLAFYFYRDNPDLKNALMQGIFVSVSATTNGGLDITGESLVPYAKDYFVQTIVMFLIVLGSIGFPVLLELKAYIKNRVTNFRFSLFTKITTTTYLFLFLFGVIVVLILEHSNAFKGLSWHQSLFYALFQSSTTRSAGLQTIDVSHFSDATNIVMGLLMFIGSSPSSVGGGIRTTTFAILILFVINFNNTGDKTGIKIFNREVHIMDVQRSFAVFTMASLITFISMIIISATEQGKLSFLQIFFEVMSAFGTCGLSLGVTSDVNDITKAVLMILMFIGRVGLISFIIMLAGRKEPEKYSYPKERIQIG

2.5E-61	217	35.7	5.4E-61	216	24.8	1.4	1	Q65KK9_BACLD	Cation transporter	ktrD BL03532	Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus subtilis group, Bacillus licheniformis, Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	279010	>tr|Q65KK9|Q65KK9_BACLD Cation transporter OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) GN=ktrD PE=4 SV=1MKVLLRKLLRVLSPVQLIALYYFLAVTVSVVLLSLPVAHKNNVEWSFIDALFTAVSAVSVTGLTVVDTADTFSTAGIWILAFVLQFG GIGVMALGTFVWLIFGKRIGLKERRLIMTDQNQSNLSGLVKLMKHVLGLILLIELFGGLILGTYFLKYFETPGEAFMHGFFTSISATTNGG FDITGNSLIPFQHDYFVQFIVMMLIILGAIGFPVLIEVKDFLLSKERKFSFSLFTKLTSVTFFLLVIGGAIGIFAMEARFAFSGKSWHEVFFF SLFQSTTTRSGGLATIDISQFTHTTILFMCMLMFIGASPSSVGGGIRTTTFALNLLALFHFARGNKSVKVFKRELHQADLMKSLIVTLMA VILVFVSTLILTVTEKHSLLELLFEVCSAFGTTGLSMGITPDLSTIGKSVIILLMFIGRIGIVTLLYLFGRKEIEANYHYPKERIIIG
2.5E-61	217	24	6.3E-61	215.8	16.7	1.6	1	R6CV96_9BACE	Potassium uptake protein TrkH family	BN697_01991	Bacteroides sp. CAG:530	531	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:530	1262741	>tr|R6CV96|R6CV96_9BACE Potassium uptake protein TrkH family OS=Bacteroides sp. CAG:530 GN=BN697_01991 PE=4 SV=1MNNYRRKTQLYKLCTIFVQRKNSFVLYFLIDMMEDNYSKFIRGNRGNSLINQRLILKILGVLLFIEGLVFLVCAGVGLLYREKDYIYF IYSLLATSGVGALFLFLGKGSENKLTRRDSYCIVTFTWLLFSCFGAMPFWLSGEVDNITDAFFETMSGFTTTGASVLNNIGSLSHGMLF WRSLTQWIGGMGIVFFTIAVLPIFGIGNQTLFSAEATGVMHDKIHPKISVMAKQLWSVYLILTVTETVLLLLGGMNLFDAVCHSFSTTST GGYSTKQVSVAYWNSPFIEYVIAVFMVLSGVSYSLYFMCLKGRFKNLLKDDEIKWFFTSVGVITLLITVSLVYHNHYGVEEAFRKAFFQ VASVHTSTGFATDDYNLWAPYTWLFIIYAMLMGGCTGSTVGGIKGIRFVIVMRNIKNEFSRLIHPRAVLPVKANGQALSSALISTVSTFIL LYFTCLFIGWFVLMVMGIDMVEAFGLSVSGLGNVGPALGAFGPEYSWDALPDAAKWFLSFLMLIGRLEIFGVLVMLAPSFWHKR
2.7E-61	217	12.8	1.4E-60	214.7	8.9	1.8	1	W0JW16_9EURY	Potassium transporter TrkH	HALLA_02450	Halostagnicola larsenii XH-48	512	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halostagnicola, Halostagnicola larsenii, Halostagnicola larsenii XH-48	797299	>tr|W0JW16|W0JW16_9EURY Potassium transporter TrkH OS=Halostagnicola larsenii XH-48 GN=HALLA_02450 PE=4 SV=1MRHYLRVDWRAGLSLVGTLLALLSLAFVVPIVVALVYGGNDLGVFVVSMILTVGFGLALRRLDPEPEPGAREAFFVVAFTWLFA AVFGAIPYVLAGNGTVAYPVNALFESMSGFTTTGATVMGDISFDTHSRAIMMWRQVTQWLGGMGIIVLAVAILSQMAVGGAQLMEAE APGPGISKLSPHIAETARVLWIAYIGFTALLIALLYALSFTVYAPNMDLYYAIAHGFSTLPTGGFSPEARSIEFFSPVVQWLIVPFMFIAGV NFVLWWHVISGDPWELLGDNEFRFYLGAVSLFSLVGTVILFFDASLQTAATGQIGGNLERSLRYSVFQITSLTNSTGFANMDFDAWG HSAKALLLFVMFIGGSTGSTGGGIKILRWLVILKSLRREVFTTIHPEAVRPVRMNGKPLDEEAIRGIYAFTLLFLALFFVGFLLLSADASRL AGFNPHTLDLLTASIATLGNIGPGFGVVGPMGSYNGFPMTSKLLMVVYMWIGRLEIFPVLVLLTAAYWRS
2.9E-61	217	20.9	5.6E-61	215.9	14.5	1.3	1	W5Y2X8_9CORY	Potassium uptake protein TrkH family	B843_10970	Corynebacterium vitaeruminis DSM 20294	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium vitaeruminis, Corynebacterium vitaeruminis DSM 20294	1224164	>tr|W5Y2X8|W5Y2X8_9CORY Potassium uptake protein TrkH family OS=Corynebacterium vitaeruminis DSM 20294 GN=B843_10970 PE=4 SV=1MRVTPSRLVAGCFAALVIIGTAILYMPVSRMGDAQADFITALFTATSAVCLTGLAVVDTATYWSHFGQAVIAVLIQLGGLGIMTLA TLAGWFISGKLGLRDRLNAEAEGRGAQLGDVRNLLVATISFTALVESITAFVLTLRFHALGSAWPAAIWEGSFHAISAFNNAGFGLRSN NLVPYVGDFGIILPISAAIIIGGLGFPLLLELYVRYRKRRAGMHVGHLSLTAIFTLIGTAVLLVLGTVGTYAIERRGVMSGFDLKTQLLASFF HSVTSRTAGFNSVDVGALHPSTLVLTDFLMFIGGGSGGTAGGIKITTAAVLLAVMVAEIRGDESVLVHCRRIPNRTVRQAMAVLMLASL FVGFAIMLMLFIAPEFATMQLSFEVISAFATVGLSTGITAALPALGKLLLVVLMFAGRVGPVALVAALAARKTTRMYSYAVERPIIG
2.9E-61	217	31.5	5E-61	216.1	21.8	1.4	1	E1R994_SPISS	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Spirs_3978	Spirochaeta smaragdinae (strain DSM 11293 / JCM 15392 / SEBR 4228)	578	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Spirochaeta, Spirochaeta smaragdinae, Spirochaeta smaragdinae (strain DSM 11293 / JCM 15392 / SEBR 4228)	573413	>tr|E1R994|E1R994_SPISS Potassium uptake protein, TrkH family OS=Spirochaeta smaragdinae (strain DSM 11293 / JCM 15392 / SEBR 4228) GN=Spirs_3978 PE=4 SV=1MKKLRSNVLVVVTLILSVITLFIEQSSLAADFAFYSNILDFIVLFLLLFEVYRDFAEAKLRWLYFRRNILSLLFVLAFVVLFVYNKLIYV GRSPDDLMGLSLGVVIVRNIFILLKTFSRIMRLNTFVESISVHPAQTILFSFLLVILTGALYLMAPFTTISPGGLGFLDALFTSTSAVCVTGL IVVDTATVFTFWGHLGILILIQIGGLSIMIISYFTIFLFRRQVSLEEKLLISYMLSEKDMTNLAKNLRTIIFSSFFLEAAGALLLYFPMKGAAG GGSESALFLAVFHAVSAFCNAGFALFSDSLEQFRGMLSVNLVVAALIIIGGISFAVISDLRHFFSVRIVALFRRRRPGIGSISLNSRLVLVG TAVLLLSGTYLVYGLEHTGALAQLPLAQQYLSAFFQSVTLRTAGFNTIPFDSLKSPTLLVMIVFMFIGAASGSTAGGVKINNIAIVWAYIR SVLRGGGQATIMRRSIEPEQVNSAFLVLLFGVSAVFGGTILLSASERAPLDRILFEAVSAFGTVGLSTGITAGLSSMGKWVIISLMFMG RLGPLTILAAVSRQGKRSPVAYPTGNIST
3.1E-61	217	21	4.8E-60	212.9	14.6	2	1	U2RJ05_9FIRM	Potassium uptake protein, TrkH family	HMPREF1546_00020	Oscillibacter sp. KLE 1745	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	1226323	>tr|U2RJ05|U2RJ05_9FIRM Potassium uptake protein, TrkH family OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_00020 PE=4 SV=1MGLTQRPFHKSWSSPFRIIIFGFLLVILLGSFLLMLPVATKEGVVTPFSDALFTATSAVCVTGLVVHDTATYWSNFGQFIIVLLIQIG GLGVVTVAGAFGILSGRRIGLMQRSTMQEAIAAPNVGGVVRLTGFILKTALVVELLGAAALFPVFWQEFGLIKGLWYALFHSISAFCNA GFDLMGIKEPFSSLVDYADNPVVSIAIPLLIIIGGIGFLTWDDIRTNRLHITRYRMQSKVILVVTGSLILLPGIYFFLFEFAREPVGKRLLLSF FQAVTPRTAGFNTADLTAMSESGQTIITMLMLIGGSPGSTAGGMKTTTLAVLLANALAVFRRNEYPHFFNRRISKETISQAATIFAMYL GLFLAGGLVISRMEGQPILDSLFETASAIGTVGLSLGLTPQLHTVSRLILIGLMFFGRVGGLTLIFAALSSTQNSSARLPQERITVG
3.2E-61	217	31.6	4.1E-61	216.4	21.9	1.1	1	K9TLF0_9CYAN	Potassium uptake protein, TrkH family	Oscil6304_3677	Oscillatoria acuminata PCC 6304	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria acuminata, Oscillatoria acuminata PCC 6304	56110	>tr|K9TLF0|K9TLF0_9CYAN Potassium uptake protein, TrkH family OS=Oscillatoria acuminata PCC 6304 GN=Oscil6304_3677 PE=4 SV=1MTVARTICLGFLVIIAIGTILLLLPVSTSDGTWNNFVTALFTATSAVCVTGLIVVDTGTHYSGLGEFFIVLLIQLGGLGYMTANTFLLL LLGRRLGLRDRVAIQQSLDTTEMSGVVPLVRSIVAMTLVFELTGMFLLLFIFSPDFGFNDSLWLSIFHSISAFNNAGFSLFADSLMAYAG SIPMNLVITFLVIFGGIGYQVIMEMYMWVRDRISRNPERVVFSLHFKIVTSTTLLLLILGTIAFFFTESSNSRTLGNADFLERLLSAWFQSV ITRTAGFNTIDFGQMTTAALFITIALMFIGASPGSTGGGIKTTTVRVLASCTRSVLQGRNQVLCFERQIPPELILKAVAVVLSSLGVVVVA TILLAITDPNIEFIQLFFEVISAFATVGLSMGITGNLSTLGQLVIIVTMYVGRVGMVMLMSAMIGDPKPSNIRYPEENLLVG
3.3E-61	217	35.8	3.3E-60	213.4	24.8	2.3	1	H1XXU4_9BACT	Potassium uptake protein, TrkH family	Calab_0113	Caldithrix abyssi DSM 13497	604	cellular organisms, Bacteria, unclassified Bacteria, Caldithrix, Caldithrix abyssi, Caldithrix abyssi DSM 13497	880073	>tr|H1XXU4|H1XXU4_9BACT Potassium uptake protein, TrkH family OS=Caldithrix abyssi DSM 13497 GN=Calab_0113 PE=4 SV=1MEQEEPRIEGLKAFWNTLKIRFYEVSDKVIHAVNISLFFVSIAALVSLALEYGFYISPQMEQIIERVNIVILVYYVLQYFVKLLFTLEK LEYIRTHWFESALVLLIITEASLVLHELGLSQFQNYLVDLNVKALTRLTIVGAQVVIILTIISGAVRLNRRIAYLRFHPAQTLMLSFFIVIVLGT LLLKLPRAVAPGHQLSWLDSLFTATSATCVTGLIVVDTGTHFSMLGQLIILTLIQIGGLGIMTISSFFALFLGRGMAIRERIMLQEMLNVER LDAITRLVKGVILITFLMEALGVVLLFFSWDLPQWSVGQRLYHSVFHSVSAFCNAGFSLNSDSLMSFNQNYPVMLTIALLIIVGGLGFVV MIDLTRGRIFEYSPKKRVHRYSVHTRLVLIITGVLLIAGTVLFLLIEPFEGSWTFKALNAFFCSVTARTAGFNTVDIGHLTTSSALLLMLLM FIGASPGSTGGGIKTTTLTGLIIASFISIIRGKTRIELFRRSISFTILNRALVVFAFAISFIMLSSFLLSLTEQADFLNLLFEEISAFGTVGLSRGI TAGLSSWGKLIIIVSMFVGRVGVLTLAFAITTPREHLRVEYPEEKNVMVG

3.3E-61	217	25	7.7E-61	215.5	17.3	1.5	1	B8CWZ7_HALOH	Cation transporter	Hore_10610	Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562)	477	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halothermothrix, Halothermothrix orenii, Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562)	373903	>tr|B8CWZ7|B8CWZ7_HALOH Cation transporter OS=Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562) GN=Hore_10610 PE=4 SV=1MNYKAILNILGTLLIIVAAAMILPVLVGLYYREKDIFAFIITSGITYLSGKLLKKCTYEGKGLQYKDGFVVVTLGWFLVSIYGALPFLISGVFKNPIDAFFESVSGFTTTGATVIMSLESVSKTVLFWRSLTHWLGGMGIIVMTMAILPELAGNMHLFKAEVPGPLHNRIQPRIQDTAKTLWLLYFFITICEIILLWISGVPFFESIIHSFGTVSTGGFSSRALSVKAYNSLLVDTIVTFFMFVAGTNFNLIYDLFRGKIRTFIKDEEFRFYIWILLIAIFLVSINLIFNVYDNPNDAIRYASFQVVSISSTTGYATVDYDTWPPFSRWILLILMFIGGSAGSTAGGIKVIRIKVLFKKGLQELYYLLHPRAIKKIKINKMVVSERVSTSILGFFFLYIMVFVMVTVVLTYFGIDLISAISAVAATLGNIGPGLELVGPLNSYLPFPDSAKLLLSFCMMLGRLEIYTILVFMFMDWR
3.4E-61	217	34.6	4.5E-61	216.2	24	1	1	I9LB69_9FIRM	Potassium uptake protein, TrkH family	FB4_3722	Pelosinus fermentans B4	451	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Pelosinus, Pelosinus fermentans, Pelosinus fermentans B4	1149862	>tr|I9LB69|I9LB69_9FIRM Potassium uptake protein, TrkH family OS=Pelosinus fermentans B4 GN=FB4_3722 PE=4 SV=1MIVHTRFANLFDISQWKLTPYQILALGFAGLIVAGALLLMTPVASTTGQGLSFIDALFTATSAVCVTGLVVVDTGTYFSIFGQMVIIVLIQAGALGIMTMATLMALIMRRKIQLRERLIMQEALNHMTVSGVVRLTQYIIFATFLLEFIGGTILAIHWYSDLGSTGIYYGYWHAVSAFCNAGFDLFGSSLTSYVDDVTVNLTVTSLIILGGLGFTVIFDVWNNRRWKKLSLHTKLVLITTFVLLIFGTVVILLLEMNNPNILGELSWKGKILASYFQSVAPRTAGYNTVDIGKMQDATLFFTIILMFIGASPASTGGGVKTTTLGVMIAAIWALITGKHDAEIFRRRINQNIIYKAFTVFFIAATLVIIVTMMMSISEEFSFLRILFEVVSAFGTVGLSTGITSSLTVHGKLWLIITMFAGRIGPVTFVLALALRSRKGAIHYPEGKINIG
3.4E-61	217	20.5	7.4E-59	208.9	14.2	2.1	1	R7HNU1_9BACT	TrkH family potassium uptake protein	BN585_00288	Prevotella sp. CAG:279	489	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:279	1262924	>tr|R7HNU1|R7HNU1_9BACT TrkH family potassium uptake protein OS=Prevotella sp. CAG:279 GN=BN585_00288 PE=4 SV=1MMIFAKNNNLNFAVVVKLLGMLLLIEAAFMLPSAIVSFAYHETAAMWSFIYSIAITVGAGALGFLLPVRNHDMGRREGFLLTSLTWVVFSFFGMLPFIFDPCGLPVPDAFFETMSGLTTTGASTMESVENQSHGILLWRSVTHFIGGMGIILFTLAVIPMLNKQSGLQLFNAEVTGLTHEKIRPRISNTAKTLWTIYIALNIILILLWAGPMNLFEAICHGMSTIATGGFSTRDSSIADFNSNYIKIVMTIFMFIAGISFSLIYRVSKGDFKSLIKNDVARWYFFIAIGAAAAITAIEYVQSDEPLSQLVVDIPFQTISDITSSGFNATDINLWHHGSIMIVIALMMIGACAGSTTGGIKIDRLVLIVKNLKNEMYRILFPNAINPVRVNGKVLSNDMTAKVCAFLLLFALSLFVGSLALSLSGINLFDAIFTSMSCLSNNGLGYGFTGQNFADINPYGKWVLSFLMLVGRLEFSAVMILLTKAFWSK
3.5E-61	217	27.4	4.7E-61	216.2	19	1	1	B1XJ81_SYNP2	Potassium uptake protein (TrkH family)	SYNPCC7002_A2268	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	422	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	32049	>tr|B1XJ81|B1XJ81_SYNP2 Potassium uptake protein (TrkH family) OS=Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) GN=SYNPCC7002_A2268 PE=4 SV=1MLPFATASGEWNSPLVALFTSTSAICVTGLIVVDTGTAFSNFGQGVILLLIQLGGLGYMTLSTFLMLLLGRRFDLAQKFAIKESFDQPYNQGTRNLIRSIIATTLIGELTGIFLLFGRFSRDFDPGEGLWLAIFHSISAWNNAGFSLFADSLVGYQDSLLVNGAISGLIIFGGIGYEAIIEMYLWLRHRLQRKSRRFTFSLNFEVVTSTTFWLLGLGTVAFLFVEWANPTTFAGMSWGDKAIAAWFQSVTTRTAGFNSIDIGKLSTAGLFITMGLMFIGASPSGTGGGIKTTTINILANCTKSVLYGQTRVTVFDREIAQSIVFKAIAVVFGSATVITIATAIISISNPEIELIAILFEVISAFATVGLSTGITASLSAVGQLTLIATMYCGRVGVLLLMSAIVGEITPRRISYPEENLLVG
3.6E-61	217	17.5	5E-61	216.1	12.1	1.1	1	D9QCB3_CORP2	Trk system potassium uptake protein trkH	trkH CpC231_1729	Corynebacterium pseudotuberculosis (strain C231)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium pseudotuberculosis, Corynebacterium pseudotuberculosis (strain C231)	681645	>tr|D9QCB3|D9QCB3_CORP2 Trk system potassium uptake protein trkH OS=Corynebacterium pseudotuberculosis (strain C231) GN=trkH PE=4 SV=1MRKTPARLVAGSFATLVIIGTLILLLPISREGDAHADVITALFTATSAVCLTGLTVVDTATYWSHFGQLVILLLIQLGGLGIMTLTSFAAWVLVGRIGVRERLNAAAEGRGRELGEVKGLLVATLAFTVVVESAVALVLTLRFKGLGYSWPASLWEGIFHSVSAFNNAGFGLRSDNLVAYVGDFGIILPISGAIILGGLGFPLLLELHRRHEHRAAGIAERRFSLTAVFTISGTLILLFIGTVGIAAFEWRGVLSELNMPTKLLASFFQSVTSRTAGFNSINIGEMHPSSLLLTDFLMFIGGGSGGTAGGIKITTVAVLLTVMVAEIRGDDNILIRGRRIPTRTVRQALAVTMLAALLVSVSLMIMLLIAPEFDFLDLSFEVVSAFATVGLSTGITPDLPSIGKLLLLVLLMYAGRVGPVSFVAALAARSNKRLYSYPVERPIIG
3.7E-61	217	15.8	5.9E-60	212.6	10.9	2	1	Q606H5_METCA	Trk system potassium uptake protein	MCA2041	Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylococcus, Methylococcus capsulatus, Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	243233	>tr|Q606H5|Q606H5_METCA Trk system potassium uptake protein OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) GN=MCA2041 PE=3 SV=1MKRLLSLARVFGLMLIVFSLTYLLPIMASLLTGDGTALLFIEDALFTIGAGALLWIATRQYRYDLKSKDGFILVVLAWTGMAAFATFPLISYIEGLSFTDAYFEAMSGLTTTGATVLAGLDQLPPAINLWRHELNWLGGMGIIVLAVAILPVLGIGGRQLFMAETPGPMKENKLTPRITETAKKLWLVYASITAACILCLKMAGMSWLDAVCHAFAAMSLGGFSTHDASVGYFDSPLIEGVLMVFMLVAGMNFATHFLAIHARSLKVYRHDIEAIPYLVLALGSCVAIALFLVAHQSYPDFWTALRHASFNVVSIATDCGFASVDYNQWPLFAPLWMLFLSSVLACTGSTGGGIKMMRTLILIKQSQLQMLLLTHPTAVNPLKIGHMVIPSNIILSVLGFIFVYFMSIVILTLLLVVSGLDMVSSFSAIIASINNAGPGLNVVGPASNYAALSDFQTWTCTIAMFLGRIEVFTALIIFTPAFWRK
4.4E-61	216	27.6	1.4E-59	211.4	19.1	2	1	R5NV75_9PORP	TrkH family potassium uptake protein	BN783_00262	Odoribacter sp. CAG:788	482	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter sp. CAG:788	1262909	>tr|R5NV75|R5NV75_9PORP TrkH family potassium uptake protein OS=Odoribacter sp. CAG:788 GN=BN783_00262 PE=4 SV=1MINIRFITNIIGKLLLIECVCFLLCVLISLLYGESDTLAFLYSAIITGITGMCMAYIVKAPDQILAKKDGYFTVTCIWLFFSLFGCLPFIIGNTIPSFTDAFFETMSGFTTTGSSILNDIESLPHATLFWRSMTQWLGGLGIAVLFLAILPSLGIEGRDLYVAEVPGPTHNKMAATFYSSARKLWLFYLSFTALETILLMFGGMSLFDAICHSFSTMATGGFSTKQDSIAYWNSPYIQYVIMLFMFIAAINFGLYLTALKGDFKRIFHDEELRWYTIIIAVCSIVIACGLYFNGWAGAEKCFRDAAFQVVTIMTTTGFATADYLLWPTLLGLLIFVLMFIGSCAGSTAGGIKVVRVVLLFKNSFTEMKRIIHPNAVINVKYDGKSVHPTVMTGVMAFFILFMIVFSIGSIIMAIFTDDIATACSAVISCMSNIGPGFGSIGPMDNFSHLSDAAKLFCAALMLIGRLEVFTVLVLFSKAFWKR
4.7E-61	216	12.7	1E-34	129.3	1.3	2	2	H9UGH6_SPIAZ	Trk-type K+ transport system, membrane component	Spiaf_0516	Spirochaeta africana (strain ATCC 700263 / DSM 8902 / Z-7692)	482	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Spirochaeta, Spirochaeta africana, Spirochaeta africana (strain ATCC 700263 / DSM 8902 / Z-7692)	889378	>tr|H9UGH6|H9UGH6_SPIAZ Trk-type K+ transport system, membrane component OS=Spirochaeta africana (strain ATCC 700263 / DSM 8902 / Z-7692) GN=Spiaf_0516 PE=4 SV=1MNYSLVIRIVGVLACLMALLLLVPALVALLYGEMSELRVFLQVAGPAAAGGGVLLLLKRGTGFSLTSHDGFLVVALAWLTMALIGAVPFVLSGAIPGYTDAFFETMSGFTTTGATILNDIEALPRSLLFWRSFTHWLGGMGIIVLTVAIFPLLGFKGLQLVRAEAPGPSVDKLTPKIAHSAKILWMLYIGLSLAETLLLLAAGMDLFDALTHTFGTMATGGFSPRNASVAAYDSAAIDAIITVFMLLAGVNFVLYYSLLTRRFDNLRRDTELKVYLGIFAAATLMTTLVLFRTSYDSLGESLRFASFQVASILTTTGYATADYLLWPTAAMAVVFLLMFVGGSAGSTGGGIKVVRVLTALFKQGMNEMKYLLHPRGVFTPQLNRAPLRKSMVLGIAGFVFLYLLLLLITTLVVALSGSSLLTSFSTALATLGNIGPGFDAIGPTENYAAFPDWLKWYLSFIMLTGRLEVYTILILFTPRYWQK
4.7E-61	216	10.9	8.2E-60	212.1	7.6	2	1	R6SH64_9CLOT	Cation transport protein	BN660_00728	Clostridium sp. CAG:448	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:448	1262808	>tr|R6SH64|R6SH64_9CLOT Cation transport protein OS=Clostridium sp. CAG:448 GN=BN660_00728 PE=4 SV=1MMGRINALILAAEAVFMIPPLVLALVDGVYGTFRGFLYGILILLAVSGVLFLLSRGAQKGFYAREGLICVGVCWVIMSLLGCLPFWLSGEIPHYVDALFEMVSGFTTTGATIVGDVEALSRAALYWRSFSHWVGGMGVLVFLLAVIPVGGQNKGFTMHLMRAESPGPDVGKLVPKMRQTAAVLYLTYVALTLLNFVFLLFGGMPVFDAVCTAFGTAGTGGFGIKNDSMASYSPYLQGVCTVFMLLFGVNFSCYYLLLLRKVRSVLRDEELRLYLGVVATSTLLIAVNLWRSVAQFAGSFGTALHHAAFQVSSIITTTGFSTASINDWPAFSQAILLGLMVIGACAGSTGGGIKCARVLLLCKGLHRNLAQLIRPREVRLIRVSGKTVDEKVMANTNAYLCAYVVILLVSTVVVSLDGLSFLANFSAVLSCFNNIGPGFAEAASNFSCFGPLSKVVLILDMLAGRLEIFPILVLLSPSVWRSR

4.8E-61	216	35.9	1E-59	211.8	24.9	2	1	I0JHK5_HALH3	TrkH family transporter (Probable function potassium uptake)	HBHAL_1246	Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	439	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Halobacillus, Halobacillus halophilus (Sporosarcina halophila), Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	866895	>tr|I0JHK5|I0JHK5_HALH3 TrkH family transporter (Probable function potassium uptake) OS=Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) GN=HBHAL_1246 PE=4 SV=1MKTRMIHMSPPQTLISVFILFITLGTFLLKLPSATSNGITFIDALFTATSAMTVTGLVVIDTGTAFTLFGQVIILVLIQVGGLGIMTFAV LIYMVLGKKIGIKERLLIQQALNQTSLGGVIRLVRKLFIFSITIETFAVVFLSLRWVPEMGMAKGIYASIFHSISAFNNAGFSIWSDSLSAYA VDPLVNIVITLLFIIGGIGFTVVFDLWKSKEFYHLSLHTKIMLVGTLCINVVSLFMIFILEYNNPDTIADFSTLGKLQAAYFQAVTPRTAGFN SIDISQMEESSLFYMLMLMFIGGGSTSTAGGIKLSTALIIVLASITFFRQKEHVTLYRRSFHFHLIMRALALTVGSVGVVFLGTFVLNLSED APFLMILFETISAFGTVGLSMGLTGQLTLIGKLTLIFIMLVGKLGPLTFAFAFARYKPDPVKYPNEDVLTG
4.8E-61	216	20.6	2.4E-60	213.9	14.3	1.8	1	A1TWM5_MARHV	Trk system potassium uptake protein	Maqu_0037	Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Marinobacter, Marinobacter hydrocarbonoclasticus (Pseudomonas nautica), Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)	351348	>tr|A1TWM5|A1TWM5_MARHV Trk system potassium uptake protein OS=Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8) GN=Maqu_0037 PE=3 SV=1MNIIPIVQILGFLLILLSFLMTLPVNLLVFGDTPDWLAFVKSSVVCFSIGAAALALAGRQKHALRQQQMFMLTVSAWVVIPLFSSLP LLLSDMKLSMTDAFFESISGVTTTGSTVLTGLDHLPDDILLWRSIMQWMGGIGIIGMAVAILPFLRIGGMRLFATESSEWNEKAVPRTS HLARSLVLIYLGLTLGCVLTYWLLGMSFFQALNHALTTVSTGGYSTSDSSMGQFDSPSILLASTVFMAMGAMPFFLFVRFIHGQRQPLI RDQQVRFFLRFLVIVAALLTIYRVLREPVDPFETFVSALFNVTSVVTTTGYASTDYSLWGPFAVVVFLFITFVGGCSGSTSGGMKIFRF QLSMLLLREQVRRLLHPRAVFARNYNGRVIGDDIVASSVAFSFIFLATLALVTAILGALGLDLVTSLSGAATALTNVGPGLGDTIGPAGN FQTLPDAAKWVLMGAMILGRLELLSVFVMLSPDFWRS
4.8E-61	216	15.9	5.9E-58	206	11	2	1	G0GB28_SPITZ	Cation transporter	Spith_0776	Spirochaeta thermophila (strain ATCC 700085 / DSM 6578 / Z-1203)	481	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Spirochaeta, Spirochaeta thermophila, Spirochaeta thermophila (strain ATCC 700085 / DSM 6578 / Z-1203)	869211	>tr|G0GB28|G0GB28_SPITZ Cation transporter OS=Spirochaeta thermophila (strain ATCC 700085 / DSM 6578 / Z-1203) GN=Spith_0776 PE=4 SV=1MIHLKGIARLLGFLLLLLAGFLLIPLGIALFEGPRTWQAFLFTMIIMAVSGLVLLFLSTGERFIKLQVRHAFLFVTLSWISAAGFGALP FTLSGSIPSYTDAFFETMSGFTTTGASILTEIEGLPRSILFWRSLTHWLGGMGIVVLTVALLPLLGVAGAQLFKAESPGPTLEKVTPTIA QTAKVLWKIYVGFTAAETVLLMLGGMDLFDALTHTFGTLATGGFSPRNQSVGAYRSAYVDVVITVFMLMAGFNFGLYHRVWSGKGR DILRNTEARAYAGIFAVSTLAVALAVRPLYGSLLNALRYAGFQVASILTTTGFATADFDAWPAFAKGVLFFLMFVGGCSGSTGGGIKVI RLVTLAKQAVVELKYLLFPYGVFRPRVNGEPVRKDFLMSISGFFFLYIAILLAVTLVVTSGGYDLTTSLSSALVTLGNIGPGFAKIGPTQN YAFFPVYIKWVLSAAMLLGRLELYTVLVVFHPRFWR
5.6E-61	216	34.9	1E-60	215	24.2	1.3	1	W0E644_9FIRM	V-type sodium ATP synthase subunit J	DESME_04130	Desulfitobacterium metallireducens DSM 15288	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium metallireducens, Desulfitobacterium metallireducens DSM 15288	871968	>tr|W0E644|W0E644_9FIRM V-type sodium ATP synthase subunit J OS=Desulfitobacterium metallireducens DSM 15288 GN=DESME_04130 PE=4 SV=1MDRFFKNLTPPRVLVIGFAIVILLGALILTLPVATVDGQGLKFLNALFTATSAVCVTGLIVVDTGTTFTLFGQLVILSLIQIGGLGFMT FATFFAIILGRKVTLKERLLLQEALNQVSLEGVVRLAKYVLQVTFAIEAAGALILAVRWSFDMSWTKAIYYGIFHAVSSFNNAGFDLFGE YSSITRYVGDPIVNITIMLLIIFGGLGFTVLSDLYMHKGKKMMLHTKMVLSMTGILIFAGAILFLIEFSNPKTLGSLDPMAKILSSLFQSVTA RTAGYNTLDMTGLRSTTLLIMIILMFIGASPGSTGGGIKTTTFASVSLYVFSLFRGESFVTFKERSIATDVIQKAVAVVIMALVLVLVVTGV LTLTEKADFLTLLFETTSAFATVGLTVGLTPTLTNMGKLMIIFTMFAGRVGPLTLVFALSHKRNGPQQKHIKYPEEKIMIG
5.7E-61	216	21.2	2.3E-60	213.9	14.7	1.7	1	A0A0F2JMR4_9FIRM	Potassium uptake protein TrkH	UF75_0038	Desulfosporosinus sp. I2	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	1617025	>tr|A0A0F2JMR4|A0A0F2JMR4_9FIRM Potassium uptake protein TrkH OS=Desulfosporosinus sp. I2 GN=UF75_0038 PE=4 SV=1MNYLLVEGILGRLMVAYATFMGAPLLVALAWQEGSVLGLLISVIVILILGVIMVSHGQKDGRMGLREGFVIVAGAWILTSLAGALP FALTGAVPTYLDGLFETVSGLTTTGASVIDNVEILPQSILLWRGMTHWLGGMGIIVLFIVFLPNITGAVHLFNAEVPGPISERVLPRIRDN ALKLWQIYLGLTLAQIILLVLAGMNWFDAINHSFATMATGGFSTKNTSIMYYDSLGLELIIIAFMMIAGGNFGLYYQAWRSGIKKILKDVE FQFYILIIVVATLMIALSLWWTMERGGGNSLRHALFQVVSIMTTTGFASDDFNQWPSVSKFILLCLMFIGGSAGSTAGGIKVSRIILLFKL AWAELKRAIHPKAVIDVRFAKRTVDPSILNTVAVFFFLFLSIFAFATLLITATGLEPFDAMSAVAATLGNVGPGFGVIGPTTTYSTINAFG ESVLILCMLLGRLELFTLLVLIQPEFWRSRKGW
5.8E-61	216	30.5	8.5E-61	215.3	21.2	1.2	1	K9RU26_SYNP3	Potassium uptake protein, TrkH family	Syn6312_1640	Synechococcus sp. (strain ATCC 27167 / PCC 6312)	453	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27167 / PCC 6312)	195253	>tr|K9RU26|K9RU26_SYNP3 Potassium uptake protein, TrkH family OS=Synechococcus sp. (strain ATCC 27167 / PCC 6312) GN=Syn6312_1640 PE=4 SV=1MAPWVVFQMLTIPRTICLGFLAVISIGTFLLVLPISTSSGAWNDPIVALFTATSAVCVTGHVVVDTGTYFSTWGQVVILALIQVGGL GYMTANTFLILLLGRKFKLKEKMAIQQALDRQGMHGGRQMIHSIIATTLIFEITGIFLLLLNFHSQYGWGHGLWLAIFHSISAWNNAGFS LFSDNLISYQASLGINLIIPALIIFGGIGYEVIFEIYTWFRDRLDHKAGLLTFSLNFKIVTTTTTRLLIFGTIALFLIEVKTSPEYFDLNFGQQVL VAWFQSVTARTAGFNTVDIGAMSNTALFMIIALMFIGGSPGGTAGGIKTTTARLLAGITKSTLQGKEEVLLYERQVPPSLIMKAVAVTV GSAVVVIFATIIISIADRDVNFIRILFEVVSAFATVGLSTGITASLSLVSKVILVITMYVGRVGILLLMAAIIGDPKPTTVHYPEENLLVG
7.1E-61	216	3.4	2.9E-60	213.6	2.4	1.7	1	D3EZC7_CONWI	Cation transporter	Cwoe_3474	Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	514	cellular organisms, Bacteria, Actinobacteria, Thermoleophilia, Solirubrobacterales, Conexibacteraceae, Conexibacter, Conexibacter woesei, Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	469383	>tr|D3EZC7|D3EZC7_CONWI Cation transporter OS=Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577) GN=Cwoe_3474 PE=4 SV=1MSLWPRPSRRSRRSSLGVDLNAVLDLLGGVLRWVGLPFIAPALVAAFAGEAIWPWLLTGAATSGTGLLLDRLTAERRVERIGTR EGFLVVALVWLVVPAFAALPFVLGGEPQLSKPVDAYFEAMSGYTATGGTVVPHVEQLGEATQFWRQLSHWLGGMGIIVLAIAVLPRL RVGGRQLLQSELAGPTETEKLGATIRDTARRLWSLYVGLTLVATLVLSLVGWLGLDPEMNPWQAFAHASSAMALGGFSPQGESVAA FAPITQWLLCLVMIVAGFNFLRLFRVLIQQRVAEFARDDEVRLYVGFLLVATALLLTELLTSDIASGETAVRLAAFQATSIMTTTGFATAD YTTWGPLATVTLLLLMFIGASAGSTGGSIKVKRHLLLFRMVRRDLAQAAHRDVVVPVRASGWVVDERALRSAVLFVLLYMFTFALGAL GLVIDSERVGGDLTPFEAIGASAACIGNVGPAFGFAGPYGSYADFSNLSTAVLTALMWLGRVEIVPVAVLLTRSFWRP

7.4E-61	216	55	5.8E-29	110.3	7.4	5.9	3	A0A0D3GKH2_9ORYZ	Uncharacterized protein		Oryza barthii	1007	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza barthii	65489	>tr|A0A0D3GKH2|A0A0D3GKH2_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1MTSIFHDLVHTKCQSFRKIGRYVLHSIVLIYRFISLHVHPFWIQLSYFLLISILGSVLLMFLKPSSPEFKPGYIDMLFLSTSALTVSGLSTVEMEVLSSSQIVVLTLLMLVGGEVFVSFLGLMLRLNHKHNPEFSGDRVSSVPIELDTIEPTRTVMSSEELQIEAAVAEVPSSTIKDLKRSKRMRWFLGFVVFSYFVVIHVVGFLLVLWYIGRVSSAKAPLKKKGINIALFSFSITVSSFANGGLVPTNENMAIFSKNPGLLLLLIGQILAGNTLYPLFLRILIWFLGKVTKLKDLKLMIKNPDELQYDYLLPKLPTAFLASTVIGIMASLVTLFGAVDWNSSVFDGLSSYQKIINALFMSVNARHSGENSIDCSLIAPAVLVLFIILMLVHDTSSIYGSWHSTYTVSFRYLPPSTTFALSNGDEKTANKKEKRKLGLVVRNLAFSQLACNAVFVIVALITERSRLRNDPLNFSALNMIFEVISAYGNVGLSTGYSCSRLQKLHPDSICQDKPYSLSGWWSDEGKLLLVFVMLYGRLKAFTKGTGEYWRLWPSNHKYNPRYVDMFFLSTSAVTVTGLATIQMEDLSSSQIAVLTLLMFLGSEMFLSFLGLVLESSKQNKHDPENRRVSSVTVCDQSHLELEEAIPQTPSMKSTDIKKRCLKYLVFVVLAYMIIILVTGSLLVFMYVAHVLSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMAVFSSNNGLLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKAEEPDFMMNNSSAVGFSHLLPNLQTTFLAAVEVALVAMTVILFCCLNWDSAVFAGLTSLQKITNALFMAVNARQAGENSIDCSLVAPAALVLFMVMMYTPSLTKLFSACQYHKRIGPESDDRTSKGKPFLKTMAFSPLAFNTTVIMLVCITERRSISTDPLNFSTFNIIFEVISASGNIGLSTGYSCSRQLQHQEGVACHDKPYSFSGWWSEPGKLILVLAMIYGRLNSKDSTSTRTR	
7.8E-61	216	5.7	5.8E-60	212.6	4	1.9	1	F2NKV5_MARHT	Cation transporter	Marky_0391	Marinithermus hydrothermalis (strain DSM 14884 / JCM 11576 / T1)	482	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Marinithermus, Marinithermus hydrothermalis, Marinithermus hydrothermalis (strain DSM 14884 / JCM 11576 / T1)	869210	>tr|F2NKV5|F2NKV5_MARHT Cation transporter OS=Marinithermus hydrothermalis (strain DSM 14884 / JCM 11576 / T1) GN=Marky_0391 PE=4 SV=1MSGFVLYVLGVSYISVALVLLGFAGLALLWGEDPRGFALAAGVGLALGGVLRARGTPKAEPRRAEGLFTVGVLWILVPLLGAIPYWVSGHLNFLDALFESVSGFTTTGATILDDFGKFNKSLFLWRGLTQWFGGIGIIVLFIAVLPHFAVAGRQLFFAEATGVQKDKLTPRLRHTAEAVLRVYLLLTALAVLGYALAGMPLYDALANALATVPAGGFSPSPTSFAAYPAAAQWVAVLFMYFAGANFLLMYKLIFGREIRPLLKDPEFKVYTLVVLAASAGFGFYHFVHHDYDLEASFRHSFFQATSILTSTGFASVDYETWVVPAQIILFFLMFISGSAGSAAGGPKLIRWLVVFAHMSRELRRTLHPNAVLPLRTGGKTVGEEVLRSVFAFMAFYFLLFGLGVLLITTAEGDFIVGFTASAAAIGNVGPGLGSVGPMGSYAALAPVSKLVMIFQMWAGRIELIPVLLLFNPETWRAVRRGR	
8.3E-61	215	12.1	1E-59	211.8	8.4	2	1	Q3IMW2_NATPD	Trk-type transport system (Probable substrate potassium)	trkH2 NP_4906A	Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) (Halobacterium pharaonis)	514	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Natronomonas, Natronomonas pharaonis (Natronobacterium pharaonis), Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) (Halobacterium pharaonis)	348780	>tr|Q3IMW2|Q3IMW2_NATPD Trk-type transport system (Probable substrate potassium) OS=Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) GN=trkH2 PE=4 SV=1MRSIRLRVDWRATASLLGTVLKYLAVALLVPLTVAVIYWEDIWVFAVAIAITVTLGFTLERLDPEPDMGPAEALLLVTVSWLAVAMVGSVPYLLAGYGTASTLANPVNALFESMSGFTTTGATVMGEISTDQHSHALLLWRQLTQWLGGMGIIVLMIAILPELAVNGAQLMKTEAPGPELQKLTPRIAETARVLWLVYFGFTVLLAALLYGLHLAGFAPNMHLYNAVAHAFTTLPTGGFSPESDSIAAFSAVVQWVIIPFMVIAGTNFALFWHLLDGDIRTLLNDAEFRVYAGAIAVLSAILAALLYGGAAPAQELGGTTAGNTENALRQAAFQVGSLMNSTGFATSDFAQWGPTAQALLLFTMFVGGSAGSTGGGIKVIRWLVVMKAIRRELSVTARPEAVKPVRLGGYVVDEDVVRGIMVFTLLYLALFGAATVFFAVDSLRVGYELSVLEAMSASIATLGNIGPGFGMLGPFGSYLGFPPETKIVMVFLMWVGRLEIIPVLAVFTGAFWKR	
8.5E-61	215	24.3	1.2E-60	214.9	16.8	1.2	1	K9VMC2_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Osc7112_4376	Oscillatoria nigro-viridis PCC 7112	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria nigro-viridis, Oscillatoria nigro-viridis PCC 7112	179408	>tr|K9VMC2|K9VMC2_9CYAN Potassium uptake protein, TrkH family OS=Oscillatoria nigro-viridis PCC 7112 GN=Osc7112_4376 PE=4 SV=1MTVSRTIALGFLAVILAGALLLMMPFSTIDGTWSDPITALFTSTSAVCVTGLSVVDVGKYYSFWGQLCLVLLVQIGGLGYMTATTFLLLLLGRRFGLKDKVALQQSLDKSGLAGVVQLVQSILATTLLFELTGVFLLMTVFVPQYGFKEGVWSAIFHSVNSFNNAGFSIYSDNLSGYISSPMVNFTVGGLIIFGGIGYQVIMEMYLWLRDRFNKSPICTVFSLNFKVVTTTTAVLLILGTLAFLVLEYDNPDTLGALNFPQKLMAAWFQSVTPRTAGFNTISIGQMTEASLFLTIALMFIGASPGSTGGGIKTTTFRILFCCTTAVIEGQEEVECYQRQIPPAMILKTISVVFGSLLVAFTSAILIELTNPQVEFIAALYEAVSAFATVGLSTGITPTLSAIGKLILIATMYIGRVGVLLLISAAFGDPKPRSFKYAEESLLVG	
9.6E-61	215	0.8	1.5E-59	211.3	0.1	2	2	Q0CMB9_ASPTN	Predicted protein	ATEG_05165	Aspergillus terreus (strain NIH 2624 / FGSC A1156)	502	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus terreus, Aspergillus terreus (strain NIH 2624 / FGSC A1156)	341663	>tr|Q0CMB9|Q0CMB9_ASPTN Predicted protein OS=Aspergillus terreus (strain NIH 2624 / FGSC A1156) GN=ATEG_05165 PE=4 SV=1MTGAGLNTVDLSILNTFQQAILLTLLIVGHAIPISITVLLVRRKAFETKFKGISHEWAQNRIFRRIRSLDPSSHRRTDASSPDWGVDQIRRPDSKGSAKVSEPVDGDAIELSTNTADDDHIRWTDDDQITLSHVRTHRHRNHHHLFHNAGVGARLDLNNHPSNVTPHLPVVEEEEEDLPPLKSMIRGTQKYFASKGSVARNSQFYGLTVEEREKLGGVEYRAISFLSIVVFLYWALFLVLGIVGMGTWLEVNHPDIPRRNGLSPFWTGAFFAVSAFVNSGMSLLDDNMTALQTSAYPIITMGILILAGNTLYPCFLRFIIWTMRHLLPGDASWKPWAVTLDFILDHPRRVYTNLFPARHTWYLLGTIIVLNGLDWAMFELLAIGNKDIEKLPPGYRVLDGLFQALAVRAGGFYVVTIANLRQGLLVLYVLMMYVSAYPVLVTMRNTNVYEERSLGIYTHDDPPEGTGSQKTPSVFMSLVRHHLLGPQLQQGPCGLFDLQHHL	
9.9E-61	215	30.3	1.3E-60	214.7	21	1.1	1	R5V5U2_9FIRM	Potassium uptake protein KtrB	BN742_00959	Firmicutes bacterium CAG:631	475	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:631	1262996	>tr|R5V5U2|R5V5U2_9FIRM Potassium uptake protein KtrB OS=Firmicutes bacterium CAG:631 GN=BN742_00959 PE=4 SV=1MKTFLRKIKNIFFGNSVAQRLFQGYLIAMLIGALLLVLPFSCAEGAEKVNFIDALFISASACSDTGLTTLQLSSQFSFFGQLVIILLVQIGGIGILTLKIMFLLFLGKKIKLKERLVGASERGSGKLGGSVDLIKTSLAVLFITEFVAAILIMIRFLTVPEYKEMFPSTGKLIWTAIFHSISATNNAGFDIFPGGTSLVVFKGDYFIQIVTMLCLIIGGIGFPIFYDIKNYFKAKRKKEFYQVSLFTKFSLKSYFIVGFGGFILVVISELLAPTSSGLLYSQDFTVMEKIFALIFQTTSARNAGFATVDLNILQPSTNLLLTILMCIGASPSSTGGGLRCTTFLLVVYLIKSVATGTDRVEIYNRSVPKNTVNKALGVFIATLFVVVGSSLLLLMVNSDNSIFTIEAVLLEVGSAFGTTGLSLGITYHLNVLSKIILIFVMFIGYVGISTSLLVWSDKKVVKNLRELPEEDITIG	
1E-60	215	34.2	1.3E-60	214.8	23.7	1.1	1	B9EAT1_MACCJ	Na+ transporting ATP synthase homolog	MCCL_0635	Macrococcus caseolyticus (strain JCSC5402)	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Macrococcus, Macrococcus caseolyticus, Macrococcus caseolyticus (strain JCSC5402)	458233	>tr|B9EAT1|B9EAT1_MACCJ Na+ transporting ATP synthase homolog OS=Macrococcus caseolyticus (strain JCSC5402) GN=MCCL_0635 PE=4 SV=1MTKLLMRLTPQQGIVLYYLVAIFISFLLLRIPYVHKEGITISYIDSLFVAVSGISVTGLSPVSIVDTYSIFGQMMIIFILNLGGIGVMAMGTLLWVILGKKIGMRERQLIMVDHNQNKMSGVVTLILEIVKTMLVIELCGALMLAFYFYKDMDSISTALFHGLFAAVSATTNGGLDITGDSLNSYADDYFVQMITMFLIVLGAIGFPVIIEVKSYLTNKIPNFRFSLFAKLTIVTYMLLFILGTLTIYVVFEYHHAFKSISWHKALFYSMFQSATTRSAGLTTIDLTQLTDATQFFMSGLMFIGSSPSSVGGGIRTTTFAILILFLINYSNGRNSIKVFNKEIDPIDINRAFAVMVLATLICFIGLLLILSFENGKYGLSEIFFEVMSAFGTCGLSLGITSDLSNLSKVVIMILMFIGRVGLISFIIMLGGKAEPEKFRYPKERIMIG	

1.1E-60	215	21.9	5.1E-31	117.1	5.7	2.1	2	R7JZH0_9CLOT	Trk system potassium uptake protein TrkH	BN584_00821	Clostridium sp. CAG:277	490	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:277	1262790	>tr|R7JZH0|R7JZH0_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:277 GN=BN584_00821 PE=4 SV=1MNYSILKYILGYVLKIEAAFMLLPCVTSLIYHEKEGRYFFLVSCVCMLLGVLMTYRKPKNTVFYLKEGCLATSLSWIILSLFGAIPF WISGEIPQWENALFETISGFTTTGATVLSNVEGLSHTALIWRSFTHWIGGMGVLVFLLAILPLSGGSSINLMRAESPGPSVGKLVPKVR YTAMILYTIYFGMTVIEFIFLLAGKMPVFDALTTAFGTAGTGGFGIKNDSIMGYSPYIQWVVAIFMILFGINFNFYFYILYRHFRKAISMEEI HYYLAMILIAVTIIFLNVRTMYPTGFEAMTHSVFQVASLATSTGFSTTDFDLWPQTSQTILIIVMFVGACAGSTGGGIKVSRIVIMFKTVLK ELNSYIHPKSVRKINVEGKPVDHEVVRSINVFFITFMIIFSLSVFAISFEDEDLVTNFTAVLTTINNMGPGLSKVGPTQNFGHFNVFSKLVL MFDMLAGRLELFPLLILFHPAIWKDSFESHRKKKQKA
1.1E-60	215	36.1	1.7E-60	214.4	25.1	1.2	1	R5X1I1_9CLOT	Potassium uptake protein TrkH family	BN488_00650	Clostridium bartlettii CAG:1329	458	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bartlettii CAG:1329	1263063	>tr|R5X1I1|R5X1I1_9CLOT Potassium uptake protein TrkH family OS=Clostridium bartlettii CAG:1329 GN=BN488_00650 PE=4 SV=1MRIRKKNIRFLKKWSSVQIITVGFLLLTLVGASILSLPISSNNGQPTNFVDSLFTATSAVCVTGLVVFDTATHWSLFGKVVIISLIQIG GLGFMTIATMISLIRGKKINLKERLLIQESLNQIDLSGIVNLTRKIIFMVFAIEAIGGIILSIIFIPRFGLITGLAYGFFHSISAFCNAGFDLMGSI SGQFSSLTSLYDNSLVMITISLLIILGGLGYPVILDVLHTRSLKKLTIHSKLVITSTIILLLIGFVFILGVEYNNPDTLGNMDMKGKLLSSMFQ TTTLRTAGFNSIDLSLTKEPTIFLMVILMLIGASPASTGGGIKTTTVAVLFLTVKDFLCGKDEIHIFERSISSESIKKAMVIFFIAIFIFIIGTLAL SLTNPQFSLIECVFEVMSAYATVGLSIGGSPNLNVVGKFIIIILMFLGRVGSLTIFTAILSINIAKKDKNIKRPKGKIIIG
1.1E-60	215	39.8	2E-60	214.1	27.6	1.3	1	E8SFM8_STAPH	Potassium uptake protein, integral membrane component, KtrB	SPSINT_0870	Staphylococcus pseudintermedius (strain HKU10-03)	434	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus pseudintermedius, Staphylococcus pseudintermedius (strain HKU10-03)	937773	>tr|E8SFM8|E8SFM8_STAPH Potassium uptake protein, integral membrane component, KtrB OS=Staphylococcus pseudintermedius (strain HKU10-03) GN=SPSINT_0870 PE=4 SV=1MYSKRQPILFYLILFLSTTFIGSLLLYLPWTGQKPISFVDAMYVATSAFTVTGLTTVDITEQFNVLGHTVIMLLIQIGGMGIVAVSLLT LMISQKKITFQNNQLFKLELNIDETINVVNFAKFIFIFTVVFEALGAMILATVFVPEYGWSKGMFISVFTSISALNNAGFSLFSDNLVSYAS DPVVNLMIAILIIVGGIGYIVLFDLMTTRHLKRLHVHTKVTLFVTFILIVVGTLGFLILEHHHALKGMSFPQQILVSFFQSVSTRTAGFNTIDF SHLAPGTLMLTMILMFIGAGPISAAGGIKVTTFTLVLLYVITSLKGHRYTQVFHRSIDQKQTQKAVAITLTAMMFIIFIIFWFAVAQPNLQF EAIAFEVISAFGTVGLSTGISTEYDTFAKALIITMIAGKIGVLTLLGVLHNRTRETFHYAKSHLYL
1.1E-60	215	30.3	6.8E-60	212.4	21	1.9	1	F0S157_DESTD	Cation transporter	Dester_1300	Desulfurobacterium thermolithotrophum (strain DSM 11699 / BSA)	480	cellular organisms, Bacteria, Aquificae, Aquificae, Desulfurobacteriales, Desulfurobacteriaceae, Desulfurobacterium, Desulfurobacterium thermolithotrophum, Desulfurobacterium thermolithotrophum (strain DSM 11699 / BSA)	868864	>tr|F0S157|F0S157_DESTD Cation transporter OS=Desulfurobacterium thermolithotrophum (strain DSM 11699 / BSA) GN=Dester_1300 PE=4 SV=1MRITVVFRYVTSLLFKLSLFFLIPAFYSLFTGDGLFFDYLYPILLCLSVFLVGIQFKKEELNIKESILSVVLIWFLFPALSALLYMETGA IPNFFDAYFESVSGFTTTGASILTDIESLPKSVLLWRSLTHWIGGIGFVVFSLSILPAFGTGGAQLMRFEASKAVEEKVLPKVKKVARAIL IVYLSLTILEIVLLKLCGLSFYEAVNHTFATVATGGFSTKNGSVGEFNSFSVEMVITIFMILGSINLSLYYRAFKRKSLKSFFSYYEVKTYLII IFLSTLFVTFMLFEDGVYSDVVTAFRYGFFQVVTAASTTGFASTDYSTWPSSVLALLMILALIGATAGSTAGGLKQFRFIVMIKTMYREL YKTAHPTLVYYRVALGNRLLDVSVLNTIWAFISLYFITTIIFGFIISLSGYDLITSFSASIACITSLGPGLGKVGPAGNFSFFSDFDKFLLSLEM ILGRLEIFSILTLLLPSFWKD
1.2E-60	215	27.4	4.6E-60	212.9	19	1.7	1	D9QUE5_ACEAZ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Acear_0391	Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Acetohalobium, Acetohalobium arabaticum, Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	574087	>tr|D9QUE5|D9QUE5_ACEAZ Potassium uptake protein, TrkH family OS=Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288) GN=Acear_0391 PE=4 SV=1MQLSDKFSLDNLTPAQFLSLGYLVVILTGTVLLSLPIATASGIRMPLIDALFTATSATAVTGLIVENTKNFFSGFGQIVILILIQIGGLG IMSMSTLFAMIVGKKITLKERLVIKQDLDQFELSGIIRLVRYVLFVTLVIEGTGALILFSRLIRDYDPLRALYLAIFHSVSAFNNAGFDIFGNS LENFTGDLTINLVITTLIILGGIGFAVIAEIYKGEKKFKNYSLQTKLVLSISGSLILLGTIVVFVLEYSNPATMGNLPLHGKALASYFMSVTPR TAGFNTVPTGSLHNTTLFFVIILMFIGASPGSTGGGIKTTTFGSVLAVVYAMMTGKEDIEAFKRRIPKDVIFKALSIIIISVLLIVVVTMILTV TEDMPFLDLFFETVSAFGTVGLSTGVTGKLSGIGKLLIILTMFAGRVGPLTLFLAIGRKRIKGNIRYPEEKVLVG
1.2E-60	215	22.8	2.8E-58	207	15.8	2.1	1	R6NX13_9FIRM	Cation transport protein	BN662_01738	Roseburia sp. CAG:45	488	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:45	1262947	>tr|R6NX13|R6NX13_9FIRM Cation transport protein OS=Roseburia sp. CAG:45 GN=BN662_01738 PE=4 SV=1MNYSMIRYILSSVICFVGIFLLLPAATAGIYQEKEGFLYLITGLACMLIGFWGRRRKPKSSVFYSKEGFAAVALSWIILSLIGALPMY LTGEFPSYIDALFETISGFTTTGSSILSDVETLSRGTAFWRCFTHWIGGMGVLVFIMAVMPLSDSSSSMHLMRAESPGPSVGKLVPKVK TTAMILYGIYVVFTVIEIIALLIAGMPLFDSMTLTFGTVGTGGFGLLNSSIASYSTAVQIIITVFMIICSINFTVYYMFLIKRPKEALMCEEMR YYLLIVFGSALLIAFNIRASFASFGKAFQQAIFQVASVISTTGFATADFNLWPEFSRMILVLLMFVGACAGSTGGGFKVSRLIIMVKSVRN EIMSVTHPRSVQKVHMDGRRIPDNVVKTVLCYLAGYVVILIVSVLLISLDNFDMTTNFTAVMATFNNVGPGLNRVGPTGNFGGFSVLSK LVLMFDMLVGRLELYPMLVIFAPGLWRIHPHRHVGKVQ
1.2E-60	215	31.1	1.6E-60	214.4	21.5	1	1	K9VWZ5_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cri9333_1616	Crinalium epipsammum PCC 9333	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Crinalium, Crinalium epipsammum, Crinalium epipsammum PCC 9333	1173022	>tr|K9VWZ5|K9VWZ5_9CYAN Potassium uptake protein, TrkH family OS=Crinalium epipsammum PCC 9333 GN=Cri9333_1616 PE=4 SV=1MTVSRTICLGFLSVIAVGTILLLMPFSNSSGNWNDPLVALFTATSAVCVTGLGVVDTGTYFSFWGQFVMVVLVQIGGLGYMTAT TFLLLLIGARFSLRDKIAIQQSLDRSSIYGSDQVLRSIIATTIIFELTGVFLLLPVFIPQHGFYQGLWIAIFHSINSWNNAGFSLFKDNLIGYQ SSVLLNFTVTGLIIFGGIGYQVIMELYLWLRDRLTKKPERLLFSLNFKVATTTTLILLLILGTISFFLIELRNPETFGQMNLVNKIMAAWFQSV TTRTAGFNTVDFGKMTTAGLFITIALMFIGASPGGTGGGMKTTTLRVLTSCTKAILQGQEQVLLYKRQVPISILILKAVGVLIGSVGTVVL ATMMIALVEPNLNFIQILFEVVSAFATVGLSTGITATISPVAKLVLILTMYVGRVGVLLLMSAILGDPKPSAIRYPEENLIVG
1.3E-60	215	33.3	1.7E-60	214.3	23.1	1.1	1	B8CXA2_HALOH	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Hore_11710	Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562)	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halothermothrix, Halothermothrix orenii, Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562)	373903	>tr|B8CXA2|B8CXA2_HALOH Potassium uptake protein, TrkH family OS=Halothermothrix orenii (strain H 168 / OCM 544 / DSM 9562) GN=Hore_11710 PE=4 SV=1MKFPQLVNKNNMTPAQVLVFGYFTVIIGTLLLMLPFATSNGQGLNIVDALFTATSATCVTGLIVVNTSTAFTVFGQLVIMVLIQIGG LGIMTMSTMIAFVIGKKITLKERLIIQEDLNQFKISGLVRLVRYVIFVTVIIEGLGALLLFVRLIKDYPFMKALYYSIFHAISAFNNAGFDLFGN SLENYTGDILMNFVVMGLIVLGGLGFAVLAELYQIRNFKKMSLQSKIVLTITLILIIAGFLSVLGLEYNNPGTMGNLNTGDKILSSLFLSITP RTAGFNTVPTGNLKSSTLFLLIVLMFIGASPGSTGGGIKTTTFGVLLITVWSLITGKRDIEIYKRRLDDEIIFKALAITMLSLGLVVAVTMILT VTEKMDFLRVFFESVSAFGTVGLSTGITSGLSTFGRILITITMFSGRVGPLTLAIAFAERKHNGVYHYPKEKIMVG

1.3E-60	215	25.8	1.6E-60	214.4	17.9	1.1	1	A0A0C2XXI3_BACBA	Potassium uptake protein, integral membrane component, KtrB	SD77_3672	Bacillus badius	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus badius	1455	>tr|A0A0C2XXI3|A0A0C2XXI3_BACBA Potassium uptake protein, integral membrane component, KtrB OS=Bacillus badius GN=SD77_3672 PE=4 SV=1MVHSKSSHFMDPPKILAGGFALVILLGAYLLTLPVATADGEGLSFLNALFTATSATCVTGLVVVDTGSTFTLFGQLVILSLIQIGGLGFMSVATLFAFLLRRKISLKERLILREAFNSLAIEGIVKLVRRVLLFTLVCEFIGGTLLAIRFSFDMPAAKAIYFGFFHAISNFNNAGFDLMGDYRSLTGYVNDPVVVLVVCSLIILGGIGFVVMNELYEYRQKKQLSLHTKIVLVTTFLLVSVGAILIFLLELHNPKTLQPLSWPGKFLGSLYQSVTARTAGSNTLNIADLTDTTLFLIIFLMFIGASPGSTGGGIKTTTFATLVGAVISQIKGKEEVVFFERRIDYKLIYKSLTIILSSLSVIVIVTMILTITETGKGFLMIVFEATSAFATTGLSMGLTPDLTPIGKAVIIFAMFAGRLGPLTLAIALTLNRQPDRFRYTEEKIMIG
1.3E-60	215	27.1	1.9E-60	214.2	18.8	1.2	1	A4J4Z1_DESRM	Potassium uptake protein, TrkH family	Dred_1616	Desulfotomaculum reducens (strain MI-1)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum reducens, Desulfotomaculum reducens (strain MI-1)	349161	>tr|A4J4Z1|A4J4Z1_DESRM Potassium uptake protein, TrkH family OS=Desulfotomaculum reducens (strain MI-1) GN=Dred_1616 PE=4 SV=1MKNNKGFLSQPSRALAVGFAGLILLGGILLSLPVASASGQPTDFLTALFTSTSAVCVTGLVVVDTGTYWSTFGQVVIISLIQVGGLGFMTMAVLFWLILGRKVTFRERLLIQQSLNVIDLSGIIKLAKQVIVLTLTIQIFIATLLAVRFVPELGLQKGIAFSLFHAVSGFNNAGFDLFGDFRSLTQYTADPIVNFAIGLDIILGGIGFTVMTDAIRYRKRKKISLHSKLALYITAILLLFGMVVFLLLEFNNTLASLSFGGKLWASWFQSVTPRTAGFNTIDLTAMRPVTLFFIILLMFIGASPGSTGGGVKTTTFGIVVLALISLARGKEDAEVFYRRISKEQVYKGLGIILLAMGWIIFATLLLGAVEKADFLKILFEVVSALATVGLSAGLTPTLSDFGQVVIMFTMFLGRLGPLTVAYALATKQQRKQQFRYPEEERIIIG
1.3E-60	215	23.7	1.9E-60	214.2	16.3	1.3	1	E5UJ54_NEIMU	Trk system potassium uptake protein	HMPREF0604_00940	Neisseria mucosa C102	497	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Neisseria, Neisseria mucosa, Neisseria mucosa C102	435832	>tr|E5UJ54|E5UJ54_NEIMU Trk system potassium uptake protein OS=Neisseria mucosa C102 GN=HMPREF0604_00940 PE=3 SV=1MYLHKGFRLGGAVSKVMPIVHVLSKLGLLFSLLLAVPTLMSYFYHDSAFFVFAYTALTVLLVSCVTWVLTLRFNRELRPRDGFTLVLMLWLAFAVVAAMPIYFYMPSMSFTDAFFEAMSGLTTTGATVISGLDTLAPSVNFWRHMLNWLGGMGIIVLAVAILPMLGVGGTQLFKAEIPGMDKESKMAPRISQVAKRLWFAYALTTAAAFVSLHIAGMGWFDALCHAMSAVALGGFSTHDDNVAFFDSLAVEWTLMFFTVWGGINFASHFTALGNRSWRVYWKDEECRTMLLVLSGSILISALYLWQQDVYQSLGEALRFVSFNFVSIGLASGFSNADFAQWPLIVSLWMFFLSNVLASSGSMGGGIKNVRALVLFKFSLREMLILLHPRAVRTVKVNNNSIPDRMALTVMSFIFIYFMTVIVFSFLLMAAGLDFLSAFTAVIACITNAGPGLGAVGPSHNYAALSDVQKWLCAAVMLLGRLEIFTVLILFTPAYWKK
1.4E-60	215	35.3	2.2E-60	214	24.5	1.2	1	A0A077J3S4_9BACI	ATP synthase	HW35_02750	Bacillus sp. X1(2014)	453	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus sp. X1(2014)	1565991	>tr|A0A077J3S4|A0A077J3S4_9BACI ATP synthase OS=Bacillus sp. X1(2014) GN=HW35_02750 PE=4 SV=1MSTIKQIQSKSRKISTFQLIVIFYLSALIISTLLLMIPFAHRPNVHLSFIDAMFTAASAISVTGLNVISVKDTFSNFGIFLLCLILQLGGLGVMSLSTFLWVVLGKKVGLKERQLIMIDHNQSNLSGLVQLAKRIFIIIVTIEFIGGIILGVHFLNYYDNALTAMKHGFFASISATTNAGFDITGESLIPFKNDYYVQIIVIFLVIIGAIGFPVIIEVYEFLITLKNKKKFHFSLFTKLTTLTFVILTVFGGLFIYLLDMNHFFANKNWHEAFFYSFFHSVTTKSAGLTTTDLNEFTPSNQLFISILMFIGGSPSSASGGIRTTTFAIVVLAIIFYAQGKGTIKVFKRELKAEDVLKSFVVIMTGSILCLVSIIILSVTEKGTILEIIFEVNSAFGTNGLSLGLTPELTTFGKILIIILMFIGRVGIVTCLLMLRGKGRKETFHYPKEKVIIG
1.5E-60	215	14.9	6.6E-60	212.4	10.3	1.8	1	A1KCP0_AZOSB	Trk system potassium uptake protein	trkH2 azo3980	Azoarcus sp. (strain BH72)	490	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azoarcus, Azoarcus sp. (strain BH72)	62928	>tr|A1KCP0|A1KCP0_AZOSB Trk system potassium uptake protein OS=Azoarcus sp. (strain BH72) GN=trkH2 PE=3 SV=1MRGANARAYFPAFNALGLIIMIFGLLMVFPLAVAWALGDGAEMAFDQAILVTFFAGLLLWAATRSRRRDLRVHDGFLLVAATWVILPVFGALPLMAFLPELTPTDAYFEAVSGLTATGGTVLTGLDRLPTSINLWRTFMHWIGGMGVIVLVVAILPLLGIGGRQLFKAEVPTPMKETSLTPRIAETAKGLWLTYILLTIACGFSLWLAGLEGWDAVIHAFSVTGLGGFSSRDESLGYFGNVAVEGVAMVFALASALNFSTHYLALSRRSFAPYLRDPEIPFFFAVLLFSIALLTVYLQQFEAHADLFSTVRYVAFHVVSISTSLGLATYDYTMWPMFAQIWVLFLGSFMACSGSAGGGIKMMRAIILYKQVLREIIRSLHPNAVRPVRLGSQPVSEGTLHAVLGFSFIYMVTIVTLTLVLSASGVELITAFSAVVACLNNTGPGLDAVGPASNYQGLSDFQTWVLSFTMILGRLEIFTFLVVLTPTFWRR
1.5E-60	215	50.9	2.4E-25	98.4	9.1	6.6	4	A0A0D9WTT2_9ORYZ	Uncharacterized protein		Leersia perrieri	959	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Leersia (cutgrass), Leersia perrieri	77586	>tr|A0A0D9WTT2|A0A0D9WTT2_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1MTSIYHEFVHSKSQSFRSIGRYVLQSIVLIYRFVSLHVHPFWIQLSYFLLISILGSVLLMFLKPSNPDFNPGYIDMLFLSTSALTVSGLSTIEMEVLSSSQIVVLTLLMLVGGGVFVSLLGLMLRLNNQVSRDFSGDKVSSVPIELNTIDSASTVISCEELQLEAAISEIPSSTIKDLKRSKRLSWCLGFVVLGYFLVFHVVGFLLVLLYIAHVSSAKAPLKKKGLNIALFSFSVTVSSFANGGLVPTNENMAIFPKNPGLLLLFIGLILAGNTLYPLFLRILIWFLGKVTKLTELKLMIKNPEELQYGYLLPKLPTMFLSSTVIGLMASLVTLFSAMDWNSAVFGGLSSYKKIINALFMAVNSRHSGENSIDCSLIAPAALLLFIIMMYLPPSTTFALSNGDEKTEDKKVKRKFSLVVQNVAISQLACNAVFVIVAFITERRGLRNDPLNFSALNMIFEVISAYGNVGLSIGYRCSRLQKLHPESICQDRPYSLSGWWSNEGKLLLVFVMLYGRLKAFSKVTVTGLATIQMEDLSSSQIVVLTLLMFLGSEMFLSFLGLVLESSKQNKNDLENRRVSSVTVCEQSQLEEAIPQTSSTSSTHIKKRCLKYLVFVVLAYMIIVLVTGFLLVFIYIAHVSSARDVLTRKSINKALFSVSITVSSFTNGGLLPTNESMAVFSSNNGLLWLIIGQILAGSTLFPVFLRLVIWALRGLRLTKAEEPDFMMNNTKEVVFNHLLPNLQTAFLAAVEIALVAMTVILFCCLNWDSAVFAGLTSLQKITNALFMAVNARQAGENSIDCSLVAPAALALFMVMMYTPALTNYFSACEDHKRSGPEHNNRTNKGNPFLKMMTLSPLAFNTTLLIILVCITERRSLSTDPGLNFSTFNIIFEVISAYGNIGLSTGYSCSRWLLLQHPEKKGMIVACHEKPYSFSGWWSDPGKLILVLAMLYGRLKGFHKKHIS
1.6E-60	215	18.3	6.1E-60	212.5	12.7	1.7	1	A0A0F2RMQ9_9PROT	Trk system potassium uptake protein	VR70_08595	Rhodospirillaceae bacterium BRH_c57	490	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), unclassified Rhodospirillaceae, Rhodospirillaceae bacterium BRH_c57	1629718	>tr|A0A0F2RMQ9|A0A0F2RMQ9_9PROT Trk system potassium uptake protein OS=Rhodospirillaceae bacterium BRH_c57 GN=VR70_08595 PE=3 SV=1MPEGTTVERAFFAPVLHIIGLLTIALGLSMAFPAMADLVVGNIDWQVFTAASITTVFLGGATVLSTRRPEISLSLKQGFLLTALSWFLLPTAAAVPFVYADLDMGIIDSIFEAVSAMTTTGSTVMVGLDSMPPGILLWRSLLQWIGGIGIIVMAIAILPLRVGGMQLFRTESSDRYDKALPRAQQMVKAITLVYLGLTVTCGLSYWAAGMTAFDALNHALTTLPTGGFSTHDASFGYFQTPLLHWLGTLFMIAGALPFTLYVATLAGRRKALLNDSQVRLFLWVVAGSVALLTVHLVGVRGFGVEEEALRLSAFNVVSVSVTTTGFATTDYSGWGALSVTLFFYLTFSGACAGSTTGGIKMLRVGVMLATLSVYIKRLVYPAGVFPRRFGGQDISSEITASVMVFTLAYASTVALAALALSAFGHDFVTSLTAAATAVANVGPGLGPIVGPAGNFAPLEPGAKLVLSVAMILGRLEIFTVLVLLSPVFWRR
1.6E-60	214	33.1	2.5E-59	210.5	23	2.2	1	F8E7R3_FLESM	Potassium uptake protein, TrkH family	Flexsi_0216	Flexistipes sinusarabici (strain DSM 4947 / MAS 10)	483	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Flexistipes, Flexistipes sinusarabici, Flexistipes sinusarabici (strain DSM 4947 / MAS 10)	717231	>tr|F8E7R3|F8E7R3_FLESM Potassium uptake protein, TrkH family OS=Flexistipes sinusarabici (strain DSM 4947 / MAS 10) GN=Flexsi_0216 PE=4 SV=1MRFSLVFKTLSVIWLILAFFMFLCSLTSLYYNEISAFKSFQITIIIIASISLLFLLLIKKSNQKILSTKGSFLLVSLAWITASFFGAMPFYLSGAIPHFTNAFFETASGFTTTGASILVDIESLPKSLLMWRSLTQWLGGMGIVVLTVAILPLLGIGGLQLIKAEAPGPSVDKISYRITTTAKYLWLIYLSLTVLLIALLVIGGMSFFDSVTHTFSTLSTGGFSPKQNSIAHYGSPFIQYVIAFFMFLASANFALHFNLITGNFKNIFNNSEFKAFIIIILTSTVIVTLNLYYNFESGGEESFRLAIFQALSFITTTGFVTDNYESWPFLSQIILFSLMFVGGCSGSTAGGIKVVRILLLFKQSLNEMKFLLHPRGIFTIKLNKMPVKKDIVYAVSGFFFLYIATNIIVTVIVASGGNSLMTSLTASLATIGNIGPAFGSAGPMDNYAGFSDYIKWVLSLAMIAGRLELYSFIIIFTPYFWKK

1.6E-60	214	29.6	3.5E-59	210	20.5	2	1	R6QRU4_9CLOT	Potassium uptake protein TrkH family	BN621_00573	Clostridium sp. CAG:352	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:352	1262798	>tr|R6QRU4|R6QRU4_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:352 GN=BN621_00573 PE=4 SV=1MIKRQNPKHKHITSFQIIILGFLSVIILGSILLMLPVATRDGKGAVCSDALFTATSAVCVTGLVIHDTATYWSMFGQSVILFLIQIGGMGIVTVAVSVAAFSGRKIGLMQRSTMQEAVSAHHVGGIVRLTKFILKTSVCIELIGAALLLPAFIRDFGITKGLWYALFHSVSAFCNAGFDLIGIKEPFSSLTSYSSQPFFNFTVMALIIIGGIGFLTWEDIKNNKLHFRKYRMQSKVILTVTGILIILPALYFFFFEYQSLPLGERILTSLFQSVTPRTAGFNTTDLTAFSETGQMLIILLMLVGGSPGSTAGGMKTTTIAVLVSSALSVFRKKENTHFFKRRISDDTVKSAATIFLLYIVLFIGGGMIISRLENIPLLPSLFETASAIGTVGLSLGITSQLGVASQFILIILMFFGRVGGLTLIFAAMKGTGTNVTKYPQEKITVG
1.6E-60	214	25.4	2.1E-59	210.8	17.6	2	1	R5UFS9_9BACE	TrkH family potassium uptake protein	BN535_00734	Bacteroides caccae CAG:21	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides caccae CAG:21	1263037	>tr|R5UFS9|R5UFS9_9BACE TrkH family potassium uptake protein OS=Bacteroides caccae CAG:21 GN=BN535_00734 PE=4 SV=1MINSKMIYRIIGFLLLIETAMLLCCGAVSLFYKENDLQSFLISSAITTGVGILMLAIGKGAEKSLNRRDGYVIVSTAWIAFSLFGMLPYYIGGYIPSITDAFFETMSGFSSTGATIMNNIESMPHGILFWRAMTQWIGGLGIVFFTIAVLPIFGMGGIQVFAAEASGPTHDKVHPRIGVTAKWIWGIYAGMTGTLIVLLVFGGMSVFDSICHAFTTTSTGGFSTKQASIEYYHSPYIDYVISIFMFLSGINFTLLLLMFNGKIKKKFIHDAELKFYFICVSFFTIFIAFWLYRTCDMGVEEAFRKSLFQVISLQTSTGFATADYMLWPSILWGCLIVVMLIGACAGSTTGGIKCIRMVILFKVAKNEFKHILHPNAVLPVRVNKQVISPSIQSTVLAFTFLYAVIAIISILIMLGFGVGFLESIGTVVSSMGNMGPGLGTCGPAYSWSELPDAAKWLLSFLMLLGRLELFTVLLLFSSDFWKKN
1.7E-60	214	20.1	3.4E-60	213.3	13.9	1.4	1	K0NHY8_DESTT	Trk system potassium uptake protein	trkH TOL2_C23740	Desulfobacula toluolica (strain DSM 7467 / Tol2)	483	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfobacula, Desulfobacula toluolica, Desulfobacula toluolica (strain DSM 7467 / Tol2)	651182	>tr|K0NHY8|K0NHY8_DESTT Trk system potassium uptake protein OS=Desulfobacula toluolica (strain DSM 7467 / Tol2) GN=trkH PE=3 SV=1MRWQFIARIIGILLLFLGFSMIVPLLVSLYYHDLALNGFLRSIAITVVAGLLLILSKSHATEDYINQKEGMTTVALAWTAIGLFGALPFYFSPDFTNFTDAFFESVSGFTTTGSSVMINIEGATQSLLFWRSFIQWLGGMGIIVLSLAILPFLGVGGIQLYKAEVPSPVPDKLTPRLSDSAKILWIVYAVFTLIEIIFLLGGGMSLFEASCHAFTTLPTGGFSPKNASIAHYDSAFFDYVIVIFMVLAGINFSLHYQMLRGKTLAFWEDTECRFFLGLTLLLTLLITWDIYGSVYTSVKDAFRFSSFQVVSIITTTGFATADYEKFPGLSQVLLFVCMFIGASAGSTGGGMKCARIIACFKYCYRELFKIIHPRSISHVKINNTVIPDEVIRSIMGFLALYIGLFILSSILLACMGIDMMTAFGAVAACIGNIGPGFGTVGPTENFAHLPVMGKWLLAWCMLLGRLEIYTVIILFVPEFWRK
1.7E-60	214	27.4	2E-60	214.1	19	1	1	K9SDI9_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Pse7367_0376	Pseudanabaena sp. PCC 7367	452	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Pseudanabaena, Pseudanabaena sp. PCC 7367	82654	>tr|K9SDI9|K9SDI9_9CYAN Potassium uptake protein, TrkH family OS=Pseudanabaena sp. PCC 7367 GN=Pse7367_0376 PE=4 SV=1MTPARTICVGFLAVIIFGTILLSLPIANVEGNWEPLIALFTSTSAVCVTGLSVVDVGQHYTPLGQLILLGLFQIGGLGYMTATTFLLVLVGRRFSLRDRIALQHALDIPGIKGGVQLVKSIISTTLLELTGVFLLLYAFSRDRSDLPFLTNVWQAIFHSVSAFNNAGFSLFSSSLVNYAGSPIVNFTITGLIIVGGIGYQVIMEVYNWLQIKLRRSNAPILLSLQFKVAVSSTVFLLAIGTLAFFLTEFTNNQTLGALSFPKQALAAWFQSVTSRTAGFNTIDTGAMTMTGLFTTIALMFIGACPGSTGGGIKTTTMFLLLGCTRSALQGREDILLFNRQVPAVLVFKAIAVAVGSMFTLVISIVLLSITEADLITKSGYSFIHILFEAVSAFATVGLSMGITPEVSDLGRLILVGTMYIGRVGVVVLMAALIAEPEPSLVKYPEETLLVG
1.8E-60	214	25	3.1E-59	210.2	17.3	2.1	1	A6L173_BACV8	Trk system K+ uptake protein TrkH	BVU_1761	Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides vulgatus, Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	435590	>tr|A6L173|A6L173_BACV8 Trk system K+ uptake protein TrkH OS=Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154) GN=BVU_1761 PE=4 SV=1MINAKMIARIMGALFFIEAGFLILCSFLAVYYNESDISAFLYSAAITAGAGSIAALAGKNAEKRISRRDGYVIVTLAWVFFSLFGMLPFYLSGYIPTITDAFFETMSGFTTTGASILDNIESLPHGLLFWRSMTQWIGGLGIVFFTIAVLPIFGVGSVQLFAAEATGPTHDKVHPRIGVTAKWIWTIYLGLTITEIILLVAGGMNFFDSVCHSLTTTATGGYSTKQNSIAAFNSPYIEYIITLFMFLAGINFTLLYLLFLKGNFKRLFQNTELHWYLGTVGFFTLFTTVTLIFTSPFSIEESFRKAIFQVVSLQTTTGFISADYMTWVPVLWTLMCIIMLFGACAGSTTGGIKCIRIAIMSRVSKNEFKHIIHPNAILPVRINRQVISSTTKSAVLAFIFLYMAIIFIGWLVLMLFGVGFEEAYSVVISSLGNVGPGIGKCGPSYSWNGLPDAAKWISAILMLIGRLELFTVLLLFMPSFWKKH
1.8E-60	214	9.9	3.3E-52	187	3.7	2.2	2	Q7UNB4_RHOBA	TRK potassium uptake system protein (TrkH)	trkH RB7675	Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1)	605	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Rhodopirellula, Rhodopirellula baltica, Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1)	243090	>tr|Q7UNB4|Q7UNB4_RHOBA TRK potassium uptake system protein (TrkH) OS=Rhodopirellula baltica (strain DSM 10527 / NCIMB 13988 / SH1) GN=trkH PE=4 SV=1MPRNGWLGNKVGIAAVGNESGHLSTAAIATVSQLVEKASSLNFPLLFRFLGTICLLIGGSMAFSLPFAFPSVADRTHLPPATEFESAAASGLLASMAICFFVGAFFRFLGRGHRGGGELYQKEAMAIVGLSWVSATVLGALPYYLSGTMIAEGSPITFIEAMFESQSGFSTTGATVLTDLETPELVPHCILFWRSWTHFLGGLGIVVLFVAILGQGSAGKAMMRAEMPGPTKDGSMPRMQHTALVFAAIYVGLNMLLTFIYMFEGMSSFDALCHAFGTMATGGFSTYNRSLGGFDSPLIEYTTVLFMILAGTNFTLLYLMLLDIPRRPLTAARRLFQDVEFRTYGLVIAVVTLGVVIFGLRAEDEGFGTLAKGVQNGLFQVVSVITTTGYGTADFDEWNNFGRGILLLLMFVGGCAGSTGGGMKVIRHVLFYKILRLEIERAHRPRVVRPLRVSGVAVDDPQLAHNILLYFCMVLAIFVMSWLALITFEPNSTWGVVMTDTPPEEVIEESAKAGKSGEDIVVVDHSQAGKKLLHGTLDEKLLDSASAVAATLNNIGPGLGVVGATRNYAGFSQGAKLLFVWLMMLGRVEIFSVLLLFVPSFWRRV
1.8E-60	214	16.5	3.3E-58	206.8	11.4	2.2	1	I0GLZ5_SELRL	Putative Trk system potassium uptake protein TrkH	trkH SELR_00740	Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421)	483	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Selenomonas, Selenomonas ruminantium, Selenomonas ruminantium subsp. lactilytica, Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421)	927704	>tr|I0GLZ5|I0GLZ5_SELRL Putative Trk system potassium uptake protein TrkH OS=Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421) GN=trkH PE=4 SV=1MDVRIVYYVLGRLVMAETVTMFIPFALALVNYENSIPGFAVALGLSASVGLVLQTNGRQRHADLSLREGIAITGFGWALATSLGMLPYVCGGYLNALDALFESISGFTGTGATVFNTLEDLPQSILFWRMMTHWFGGLGIIVIFIALLPQTGQSTIYMYNAETTGPTDDRVLPRLRDMTKALFQMYMLFTLVAAAVYMVCGLNLYEALTHAMSTIGAGGFSTYDESAMHFDSPAFEWCMTFFMILAGGNFGLYYRIWQKGPGVIKRNSEFKAYLWILGIAIVLITLNLLVKMDFGLGDALRYAAFQVGSLSTTGFVSADFEQWPPFSKGIILFLMVCGGCAGSTASGMKVVRVLLLLKNAWAVVHQKMSPRRVVEVRLNGSRVSEETLLRVGQFFFLYIFFIAFWALLLTLDGLTVFDAIGLSVSTMGNIGPAFGIAGATCTYAGLSVFSKSILCISMLLGRLEMFTLLVMLTPDFWQKGNRW
1.9E-60	214	39.3	2.1E-59	210.7	27.3	1.9	1	A0A090HXV9_9FIRM	Potassium uptake protein KtrB	ING2D1G_0853	Peptoniphilus sp. 1-1	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptoniphilaceae, Peptoniphilus, Peptoniphilus sp. 1-1	875453	>tr|A0A090HXV9|A0A090HXV9_9FIRM Potassium uptake protein KtrB OS=Peptoniphilus sp. 1-1 GN=ING2D1G_0853 PE=4 SV=1MKNLFEFKLFKILKKPPLILCMSFLVVIFVGAFLLNLPIASNNNESMGFVNALFTSTSATCVTGLVVVNTAEFFSTFGKIVILFLIQIGGLGTMVLFSMLLVITGKKIGLKDRILIREQLNTDSLSGLVKFSKYVLEVSILIEIIGALFLSTVFISDFGLLRGIWFSIFHSISAFCNAGFDILGNSIVPYKTNYIINLTIMFLIILGGLGFGVYMDIYKHKKFSKLSTHSKMVLIMSGILLIVGTLLFLIIEYNNSSSIANFNLKDKILISAFQSTITRTAGFNSIDISKIFDSTAFVMIILMFIGGSPASTAGGLKTTTFGVLLFTTVSVIRGERDVVFMKRKISLSIVLKALAICIICLILVVLVALLLSIIEADRFNFIDILFETVSAFGTVGVTRGITPLLDDASKIILSMTMFLGRVGPTTLAIGFLGKNYSNGLKYAKGNIIVG
1.9E-60	214	38.7	2.5E-60	213.8	26.8	1	1	B1HP44_LYSSC	Uncharacterized protein	Bsph_1288	Lysinibacillus sphaericus (strain C3-41)	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus sphaericus (Bacillus sphaericus), Lysinibacillus sphaericus (strain C3-41)	444177	>tr|B1HP44|B1HP44_LYSSC Uncharacterized protein OS=Lysinibacillus sphaericus (strain C3-41) GN=Bsph_1288 PE=4 SV=1MPWKKTSNRLVTPFQVLVSYYFIAIAISFLLLRLPGVHQEGVKVSFLDSLFTAVSAVSVTGLTTINISETYTKFGLVMILVILQLGAIGIMSLGTFVWLLVGKKIGMRERQLIMIDHNQYNLSGVVKLIREILKILIGIEVAGTVILTLHFTNYFDTLEEAFLHGIFASISAITNGGFDITGMSLLPFHDDYFVQLVTMVLIVLGAIGFPVLIELKTFLLKRHANFRFSLFTKITTSTYAILFVVGALVILLLESFHSFKEMSWHEALFSAMFHSVSTRSAGLTTYDVTTFSEATDIFMSFLMFIGSSPSSVGGGIRTTTFAIAILFLITFARGREDIQVFGREIHLIDVFRSFVVILLAFFMVLIATIILLITEPHASLIQIIFEITSAFGTCGMSLGITSDLSVIGKIIIIILMFIGRVGLISFLYTLGGGGRGKKSKFHYPKERVIIG

2E-60	214	39.2	2.6E-60	213.8	27.2	1.1	1	A0A0B4RE37_9BACL	Uncharacterized protein	Plano_2062	Planococcus sp. PAMC 21323	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Planococcaceae, Planococcus, Planococcus sp. PAMC 21323	1526927	>tr|A0A0B4RE37|A0A0B4RE37_9BACL Uncharacterized protein OS=Planococcus sp. PAMC 21323 GN=Plano_2062 PE=4 SV=1MNKSFQKVRNLTPAQAIVSYYFVAIAVSFLLLRLPNVHKPGMTIPLIDSLFTAVSAVSVTGLTVINVVDTYTVFGIIVLMIVLQLGGIGIMSIGTFIWLLFGKRIGLRERQLIMVDHNQSSMSGVVKLIREIVKIMLLIEAVGAVILTIYFTQYFPTFQEALLHGVFGSITATTNGGFDITGESLMPYFNDYFVQIINMILIILGAIGFPVLIEVKEFISNKQKYFRFSLFTKITTTIFAVLLAVGAIGIFLLESVKAFKGMTWHESMFASIFHSVSSRSGGLVTVDITQFSDATNAFMSALMFVGASPSSAGGGIRTTTFAIAILFLINFARGKNTIQIFNRREIELIDVFRSFAVIFLAFFIVFASTLALLITEPTATIVEIIFEITSAFGTCGMSLGITSDLSEIGKFIIMALMFVGRVGLISFLFTIGGKTDPTKFHYPKERVIIG
2E-60	214	41.7	4E-60	213.1	28.9	1.4	1	A0A0F0CXB4_9BACT	Potassium uptake protein, TrkH family	OMAG_000033	Candidatus Omnitrophus sp. SKK-01	449	cellular organisms, Bacteria, unclassified Bacteria, Omnitrophica, Candidatus Omnitrophus, Candidatus Omnitrophus sp. SKK-01	1609969	>tr|A0A0F0CXB4|A0A0F0CXB4_9BACT Potassium uptake protein, TrkH family OS=Candidatus Omnitrophus sp. SKK-01 GN=OMAG_000033 PE=4 SV=1MKFILTPPRLVVFSFLAAIIVGTVCLSLPIATPKEVSISFIDRLFTVTSAVCVTGLSVNDFSTTFTGFGKAVILILIQIGGLGIMTLSTLFALVIGKKIGFYGDEVIRRTLNEQDIISVRKLIFFILIITFFIEGIGAMLLYFRWTAITDWSVFAVVWQSVFHSVSAFCNSGFALFSNNLESYRADWIVNLIIMGLIIFGGIGFVVIMDIIGLLSWRKTRKKLSLQSKTALIMSLILIIAGAACLFIFEFNNVFKGRPVSEGVLCSFFQSVSSRTAGFNTIPIGNLTSPSLMVLIILMFIGASPASTGGGIKTTTFAIVILSVIWSTIRGRDEVTIFSRSISQKSVREAVIIFFLYLAWVIVFSIILSFIHFMIHGEDAPFLKLMFEVVSAIGTVGLSAGITPGLDALSKLCIIITMFIGRIGPLTLVMAIAFKNQKENYVFPEENVMIG
2.1E-60	214	22.1	3E-60	213.5	15.3	1.1	1	A3UAH0_CROAH	Putative potassium uptake protein	CA2559_12238	Croceibacter atlanticus (strain ATCC BAA-628 / HTCC2559 / KCTC 12090)	498	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Croceibacter, Croceibacter atlanticus, Croceibacter atlanticus (strain ATCC BAA-628 / HTCC2559 / KCTC 12090)	216432	>tr|A3UAH0|A3UAH0_CROAH Putative potassium uptake protein OS=Croceibacter atlanticus (strain ATCC BAA-628 / HTCC2559 / KCTC 12090) GN=CA2559_12238 PE=4 SV=1MPRLNFKIILYIMGLLLLCNGGFMLLSVIVSWYYNDGVTLELFSSSLLTLIIGTLLMFTTRNHSKRIDKREGYIIVTFGWIFMALSGMIPYLLSEAIPGFTNAFFETMSGYTTTGSTVLSDIEIVPKGVLFWRSLTHWIGGMGIIVLAIAILPLLGIGGMQLFAAEAPGPSADKLKPRITDTAKRLWLIYVGFTFSETILLKVAGMGWFDAVNHSLSTLSTGGFSTKNASLAYWNDTPIIQYIVIVFMFLAGMNFVMSYFALKGKFSRLLQDDELRWYFVFITGFTIIASVLVYLFADVSISSIAHPMVVWGEAESSFRHSLFQVLAIITTTGFVTADYTLWTPFLTIFFFGMFFLGGSAGSTSGGVKVVRHLILIRNGITEFKRTLHPNAILPVRYRQKAIPKEIVFNILGFFILYMLAFIIGAIGLAALGLDFETAIGGAATSIGNIGPAFGDLGPVNNFNGLPNFGKWWCSFLMLIGRLELFTVLIILTPFFWRNR
2.2E-60	214	31.9	2.8E-60	213.6	22.1	1.1	1	Q2FZP1_STAA8	Putative uncharacterized protein	SAOUHSC_00959	Staphylococcus aureus (strain NCTC 8325)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus aureus, Staphylococcus aureus subsp. aureus, Staphylococcus aureus (strain NCTC 8325)	93061	>tr|Q2FZP1|Q2FZP1_STAA8 Putative uncharacterized protein OS=Staphylococcus aureus (strain NCTC 8325) GN=SAOUHSC_00959 PE=4 SV=1MSIFSQFLKRSSPQQGIVLYYIVAIVIAFLLLNLPYVHKPGVEVNPIDTLFVAVSGISVTGLSPISIVDTYSTFGQLIILVILNIGGIGVMAIGTMLWVVLGKHIGIRERQLIMLDNNKNTMSGTVKLIIDIVKSIFVIELVGAMLLAFYFYRDNPDLKYAIMQGVFVSISATTNGGLDITGKSLIPYAHDYFVQAIVIFLIILGSIGFPVLLEVKAYIQNRVTNFRFSLFTKITTSTYLFLFIVGVLAILLFEHNHAFKGLSWHQSLFYSLFQSATTRSAGLQTIDVTTLSDPTNIIMGILMFIGSSPSSVGGGIRTTTFAILILFLINFSNNADKTSIKVYNREVHIMDIQRSFAVFTMATILTLFGMLIISATENGKLTFLQVFFEVMSAFGTCGLSLGVTSDISDISKVVLMILMFIGRVGLISFIIMIAGRREPDKFHYPKERIQIG
2.3E-60	214	23.3	3.3E-60	213.4	16.1	1.1	1	A0A0D5NLI5_9BACL	ATP synthase subunit J	VN24_16075	Paenibacillus beijingensis	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus beijingensis	1126833	>tr|A0A0D5NLI5|A0A0D5NLI5_9BACL ATP synthase subunit J OS=Paenibacillus beijingensis GN=VN24_16075 PE=4 SV=1MKELRKRGIWDWSPPRVLSAGFVMIILLGGLLSLPYASADGEGTNLLDAIFTATSATCVTGLVVVDTGTHYSVAGQIVIMLLIQTGGLGFMTMTTLFALVIRKRISYKERLILQEAMNQQSMEGIVRLIRKVIFYSLSIELTGALLYAIRFAADMPLGRAAYLGLFHGISMFNNAGFDLFGDFRSLTGYVNDPAVNIITMLLIVLGGLGFVVLSDLLHFRGIRKLSLHSKVVLSMTGVLIVTGAAVIFLFESNARTLGSLGPGGKVLAAFFQSVTTRTAGANTVDIGALRQGTVFFMIILMFIGASPGSTGGGIKTTTFMTLIGAAIAMMRGREDVVLFRYRLERGRIYKALTLTILSLGLVIAVTMILCTTEDRDFLRILFETTSAFGTVGLSTGITSTLTPVGKIMICLTMFAGRLGPMTLAYALGPKAEKELYRHPEGKIIIG
2.3E-60	214	25.8	3.1E-60	213.5	17.9	1	1	K9WLY5_9CYAN	Potassium uptake protein, TrkH family	Mic7113_5160	Microcoleus sp. PCC 7113	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	1173027	>tr|K9WLY5|K9WLY5_9CYAN Potassium uptake protein, TrkH family OS=Microcoleus sp. PCC 7113 GN=Mic7113_5160 PE=4 SV=1MTISRTICLGFLAVITVGTFLLMLPISTSAGTWNDPLVALFTTTSAVCVTGHIVVDTGTYFSFWGQLFILILIQMGGLGYMTTTTFLILLVGYRFELRHKRAIQEELSRPGLQDSAQLIRSIIATIIIFEITGIFLLLPVFAPKYGLDYGLWLSIFHSVSAWNNAGFSLFSDNLIGYKSSVTVNLVITSLIIFGGIGYQVIIETYLGVRDRFRKEPKRINFSLNFKVVTSTTLILLIVGTIAIFLTELNNPQTLGSLNFKDQLLAAWFQSVVPRTAGFNSVDYSKMTTAALFLTIGLMFIGGSPGGTAGGIKTTTLRVLTSCTRSILQGKEEVHLYERQVAINLVLKAVGVLLGSATTVIISTMLITLTDPNVEFIRILFEVVSGFCTVGLSTGITAGLSAGAKLVLIATMYIGRVGVLLLMTALLGDPRPSRIQYPEENLLVG
2.6E-60	214	32.2	4E-60	213.1	22.3	1.2	1	W0GS18_9MOLU	TrkH family potassium uptake protein,transmembrane component (Uncharacterized protein)	P344_06360 SMM_1068	Spiroplasma mirum ATCC 29335	534	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma mirum, Spiroplasma mirum ATCC 29335	838561	>tr|W0GS18|W0GS18_9MOLU TrkH family potassium uptake protein,transmembrane component OS=Spiroplasma mirum ATCC 29335 GN=P344_06360 PE=4 SV=1MRVYQPFFKNIFKKRKELLNQRNEDDIAAPIKKRRIHFIPFSKVAGKLFLIYVLVVLISGFLLCIPGVVYNGARDITNGSGTPLGQYDFRWNFLIGLFTASSAFSDTGLTIPVTAADYTFFGQLIIIILIQFGGFGVLTFKIMILVLLGRKISIKDRMLVQGERGNNSFGHTLDLIKSSFYFLIIVEVIAVILLFFNFYFSPGSTTGKFMIDNVTYHRFWASLWSGVFHSISAINNAGFDIVGNSSLMPYNTNYFLQFIFMIEFVMGGIGFPTFYDIKRKIAAWKRKEKVKFSLFTKINFISYSLVSIVGVFLVWLVEYVNLNMTTMDAFGNTVVYIETILRDAPTKWNGFMNILFNTMSTRNAGFSTIDCTKLLPGSRAIMSIMMFIGSAPSSTAGGIRTTTFAIVLITIWSIMRNNNSVNAFKRKIPNETVKRALVVTIISVMLVGGTVLGISIENPTLDYLNILFVVCSAFGTTGLNAFNFLQTYGLGAFSLLLLIANMFIGQLGISSTLLVSIKGTGDKEYSYVEEDVTIG
2.6E-60	214	17.7	2.5E-58	207.2	12.2	2.1	1	R5AQI1_9FIRM	Uncharacterized protein	BN455_00922	Firmicutes bacterium CAG:103	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:103	1262999	>tr|R5AQI1|R5AQI1_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:103 GN=BN455_00922 PE=4 SV=1MNFRMIGQVVGRVLCIEAALMLLPMIAAVIYDESPVPFLITIGITGGVGLMMWRVRAKSGSITARDGFLIVGLSWIAMSLLGAIPFVLTGDIPNYIDALFETISGLTTTGASVVTSPESMTRGGMFWRLFTHWIGGMGILVFVLAVLPMSGNRSMHIMRAEVPGPTVGKLVPRIRKTASILYLLYIALTLVETVLLIAGGMSFYDALLHSFATAGTGGLSTRALSIGYYNSAYIDIVVGVFMILFGANFSLYYLILLGNIRTALRNEELRWFLGVIAFSVITIAVDIRNLYGGVGHALRYSFFQVTSIISTTGFATADFNLWPEYSKFLLVLLMFVGGCAGSTAGGLKVSRVMLLFKSCTIEVKKMLRPRCVENVRLDGKPVDAQTVYNALTYFTFYIIIMLIAGLIVSLDGLDFTTNFTAALSCLSNVGPGLSLVGPTGSFAIFSPLSKIVLMICMLLGRLEIFPLLLLFVPFTWRWK

2.7E-60	214	23.9	2E-59	210.8	16.6	1.9	1	F2K003_MARM1	Trk system potassium uptake protein	Marme_2893	Marinomonas mediterranea (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1)	472	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Marinomonas, Marinomonas mediterranea, Marinomonas mediterranea (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1)	717774	>tr|F2K003|F2K003_MARM1 Trk system potassium uptake protein OS=Marinomonas mediterranea (strain ATCC 700492 / JCM 21426 / NBRC 103028 / MMB-1) GN=Marme_2893 PE=3 SV=1MPLLWMGIVQLSFAELSYFFFKDNVGDAFFESAAVVTLLATFFLLYMRRFPFNAVSTKEAILFAVLTWFTVGFLGAVPIFIITGVS WTDAVFESISALTTTGATVLSGLDYMPKTFLLYRQFLQWMGGLGVVIFVVAVLPMLNVGGMKLLKAETPGPMKDDKLSPRIKNSADR LWYVYLALTLICALAYWLGGMSAYDAIAHSLATISTGGFSTHDSSMGYFDSSLLLWLCNFFMIAGAISFALHYRVFKAKRFKQYIKDEE CLFFLWIILAFSLVAAGVLYFSGYHHSVYEAISQATFHVISFITSTGFGAGDFSSWPMSLMLLLIVVGYIGGCAGSTAGGNKVIRSVIAFR TLVIELKQMVHPNAVFVLKYQKRPVADQIRNSIIAFMWLVFVTSIIFTFLVMLTGEDFVTSFSAVSACVNVLGPGFGDISSNFAPLNSFA KWLLSFAMVFGRLEYFTVIVLLTPYLWRS
3.1E-60	214	23.7	3.8E-60	213.2	16.4	1.1	1	T0UF01_9STRE	Potassium uptake protein, integral membrane component, KtrB	HSISB1_1781	Streptococcus sp. HSISB1	404	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus sp. HSISB1	1316409	>tr|T0UF01|T0UF01_9STRE Potassium uptake protein, integral membrane component, KtrB OS=Streptococcus sp. HSISB1 GN=HSISB1_1781 PE=4 SV=1MVCVTGLSVFPVADVYNGLGQVISVILMQIGGLGLVTLIAVSTYLLRRRMNLSSQNILQSALSYDNSGHLKRYLFNVYKITFIIESLI AILFLIDFIPRFGMSHGIFNAIFLAVSAFCNAGFDNLGGDSLKPFVLNPLLNLLFMILIVSGGIGFAVWVDIKRAIKAFLTDRPYRLKTFTRK LSNQTRLVLNTTAVILILGTAITWLLEANNPKTIGLYNPFQQFMVSLFQTVTMRTAGFATISYLDTHTATNILYMIQMIIGGAPGGTAGGIK VTTVAITFLLFKSELAGQSEVTYRHRIIANKVIKQTLTVLIFFFSILIVGYILLLQFEPHHDPIALLFEAVSAIATVGVSMDLTPQLSTSGRLVI MALMFIGRVGPLTVLLSLLQKKEKEIQYAQTNITVG
3.1E-60	214	33.8	5E-60	212.8	23.5	1.2	1	K9YMF0_CYASC	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cyast_1303	Cyanobacterium stanieri (strain ATCC 29140 / PCC 7202)	443	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobacterium, Cyanobacterium stanieri, Cyanobacterium stanieri (strain ATCC 29140 / PCC 7202)	292563	>tr|K9YMF0|K9YMF0_CYASC Potassium uptake protein, TrkH family OS=Cyanobacterium stanieri (strain ATCC 29140 / PCC 7202) GN=Cyast_1303 PE=4 SV=1MTIARTICLGFLAVIAVGTLLLSLPFSSVEPGWSSFTTALFTSTSAVCVTGLIVVDTGSYYTFWGQLFILCLIQVGGLGYMTTTTFLI LLIGRKFDFREKLAIKESFDRPFLHGSKNLLKSVFATTIALETLGSIVLFFIFQQDYGNRESLWLAVFHSISAWNNAGFSLFADSLTGYQT SIPLNTIICFLIVFGGIGYQVIIEFYLWLKEKLDTSSKREYRFSLNFKVVTSTTIFLLIFGTVAFFVTEYNNLLAEYSLNQKILLAWFQSVTTR TAGFNSVDLGAMTIASLFLTIGFMFVGGSPSGTAGGIKTTTLRILYESTKAVLQGKQEVITYEREVPPSLILKAMAVVFGSTITVLVVTFSI SFLHSNFNFINIFFEVVSAFATVGLSTGITSDLSQLAQLLIILTMYLGRVGVLLFMSAILGDPRPTRIHYPEENLLIG
3.4E-60	213	21.7	2.1E-58	207.4	15	2	1	R7JRM7_9FIRM	Trk-type K+ transport systems membrane components	BN630_01604	Blautia sp. CAG:37	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:37	1262757	>tr|R7JRM7|R7JRM7_9FIRM Trk-type K+ transport systems membrane components OS=Blautia sp. CAG:37 GN=BN630_01604 PE=4 SV=1MWSIKLRYRKQWSSFEIIILGFAGVILAGALLLMLPVASREGNVTPFTETLFTATSAVCVTGLAVRDTGSYWSVFGQSVILLLIQIG GLGVVTIAVSIAMLSGRKISLMQRSTMQDAISAPKVGGIVRLTRFILKGTFGIELLGALFLLPVFLRDYGGKGIWMALFHSVSAFCNAGF DLLGKTDHLYPSLTSYVGNPLVNLTIMGLIVTGGIGFLTWDDIYTKKYHFRQYCMQSKVILLTSLFLIFVPAAFFFRDFAGMPVKERTL CALFQSVTTRTAGFNTADLSGMTGASQAIMIVLMMIGGAPGSTAGGMKITTFAVLTANASATFRQREDTQMFGRRVGQEVLKNASTI LMMYLFLVLMGGMVISVAENLPISECLFETASAVGTVGLTLGITPRLGVLSKGILIALMFLGRVGGLTLVYAAMPGRKSAHAKMPLEKIN VG
3.4E-60	213	18.8	7.7E-60	212.2	13	1.5	1	A0A068JHG5_9DELT	Trk system potassium uptake protein	GY33_03565	Desulfonatronum thiodismutans	483	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfonatronumaceae, Desulfonatronum, Desulfonatronum thiodismutans	159290	>tr|A0A068JHG5|A0A068JHG5_9DELT Trk system potassium uptake protein OS=Desulfonatronum thiodismutans GN=GY33_03565 PE=3 SV=1MHWRGIFSYTGAIIAAVGLLMIPALACSLYYGDAGVTPLLFSMVSVSLGGGALYLVWRKHAPEIVTSREAMAVVALCWVSAGLV GALPFYLGGMFDTFADAFFESVSGFTTTGSSVLTDIEAVAPGLLFWRSMTQWIGGMGIIVLSVAVLPILGVGGMHLYRAEFSGGRQD RIKPRVRAAALSLWKVYLLFSTVLVVLLLGGMNLFDALCHMFATIATGGYSTKNLSMGHYQSVYLQLVVTVFMFLGAINFALHYQALR GRPLALWRNSEVRFFTLLVLGTVTVIALTLWANRSYETLGEAFLYSAFNLVSIITTTGYATADFALWPPLAVAVLFLTMFIGGCAGSTAG GVKCMRLLLAAKHMYREGFRVIHPQAVVQVKMSGKPVEESVISGVWGFLGLFAALYLVLSLMLAAMGLDLITAFSAAIAAMGNIGPGF GGVGPAQNFAHLPAAAKWLLAWGMLLGRLELYAVIIFLLPAFWKA
3.4E-60	213	11.1	4.2E-60	213.1	6.6	1.8	1	C4KDD3_THASP	Trk system potassium uptake protein	Tmz1t_3505	Thauera sp. (strain MZ1T)	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Thauera, Thauera sp. (strain MZ1T)	85643	>tr|C4KDD3|C4KDD3_THASP Trk system potassium uptake protein OS=Thauera sp. (strain MZ1T) GN=Tmz1t_3505 PE=3 SV=1MQAYFPVLGVLGMMLMLFGLVMGFPLAVSFALEDGATEAYDLAILATFATGLLMWAAGRRARRDLHVSDGFLLVAATWLITPVF GALPLLFYLPELSFTDAYFEAASGLTTTGATVLTGLDTMPVSINLWRCFMHWVGGMGVIVLMVAVLPLLGIGGRQIFRAETPGPMKES SLTPRIAETAKGLWGVYVVLTAGCTLALLQAGMAPWDALIHAFSIMGLGGFSTRDASLGAFDSVPIETVTIVFALLSGINYATHYLALVR RTPRPYGEDPELRWFFGVLGVTVVFLTVYLLESGAYRDGALAFRHVSFHAVSLATSLGLATYDYTVWPMFAQVWILFLSSFAACSGS TGGGIKMMRAIILYKQVHREIVRSLHPSAVVPLRLGRQPVSDNVLHAVLAFSFMYMVSIVSLTLILAASGLDLITAFSGVVACINNAGPGL AALGPAGNYQGLGDFQTWVMSFAMILGRLEIFTLLVVLTPAFWRR
4.4E-60	213	36.5	2.2E-59	210.7	25.3	1.8	1	E4RKH7_HALHG	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Halsa_1258	Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	440	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	656519	>tr|E4RKH7|E4RKH7_HALHG Potassium uptake protein, TrkH family OS=Halanaerobium hydrogeniformans GN=Halsa_1258 PE=4 SV=1MKLTKKKFSPAQYLVIGYFVVILLGSIMLMLPIATIDGQGLNIIDAVFTATSATCVTGLIVVNTKETFTLFGSTVIMMMIQIGGLGIMS MSTLFAFIIGKKISLKERLIIQEDLNQYKISGMVRLVQYLLGFTFAIEGIGASILFLRLSQDHDFLRAVYLSIFHAVSAFNNAGFDLFGNSLE SFTGDITINFVIMALIILGGIGFGVMLEVYNRVKFKKATLQTKIVLVVTAALLIFGFVVFFALEYNNTMEGLPFLDKVLSAMFLSVTPRTAG FNTLPTGALRQSSLFLIIVLMFIGASPGSTGGGIKTTTFGVMLVTLKNMVSGKSDMEVYNRRFETQIIYKAFTITMLAAALVILMTTLILIIE DFQFIDVLFETVSAFGTVGLSTGITGSLSNISRVLITITMFAGRVGPLTLAVAFGDKVRKGIYHYPTEKVMVG

4.4E-60	213	22.1	3.9E-58	206.5	15.3	2.1	1	L0F8C0_DESDL	Trk-type K+ transport system, membrane component	Desdi_1997	Desulfitobacterium dichloroeliminans (strain LMG P-21439 / DCA1)	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium dichloroeliminans, Desulfitobacterium dichloroeliminans (strain LMG P-21439 / DCA1)	871963	>tr|L0F8C0|L0F8C0_DESDL Trk-type K+ transport system, membrane component OS=Desulfitobacterium dichloroeliminans (strain LMG P-21439 / DCA1) GN=Desdi_1997 PE=4 SV=1MNYSLVQGILGRLLIGYSLTMLVPLILAFFSKESSQWALLLSLVITACIGLLMYRFRESTDGKMGIRESFVIVAGAWFLTSFLGALP FWISGSVPTYIDALFESVSGLTTTGSSVINDVEILPSSILLWRSITHWLGGMGIIVLFIILLPKTGFGAVHLFNAEVPGPLSKRTMPRIRDT AITLWRIYTFFTLVLIGLLLAAGLDLFDAVNHAFSTVSAGGFSTKNTSIMHYNNLAVESIIIVFVIIAGGNYRLYLEAWTKKSLKPFRNTEFI TYLIIIIVSTLLIMGGLWLTHDKTPDYALRHALFQVVSMVTGTGFVSTDYDLWPAITKLILFVLMFIGGCAGSTTGGMKIARIMLLAKHTW SMLTRGLHPQAVSSIKLDGKPINAAAVNMVSLFFFLYVGIFAIATILIAGTGLEPMDAMSSVAASLGNVGPGFGIVGPTTTFASITLFGKS VLILCMLLGRLELFTLLILLRPEFWKTKSRW
4.6E-60	213	12.2	2.5E-58	207.2	8.5	2.1	1	A0A052IQK8_9BORD	Trk system potassium uptake protein	L539_0284	Bordetella hinzii 5132	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella hinzii, Bordetella hinzii 5132	1331257	>tr|A0A052IQK8|A0A052IQK8_9BORD Trk system potassium uptake protein OS=Bordetella hinzii 5132 GN=L539_0284 PE=3 SV=1MKRLLATFYVLGLTMVVFALTMLIPLGVAWLGEDDGLRAFAEGFGIAMGIGAGVWLLTHRWRSELHARDGFLLVSIVWAGLPLL AAIPLLLYYSQAGQPLSFTHAYFEAMSGLTTTGATVLTGLDHLPPSINLWRATLIWIGGMGILVLAVAILPLLGVGGHQVVRAETPQPM KDERLTPRIASTAKALYAVYFGFSILCFLAYRAVGLSWFDAWAHMATTMGLGGFSTYDEGFLKFDSVPVEIVAIVFMLISGINFATHFN ALRQRSFRPYLSCPQTIPYLAVVLGTGLVISVYLFLKHVYTDPLQALRYGMFNTISVATTTGYANTDYAAWPLFAPLTMLLLSAFATSA GSTGGGIKMIRVMLLIKQARNELITMLHPHAVSPVRIGSRIVDQRVMFSVLAFMLVYGLSVGVLSSLLLLSGLDLTTAFSAVMAMINNTG PGLGVLGPMGHYGVLTDFQVWVCTFAMLIGRLELLTVLVLFTPWFWRK
4.7E-60	213	19.6	6.5E-60	212.4	13.6	1.1	1	B1VDX0_CORU7	Potassium uptake protein, TrkH family	cu1058	Corynebacterium urealyticum (strain ATCC 43042 / DSM 7109)	453	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium urealyticum, Corynebacterium urealyticum (strain ATCC 43042 / DSM 7109)	504474	>tr|B1VDX0|B1VDX0_CORU7 Potassium uptake protein, TrkH family OS=Corynebacterium urealyticum (strain ATCC 43042 / DSM 7109) GN=cu1058 PE=4 SV=1MNRLSASLTQNPARLVSVGFLSLIVLGTFLLLMPFSAPDGNSVSPLEAFFTATSAVTLTGLGVRDTGTGFTAAGQVVILALIQIGG FGIMSLTSLAGLILSGRLGLKTKLYTVAERRTLTVGSVKSTIIGAIVLTVICELLVAGVLAIRMFTGGYVDSLGSAAWMGIFHAVSAFNNA GFGLNAGSLIPYVGDAWIVLPIGLAIVFGGLGFPVLDELIARVRLRRQRRKPPRLSMTARITLDGTAVLLIGGFVMFWVLERNHAFAELS SWDAALAAVFQSITTRTAGFQSVDFGEMSPNTLMGTDILMFIGGGSGGTAGGLKITTFFVVLAAIVAEIKGDKDTVVGGRRVDHTVIR QALTVGAVAVGVITFVIACLRTFNSQFSADQIHFEVISAFATVGLSTGITADLSGASQILLCVLMFMGRVGPITLVAALATTTPSKHYSYP AERPYIG
5E-60	213	21.1	3.8E-57	203.3	14.6	2.1	1	R5PWD2_9FIRM	Uncharacterized protein	BN766_00001	Ruminococcus sp. CAG:724	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:724	1262966	>tr|R5PWD2|R5PWD2_9FIRM Uncharacterized protein OS=Ruminococcus sp. CAG:724 GN=BN766_00001 PE=4 SV=1MNYKSVYNIVCRMLAVEAVLLLIPAGVSLAYGEMRSFFCFLITAGITAVLSIPAIIIFRKGDRHALYAKEGLVTVSLAWILWSALGAL PFVLEGCIPNYIDALFETVSGFTTTGASILKNIEALPKGMLFWRSFTHWIGGMGVLVFVMTIVPLSDDHSMLLMRAEMPGPTVGKLVPK GKSTAKILYLIYICMTLAEIVFLLFGGMSVFDAFIHAFGTAGTGGFSSYNASIAHFNSIYIEMVIAVFMLLFGINFNIYFFILIRKIKGVLRNDE WKVYLSIIAVATGIIAVATLGIYGAFGTSLRYAFFQVVSFITSTGYVSTSFVAWPAVCRSILLMLMVIGACAGSTGGGLKVSRAIILFRGL KKELHQMELHPKAVSHVKMDGAIVDEKAVKSAAIYFFALFAIIGVSAFAISTDNLSLETNLSAVLSCTGNTGPGYGAASSNFACFSWFSKI ILSLDMLFGRLEIFPLLIALTPGVWKKKFF
5E-60	213	21.8	1.2E-59	211.6	15.1	1.5	1	X2HGJ9_9NEIS	Trk system potassium uptake protein	SALWKB2_1279	Snodgrassella alvi wkB2	501	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Snodgrassella, Snodgrassella alvi, Snodgrassella alvi wkB2	1196094	>tr|X2HGJ9|X2HGJ9_9NEIS Trk system potassium uptake protein OS=Snodgrassella alvi wkB2 GN=SALWKB2_1279 PE=3 SV=1MSHFTNRFVLHHKESGFLNKIAPTAHIVAKTGFLFSLLLLAPTIVSLIYMDHVFPAFAFTAGICMSVCVVAWLLTMRYNRELRPRD GYTLVFMLWIGFALIACLPFYIYLPGLGFTNAYFEAISGLTTTGATIITSLDSLAPSLNFWRHMLNWLGGMGIIVLAVAVMPMLGVGGTQ LFKAEIPGVNKDSKMAPRISETAKRLWGVYVLFTIVALLALRLAGMSWFDAVCHAMSAFSLGGFSTHDNSISYFHSVPIEIILSIATLLGA INFSNHFNALQKGSLRYYWRDEEVRVLLCVLLFSIVGISLYLVWWHSFYSFSEAFRYTSFNLISIGLANGYSNTDFAKWPLIASLWMFFL SNILSNGGSAGGGIKTVRAIVLFKFSLREMLLMLHPNAVSMVKINGSNIPDRRALTVMAFVFVYVLTIILFSFALMISGLDFLSALTAAISCI TNAGPGLGAVGPANNFAFLSDIQKWLCIMIMLLGRLEIFTVFILFTPAYWKK
5E-60	213	21.8	1.2E-59	211.6	15.1	1.5	1	X2HGJ9_9NEIS	Trk system potassium uptake protein	SALWKB2_1279	Snodgrassella alvi wkB2	501	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Snodgrassella, Snodgrassella alvi, Snodgrassella alvi wkB2	1196094	>tr|X2HGJ9|X2HGJ9_9NEIS Trk system potassium uptake protein OS=Snodgrassella alvi wkB2 GN=SALWKB2_1279 PE=3 SV=1MSHFTNRFVLHHKESGFLNKIAPTAHIVAKTGFLFSLLLLAPTIVSLIYMDHVFPAFAFTAGICMSVCVVAWLLTMRYNRELRPRD GYTLVFMLWIGFALIACLPFYIYLPGLGFTNAYFEAISGLTTTGATIITSLDSLAPSLNFWRHMLNWLGGMGIIVLAVAVMPMLGVGGTQ LFKAEIPGVNKDSKMAPRISETAKRLWGVYVLFTIVALLALRLAGMSWFDAVCHAMSAFSLGGFSTHDNSISYFHSVPIEIILSIATLLGA INFSNHFNALQKGSLRYYWRDEEVRVLLCVLLFSIVGISLYLVWWHSFYSFSEAFRYTSFNLISIGLANGYSNTDFAKWPLIASLWMFFL SNILSNGGSAGGGIKTVRAIVLFKFSLREMLLMLHPNAVSMVKINGSNIPDRRALTVMAFVFVYVLTIILFSFALMISGLDFLSALTAAISCI TNAGPGLGAVGPANNFAFLSDIQKWLCIMIMLLGRLEIFTVFILFTPAYWKK
5.1E-60	213	19.6	2.8E-58	207	13.6	2	1	R5JRZ8_9BACE	TrkH family potassium uptake protein	BN523_03503	Bacteroides sp. CAG:189	478	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:189	1262737	>tr|R5JRZ8|R5JRZ8_9BACE TrkH family potassium uptake protein OS=Bacteroides sp. CAG:189 GN=BN523_03503 PE=4 SV=1MIYRITGFLLLIETAMLLCCGGVSLLYHEDDLISFLQSASLTALMGVVLLFIGRGAEKQLGRRDGYVIVTVAWLAFSLFGMLPFYLS GYIPSITNAFFETMSGFSSTGATILNDIEKLPHGLLFWRSMTQWIGGLGIVFFTIAVLPIFGVGGIQVFAAEASGPTHDKVHPRIGITAKW IWGIYAGLTGTLIILLMFGGMNIFDSICHAFATTSTGGFSTKQASIEYYHSPYIEYVISIFMFISGINFTLLLLFVNGKLKKFVHDAELKWYF WSVTGFTIGIAAILYYNSSMGVEEAFRKSLFQVASLHTSTGFATADYMTWPAITWGMLTVIMIMGACAGSTTGGIKSIRLVILAKVSRN EFKHIIHPNAVLPVRVNKQVISPSIRSTVLAFTFLYTVLIAGTLAMLGLGVGLTESLGCTISSLGNMGPGLGLCGPAYSWNELPDAAKW LMSFFMLLGRLELFTVLLLFSSDFWKKN
5.3E-60	213	29.8	2.5E-30	114.8	7.5	2.2	2	B9L7Q4_NAUPA	Trk system potassium uptake protein	NAMH_0238	Nautilia profundicola (strain ATCC BAA-1463 / DSM 18972 / AmH)	484	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Nautiliales, Nautiliaceae, Nautilia, Nautilia profundicola, Nautilia profundicola (strain ATCC BAA-1463 / DSM 18972 / AmH)	598659	>tr|B9L7Q4|B9L7Q4_NAUPA Trk system potassium uptake protein OS=Nautilia profundicola (strain ATCC BAA-1463 / DSM 18972 / AmH) GN=NAMH_0238 PE=3 SV=1MDRSTVKNILKFLSLVGLMTEFFFLIPIITGVIYKENVTSFIIYSAVATTIFFLILFWLKNHDMKMKIKDAILSVNLVWIMLGVLGAIPL MLETNVTFIDGFFEAASGFTTTGATIYSDITDLPKNILMLRSTMHWIGGMGIIVLGVGLLSLINPTGSLALFKGESTGITPDKVTPKIKHTA LKLWGVYFTITVIDAIMLKFEGMSIFDAINHAFATISTGGFSTRSESLGFWSNNPWILWTTTLFMFISGINFIAHIKFLKKDYSGYKSEEVI WYTLIFIILAIGVSLVHYINSNDSLFYALTHGFFTISSILTTTGFATVDYSQWGQTAIALIFIAMLVGGNAGSTAGGIKVIRFVVMFKNLNYQ IKKILFPNAIISVKVDKKTIPQPIINNVSAFIFLYILTVTSIALYLFANGYDTLTSLSASIACVGNIGPGFGHVGPVDNFAFFTQPQKLILAIGMI IGRLEFFTVLILLSRDFWKKF
5.4E-60	213	18.9	1.1E-57	205.1	13.1	2	1	R6G5I6_9FIRM	Uncharacterized protein	BN690_01021	Blautia sp. CAG:52	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:52	1262758	>tr|R6G5I6|R6G5I6_9FIRM Uncharacterized protein OS=Blautia sp. CAG:52 GN=BN690_01021 PE=4 SV=1MNYRIITYVIGWVLNLEAICMTLPAVTGLIYGEKTWTSFLITGLISALAGTLLVVRRPEKPHFFMKEGCVSVALSWIALSLIGSLPFM ISGTIPHFVDALFETVSGFTTTGASIMASVEDAPRCILMWRSFTHWIGGMGVLVLLLSIIKMSGGSQMNLMKAESPGPSVSRLAPTVRS TAKILYTIYLLMTVLETVILLLCGMPIFDALTTAFGTAGTGGFGIKNDSMGGYSVTIQIVVTVFMILFGINFNVYFLLLSKKWKQALKNEEV RWYLAIILGAVLLIGWNIRGVYGSMGKAIQQAAFQVASIITTTGFATVDFNIWPEVSRTILVLLMFVGACAGSTGGGIKVSRFIILLKAMK KEIKQYLHPRQIRKIRMDGRVVEHEVVRNVNVFMVVYIMIFATSVFILAFDNLDLITNFTAVAATFNNIGPGLELVGPTANFNVFSDVGKY VLIFDMLAGRLEIFPLLLVFFPDTWRKF
5.6E-60	213	31.8	4.1E-59	209.8	22	1.9	1	B1MWC0_LEUCK	Trk-type K+ transport system, membrane component	LCK_01662	Leuconostoc citreum (strain KM20)	467	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Leuconostocaceae, Leuconostoc, Leuconostoc citreum, Leuconostoc citreum (strain KM20)	349519	>tr|B1MWC0|B1MWC0_LEUCK Trk-type K+ transport system, membrane component OS=Leuconostoc citreum (strain KM20) GN=LCK_01662 PE=4 SV=1MSRKIELPSAAEMKKFHNQSRKHTFWTHISMPQRLTLGFLSVITIGALLLMMPISHYGNMHHSFMDALFTATSAASVTGLTVVDT ATHWTVFGQTVIMFLIEVGALGFMSFSVLLFTATRRQMDLRNKMMVQEVYSLESLYDTRVVFGYVIKLSVIIQFVGAILLAPFFIQDFGL KRGLFYAIFHAISAFGNAGFTILPAGSIAYANRPFVLLIIALLIAGSLGFLVWRDLLLYHHKHKLSLHSKLALMMTGLLIIGGWLLFELTES NLALAQTLSPINRIVNTLFMSISYRTAGFSQFSFSQMTPATILLTMMLMYVGGTPGSTAGGIKTTTLGVLLLKTHAALRGKKDVTFAHRR LTDENITRSLLLVFVSLVFLAILSFLLMLTQGNDSRFGLEYVIFEVISAFATAGLTLGLTPHLTDFGQCVIMLTMFIGRVGVYTVMFSVLNV HGEHAPYRYPEESVIIG

5.7E-60	213	22.1	9.1E-58	205.3	15.3	2	1	R5QSL2_9FIRM	Cation transporter	BN526_01749	Firmicutes bacterium CAG:194	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:194	1263008	>tr|R5QSL2|R5QSL2_9FIRM Cation transporter OS=Firmicutes bacterium CAG:194 GN=BN526_01749 PE=4 SV=1MNYAVIRRILGLILLFESAFLLLPCMVAVIYREKQGLSYLAVAFICLVIGFLLTRRKTENQMFYAKEGFVIVALSWIVMSFFGAMPYYLSGDIPDVSQALFEAVSGFTTTGASTLSSVEVLSHCTLVWRAFTIWIGGGMGVIVFLLAVLPLTGGYNMHLMRAESPGPSVGKLVPKVRETAKILYLIYISLTVIEIVLYILAGMPVFDAVTTGFSTAGTGGFGIRNDSMGSYSTVLQILITIFMILFGVNFNFYYFLLGKEKKEAFKMEEVRWYFTIIVVAALLIAVDIRGMFDNIGIALQQAFFQVGSIITTTGFSTIDFNLWPQGSKTILVLLTFLGACAGSTGGGIKVSRLMILVKSIRQEIAYFIHPRSVKVIKMDQKAIDKSTVRGVHAFFATYMMIIVVSVFLISFDGLDLVTNFTAVATAFNNVGPGLELVGPAGNFGCFSDFSHYVLMFDMLAGRLELYPILLLFTPAVWKKN
5.9E-60	213	19.3	1.4E-58	208.1	13.3	2	1	Q8PU49_METMA	Trk system potassium uptake protein	trkG MM_2500	Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) (Methanosarcina frisia)	476	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina mazei (Methanosarcina frisia), Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) (Methanosarcina frisia)	192952	>tr|Q8PU49|Q8PU49_METMA Trk system potassium uptake protein OS=Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) GN=trkG PE=4 SV=1MNIKIVFYVLGGLLRLLGIIMVVPLGVAYYYGEDLTPFLVSIAITVITGLILLSYKTDEEWMRKEGFAIVGLGWLIAAVFGAIPFVLDGISPLNALFESMSAFTTTGSTILTDIESHPKGILFWRGMMQWLGGMGIIVLFIAILPKLGVAGRQLFRAEAPGPTEDKLKPRIRETAKILWMVYFVISFAQVVTLLLAGLSLYDAVNHTFTTMACGGFSNYGLSIGAFNSPLVEYIITFFTFVAGANFALHYRAIYVDRDFLLKDDEFRFYTALVLSASGLLTLLLWRDLNTGFFDSFRLAIFHVVTIMTSTGFAIADFNLWSESSKMVILLVMFIGGCAGSTGGGIKVVRILILLRHSRTELFKALHPRAIKSVKFNNKAVPDEIISSIISFVVIYLLIFISSALILSVLGMDIITSITASIATLGNIGPGLGVVGPMGSFDPIPPLGKLILIANMWIGRLEIYTVIVLFTPEFWNK
5.9E-60	213	25.8	9E-60	212	17.9	1.2	1	A0A075LGE3_9BACI	Ktr system potassium transporter B	GZ22_00810	Terribacillus aidingensis	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Terribacillus, Terribacillus aidingensis	586416	>tr|A0A075LGE3|A0A075LGE3_9BACI Ktr system potassium transporter B OS=Terribacillus aidingensis GN=GZ22_00810 PE=4 SV=1MATRRRKLFHRIKINPPQFFALGFLVLIALGTFLLMLPMATADRHHLSFIDALFEATSAVCVTGLVVVDTQTTFTLFGQIVLLCLIQIGGLGFMTLTVFIALLLRRNISFEERHLVKESLNQNSYEGIVRMVRFVLLFTVICEVIGTIILGIHWGDEFGYLKSFYYGLFHSISAFNNAGFDIMGDFSSMTAFVGDPIVNLTLTSLLILGGIGFIVVADILQKKKGKRLMLHTKVVLWMSAILVAIGTILIFLLEYGNPATIGNLPWNDKLLASYFHGVVPRTAGFNSLNTADLTLGSQLVTMALMFIGGGTGGTAGGIKVTTFAILLFAVWALIKGKQEVNIRNRRIPGDLVFRAFSITTYSVLLVSLFVFLLAITEKGAALNYIAFEVLSAFGTVGMTLGLTPELSEPGKMLLSLLMFMGRVGPITIAFALAFRIKKTAVRNPEERIIIG
5.9E-60	213	27	9.9E-60	211.8	18.7	1.2	1	G4Q580_ACIIR	Potassium uptake protein ktrB	Acin_0832	Acidaminococcus intestini (strain RyC-MR95)	442	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Acidaminococcaceae, Acidaminococcus, Acidaminococcus intestini, Acidaminococcus intestini (strain RyC-MR95)	568816	>tr|G4Q580|G4Q580_ACIIR Potassium uptake protein ktrB OS=Acidaminococcus intestini (strain RyC-MR95) GN=Acin_0832 PE=4 SV=1MLKGKHFSPNQVVALTFLGLILAGAFLLMLPISHRDGMWMPFLDALFTATSASCVTGLVVCDTGKVFSLFGQLVIIGLIQLGGLGLMLFATLFSVALGRRINLQDRMLIQASLNQNDMSGVVRMSLRVAKYTAVVEGVLGTALALRFYQQFGLKGIYYGYWHAISAFCNAGFDLFGNYQSLVGYVHDPVVNGLIALLIILGGIGFAVMSDVVHTRHFRNYRLHTKLVLVSTVALIALGTLLIQVMEFDNGRTLGTLSVGDQWMASFFQSVSARTAGFNTFDLMQMRTSTILVMVLLMVIGASPASTGGGIKTTTAALLILSAHQVLFQKPECVIFGRRIDQETIHRAFAITTLSIIWIFLAIIGITYLEETSLVEALFEVVSAYATVGLSSGLSQHLTAGGKIIMILSMYAGRVGIMTFVMALTARRREALIRYPEEKIIIG
6.5E-60	212	32.2	8.6E-60	212	22.3	1.1	1	Q49WF2_STAS1	Putative cation transport protein	SSP1762	Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus saprophyticus, Staphylococcus saprophyticus subsp. saprophyticus, Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229)	342451	>tr|Q49WF2|Q49WF2_STAS1 Putative cation transport protein OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229) GN=SSP1762 PE=4 SV=1MSIFNQLFKKSSPQQGIVMYYIVAIIVAFLLLNLPYVHKAGVSVDPIDSLFVAVSGVSVTGLSPVNIVETYTTFGQIIIMIILNIGGIGVMAIGTMLWVVLGKHIGMRERQLIMLDNNKDTMSGTVKLILDIVRTILIIEVVGAALLTFYFYRDNPDLQYAIMQGFFVAVSATTNGGLDITGQSLIPYANDYFVQTIVMFLIILGSIGFPVLIEVKAYIKNRIPNFRFSLFAKITTVTYLVLFVFGVIIILLFEYNHAFQNMSWHKSLFYALFQSATTRSAGLQTIDVSHFGEGTNVIMSILMFIGSSPSSVGGGIRTTTFAILILFLLNFNNNSEKLSIKAFNREIHTTDVQRSFAVFTMAGILTFAATIFILVVENGKISFLQGFFEVMSAFGTCGLSLGVTGDFNDMSKVTLMILMFIGRVGLISFIIMIGGRREPDKFHYPKERVQIG
6.9E-60	212	21.5	1.1E-57	205.1	14.9	2	1	R7CNM2_9FIRM	Uncharacterized protein	BN806_02465	Ruminococcus sp. CAG:9	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:9	1262967	>tr|R7CNM2|R7CNM2_9FIRM Uncharacterized protein OS=Ruminococcus sp. CAG:9 GN=BN806_02465 PE=4 SV=1MPEKMCKKKHLTSFQLIILGFAGVILLGSILLMLPVSSLDKVPTPFHEALFTATSAVCVTGLVVKDSGSYWSVFGQTVILALIQIGGLGVVTVAAAVSLLSGKKISLMQRSTMQDAISAPKVGGIVRLTRFILKGTLLIEAAGAMLLLPVFVSDYGLKGIWMAVFHSISAFCNAGFDILGTADNAFPSLTGYSGNILINVVIMLLIITGGIGFLTWDDIYRNKMNFKRYRMQSKIILMTTVCLIVFPAVFFFACDLKNLPAGERLLAAMFQSVTTRTAGFNTIDISEMSEASKAVMILLMLIGGSPGSTAGGMKTTTFTVLILNAIATFRSQENAGAFGRRLEYHVIKNAATIAMLYFTLFFCGGVAISVYEGLPLLDCLYEAASAVGTVGLTLGVTPGLHVFSQVVLIILMYLGRVGGLTLIYAVFSGRNKGNAKLPLEKITVG
7.3E-60	212	18.4	1.5E-59	211.2	12.7	1.4	1	C4XTL7_DESMR	Putative potassium uptake system membrane components	DMR_01730	Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	457	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio magneticus, Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	573370	>tr|C4XTL7|C4XTL7_DESMR Putative potassium uptake system membrane components OS=Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1) GN=DMR_01730 PE=4 SV=1MWLKKIYTPLALPIHFFAAAIFLGAGLLCQPISCVGEPVSFLDALFTATSAACVTGLTVVDTGTAYNRFGQTVILALIQLGGLGIMTFSTLIFYLWRRRVSLADHIAVGQSLLHDASFHLGRFLVRMAAVTVFIEAVGALSLYAFDPVGFAPFSAVFHSVSAFCNAGFGLRPDNLVAYAGNPGVNGVIMWLIVSGGLGFAVLIEGYRVVKDRLVILVTAPGRRPLALSWQARTIFGVSAFLIFAGAAMIYCGEFLGGRYGELSLLDKAMAALFQSVTCRTAGFNTIDIGRMADASLVIMILLMFIGGSPGSCAGGIKTTTFRVLVAFGRAKMFGRKQSVVGRYAVDDDTVDRAVTLTIFALGLVLASVLLMCFTEGAVAPHVEAGGRFLEILFEVVSAFGTVGLTTGITTSLTPAGKLVIIMLMFVGRLGPILFLSVLQGFEEPRRYRWPEQGMMIG
7.5E-60	212	35.5	1E-59	211.8	24.6	1.1	1	F4LW84_TEPAE	Ktr system potassium uptake protein B	ktrB TEPIRE1_0733	Tepidanaerobacter acetatoxydans (strain DSM 21804 / JCM 16047 / Re1)	455	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Tepidanaerobacter, Tepidanaerobacter acetatoxydans, Tepidanaerobacter acetatoxydans (strain DSM 21804 / JCM 16047 / Re1)	1209989	>tr|F4LW84|F4LW84_TEPAE Ktr system potassium uptake protein B OS=Tepidanaerobacter acetatoxydans (strain DSM 21804 / JCM 16047 / Re1) GN=ktrB PE=4 SV=1MDFSEAVEIKILHFGLRKLKPTQILVFGFAALILVGGILLNLPSASKSGQSIGFLNALFTSTSAVCVTGLVVVDTQTQFSTFGQIVIMCLIQMGGLGIMTMATLIFLLLGKKITLRERIVMQEALNQSTLSGLVKLTRHILLTTFIFEGIGAILLSIRFTQIYGISKGIYYGVFHAVSAFNNAGFDLIGGFKNFTPFVEDPIINGVIMGLIIFGGLGFTVIHDLLLLKRNFKHLSLHSKVVITMTLLLLVSGFITFYCLEYSNLKTLGNLSPTGKILAAAFQSVTARTAGFNTLNLSDLTMPSKYFTIFLMFIGASPASTGGGIKTSTFAIIIMMIYTILASKEDVEIYQRRVPMDNIFKAVVIGVIALLLVFTSSFLLTITEKADFLSILFETTSAFGTVGLTLGITTELTSIGKIIIILTMFAGRVGPLTLAMALGSRINKAMIRFPEERILVG

7.8E-60	212	22.9	1.6E-58	207.9	15.9	2	1	R6TAN7_9FIRM	Cation transport protein	BN714_02107	Ruminococcus sp. CAG:57	489	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:57	1262962	>tr|R6TAN7|R6TAN7_9FIRM Cation transport protein OS=Ruminococcus sp. CAG:57 GN=BN714_02107 PE=4 SV=1MNSSIIRYILGNVMRMEACFLLLPCIVSLVYGEGVGLYYLGTAIVCLAFGVVMAWKKPKNYVFYLKEGCIATSLSWIVMSLVGCM PFWISGEIPSFTDAMFETVSGFTTTGASILTNVEALSHTALFWRSFTHWIGGMGVLVFLLAIIPLSGGSNINLMRAESPGPSVGKLVPK MKYTARILYIIYFGMTILEFIFLIIGKMPVFDSICTAVGTAGTGGFGVKNDSLGSYSPYLQWVVAIFMILFGVNFNAYYYIIYRHFKKAFKM EEVRCYFAIILIATAIIFANILDRCVSIFDALTKSVFQVASLITSTGFSSTDFNLWPQICRTVLVLIMFIGACAGSTGGGIKVSRVIVLFKTMIK ELHSYIHPKSIRKVNLDGKPVEHEIVRSINVYIVTFVIIFASSVFMVAFDGKDLVTNFTAVLTTINNMGPGLAEVGPAGNFSNFSVFSKFV FMFDMLAGRLELFPLLILFHPSAWKDLISKRAEARKF
7.9E-60	212	14.2	3E-59	210.2	9.9	1.7	1	C7RIU0_ACCPU	Trk system potassium uptake protein	CAP2UW1_0052	Accumulibacter phosphatis (strain UW-1)	484	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, unclassified Betaproteobacteria, Candidatus Accumulibacter, Candidatus Accumulibacter phosphatis, Accumulibacter phosphatis (strain UW-1)	522306	>tr|C7RIU0|C7RIU0_ACCPU Trk system potassium uptake protein OS=Accumulibacter phosphatis (strain UW-1) GN=CAP2UW1_0052 PE=3 SV=1MQRYYPVIRVLSMVIVMFGLTMLVPWGLSWFMHDGAESAFDEAVLLTVGTGAGLWYATRKEKRDLTIRDGFLMVALVWTVLP VYAALPLVIQLNASFTDAYFEAVSGLTTTGATVFEGLDNLPVSINFWRTQLVWLGGMGLIVLAVAILPLLGIGGRQMFKAETPGPMKDS KMTPRMAETAKGLWVVYTLISVCCVLGYQWAGMTWLDAIMHMFATMGLGGFSSHDASYGYFNSPLIEAVAILFMLIAGCNFATHYVV LSGRSLRPYATDPEAGMFLLVTLGSVVGIAIFLDVHEVYPTFSEALRFSAFNVVSIATTTGFANTDYALWPFFAPLWMLFLSSFATSAG STGGGIKMIRAIVLYKQVYRELARAMHPNAVHPVKVGNEVVPPNILFAVLAFGFMYMVCIASMTLLLSFSGLEIITAFTAVVASINNTGP GLGQVGPANNFSVLTDFQTWVCTFAMLIGRLEIFTLLVVLTPAFWRK
7.9E-60	212	19.8	8.7E-58	205.4	13.7	2	1	R6MFF9_9FIRM	Potassium uptake protein TrkH family	BN524_01498	Coprococcus comes CAG:19	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus comes CAG:19	1263070	>tr|R6MFF9|R6MFF9_9FIRM Potassium uptake protein TrkH family OS=Coprococcus comes CAG:19 GN=BN524_01498 PE=4 SV=1MNVKMIRYIISKMMGAEGLLMLLPMMVGIIYGEHTSVYFLITAAILTAIYLLFGRKCPENMTIYAKEGLIIVATAWIFWSLAGALPFVL SKSIPSYVDAFFETVSGFTTTGSTILTEIEGLPKGILFWRSLTHWVGGMGVLVFVMVLTSLDEKNSMHLMRAEVLGPEADKLVPKARG TARILYGMYFALTTIEVVFLLAGGMNLFDAVTHAFSTAGTGGFSGYNASVAHFNSAYIDGVITVFMILFGINFNLYFFLLLKEFKSVFKNE ELRAYLGIIAGATVVITCNIAGGYHSLLKAFRYAAFQVASVITTTGFVTADFNKWPELSKCVLLLVMVIGASAGSTGGGIKVSRLLILVKSI RRELKTMIHPKAVNIVKVNGKKVKEETMRGVYIYFIAYILILIVSVLLISINNFDFTTSFTGVLTTLNNVGPGLNLVGPVENFAKFSDFSKIV FCVDMLIGRLEIFPFLMLFSPSLWSRKF
7.9E-60	212	22.3	1.1E-59	211.6	15.5	1.1	1	F8E24_CORRG	Potassium uptake protein (EC 3.6.3.14)	trkH CRES_1005	Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	456	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium resistens, Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	662755	>tr|F8E244|F8E244_CORRG Potassium uptake protein OS=Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026) GN=trkH PE=4 SV=1MQTNATTPRLHPTQVVAVGFIVLILLGALVLMLPAASESGESTEFLPSLFTATSAVSLTGLIVVDTATHWSTFGQVVIICLIQLGGF GVMSLTSLAAMMLTGRLSLRSQLNTLAEGRAQDASGVRKTLIMTLAFMAGTEILVAGILALRFVFGYHEPLGRATWYGIFHAISAFNNA GFSLFSDNLISLATDAVVILPIAFALIVGGLGFQVLLEIFKKAQRRFNNPKNRGDNIRFSVTATVTLWGTLILLVSGAAWYAFFEWRNTLA SLDPAHKVLLSFFGSATARTAGFNAVDYSQLNPSTLMGTDILMFIGGGSGGTAGGIRITTTAIILAAMITEFRGENSVIINRRTISPSTVR RALTVVSFGMVLVVAAIVAIRTLDPQFTADQVVLETVSAFSTVGLSTGITANLSGASQGILIAIMYLGRIGPITLVTAMALKRFKRRFEYP EERPFIG
7.9E-60	212	31.6	1.1E-59	211.7	21.9	1.1	1	K9PEA3_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cal7507_0599	Calothrix sp. PCC 7507	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix sp. PCC 7507	99598	>tr|K9PEA3|K9PEA3_9CYAN Potassium uptake protein, TrkH family OS=Calothrix sp. PCC 7507 GN=Cal7507_0599 PE=4 SV=1MTVSRTVCLGFLAVIAVGTILLMMPFSTSSGTWNNLIVALFTSTSAVCVTGLSVVDPGTYFSFWGQLFIALLAQIGGLGYMTSTT FLILLIGRKFDMRQKIAIQQSLDRPGMSGSTQVIRSIIATTLIFEITGVFLLLIAFVPDYGWSQGLWLAIFHSINAWNNAGFSLFKDNLIGY QSSGLVVFTITGLIIFGGIGYQVILEMYLWMRDRLLKKTGSQVFSLDFKVAISTTLILLALGTIAFLCIEIRNPQTFGGLNFQNQLLVAWFQ SVTPRTAGFNTIDIGKMTTAGLFIMIALMFIGASPGGTGGGIKTTTLRVLTSCTKAILQGKEEVLLYDRKIAISLILKAVGVLVGSVATVIIAT TLIALTDPKLDFIQILFEVVSAFATVGLSTGITGSVSVAAKLILIATMYLGRVGVLLLMSAILGDPRPSRIHYPEENLLVG
8.1E-60	212	13.1	8.6E-58	205.4	9.1	2.1	1	M1Y5G5_NATM8	Trk-type transport system (Probable substrate potassium)	trkH1 Nmlp_3693	Natronomonas moolapensis (strain DSM 18674 / JCM 14361 / 8.8.11)	511	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Natronomonas, Natronomonas moolapensis, Natronomonas moolapensis (strain DSM 18674 / JCM 14361 / 8.8.11)	268739	>tr|M1Y5G5|M1Y5G5_NATM8 Trk-type transport system (Probable substrate potassium) OS=Natronomonas moolapensis (strain DSM 18674 / JCM 14361 / 8.8.11) GN=trkH1 PE=4 SV=1MSRGVNWKASVGLLGVGIKYLAVTMVIPLIVAVAYGEDAWVFLVSMALVAVIGLVVERVDPDPDLGPREALLFVSLAWLAAAAIG TIPYLLAGYGTASTVAHPVNALFESMSGFTTTGATVLGEISTERHSHAILMWRQLTQWLGGMGIIVLMIAILPEIAVNGAQLMESEAPG PELQKLTPRIEETARALWLIYFGFTVVYILILYGLHLLGMAPNMDLFNAIAHGFTTLPTGGFSPEADSIAAFSAAVQWVVIPFMIVAGVNF ALFWHVLRGEAEVMLENAEFRTYAGAIAVVTAVLAVMLFRGAAPAIELGGATQGMAENSLRQAAFQIGSLLNSTGFATADFAQWDAD AQILLMLTMFIGGSAGSTGGGVKIVRWLVVGKAIRRELFTSAHPDVVQPVRLSGNVVDEDAIRGIMAFTILYVVLFGVSAVFLSLDAARI GVQLTMLESTSASLATIGNIGPGFGRFGPFGSYLFLSDASKLLLIFLMWIGRLEIVPVLAVFVSAIDGQ

8.1E-60	212	9.8	1.8E-57	204.4	6.8	2	1	D8J647_HALJB	Trk-type transport system (substrate potassium) 1, subunit 2.1 (Trk-type transport system (Substrate potassium) 1, subunit 2.1)	HacjB3_11910 C497_10718	Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	498	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halalkalicoccus, Halalkalicoccus jeotgali, Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	795797	>tr|D8J647|D8J647_HALJB Trk-type transport system (substrate potassium) 1, subunit 2.1 OS=Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3) GN=HacjB3_11910 PE=4 SV=1MRINVDWRVSATLVGVVLKWLSVPLAFPLLVAVYYREALAPFLVAMAISVLAGEALVRVGHEARLGPREAFLMVAVTWFVVPLIGAVPFVLAGVGSVAHPINALFESMSGITTTGATVLVDFEIHARSIMMWRQVSQWLGGLGILVLATAILSQIGVGGAQLMESETQTRDVNKLDPRIARTARLLGGLYIGMTLLLVAILYSLSLAGLAPNMGLYNAIAHPLTTVSTAGFSPEPDSIMAFSPAVQWVITLFMIIGATNFVLIYFALQGDWRRLVDSEEFRFYIALLALLAAITAVLLAFESDYAGGVERTVRHAVFNTVSMLTTTGYANVDFDRWEAGAKHVMFVCMFIGGMAGSTTCSIKTLRWLVVLKGFRRDLFTSIHPEAIRPVRLSDEVIDEETVRDIYAFALVNLLLFSAATILVVVDGARVGLPLNEFEAMGAAAATFLNIGPAFGIAGPFGTYEAFPATTKLAMILLMWIGRIEVIPVLVLLTKAFWTS
8.4E-60	212	20	9.7E-59	208.6	13.9	2.1	1	R5C310_9BACE	TrkH family potassium uptake protein	BN727_00437	Bacteroides sp. CAG:598	501	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:598	1262743	>tr|R5C310|R5C310_9BACE TrkH family potassium uptake protein OS=Bacteroides sp. CAG:598 GN=BN727_00437 PE=4 SV=1MEGFNTETLYNQSKRKHSLINKKIIARVLGILLFLEAIMFLICALVSWYYQEKEAFTFLQTAGINTLVSIILILLSRGAERRMNKRDGYCIASLAWVLFSAFGMLPFYLSGSVDSITNAFFETMSGFTTTGATIMDNIDSQPHGILFWRNLTNLIGGLGIVSFALVLLPIFNEGNVQLFSAEATGVTQNKLHPKISIMIKQIWGVYLLITLLAAVLLRVGGMNWFDAVCHSFATIATGGYSTRQASVAYWNSPFIEYIISIFMIIGGLNFSLIFLAAKGKVSKIWHDEETRWYLWSVVILTVACTAALVIGNGYGTEEAFRKALFQVTTVHSSCGLSTEDYSSWPPFTWVLLIFAMLAGGCTGSTAGGIKAVRLQMMAKGIRGCFRRMLHPNAILPIRINRQTIASNTVLAVAFFVFLYLVLIMTGWLALMILGVEFSDAFGVVVSSIGNTGIAIGHYSPAYSWNALPEAAKWISAFLMLVGRLEIYCVLLLFYPSFWKNR
8.5E-60	212	22.4	1.6E-58	207.8	15.5	1.9	1	Q1IY06_DEIGD	K+ transporter Trk	Dgeo_1583	Deinococcus geothermalis (strain DSM 11300)	458	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus geothermalis, Deinococcus geothermalis (strain DSM 11300)	319795	>tr|Q1IY06|Q1IY06_DEIGD K+ transporter Trk OS=Deinococcus geothermalis (strain DSM 11300) GN=Dgeo_1583 PE=4 SV=1MPDVPAPRIRKPLLSRISPPQLIALSFALAILTGGVLLSLPLTHGAGRQVNFLQALFTSTSALCVTGLNVVDPSRDFNRLGQVIIMLLIQLGGLGIITFGTVFALLMRRRVNYSERIRLAQQVSAFSAGDVVPLIRNIFLYTFVLEAAGAALLAFRFVPLEGWGRGLFYAVFHAISAFNNAGFALYSDNLMRFVGDPLISLVIALLIILGGMGFLVQLNVVAHLLNPRRNRLLVHSKLVLTMMSALLLIGTLTYLGLEWNNPKTLAPLPFGDKLLASFFQSVTTRTAGFNTIDIGAISLGTAFITIILMFIGANPGSTGGGIKTSTFYVMMASAWSMVRGHRDVTLFKRRIDQTTILRAMTVGLLSIGLVNTMLILLLLLNTNLQVSFVNLFFEAVSAFGTVGLSMNTTPLLNAEQQVIIILLMYLGRIGPLTFAVAFNNQEPGDPVRYPAEKDILIG
8.8E-60	212	35.2	1.2E-59	211.5	24.4	1.1	1	Q8ERB8_OCEIH	Na(+)-transporting ATP synthase	OB1388	Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)	455	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Oceanobacillus, Oceanobacillus iheyensis, Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)	221109	>tr|Q8ERB8|Q8ERB8_OCEIH Na(+)-transporting ATP synthase OS=Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831) GN=OB1388 PE=4 SV=1MSKNKYQRNVLNQLSPVQLLLLFYGIAVVFSTVLLSLPVAHKPDVNIPFIDIMFTAVSAISVTGLSTITIVDSFSTIGIVFLAIIMQLGAVGIMAIGTLIWLILGKRIGFKERSMIMTDQNQTHFDGMVRLIKGIIYVLLIIELIGFLILGTYYLQYFPTAREAYIQGFFGTISAISNGGFDITGQSLVLFKDDYFVQFIQILLIIFGAIGFPVLIELKEYLFRKRTERNLFHFSLFTKVTTVTFFVLIVIGALGIYLLDMNAFFKGLTWHESLFYALFQSVTTRSGGLSTMDVSLLTETNQLFMSGLMFIGASPSSAGGGIRTTTFALAIIFVFTYIRGGNSVRIFNREVYNDDLIKAVSITLFAITLVIFSTLVLTALEPLFTLEEILFEVTSAFGTVGLSLGITSELSNISKILIMLLMFIGRIGIVTFLLIFKRKKKKAKYHYPKERIIIG
9.2E-60	212	7.9	5.6E-36	133.5	0	2.1	2	A0A0H3LGU3_BORBR	Trk system potassium uptake protein	trkH BB0267	Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella bronchiseptica (Alcaligenes bronchisepticus), Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	257310	>tr|A0A0H3LGU3|A0A0H3LGU3_BORBR Trk system potassium uptake protein OS=Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) GN=trkH PE=4 SV=1MKRLLATFYVLGLTMVVFALTMVIPLAVAYIGQDAGFTAFLEGFLLALGIGAGTWLATRRGRSELHARDGFLLVSTVWAALPALAAIPLLLYYDDVGIPLSFTDAYFEAMSGLTTTGATVLSGLDALPASINLWRATLIWIGGMGILVLAVAILPLLGVGGHQVVRAETPGPMKDERLTPRIASTAKALYAVYFGFSMVCLLAYRAVGLSWFDAWCHMATTMGLGGFSTYDDGFAHFDSLSVELVAIVFMTISGINFATHFNALRQRNWRAYVVCPQTIPYLTVMLGAGLVISVFLYIKGVYGDPWEALRYGMFNTISVATTTGYANVDYASWPLFAPLTMLLLSAFVTSAGSTGGGIKMIRIILLVKQARNELVTMLHPHAVSPVRIGSRVVDQRVMASVLAFMLVYGLSVGVLSSLLLLSGLDLITAFSAVMAMINNTGPGLGPLGPMGNFSVLNDFQTWVCTFAMLIGRLELLTVLVLFTPLFWRK
9.3E-60	212	13	8.1E-58	205.5	9	2	1	Q2L0C7_BORA1	Trk system potassium uptake protein	trkH BAV0233	Bordetella avium (strain 197N)	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella avium, Bordetella avium (strain 197N)	360910	>tr|Q2L0C7|Q2L0C7_BORA1 Trk system potassium uptake protein OS=Bordetella avium (strain 197N) GN=trkH PE=3 SV=1MKRLLATCYVLGLTMVVFALTMLIPLGLAVWENDAGQQAFARGFAIAIGSGLAVWLLARRWRSELHARDGFLLVSVVWAALPLLAALPLLLYFHDVGKPLSFTHAYFEAMSGLTTTGATVLTGLDELPHSVNLWRVTLIWIGGMGILVLAVAILPLLGVGGQQVVRAETPGPMKDERLTPRIASTAKALYAVYFGFSILCFLAYRAVGLPWFDAWAHMATTMGLGGFSIYDSGFLKFDSVSVEMVAIVFMLISGINFATHFNALRQRSFKPYLSCPQTLPYLTVVLGVGLLISAYLYIRHVYTDPLQALRYGMFNTVSVATTTGFANTDYATWPLFAPLTMLLLGAFATSAGSTGGGIKMIRVILLVKQARNELITMLHPHAVSPVRIGSRIVDQRVMFSVLAFMLVYGLSIGVVSSLLLLSGLDLSTAFSAAMAMINNIGPGLGILGPMGNYGVLSDFQIWVCTFAMLIGRLELLTVLVLFTPWFWRK
9.6E-60	212	27.6	1.3E-59	211.4	19.1	1.1	1	E8SER3_STAPH	Potassium uptake protein, integral membrane component, KtrD	SPSINT_0719	Staphylococcus pseudintermedius (strain HKU10-03)	434	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus pseudintermedius, Staphylococcus pseudintermedius (strain HKU10-03)	937773	>tr|E8SER3|E8SER3_STAPH Potassium uptake protein, integral membrane component, KtrD OS=Staphylococcus pseudintermedius (strain HKU10-03) GN=SPSINT_0719 PE=4 SV=1MYYLVAIVGAFLLLNLPGVHKPGVKVAPIDTLFVAVSGVSVTGLTPVNISETYSAFGYIVLLVILNIGGIGVMAIGTLLWVVLGKHIGIRERQLIMLDNNREAMSGTVKLILDIVRTILVIELVGATLLAFYFYQDIHDLKEAILQGVFVSISATTNGGLDITGDSLIPYANDYFVQTIVMFLIVLGSIGFPVLLEIKAYIKNRIPNFRFSLFTKVTTVTYLLILIVGMLGILLIEAHGVFANESWHKTLFYAMFQSVSTRSAGLQTFDVSQFSDATNLLMGGLMFIGSSPSSVGGGIRTTTFAIIILFVINYKPNAEKSSIKVFNREIHNQDIQRSFAVFCIAIVMTFVGTFIIMLNEGHHIDFIKIYFEIMSAFGTCGLSTGITSELGSVSKVVLMILMFIGRVGLISFIIMMSGNREPAKYHFPKERIQIG

9.7E-60	212	28.5	1.3E-59	211.5	19.8	1	1	K9XT59_STAC7	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Sta7437_2169	Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	444	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Stanieria, Stanieria cyanosphaera, Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	111780	>tr|K9XT59|K9XT59_STAC7 Potassium uptake protein, TrkH family OS=Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437) GN=Sta7437_2169 PE=4 SV=1MTIARTICLGFLAVIVIGTLLLTMPFATSNGEWNDPIVALFTSTSAVCVTGLVVVDTGSYFSFWGQLIIALLIEIGGLGYMTITTFLILLIGRKFDLKQKFAIQESFDRPFLQGSSNLIRSIIATTLLFEITAIFLMLPIFTKDFGLSQGLWFAIFHSISAWNNAGFGLLPDNLIQYASSWTINLVIPGLIIFGGIGYQVIIEMYIWLLNRIQKRKEKFCFSLNFKVVTSTTLILLILGTIGFWLIEFDNQNTLGNLDIQGRFLTAWFQSVTTRTAGFNSIDIGKMTTAGLFLTIGLMFVGASPSGTGGGIKTTTLRILFNCTRSVLEGKDEVILYQREVPYPLILKAVAVVFGSAASIVFITIIISSIDGSIDLIAILFEVVSAFATVGLSTGITASLSKLSQLMLIMTMYAGRVVGILLLIAAIIGDPRPTTLNYPEENLLVG
9.8E-60	212	18.3	2.9E-58	207	12.7	2.1	1	R7EJN7_9BACE	TrkH family potassium uptake protein	BN594_03320	Bacteroides uniformis CAG:3	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides uniformis CAG:3	1263055	>tr|R7EJN7|R7EJN7_9BACE TrkH family potassium uptake protein OS=Bacteroides uniformis CAG:3 GN=BN594_03320 PE=4 SV=1MINFKTIIRIIGILLLLETVMFLVCSGVSFYYRESDMLDFWKAGGITAGVGLLLAALGKGGERQLTRRDGYVLVSFAWVAFSLFGMLPFYIGGYIPDIANAFFETMSGFSSTGATILDDIESLPHGILFWRSMTQWIGGLGIIMFTIAVLPIFGVSGLQVFAAEASGPTHDKVHPRIGITAKWIWSIYAGITALLVGLLMLGGMDWFDSICHAFATTGTGGFSTKQASVAYYKSPYIEYVISIFMFISGINFTLLLLFVNRKFKKFIGNAELKFYFGSVVLFTAVIAIVLYYTSPMGMEESFRKSLFQVISLQTSTGFATDDYMQWTPVLWGLLTIIMLMGACAGSTTGGLKCIRMVILTKVSRNEFKHILHPNAILPVRINKQVISPSIVSTVLAFCFIYIAIIVISTLLMMAMEVGAEESMGCVISSIGNMGPGLGKTGPAYSWNALPDAAKWLLSFLMLLGRLELFTVLLLFTPDFWKRN
1E-59	212	8.1	5.6E-36	133.5	0	2.1	2	Q7VS69_BORPE	Trk system potassium uptake protein	trkH BP0574	Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella pertussis, Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	257313	>tr|Q7VS69|Q7VS69_BORPE Trk system potassium uptake protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) GN=trkH PE=3 SV=1MKRLLATFYVLGLTMVVFALTMVIPLAVAYIGQDAGFTAFLEGFLLALGIGAGTWLATRRGRSELHARDGFLLVSTVWAALPALAAIPLLLYYDDVGIPLSFTDAYFEAMSGLTTTGATVLSGLDALPASINLWRATLIWIGGMGILVLAVAILPLLGVGGHQVVRAETPGPMKDERLTPRIASTAKALYAVYFGFSMVCLLAYRAVGLSWFDAWCHMATTMGLGGFSTYDDGFAHFDSLSVELVAIVFMTISGINFATHFNALRQRNWRAYVVCPQTIPYLTVMLGAGLVISVFLYIKGVYGDPWEALRYGMFNTISVATTTGYANVDYASWPLFAPLTMLLLSAFVTSAGSTGGGIKMIRIILLVKQARNELVTMLHPHAVSPVRIGSRVVDQRVMASVLAFMLVYGLSVGVLSSLLLLSGLDLITAFSAVMAMINNTGPGLGPVGPMGNFSVLNDFQTWVCTFAMLIGRLELLTVLVLFTPLFWRK
1E-59	212	31.1	1.8E-59	211	21.5	1.3	1	B4S454_PROA2	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Paes_1834	Prosthecochloris aestuarii (strain DSM 271 / SK 413)	633	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae, Prosthecochloris, Prosthecochloris aestuarii, Prosthecochloris aestuarii (strain DSM 271 / SK 413)	290512	>tr|B4S454|B4S454_PROA2 H(+)-transporting two-sector ATPase OS=Prosthecochloris aestuarii (strain DSM 271 / SK 413) GN=Paes_1834 PE=4 SV=1MGNIHVKPGLLNGGEDGPRLLPGKDNNRFLAVIDWIVILLAFPAVFSLVAEYGFYLTSDQTSLIQILDLGILWIFAVCGFIRILLISDKTGYLKSHWSDVLILFLISMLLFFPVNIAAIMQSFIPGLVPKVIAKISIVLTQVLLILALVPPALRYSQRLMSFNVQPAALIIMSFLLFIFLGTLFLLLPKATLNGSISVIDALFMSTSAVCVTGLVVVDTAKDLTMFGQTVIMILMQLGGLGIMTMTTFFAYMVGSGSGLKEYATLQTLLGEESLGRIRSTIFQVALFAFSFEVLGAWILFEQFDRYSFASAPDRLFFAIFHSVSAFCNAGFSLWSENLMAPGVQNDMLILSVIMVLIVLGGLGFPVIANINAIVAHRFRRRFFSMISDEPVVENLHSPDVVQKERLRERRVRLGLHSKLVLMTTGVLLVTGTLGIYLLEVHRTLEGLPVTEQVFASLFHSVSARTAGFNTLDIGHFTMPTLFFIIVLMWIGASPGSTGGGIKTSTLAVAVLNILAIVSGRNRIEIFRKQIAQVTVTKAFSTVILSIFYISCALFILLVTENLPFEQLLFEVVSAVGTVGLSTGITPALSMTGKCVIIVSMFIGRIGMLAVLGAVIRQRSYGRYSYTEENVMIS
1E-59	212	27.3	2.2E-58	207.4	18.9	2	1	R2PYM7_9ENTE	TrkH family potassium uptake protein	UAS_01039	Enterococcus asini ATCC 700915	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus asini, Enterococcus asini ATCC 700915	1158606	>tr|R2PYM7|R2PYM7_9ENTE TrkH family potassium uptake protein OS=Enterococcus asini ATCC 700915 GN=UAS_01039 PE=4 SV=1MKKRMYRRYDLTTPQLISMGFASLILLGALLLMLPISSRTGEVTPFIDALFTTTSATCVTGLTTVNTAEHWSLFGQAVIITLIEIGGLGFMSIPVVFYFISRKKINLSTRMILRDSLNMPTMSGEVGLMRYILKTAFVIQALGMTALAIDFVPRYGWAKGLWFSFFHAISSFCNAGFDLFGDSLVPFQEDPWVLFIVMFLIIAGGLGFLVWYDLVGLRKKRRMTLHSKIALTITGGLLLFGTLGFFITEGTDTALINSDHFLSRFANTLFMAVTPRTAGYYSVDYFQMSHAGLILTMILMFIGGTSGSTAGGLKTTTFGVLLLKVKSIFKGRSHVEFSGRTIREAAVNRAMTLFFITLTLCIFATMVLSVTETIPNVDQLGLEYIAFEVISAFGTVGLTMGITPDLTIVGKLIIISLMFIGRVGIMTVVFSLVRRPEKEGNFKYPDESVMIG
1.1E-59	212	15.3	1.4E-58	208	10.6	2	1	G2KSK0_MICAA	Trk system potassium uptake protein	MICA_952	Micavibrio aeruginosavorus (strain ARL-13)	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, unclassified Alphaproteobacteria, Micavibrio, Micavibrio aeruginosavorus, Micavibrio aeruginosavorus (strain ARL-13)	856793	>tr|G2KSK0|G2KSK0_MICAA Trk system potassium uptake protein OS=Micavibrio aeruginosavorus (strain ARL-13) GN=MICA_952 PE=3 SV=1MDLRPIFYVVGALLCILAISMSVPMFVDMVHNHPDWKVFLLCMSITAFFGGTTVLTNASDKPFQLTIKQTFLLTAISWFALAGFGALPFWLASETDIGFTDAFFESVSGITTTGATVLTGLDTMPPGILMWRCMLNALGGIGFIVAAMAVLPFLRVGGMQLYRTESSDKSDKVLPRMQKVATAIAYIYFGLIAICALCYWMAGMSGFDAITHAMSSVATGGFANYDSSFGAFLEHPHILWIAMIFMILGGLPFVLYIKVLGGNFNALIRNTQVRTFLGLLGGSILISTLWLSMKGVLPFGEALLQSAFNIVSVVTTTGYASADYMQWGPFFVVFFFILTFFGGCTGSTSGGVKIMRYQVMALILGRHFQKLQQPNAIIALHYDGRTLPDDVPYSVMVFIFGFLGAFIVLALALSMCGLDFITSISGAATALTNVGPGLGPVIGPAGNFSTLPDPAKWLISGGMLLGRLELFTLLVLVMPSFWRK
1.1E-59	212	20.4	1.6E-58	207.9	14.1	2.1	1	D1Z1K5_METPS	Trk system potassium uptake protein	MCP_2505	Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE)	481	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanocellales, Methanocellaceae, Methanocella, Methanocella paludicola, Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE)	304371	>tr|D1Z1K5|D1Z1K5_METPS Trk system potassium uptake protein OS=Methanocella paludicola (strain DSM 17711 / JCM 13418 / NBRC 101707 / SANAE) GN=MCP_2505 PE=4 SV=1MSWRDLHIVVGNLKGLFTTVAILMAVMAAMSIAFGDRVSMAGFTAGLLVSGAIALAIHLAVAPDETIELKHAMVIAALAYLLVPALSAIPYVYHGVPSIDAFFEGISGWTGSGFSMIPSPETATHTIQLWRSLTQWVGGAGVILLMVTILIRPGTSAFTLYTSEARKERIKPSIRSTLNIIWKLYLGLTLFAVLLLLAAGMPAWDALNTAMTAISTGGFSIYADSIGHYGSLSVELALIPIMVAGSLPFAAMYRALKPDLRALLDDVQVRAFIGLVIAGCAVLAIQNMLFPVGASVADSVFQFASAVTCTGLQSADLSQWSPTSMLILSIAMVIGGCAGSTSGGIKIARALFLVAEARLWLAQTLLTKKAVIVVRMGDRKLTGQEMSRELADAALISFLWVVTLLASVMLLSNIVLGQASLSQVIFEVCSAMGNVGLTAGIVSPGMSLAAKLIIMFDMWVVGRLEIIPVLVLLRAILKGLRP
1.1E-59	212	14.8	3.3E-39	144.1	0.7	2	2	C7RIU1_ACCPU	Trk system potassium uptake protein	CAP2UW1_0053	Accumulibacter phosphatis (strain UW-1)	486	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, unclassified Betaproteobacteria, Candidatus Accumulibacter, Candidatus Accumulibacter phosphatis, Accumulibacter phosphatis (strain UW-1)	522306	>tr|C7RIU1|C7RIU1_ACCPU Trk system potassium uptake protein OS=Accumulibacter phosphatis (strain UW-1) GN=CAP2UW1_0053 PE=3 SV=1MIKRFAPVLFVLGILILGFGFLMLVPLSLSWLSADGAHGAYDEAVLITMASGALLSLSVRRQKREIRVRESFLLVALIWSLLPAFGALPLYLHIKELSWTDAYFEAVSGLTATGATVLSGLDTLPLSINFWRTFMHWIGGLGVVVLAVAILPMLGFGGRGMLKAETPGPMKDAKITPRITETAKGLWVVYVILTISCGVSLYQVGMEPWDALMHAFSIMGLGGFSTKDASLGHFDSLDIELVVIFFALLAGINFSTHFLVLSQRSLRAYRFDIEAHYFLGFLALSSVALALYLWPDDVYEDFLTTLRYVAFHSVSLATSLGFATTDYAQWPLFAQLWILFLGSFVACSGSAGGGIKMIRAVVLYKQVSRELMRAMHPRGLQTVRFGATVVPDPVLHSILGFMFIYVVTIVILTLLLIATRLDVITAFSAVVACINNTGPGLNLVGPSTTYAVLTDFQTWVCTWAMLLGRLEIFTLLVILMPAFWRR

1.1E-59	212	13.4	2.6E-30	114.8	1.6	2.1	2	R7ID97_9FIRM	Trk system potassium uptake protein TrkH	BN770_02007	Faecalibacterium sp. CAG:74	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, environmental samples, Faecalibacterium sp. CAG:74	1262897	>tr|R7ID97|R7ID97_9FIRM Trk system potassium uptake protein TrkH OS=Faecalibacterium sp. CAG:74 GN=BN770_02007 PE=4 SV=1MNKRLVAYMQGAVLLIEAACMTPALVIALFQQDGDAWALGATMLILIAIGAPLRFLVRPGERNLRAREGFLTVALAWIALSCFGALPFVFSGMIPNYIDALFESVSGFTTTGATVLENFDNLPQGIMFWRSFTHWIGGMGVLVLTLALVPQLSERTSHLVKAESPGPTLSKIVPKMGDTAKIFYIILTILEFIVLMIAGMNPYDAAIHAMGTAGTGGFSNYAASVGAFASPVIDVTITVFMVMFGINFALYYCAITGNWRGIVKSEELRWYLGIFLTVTAAITVVILPQYGTVGNALRYASFQVASIMSTTGYATADFSLWPVAARMLIFMLMFIGACAGSTAGGMKICRIAMLWKQGVRSVRHTFQPRKVQVVRFEGKGVDDTLLRETASFAFVYIAMILIGAVLIAFEGKYDIETNLSAALTCVSNVGPGFNAVGPAGNFAGYGSFAKVVLSLLMLAGRLELYPMLALLYPALWRKQ	
1.2E-59	212	31.1	2.4E-59	210.6	21.6	1.4	1	Q838Y7_ENTFA	V-type ATPase, subunit J	EF_0295	Enterococcus faecalis (strain ATCC 700802 / V583)	455	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus faecalis (Streptococcus faecalis), Enterococcus faecalis (strain ATCC 700802 / V583)	226185	>tr|Q838Y7|Q838Y7_ENTFA V-type ATPase, subunit J OS=Enterococcus faecalis (strain ATCC 700802 / V583) GN=EF_0295 PE=4 SV=1MKHQIKRRLYISPVQTIVLGFFLLIVVGTILLMMPFSAQAGQKTQWIDAFFVATSAVCVTGLSPLNTAEHWSPIGQVIIMILIELGGLGFLTVATIFFSLLRKKASLSVRMLYQEALNVSEVSGVFRLMKYIMKFAAIIQLLGAFLLSFQFVPTFGWKKGLFFSLFHAVSAFCNAGFDLLGDSMVPYQNSPYLLLVISFLIIAGGLGFIVWRDIFAMIKGYKNKIKHRVSIHTRLALTVTATFLVLGTVIFYISEYRHFPADMSFWQRLVNSWFLSVTPRTAGFYSVDYLKMSNPGLIVTILWMFIGGTSGSTAGGLKTTTFGVLFLQFRAIFKGKQRVEFHERTIPERVVLQAFTLFFLATFLCVTASVILSFTETLPLKNGIEYIVFEVISAFGTVGLTMGLTPDLTVFGKLVIIFLMFVGRVGVYTVLLSLIKKGLESQSKVQYPKESVMIG	
1.2E-59	212	19.5	2.9E-58	207	13.5	2.1	1	E6SU08_BACT6	Cation transporter	Bache_1302	Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides helcogenes, Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	693979	>tr|E6SU08|E6SU08_BACT6 Cation transporter OS=Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108) GN=Bache_1302 PE=4 SV=1MINFKTIIRIIGVLLLETVMFICCSGVSWYYGESDIVDFWKAGAVTAGAGLLLAALGKGGERQLTRRDGYVLVSFAWIAFSLFGMLPFYIGGHIPDITNAFFETMSGFSSTGATILDNIESLPHGILFWRSMTQWIGGLGIIMFTIAVLPIFGVSGLQVFAAEASGPTHDKVHPRIGITAKWIWSIYAGITGLLVVLLMIGGMGWFDSICHAFATTGTGGFSTKQASVAYYNSPYIEYVISIFMFISGINFTLLLLFVNRKFGKCISNAELKWYFWSVVSFTAVIATTLYYTSPMNAEESFRKSLFQVTSLHTSTGFATDDYMLWPPVLWGLLTIIMIMGACAGSTTGGLKCIRMVILTKVSRNEFKHIIHPNAILPVRINKQVLSSSTVSTVLAFCFIYLVIIIISTLLMMAMGIGFEESIGCVISSIGNMGPGLGECGPAYSWSALPIAAKWLLAFLMLLGRLELFTVLLLFNPEFWKRN	
1.2E-59	212	26.5	4.4E-58	206.4	18.3	2	1	A8MM67_ALKOO	Cation transporter	Clos_0674	Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus oremlandii, Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	350688	>tr|A8MM67|A8MM67_ALKOO Cation transporter OS=Alkaliphilus oremlandii (strain OhILAs) GN=Clos_0674 PE=4 SV=1MNYGIVLKVLGNILLVESTLMVPALCIAFYTGGYDKFGFMITILITLLIGSIMSRAKSSRSTISARAEGLTIVTLGWVLASLLGALPFYISGSIPAYIDAFFETVSGLTTTGSSILTNVEALPYGSLFWRSFTHWIGGMGILVFTIALLPALGIGGFQIFKAESPGPIADKIAPRIKDTAKILYVTYFALTIVTVISLRMGGMALFDSLLHAFGAVGTGGFGMRNNSVGFYSSSYIHIVLGTFMLLSGTNFSLYYAIFKGKWRDVLKDEELRLYLGIIFISVVAIGVNLALTSYSSIFLAFRDSYFQVTSIITTTGYSTADFDLWPSFSKAILFVLMFIGGSAGSTAGGMKIIRVLILGKLIKRDVAKMFHPRAYISIKNGGRTVPNETIVSINTFFALYMIIFAISTILISLEGIDLVSASSSVAATLGNIGPGLGFVGPMRSFSEFSFASKALFSFLMLLGRLELFTILALMAPKRWASEA	
1.2E-59	212	31.1	1.6E-58	207.8	21.5	2	1	F0P2C8_WEEVC	Cation transporter	Weevi_0011	Weeksella virosa (strain ATCC 43766 / DSM 16922 / JCM 21250 / NBRC 16016 / NCTC 11634 / CL345/78)	511	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Weeksella, Weeksella virosa, Weeksella virosa (strain ATCC 43766 / DSM 16922 / JCM 21250 / NBRC 16016 / NCTC 11634 / CL345/78)	865938	>tr|F0P2C8|F0P2C8_WEEVC Cation transporter OS=Weeksella virosa (strain ATCC 43766 / DSM 16922 / JCM 21250 / NBRC 16016 / NCTC 11634 / CL345/78) GN=Weevi_0011 PE=4 SV=1MKSFNFKIVFYLSGILLLLNTFFMLLCSVLSLIWKDDLSFSFLISGLITGSIGGFMYISGKKASRTVRKREGYLVVSFGWVILILTGVLPYYFSESYLPLSVYYSNDITTINLFYETVSGYTATGTTIFQNIDYLPKTILFWRSLTHWIGGMGIIVLTIAIMPFLGIGGMQLFSAEYTGNVSPDKIHPRIADTAKNLWLIYIVLTFAETILLYFAGMNFFDAINHSFSTMSAGGFSTKDNSIAYWRNNELIQYILTFFMALSGTNFVILYFLSRLKWKKAWQNEEFKSYLAIILIISAIISIVYYFHYYKEDSFNFDNLENAFRFSIFHTTSILSTTGFIFTDYTTITPLVTLLLFSLFFVGGSAGSTAGGIKIIRQVILLKNSIIEYKRILHPNAVIPVRYGGKAISQKIVYNILAFFVMYMFIWVSSAILFSLINDDLSKDYESILSSLTVTASSLGNVGPGIGVYGPTSNMSNLTNAAKLLCNVLMILGRLEIFTFVIIFTPYFWKSN	
1.2E-59	212	28.2	1.1E-58	208.4	19.6	2	1	Q28LE6_JANSC	K+ transporter Trk	Jann_3549	Jannaschia sp. (strain CCS1)	449	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Jannaschia, Jannaschia sp. (strain CCS1)	290400	>tr|Q28LE6|Q28LE6_JANSC K+ transporter Trk OS=Jannaschia sp. (strain CCS1) GN=Jann_3549 PE=4 SV=1MARGRVRFEISLQKARLSPPALLACIYGLFIVFGAIILWLPVSQTGEVTLSDAFFTAASAVTVTGLVVVDTGSDFTLIGQIVIALLIQVGGLGLMTFAALLLTMLGMTIGMPQRLALRDELGQTGLSELSALIRIVILVAFTAEAIGTAALMFVFVPDYGWSAGFWQALFHAISAFNNAGFSLFSDSLSAYVADPVVNITITALFIVGGLGFVVLADINKQRRWSKLMLHSKLMLSGTLFLIVFAWLMFALLEWNNPATLAGLQTDGARIWASWFQAVTPRTAGFNTLDYAQMNDSTTIMTLALMLVGGGPSSTAGGIKVTTLIVLALATLAFFRRQERLDMFGRSIGVSEIMKVLALTALSIFLVLTGLFLVSLTYEGEFIDLVFEVFSAFGTVGLSRGATGELDEFGRLVIVVMMFVGRLGPLTLAFFLATQTKPKVRYPEGRVFLG	
1.3E-59	211	29.4	2.5E-59	210.5	20.3	1.3	1	K9TTI7_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Chro_0308	Chroococcidiopsis thermalis PCC 7203	444	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Chroococcidiopsis, Chroococcidiopsis thermalis, Chroococcidiopsis thermalis PCC 7203	251229	>tr|K9TTI7|K9TTI7_9CYAN Potassium uptake protein, TrkH family OS=Chroococcidiopsis thermalis PCC 7203 GN=Chro_0308 PE=4 SV=1MTVPRTISLGFLAVIAVGTLLLMIPFSSSSGDWTNPIVALFTSTSAVCVTGLSVVDVGTYFSFFGQVILVALVQIGGLGYMTATTFLLVLIGVKFGLRDKVAIQQALDRTGLSNSADLIRSIIGVTLIFEITGIFLLLPVFTPQYGLDRALWLAIFHSVNSWNNAGFSLFKDSFIGFQSSILLNLVVTGLIIFGGIGYGVLFQIYIYLRDRLQRKSERVVFSLDLKVAISTSLILLIAGTVAFFLIESRNPNTFGNLSWQNKILAAWFQSVTPRTAGFNTIDIGKMTNAGLFLTIAFMFIGASPGGTGGGIKTTTLRVLTSCTKAILQGKEDVLLYERQIPLNLILKAVGVLVGSIATVILATILISLTDPNIDFIQILFEVVSAFATVGLSTGITANVSAAAKLVLIATMFIGRVGILLLIGAVLGDPRPTAIHYPEENLLVG	
1.3E-59	211	25.8	5E-59	209.5	17.9	1.8	1	R6T1Z6_9BACE	Trk system potassium uptake protein TrkH	BN532_00671	Bacteroides finegoldii CAG:203	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides finegoldii CAG:203	1263045	>tr|R6T1Z6|R6T1Z6_9BACE Trk system potassium uptake protein TrkH OS=Bacteroides finegoldii CAG:203 GN=BN532_00671 PE=4 SV=1MINSKMIFRILGFLLLIETAMLLCCGGVSLFYEEGDLKSFLISSALSAGIGVVLLAIGKGAEKSLNRRDGYVIVSVAWVTFSLFGMLPYYIGGYIPNVADAFFETMSGFSSTGATILNNIESMPHGILFWRAMTQWIGGLGIVFFTIAVLPIFGVGGIQVFAAEASGPTHDKVHPRIGVTAKWIWGIYAGMTGTLIILLTVGGMSIFDSVCHAFTTTSTGGFSTKQASIEYYHSPYIDYVISIFMFLSGINFTLLLLMFNGKIKKKFIHDAELKFYFLCVVSFFTIFIAVWLYQTSPMSVEEAFRKSLFQVISLQTSTGFATADYMLWPSILWGCLLIVMIIGACAGSTTGGIKCIRMVILFKVVKNEFKHILHPNAVLPVRVNKQVISPSIQSTVLAFTFLYAVISIISILIMMGLGVGFLESIGTVISSMGNMGPGLGTCGPAFSWSELPDAAKWLLSFLMLLGRLELFTVLLLFTSDFWKKN	

1.4E-59	211	33.5	2E-59	210.8	23.2	1.1	1	B0K7C0_THEP3	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Teth39_2062	Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Thermoanaerobacter, Thermoanaerobacter pseudethanolicus, Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	340099	>tr|B0K7C0|B0K7C0_THEP3 Potassium uptake protein, TrkH family OS=Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) GN=Teth39_2062 PE=4 SV=1MIFIIKIKLTPTQVLALGFATIILIGTLLLMLPVATKSGERTDFLTALFTATSATCVTGLVVVDTKTYWSVFGQIVIMLLIQVGGLGIMTMSTLFALILGRKITFKERLVMQEAFNTNSLGGIVKFAKYILMVSFLFESIGAIMLTLRFLPQMGLKKAVYYGLFHSIASFNNAGFDLMGNFKSLTGYVSDWVVNLVVMGLIIFGGLGFYVLLDIYEHRHFNKFTLHSKIVITITLLLIAIGTLLIFLFEYNNPKTLGPLDFPTKILAALFQAVTPRTAGFNTLSLSDMTIASKFLTIILMFIGASPAGTGGGIKTTTFAVILYTVLSVIQGEEETVLYKRTISRNIVYKAVAISFISVFIIFSVTMVLSITETSNFLTVLYETTSAFGTVGLSLGLTPELSTVGRIIIIFTMYTGRVGPLTLALALAKRQRRPKPIIKYAEEKIMVG
1.4E-59	211	32	1.9E-59	210.9	22.2	1.1	1	A0A0C2YEY0_BACBA	Potassium uptake protein, integral membrane component, KtrB	SD77_2552	Bacillus badius	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus badius	1455	>tr|A0A0C2YEY0|A0A0C2YEY0_BACBA Potassium uptake protein, integral membrane component, KtrB OS=Bacillus badius GN=SD77_2552 PE=4 SV=1MRIIRKKALKPSQIIVAFYLIATIVSTALLSLPIALKPGVHLSFLDALFTAVSAISVTGLSVVPIVDTFSTAGIFILMFILQFGGIGIMTLGTFIWMLARKRIGLKGRQLIMTDQNQSQLSGLVNLMRQILAIIVLIELIGTMILGTYFLNYFPTWQEAYYQGLFAAISATTNAGFDITGSSLVPFAQDYFVQFVHIILLILGAIGFPVLIELKNFMVSKKNQSGPFFSLYTKLTTITFFSLLVFGTIMILLLEANHFFQGKSWHESFFYALFQSATTRNGGLATMDVSEFSDPTLLVIAFLMFIGASPSSVGGGVRTTTFAVNLLFLYSFAKGYKNTKVFKRELHIEDVRKSFVVTFTAFFICFIATIALSATEPFSLMEISFEVSSAFGTTGLSMGITPELSSAGKCVIILLMFIGRIGILSFIFLLSKGTPQENYHYPKERVIIG
1.5E-59	211	20	3.3E-58	206.8	13.8	2	1	R5MLQ6_9BACE	Potassium uptake protein TrkH family	BN711_02215	Bacteroides intestinalis CAG:564	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides intestinalis CAG:564	1263049	>tr|R5MLQ6|R5MLQ6_9BACE Potassium uptake protein TrkH family OS=Bacteroides intestinalis CAG:564 GN=BN711_02215 PE=4 SV=1MINFKTVIRIIGILLLLETVMLLACSGVSFYYQDEALVDFWVSAGITAGAGLLLAAMGKGGDRQLTRRDGYVLVSFAWIAFSLFGMLPFYISGYIPSITNAFFETMSGFSSTGATILDDIESLPHGLLFWRSMTQWIGGLGIIMFTIAILPIFGVSGLQVFAAEASGPTHDKVHPRIGITAKWIWSIYAGITCILVALLMLGGMDWFDSVCHAFATTGTGGFSTKQASVAYYQSPYIEYVISIFMFISGINFTLLLFFVNRKFKKVIHDAELKWYFWSVILFTGLIAVILFYSKPMGMEDAFRKSLFQVISLHTSTGFATDDYMLWPAVTWGLLTIVMLMGACAGSTTGGLKCIRMVILGKVARNEFKHILHPNAVLPVRINKQVISPSVQSTVLAFCFIYAVIIISVLIMMGLGIGFVESVGCVVSSIGNMGPGLGETGPAFSWNALPDIAKWLLAFLMLLGRLELFTVLLLFTPEFWRRS
1.5E-59	211	25.4	2.1E-58	207.5	17.6	2	1	R5UW80_9PORP	TrkH family potassium uptake protein	BN709_01805	Odoribacter laneus CAG:561	482	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter laneus CAG:561	1263089	>tr|R5UW80|R5UW80_9PORP TrkH family potassium uptake protein OS=Odoribacter laneus CAG:561 GN=BN709_01805 PE=4 SV=1MINIRFIINLLGKLMLIESACFLLCVLISLLYRENDTLAFLYSTLITGGTGAIMVFGIKANDKVLAKKDGYFTVTFIWLFFSLFGCLPFILGNTIPSFPDAFFETMSGFTTTGSSILNDIEALPHASLFWRSMTQWLGGLGIAVLFLAILPSLGIEGRDLYVAEVPGPTHNKMAATFYSSARKLWLFYLFFTLLEAVLLSIGGMGIFDAICHSFTTMATGGFSTKQDSIAYWNSPYIQYVIIVFMCIAATNFGLFYAALKGDVKKLLLDEEFRWYMILILGATTIIATGLYWANWGEEEKCIRDALFQVVSIMTTTGFATADYLYWPTLLGLILFILMFIGSCASSTAGGIKVIRVVLLFKNSFTEMKRIIHPNAVINVKYNDKSVHPTIMTSVMGFFILFIIVFSIGSVIMAFFTEDIATACSAVITSLSNIGPGFGSLGPMDNFAHLSDVAKLFLAALMLIGRLEVFTVLVLFTKAFWKK
1.5E-59	211	35.9	3.2E-59	210.2	24.9	1.4	1	C9AB21_ENTCA	Cation transporter	ECBG_02349	Enterococcus casseliflavus EC20	468	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus casseliflavus (Enterococcus flavescens), Enterococcus casseliflavus EC20	565655	>tr|C9AB21|C9AB21_ENTCA Cation transporter OS=Enterococcus casseliflavus EC20 GN=ECBG_02349 PE=4 SV=1MNFTRFARLTQRRSKTFISQNVSSIQVIVFYYIVMTVVSLGLFSLPFFREPGSHVAFIDLFFMAVSTVSVTGLTTFPINDVFNDHGVILLEVLFQVGGLGIMMISTFFAIVSRRKISLKQRQLIMTDMNQPKLSGIVRMIRTTFTIIILLCQVVAGTIFAVYFHLYGYYDNWRDAIFYGFYQAISAVTNSGFDVTGNSILPFSHDYFFLTCIMILIFIGGIGFPVIMDFREWVLFKMKKQRRRLPFRFSLFTKIAVLAFVILFVGGTLAIFFLEKDYLFKDYSFSGMWMNSMFYSMTTRNAGLQIHDLGNFQTTTLIVFSLLMFIGCSPSSVGGGIRTTTIAIIGLYLYAFLKSEDNINIFGRRIDQDDVRKSVVVFMLSMGMCFFCVLFLTAIEDIPLIAIIVEVSSAFGTTGLSLGITGDLSTIGKLVIALLMFIGRVGMLYTLMLFVPKETRDLGYEYPTEKIIIG
1.5E-59	211	32.3	2.1E-59	210.7	22.4	1.1	1	K9QY86_NOSS7	Potassium uptake protein, TrkH family	Nos7524_4362	Nostoc sp. (strain ATCC 29411 / PCC 7524)	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain ATCC 29411 / PCC 7524)	28072	>tr|K9QY86|K9QY86_NOSS7 Potassium uptake protein, TrkH family OS=Nostoc sp. (strain ATCC 29411 / PCC 7524) GN=Nos7524_4362 PE=4 SV=1MTVSRTICLGFLAVITVGTILLMMPFSTSSGNWNDPIVALFTSTSAVCVTGLAVVDTGTYFSFWGQLFILMLAQIGGLGYMTTTTFLILLIGRRFDLRQKVAIQQALDRPGMSGSTQVIRSIIATTLIFEITGIFLLMPAFVADYGWNQGIWLAVFHSINAWNNAGFSLFPDSLIRYQSSWLVVLTITFLIIAGGIGYQVILETYIWLRDRLLKKKATLVFSLDFKVATSTTMILLFLGTVAFLCIEIRNPETFGNQSLSHQLLLAWFQSVTPRTAGFNTIDIGKMTTAGLFITITLMFIGASPGGTGGGMKTTTLRVLTSCTKSILQGKEEVLLYERKIAISLILKAVGVLVGSVATVMLATILIAVTDPKLDFIEILFETVSAFATVGLSTGITGTVSTVAKFILIITMYVGRVGVLLLMSAILGDPRPTRIHYPEENLLVG
1.5E-59	211	25.7	2.3E-29	111.6	7.5	2	2	Q899E6_CLOTE	Potassium uptake protein trkH	trkH CTC_00235	Clostridium tetani (strain Massachusetts / E88)	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium tetani, Clostridium tetani (strain Massachusetts / E88)	212717	>tr|Q899E6|Q899E6_CLOTE Potassium uptake protein trkH OS=Clostridium tetani (strain Massachusetts / E88) GN=trkH PE=4 SV=1MNYGIIIKVLGNILSVEAILMVPSLLVSLYYNQSDKLSFIISIVLISIIGIILSKKTVYKKSIKAKEGLAIVALGWVLCSFFGSLPFVFSGSIPFWIDSFFETVSGLTTTGATLIDNIEVLPKGILFWRSFTHWIGGMGILVFTVALLPTIGVGGFQIFKAESPGPTAERIVPRIKDTAKILYITYVTITILEIILLRIGGMSLYESTVHTFATVGTGGFSTRNSSVGAFNSTYIHIIISIFMLLSGISFSLYYALFKGRWKDALRNEELKLYLGIVLSSVVLIALNINSEIYHNIGLALRDALFQVSSIITTTGYATTNFDEWPTFSKSILFLLMFVGGCAGSTSGGIKSIRILVLAKLVKREFYKILHPRAIIPIKNRERAIPNETVASISSFFILYMAIFILGTILISLEGINFESAASATASMLGNVGPGFGFVGPTCTYSGFSGISKLLLSLLMLLGRLELFTIIALFMPTTFKNNFDS
1.6E-59	211	29.5	2E-59	210.9	20.5	1	1	D3QZV4_MAGIU	Potassium uptake protein, TrkH family	HMPREF0868_0109	Mageeibacillus indolicus (strain UPII9-5) (Clostridiales genomosp. BVAB3 (strain UPII9-5))	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Mageeibacillus, Mageeibacillus indolicus, Mageeibacillus indolicus (strain UPII9-5) (Clostridiales genomosp. BVAB3 (strain UPII9-5))	699246	>tr|D3QZV4|D3QZV4_MAGIU Potassium uptake protein, TrkH family OS=Mageeibacillus indolicus (strain UPII9-5) GN=HMPREF0868_0109 PE=4 SV=1MYHISPSRKIALSFFLIIVAGSILLYLPWLQQPGQHVSFLDCFFTATSATCVTGLSSVTIATAFNNWGHLVIMLLIQFGGLGFMTIMAGFILLLKNRISLTQQLAVRDLLNRRGLFNINSFLKEIVLITIFIESFGAVFMSIALIPQFGILHGIWQAVFLAVSAFCNAGFDILGSTSLIAYRDNWLICGIVMLLITIGGIGFAVWYDVKEYYANLRLRRQKELPRRAWQSLSTHSQIALIASAVLIVLPALLILLQETTNPKTLAGETYGGKILQALFQSVTLRTAGFASVDIGSLTSATKLLMLPVMFIGGSPGGTAGGIKTTTAVLIFCFIISLIKNRAHVSIFKRTIPTALLHKSLAVGGISVVFLSISIYLLSLTETAPIFDLAFEAVSALATVGLSTGITATLSGWGKLIIIILMFAGRIGIVTLIFSLIDPSEVVSRRQYPSGHVLVG

1.6E-59	211	34.3	2.3E-59	210.6	23.8	1.1	1	A0A0A7FYY1_9CLOT	Potassium uptake, TrkH family protein	U729_2894	Clostridium baratii str. Sullivan	448	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium baratii, Clostridium baratii str. Sullivan	1415775	>tr|A0A0A7FYY1|A0A0A7FYY1_9CLOT Potassium uptake, TrkH family protein OS=Clostridium baratii str. Sullivan GN=U729_2894 PE=4 SV=1MRKIFMKKIKLDAVQILALGFGLVILIGGIILSLPISSASGKSTDFLDALFTSTSAVCVTGLITLDTGTYWSQFGQIVIMLLIEVGGLGFMSFATFIAVLLGKKITLRDRLVMQEALNTFSIQGLVKMVRYVLGFTFAVQFFGALLLSTQFIPQFGLAKGIYFSIFHSISAFCNAGFDLMGGFSSVTAYSSNAVILITISSLIIIGGLGFTVWLELYNYRGLKKLSVHSKVVLLITVILLIGGTILMFLFEMNNPETMGHMSFGDKVLNSYFASASPRTAGFNSVVSTDGMTNSGKFLTIILMFIGGSPGSTAGGLKTATFGVILLTVISVIRGREDTQVFGRRFSKDLVYKAFSLLIIGMSLVIGVTLILSITEPNESFINILYEATSAFGTVGLTTGVTQRLSSIGKVIILITMYFGRVGPMTVALAFLRNKKKQTHKYPEGKILIG
1.6E-59	211	30.5	2.1E-57	204.2	21.2	2	1	A0A0F2QBV3_9CLOT	Uncharacterized protein	VR72_02135	Clostridiaceae bacterium BRH_c20a	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, unclassified Clostridiaceae, Clostridiaceae bacterium BRH_c20a	1629719	>tr|A0A0F2QBV3|A0A0F2QBV3_9CLOT Uncharacterized protein OS=Clostridiaceae bacterium BRH_c20a GN=VR72_02135 PE=4 SV=1MKYDLILASISRILIVVGISMIIPLLWSFFYGDGSAKAILYSIFTIIAVALSLFYFFPLKIRQITYIEGYLIVTISWLAISLFGTLPYLFSGVMNFTDAFFETVSGFTTTGASILSDIESLPKGILMWRALTQWLGGMGVIVLFVALVSQFGVGANKIFAAEAPGTVVEKVTPRISDTARSFWSIYMIFTVLQIISLYLAGMNFFDSMAHTFTTIATGGFSTKNTSIGYFMDNTAIQIVITLFMFLGGTNFALFYYLYKEKSFKVFWRNEEFKLYFKVVLVATSIILLSLYLGNPEKHGILPVTALFQVVSITTTTGFATVDYDAWPNLARNIMFLLLFVGGSLGSTAGGIKMARFLILLKATGAEIKRFLHPRLVTGIKINKIPITEKVISNTFVFFFVYLGIVSISTLILSFADYDLETSLTAVLACIGVIGPGLANVGPAANFSDFPIWSKYFLSLLMLIGRLEFFTILVLFYSTPLNKKN
1.7E-59	211	24.4	1.3E-58	208.1	16.9	1.9	1	R5YIZ1_9BACE	TrkH family potassium uptake protein	BN496_01264	Bacteroides sp. CAG:144	487	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:144	1262736	>tr|R5YIZ1|R5YIZ1_9BACE TrkH family potassium uptake protein OS=Bacteroides sp. CAG:144 GN=BN496_01264 PE=4 SV=1MAEINYRIILKIIGVLLWLEAASMLMPLGISIYYGENDTTAFLITIGIAAVIGSILFFQYPNTERKTLGKRDGIMVVSLCWICFSLLGSLPFILSGAVDNMAEAFFETVSGVTGTGASIITDVEKLPHGILLWRSLIQWLGGLGIILLTLAILPLINSGGSMQLFNAETTGIMNDKLGPRIGQTAKLLWTTYLGLTIVLIILLKLGPMNLFDAVCHAFTTAATGGFSTKNDSIAYWNSAYTEYVITIFMLISGINYALVYRAIRGEIKKTFGNEEVKWYLTIVVVLFTILIVIGLFFNGVYERLGLEATIRASLFQVSSIITSTGFISADYVSWGPFFCILICLLMFCGGCAGSTSGGAKVIRIVVVLLKNTIYEFYRQVHPNTIVPVRINQQAISHEIITKILAFLFTYAIIVIIGALTLATMGLTIDEAFGCSLSCIGNIGTGLGRTLYSFAIIPDAGKWLLSFIMLIGRLEIFTILILFTSYFWKK
1.7E-59	211	23.7	4.2E-59	209.7	16.4	1.5	1	G4R8T4_PELHB	Trk system potassium uptake protein	KKY_325	Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	481	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Pelagibacterium, Pelagibacterium halotolerans, Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	1082931	>tr|G4R8T4|G4R8T4_PELHB Trk system potassium uptake protein OS=Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2) GN=KKY_325 PE=3 SV=1MDFRTIFSAIGALTAALGLAMLLPALADLVVGNEDWLVFLTASLITMIFGAGLWASSTGHKSELNLRQAFLMTVSIWVVLTIFGALPLYMSNLGLSFTDAMFEAMSGITTTGSTVITTLDTTAPGILLWRGLLQWFGGLGVVVMAIAVLPMLRVGGMQMFRAEAFETPDKILPAAAQIATAMVIVYCILTFACAVAYWLAGMGAFDALVHSLSTVATGGFSTRDASLGAFDQPAIHYVSVVFMILGALPFVLYVGMLQGSFGELFRDSQVRLFLYLIGLATMIVVFVQLTGDIARGEEAFRHGLFSVVSIITGSGFGVADFSTWGPLAASLFFVIMFIGGCTGSTSCGIKIFRFQVLARDLYQHIREIVFPSLVYVKRYNGRPLPDTVSTSVQSFVFIYFSSFLLLAVLLSLSGLEPLDALGAAATAISNVGPALSPELGPAGSFAGVSDVTKWLLTIGMLVGRLEVLMVLVLFTPRFWRA
1.7E-59	211	12.6	2.6E-59	210.5	8.7	1.1	1	D1C995_SPHTD	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Sthe_2985	Sphaerobacter thermophilus (strain DSM 20745 / S 6022)	492	cellular organisms, Bacteria, Chloroflexi, Thermomicrobia, Sphaerobacteridae, Sphaerobacterales, Sphaerobacterineae, Sphaerobacteraceae, Sphaerobacter, Sphaerobacter thermophilus, Sphaerobacter thermophilus (strain DSM 20745 / S 6022)	479434	>tr|D1C995|D1C995_SPHTD Potassium uptake protein, TrkH family OS=Sphaerobacter thermophilus (strain DSM 20745 / S 6022) GN=Sthe_2985 PE=4 SV=1MVEQCEASSGVSDPGQPRSGTPPRYTRRPGDRVVRRAVLRPEAVTLAAPKARRRPRPPALVPVLGFAGVILVGAILLSLPIATTSGRSTPFIDALFTATSAVSVTGLVVVDTGTHWNAFGQAVVLALIQIGGLGFMATSTLLLMLVGRRATLRDRMALGLTMGTPEPGGAMRLLRRIALMTLIIESVGVLLLFLRFTQEMPPGRALWWGLFHGISAFNQAGFDIVGGFQSMIPFQRDPWILLTMAVLITLGGIGYTPLADVLRCRTWRRLTVDTKLVLSTTAALLAVGMVGYLIMEWNNPATLGHLPWGDRLLNGYFQSVTPRTAGFNAIPIGEMRDQSLVFTIALMFIGGASGSTAGGVKVQTFSLLFFAILAAISGRESVVAFGREIPPRQIYQALAVVLLAIAVVFLVALGLTVFEPFDAIDVAFETVSGFGTVGLSTGITPQLGPGSRLFLIAIMFTGRLGPLTLALALAARPTRRGIGYARENVKIG
1.9E-59	211	23.1	2.4E-59	210.5	16	1	1	R7FQ61_9FIRM	Potassium uptake protein TrkH family	BN651_01413	Dorea longicatena CAG:42	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea longicatena CAG:42	1263074	>tr|R7FQ61|R7FQ61_9FIRM Potassium uptake protein TrkH family OS=Dorea longicatena CAG:42 GN=BN651_01413 PE=4 SV=1MKKTGKQNIRWNTMKILAVGFLSVIFLGAVLLWLPVSNEKSISFLDALFTSTSSVCVTGLVTIVPKYQFTITGKVILLIIQIGGLGVIACITAFFMLLKRKITVKERVVIQEAYNMNSLGGLVGLVRKILIGTVVVEGIGAVFYAIQFIRDYGVAKGIWYGIFHSISAFCNAGIDILGDDSLARYATDPLINIITMLLIILGGIGFTVWYDVIDNGKKIWHREIPGKCWFTRLKLHSKIAIITTGFLLIAGTVLNFALEYHNPATIGHLNTGQKLMVSAFQAVTTRTAGFSTFQQSGMYEETGFLNIILMFIGGSPGGTAGGLKTTTFALLFLAFHTMLRGGHDIECFRRKVDEKNFHVAFVTIMLALAIYITGTTFVAVIEPDTISFQRIMYETASAMATVGLSQDLTTHLRTGSKIVLMIMMYIGRVGPMTIALLFAGKVNLKEKMRTLPTEKIMIG
2E-59	211	22.7	9.2E-58	205.3	15.7	2.1	1	D2RGJ9_ARCPA	Potassium uptake protein, TrkH family	Arcpr_0354	Archaeoglobus profundus (strain DSM 5631 / JCM 9629 / NBRC 100127 / Av18)	470	cellular organisms, Archaea, Euryarchaeota, Archaeoglobi, Archaeoglobales, Archaeoglobaceae, Archaeoglobus, Archaeoglobus profundus, Archaeoglobus profundus (strain DSM 5631 / JCM 9629 / NBRC 100127 / Av18)	572546	>tr|D2RGJ9|D2RGJ9_ARCPA Potassium uptake protein, TrkH family OS=Archaeoglobus profundus (strain DSM 5631 / JCM 9629 / NBRC 100127 / Av18) GN=Arcpr_0354 PE=4 SV=1MNFGLVINTLGKISLAFFALMVGLTILAIYFNEDPVPFLTSSLFSLGLGILLTAKKAESDVLRFKEGFAIVGLGWLLVSFLGSIPFMYYIHPINAFFESISGFTTTGASVIDKPELLPRSILFWRSLTQWIGGIGIIMIFLLIIPNIATGAVFQAEYPGITLVKIKPRIRDTALRLYLIYVSLTVAEIVILKFLGVPIFDAVTHAFTTLSTGGYSTHSQSIAYFKDWRVEFSIAIFAILGGSNFSIFYFLCLRRFEVLRDREFIIYILLVTILTLVTITLLNLDRYDLINSFRYSFFQVASIITTTGYTTTDFDKWGSGAKMLLLIAMFIGGCSGSTAGGMKVIRLYIMSKYAISQVVKSAEPKVVRIIKYGDRALRSDIVESVVAFFVLYIFIFTISSLIIALHGYDIVTSLSATAACLGNVGPGMGLAGASETYSHFPWTIKILLCLDMWIGRLEIYTVLALFIPSFWR
2E-59	211	32.7	3E-59	210.2	22.7	1.2	1	B0JWK8_MICAN	Trk system potassium uptake protein	MAE_18660	Microcystis aeruginosa (strain NIES-843)	421	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Microcystis, Microcystis aeruginosa, Microcystis aeruginosa (strain NIES-843)	449447	>tr|B0JWK8|B0JWK8_MICAN Trk system potassium uptake protein OS=Microcystis aeruginosa (strain NIES-843) GN=MAE_18660 PE=4 SV=1MPVSTTSGTWNDPIVALFTSTSAVCVTGLAVVDTGTYFSFWGQLFIALLVQVGGLGYMTTTTFLMLLVGRKFDLRQKLAIQESFDRPFLQGSQSLMKSVIATTLVFELTATLVMLTVFAQKYDFRYAVWLSLFHSISAWNNAGFGLFKDNLMSYQSSIIINLSITGLIIFGGIGYQVIIEFYTWFEIYRFQYKRKGFVFSLNYKVAISTTIFLLVMGTLAFLFTEQGNGDTLANLSIKDKLLAAWFGSVTSRTAGFNTIDIGKISVEGLSITMALMFIGASPSGTGGGIKTTTFRILYNCTRSVLRGREEVTLYQRRIPTPLILKSMAVVFGSVIAIIISTLAISFVETDFQMIQLFFEVVSAFGTVGLSMGITAALSPISKLIIVFMMYLGRVGVILLIAAIIGDPKPTVINYPEENLLVG
2.1E-59	211	28.8	2.6E-58	207.1	20	2	1	R6DJH5_9BACE	Trk system potassium uptake protein TrkH	BN772_03401	Bacteroides sp. CAG:754	478	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:754	1262750	>tr|R6DJH5|R6DJH5_9BACE Trk system potassium uptake protein TrkH OS=Bacteroides sp. CAG:754 GN=BN772_03401 PE=4 SV=1MIFRILGFLLLIETVMLLCCSVVSLFYKEDDLQSFLISSAITASIGFILLAIGKGAVKSLNRRDGYVIVSAAWVAFSFFGMLPYYIGGYIPSLTDAFFETMSGFSSTGATILNNIESMPHGILFWRAMTQWIGGLGIVFFTIAVLPIFGVGGIQVFAAEASGPTHDKVHPRIGITAKWIWGIYAGMTGTLIVLLVFGGMGVFDSICHAFTTTSTGGFSTKQASIEYYHSPYIDYVISIFMFLSGINFTLLLLMFNGKIKKFIHDAELKFYFICVSFFTIFIAAWLHFTSSMGIEEAFRKSLFQVISLQTSTGFATADYMLWPSILWGCLIIVMIIGACAGSTTGGIKCIRMVILFKVVKNEFKHILHPNAVLPVRVNKQVISPSIQSTVLAFTFLYAVIALISILVMMGLGVGFLESVGTVISSMGNMGPGLGTCGPAFSWSELPVVLAKWLLSFLMLLGRLELFTVLLLFTSDFWKKN

2.1E-59	211	31.3	2.9E-59	210.3	21.7	1.1	1	A0A0A2TVP5_9BACL	ATP synthase subunit J	P364_0123380	Paenibacillus sp. MAEPY2	444	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. MAEPY2	1395587	>tr|A0A0A2TVP5|A0A0A2TVP5_9BACL ATP synthase subunit J OS=Paenibacillus sp. MAEPY2 GN=P364_0123380 PE=4 SV=1MNVQWMRLSPPRILVLGFAGIILLGTLLLMLPASSRSGVSLPFIDALFTATSAVCVTGLVVVDTGTHFSTLGQVVIAILIQIGGLGF MTMSTLVAIAFKRRISLRERLILQEAMNQSTMEGIVRLIRKVVVYSLILEGICGTLFAIRWSFDMPVGQAIYYGYWHAISMFNNAGFDMF GEFRSFTGYVYDPLVNFTAMFLIVSGGIGFVVLSDLVEYRRTKKLSLHSKVVLLTTGLLIVCGALVIFVFEFSNPRTLGGLNWGGKILGS FFQSITPRTAGANTVDIAGLRQATQFFIIILMFIGASPGSTGGGIKTTTFMMIMIGAVVAMIRGREDIVFFRYRLLQERIFKALTITLLALLLIIA VTMVLSTTEDSSFLTILFETTSAFSTVGLSMGLTLKLTTIGKILICFTMFAGRLGPITLAYALGQKKGKELYRYPEGKMIIG
2.2E-59	211	29.1	1.4E-57	204.8	20.2	2.1	1	R5UN70_9FIRM	Uncharacterized protein	BN518_00789	Roseburia sp. CAG:18	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:18	1262941	>tr|R5UN70|R5UN70_9FIRM Uncharacterized protein OS=Roseburia sp. CAG:18 GN=BN518_00789 PE=4 SV=1MSKVVHRKKRLSSFKLIVLGFAAVIFVGALLLMLPVSSVSGTQTPFHEALFTSVSAVCVTGLVVQDTGSYWSSFGQAVILLLIQT GGLGVITVAVSFAILSGRKISLMQRSTMQDAISAPKIGDIVRLTKFSVQGTLFIELLGMTAMLPVFFRDYGIKGIWMAAFHSVSAFCNAG FDLLGTSNQPFVSLSRYIANPLINLVIMLLIIIGGIGFLTWDDICTHKWHIRRYRVQSKVILWTSALLIIIPAVFFFVVDFTGSSTGTRLLAST FQSVTTRTAGFNTADLTAMTPTSKSVMIMLMLIGGSPGSTAGGMKTTTFAVLILNMVATFRQKEDIEIFGRRLDSHAIKNAATIVALYIIF FFIGGIAISSIEHLPLLDCLFETASAVGTVGLTLGITPTLGIPSQLILILLMFFGRVGGLTLIYAAISVKQNGVKLPLEKITVG
2.2E-59	211	29.7	1.5E-57	204.6	20.6	2	1	R6EGV1_9FIRM	Trk-type K+ transport systems membrane components	BN710_00433	Ruminococcus sp. CAG:563	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:563	1262961	>tr|R6EGV1|R6EGV1_9FIRM Trk-type K+ transport systems membrane components OS=Ruminococcus sp. CAG:563 GN=BN710_00433 PE=4 SV=1MFHNIRFKKHISTFQIIILGFFSIILVGALLLMLPISSVSGKVTPFNESLFTATSAVCVTGLVVHDSGSYWSIFGQAIILLLIQIGGLGV VTVAASFALLSGRKISLMQRCTMQEAIAAPKVGGIVRLTGFILKATLIFELCGAVIMMPAFCKNFGVKGVWFAFFHSISAFCNAGFDILG TESLQYVSLTQFENSISINLAVIFLIIIGGIGFLTWEDIYTNKLNFKKYRMQSKVILVTSAVLVIIPALYFFFFDFTNLPIKQRILPSLFQSVTT RTAGFNTVDLTALREPSIAIMIVLMIIGGSPGSTAGGIKTTTVAVLIANASATFGRKDSAHYFKRRIDNQVVKNASTILIMYLILSFTGAIAIS TVEKMPFLNCLFETSSAIGTVGLTLGLTPELSLFSQLILIVLMFCGRVGGLTLIYAALSNTKKTMSKFPLERITVG
2.4E-59	211	11.1	2.3E-30	115	0.9	2	2	R6GXV7_9FIRM	Uncharacterized protein	BN557_00177	Oscillibacter sp. CAG:241	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, environmental samples, Oscillibacter sp. CAG:241	1262911	>tr|R6GXV7|R6GXV7_9FIRM Uncharacterized protein OS=Oscillibacter sp. CAG:241 GN=BN557_00177 PE=4 SV=1MNYRIIFHTTGKVLLAEAGLLVLPLLVSVLYHERCAWAVLASMAAAAVIGGLLTLLARPRRHTFFNREGYIIVALAWVLLSAVGALP FWFSREIPSYADAFFETVSGFTTTGASILTDVEAMSHGLLFWRSFTHWVGGMGVLVFITMISGSSDRSMNILKAEMPGPVVGKLTPR TRDTARVLYLLYFLITTVLVGMLLLGGMPLFDSLVHAFGTVGTGGFGIKADSIASYSPYIQGVITVFMILCGINFNLYYLLLLRQWRSVLR SDELWTYLGLVVVATGVITLDLRGVYGGLGTCLRQAAFQVGSVITTTGYATADFNVWPGLSRAILFALMFIGGCAGSTAGGLKVSRA MILLRTIRREINRLVHPRRVTAVRCDGKALGSEVQRGVSIYFALYCLCILVAFLCLSGEPFTLETNLSAVVSCFNNVGPGLGAVGPAGS YADYSVLSKLLLSMAMLMGRLEIYPMLVALSPSVWRKD
2.4E-59	211	20.1	4.5E-59	209.6	13.9	1.3	1	U7MTS3_9CORY	Uncharacterized protein	HMPREF1290_00673	Corynebacterium sp. KPL1989	451	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium sp. KPL1989	1203622	>tr|U7MTS3|U7MTS3_9CORY Uncharacterized protein OS=Corynebacterium sp. KPL1989 GN=HMPREF1290_00673 PE=4 SV=1MIFHSGAHRRRGFSPAQLVSVSFLLLILAGTVLLLPVSRSGVDNPEFTTALFTATSAVCLTGLTVVDTATYWSHFGQIIILVLVQI GGLGIMTLATVVSFVLAGQMGVKGRLRAVAEQRGRNLGEVRTVILGTIGFSLAVELVITVVLAIRFATKYGYALLPAVWQGGFHAISAF NNAGFGLQSNNLIPYVNDSGIILPVAAGVIVGGLGFPVLLEIKERRCSKVQRPRSLTLLFTLVGTAILLVVGTIGFGIMEWTNSLRELSPW SAVQAAFFHSVSTRTAGFNSVDLSNLRPSSLMLTDFLMFIGGGSGGTAGGVKVTTAAVLVAVLIAEVRGDDELLVAGRRIPGRIVRQS MAVFMMAFILIAGSIMGLQMLLPQFNSHQITFETISAFATVGLTTGITPELPEFARVWLVVLMYAGRIGPITVVAALAARTNQRRYSLPV ERPFIG
2.4E-59	211	13	3.9E-59	209.9	9	1.2	1	A0A0F7NEY8_9ACTN	ATPase	AA958_27095	Streptomyces sp. CNQ-509	457	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. CNQ-509	444103	>tr|A0A0F7NEY8|A0A0F7NEY8_9ACTN ATPase OS=Streptomyces sp. CNQ-509 GN=AA958_27095 PE=4 SV=1MRGWLRSTSRSLLATHPARLVVVAFGLVVLIGTLLLSLPVAAEDRSATGFVPSLFTATSAVCVTGLTVVDTGTHWSAFGEGVILA LIQVGGFGIMTLASLLALLVVGRLRLRLQLTAQVETKTLGLGDVRRVLLGVAGTTLIVELSVAALLALRFRFGYDQGVGESAYSALFHAV SAFNNAGFGLHVDSLTRYATDPWVTVPVAAAVICGGLGFPVLLEVLRYRHRRRVSGRRGWSLHAKLTLTTTAVLLVAGAALTCALEW SNGATLGPFGTGEKLLSGFFHSAMTRTAGFNAVDIGALHPATLLVTSVLMFIGGGSAGTAGGIKVTTFAVLAVAMVAEVRGEPAAETM GRRIPPAALRQALTVALLAIGLVISATVVLLTMTQERFEAVLFETVSAFGTVGLSTGITADLPAAGQVVLVLLMFVGRVGPITLVSALALR ERTRRFQLPEERPVIG
2.6E-59	211	22.8	2.4E-58	207.3	15.8	1.9	1	A4J8L3_DESRM	Potassium uptake protein, TrkH family	Dred_2912	Desulfotomaculum reducens (strain MI-1)	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum reducens, Desulfotomaculum reducens (strain MI-1)	349161	>tr|A4J8L3|A4J8L3_DESRM Potassium uptake protein, TrkH family OS=Desulfotomaculum reducens (strain MI-1) GN=Dred_2912 PE=4 SV=1MHIHLVLKTMGLVLLFEAAAMVPSLFIGVYYDGTNLNPFLASIGVTGLIGFVLYLIPIRSKNVGYREGFAIATFGWLLLAIFGALPFTI AGAVPSYVDALFETMSGFTTTGASVISDVEALPKSILFWRSFTHWLGGMGIIVLTLALIPSLNIAGLQMFKAEVPGPTKSKVLPRIAQTS RQLYKVYLIITLTQLVALKLAGLTWFDSAIHTFGSVATGGFSNYNSSVGHFQSLSVELIIIFFMLICGINFSLHYSVLRGNFKTLYKDTETK FYLGIIALSCLAIMLNLIHDLDYTAGKALREAAFQVATIITTTGFATADFEQWPSFSKFILLLLMFCGGCAGSTSGGLKVGRILILIKTFSRQ LMRLIHPKAVIPVRLGTFVASNEVIESAHTFFTLYILIFAVGTGIMTALGLDLISAASATVATLSNIGPGLGLVGPMSNYAAALPDLGKIILTFL MLIGRLEIYTVLLVFSVRFWR
2.6E-59	211	19	3.6E-59	210	13.2	1.1	1	T2GDB0_DESGI	Putative H(+)-transporting two-sector ATPase	DGI_2145	Desulfovibrio gigas DSM 1382 = ATCC 19364	453	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio gigas, Desulfovibrio gigas DSM 1382 = ATCC 19364	1121448	>tr|T2GDB0|T2GDB0_DESGI Putative H(+)-transporting two-sector ATPase OS=Desulfovibrio gigas DSM 1382 = ATCC 19364 GN=DGI_2145 PE=4 SV=1MRVSLASPLMLPIVSFAAAILLGGILLAHPVSEGSTEVSLLDGLFTATSAVCVTGLAVVDTGTAFSPVGHGVLLSLIQAGGLGIMTF ASLAFYLWRHRVSLTDRIAVGQTLLHDQGFHLGRFLVALFAGVFGIEALGALALHLADPQGFPVFGAVFHSISAFCNAGFGLYSDSLM QWRGDWAVNGIVMLLIILGGLGFSTLTELAMVLPRRLRHRHMTLQPRLSFHTRLVLRASAWLIVGGWVAILFMEVMTDIRIGHLETDD FLLAALFQSVTCRTAGFNTVDIASLSSITLLFMMFLMFVGGSPGSTAGGIKTTTFRVILGFIGSQLRRREQTVVGNRAVDADTLNRAIILT IFSVLAVLAAIMALCITEAGGTDRMVRERFLDLAFEAVSAFGTVGLSTGVTPTLSAPGKVVIMLLMFTGRLGPIVFLSVMQSWQRSPRY RWADERCMIG
2.6E-59	210	15.3	2E-58	207.6	10.6	1.8	1	G4KU25_OSCVS	Trk system potassium uptake protein TrkH	trkH OBV_06680	Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	478	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	693746	>tr|G4KU25|G4KU25_OSCVS Trk system potassium uptake protein TrkH OS=Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20) GN=trkH PE=4 SV=1MIAYILGKILLVEAALLTLPMVVAMFYRESAEPFLIPMLTLILCGILLSHISPKSRALYARDGLAIVALAWIAMSLFGAMPFYISHSMP TFVDCFFETVSGFTTTGASILTEIEHLGRGVLFWRSFTHWVGGMGVLVFVMAIFPASDGHGMHLLRAEVPGPAVGKLVSRLGDTAKIL YGIYLVMTVAEIVLLLLGGMPLFDACVHAFGTAGTGGFSCRNLSVGAYNSPYFDLVIGVFMLLFGVNFNLYYFLLIGKVREVLRSEELR TYFLIVAAATVTIAWNISHLFESFSTALRYAFFQVSSIITTTGYATADFNLWPPYSRVVLVFLMFAGACAGSTGGGIKIARLVILGKTAVS DMRQMLHPNAVATVRIEGRPVSSKILRSTHVFLVVYLLIMSISTLLLSLDGFDLVTTFTAVVSCINNIGPGLGQVGPMGNFAAFSPASKIL LAFDMLAGRLELFPMLLLAPSLWRRHSFLR

2.6E-59	210	27.8	4.6E-59	209.6	19.3	1.3	1	X5A5R1_9BACL	TrkH family potassium uptake protein	PSAB_21250	Paenibacillus sabinae T27	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	1268072	>tr|X5A5R1|X5A5R1_9BACL TrkH family potassium uptake protein OS=Paenibacillus sabinae T27 GN=PSAB_21250 PE=4 SV=1MFLKGLKMVTGKLSLTSSRIILLGFAIPILLGALLLALPISSSTGNSVGWLNAWFTSTSAVCVTGLVVLDTGTAFSPFGQIVILCLIQIGGLGFMTFGVLIAVVMGRRIGLKERLLIQESANSVTTQGVVRLSLSIFLIAFIVETLGAALLTIRWADELGPTRAIYYGIFHAVSAFNNAGFALWPDSLSRYVGDPSINLVISSLFIVGGIGFTVILDLYRKKRWRDLAFHSKVVVITSGLLCLVGFLVIFVIELFNTRTFGGLSWTERLWAGYFQGVVTRTAGFNSIDVASMMPASQFFMIFLMFIGASSGSTGGGIKTSTFAVLVLSIMATVKGNEDVQLLKKRISQKMIFRALAVMTISVGVVIAAAFLLTITEYRLHKDFLVLLFEATSAFGTVGMSMGLTPELSPLGKLVIIITMFIGRLGPLTLAFALAQRNKKQKYRYPEEKLLIG
2.7E-59	210	36.6	3.9E-59	209.9	25.3	1.2	1	C0Z4U0_BREBN	Probable potassium uptake system membrane components	ktrD BBR47_08400	Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus brevis (Bacillus brevis), Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	358681	>tr|C0Z4U0|C0Z4U0_BREBN Probable potassium uptake system membrane components OS=Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599) GN=ktrD PE=4 SV=1MLSSNQKRRLTSVQIIVFAYVGLILISAFLLSLPFFHLPGASLSFIDSLFTAASAISVTGLTVITIHEVFNQWGILFLTLLFQVGGVGIMTLGTFIWILMGQKIGLEQRIWIATDHNRSTLSGLVDLMRNILVIALMIELVGTILLGSHFIYAGYYDDWYTAFYHGYFASVSAFTNAGFDLHGNSMLDFTHDYVFQTIVMILIICGAIGFPVLVELRTYFSYRRAKVRFTFSLFTKITTLTFFSLIAIGALLIFVFERNHFLVDKSWHEMLFYSLFHSVSSRSGGLATMDISLLSTTTLIMLSGMMFIGASPSSVGGGIRTTTFFVLIASVFANMRGYKDVKVFGRELVDEDIQRSFIVFFIAIILVFTAVMLLVWLEDLPFQYVLFEVCSAFGTTGLSTGITAQMGIGGKLILIITMMIGRIGIINLLLFLKRNDRIVRYHYPKERIIIGQ
2.9E-59	210	33.4	3.8E-59	209.9	23.1	1.1	1	B2IU26_NOSP7	Potassium uptake protein, TrkH family	Npun_F6024	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	63737	>tr|B2IU26|B2IU26_NOSP7 Potassium uptake protein, TrkH family OS=Nostoc punctiforme (strain ATCC 29133 / PCC 73102) GN=Npun_F6024 PE=4 SV=1MTVARTICLGFLAVIAVGAILLMMPFSTSNGTWNNLIVALFTSTSAVCVTGLSVVDPGTYFSFWGQLFIALLAQIGGLGYMTTTTFLILLIGRRFDMRQKIAIQQALDRPGMSGSAQVIRSIIATTLIFEITGTFLLLPAFVPEYGWSKGLWLAIFHSINAWNNAGFSLFKDNLIGYQSSFLVVFTITMLIIFGGIGYQVILEMYLWLRDCLFKKNHNQIFSLDFKVATSTTIILLVIGVIAFFCIEIRNPETFGSLNFRDQILLAWFQSVTPRTAGFNTIDISKMTTAGLFITIAMMFIGASPGGTGGGMKTTTLRVLTSCTKAILQGKEEVLLYDRKIAISLILKAVGVLVGSIATVILATILISLTDPTLDFIQILFEVVSAFATVGLSTGITGSISIIAKLILIIITMYIGRVGVLLLMSAVLGDPRPTRIHYPEENLLVG
2.9E-59	210	18	6.3E-59	209.2	12.5	1.5	1	C0QA06_DESAH	Trk system potassium uptake protein	trkH HRM2_36660	Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2)	482	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfobacterium, Desulfobacterium autotrophicum, Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2)	177437	>tr|C0QA06|C0QA06_DESAH Trk system potassium uptake protein OS=Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2) GN=trkH PE=3 SV=1MRWPYIANVIGILLVFLGLSMVFTLVCSLIYADTSLVALIESMGVTIAAGLLLYFGSRRPTIDYISPREGIAIVALGWTVMGLFGALPFYLGDGLPHFTDAFFESVSGFTTTGSSVLTNIEGLSRSLLFWRSFIQWLGGMGIIVLSLAILPFLGVGGMQLFKAEVPSPVPDKLTPRLSDSAKILWYLYALISVAEVIFLLAGGMDFYDALCHTLTTMPTGGFSTKNTSMAHYDSAYLDYVVVVFMVIAGINFSLHYQMLRGRTLIFWRDSECRFFLGLCLVLSLVIAFNIHGTVYDSFGKAFQYASFQVVSIVTTTGFATADYETWPGLSQAIIFICMFIGASAGSTGGGMKCARVMVCFKYCYRELFVLVHPRSIVQVKLNAAVVPDSVLRSIMGFLALYMGLFVFSSLCLAALGMDMVSSFGAVAACIGNIGPGFGTVGPVDNFAHISAAGKWILIWCMLLGRLEIYTVIVLFVPEFWKK
3E-59	210	24.9	4E-59	209.8	17.3	1.1	1	A5D535_PELTS	Trk-type K+ transport systems, membrane components	TrkG PTH_0457	Pelotomaculum thermopropionicum (strain DSM 13744 / JCM 10971 / SI)	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Pelotomaculum, Pelotomaculum thermopropionicum, Pelotomaculum thermopropionicum (strain DSM 13744 / JCM 10971 / SI)	370438	>tr|A5D535|A5D535_PELTS Trk-type K+ transport systems, membrane components OS=Pelotomaculum thermopropionicum (strain DSM 13744 / JCM 10971 / SI) GN=TrkG PE=4 SV=1MGFVEQEERIVIKKNSERRLTVGATPPQVLVVGFAAIILAGALLLTLPASVRPGGEINFLTSLFTATSAVCVTGLVVVDTGTHWTFFGQLVILTLIQVGGLGFMTMATFFAILMGRRIGLRQRLIMQESLNQTSVSGIVRLARHVLVFTFSAELVAATILSVRWAADLGWQKGIWYGLFHSISAFNNAGFDLFGEFRSLTGYVEDVTVNLCITTLIILGGIGFSVIVDLFRNFRSPGRLSLHTKLTLSVTGILLLAGTVLIYCLELSNSLAPLSPQGKLLAAYFQAVTPRTAGYNTLNMAALRSATQFLIVVLMFIGASPGSTGGGIKTTTIGTLAVSIWSMARGRTDSVVFKRRLGQEQVYKSLAILFMATTLVITVSLLLSVTESADFLAVLFETTSAFGTVGLTMGLTPDLSTAGRLLIILTMFLGRVGPLTVAFALARPRHKFPLRYPEEKIMVG
3E-59	210	26.8	2.9E-58	207	18.6	2	1	Q8A0C4_BACTN	Trk system K+ uptake protein trkH	BT_4097	Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides thetaiotaomicron, Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	226186	>tr|Q8A0C4|Q8A0C4_BACTN Trk system K+ uptake protein trkH OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) GN=BT_4097 PE=4 SV=1MINSRMIYRIMGFLLLIETAMLMCCGGVSLFYKEDDLNSFLLSSAITAFVGVIMLAIGRGAEKSLNRRDGYVIVSVAWIAFSFFGMLPYYIGGYIPSVTDAFFETMSGFSSTGATIMNNIESMPHGILFWRAMTQWIGGLGIVFFTIAVLPIFGMGGIQVFAAEASGPTHDKVHPRIGVTAKWIWGIYAGMTGTLIILLVFGGMGLFDSICHAFTTTSTGGFSTKQTSIEYYHSPYIDYVISVFMFLSGVNFTLLLLLMFNGKIKKFIHDAELKFYFMSVAFFTVFIAVWLYQTSSMGAEEAFRKSLFQVISLQTSTGFATADYMLWPSILWGCLLIVMIMGACAGSTTGGIKCIRMVILFKVAKNEFKHILHPNAVLPVRVNKQVISPSIQSTVLAFTFLYAIIAIISILVMMGFGVGFLESIGTVISSIGNMGPGLGTCGPAFSWSELPDAAKWLLSFLMLLGRLELFTVLLLFSSDFWKRN
3E-59	210	21	7.4E-59	208.9	14.5	1.5	1	A0A0A7KJU0_9DEIO	Potassium transporter KtrB	QR90_03830	Deinococcus swuensis	455	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus swuensis	1182571	>tr|A0A0A7KJU0|A0A0A7KJU0_9DEIO Potassium transporter KtrB OS=Deinococcus swuensis GN=QR90_03830 PE=4 SV=1MPTGPRRKPWLSRLRPPQLIALTFALAIVVGAGLLLLPISLEPGQSLRPIQALFMATSAVCVTGLGVVDVGSTFSTFGEVVMLLLIQIGGLGLITLGTLFAIAVRRRVGISDRIQVAQQLNTLELGGVVKLVRTIVLSSVLVELAGTVLLSSVFVPEEGLGRGLYFSLFHAVSAFNNAGFSLYATGLTGFVTNPVINLVIPLLIVLGGMGFLVQLNVLAYLRHRRRNRLNANSKLSLVMMAALLLIGTLSFALLEWTNPATLGTLPLGDKLLAAWFQGVTPRTAGFNTLDYSTMHYGTIFVTILLMFIGANPGSTGGGIKTTTFYVMMASAWGMVRGRHDTTLFRRRIGTTTILRAMTVGLLSLGLVNLGFLLMLLLNTNPEVKFVQLFFETVSAFATVGLSMNATPLLNADQEVVLIFLMFLGRIGPLTFAVAFSRPDSRTLVRYPQEHDILIG
3.1E-59	210	24.6	1.4E-57	204.8	17.1	2.1	1	R6MTN9_9CLOT	Cation transport protein	BN565_01399	Clostridium sp. CAG:253	491	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:253	1262785	>tr|R6MTN9|R6MTN9_9CLOT Cation transport protein OS=Clostridium sp. CAG:253 GN=BN565_01399 PE=4 SV=1MNRSIIRYILGSVLKIEAAFMLLPCIVAVCYGEKQGFVYLGVGIVTFLLGMLMTHKKAGSSVFYLKEGCVATSLSWIFMSFFGGIPFILTGEIPSLIDALFETVSGFTTTGASILSDVEALSHCSLMWRSFTHWLGGMGVLVFLLAIIPLGGGSRINLMRAESPGPSVGKLVPKVKHTAQILYIIYITLTVVQIIFLLIGRMPLFDSLAMAFGTAGTGGFGIKNDSAASYSPYIQWVLTIFMILFGVNFNAYYFILYKQFKKAFKMEEVRYYFLIIIAAVGIICFHIIDTTKSFFEALTQASFQVASIITTTGFSSVDFDKWSQTCKTVLIFLMFCGACAGSTGGGIKVSRFIILVKTIIKDLESYIHPKCIRKIQIDKKPVEHEVVRSVNVFFITFFIIFAASIFILSFEGKDFITNFTAVAATMNNIGPGLALVGPTCSFGHFTVISKLVLIFDMLAGRLELFPLLILFHPAIWKEMFKIKNNRKCMRE

3.2E-59	210	42.7	4.1E-58	206.5	29.6	1.9	1	A7GMK5_BACCN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Bcer98_1037	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	439	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cytotoxicus, Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	315749	>tr|A7GMK5|A7GMK5_BACCN Potassium uptake protein, TrkH family OS=Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98) GN=Bcer98_1037 PE=4 SV=1MKQINMKMSPPRVLILSFMMLSIAGTCLLKLPVSTTTSISWLDALFTTVSACTVTGLGVVDTGKIFTTFGQCVILFLIQVGGLGIMS FAVFIAIMLGRKIGLQNRILLQQALNQTNIGGVIGLVKSLFIFSFTVECIAALFLSFEWIPKYGIKKGVYYSLFHSISAFNNAGFSIWSDNLM SQSHSILVNIVISTLIILGGMGFTVIVDIKRKKSFKTLTLHSKLMLSSTLIINIIATLLIFIFEFHNSISMKGFTPFEETLAAYFQAISTRTAGFNT VDIAQLSTPSLLLMMLLMFIGAGSASTGGGIKLTTFLIMLFGVFKFLQEQDDIVIFKKSIKDTLIVKSLTITVISISFIFFSILILSITEQTPLFMS AFEVFSAFGTVGLSMGLTPQLTVIGKFIIIFMMFFGKMGPLTLAFSFARKKQKKIKYPNEDLLTG
3.4E-59	210	32.7	4.9E-59	209.5	22.7	1.1	1	K9RP17_9CYAN	Potassium uptake protein, TrkH family	Riv7116_6709	Rivularia sp. PCC 7116	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Rivularia, Rivularia sp. PCC 7116	373994	>tr|K9RP17|K9RP17_9CYAN Potassium uptake protein, TrkH family OS=Rivularia sp. PCC 7116 GN=Riv7116_6709 PE=4 SV=1MTAPQKICFGFLAVIAVGTVLLMMPFSTATNTWNSPIVALFTATSAVCVTGLAVVDTGTDFSFWGQLFILLLAQVGGLGYMTFTT FLIMLTGRRFDLRHKIAIQQALDRREMEGSGNIIRSIIAVTLFFEITGIFLLLLVFVPDFGWDKGMWLAIFHSISAWNNAGFSLFSNSLVDY NSSGLLVFTISGLVIFGGIGYQVILEMFFWLRDRLRRRPRNIVLSLDYKVATSTTIFLLVLGLVAFFFVEVRNTQTIENFSFRSQLLAAWF QSMTTRTAGFNSIEIGSMTTAGLFITIALMFVGASPGGTGGGMKTTTIRVLSSCTKSILQGKEEVLLYERRIAVSLILKAVGVIVGSVTVVI ICTILISLTDPVFDFIQILFEVVSAYATVGLSTGITSKFSIWGKLILILTMYMGRVGVLLLMSAVLGDPKPTQIHYPEEDLLVG
4E-59	210	32.6	4.8E-58	206.3	22.6	1.9	1	A5I6L4_CLOBH	Putative potassium uptake protein	CBO3134	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum A, Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	441771	>tr|A5I6L4|A5I6L4_CLOBH Putative potassium uptake protein OS=Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A) GN=CBO3134 PE=4 SV=1MKIPHIGRRFTPVQILAIGFAIVIFVGAVLLSLPISSQSGQRTPFLDCLFTSTSSVCVTGLIVVDTGTHWTYFGKTVIMLLIEIGGLGF MSFATLLAILLGKKITLKERLVMQEALNTFNIQGLVKMAKYILLFTFSIQGGGALLLSTQFIPRYGLAKGLYYSIFHSVSAFCNAGFDLFG NFSSLTSVYNNPVIILVIAFLIIIGGIGFYVWYEIYHYKGRRKLSTHSKLVLVAFIVAGTFLLLTVGTILMFIFESNNPGTMANMTFNNKILSSFFAA VTPRTAGFNSISTSDMTMAGKFLTILLMFVGGASGSTAGGIKVTTAGVLIMTVVCVVKGKQDTEINKKRISKEIVYRALAITVIGLALVITV TMILSITEVKVPFEYYLYEATSAFGTVGITLGLTTKLSSIGKIVILLTMYAGRVGPLTLAIAFARKLKNSSIKYPEEKILVG
4.1E-59	210	21.6	1.1E-58	208.4	14.9	1.5	1	A0A0B4XU93_9PROT	Trk system potassium uptake protein	TH3_00645	Thalassospira xiamenensis M-5 = DSM 17429	472	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Thalassospira, Thalassospira xiamenensis, Thalassospira xiamenensis M-5 = DSM 17429	1123366	>tr|A0A0B4XU93|A0A0B4XU93_9PROT Trk system potassium uptake protein OS=Thalassospira xiamenensis M-5 = DSM 17429 GN=TH3_00645 PE=3 SV=1MVIIIGVSMMIPAAVDLYYGNPDWKIFAQASMTSIGLGGMACLACRSEMGPRVTARQGYVLTVFSWVAISLTGALPLWFSSLDIS FCDAVFETVSGLTTTGSTILSGLDDMPPGLLLWRSILQWLGGIGIIVTALALLPMMRVGGMQLFQMESSDRSEKLSPRIRDMCLQIVMI YVGLSIICMVLYRIFGMTWFDAINHGMSTLATGGYSTSDLSFAKFDSSLALHWVGIIFMFAGALPFTAYAVLIRKRDISAIISNQQIRLFLL VIAVFTGLLTLRLMHISDDGFFRSLTMAAFNLVSVITTTGYASGDYLQWGPAAIMLFFFATFIGGCSGSTAGGFKMFRLYVVFTGLKAH FMRLRSPSAVIVSRIDKHEITSDIYNAVTVYVFLLTISYIAISVALAFTGLDLVTSMSAAATSLANVGPGLGPIVGPAGNFQSLPDAAKWIL DIAMVLGRLEFETFLVLLMPAFWRD
4.1E-59	210	29.6	4.2E-57	203.2	20.5	2.2	1	R5JYW5_9FIRM	Potassium uptake protein TrkH family	BN781_00703	Coprococcus sp. CAG:782	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus sp. CAG:782	1262863	>tr|R5JYW5|R5JYW5_9FIRM Potassium uptake protein TrkH family OS=Coprococcus sp. CAG:782 GN=BN781_00703 PE=4 SV=1MQQTNRSRHRHITSFQVISLGFLSVILLGSLLLMLPIATKSGRSTSFLDALFTATSSVCVTGLVVNDTATYWSLFGQGVILLLIQIG GMGIITIAIAIAVVSGRKIGLMQRSTMQEAISAPTVGGIVRRTQFIIRTTILIEIIGAVLLAPVFCRDFGFWKGIWYSLFHSISAFCNAGFDLF GIRSHFSSLTSYSVQPIVNLVIMMLIIVGGIGFLTWEDIKNHKWHFKKYRMQSKVIFMVTGILIFLPALYFFCFEFSNLPLTERVWVSLFQ SVTPRTAGFNTADLTLLSEVGQMLIIMLMLIGGSPGSTAGGMKTTTLAVLVSSALSVFRKKEHTNFFRRQIPDGTIRNAATIFLMYIVLFL VGGMVISRTEDIPLMTALFETASAIGTVGLSLGITPDLGLVSHIILICLMFLGRVGGLTLIFATISEKKPNGSKYPQEKITVG
4.2E-59	210	32	4E-58	206.5	22.2	1.9	1	W6S4I1_9CLOT	V-type sodium ATP synthase subunit J (EC 3.6.3.14)	ntpJ CM240_2094	Clostridium bornimense	455	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium bornimense	1216932	>tr|W6S4I1|W6S4I1_9CLOT V-type sodium ATP synthase subunit J OS=Clostridium bornimense GN=ntpJ PE=4 SV=1MSKHILGRIKIKPVQVLALGFMAVLLIGAGILMLPISTATGEKTSFIDALFTSTSAVCVTGLVTVDTASHWSYFGKTVIIFLIQIGGLG FMSFATLFALILGKRVSLKERLILQEAVNATYISGIVKLVKYILSFTFAIEGIGAAILATQFIPEHGLLKGIYFSIFHAISAFCNAGFDLIGDSL FPYQNNAVVILTISALIIIGGIGFAVLLDLFNASQSTRLYTHTKFVLVLTAILLVTGTVFIFIMEYNNPETIGNMGFGGKLLNSFFASVSSRT AGFYSIPLEYLTTGSIFLYFILMFIGGSPGSTAGGVKTTTIGLICLTVVSGLRGKEDTELFKRRISKDVIYKAFSILFLSLMIVVAITMLLSNT EADTLVNGELVPLEGIIFEAISAFGTVGVTLGITPYLSFVGKLLIILTMYIGRVGPITLVMAITRQKKKNAGNIKYPEAKILIG
4.2E-59	210	23.8	3.2E-57	203.6	16.5	2	1	R5JZD0_9CLOT	Uncharacterized protein	BN743_01358	Clostridium sp. CAG:632	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:632	1262830	>tr|R5JZD0|R5JZD0_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:632 GN=BN743_01358 PE=4 SV=1MLEGLYKKKQLTSFQLIILGFAGVILLGTILLMLPVSTVEEVPTPFREALFTATSAVCVTGLVVKDTGSYWSMFGQVVILVLIQIGG LGVVTVAVSGSLLSGKRISLMQRSTMQDAISAPTVGGIVRLTKFILRGTFLIETIGAMLLLPVFLSDYGLKGIWMAVFHSISAFCNAGFDI MGTVDNTFPSLMRYSGNVLVNVVIMLLIIIGGIGFLTWDDICMNKIKFKCYRMQSKIILVTTVCLILFPTVFFFICDMKNLSAGEGLLAAIF QSVTTRTAGFNTINISEMNETSKAVMIFLMLIGGSPGSTAGGMKTTTFAVLLLNAIATFRNQENAEAFGRRLEYHVIKNAATITLLYFALF FLGGSVISIYEEELPLLDCLFEAASAVGTVGLTLGITPELHVLSQIVLIILMYLGRVGGLTLIYAVFLKRNKGNAKLPMEKITVG
4.2E-59	210	15.4	8.1E-52	185.7	10.5	2.7	2	A0B6I5_METTP	Cation transporter	Mthe_0518	Methanosaeta thermophila (strain DSM 6194 / JCM 14653 / NBRC 101360 / PT) (Methanothrix thermophila)	524	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosaetaceae, Methanosaeta, Methanosaeta thermophila, Methanosaeta thermophila (strain DSM 6194 / JCM 14653 / NBRC 101360 / PT) (Methanothrix thermophila)	349307	>tr|A0B6I5|A0B6I5_METTP Cation transporter OS=Methanosaeta thermophila (strain DSM 6194 / JCM 14653 / NBRC 101360 / PT) GN=Mthe_0518 PE=4 SV=1MNVKILLYSFGDLLRIIGIAMVFPGIAAACYREPHGVVAFAFTSMIAMMIGSFFRRHGEIGDLSIKDGFALVAFGWLAAAMIGAIPY MMLGMGSIDSLFESMSGFTTTGASVLTDSNSEGYWIIDGELANQSVAFIVAGSVEYLLWATTNTTVSAMIPEHPTYYGLLFWRSFSQ WLGGMGIILLFIAILPRLGVAGRQLYRAEVPGPEKESLTPRIRQTAELLWGIYLSLSIIEVILLKVAGMPLYDALCNTFATVATGGFSPQS MSIEAYGSPMIEYIIVLFMFLAGANFALHYMTIHQDRRCLIRDPEFRFYSFIIVVSTLFIAATAGMMSPLPDRIRCALFQVVSIMTTTGFST TNFDTWYPAAKIVLLLLMFVGACAGSTGGAIKVVRVLVILKYVHRELMLAMHPKAVIQVKLHDITVKEEIVRSTISFFGVYMLTFALASIVL AAISYSDQAMNLEAIISAVASCLGNVGPGFGPVGPYMNFAEIHPLGKLVLILCMWMGRLEIMTVLVLLLPDFWKK
4.3E-59	210	24.7	5.6E-59	209.3	17.1	1	1	G5K840_9STRE	Cation transport protein	STRPS_1438	Streptococcus pseudoporcinus LQ 940-04	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pseudoporcinus, Streptococcus pseudoporcinus LQ 940-04	875093	>tr|G5K840|G5K840_9STRE Cation transport protein OS=Streptococcus pseudoporcinus LQ 940-04 GN=STRPS_1438 PE=4 SV=1MRLPPIRTWTVTQKLTLSFASVILIGSTLLSSPLTHSPSAHQATFLDHLFNVVSMVCVTGLSVIPVSEAYNTLGQTIVICLMQIGGL GLVSFIAFSTFALKRKMDLSGHTLLQSALNRKDSKNLKDFLFFAYKMTFIIEILACAIIAIEFVPRFGWKNGLFNSLFLAVSAFCNAGFDN FGSSSLKDFVLNPTINVVVSALIIFGGIGFAVWHDVMENLKRYFVEKPKCHGLFYRKLSNQTRLVLQTTGLILVLGTLLTWFLEKDNPKT IANYTFIEQMMVSFFQTVTMRTAGFATLSYLDTLAPTNFLYMIQMVIGGAPGGTAGGIKVTTVAITILLLKAELAGQSQVTFQNRIITSRT VKQTMSVLIFFMSVFIIGYTLLLSVEPTLDPVALLFEAVSAIDTVGVTMDTTPKLSTPGRVIIMFLMFIGRVGPITFLLSLIQRKEKTIRYATT DILVG

4.7E-59	210	24.7	7E-59	209	17.1	1.1	1	C0QAF8_DESAH	TrkB (EC 3.6.3.14)	trkB HRM2_16340	Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2)	461	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfobacterium, Desulfobacterium autotrophicum, Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2)	177437	>tr|C0QAF8|C0QAF8_DESAH TrkB OS=Desulfobacterium autotrophicum (strain ATCC 43914 / DSM 3382 / HRM2) GN=trkB PE=4 SV=1MFRQRFSTMVNRFFSSPGPATVFGFLAMIFAGSGLLLLPQATTGTGRGLTFVDALFTSTSSVCVTGLSVTDTGTSFTLFGQTIIL TLIQTGGLGIMTLSTLFLMLSGKRLSFSSHTAIRESFTPFQERHPWAILKDIFLFTLVLEGVGAMALFTQFIRTATPSKAFFLSIFHSISAF CNAGFCLFPDSFTAFRSSIVVNLTIGFLIILGGIGFPVMSELKWRLLRGDRQRSPMSLHSKIALSMTAILLVSGTLVFLTMESRVTLDRLP WGQRVLASFFMSVNARTAGFNSLTLENMANETLFFIILLMFVGASPGSCGGGIKTTCFASLIALGQSRLKGEKKPNLFGRAIPEQTIGK AVSILMVSTVIVCLGTMALLMTELGDVSHPQSRGMFLELLFEVVSAFGTVGLSTGVTASLTNPGKLLVVTIMFMGRLGPLLIAMAVSRP LRLGYTHAEEDFIIG
4.8E-59	210	18.9	9.2E-52	185.5	8.1	3.4	2	D8QVJ8_SELML	Putative uncharacterized protein	SELMODRAFT_79151	Selaginella moellendorffii (Spikemoss)	537	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8QVJ8|D8QVJ8_SELML Putative uncharacterized protein OS=Selaginella moellendorffii GN=SELMODRAFT_79151 PE=4 SV=1MPVSRRRSSTVTLARKHLTFFRLHLAYFIAIAIAGTWILWGIGARRHSKISHLKFIDCFYLITSALCITGLASVPIESIPPGGQVVLML MMILGGQVVTSVVPLFVKKQRYCDVARQVLAQDDRTRPSGSMKLRSKEDVWMREMASKKHAQHLREIFQEHSATVSLTWIVVWYYI LVHLTGFFITWRCILGDASAKSSLESKNINIGFFALFLTVSSFANAGFVLVDENMTLFSSSTVLLLALAAIILLGNTMFAPSLRGIIWLLHR VDATRREDYEFLLEHPRKCYTHLFPRTTTLWLVLAVTGFNGFECLMFYILDWKSKALEGFGTGDKVVNGIFQSVNTRSAGMNSMNLA DLSPSMLFLYCGMMYIAAYPVFLSRQYSRHYEAKEQRASRLLAQDWAYLFLATFFICVSDNKQLKSDPRNFTIFSVIFEVISAYGNVGL TLGYSCSLRIDSAPCTDVPYSFSGKWGVVGKLLLILVMFLGRHRGLPDSIDSAILLPEDKFYSMLRSQTVAQPDGSITIIAPPRSECTDL VDLS
4.9E-59	210	29.4	6.7E-59	209.1	20.4	1.2	1	D4ZMP1_ARTPN	Putative cation transporter family protein	NIES39_D02710	Arthrospira platensis (strain NIES-39 / IAM M-135) (Spirulina platensis)	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Arthrospira, Arthrospira platensis (Spirulina platensis), Arthrospira platensis (strain NIES-39 / IAM M-135) (Spirulina platensis)	696747	>tr|D4ZMP1|D4ZMP1_ARTPN Putative cation transporter family protein OS=Arthrospira platensis (strain NIES-39 / IAM M-135) GN=NIES39_D02710 PE=4 SV=1MTVPRTICLGFLAVIAIGTFLLWMDDTIYHSSFGNPITALFLATSAVCVTGLSVVDVSNFYSFWGHFCLLSLVEIGALGYMTANTM LLLLIGRKFGLRDKLALQKSLDTAGIAGVMPLLRSIIATMALFQIAGVILLMMVFLPDYGLKNSLWLAIFHSVNGFNNAGFSLLEESLVDY VSSPIVNITMSILIIFGGLGYQVIMELFLWIKTTLNKEPMRRDFSLHFKVVTSTTIILLFSGSFLFFITEFNNPQTLQSLTIFGKMQAAWFQS VTSRTAGFNTISIGDMTYSSILITMILMFIGASPGSTGGGLKTTTSRILVNCTKAALQGRDEVLCYQRKIPSPLILKAVGVLVGSITVVCVA TLLIVIMQPELGFGSIFFEIVSAFGTVGLSTGITGDFSMLSRLIIIATMYIGRVGVLLLMSAVLGDPQPSSIDYPEENLLVG
4.9E-59	210	20.1	1.1E-58	208.4	13.9	1.5	1	K4MSN8_9EURY	K+ transporter Trk	Mpsy_2553	Methanolobus psychrophilus R15	477	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanolobus, Methanolobus psychrophilus, Methanolobus psychrophilus R15	1094980	>tr|K4MSN8|K4MSN8_9EURY K+ transporter Trk OS=Methanolobus psychrophilus R15 GN=Mpsy_2553 PE=4 SV=1MNTSIIFNVLGGLLQFLGLVMVIPLLVAVYYNDPLLPFAVAVLITGVTGILLSRRYGAEGEWKVKEGFAIVAFGWLSVAFFGSIPYV LDGITPINSFFESMSGFTTTGATILQDIESHSKSILFWRSMTQWLGGMGIIMIFIAILPKLGVAGRQLFRAEAPGPTEDKLKPRIRGTARIL WAVYVVISVVQVILLKLAGMSLYDAVTHTFTTMSTGGFSPYGAGIAEFNSPLIEGIIVVFMFIAGANFALHYRVLYVDHNNFMKDNEFKF YTAIILIATVILTFSLWKDMGQSIETAFRYAVFQVISIITTTGYASADFDIWSDSARIVLLAVMFIGGCAGSTAGGIKVVRILLLLKYGKNVLF KSLHPKAIKPVKYNGKAVPEDIMHSIVSFVVLYMMIFAISTGILALMGMDLISSITASITTLGNIGPGFNAVGPMANFDVVPDLGKLLLIAN MWIGRLEVFTVLVMLTPEFWKD
4.9E-59	210	29.9	7.5E-59	208.9	20.7	1.2	1	I0JLT6_HALH3	Cation transporter family protein	HBHAL_2758	Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Halobacillus, Halobacillus halophilus (Sporosarcina halophila), Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	866895	>tr|I0JLT6|I0JLT6_HALH3 Cation transporter family protein OS=Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) GN=HBHAL_2758 PE=4 SV=1MWVRRKSLRWLNELSPFQLIAIYYLIAVTISSILIALPVAHKPGVKLDFIDVLFTAVSAVSVTGLTTVPTAETFSTTGVFILALVLQFG GIGVMTLGTLIWLVLGKKIGLKERRLIMTDQNRTSFQGMVQMVKEIVLVVLLIEFIGFLTLGTYYLQYYDPGEAYLQGFFGAISAMTNGG FDITGQSLIPFKDDYFVQFINMILIIAGAIGFPVLIEVKQYLFNNNDVKTIRFSLFAKLTTFTFFVLVLLGTGMIILLEFNHFFAGKDWHEVFF YALFQSVTTRSGGLSTMDINQFTEQTQLFMSSLMFIGASPSSVGGGIRTTTFALVVIFILTFARGGSRIRLFRREVHNEDLNRAVVVMM MALLLCFIALMALSISEPFTLNELLFEVCSAFGTVGLSLGITPGMTTFGKFVLMLLMFLGRIGILTLFSFQKDRTKGDYHYPKERLIIG
4.9E-59	210	20.1	9.8E-58	205.2	13.9	2	1	R5A8Y6_9FIRM	Trk system potassium uptake protein TrkH	BN453_00628	Firmicutes bacterium CAG:102	483	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:102	1262998	>tr|R5A8Y6|R5A8Y6_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:102 GN=BN453_00628 PE=4 SV=1MNFNMIAYILGNIIRIEAALLAVPAFVSIWYQEAKAASAFVATIIACLMVGTVLVSREPENKRIYGREGFVVVALSWIVMSVLGALPF YLSGSISGYVNCFFETVSGFTTTGASILQEIETLPKSIQFWRCFTHWIGGMGILVFMLAIMPLGDERTMYLMKAEAPGPLVSKLVPKVK STAKILYTIYIVLTLVEMILLFAGGMPFFDSVVHALSTAGTGGFSVKNSSIAEYNSAYFEYVITAFMLLFGVNFNLFYLMLMKDFKNVWK NEELRCYIAIVCIATALITIDISRYYSTVEGAFRHAIFQVAAIMSTTGFVTANFDLWPEFSKTLLYCLLILGACGGSTAGGIKVSRFVILLKMI RREISHIVHPRSVNLIKLDGYKVDEDSIRSVTGFIILYVLILLGSFMLVSLDNFDFITNVTAVTTCLSNVGPGLAMAGPVENLSFFSGFAKI VLCLDMLLGRLEIFPIIMLFAPSIWRKSYM
4.9E-59	210	29.2	7.7E-59	208.9	20.2	1.2	1	F3Z0V2_DESAF	H(+)-transporting two-sector ATPase	Desaf_2715	Desulfovibrio africanus str. Walvis Bay	451	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio africanus, Desulfovibrio africanus str. Walvis Bay	690850	>tr|F3Z0V2|F3Z0V2_DESAF H(+)-transporting two-sector ATPase OS=Desulfovibrio africanus str. Walvis Bay GN=Desaf_2715 PE=4 SV=1MFFKNLFSPFTLPIYFFGLAIAIGAILLNQPFSLAAGNISWIDALFTATSATCVTGLAVVDTGTAFSRVGQSIILALIQVGGLGIMTFA SLFFYLWRRRVSLADRIAVGQNLLHNPAFHLGRFLTHMVLWTLMIEVSGALLLHFFDPEGFTLYSALFHSISAFCNAGFALHADSLVRF QDNVGVNMVIMSLIILGGLGFSVLVELEGFVHQRLARGGKRRLSWYTRIVLQTSLWLIVIGWIFIYITEFLGERSLLDPLSKILSSLFQSV TCRTAGFNTLDIGQMTNASLLFMMMLMIIGGSPGSTAGGIKTTTFRTLLAFAISQIKDRRQTVIGKHAVDLVTVNKALTLVIFAVTIIGTS MLILTITEGGDTSHAQASGNIFMDILFETISAFATVGLSTGITPKLSTQGKIVISLLMFIGRIGPIVFLSALQSLREEPYYAWPERNMLIG
5.1E-59	210	37.1	1.2E-58	208.2	25.7	1.4	1	R4KL63_9FIRM	Potassium uptake protein, TrkH family	Desgi_4144	Desulfotomaculum gibsoniae DSM 7213	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum gibsoniae, Desulfotomaculum gibsoniae DSM 7213	767817	>tr|R4KL63|R4KL63_9FIRM Potassium uptake protein, TrkH family OS=Desulfotomaculum gibsoniae DSM 7213 GN=Desgi_4144 PE=4 SV=1MVIKKRINPPLFIILGFAVIILIGTVLLALPVSSSSGNSLGLLDSLFTATSAVCVTGLVVFDTGTKYSSFGEIIIMILIQLGGLGFMIFGV TTAVLLGKKIGLKQRLLIQESTHAISTAGLVKLSLNILIITLVFETVATIILTVRWYGEMGLFKAVYYALFHSVSAFNNAGFSLWPDSLTRY VGDPVVNLVISALFITGGIGFIVIMDLYVKRQWQKLSLNSKIVLVTSGLLSVAGFVVVFILESFNSQTFGELNFSQRLWAAYFQGVVPRT AGFNTIEIGQMIAASQLFIIFLMFIGASSGSTGGGIKTNTFAILILSLFAITRGRNEISVFHRTVTVEIILRSLAVIIASMGVIITASFLLTITEHS TQRDFLEILFEATSAFGTVGLSMGLTGDLSPLGKLIIIITMFIGRLGPLTMAFALAQKGIKPKIRYTEEKILIG

5.1E-59	210	30.3	2.9E-57	203.7	21	2.1	1	D0RQ64_9PROT	Trk system potassium uptake protein	HIMB114_00009520	alpha proteobacterium HIMB114	481	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Pelagibacterales, Pelagibacteraceae, unclassified Pelagibacteraceae, alpha proteobacterium HIMB114	684719	>tr|D0RQ64|D0RQ64_9PROT Trk system potassium uptake protein OS=alpha proteobacterium HIMB114 GN=HIMB114_00009520 PE=3 SV=1MNSGLKTTFLIIGYLIIILSGFMIIPHIVEMTIGDKSQHFLVTGILSAFIGTLLVLISQTKDRSLNVQQAFLMTNLAWLSICFFGAIPLYFSSLDLTFTDAFFESVSGITTTGSTILPDIERASKGILVWRSLLQWLGGIGIIVMAITILPLLNIGGMQLFRSEGMEVEKVVPKVTEIALSITKIYIFITILCSLAYWLAGMNVFDAINHALTTVSTGGYSTHSQSIGYFNSSLIEVVAIIFIITGSVPFLAYIKFIRGDLFVFFKDKQIIGFFLILVGSILIITIHSYVNRSDALILALRDAAFNVTSIITGTGYTTKDFSAWGNFSVFFFLVLMFVGGCSASTTCGIKVFRFQIILSFIDQQVKKIFYPNGVFPIKYNNQNINDQFLTSVLAFVCLYIFIFFILTLLLSLTGLDLITSVSAAATSISNVGPGLGHVIGPDGNFFILSDSAKWLLSLGMLLGRLELLTVLVLFLPAFWRN
5.4E-59	209	17.4	7.4E-59	208.9	12.1	1.1	1	A0A059MVT5_9NOCA	ATPase	N505_0102695	Rhodococcus sp. BCP1	458	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. BCP1	191292	>tr|A0A059MVT5|A0A059MVT5_9NOCA ATPase OS=Rhodococcus sp. BCP1 GN=N505_0102695 PE=4 SV=1MRTRTGAFAPSLLRRMAARATLTPVRVVALSFAAAIAVGTLLLLTPAASLPGTATSLVDALFTATSAMCLTGLVVVDTPTHWSGFGQGIILALIQAGGFGIMTMASLVGLLLANRIGLKARLNTAAEVRASGLGDVRSVVVGVVRMSVFIESVTAVALALRFALGYEEPPLRAVWLGVFHSVSAFNNAGFALYSDNIIGFADDPWICVPLMLAVILGGIGFPVLFEVTRHLRGRSHRWSLHTRLTVTVTAVLLVVGPMLVLVLEWTRTLQHYHFGQKLLVAAFQGVMPRTAGFNSVDYAQMDPATLLVTDVLMFIGGGSGGTAGGIKVTTFVLLLFVILAEAARGERSVSVFDRRIDTRVQRQALSVALIGVALVMVPTIALLAGTSFDLNVLLFEVTSAFATVGLSTGITAQLPVWGQLILVLLMYLGRIGSITLVSALAARDRGRRYELPEERPFIG
5.8E-59	209	20.6	7.3E-58	205.7	14.3	2	1	R6MCL6_9BACE	Potassium uptake protein TrkH family	BN507_00881	Bacteroides clarus CAG:160	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides clarus CAG:160	1263039	>tr|R6MCL6|R6MCL6_9BACE Potassium uptake protein TrkH family OS=Bacteroides clarus CAG:160 GN=BN507_00881 PE=4 SV=1MINFKTIIRIIGILLLLETVMLLACSAISYYYNDEALLDFWKSAGITAGAGLLMAIAGKGGEKQLTRRDGYVLVSLAWVAFSLFGMLPFYISGYVPDITNAFFETMSGFTSTGATVLDNIESLPHGLLFWRGMTQWIGGLGIIMFTIAVLPIFGVSGLQVFAAEASGPTHDKVHPRIGITAKWIWSIYTGLTLILVVLLMLGGMDWFDSVCHAFATTGTGGFSTKQASVAYYNSPYIEYVISIFMFISGINFTLLLFFVNRKFKKVIDNAELKWYFWSVVGFTTVIAVVLYYTSSMGVEEAFRKSLFQVISLQTSTGFATDDYMLWTPMLWGLLTVVMIMGACAGSTTGGLKCIRMVILAKVSRNEFKHILHPNAVLPVRVNKQVISPSIVSTVLAFFFLYIIIIIIGILIMMGMGIGAEESIGCVISSIGNMGPGLGDTGPAYSWNALPDAAKWLLSFLMLLGRLELFTVLLLFTPEFWKRN
5.8E-59	209	31	1.4E-58	208.1	21.5	1.5	1	R2QI29_9ENTE	TrkH family potassium uptake protein	UAU_00901	Enterococcus pallens ATCC BAA-351	454	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus pallens, Enterococcus pallens ATCC BAA-351	1158607	>tr|R2QI29|R2QI29_9ENTE TrkH family potassium uptake protein OS=Enterococcus pallens ATCC BAA-351 GN=UAU_00901 PE=4 SV=1MDIKDKLTKFRLHPLQFLALGFMLVILTGALLLSLPISSNSGEATNFIDALFTATSATCVTGLTTLTTIEHWNFFGQAVILTMIELGGLGFMMMPILFFTVFRKKVGLKTRIVLQEALNLEAMSGVMDLMVYILRLATIIQCIGAVLLAIHFIPEYGWRLGAWYAVFHSVSAFCNAGFDLFGDSLVSFQSNPYVLLVISSLIVAGGLGFYVWKDIISFPKRRKLSLHSKIALGMTFILLVGGTLLFYITEHNAYSLAAGSNGMERFANTIFMAVTPRTAGYFSIDYLRMSQAGILLTIILMFIGGTSGSTAGGLKTTTLAVLIIQTISMLKGRQHAELKGRTIRSATVFRAMSLFFITLSLCVASTMILSITEAIPETSGIEYIAFEVVSAFATVGLTMGLTPDLTLFGKLLIILLMYVGRVGILTVGFSISMRLAQDKSHGTYKYPEETVIVG
6.2E-59	209	33	2E-57	204.3	22.9	2	1	B2TMP1_CLOBB	V-type sodium ATP synthase subunit J (EC 3.6.3.14)	CLL_A1845	Clostridium botulinum (strain Eklund 17B / Type B)	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum B, Clostridium botulinum (strain Eklund 17B / Type B)	935198	>tr|B2TMP1|B2TMP1_CLOBB V-type sodium ATP synthase subunit J OS=Clostridium botulinum (strain Eklund 17B / Type B) GN=CLL_A1845 PE=4 SV=1MSMINNKFKLNPVQILAIGFIILIFVGGLLLSLPMSSASGESTNFLDALFTSTSASCVTGLVVKDTGTYWSTTGQVIILILIEIGGLGFMSFATFIAMLFGKKITLKNRLVMQEAMNTLSIQGLVKMLRYYVMGITFSIQILGASILSTQFVPEFGLKKGSFYSIFHSVSFFCNAGFDVIGNFESLTRYYNKPVVLLTVSSLIIIGGLGFTVLLEIYNFKGIKKLSSHTKLVLLVTVALILFGSVFIFALEYTNLNTIGNMNLRDKIFNSLLASVSPRTAGVNSIPIDEMHTASKFFTIILMFIGGSPGSTAGGLKTTTFGIIILTVVCVIKGKEDTELFGRRFPKELVYKAFSLLFIGMTLVMVVTMVLTITDPNESLISLLYEATSAFGTVGLTTGVTQRLSSMGKIMIIVMMYLGRVGPLTVALALTKRRKRTLYKYPEAKILIG
6.7E-59	209	42.2	1.3E-58	208.1	29.3	1.4	1	A0A075RIJ3_BRELA	Ktr system potassium uptake protein B	ktrB_2BRLA_33p000180	Brevibacillus laterosporus LMG 15441	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus laterosporus (Bacillus laterosporus), Brevibacillus laterosporus LMG 15441	1042163	>tr|A0A075RIJ3|A0A075RIJ3_BRELA Ktr system potassium uptake protein B OS=Brevibacillus laterosporus LMG 15441 GN=ktrB_2 PE=4 SV=1MLLSYKKRRLSSVQIIVMFYLSSVILAALLLWLPIFHQPGVSISFVDSLFTAASAISVTGLTVIQISEVFNQSGIILLTLFFQIGGIGIMTLGTFLWMMLGQRIGLEQRKWIATDHNRPTLSGLVKLTRSILLLTILIELIGTLLLGSYFFWTGYQTDWYTAYYYGYFVSISAFTNAGFDIFGNSLLSFSGDYFVQSINMILIICGAIGFPVLIELVSYATHRQGQYRFTFSLFTKVTTLTFFTLIVVGTLLFYFFEKNAFLQDKTWHEALFYSLFQSVSTRSGGLATMDIGLLSTPTLVMLSGMMFIGASPSSVGGGIRTTTFFVLIATIYTYMRGQKDVKVFGRELVQEDVIKSFMVFFVAIIMVFTAVIFMVWFEDLSMQAILFEVCSAFGTTGLSMGITSELSTPGKLILIIMMVIGRIGIINLLLFLKKDAPSVRYHYPKERMIIGQ
6.9E-59	209	23.9	2E-57	204.2	16.6	2	1	R6Q524_9FIRM	Uncharacterized protein	BN668_02055	Firmicutes bacterium CAG:466	444	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:466	1263025	>tr|R6Q524|R6Q524_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:466 GN=BN668_02055 PE=4 SV=1MVRSRMRLSNLQIVALGYFLVILTGTLLLMLPIATQEGQPPTSVLDALFTAVSASCVTGLVVVDTGTHWTVFGQLVILGLIQIGGLGFMTISLGFLLLMRKRIGLRHREVMVESINSIQLGGIVRLTRKILYGTLLFEGLGALLLAIRFVPQFGWKQGAYFSVFHSISAFCNAGFDLFGNYNSIVAYADDALVNFTLMGLITMGGLGFLVWEDLWQKKWSFHHLRLQTKIVLSTSFALTVGGGFLLLLLERNNLNVDMSNSERLLTAFFQSCTARTAGFNSVDPGAMTSGSKMLMMLLMFIGGSPGSTAGGIKTTTLMVILMYTLAGVRHARSANIYGRRLEEDALHKAIYVFFVNLIFVILGTIAICSVQNLELTDVLFEAFSAMGTVGISTGITRELEVFSRLIIIFLMYCGRVGSISFAVALMERKAAPPVTMPLEKITIG
6.9E-59	209	26.1	5.2E-58	206.1	18.1	1.8	1	D5DK47_BACMD	Potassium uptake protein, TrkH family	BMD_3602	Bacillus megaterium (strain DSM 319)	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus megaterium, Bacillus megaterium (strain DSM 319)	592022	>tr|D5DK47|D5DK47_BACMD Potassium uptake protein, TrkH family OS=Bacillus megaterium (strain DSM 319) GN=BMD_3602 PE=4 SV=1MIISKPRKKHKVKHLEPASILFVGFLGLILLGTCLLMIPAATSDRHHLSFIDALFEATSAVCVTGLAVVDTGTTFTLFGQLILLVLIQVGGWGFMTIGILMFIVLGKKIGLQQRLILKESLNAFSLQGVIALVQRVVLITLAVEGIGALILAIRWSQEMSWGRAIYYGIFHSVSAFNNAGFGLEPDNLSKWVGDPTVNIMITSLFIIGGTGFFVIADIFRKRNIRKFSLHTKIVLVSTILLNVVSTLIIFALEYHNPHTLGELSMGDKWWAAYFQGVVPRTAGFNTVDIGALTLPSKVYMMGLMFIGAAPGSTGGGIKITTFVLILFALWSVLTNKEEINVFRRRIPKSLVYRAFSITTSGIIFVSIIFFLLTITEKGVDMATLLFETFSASGTVGLSANFTGDLSPIGRILITIMMFIGRVGPLTIGFVLAIRSNKQAKIRYAEEKILIG

7E-59	209	34	1E-58	208.5	23.6	1.2	1	B9KEL7_CAMLR	TrkB system potassium uptake protein TrkB, putative (EC 3.6.3.14)	ktrB Cla_0138	Campylobacter lari (strain RM2100 / D67 / ATCC BAA-1060)	447	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Campylobacter, Campylobacter lari, Campylobacter lari (strain RM2100 / D67 / ATCC BAA-1060)	306263	>tr|B9KEL7|B9KEL7_CAMLR TRK system potassium uptake protein TrkB, putative OS=Campylobacter lari (strain RM2100 / D67 / ATCC BAA-1060) GN=ktrB PE=4 SV=1MAKLSLDRKNIRILFIGYILVALFGTFILMLPIMHTKPISFLDAFFTSASAVSMTGLIVLNTSLDFSFYGQLVILLLIQIGGLGYMSIAMALYILVRKKMSFGEKNLLRESLIYPESDGLVGFLKKVLFFVFAIEFTGAILLFLRFKLDMNLTEALWASVFHSISAFNNAGFSIFESGMMPYRDDFWINFIITSLIIVGGLGYFVLLELYFFSKKRFASLSLHTKLVLISTIILIIFASLIVFLFEYHNPKSIGEFSLFDKIMSAYFTAVNYRTAGFNTLDLSTFKDASLFFGSLFMIVGGAPGGTAGGIKVTTVAVLLIYAYWSIKDSNARIFNFEIPTETINKAFIIAVSSIVYIITCVLILSLIEDDKSFLPLLFETSSAFATVGVSVGDGGTLSFSALFNSESKLLIILLMLSGRVGVLAFLFSIFFKEKEKYLNYPKGKIIL
7.3E-59	209	17	1.4E-57	204.7	11.8	2	1	R5PK58_9BURK	Trk system potassium uptake protein	BN489_00192	Sutterella wadsworthensis CAG:135	487	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Sutterellaceae, Sutterella, environmental samples, Sutterella wadsworthensis CAG:135	1263111	>tr|R5PK58|R5PK58_9BURK TRK system potassium uptake protein OS=Sutterella wadsworthensis CAG:135 GN=BN489_00192 PE=3 SV=1MFRYLLFPVLNALGSVLAAFAALMLVPALYSWAEGDGAVWDFLYSVGITFAAGTILFFTCLPFRRELTARHGFLLVTLSWTLTSAFATIPLLLNQPQYNFSELYFETVSCITTTGSTVITGLDSLPPSINGWRCFLSWVGGMGLIVFSVAILPLLGIGGAQLMKAETSGPMKETRLTPRVAETARALYIIYLGISAICVIAYHLAGMNWRDAVMHMMTTVSLSGIATHDASFAFFKSAEVETVAIFFMLICSLNFALHFVAWRRKSLLAYWRSTEARCCLAAFLMLAAGTAFALYYTGAYPEPLEAFRTAFFAVASTASTTGYASADWSNWPYGIPFILLLSSAVVSCAGSTGGGLKMLRVAIIFSQLRHEFTRLLYPNAVTPVTIDAAEIPNKIVFSVLSYAFIWLLSALTGVLLLLGSGMSPLESFSAAVASITNLGPGLGSVGPAGNYQALSDLQLNILSSLMLIGRLELFTVFVLFSRAFWKP
7.4E-59	209	37.5	8.2E-58	205.5	26	1.9	1	Q9KF87_BACHD	Na+-transporting ATP synthase	BH0598	Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus halodurans, Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)	272558	>tr|Q9KF87|Q9KF87_BACHD Na+-transporting ATP synthase OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) GN=BH0598 PE=4 SV=1MARLLSKSALKGKVIHLSPPQILALSFLVFIMIGTLLLKLPIASTTYISWVDAMFTATSAITVTGLVVVDTGTDYTVFGQVVIMILIQLGGLGLMTFAVLAVMMLGKKIGLQQRILIQEAMNQTSLGGLIRLVRVLLLFTLVMETIAFILLSIRWVPEFGWREGMYQSLFHTISAFNNAGFSLWSDSLSAYVGDPAINLIITILFITGGIGFTVLADLWYKKTFRALSLHSKIMLLGTLALNCIAFIAIFILEYANPHTLGGLAQSDRFWGAYFQAVTPRTAGFNTLEIADMTTASIVLILLLMFIGAGSASTASGIKVTTFFVMILATWSFLKGRAETVVFERTIKLHTILRALAIIVISMMIVFIAVFILAITEDAPFIVKVFEVFSAFGTVGLSMGLTGELTTLGKMTIMVVMFIGRVGPLTMAFTLARPKQSNIRYPEDEVFTG
7.4E-59	209	38.4	7.4E-59	209	26.6	1.7	1	R2QNF0_9ENTE	Cation transporter	UAU_00722	Enterococcus pallens ATCC BAA-351	465	cellular organisms, Bacteria, Firmicutes, Bacili, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus pallens, Enterococcus pallens ATCC BAA-351	1158607	>tr|R2QNF0|R2QNF0_9ENTE Cation transporter OS=Enterococcus pallens ATCC BAA-351 GN=UAU_00722 PE=4 SV=1MNFSRRLNFVKRSLRRLDNRFSSIQIIVFYYLIMTLLSLLLFYLPVFRQQDSHVPFLDMVFMAISTVSVTGLTTFDINSVFNEAGVVMLEILFHVGGLGIMMISTFFFIVSKRRITLKQRQLIMTDMNQPRLSGVVLLIKITLTMLLCTELVFGTIFSIYFYMMGYYSKIGEAIFYGFYQSISAVTNSGFDVTGNSIIPLANDHLFLIVIMFLIFIGGIGFPVLMDFYGWIMHRRRSTSKIPFRFSLFSKIALLAFVVLFVGGTIIIWLLEKNHSFHQLSFGDQWLNSAFYSMTTRNAGLQIHDLNQFQNTTLLIFSMLMFIGASPSSVGGGIRTTTVAIIGLYLYSFLKNEEDINIFNRRIPQNDVRKSVVVFMLSMGMCFFSILFLTATEEHSLISIIVEVTSAFGTTGLSLGITDDLSATGKIMIAILMFIGRIGMLYTLLLFVPKETRDLGYEYPEEKIIIG
7.4E-59	209	26.5	7.4E-56	199.1	15.3	2.7	2	F4Q314_DICFS	Transmembrane protein	DFA_08574	Dictyostelium fasciculatum (strain SH3) (Slime mold)	1208	cellular organisms, Eukaryota, Amoebozoa, Mycetozoa, Dictyosteliida (dictyostelid cellular slime molds), Dictyostelium, Dictyostelium fasciculatum, Dictyostelium fasciculatum (strain SH3) (Slime mold)	1054147	>tr|F4Q314|F4Q314_DICFS Transmembrane protein OS=Dictyostelium fasciculatum (strain SH3) GN=DFA_08574 PE=4 SV=1MIEYLKRPFEWSFWRKCLTLALVYVDQNYFYRLHFLYIVMVGLLGACVISLAERDHRFLDCLYHSYSAITSTGLASIDMSKVSAFTQVVTFVLMQLGSSVLLTLPVVLIKRHYLRKRFARRLEKARVATSSLSDNNNNNNNNKPRRKHKQKDPAKQPLQGTVDITPGDDHDEEEEESIPATRYNSEPDDHIGIGIGMVIHHDHDHHHDYHDGIDVVQHHFNLDEHRRHEHEDHHDDDDDHDNDDEDDDYIDDDQDDSMVGLEHIVDSPTTKESSGGVSTITTSATTGLVHSIETNLEYRSLGKLLYIIPLYQLIVYAIGSTLLYILTSATSVHNVMLKNNVASWWWSIFESVSAFNNCGFVLFTDNLVQLNNRPLILVTISFLIAMGNTLYPVFLRIIISVLKKVSKDPVPYEHLAENPRSLYTHLFPVRQTVILTIVWWVFTISQMSLMAILETNDKAFEGISSSNTFFNYFFQSVSTRTAGFNSVDISLLSSSVLILFVGLMFVSSYPLVISLKGSAVNGKYSYQDTELKTKSVMKDILIRDIFIIYVCILLIGIIEEHRLDDAGNPTFTVFHIIFEVISAFGCVGLSMGFPGAVSFSAILKSSSKLVIIVVMLLGKHRALPDSIDTAVVIKEKAVISKLFLRRRKARQYIYLSFSKIQHNHFYYYLSNNQKSNHLFYIHYPIMNPLIIIFILCIVVSSVFANLSCNNQYVFVNDTNSLSSFSLFDHVEQQSNIIQNKNISLSMMMQPSSVSLSSFNHFEHPIILNKNKNNKNNTNYNNNNSNNNNDIDSSISQTQFDSDNHIVSQCHLPSNHTFIPIYNNKKNNNNNLSFNSSVSISIPFNVLSQSHFQSPLNHSTNNHIIFYGDKEEEEEEYVQLNSNNNTISCFNHVEHQLISHNIHFNSSHVLFISNHSTTKNHIILEEEEEDFNNSRPISISCFNVNHQSNLILEEEESVQLNSNNNTISFSYFNQSIPIDNNTISFFNDHQSSIPCFKSSDLYTRSTTNNHILVEEEFVQLNKSSINIINSLTCLDNVKHQSIPINNQSNNNNNYFSLIQSSSLISPIPFSSDYFNSSNTSTSSSSSSTLYLLSNTINSTRSNTSPFSRYSSNISRIENNNNAVTSSDNLKHSTDSSSFIFIDTKVANNYFDSLNCFGTNHSNHTTIQQQQPSSSPINHDTILTTIHTHKSTHNQYSQITPPSSNNNNNNKK
7.4E-59	209	18.1	3.9E-57	203.3	12.6	2	1	D7E6G7_METEZ	Cation transporter	Metev_0261	Methanohalobium evestigatum (strain DSM 3721 / OCM 161 / Z-7303)	479	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanohalobium, Methanohalobium evestigatum, Methanohalobium evestigatum (strain DSM 3721 / OCM 161 / Z-7303)	644295	>tr|D7E6G7|D7E6G7_METEZ Cation transporter OS=Methanohalobium evestigatum (strain DSM 3721 / OCM 161 / Z-7303) GN=Metev_0261 PE=4 SV=1MNVHIIFNIIGRLLLLLGFIMIIPLFVALYYGEPIEPFTVAITMTILVGTVFLFLFRSTEDEWHHREGFAIVALGWLFAAIFGSIPYMLDGVTPLNAFFESMSGFTTTGSTVFVNIEAHPKGILFWRNMTEWLGGMGIIVLFIAILPKLGVAGRQMFRAEVPGPQEDKLKPRIRETSKILWMVYLVVSIAEAIALKLAGLSVYDAVTHTFTTVSCGGFSPYARSIEAFGSPLVETIIMVFIFISGANFALHYKTLYASRKSLIKDDEFKFYSFVIFSAIALLTLILWRDINIPIIESLRYAAFQVLTIITTTGYATTDFIAWPHSAQMILLILMFAGGCAGSTAGGPKMVRWLLMLKYSRREIFKVIHRRAVTRIKFNKKSVPEDIMQSVISFIAIYFLIFAASSVLLGLLGMDLVSSITASIATLGNIGPGLGAVGPMDNFDVVPALGKVALIGNMWMGRLEIFTVFVMLTPEYWKKW
7.5E-59	209	20.5	2.4E-58	207.2	14.2	1.7	1	R7D038_9BACE	Trk system K+ uptake protein TrkH	BN666_00481	Bacteroides sp. CAG:462	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:462	1262740	>tr|R7D038|R7D038_9BACE Trk system K+ uptake protein TrkH OS=Bacteroides sp. CAG:462 GN=BN666_00481 PE=4 SV=1MINYKIVAKILGILLFLEAILLLGCSIFPICFGESDLVPFLASAGITCLIGLILFWIGHDADKKVNRKDGYIIVTFSWVLFSLLGMLPFLFGRYTESVANAFFETMSGFTTTGATVLDNIESLPHGILFWRSLTQWFGGLGIVFFTIAVLPIFGSGGMKLFAAETTGPTHSKLHPRLDVTAKWIWTIYLIITLTHGALLLLGDMPWFDSLCTAMSTAATGGYSVKQSSLMAYNSPYIEYITTLFMLISGVNFTLLYVAILKRQPVRLLKDTEFRWYIGSYSVFTLFITIALLVDTPMGLEESFRLASFQVATAQTTTGFGTADYMLWPSCTWLVLCIAMMVGACAGSTTGAMKSIRLAMLFKIVRNQFRHMLHPNAVLPLRISGVVISNEIKTTLLAFFFAYIGIILVGWVFMLTLGVGFMEAFGITVSSLGNVGPGLGNCGPAYSWNNLPDAAKWGCSFLMLIGRLELFSVLLLFSPSFWKKH
7.7E-59	209	42.1	2.9E-34	127.8	12	2	2	R5RAD4_9FIRM	Potassium uptake protein	BN521_00558	Coprobacillus sp. CAG:183	434	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:183	1262853	>tr|R5RAD4|R5RAD4_9FIRM Potassium uptake protein OS=Coprobacillus sp. CAG:183 GN=BN521_00558 PE=4 SV=1MHGLTPMKIIFYGFCIIILMGTILLSLPISLKENQEVSIMTSFFTATSATCVTGLIRVDTYSHWSWFGQFIIILLIQIGGIGFMTFCIYALTLAKKKIGIISRSIMQNSISSPHVGGIVKMTKFIILATFFIEALGAFFLSFIFCPKLGLVKGLWFSIFHSISAFCNAGFDLMGNFEPYSSLVSFQDNWYLNMIIIMLLIIIGGLGFLVWKDIIDNRGHFSKMRLHTKIVITTTIILIFGGALFIYFCEQGNATILSSLFQSVTARTAGFNTVDLSKIRETTQLIIIILMFVGGSSGSTAGGIKTTTIAVMLVNIISMFKQKKGVEVFKRRISDEIVKMASCVLMAYLVLTLIVSLIICQLENISYITVLFECVSAIATVGLTIGITSQLGVISQCLLALLMLFGRVGSITFLLAFASNRVTPLAKAPAEKIQIG

7.9E-59	209	33.8	1.3E-58	208.2	23.4	1.3	1	U5L514_9BACI	ATP synthase	N288_01930	Bacillus infantis NRRL B-14911	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus infantis, Bacillus infantis NRRL B-14911	1367477	>tr|U5L514|U5L514_9BACI ATP synthase OS=Bacillus infantis NRRL B-14911 GN=N288_01930 PE=4 SV=1MKTFIEKVLERLSSAQLIVLFYLFAVILSAVLLELPITLKEGVELSFIDAFFTSVSAISVTGLSTVNVSEILSVPGTFIFAFILQFGGIGIMTLGTFFWLLVGKKIGLRKRKLIMTDQNQYNLAGLVVLIRRILVIFITIELIGAIILGFHFLRYFPTWQEAFLQGFFASVSATTNAGFDITGQSLIPFADDYFVQLINIILLIVGAIGFPVLIEIREFIRHRGTIPYKFTLFTKVTTVTFFLLVVLGTAFICLFEYNHFFADKSWHESFFYALFQSVSTRNGGLATMNISDFSEPTLFFISILMFIGASPSSVGGGIRTTTFAIMVLSIYTYAKGNTHIKVFKKEIMQEDVIKSYIVFATAILICSLAVILLTFTDPKFTFLQIAFEVASAFGTTGLSMGITADLTDAGKIIIILLMFIGRIGILSFLFLIRGTPNKERYHYPKEKIIIG
7.9E-59	209	14	4.5E-57	203.1	9.7	2	1	R6UQE1_9FIRM	Trk system potassium uptake protein TrkH	BN503_00545	Oscillibacter sp. CAG:155	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, environmental samples, Oscillibacter sp. CAG:155	1262910	>tr|R6UQE1|R6UQE1_9FIRM Trk system potassium uptake protein TrkH OS=Oscillibacter sp. CAG:155 GN=BN503_00545 PE=4 SV=1MIAFVIGRILLTEAALLVIPLVVALLYGESLKPFLLPMALLVLLGALMSFRRPRSTALFARDGLAVVALAWIAMSAFGALPFYLSGEIPSYVDCFFETVSGFTTTGASILQEVESLSKSLLFWRSFTHWVGGMGVLVFVMAILPMTDGHGMHLLRAEVPGPTVGKLVSRMGDSAKILYGIYLVMTVLEIILLLLGDMPLFDACINSFGSAGTGGFSCRNLSIGAYDNAYYDIVIGIFMLLFGVNFNLYYFLLVRKFRDVFHSEELRTYLIIVATAVAAITLDILHIYHSVGTSLRHAFFQVSSIITTTGYATVDFNAWPAFSKAILVMLMFIGACAGSTGGGIKVARLVILTKSALCDMKRMLHPNAVTTVRFEGRPLAEKNVRGVHMFLAVYLLVFCASCLLVSLEQVDLVTVFTAVASCINNIGPGLEIVGPMGNFSSFSDFTKLLLSFDMLVGRLEVFPMLLLFAPSIWRQKLPIRQIRL
7.9E-59	209	34.3	1E-58	208.5	23.7	1	1	F2JIB9_CELLD	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Clole_2582	Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	473	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Cellulosilyticum, Cellulosilyticum lentocellum, Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	642492	>tr|F2JIB9|F2JIB9_CELLD Potassium uptake protein, TrkH family OS=Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) GN=Clole_2582 PE=4 SV=1MKQSEAPGFIKVKRGFIQRQNLHPAQILVGGFLIVILLGTLLLSLPISAANGEATSLIDALFTTTSAVCVTGLTVVNTSMHWSSFGKTVILFCIQIGGLGFMTLVSMLFIVLGKRITLKNRLIMQEALNFNTTAGIVRFTTHIVKGTLLVEGIGAFLLCFAFIPDYGFIKGIIYSIFHSISAFCNAGFDLIGTRSLTPYVGNSIVNLVIMSLIVVGGLGFSVWIDTYKMIRGKLKAPKHFKWKQAFNKMSVHTRLVWILTISLLLIGFIVIFVLEYKNPGTLGPLTFKEKIYAAMFQSVSPRTAGFNTVDLASLTDTSKLVTILLMFIGGSPAGTAGGIKTVTVGVLMLCAISTIRGNEQTTVFKRRIPLQIITRALTIIAMISIMVVFTVVGILSLSENFTFMEILFETISAFATVGTTLGITPLLSITGKITIIIVMFIGRLGPITMAMALMVRQSKNKGNIQYPEEKVMVG
8.2E-59	209	28.2	1.1E-58	208.3	19.6	1.1	1	B1HTK4_LYSSC	V-type sodium ATP synthase subunit J (EC 3.6.3.14)	Bsph_3724	Lysinibacillus sphaericus (strain C3-41)	415	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus sphaericus (Bacillus sphaericus), Lysinibacillus sphaericus (strain C3-41)	444177	>tr|B1HTK4|B1HTK4_LYSSC V-type sodium ATP synthase subunit J OS=Lysinibacillus sphaericus (strain C3-41) GN=Bsph_3724 PE=4 SV=1MPLSTEDGKGLSFLDALFTATSATCVTGLIVVDTGDTFSVFGEVVILCLIQIGGLGFMTFATLLFLLLGKKISLKERLLLKEAFNNISIAGLVKLVKRILLFTALIEIIGGLILSIRFSFDMPIGKAVYFGFFHAISNFNNAGFDLMGGFNGMTAYVDDPFVVLTICVLITIGGLGFIVMNELYEYRVTKRLSVHTKIVLASTIILTVSATILIFLFEFGNDKTLGPLTEWGKVLGSFYQAVTPRTAGSNTLAIGDLTHSTLFLIILLMFIGAGSGSTAGGIKITTFAVLVATMWSQIRGKEDVVLFKRRIVTETILKALTVTMCGVLIVVVVTIILSITEQRHSFMMYLFEATSAFGTVGLSMGLTPELSPTGRILIILTMFAGRLGPLTIAFAITKRRKTEAFRHPKGNIMIG
8.5E-59	209	23.7	4.7E-58	206.3	16.4	2.1	1	B0ECJ7_ENTDS	Sodium transporter, putative (EC 3.6.3.14)	EDI_263660	Entamoeba dispar (strain ATCC PRA-260 / SAW760)	717	cellular organisms, Eukaryota, Amoebozoa, Archamoebae, Entamoebidae, Entamoeba, Entamoeba dispar, Entamoeba dispar (strain ATCC PRA-260 / SAW760)	370354	>tr|B0ECJ7|B0ECJ7_ENTDS Sodium transporter, putative OS=Entamoeba dispar (strain ATCC PRA-260 / SAW760) GN=EDI_263660 PE=4 SV=1MNNKKPEGKVVSEIGNTEPNKVSDENVTPVTSSFNKYPDKQESVEIEMDNRVNDSRSYDHSQNDNEGVVQQPRRWYSNNVSPSLRSGFSEQGQMGRENCQSEMAEGVNSEDSSETSIASVSNQISKRVRPAVVLNDGSKEDEEQGRSDDNFEDENEIKEDKSLPPHDLGYYVARLRTIIYPNFLNYYLMHFLFFTALCFVGAIIMILIDSKLNYIDALYTAVSSYTGSGLTVIDLTKVKFGIQFISYLLTFIGSIVLDSSYYILIKLFRMGTKKQTKSLEGTAPQVVIDAAIAQARHINSTETKTSILLLVVIWLYNIIVQVIGFLLLLIAFAKDKDKIEATGVNWVWFTLYQTNSAFNNCGIVLSSNSLVSFSNNAGVTIIVSILTVLGNTCYPIVLRGIIELLGIILKCTRYDKIIQYILRYPRRCSTHIYPRKATIWLIIVFFMITFSEFIIQMSLDFNNFKDIPVGYRTIDIFAQSISTRTAGFAILDFSKISSSGCYVMMIGFMYLSSYPITVTLRETNPYLRHKENSNQDSGIVYQAKNMLAWDVVCFYSFYFLICCCEQDALRKDYTYTEFMILFEVISAYGTVGYSLPMTNGAYSVSGGFRPICKLFICCVMMFGKHRGFPERVDRGFTPYQIVINRKENEDSSLECQVNDRNEKKIRKEEKTKVQAENNKEGNTSTSVISALDTPLSLPQRNQVSSRNFDEITFRDNDL
9.1E-59	209	21.6	8.6E-58	205.4	15	1.9	1	R5Y9L6_9FIRM	Potassium uptake protein TrkH family	BN695_01533	Anaerotruncus sp. CAG:528	452	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Anaerotruncus, environmental samples, Anaerotruncus sp. CAG:528	1262700	>tr|R5Y9L6|R5Y9L6_9FIRM Potassium uptake protein TrkH family OS=Anaerotruncus sp. CAG:528 GN=BN695_01533 PE=4 SV=1METNNAKRRKFKLNTFQTIILGFAGVILLGSFLLSLPFATKSGDPVPYIDALFTSTTSVCVTGLITRDTGTYWSLFGQIIILILIQIGGMGVMTVTIMLGLISRRRFSIMQKYTMQDAISAPVFGDTIKLTKYIICVTACTEAAGALCLLPVFKQHYGWLKAIWYSVFHAISAFCNAGIDLNGVEQPYCSLTHYYNNPVVNFVIMFLIVFGGIGFITWDDMRRNGFKFKKYRLQSKIALLMTAILIILPALYFYIYEFHRVRWDWMSEGGRIMASLFQAVTPRTAGFNTIDLNMMSDVSKMIIIVLMLIGASPGSTAGGMKTTTVAVLISSAFSVFKKREDPEAFHRRLSADVVRSASAVLSMYVALFMLGSIVICQLEDVPIMPAMFETASAIGTVGLSLGITPGLCTVSKVVLISLMYFGRVGGLTLIFAAASGIQKKRSKYPLEKVAVG
9.2E-59	209	25.1	1.6E-58	207.8	17.4	1.3	1	K9UA89_9CHRO	Potassium uptake protein, TrkH family	Cha6605_0454	Chamaesiphon minutus PCC 6605	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Chamaesiphon, Chamaesiphon minutus, Chamaesiphon minutus PCC 6605	1173020	>tr|K9UA89|K9UA89_9CHRO Potassium uptake protein, TrkH family OS=Chamaesiphon minutus PCC 6605 GN=Cha6605_0454 PE=4 SV=1MTVSRSICLGFMAVISFGALLLMLPISTSNGQWNDPIVALFTATSAVCVTGHVVVDTATYFSRLGQLAILLLIQVGGLGYMTVTTFLLLLLGRRFGLKDKVAIQQSLDRRSLQGSTQILQSIVATTMLFELTGAFLLLVFVPDLGWQKGLWFALFHSISAWNNAGFGLFSDNLVGYQGSWLVNGVITGLIIFGGIGYEVILELYLRGRARLQCQRSGISRSLNFQVAVSTTLFLLLGGTLAIWAIEIRNPQTLGALSFPQQVLAAWFQSVTSRTAGFNTIDISKMTTAGLFVTIALMLVGGSPGGTAGGIKTTTARLLASCTYAILRGKESVILYRRQVPNSLLLKAIAVTFGSLLTVVFATMAIALADPKLDFIRILFEVVSAFATVGLSTGITAGLTPFSKLVLIATMYIGRVGILLLIAALLGDPRTTTVKYPEESLLVG
9.3E-59	209	32.3	1.6E-58	207.9	22.4	1.2	1	V9W6Q6_9BACL	Ktr system potassium uptake protein B	ktrB2 ERIC2_c29500	Paenibacillus larvae subsp. larvae DSM 25430	460	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus larvae, Paenibacillus larvae subsp. larvae, Paenibacillus larvae subsp. larvae DSM 25430	697284	>tr|V9W6Q6|V9W6Q6_9BACL Ktr system potassium uptake protein B OS=Paenibacillus larvae subsp. larvae DSM 25430 GN=ktrB2 PE=4 SV=1MPFFVFQEEMMNIPGKIFRLKPPQILVLGFASIILIGALLLMLPISSADGYSMPFIDAVFTATSATCVTGLVVVDTETHFTVFGKVVIILIQVGGLGFMSMATLIAFLRKKRISLRERLVLQEALNQSSMEGIVRLFRKVLVYSLTIEGIGAALFTIRWSFDLGFPKALLFGIFHGISFFNNAGFDLFGSISGPFSSLTSYKNDFIINFTSMALIVIGGIGFIVMSDIMEYKKTRRLSLHTKVVLSATAFLIVFGALVIFIFEYTNQATMGQQGFFGKVLSAFFQSVTPRTAGANTLDISSLRQATQFFIIILMFIGASPGSTGGGIKTTTFFMTIIGAMIAMVRGKEDIVFFRYRLGKDRILKAITLSMICLFLVIFVSMVLSTTESQQFLKILFEVTSAFGTVGLTMGITPYLTIFGKIMISLTMFAGRLGPLTLAYALGPKPDKELYRYPEGKITIG

9.3E-59	209	9.5	1.5E-58	207.9	6.6	1.2	1	L0JNI1_NATP1	Cation transporter (Trk-type K+ transport system, membrane component)	Natpe_2092C488_06430	Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	515	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrinema, Natrinema pellirubrum, Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786)	797303	>tr|L0JNI1|L0JNI1_NATP1 Cation transporter OS=Natrinema pellirubrum (strain DSM 15624 / JCM 10476 / NCIMB 786) GN=Natpe_2092 PE=4 SV=1MIGRIHVDVRSSCSLLGTVLKFLSLSLLVPTAVALFYRESPLPFLVALVVAVGVGTGLERLEPEPDLEHREAFLLVALTWLVLPLV GTIPYLVAGTGTIAQPINALFESMSGFTTTGATVMGEISVETHSHSIMLWRQLTQWLGGMGIIVLMVAILSELSVGGTQLIREEAPGIQV EKLTPRIRQTARALWLIYVWFTLAAVVVYYGLHLVGLAPNMTFYNAVSHALTTLPTGGFSPEGRSVEAFEPIVQWAVMPFMIVAGTNF ALYWHVWRGKPDRLTGNAEFRSYLLSMGVVGVLLSAPLFLGVGLATVPDGVAAIPGSLERSLRHGLFQTLAIVTTTGYASMDFNTWS ESTQVILLFAMFLGGSAGSAAGSIKIIRWYVVGKSIERELFTTVHPQAVRPVRMGDTGDVIDEEAIHGIFVFIVLFLTLFAVSTVLLFLDAY RTPGLELTALEAISATIATLGNVGPGVGVVGPMNSYEPFSGAAKLYMTFLMWIGRLEILSVLVILTPAYWRS
9.3E-59	209	11.9	2.7E-58	207.1	8.2	1.7	1	D8J4T8_HALJB	Cation transporter	HacjB3_10860C497_11807	Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	510	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halalkalicoccus, Halalkalicoccus jeotgali, Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3)	795797	>tr|D8J4T8|D8J4T8_HALJB Cation transporter OS=Halalkalicoccus jeotgali (strain DSM 18796 / CECT 7217 / JCM 14584 / KCTC 4019 / B3) GN=HacjB3_10860 PE=4 SV=1MSLHIDWRASVGLVGTVVKYLSLTMLVPLFVAIIYREDVWVFVVSILITISIGLALERIEPDPDLGPEEALLLVTLAWLAAALIGTIPY LLAGYGTASTLSHPINALFESMSGFTTTGATVMGEIGVERHSHALMMWRQLTQWLGGMGIIVLMIAILPELAVNGAQLMGSEAPGPTL QKLTPKIAQTARALWMVYFGFTIALICLLYALHVLGLAPNMDLYNAIAHGFSTLPTGGFSTRADSIAAFSAAVQWALVPFMVIAGVNFAL FWQVLRGEWRALFEDTEFRVYTGAIAVLVAVLAVVLFRGGAPVLELGGATEGVSENALRQAAFQIGSLLNSTGYATSDFAQWDAHA RMVLLFAMFIGGSAGSTGGGIKVIRWLVILKTLRRELFVAAHPRAVRPVRLAGRVVDEDVIRGLVAFTFLYLLLFGLSAVFLSLDAARIG YELTPMEAITASLATIGNIGPGFGSLGPFGSYLAFSNVSKLLMTFLMWVGRLEIVPVLALFVLSIEE
9.4E-59	209	21.2	6.8E-58	205.8	14.7	1.9	1	A0A0F5VHZ4_9GAMM	Trk system potassium uptake protein	KY46_04820	Photobacterium halotolerans	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	265726	>tr|A0A0F5VHZ4|A0A0F5VHZ4_9GAMM Trk system potassium uptake protein OS=Photobacterium halotolerans GN=KY46_04820 PE=3 SV=1MVNPRNTFRLLAMPMLWMGFVQLSFGLLSLFIFNDHISRLFLAPGLFMVLGSAIVSVILRQSKLDKVTFRDALIFASLTWVLTGIL GAIPIHLVTDVNYSDAVFESISALTTTGATILSGLDNMPKSFLLYRQFLQWMGGLGVVIFVVAVLPMLNVGGMRLLKAETPGPIKDDKLS PRISKTAHYLWGVYLAITAACAFAYYLAGMSAYDAIAHSFTTVSTGGFSTHDASMWYFESHLILMISNVFMLLGAINFGLHFRVFRAGL SGIKLYLRDEEVRVFVLIVLALSFILGWYLYRQSAYEHILISFSFAMFHVISFITSTGFGAADLSAWPAATALFLVFCAYLGGCSGSTAGG NKIVRDILTFKVIRREIRQLIHPRGILPIRYQGRVVASDITNAVMAFMSLAALTTLVFTLLLMATGLDFWSSFTAVVACINVLGPGFGQVG SNFQPVSDTGIWFLNLAMILGRLEYFTVLAMLLPHFWKK
9.8E-59	209	19.9	2.5E-57	203.9	13.8	2	1	R6KJN8_9BACE	TrkH family potassium uptake protein	BN506_01679	Bacteroides cellulosilyticus CAG:158	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides cellulosilyticus CAG:158	1263038	>tr|R6KJN8|R6KJN8_9BACE TrkH family potassium uptake protein OS=Bacteroides cellulosilyticus CAG:158 GN=BN506_01679 PE=4 SV=1MINFKTVIRIIGILLLLETVMLLLCSGVSFYYQDEALVDFWVSAGITAGAGLLLAAMGKGGDRQLTRRDGYVLVSFAWVAFSLFG MLPFYISGYIPSITNAFFETMSGFSSTGATILDDIEALPHGLLFWRSMTQWIGGLGIIMFTIAILPIFGVSGLQVFAAEASGPTHDKVHPRI GITAKWIWSIYAGITCILVALLMLGGMDWFDSVCHAFATTGTGGFSTKQASVAYYQSPYIEYVISIFMFISGINFTLLLFFVNRKFKKVIH DAELKWYFWSVVLFTGLIAVILYYSNPIGMEDAFRKSLFQVISLHTSTGFATDDYMLWPAVTWGLLTIVMLMGACAGSTTGGLKCIRM VILGKVARNEFKHILHPNAILPVRINKQVISPSIQSTVLAFCFIYAVIIIISVLIMMGMGIGFVESVGCVVSSIGNMGPGLGETGPAFSWNAL PDVAKWLMAFLMLLGRLELFTVLLLFTPEFWRRS
9.9E-59	209	13.9	3.1E-57	203.6	9.7	2	1	R6I577_9FIRM	Uncharacterized protein	BN556_01893	Firmicutes bacterium CAG:240	480	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:240	1263013	>tr|R6I577|R6I577_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:240 GN=BN556_01893 PE=4 SV=1MKIKLVFHTVGRVLLLEAALMLLPLAVSLIYGESCSLSFVISAAAAAVVGAALKFFCRSDSKNLYTRDGLAIVALSWIGISLFGALPF VISGSIPSFIDAFFETVSGFTTTGASILTDVEALSHGLLFWRSFTHWVGGMGVLVFIMAVMEKTPERSVNILRAEMPGHNVDKLTPRAS GTAKILYYIYLALTVLETVLLLCGGMPLFDSIVHALGTAGTGGFGIKADSIASYSHFCQWVITVFMLLFGVSFNMYYLLLIKRWREVLKSN ELKCYLGISLAAMIIVVLSIMPLYGSIADAVRLSAFQVSSIVTTTGYATADFDAWPSLAKAVLLILMFFGGCMGSTAGGLKMSRVTVLAQI ARNDLRHALRPREVSTVILNGRRVDAQGERQILSYFALYIAVIGAVFLLISFEPFGIETNFSATVSCVNNIGPGFGQVGPSLSYADYSAF SKLVLSFAMLLGRLEIYPLLLLLSPQLWTKR
1E-58	209	28.6	1.3E-58	208.2	19.8	1	1	A9KHD5_CLOPH	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Cphy_0415	Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) (Lachnoclostridium phytofermentans)	455	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Lachnoclostridium phytofermentans, Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) (Lachnoclostridium phytofermentans)	357809	>tr|A9KHD5|A9KHD5_CLOPH H(+)-transporting two-sector ATPase OS=Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) GN=Cphy_0415 PE=4 SV=1MFQKKRRFSTTRMIATGFLAGIMLGALLLSLPIATKAGIVTPLEDSFFTATTSICVTGLTTVTTGEHWSFFGQLVILLLIQFGGLGV VTFTTTIFLLLGKRVKLSDRLVIQNAYNIDTLSGLVKLTKKIIKFTLIVEGIGAFCYLFQFVPEFGVVDGVWYSIFHAVSAFCNAGIDLVGG NSFIPYRDNLWINLVTMGLIVLGGIGFPVWWDVFHISKQAVKKDIKVRSMFRRLTLHSKIAITVTVVMIVLGAVLTFILEFNNPATIGELSI GKKMLSSLFQSVTTRTAGFATIPQQNFKDATSIVYLVWMFIGGSPSGTAGGIKTVTVAVILLSTISIVRGKKDIEIFQRRISDQYLKKGLA VVMVSFLVLMVTTISLSAIQNSSFLDTLYETTSAIGTVGLTRNMTGSLMTAGKIIVMITMYLGRIGPITMALAINAGKHQGEKSLPEGKILV G
1E-58	209	40.7	8.9E-58	205.4	28.2	1.9	1	Q81TF4_BACAN	Ktr system potassium uptake protein B (Potassium uptake protein, TrkH family)	ktrB GBAA_1323 BASH2_04538 BF27_654	Bacillus anthracis	439	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus anthracis	1392	>tr|Q81TF4|Q81TF4_BACAN Ktr system potassium uptake protein B OS=Bacillus anthracis GN=ktrB PE=4 SV=1MKRINIRMSPPRVLTLSFIMLSIIGTCLLKLPIATTTSISWLDALFTTVSACTVTGLGVVDTGKVFTLFGQCVILTLIQVGGLGIMSFA VLIAIMLGRKIGLQNRILLQQALNQTNIGGVIRLAKALFLFSFTVECIATLILSFEWIPKYGIAKGLYYSFFHSISAFNNAGFSVWSDNLMS HSHSILVNVVISSLIILGGIGFTVIVDIKKKKNFKNLTLHSKLMLSSTLIVNIIATVFIFIFEFHNSLSMRGFTPFEEGMAAYFQAVSTRTAGF NTVDISALSKPSLLLMMLLMFIGAGSASTGGGIKLTTFLIMFFGVFKFLQEQDDIVVFKKSIKDTLIVKSLTIAIISISFIFFAILILSITERVPLL MSAFEVFSAFGTVGLSMNFTPHLTIIGKAIIIFMMFFGKMGPLTLAFSFARKKNRKIKYPNEDILTG

1.1E-58	208	16.7	1.1E-28	109.4	5.6	2	2	W0JUG6_9EURY	Potassium transporter TrkH	HALLA_19735	Halostagnicola larsenii XH-48	499	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halostagnicola, Halostagnicola larsenii, Halostagnicola larsenii XH-48	797299	>tr|W0JUG6|W0JUG6_9EURY Potassium transporter TrkH OS=Halostagnicola larsenii XH-48 GN=HALLA_19735 PE=4 SV=1MRIRVDWRSSCSLSGTVLKWLAVPLSAPLVLAVIDGSDPTPFVVAVIVTALVGLSLERLSVDRDLGQREAFLMVALTWLCVAVIG AIPFFVAGVGTLAHPINALFESTSGLTTTGATVLEDFDAHSRAIMLWRQLLQWLGGLGILVVAIGLLSNLMVGGAQLMETETQTRNVRK LRPHIADTARLIWGLYVGLTVLAAATFYALNRLGVAPEMTLFNAVSHALTSVSTAGFSPEAESVGAFSPIVQWSFVPFMILGATNFVLL YYVVQGNYFQPLKNEEFRFYVGVLAAFSLLVVGVLSVDSSSFDRGLEPTIRHGVFNVVSMVTTTGYASVDFDLWSSGAKHILFLCMFL GGMAGSTTCSIKLLRWLVVLKTLYRNLFTSIHPQAVRPVRLGDSVVDEDTITDIFSYVLLVLVIFFLLTIVVVVDAARDPSTAVSEFDALG AAASIFLNIGPAFGMAGPMGSYEGFSVFSKSVMIVMMWIGRIEIIPVLVLLTPAFWKS
1.1E-58	208	36.9	1.4E-58	208	25.6	1.1	1	Q8RI86_FUSNN	Potassium uptake protein KtrB	FN1725	Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131)	448	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Fusobacterium, Fusobacterium nucleatum, Fusobacterium nucleatum subsp. nucleatum, Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131)	190304	>tr|Q8RI86|Q8RI86_FUSNN Potassium uptake protein KtrB OS=Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131) GN=FN1725 PE=4 SV=1MRKLSLLKKWDSLSPYRKLIFGFLVAIFIGVILLKMPFSLRENQNITVLDSLFTIVSAICVTGLSVVDISQVFTSTGQLIILFFIQLGGL GVMTVSIIVFLLVGKKMSFETRELLKEERNSNSNGGITNFIKNLLLTVSLIEILGASILAYGFSRYYPLKKSIFYGLFHSVSAFCNAGFSLF TNNLEDFRYDKLISLTISFLIILGGIGFVTVNSLFIIKKKKLKNLSLTSKFALLITFFLLTFGTMLFLVFEYNNSSTLKGMNFVDKIINSFFQSV TLRTAGFNTVPLENIGPATVFISYIFMFIGASPGSTGGGIKTTTFGILIFYAFGVLKRKEYVEVFKRRIDWELINKALAIVIISLFYIIVVITILL SIESFSADKVIYEVISAFSTTGLSMGITASLGIISKFLIIITMFIGRLGPMTVALAFTNNKKSLVKYPKEDILIG
1.1E-58	208	31.4	2.7E-58	207.1	21.8	1.5	1	R2THY6_9ENTE	TrkH family potassium uptake protein	UAW_00887	Enterococcus haemoperoxidus ATCC BAA-382	454	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus haemoperoxidus, Enterococcus haemoperoxidus ATCC BAA-382	1158608	>tr|R2THY6|R2THY6_9ENTE TrkH family potassium uptake protein OS=Enterococcus haemoperoxidus ATCC BAA-382 GN=UAW_00887 PE=4 SV=1MKKKKITSIVKKRLSAVQVLALGFIVLIFIGGALLSLPLFSRSGNATPFIDALFTSVSAVCVTGLTTVNTALHWNAYGQLIIMILIEIGG LGFMTMPVLLYFILRKKITLSTRILLREALNLDDMSGAFRLMIYVVKLAAIIQIVGAILLSIQFVPEFGWRKGLFFGLFHSISSFCNAGFDLL GDSLTPYQTNPFVLLVIGGLIISGGLGFIVWQDLLQLKKIRRFSLHTKIALITTFSLLVGGFILFFVTEHNASDLTAGTNFFDRLANTFFMS VTPRTAGYYSIDYMQMTNAGLITTIFLMYVGGTPGSTAGGLKTTTFAVLVIQIVSIFKGRTRAEFQGRTIRNSTVFRALTLFFITLTLCVF SIMLLTITENIPESSGIEYVAFEVFSAFGTVGLTMGLTPELSVLGKVIIMLLMYIGRVGIYTVGFSLLTRGQKQQAKYKYPDESVMIG
1.1E-58	208	30.6	2.4E-58	207.3	21.2	1.4	1	A2U3E8_9FLAO	Potassium uptake protein TrkH	trkH MED152_12369	Polaribacter sp. MED152	499	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Polaribacter, Polaribacter sp. MED152	313598	>tr|A2U3E8|A2U3E8_9FLAO Potassium uptake protein TrkH OS=Polaribacter sp. MED152 GN=trkH PE=4 SV=2MNNLNLKIIYRFLGITAILNGCFMFIAFPFSFFSEEKEAWGILNAGIITVFIGLLLFFFNKPTHKNIQKKEGYLIVTFGWLILSITGMLP YLLSGAIPTVSDAFFETISGYSTTGSSILTNIEAMPKGILFWRSATHWIGGMGIIVLTIAILPLLGIGGMQLFMAEAPGPSADKLHPRITDT AKRLYLIYVVLTFAEFFLLKAAGMTWFDAINHAMATVSTGGFSTKTDSIAFYNGSPIIQYIIIFFMFIAGTNFVLTYFALKGKVKKVYESEE FRYYFFGILGISMIISVIIIFFKDETMVTTLAHPEVLGKTESAIRHSLFMVTSVVTTTGFVSADFTMWNFFATGIFFALFFTGGSAGSTSG GVKVVRHIVMLKNSFLEFKKALHPNAIIPVRYDGKSVNQTIVFNIISFFIIYMLIFIMASVTLTLLGLDFLSALGAAASSLGNIGPAIGSVSPV DNFAHLTAPAKWFCSFLMLIGRLELFTVLILFTPFFWRKN
1.1E-58	208	26.7	9.5E-57	202	18.5	2	1	D4M4N7_9FIRM	Trk-type K+ transport systems, membrane components	RTO_16070	Ruminococcus torques L2-14	413	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, [Ruminococcus] torques, Ruminococcus torques L2-14	657313	>tr|D4M4N7|D4M4N7_9FIRM Trk-type K+ transport systems, membrane components OS=Ruminococcus torques L2-14 GN=RTO_16070 PE=4 SV=1MLPIATKSGQCTSFLDALFTATSAVCVTGLVVNDTATYWSLFGQGVILLLIQIGGMGIITIAIAIAVVSGRKIGLMQRSTMQEAISAP TVGGIVRRTQFIIRTTILIEIIGAVLLAPVFCRDFGFWKGIWYSLFHSISAFCNAGFDLIGIRTPFSSLTSYSVQPIVNLVIMMLIIAGGIGFLT WEDIKNRKWHFKKYRMQSKVIFMVTGILIFLPALYFFYFEFSNVPLTERVWVSLFQSVTPRTAGFNTADLTLLSEVGQMLIIMLMLIGG SPGSTAGGMKTTTLAVLVSSALSVFRKKEHTHFFGRQIPDGTIRNAATIFLMYIVLFLVGGMVICRTEDIPLMTALFETASAIGTVGLSLG ITPDLGLVSHIILICLMFFGRVGGLTLIFATISEKKPNGSKYPQEKITVG
1.2E-58	208	32.4	2.6E-58	207.2	22.4	1.5	1	A8FCF8_BACP2	Trk family potassium (K+) transporter, NAD+ binding protein	ykrM BPUM_1242	Bacillus pumilus (strain SAFR-032)	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus pumilus (Bacillus mesentericus), Bacillus pumilus (strain SAFR-032)	315750	>tr|A8FCF8|A8FCF8_BACP2 Trk family potassium (K+) transporter, NAD+ binding protein OS=Bacillus pumilus (strain SAFR-032) GN=ykrM PE=4 SV=1MNPIKKLIDRLSAFQLIALYYFLAVTVSLILLSLPVAHQDGVKWTFIDALFTAVSAVSVTGLTVVDTSQTFSVAGMWILAFVLQIGGI GIMTLGTFVWIVMRKRIGIKERKLIMADQNQSNLSGIVKLMKQVLYLILLIEFVGGLILSMYFLKYYDVQTAFLHGFFSSISATTNGGFDIT GNSLIPYKDDYFVQFITMLLIIFGAIGFPVLVEVKDYLFNQDRKHASFSLFTKITTITFGSLVIVGAIGIYALEARFTFLGKSWHEVLFYSLF QSTATRSGGLSTLDITQLTEPTLLFLCLLMFIGASPSSVGGGIRTTTFALNLLALFHFARGNKSIKIFKRELHQADINKSLMVTMMAFILVF GATFLLTLSEHNTLLQNLFEVCSAFGTTGLSLGITSELSVFGKCIIMMVMFIGRIGIPSFLYLIGRRESEANYHYPKERVIIG
1.2E-58	208	30.8	2.3E-58	207.3	21.3	1.3	1	KTRD_BACSU	Ktr system potassium uptake protein D (K(+)-uptake protein KtrD)	ktrD ykrM BSU13500	Bacillus subtilis (strain 168)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus subtilis group, Bacillus subtilis, Bacillus subtilis subsp. subtilis, Bacillus subtilis (strain 168)	224308	>sp|O31658|KTRD_BACSU Ktr system potassium uptake protein D OS=Bacillus subtilis (strain 168) GN=ktrD PE=3 SV=1MRLKFGKLIQALSPAQLIALYYFLAVTVAVILLSLPAAHKPGADWTFIDALFTAVSSVSVTGLTVVDTADTFSTIGIFILAFVLQFGGI GIMTLGTFIWLIMGKRIGLKERKLIMVDQNQSQFSGIVNLMKQVLFLILWIEFFGGLILGTYFLTYYDSYQEAYLHGFFASISATTNGGFD ITGNSMIPFRHDYFVQFITMLLIIFGAIGFPVLVEVKDFLFSKHRRYPFTLFTKITTITFGSLVLFGAIGIFALEANHAFAGKSWHDILFLSLF QSTATRSGGLATIDISQLSDSTLFFICALMFIGASPSSVGGGIRTTTFALNLLALFHFARGNKAVKVFKRELHPADLMKSLVVTMMAILLV FGATLILTITEKHSLLELLFEVCSAFGTTGLSLGITADLSSVGKCVIMIVMFIGRIGILTFLYLIGRKEIEANYHYPKERVIIG
1.3E-58	208	24.9	1.9E-58	207.6	17.3	1.1	1	B0C2B6_ACAM1	TrkH family potassium uptake protein, putative	AM1_3578	Acaryochloris marina (strain MBIC 11017)	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Acaryochloris, Acaryochloris marina, Acaryochloris marina (strain MBIC 11017)	329726	>tr|B0C2B6|B0C2B6_ACAM1 TrkH family potassium uptake protein, putative OS=Acaryochloris marina (strain MBIC 11017) GN=AM1_3578 PE=4 SV=1MTVSRSICLGFLVAILVGAGLLLLPISTASGDWNSPVIALFTATSAVCVTGHVVVDTGSYFSPVGQVFILTLIQLGGLGYMVSTTFL LLLLGRKFGLRDKIALQQALDRSKLQGSNQVVVSIIATILVFELMGMIFLFGVFSQQYPTPLALWYAVFHSISAWNNAGFSLFPDSLSSY QFSWIVNLTISGLVIIGGIGYEAIFEVYLWLRDRLAGKQKRTLFSLNFRVVTSTTAMLLTLGTIAFYLTESRNPDTLQALSWNDQLISAWF QSMTTRTAGFNTIDIGSMTNAGLFLAIAFMYVGGSPGGTGGGVKTTTIRVLSSCTKAILRGKESVTMYERQIPLSLILKAVGVVVGSITTI VSATTLMSIADPGVEFINILFEVVSAYATVGLSTGITAALTGSSKLILAATMYMGRVGVLLLMAALLGDPRPSTVRYPEESLLVG

1.3E-58	208	9.9	3.7E-58	206.6	6.9	1.6	1	Q9HMF7_HALSA	TRK potassium uptake system protein	trkH3 VNG_2565G	Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	515	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halobacterium, Halobacterium salinarum (Halobacterium halobium), Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) (Halobacterium halobium)	64091	>tr|Q9HMF7|Q9HMF7_HALSA TRK potassium uptake system protein OS=Halobacterium salinarum (strain ATCC 700922 / JCM 11081 / NRC-1) GN=trkH3 PE=4 SV=1MHVAVDTVGRDVGRILQAVSLLLAASVAVVAVNGEFFAIPAFVVSAAVMGGIGTGLARLCRGARPPKKPDAMVTAATAWAVVG VLGALPFVLVAWTMRLHLLPGLTPPLNATTRVFLHPLNAVFETISGFTGTGLTMATTEGDLPRALHWWRSLTEWVGGVGVIVLTVAIL RRGDGSSGSYTLYESEARSEKIHPSIITTVQEIWRLFVGLTLGAIALLLLAGMPPWDAINHGMTGIATGGFAVRAGSIGAYNSPAIEYAT VPIMIAGSIAFPVHYLLFTGDLRNVYADLQTRWVVAWFAVGAAVLSALLFYTGQYDSLAASFRIGLFQFVSATSNTGFGTTTIGRGTER VWQTGPTLFACLGMLTGAAAGSTVSGIKLIRVITLIKGTAWQIRDVFRPASAIRSLRIGDRKLSEHQAQREYAEATLVFVLWLAFLAIGV AVLLAALSPQHPLEYVLFDVMSAQSNVGLDAGITSPGMPALAKGMLIINMWVGRLEIIPIAVLISAVLRHGDFYR
1.3E-58	208	31.2	6.9E-57	202.5	21.6	2	1	Q65DQ0_BACLD	K+ transporter integral membrane subunit	BL03955	Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus subtilis group, Bacillus licheniformis, Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46)	279010	>tr|Q65DQ0|Q65DQ0_BACLD K+ transporter integral membrane subunit OS=Bacillus licheniformis (strain ATCC 14580 / DSM 13 / JCM 2505 / NBRC 12200 / NCIMB 9375 / NRRL NRS-1264 / Gibson 46) GN=BL03955 PE=4 SV=1MPKLVSSNLVKGKIINISPPQTLALSFLIIIAIGACLLKLPGASTTYISWVDALFTATSATTVTGLVVVDTGADFTVFGQTVIMCLIQIG GLGLMTFAVLVVMMIGKKIGLQQRILVQEAFNQTSLGGLVRLVKHLFIFTIVIEFVAFLILSIRWVPEYGLQKGLFHSLFNTISAFNNAGFS LWPDNLSQYVGDPIVNLVITGLFITGGIGFTVLLDLWTKRNFRKLSLHSKLMIVGTLIINTTAALLIFILEYSNPGTLGGLPLADKMWGAYF QGVTPRTAGFNTLDIAQMTTPSLLLIIVLMFIGAGSASTGSGIKLTTYIVMILATITFLRGKSETVVFKRAIKMKTILRALAIIVISFLFVLFAL FILTITENAPFLKIVFEVFSAFGTVGLSMGLTPDLTAAGKAVIMMMMFIGRVGPLTMAFTLAKPKKAPIRHPEDEVITG
1.3E-58	208	34.2	1.7E-58	207.7	23.7	1.1	1	D5DCX9_BACMD	K+-transporting ATPase	ktrD BMD_1217	Bacillus megaterium (strain DSM 319)	440	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus megaterium, Bacillus megaterium (strain DSM 319)	592022	>tr|D5DCX9|D5DCX9_BACMD K+-transporting ATPase OS=Bacillus megaterium (strain DSM 319) GN=ktrD PE=4 SV=1MSSAQIIVTFYIVAVTLGFLLLSIPEALKPGVKLAFIDRLFIAVSAVSVTGLTPVSTPDTFSTTGYFLLAFIFQIGGIGVMTLSTFIWMI LGKKIGLKERQLIMTDHNQSRLSGLVDLMRNILFIIFAIELVGAIVLGLHFLRYYSSWTDAFLHGFFASVSATTNAGFDITGSSFIPYAHDY FVQVVTVILITLGAIGFPVLIEIKHYFLTFKDKRKFQFSLFTKLTTIMFFLLLAGGTILILVLEHSGFLADKSWDESFFYAFFQSAATRSGGV ATMNINEFSLPTLIMMSAMMFIGASPSSVGGGIRTTTFALNILFLFYYVRGNKTIKIFRREIHEDDIIKSVAVSMLAVIICSISLLILSITEHFS LIELIFEVCSAFGTTGLSMGITGGLSDIGKCVIMILMFIGRIGMFSFILMLRRPTSGPDYHYPKERIIIG
1.3E-58	208	39.4	1.9E-58	207.6	27.3	1.2	1	A0A075JV42_9BACI	ATP synthase	X953_12845	Virgibacillus sp. SK37	454	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Virgibacillus, Virgibacillus sp. SK37	403957	>tr|A0A075JV42|A0A075JV42_9BACI ATP synthase OS=Virgibacillus sp. SK37 GN=X953_12845 PE=4 SV=1MKLRYPFLYWMNKLTPVQVLLIFYFLAVLLSTAVMSLPIAYQEGVDIPFIDVVFTAVSALSVTGLSSITIADTLSTTGIIILALILQLGA VGVMAIGTFIWLLLGKKIGLKERRLIMTDQNQHTFEGMVRLIKQIVYVLLTIELIGFIVLGTYFLQYFPTAKEAYLNGFFGTISAISNGGFDI TGQSLIPFKDDYFVQFINILLIVFGAIGFPVLIEVKEYIFSKSVNQRFMRFSLYTKVTTSTFAILIVIGTLFIYLFDMNNFFVGKTWHESFFY SLFQAVTTRSGGLSTMDVSQLTEQNHLFMSLLMFIGASPSSAGGGIRTTTFALAVIFLITYSRGGDSIRIFKREVYEEDLLKAVTVVMMA FILVFSSVLIITIVEPFSLTQILFEVTSAFGTVGLSLGITSEITTFSKIVLMILMFIGRVGIISLLFIFKSNKKSGKYHFPKEKIIIG
1.3E-58	208	31.3	2.6E-57	203.8	21.5	2	1	Q040A5_LEUMM	Trk-type K+ transport systems, membrane component	LEUM_0065	Leuconostoc mesenteroides subsp. mesenteroides (strain ATCC 8293 / NCDO 523)	467	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Leuconostocaceae, Leuconostoc, Leuconostoc mesenteroides, Leuconostoc mesenteroides subsp. mesenteroides, Leuconostoc mesenteroides subsp. mesenteroides (strain ATCC 8293 / NCDO 523)	203120	>tr|Q040A5|Q040A5_LEUMM Trk-type K+ transport systems, membrane component OS=Leuconostoc mesenteroides subsp. mesenteroides (strain ATCC 8293 / NCDO 523) GN=LEUM_0065 PE=4 SV=1MSRKIDLPTAAEMQKFHDKSQRHTFWSRISMPQRLSLGFLTVITVGALLLMLPLSYHGNVGHTFMDGLFTATSAASVTGLTVVD TATHWTTFGQIVIMVLIEIGALGFMSFSVLLFTATRKKMDLRSKMMVQEVYNLESLYDTRVVFGYVIKLSVIIQSIGAVLLAPFFINDFGW KHGMFYAVFHAISAFGNSGFSILPHGTAAYNNQPWILLIAFLIIAGSLGFLVWRDLLIYRTTHRLTLHSKLALVMTGVLIVGGWLLFELTE RNMNSAQDIQPINRIFDTLFMSISYRTAGFAQFGFDSMSSATVLLTMMLMYIGGTPGSTAGGIKTTTLGVLILQTHAALRGKKDVVFSH RRLSHENIVRALLLVFVSLAFLGILSFLLMLTQEHTAHYGLEYIIFEVVSAFATTGLTLGLTPHLTTFFGQLIIMLAMFIGRVGIYTVMFSILNV HDDKAPFRYPEESVIIG
1.3E-58	208	36.3	2.1E-58	207.4	25.2	1.2	1	R6GQB0_9CLOT	Potassium uptake protein	BN542_01552	Clostridium sp. CAG:221	448	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:221	1262780	>tr|R6GQB0|R6GQB0_9CLOT Potassium uptake protein OS=Clostridium sp. CAG:221 GN=BN542_01552 PE=4 SV=1MQYKFNKGFKLNPMQILSLGFLLIILIGGILLSLPISSSTGEYTSFIDAVFTSTSAVCVTGLVTVDTGTHWNLFGQTVIMLLIEIGGLG FMSFTTLIAILLGKKITLRERLILQNAMNTFNIQGVVKMVKYILLFTISIQAIGALIFCTQLIPEYGLGKGLFYSIFHSISAFCNAGFDVFGGG VSLTTHNTNALVILTAAALIIIGGLGFGVWTELYNVKRIRRFSVHTKIVLLVTGFLVIGGTILMLLFEYNNPETIATMNGGEKVLNSFFAAVT PRTAGFNSISTSGMTSAGKFLTMILMMIGGSPGSTAGGIKTTTVGVLILTVICVIKRREDTEVFSKKISKDLVYKAFTLFFIGSGLVIVVSLI LSFTETGASFTAILYETVSAFGTAGLTIGLTPNLSVIGKVLIMLMMYIGRVGPLTVVLSLTKEKIKSGIKYPEGKILIG
1.4E-58	208	21.8	1.1E-57	205.1	15.1	1.9	1	E3GP29_EUBLK	Uncharacterized protein	ELI_2652	Eubacterium limosum (strain KIST612)	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium limosum, Eubacterium limosum (strain KIST612)	903814	>tr|E3GP29|E3GP29_EUBLK Uncharacterized protein OS=Eubacterium limosum (strain KIST612) GN=ELI_2652 PE=4 SV=1MNYRMVFYVIGNMMKSEAALMLLAIIVALVYGEADTIVWFVIPMFILVSLGFILSNKMPEYRNFYARAEGFVVVALSWLVMSFFGG LPFFLSGQIPSLVDSFFEAVSGFTTTGSTILTNIEALPNSMLFWRSFTHWIGGMGILVFVLTIMPKTEGNSIYLMRAEMPGTSVEKLVSK VRPTVRILYGIYLGMTILLIILLVIGGMPLFDSIINAMGTAGTGGYSLKNDSIAYYNSAYIDVVLTIFMLMFAVNFNLYHLVFIKKGKDFFKS EELRWFIGIVAVAIALITIDLLPQYGNRVLETLRYSSFQVASIITTTGFATTNFDLWPSFSKYILLFLMFVGACAGSTGGGIKVSRWLIIVKT AANELKKMIRPRQVTTVKFEDKPLGAQVVASVYTYLAVYILIFAASLLVLSLDQYDFLTNFSAVATCINNVGPGFNAIGPIENFSDFSVVS KLVLCFNMLAGRLEIFPILMLFAPHTWKN
1.4E-58	208	29	3.7E-58	206.6	20.1	1.6	1	C0Z9D0_BREBN	Probable potassium uptake system membrane components	ktrB BBR47_16230	Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus brevis (Bacillus brevis), Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	358681	>tr|C0Z9D0|C0Z9D0_BREBN Probable potassium uptake system membrane components OS=Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599) GN=ktrB PE=4 SV=1MIKKIVEKLHLDPPKTLVLGFSLIIFLGALLLTLPVATVDGLGLHWLDALFTATSATCVTGLVVVDTGTTFTTFGQLVILSLIQIGGLG FMTFATTFALIMRKKISLRERLILQESLNQMSMEGIVRLAKMILVFTALTELIGGVLLSIRFAFDFPLPKAIYFGFFHAISNFNNAGFDLMG EFSSLTAYVDDPVVTLVVCLLIILGGIGFMVVSELYDYRQTRRLSLHTKVVLSTTGILVVAGTALIFILEYANPKTLQPLSMMGKVLGSLY QSVTARTAGSNTLNIGDMYQSSLFLIILLMFIGASPGSTGGGIKTTTFATLIGAVVAQMKGKEDVIFFRQRILPHMVYKSLTLTMISLFIVL VMTMVLSITETSARFEMILFEVTSAFATTGLSMGLTPHLTPIGKILIVLTMFAGRVGPLTIAFALAQRKQKEYFRYPKGKITIG
1.5E-58	208	23.1	1.8E-58	207.6	16	1.1	1	S5QZ02_9STRE	Potassium uptake protein KtrB	KE3_16091	Streptococcus lutetiensis 033	404	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus lutetiensis, Streptococcus lutetiensis 033	1076934	>tr|S5QZ02|S5QZ02_9STRE Potassium uptake protein KtrB OS=Streptococcus lutetiensis 033 GN=KE3_1691 PE=4 SV=1MVCVTGLSVFPVAEVYNGLGQVISIILMQIGGLGLVTLIAVSTYLLRRRMNLSSQNILQSALSYDNSGHLKRYLFNVYKITFIIESLIA ILFLIDFIPRFGVSHGIFNAIFLAVSAFCNAGFDNLGGDSLKPFVLNPLLNLLFMILIVSGGIGFAVWVDIKRAIKAFLADRPYRLKTFTRKL SNQTRLVLDTTAVILILGTAITWLLEANNPKTIGLYNPFQQFMVSLFQTVTMRTAGFATISYLDTHTATNILYMIQMIIGGAPGGTAGGVK VTTVAITFLLFKSELAGQSEVTYHHRIIANKVIKQTLTVLIFFFSILIVGYILLLQFEPYHDPIALLFEAVSAIATVGVSMDLTPQLSTSGRLVI MALMFIGRVGPLTVLLSLLQKKEKEIQYAQANITVG

1.5E-58	208	27	1.9E-58	207.6	18.7	1	1	U5SAC1_9LACT	Uncharacterized protein	Q783_08510	Carnobacterium sp. WN1359	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium sp. WN1359	1266845	>tr|U5SAC1|U5SAC1_9LACT Uncharacterized protein OS=Carnobacterium sp. WN1359 GN=Q783_08510 PE=4 SV=1MFLKRLRRLPPAAKIVISFATVIFIGSLLLTLPISNLESSETTYFDNLFTAVSMVCVTGLFTLPVATSFTVFGQIVCIVLMQIGGIGLM TILATFIMRIGRKMRFSDTIAVKEALNRDELGDFKTYLASIIKYTAIIEGTGMLLLALRFVPEFGFASGLFVSLFLAVSAFCNAGFDNLGAY SLQEYVQDPLINLVITTLIILGGIGFSVWFDVTHNIQSIIKNKCKSGWKRSYRMLKIHTRLAINMTLGLIVIGTLVFLVVEWNNPNSIGNFTF GEKVLASFFQYTVTMRTAGFATLDYELIKPFSLFFFIGTMFIGGSPGGAAGGIKTTTFALVALLVISEIKGQKHVNYSHHTIPIEIIRRAIVIV ATFSLFLIAGVSVLMLVEDQPFLYLLFEAVSALATVGVSVNLTPELSHISQVVLMILMFIGRIGPITILLSLSRKSKKTKDQLYAKTTILIG
1.5E-58	208	32.3	1.3E-57	204.9	22.4	1.9	1	N0AWY8_9BACI	Trk-type K+ transport system, membrane component	B1NLA3E_03720	Bacillus sp. 1NLA3E	442	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus sp. 1NLA3E	666686	>tr|N0AWY8|N0AWY8_9BACI Trk-type K+ transport system, membrane component OS=Bacillus sp. 1NLA3E GN=B1NLA3E_03720 PE=4 SV=1MIMKNWYKPISLNPPQMLAIIFFTLVFAGGLLLKLPMATEKGITWVDAFFTAASAATVTGLATIDPGSTFTLFGEIVIMFLMQLGGL GIMTFTVLVMIMLGKRIGIRQRLIMQEALNQPSVGGVVRLVRKILIFTFTVQIISVIILSLRWIPDLGIGKGVYYAIFHTIAAFNNAGFSLWP DNLSRYVHDPTVNIMITSLIVGGLGFTVIFDLVTVKNFKKISLHSKVMLISTLVVNLLAFLFILLAEFHNPNTLGKLDFPSKLWASYFQAIT TRTAGFNTIDIGSLEPGTALFMMFLMFVGAGSTSTGGGIKLTTFVIISAAVITFLKGKQETNILHRRIRDEAIIRSLAITTVSILFIFLVTIVLAI SEKGTFLQILFEVISAFGTVGLSMNFTSSLSILGKIIVILIMFFGKLGPLTLVYSFTKREKSKLSYPTGELYT
1.6E-58	208	17.2	2.3E-58	207.3	11.9	1.1	1	Q6NFG0_CORDI	Sodium transport protein	DIP1931	Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium diphtheriae, Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis)	257309	>tr|Q6NFG0|Q6NFG0_CORDI Sodium transport protein OS=Corynebacterium diphtheriae (strain ATCC 700971 / NCTC 13129 / Biotype gravis) GN=DIP1931 PE=4 SV=1MRKTPARLVAGCFAALVLLGTVLLLLPVSREGHAQADVVTALFTATSAVCLTGLTVVDTATYWSHFGQLVILALIQVGGLGIMTLT TFAGWVLVGRIGVKGRLNAAAEGRGRELGEVTGLLIATIGFTLVVESAVAVALTLRFHAMGFDWWASLWEGVFHAVSAFNNAGFGL RSNNLMPYVGDGWIILPISAAVIVGGLGFPMLLELHRRATFRRQGQAIRRMSLTSLFTIAGTIVLLAAGTVGIAVLEWRGVLAPFDGPTK MLAAFFHSVTSRTAGFNSIDMSQLHPTSLLLTDSLMFIGGGSGGTAGGIKITTVGVLLAVMVAEIRGDDQILIRGRRIPNRTVRQALAVT MLAVLTVGVAVGLVLVLAPEFGVLDLSFEVVSAFATVGLSTGITGSLPSAAQLVLVVLMYAGRIGPVSLVAALAARSSKRQYSYPVERLI IG
1.6E-58	208	22.2	5.8E-58	206	15.4	1.7	1	R6GX55_9FIRM	Trk system potassium uptake protein TrkH	BN704_00611	Firmicutes bacterium CAG:552	485	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:552	1263029	>tr|R6GX55|R6GX55_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:552 GN=BN704_00611 PE=4 SV=1MNYKAVFNIIGKVLLLVAALMVLPAATALIYAEYRAAVSYVSVAVLSAAIGFALSFLKPKDSIIYAKEGLVAVALAWIAVSVIGAIPFV VSGDIPNVVDALFESVSGFTTTGATVVVVTEDLTHASLLWRALAHFVGGMGVIVFVIAVVSRSPGRSMNILRAEMPGPIVDKFVPKAR DTAKILYMIYAGMTLVMTVMLLCGGMPLFDSIVHAISTAGTGGFGVKTSSIATYNDYSQWVIAVFMLLFGVNFNVYYLIIIKKFSQAVKS SELRCFLIIILVSTALIASNIYSQVGNLYTAIKNAFFQTTSYISTTGFAIADTSQWPTMSKTVLIVLMFIGGCAGSTAGGLKVSRLMIVFGKI GSELKKAVHPHKATIEKLEGKRLDEKTVTQTHSYFALYFVAFFAILLLVTFIEQFFTDFSFEANFAAVASCFNNVGPIFDNVVGYGTFAN YSGLSKVLLTLAMLLGRLEIYPLLLTLAPSTWAKR
1.6E-58	208	8.3	4.6E-58	206.3	5.8	1.6	1	W0K0N1_9EURY	Potassium transporter TrkH	HALDL1_13400	Halobacterium sp. DL1	522	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halobacterium, Halobacterium sp. DL1	751944	>tr|W0K0N1|W0K0N1_9EURY Potassium transporter TrkH OS=Halobacterium sp. DL1 GN=HALDL1_13400 PE=4 SV=1MKVRVDWRASLALVGTVVKWLSVPLVAPLVVALYYGDGGIAAFGATIVVAFTAGVALESLGDPEEMRAREGFLMVAVTWLAVS IVGAVPYLLAAHGVPGVLPATAPGSTLANPVNAVFESMSGFTTTGATVLGSISFETHSHSVLLWRQLTQWLGGMGIVVLAVAILPELS VGGAQLMDAEVPGPGIQKLTPHIAETARVLWLAYAGITALEIVLLYGLHVGGFAPNMGVYNAIAHGLTTMATGGFSPEARSIEAFSAAV QWLIVPFMVAAGTNFALFWHVIQGDTQELFEDAEFRFYVGVVGTLTALLAAILFTGPALGLGDAVAPVAGNAEDALRHAAFQAASIVT TTGYASMDFNQWSQPGKMVLFVALFLGGSAGSTGGAVKMVRWLVILKSLKRELFVTVHPDAVQPLRLAGQALDERGVRGIYAFTAV YFSLFVFGTVFVAIDAGRIQETVTGFEAMSAVAATLGNVGPGFGIVGPMNSYLPFPNSSKLLMVGLMWVGRLEILPVLVLFTGSYWQS
1.6E-58	208	29.4	5.6E-58	206.1	20.4	1.7	1	A0A0B4R914_9BACL	Potassium uptake protein	Plano_0475	Planococcus sp. PAMC 21323	442	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Planococcaceae, Planococcus, Planococcus sp. PAMC 21323	1526927	>tr|A0A0B4R914|A0A0B4R914_9BACL Potassium uptake protein OS=Planococcus sp. PAMC 21323 GN=Plano_0475 PE=4 SV=1MWSWKKKRLTVSPPLVISGSFLFLIVLGTFLLKLPFATTESISWTDALFTATSATTVTGLSVFDPGTVLTAFGELVLLVLIQCGGIG LMTFAVAILILFRKKVGLQNRIYLQESLTQSSIGGIVKLVKLILTFALTVEAVATVFLTIYWIPQFGFKDALNYSIFHVISAFNNAGFSLFPD NMIGFAGDPVVTLLISSLFIIGGIGFTVVMDVSQKKSIRRWSLHTKLMVGGTLILNCLAMLVIFLLEYNNPGTLGPMSIFDKLVTSYFSAV TPRTAGFNMLDYGQLEDPTLLFTMLLMFIGGGSASTASGIKLTTFIVVILATVSFLRSRREPEIFGRSIRLETVIRSLAITTISVLLVVLFLFL LTVSETIPFLPLAFEVVSAFGTVGLTMGITGDLSSIGEVLLSIVMFTGRIGPLTLFFILMKPRKENYRYPYDPVFTG
1.7E-58	208	37.9	2.3E-58	207.3	26.3	1.2	1	A0A024QDF4_9BACI	Ktr system potassium uptake protein B	ktrB_1 BN990_02612	Virgibacillus sp. Vm-5	454	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Virgibacillus, Virgibacillus sp. Vm-5	1462526	>tr|A0A024QDF4|A0A024QDF4_9BACI Ktr system potassium uptake protein B OS=Virgibacillus sp. Vm-5 GN=ktrB_1 PE=4 SV=1MQYQKSIIRWANRLSPVQILLLFYFFAVLLSTIIMSLPFVYQEGVEMPFIDILFTAVSALSVTGLSSISIADTLSTTGIILLAAILQLGAV GVMAIGTFIWLLLGKKIGLKERRLIMTDQNQTTFEGMVRLIKQIVYVLLTIEFLGFMILGTYFLQYFDTAKEAYLHGFFGTISAVSNGGFDI TGSSLIPFKDDYFVQFINMLLIIFGAIGFPVLIEVKEYIFAKSDNRKHVRFSLFTKVTTSTFLFLIIIGALFMYLLDVTHFFADKSWHEAFFYS LFQSVTTRSGGLSTMDVSQLTEENHLFMSLLMFIGASPSSAGGGIRTTTFLLVVIFIITYARGGKSIRLFNREVYDEDLLKAVTVTLMALI MVFTSIILISIAEPFSLTQILFEVTSAFGTVGLSLGITSELTSFSKVILMLLMFIGRVGIITFLFIFKNNKKSGNYHYPKEKLIIG
1.7E-58	208	10.2	1.6E-57	204.5	7.1	1.9	1	D1B9K7_THEAS	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Taci_0727	Thermanaerovibrio acidaminovorans (strain ATCC 49978 / DSM 6589 / Su883) (Selenomonas acidaminovorans)	429	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Thermanaerovibrio, Thermanaerovibrio acidaminovorans, Thermanaerovibrio acidaminovorans (strain ATCC 49978 / DSM 6589 / Su883) (Selenomonas acidaminovorans)	525903	>tr|D1B9K7|D1B9K7_THEAS Potassium uptake protein, TrkH family OS=Thermanaerovibrio acidaminovorans (strain ATCC 49978 / DSM 6589 / Su883) GN=Taci_0727 PE=4 SV=1MVYGFLLLIAAGALALWGIGELVGRPLDPIDALFTATSAVCVTGLSTVDVGTALPLPSQLVLLLLIQLGGLGVMAATTSFYLMLGA KVGFKERLAWAESMGLDTPRGAIRLLLLVIRVSLIAETVMAVPLFVGFARREGAVRGAYMAIFHSISAFCNAGFSPYSDSLVSFATEPL VMLPITVLIVVGGLGFPVLDDVLKSVRSRRWRPSSYTRVVLTFTPVLILLGSVVFLLGEINGVLRDMPWPHKLINALFMSVTPRTAGFN SVPLGRMSGVSLLFTSFLMWVGANPSSTGGGVKVTTFAVLWSSCTSEIRGRSDVCLARRHVDWRTQRKAITVAVLYTLAVFVAVFM LAVFEPEVDISSLVFEAISAMGTVGLSLGVTPHLSPDGKMVLIFLMYWGRVGIVTFLYSIFRRHEPGRVSLPNLDMPIG
1.8E-58	208	23.6	2.2E-58	207.4	16.3	1	1	A0A0D5NFX3_9BACL	ATP synthase subunit J	VN24_03690	Paenibacillus beijingensis	442	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus beijingensis	1126833	>tr|A0A0D5NFX3|A0A0D5NFX3_9BACL ATP synthase subunit J OS=Paenibacillus beijingensis GN=VN24_03690 PE=4 SV=1MRPMMKPHLLTPPRALAGGFALIIAIGTLLLSLPVAVNGNGLPFIDALFTAVSATCVTGLTVVDTASQFSYFGKIVLLALMQIGGLG FMTTATWFAIAFNRRISLRDQLILKESMNQSNMEGLVRLAGKVFLFSAVIELCGTIGFALRWAAEMPLGQAVWHGFFHAVSIFNNGGF ELFGGFTDYAEDPFINLVTIVLVIFGSLGFIVLSELIEYPKTRSLSLHSKVVLTASGILIGAGAIVLAVFEFTNARTLGTLDWEGKLLAPLFQ SVGLRSAGINTLPIAELRSATQFFMILMMFVGAAPGSTGGGIKITTFVVLLAALVAMTRGREDVVLFRRRIDRGDIYRAIAVTMLSVFVVI VATLILTAVQHENFLMLLFEAASAFGTVGYSMGLTPKLSLAGKIVVIVLMFTGRVGLITFALALQPKPRKELFRYPEGKITIG

1.8E-58	208	11.3	1.6E-53	191.3	6.4	3	3	D8S0R1_SELML	Sodium transporter	HKT2SELMODRAFT_447883	Selaginella moellendorffii (Spikemoss)	745	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8S0R1|D8S0R1_SELML Sodium transporter OS=Selaginella moellendorffii GN=HKT2 PE=4 SV=1MSQEDEAQCDSLKRSPPRPPPPPLAPLPENSSSATTTTTAHGYPIDQFLQQHEIVRSSATTPLRLLLSRLRWGIIRPPFPASAFSIDGDEEERIKRSSSKERGRSYVLLPRWISSRLTFYRLHLAYFVTIAWVASICLWLFPKSDRAGADKLAFIDCVYNAVSSVCTTGLISVRMTSFSLPDNILIMILFTLGSPIFTSVLPLYIRLFQFRKNIVEIEHHLGQPEVAAAAELESEGEPEAKSEIESVVSEMEAEVVPEVVGHRIITRRRSAKNIHAANAVTKLRDALATMRLEHDALVSLNWVVSIYFVVWTILGFLVLEILLQCSAKDMAVLEQRSVNHLFFSLFASISTFTNSGILPLDDSIAAFRENNGILLWLSILILVGNTLFAPCLRTTIWCLKSLSATPARRAIYDYLLKNPRRCFTHLFPRNQTIWLVVTVMGFNAFESAFFYILSWRSQALDGLTTPQKLVNGIFQSITTRSAGENVVSISALSPSMLVLYIAMMIAVYPVYLSRQNSQAQDESVEKTSKKIQDHGKKKKKKKKGDFSIASQSKRLIATDTAYLFISIFVLCIIENRKINDDPLNFSIFNIIFEVISAYGNVGLSLGYSCSLLRKLTSFSSDTSCEDVPYSFSGTWSVPGKLLMIVIMFLGRHRGLPDNMDSALQIPKSFFTTTKRDQNYQHHHENGISLDHQPVEIHPEYVVEIPAAVDFSVVEIDGDQARQQCSCGPDHPDRLELQKLDRFPVV
1.9E-58	208	30.9	3.6E-57	203.4	21.4	2	1	A0A077J632_9BACI	Ktr system potassium transporter B	HW35_07540	Bacillus sp. X1(2014)	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus sp. X1(2014)	1565991	>tr|A0A077J632|A0A077J632_9BACI Ktr system potassium transporter B OS=Bacillus sp. X1(2014) GN=HW35_07540 PE=4 SV=1MEVSRQWVKINPAQTLSLGFFFLIILGTLLLMLPFATKDRHHLSFIDALFEATSAVCVTGLVVVDTQSTFTLFGQIVLMVLIQIGGLGFMTVAILIALFLGKNIGLKGRLMIQESLNQLSLEGMVRLVKFVVFFTLLIEGLGAVILAIRWSSDFGFPQSIFYGIFHSISAFNNAGFDIMGGFKSITGYVGDVTVILTLSSLLIIGGIGYTVIVDLLKKKSLRKLSLHSKLVLLVTLILNVLATILIFVLEYNNPGTLGNLSFKDKLLGAFFHGVVPRTAGFNSLNMPDLTLSTQFVTMFLMFIGGGSGGTAGGIKVTTFVILILAVWTLIRGRDEVNILGKRLPNDIIFRAFSITVYSTAIVSLVIFILTITEEAPLNMILFEVISAFATVGMSLGLTTELSPVGKILISLMMFIGRVGPLTIAFALARANKKLPYKYAEEKIMIG
2E-58	208	15.7	1.2E-33	125.8	2.5	2.1	2	A0A077FER5_9PSED	Trk system potassium uptake protein	PSAKL28_38500	Pseudomonas alkylphenolia	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas alkylphenolia	237609	>tr|A0A077FER5|A0A077FER5_9PSED Trk system potassium uptake protein OS=Pseudomonas alkylphenolia GN=PSAKL28_38500 PE=3 SV=1MALPTLRIIGFIIGIFLITLAISMVVPMATLVIFDRTGDLPSFLWASMITFVAGLALVIQGRPEHVHLRPRDMYLLTVSSWLVVCIFAALPFLLTQHISYTDAFFESMSGITATGATVLSGLDNMSPGILMWRSLLHWLGGIGFIAMAVAILPLLRIGGMRLFQTESSDRSEKVMPRSHMVAKSIVAVYVGFTALGGVAFWLAGMNVFDAINHAMSAISTGGFSTSDQSLAKWDQPAVHWVAVVVMILGSMPFALYVATLRGNRKALIKDQQVQGLLAMLLATWLVLGTWYWATTDLHWLDALRHVALNVTSVVVTTTGFALGDYSLWGNFSLMLFFYLGFVGGCSGSTAGGIKIFRFQVAYILLKANLNQLIHPRAVIKQKYNGHRLDEEIVRSILTFSFFFAITICIIALLLSLLGVDWMTALTGAASTVSGVGPGLGETIGPAGNFATLPDAAKWILAAGMLLGRLEIITVLVLCMPAFWRH
2E-58	208	22.7	1.6E-57	204.5	15.7	1.9	1	K4RJU0_HELHE	Potassium uptake protein, integral membrane component, KtrB	BN341_900	Helicobacter heilmannii ASB1.4	441	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter, Helicobacter heilmannii, Helicobacter heilmannii ASB1.4	1216962	>tr|K4RJU0|K4RJU0_HELHE Potassium uptake protein, integral membrane component, KtrB OS=Helicobacter heilmannii ASB1.4 GN=BN341_900 PE=4 SV=1MRKVFGMIVGSYALLALVGALVLDLGPMHTKPIAFLDLFFTATSAVCLTGLITANPATDFTHYGQAVLLGLIQAGGFGYMGLAGLLFLLLGKKMDFQGRLMLKESLDYPSMQGVLLYLKQILLFTLAIEGVGVLLLSACFAMRLPFKQALWAGLFHSISAFNNAGFSIFASNLMDYQQNAPINFVVCALIILGGLGFLVLSECANYRKNTRLSVHTRIVLWATLGCLVLGVAVVLLFEWDNPKSIGSLSTWAKVMAAFFLSVNLRTAGFNTIDMTNLHDESLFFSSLLMVIGAAPGSTAGGIKITTLTILLAYAYHALKGQEVVLFKRTIPQSTVKKSFLIFIVALFYIVISAMLLSATEDHQNKFFLHLFFEICSAFGTVGVSTGNGGDLSLVAKFSSFGKLYLMLLMFMGRVGVLVFSLALVGKSKTRHVHYPEEEVVL
2.1E-58	208	26.1	1.9E-56	201	18.1	2	1	R5QX55_9FIRM	Potassium uptake protein TrkH family	BN747_02093	Firmicutes bacterium CAG:646	456	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	1262995	>tr|R5QX55|R5QX55_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:646 GN=BN747_02093 PE=4 SV=1MKDAIKGYKKMQATGKKRHRHITSFQVIIFGFFSVILLGSFLLMLPWATQDGQGASFGDALFTATSAVCVTGLVLHDTATYWTVFGQAIILFLIQIGGMGVVTVAVAIVSASGRKIGLMQRSTMQESISAHQVGGIVRLTKFILKTGIVIEMTGAILLAFVFCKDFGVGKGIWYAIFHSISAFCNAGFDLIGIREPFSSLTTYVAQPIVNVTIMALIVTGGIGFVTWADIKKNKWHLKKYRMQSKVILSVTAGLILIPAVYFFFCEFSSLPLGERIWSSLFQSVTPRTAGFNTADLTLLTETGLMIMILLMLIGGSPGSTAGGMKTTTIAVLVSSALAVFKKKESAHFYGRRIPDETVKHAVTILLMYLILFLGGGMVISSLEDIPLLSALFETSSAIGTVGLSLGITPTLGRVSQAILIGLMFFGRVGGLTLIFAALSERKITNARLPQEKITVG
2.2E-58	207	4.6	1.4E-55	198.1	0.5	2.9	2	B6HPU2_PENCW	Pc22g06520 protein	Pc22g06520 PCH_Pc22g06520	Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)	642	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium chrysogenum complex, Penicillium rubens, Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)	500485	>tr|B6HPU2|B6HPU2_PENCW Pc22g06520 protein OS=Penicillium chrysogenum (strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) GN=Pc22g06520 PE=4 SV=1MKGEFKFFTEKNKQKYFWLLQGPYNPIILYMVWGIPALNSDNAYDSHISMPIMADLLAFSPLTLHYAYFILTPAIGSAIFYTASSHIHDLHYSDALFMCFSAMTGAGLSVMDLSTLNSLQQGTLFCLLILGHAFPIIAIISLFRAWKLRSALRDNSNGEKQNQVACNKQGALSAKDTCNAKATTVVREVQPDVSSPCEPEGSSGDYGFIVVTDLKHPEQSQQVTSLIVDKEKVLGNRKAHISWLKGIVQRASKHLSCKKPTNYRELDEVEYRALALTAVLIILYFIGFLILGIVSIGLWSKFVRPDIPREDGASPFWAGAFLATSALCNNGMSLIDTNMGAYQKEPFPLLACGVLILAGNTLFPCLLRFLIWALRQMLPNKPTWQEWRRSFDFTLTQSQKACAYLYPAWHTWFILGTVVVLNAIMWGAFEVSAINNEEIGSLPVKFRVLDGLFQALAVRGGGFTVVAFDRLPQGLLILYGTSTKITNTQFTAPPQKESHRSSLSGLPHARFVYQQLRSQFSHDIWWLSLAILLITITESDHFEADPLAFSTFRIIFEAVSAYSYVGVSFGCPGQTYSFCGAWHTFSKVLLIAVALRGRHRGLSAIFGNADLFPQSRGGTGEENMELEKNGHVNTKEMSVGCV
2.2E-58	207	37.9	2.4E-57	203.9	26.3	1.9	1	C2W5H0_BACCE	Potassium/sodium uptake protein	bcere0022_10370	Bacillus cereus Rock3-44	442	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock3-44	526986	>tr|C2W5H0|C2W5H0_BACCE Potassium/sodium uptake protein OS=Bacillus cereus Rock3-44 GN=bcere0022_10370 PE=4 SV=1MYAMKRINIKMSPPHVLTLSFIALSIIGTCLLKLPISTTTSISWLDALFTTVSAFTVTGLGVVDTGKVFTMFGQLVILTLIQVGGLGIMSFAILIAIMLGRKIGLQNRILLQQALNQTNIGGVIRLAKSLFLFSFTIECFATLLLAFEWIPKYGVARGLYYSFFHAISAFNNAGFSIWTDNLMSQSHSILVNIVISSLIILGGIGFTVIVDIKRKRNFKNLTLHSKLMLSSTLIVNIAATILIFIFEFHNPNSMKGFTPFEEGLAAYFQAVSTRTAGFNTIDMAQLTKPSLLLMMLLMFIGAGSASTGGGIKLTTFLIMLLGVLKFLQEQDDIVIFKKSIKDGLIVKSLAIVVISISFIFFAILILSITEHVPLLMSAFEVFSAFGTVGLSMGLTPKLTIIGKLTIIFMMFFGKMGPLTLAFSFARKKQRKIKYPNEDILTG
2.2E-58	207	28.7	7.7E-58	205.6	19.9	1.6	1	R6LMY6_9FIRM	Potassium uptake protein TrkH family	BN524_01741	Coprococcus comes CAG:19	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus comes CAG:19	1263070	>tr|R6LMY6|R6LMY6_9FIRM Potassium uptake protein TrkH family OS=Coprococcus comes CAG:19 GN=BN524_01741 PE=4 SV=1MTVIYKKMTQTQMIVVGYLLLILLGSILLMLPVSSRDGNMTSFADALFTSTSASCVTGLVVQDTYLHWSFFGQLIILILIQIGGMGFMTIGVCVAILLRRKIGLKVRGILQESINSIQIGGIVKLTKKIIKGTLFFESIGAVLLMIRFIPEFGIGRGIWYGIFHSISAFCNAGFDLMGENGAYQSLIRYSDDWLVNTVIMLLIIIGGIGFLVWDDLSVKKFQWKKYHLHTKIVLSTTGFLIIGGAVLFLILEKNNVLAGMPVKEQILCSLFHSVTARTAGFNTTDTGALTEGSKLVTMILMFIGGSPGSTAGGIKTTTVVVLIVFVRANLMEAAGCNVFNRRLDETAIRKASVVMCTNLFLILTGTIFMEIMQPFSLSDVMFEVFSAMGTVGMSAGITRDVCMASRMVLVFLMFCGRIGSLTFALSLKGHRHGAPIRKPVEEITIG

2.4E-58	207	28.3	3.1E-57	203.6	19.6	1.9	1	R5WSS9_9FIRM	Potassium uptake protein TrkH family	BN568_00628	Blautia sp. CAG:257	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	1262756	>tr|R5WSS9|R5WSS9_9FIRM Potassium uptake protein TrkH family OS=Blautia sp. CAG:257 GN=BN568_00628 PE=4 SV=1MNYTGNRKHRHFTSFQVIILGFFSVILLGSLLLMLPLSTRDGNGASFADSLFTATSAVCVTGLIIHDTATYWSEFGQAIILTLIQIGG MGVVTIAVAIAVASGRKIGLMQRSTMQEAISAHQVGGIVRLTKFILKTSIFIELIGAALLMPVFCKDFGILKGLWYSLFHAVSAFCNAGFD LLGVREPFSSLTSYASNPLVNFTIMALIVTGGVGFVTWADIKKNKLQFKKYNMQSKVILTVTAVLIAVPAVYFFFCEFSGLPLGERIWTS LFQSVTPRTAGFNTADLTLLTETGLMLMIILMLIGGSPGSTAGGMKTTTIAVLFSSALSVFRKNDSAHFFRRRVPDSVIKNAATILLMYLV LFLGGGMIISYIDKVPLISALFETSSAIGTVGLSLGLTPTLGMVSRLILILLMFFGRVGGLTLIFAALSERNSYGSRYPQEKITVG
2.5E-58	207	21.3	6.7E-58	205.8	14.8	1.6	1	Q7MSZ1_PORGI	Potassium uptake protein TrkH	trkH PG_2219	Porphyromonas gingivalis (strain ATCC BAA-308 / W83)	487	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, Porphyromonas gingivalis, Porphyromonas gingivalis (strain ATCC BAA-308 / W83)	242619	>tr|Q7MSZ1|Q7MSZ1_PORGI Potassium uptake protein TrkH OS=Porphyromonas gingivalis (strain ATCC BAA-308 / W83) GN=trkH PE=4 SV=1MLQHINFKFVLKVVGSLCLSEILFLLICLGISVYYKGSDLLPFVYTIGVMAAVGSCFYLLGRRARMNNASRREGMLTVTLTWLILSL VGMLPFVFGGYTPSVTDAFFETMSGFTTTGATIFPEVESLPRGILFWRSIMQWQGGIGIVVFTVGLLPMLGAGSAVSQIYNAETTGIIH DRFLPRIRQVARRLCGVYILGTAVLILLLWLGPMGLFDAICHAFTCISTGGYSTRNGSIAEFQSSYIEYVTSFFMFYGSLSITLQYFLLVG KPGKLIRDEEMRTFVVLTLCAVLITTLWLLYRGEYPSLEENFRHALFQTYSIISTTGYTTADYFSWGPFFWSIAIVMMIVCGCAGSTTG GIKISRLVVLMKNLRNEFKKRTHPNLMVPVRINGIIITGQLVSQVLAFAFLYFLLIFCSIILLTLDGMDFVAAVGSAVSAMGNVGPGFGDY FGNFSQAGDFSKWILSFLMLTGRLEVFTVISILHPAFWRR
2.6E-58	207	12.9	4.8E-28	107.3	2.3	2	2	B9LN41_HALLT	Cation transporter	Hlac_1185	Halorubrum lacusprofundi (strain ATCC 49239 / DSM 5036 / JCM 8891 / ACAM 34)	502	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Haloferacales, Haloferacaceae, Halorubrum, Halorubrum lacusprofundi, Halorubrum lacusprofundi (strain ATCC 49239 / DSM 5036 / JCM 8891 / ACAM 34)	416348	>tr|B9LN41|B9LN41_HALLT Cation transporter OS=Halorubrum lacusprofundi (strain ATCC 49239 / DSM 5036 / JCM 8891 / ACAM 34) GN=Hlac_1185 PE=4 SV=1MPTNTRIRVGWQASVGLTGDVLAALPVPLAFPLLIAIYYGESPLPFLAAIAVSLALGAAFRRVQDPSVDLGPREAFLAVALIWFLV AAIGAIPFVVAGVGTVAHPVNAMFESMSGLTTTGATVLEEFSIHSRSVMMWRQVIQWLGGLGILILATAVLSEVGVGGAQLMETESQT QDVNKLTPKISQTAQLIWGIYFGLTGLAVVVYFLLGLAFDPQMDLYNAVAHAFTSVATAGFSPEPLSVGAFHPIIQWAVVPFMVIGSTS FVLIYFAINGEPMRLLRNEEFHFYLGVMGTLATIVAVGLFLDPGTNFGAEGTIRHAVFNVTSIVTTTGYASTDYVLWAPAAKHMLFMGM FIGGMVGSTTCSIKSLRWLVALKSFRRNLYTAIHPEAVRPVRISGKSIDEGAIRDIYAYLLLSLIIFFLLAVFIVVDAERANLRVDEFEALGA AATTFLNIGPAFGDAGPYGTFASFPMSTRAVMIVLMWIGRIEIIPVLVLFTKAFWTS
2.6E-58	207	23.9	4.9E-58	206.2	16.6	1.3	1	B8FDP8_DESAA	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Dalk_5008	Desulfatibacillum alkenivorans (strain AK-01)	459	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfatibacillum, Desulfatibacillum alkenivorans, Desulfatibacillum alkenivorans (strain AK-01)	439235	>tr|B8FDP8|B8FDP8_DESAA Potassium uptake protein, TrkH family OS=Desulfatibacillum alkenivorans (strain AK-01) GN=Dalk_5008 PE=4 SV=1MQSNPEKSVHPFRPNANQLAVMGFMGLIVLGALLLMLPISSRGESLNLLDALFTATSAVCVTGLTVVDTGTHFTGFGQAVILILIQ AGGLGIMILTSSILFMLGKRLSLTLSDGVSGAFLPARHISMGGMIKITLAWTFLFELTAAVILFARWAVDFSPGKALWLAIFHSVSAFCNA GFSLFPDSLSGYVGDPLINGVIMALIICGGIGFFVMIDFWVCARSRFRPGRRLSFHSRIVLTATLFLIFFGALALWAIEHNHNLQGLSLHQ SIMRSLFQSVTARTAGFNTMEIPELANASLFLLIMLMFIGGAPGSTAGGIKVTAASVLVIAVRSRLQGMQKASWAGRSLSRADLERALV LILLSGALVGLITMLLLITELGGAAHTHSRGLFLELLFESVSAFGTVGLTTGVTPGLTPTGRLLVIFAMFIGRLGPFTLVYAMESRREPVR MQFPEEKIMIG
2.7E-58	207	32.1	8.7E-57	202.1	22.3	2	1	R5KPP9_9FIRM	Potassium uptake protein KtrB	BN508_01656	Eubacterium sp. CAG:161	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:161	1262881	>tr|R5KPP9|R5KPP9_9FIRM Potassium uptake protein KtrB OS=Eubacterium sp. CAG:161 GN=BN508_01656 PE=4 SV=1MEKRRIHLSTAQFILLGFVGMIIIGSLFLMLPCSTRSGEGASFLDSLFTATSAVCVTGLVVQDTATYWSDFGQAVILFLIQIGGMGI VTIAVAFAAMSGRKIGLMQRTVMQEAISAPKLEGIVRLTRFIIKMAFVIELTGAVLMYPVFAVKMGALKGIWYSIFHSISAFCNGGFDLM GINEKYSSFTSFSGNIVINLVIVLLILLGGIGFMTWDDIRTHKFKFSKYRMQSKVILSATIGLIVIPFVYFYFCEFSGAKWHMSGADRALAS LFQTVTPRTAGFNTVDLTKISGAGQLIMIVLMMVGGATGSTAGGMKITTIAVLLASSISVFRRKSSPHLFRRRIAEEVIKSAAAILLLYSFL FLMGGIIICAVDGFNIIDTLFESASAVCTVGVTLGITPHTGVISRIVLIVLMLFGRVGGLTVIFATVSSKRKDVAKFPEEKIMVG
2.7E-58	207	27.2	2.3E-56	200.7	18.8	2.1	1	X5DFW9_9BACT	Potassium transporter	FH5T_11200	Draconibacterium orientale	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prolixibacteraceae, Draconibacterium, Draconibacterium orientale	1168034	>tr|X5DFW9|X5DFW9_9BACT Potassium transporter OS=Draconibacterium orientale GN=FH5T_11200 PE=4 SV=1MNIALILHIISIVITFESLFMLFALIVSFIYKESVFADLSHTFLITFVLGVVLNLLTKKQRQVEPSLRESFIIVTLAWVVMALDGTLPYLL TGSIPNFTNAFFESISGFTTTGSSILADIEALPKSILFWRAETHWIGGMGIIVLVVAIMPFLKINGIYLFYSEVSSVASEKVSTRIRQVARRL WLIYMGLTVAETIILWFGGMSLFDAVCHSFATIATGGFSTKNDSLAGFSPFIQYTVTFFMLLSGINFVVHVFWLRGDFKTAFKNEELRL YLKIILVAGTIITLSLFFHHQDMGFEPAFRHAFFQVISIITATGFATADYLQWPLQSIGIIAILMLIGASSGSTGGGVKVIRHLVVFKHIRTLY KEYFSSSAVVRVVHYNKNIVRPELINRVFTFVLFYYLILIISTMIMMLWTNDLKTSFGAVATSMAGIGPGFGTVGPVSNFLHLPDGAKYF LTALMVIGRLEIYSVLVLFTPSFWLD
2.8E-58	207	11.2	2.5E-56	200.6	7.8	2.1	1	X4Z4P6_9BORD	Trk system potassium uptake protein	D560_1157	Bordetella holmesii ATCC 51541	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella holmesii, Bordetella holmesii ATCC 51541	1247649	>tr|X4Z4P6|X4Z4P6_9BORD Trk system potassium uptake protein OS=Bordetella holmesii ATCC 51541 GN=D560_1157 PE=3 SV=1MKRLLATFYVLGLTMVVFALTMLIPLGVAWLGEDAGLRAFVEGFGLAMGIGTGVCLAAHRWRSELHARDGFLLVSIVWVGLPLL AAIPLLLYYSQIGQPLSFTHAYFEAMSGLTTTGATVLTDLNHLPPSINLWRATLIWIGGMGILVLAVAILPLLGVGGHQVVRAETPGPMK DERLTPRIASTAKALYAVYFGFSILCFLAYRAVGLSWFDAWAHMATTMGLGGFSTYDEGFLKFDSIPVELVAIVFMLISGINFATHFNAL RQRGFRPYLTCPQTIPYLAVVLGAGLVISVYLFFKHVYTDPLQALRYGMFNTISVATTTGYANADYGAWPLFAPLTMLLLSAFATSAGS TGGGIKMIRVILLIKQARNELVTMLHPHAVSPVRIGSRIVDQRVMFSVLAFMLVYGQSVGVLSSLLLLSGLDLTTAFSAIMAMINNTGPG LGVLGPMGHYAVLSDFQIWICTFAMLIGRLELLTVLVLFTPWFWRK
2.8E-58	207	15.6	3.5E-58	206.7	10.8	1.1	1	X5DNV0_9CORY	Trk system potassium uptake protein TrkH	trkH CGLY_11990	Corynebacterium glyciniphilum AJ 3170	467	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium glyciniphilum, Corynebacterium glyciniphilum AJ 3170	1404245	>tr|X5DNV0|X5DNV0_9CORY Trk system potassium uptake protein TrkH OS=Corynebacterium glyciniphilum AJ 3170 GN=trkH PE=4 SV=1MPVELSRPHRYPRHLRMPQITLSPAQAVALGFLALIVIGTLVLSMPAASASGVGTDLLSSLFTVTSAVTMTGLVVLDTGSHWSGL GQVIVLVLIQVGGFGIMSVTSLAGMLLTGRIGLRSRLYTRAENRSLDTGDIGRTVLATLLITVICEAIVAVITTVRFATTYGMSLPQASWE GMFHAVSAFNNAGFGLRSDSLVPYVGDGWIILPLACALIIGGLGYPVVSELWDRARLSMQRRGHRGARKLSVTTRITVTGTVILIVAGV AMVGVLEWNNTLAALPAGTRVLAAFFQGVSPRTAGFNSLDYGEFHPVTLMGTDLLMFIGGGSAGTAGGIKITTAAVLLAAIIAEVRGH HATTIGHRTISQPVVRQALTVAVLSVVLVVVAVGTLRLLDPVFTGDQITFEVISAFATVGLSTGITADLSSPCQLVLCALMYLGRIGPVTL VVALAAKHSARRFHYPEERPFIG
2.8E-58	207	3.7	4E-58	206.5	2.5	1.1	1	G2MIV3_9ARCH	Cation transporter	Halar_1289	halophilic archaeon DL31	535	cellular organisms, Archaea, unclassified Archaea, unclassified Archaea (miscellaneous), halophilic archaeon DL31	756883	>tr|G2MIV3|G2MIV3_9ARCH Cation transporter OS=halophilic archaeon DL31 GN=Halar_1289 PE=4 SV=1MSLRVDCRASLSLVGTVLKYLAVPLSLPTLVAIAYGESTIPFLTTIALTVAVGYSLERLRPNPDIGAREGFLMVSSTWLAVALVGM VPYLVAAHGIPFLLEPIYAASTLANPVNALFETMSGFTTTGATVLGSISVEDHTYSIMLWRQLTQWLGGMGIVVLAVAILPELSVGGAQL MDAEAPGPGIEKLTPKIAETARVLWGAYLGITLAEIALLYGVHLLGMAPSMDAFNAVAHGLTTMPTGGFSPQARSIEAFSAAAQWVIIP FMAIAGTNFALVWHALSGSPERLWKDTEFRAYMGAVGVLTAILTGLLFTGGMTNPATIPPGSTFDAAYVQEYAAVLTGNVEPALRHAL FQALTVITTTGYASMDFDAWSEAARYVLLFGMFIGGSAGSTGGAVKIIRWIVIAKAARRELFTTAHPEAVRPVRLNGNALDDRAIRGIVT FTLLYLIIFFVGSLLLFLDAVRAGVDLTVLEVMAASASTLGNVGPAFYRLGPMGNYLPFSDASKLFMLLLMWAGRLEILPLLVCLTPEYW RR

2.9E-58	207	30.8	1.7E-57	204.4	21.4	1.8	1	A6TTC1_ALKMQ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Amet_3310	Alkaliphilus metalliredigens (strain QYMF)	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus metalliredigens, Alkaliphilus metalliredigens (strain QYMF)	293826	>tr|A6TTC1|A6TTC1_ALKMQ Potassium uptake protein, TrkH family OS=Alkaliphilus metalliredigens (strain QYMF) GN=Amet_3310 PE=4 SV=1MQSKIKPRFDLTYAKLSAIGFLIIILVGAILLSLPIASRSGDGTPFLNALFTATSATGVTGLVVYDTYSHFSIFGQSVILVLIQIGGLGFMIIATMFLLLLRKKIGIRERSFLQESVNTIHIGGVVRLVKHILVGTLIFEAIGAIILAIKFSREMGIKPGIFNGIFHSVSAFNNAGFDLMGRYEAYSSLTRYSGDAVINITIMTLVVVGGIGFIVWEDIYKNKYKFKKYQLHSKIVLFTTALLIFGSAIAFYVFERNNLLVDTGVKESVLSSLFQAITPRTAGFNTIDTAALSEGSKLLTMMLMIIGGSSGSTAGGIKTTTFFIITILSVISLVRHSEDLNIFGRRLEDSVLKRAYSIITMYIIGACVGMLLISLIQPGLALSDITFEVLSATGTVGLSTGITRDLNVLSRLIITVLMFCGRIGSLAVLMAVVESKNSVLVKNPLEKIVIG
2.9E-58	207	20.8	1.9E-55	197.7	14.4	2.1	1	R5J1A1_9FIRM	Trk system potassium uptake protein TrkH	BN738_00258	Peptostreptococcus anaerobius CAG:621	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptostreptococcus, environmental samples, Peptostreptococcus anaerobius CAG:621	1263100	>tr|R5J1A1|R5J1A1_9FIRM Trk system potassium uptake protein TrkH OS=Peptostreptococcus anaerobius CAG:621 GN=BN738_00258 PE=4 SV=1MNYEMMLFVIMNIARVEGALMLLPALVALIYGENTVAGKILIIAVLCICLGSVFSRKRPKRSDIFVKDGLMIVGLAWVMFSLLGALPFYFTGAIPRFVDAFFETVSGFTTTGSTILTDIESLPYGIHFWRAFTHWVGGMGVLVFVMAVIPLAGSKSLNIMKAEVPGPTMDKIVPKTRQTAKILYLIYVVMTVAEVVLLVLGGMPLFDALIHTFSTAGTGGFSNKADSVSFYDSAYIDGVITVFMALFGVNFNLFYLLLLGKFARVFKSEELRTYIGIIAVATLLITINIYPMYGSFLTSFRYSSFQVTTIITTTGMMTTDFNLWPSFSKGILLMLMFVGACAGSTGGGLKVSRVLLLGKYIKSEIRKIVHPRSIVSVKVDGKVMDDTVIRSVVTAYIMIYMSILVVSYLMISLNELDLETTLTSVITCINNVGPGFGEIIGPTQNFSTLSDFSKLVLILDMLIGRLEIYPILFIFSPRMFKRRF
3E-58	207	23.4	1.3E-56	201.5	16.2	2.1	1	R5LRS1_9FIRM	Trk system potassium uptake protein TrkH	BN569_01649	Butyrivibrio crossotus CAG:259	488	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, environmental samples, Butyrivibrio crossotus CAG:259	1263062	>tr|R5LRS1|R5LRS1_9FIRM Trk system potassium uptake protein TrkH OS=Butyrivibrio crossotus CAG:259 GN=BN569_01649 PE=4 SV=1MNSSIIRYILGSVLKLEGALMALPCLVSVIYKEEEGLSYLAVALGCLAFGFLLTFKKPKDTVFYLKEGCVSTALSWIMLSIFGCIPFVLTKEIPSFTNALFETISGFTTTGATILDDVESLSHTSMFWRSFTHWIGGMGVLVFLLAVVPLSGGSNVNLMRAESPGPSFGKLVPKLKTTARLLYLIYFGLTIIQIILLICGRMPVFDAITTSFGTAGTGGFGIKNNSISGYSLYIKWVVTIFMILFGVNFNAYYLILYKKFKSAFAMEEVKAYLIIIIVSVVCIFFNILKMSTSAVNAITDSAFQVASIITTTGFSTTDFNLWPEASKTILVILMFIGACAGSTGGGIKVSRLVILIKSLGKETDSYIHPKIIKKIKMDGKPVEHEVVRSVNVYFLTFMIIFTVSVLLVSLENKDFTTNFTAVAATINNVGPGLSKVGPICNFGGFSALSKYVMMFDMLAGRLELFPLLILFHPAIIREIFSGKRKSKA
3E-58	207	25.8	4.9E-58	206.2	17.9	1.2	1	F4LN64_TREBD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Trebr_1405	Treponema brennaborense (strain DSM 12168 / CIP 105900 / DD5/3)	445	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema brennaborense, Treponema brennaborense (strain DSM 12168 / CIP 105900 / DD5/3)	906968	>tr|F4LN64|F4LN64_TREBD H(+)-transporting two-sector ATPase OS=Treponema brennaborense (strain DSM 12168 / CIP 105900 / DD5/3) GN=Trebr_1405 PE=4 SV=1MRIKWSFDKILLFSYFGLLAGTGTVLLLLPFSVTQPLSVPDALFTSVSAVCVTGLCTVPMSTFTVFGKVVILFLIQFGGLGIITFFSLYIGIGSRRRVSFMNRKMIRSFFIDEVESDHKKIVRNIVSITLGIELAGAVCLYGAFSAAGVPNPAFTAVFHAVSSFCNAGFSTFNDSLAGFADNPAVLVPIAVLIFLGGIGFIVMKDVFRFVKTFGRERVSYHAKLALGMTAFLIVGGTVLFLILEWNQGFAQYGAGGKILSAFFQSVTTRTAGFESVAQAQFSPVSGFVTLLLMFIGGSPGSIAGGVKTTTFLIVMAYALNERDDSTSMLLGRKSISAGILEKAFNIISKSIIFLCIAVFLLMCTEERLLLAGTASVFDVLFESFSAFGTVGLTRGLTPHLSDLGKIVIIATMFIGRTGVFAMILKIPGKKEERLIRYPDEQVMLG
3.1E-58	207	22.1	8.8E-58	205.4	15.3	1.7	1	F0R935_BACSH	Cation transporter	Bacsa_3635	Bacteroides salanitronis (strain DSM 18170 / JCM 13567 / BL78)	501	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides salanitronis, Bacteroides salanitronis (strain DSM 18170 / JCM 13567 / BL78)	667015	>tr|F0R935|F0R935_BACSH Cation transporter OS=Bacteroides salanitronis (strain DSM 18170 / JCM 13567 / BL78) GN=Bacsa_3635 PE=4 SV=1MEETIAKNVYVGGSRKNSLINQKMICRILGFLLFIEGVMLLVGSAVSLYYHESDYIYFIYSTLITVGAGSLLVFLGRKAENKLSRRDGYCIVAFTWILFSVFGMLPFYISGAIPSIPDAFFEIVSGFTTTGATILDNIESLSHGILFWRCFSHWIGGLGIVFFTIAVLPIFGVGNQVLFSAEATGVTHDKIHPKVSIMAKWLWTVYLILTVSETLLLVWGGMGWFDAICHSFSTTATGGFSTKQSSVAYWNSPFIEYVIAIFMMLSSLNFSLYFMCLKGKFRHLLKDDEVKGFLISVFTVTLFITVALIINNHYDVEKAFRKALFQVVTVHSSSTGFTTDDYNFWPPFTWMLIMYATIVGGCTGSTSGGIKVMRLLILLRNAKNELARLIHPRAVFPVKINRQTVDPLTISAVTTFTLLFLICGFVGWVLLMMMGVELTDAFGVVYSSMGNAGVALGHYGPAFSWSGLPDGAKWILSFLMLLGRLELYAILLMFVPSFWHNR
3.1E-58	207	15.9	4.1E-58	206.5	11	1	1	Q7NN96_GLOVI	Glr0515 protein	glr0515	Gloeobacter violaceus (strain PCC 7421)	453	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter violaceus, Gloeobacter violaceus (strain PCC 7421)	251221	>tr|Q7NN96|Q7NN96_GLOVI Glr0515 protein OS=Gloeobacter violaceus (strain PCC 7421) GN=glr0515 PE=4 SV=1MPTLSPARTICLGFLLVIAIGTSLLLLPWSTASGEWTPWLVALFTSTSAVCVTGLAVVDTGSYYSFFGQLVILLLIQVGGLGYMSATTFLLLLVGRRISLRNRLALQEALGSLGDKAVPRLVARVAILTLGFELVGALVIAPTMVRQEGLLPGLWSAIFHSVSAFNNAGFGLRSDNLIPWQNNFWVLGGLGFLILAGGLGYQVWIELYEKILLRLVRQIFGKQPAPPAPLSLHTRVVLLTSAILVVVGSVGFFLIERTNALTLGRLSLDAQVAGAIFHSISARTAGFNAVPFDGLLEAGLFWIILLMLIGASPASTGGGLKTTTFAILVSNMLAVIQGREDVLLFDRRLGVGAVRKASAVLLGSIAAIAVALVGLTLSDPEPGFVQVLFEAVSAFCTVGLSTGITPKLSVVGQLILVFSMYLGRVGVLLLAEALLSQKPTFPYRQPEEQILIG
3.2E-58	207	23.9	7.6E-58	205.6	16.6	1.5	1	F8F2F5_TRECH	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Spica_2844	Treponema caldarium (strain ATCC 51460 / DSM 7334 / H1) (Spirochaeta caldaria)	444	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema caldarium, Treponema caldarium (strain ATCC 51460 / DSM 7334 / H1) (Spirochaeta caldaria)	744872	>tr|F8F2F5|F8F2F5_TRECH H(+)-transporting two-sector ATPase OS=Treponema caldarium (strain ATCC 51460 / DSM 7334 / H1) GN=Spica_2844 PE=4 SV=1MRPRFRSDSWYLVALFITLISVGSILLVLPLSQAGYPGNATHISYIDALFMATSAVCVTGLTTVDMATFSLFGQTVLLLLIQLGGLGIISFTSLLLILPGGRIPFRRISTIRSFYVDGVEYDPKKIISTIVVTTLGIEAIGALLLAWFFMQAGVLNYGYYGVFHAVSAFCNAGFSLFSDSLEGFSKNPAILTIIMLLIISGGLGFIVLQDVYQRITKRRRYLNYHSRVVLGMTAGLILFGFLIFFFFESKGTLSDFSLRDRIMNALFQSVTPRTAGFDTIPQYALSQPSKVFTILYMLIGAGPGSIAGGIKVTTIFIIIILMIRYPDPAGDIRIGKHRITSYTLNRATVYFLKALSLLLLGALALSLIEGHRGVAFDAIVFEVVSAFGTVGLSLGLTPQLSVAGKMVIIGIMFAGRIGLVALSFSLIRAKNYDITYPEGSVLLG
3.2E-58	207	18.3	1.2E-56	201.7	12.7	2.1	1	D5EFS6_AMICL	Potassium uptake protein, TrkH family	Amico_1288	Aminobacterium colombiense (strain DSM 12261 / ALA-1)	483	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Aminobacterium, Aminobacterium colombiense, Aminobacterium colombiense (strain DSM 12261 / ALA-1)	572547	>tr|D5EFS6|D5EFS6_AMICL Potassium uptake protein, TrkH family OS=Aminobacterium colombiense (strain DSM 12261 / ALA-1) GN=Amico_1288 PE=4 SV=1MKLRLVARVLALLSAMISIFMFWPLFWAFLDGTPDVKAFSVSIAIGFLIAAFLYIWGRQDSFQDIGIREAFAVVTLSWVTASIIGGLPYLLNGTAATFTDAFFEAMSGFTTTGASILTNIEAEPRGILFWRDLTHWLGGMGIIVLSLAILPFIGVGGMELYKAEVPGPIPEKMTPRIQQTALLLWGVYIFLSALQSILLLFGGMNLFDALTHTFGTMATAGFSPKNASVAHYGSAYIDWVITIFMFLAGSNFALHYHFLQGKWDAWWKDGEFRVYFSITTCCTFIITLLLRKGIYSNIFEALRYAAFQVVSIITTTGFVTADYELWPIFTQFLLLILMFIGGCAGSTSGGIKNLRIMVLVRHAYTELYRLLHPKAIIHTKIGDRTLSKEIVGSITAFFLLYIGLFTLATLLMTGLGLDLVSAISSVAATLGNIGPGLAIVGPTKNYALIPDIGKWILSFCMLLGRLELYTVLILCVPATWRR

3.3E-58	207	29.1	3.8E-58	206.6	19.8	1.2	1	W6AIJ1_9MOLU	Potassium uptake protein KtrB	ktrBSSABA_v1c01120	Spiroplasma sabaudiense Ar-1343	578	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma sabaudiense, Spiroplasma sabaudiense Ar-1343	1276257	>tr|W6AIJ1|W6AIJ1_9MOLU Potassium uptake protein KtrB OS=Spiroplasma sabaudiense Ar-1343 GN=ktrB PE=4 SV=1MFLLLEGQENGKFIKKNESDENPGLSLKEKRRRHKELKKERLEERRRKFKEEGQERKSFITKFKNWWPLSKVSGKILLIYFLTVL VGGLLLAIPGVILNSQFHWDFLTGIFTASSAFSDTGISISNAAADYSFWGQLLILIMIQIGGIGILTFKIVLLISLGKKVSINDQSVAQSERG SSQFSSTVEMIKDGFIFLTFVEIIGMVMLFFGFYFTPLTFENYNSIYKDNFSYQYVDVYHDFGGSLWAAIFHSISAVNNAGFDIISGSSLQ PYNLSDNQGYLIQSVFLVQWVIGGLGYPTFHDIKQKIKARRTGQVVKWSLFTKLNFTVYLTLFLVGPLLVFLSELSQGKDSYILNYYNV TRDETFYDVILSYEYIDIGPKPVGQAFMDIFFNVTSSRNAGFTTVDINQFNAGSKLIMSVWMFIGSAPSSTAGGIRTTTFAIVILTIISIMR NRRSVVAFRKKIPEETVRRSLAVAFVGVMVIVGATAIIYIDSNKVLANRTNGDKTIIELITLICSAFGTVGLNPFTTGQMIGLGAFSKITLIFI MFIGQLGISNTLLAFIKPNNKKSYEFLEEEVVIG
3.6E-58	207	26	4.7E-58	206.3	18	1	1	F2I7J0_AERUA	Potassium uptake protein, TrkH family	HMPREF9243_1781	Aerococcus urinae (strain ACS-120-V-Col10a)	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Aerococcaceae, Aerococcus, Aerococcus urinae, Aerococcus urinae (strain ACS-120-V-Col10a)	866775	>tr|F2I7J0|F2I7J0_AERUA Potassium uptake protein, TrkH family OS=Aerococcus urinae (strain ACS-120-V-Col10a) GN=HMPREF9243_1781 PE=4 SV=1MLNFFKRLNVSQKIAFSFMIVILVGSLLLSLPIAHTATSTATYLDHLFISVSAVCVTGLWTESIYDSYNIIGQMVMLALIQTGGLGLM TIIGSIYHTIGQNIGLKNQIATGAALNHSENYKIGDFLTRIIRYTAIIEGAGFILLSTYFVPRFGWVKGLWNSLFTAISAFCNAGFDIMGNNS LIDLKTVPVLNWTIMALIVLGGIGFSVWFDITNQIKNYAKKSNGHKLSFYFKHLSPHTKLVLIVTSLVILTGTSLFLLVEWNNPGTIGPLSL GDKIMTAFFQTITMRTAGFATVDYTACRPVSLLLFVLTMFIGGGAGGTAGGLKVTTFALTIMLALREVRQIKHVNFERHTIPDAAVRQSF TIALMYVSALFIGSALLLTFDPGQRYLHLLFEAISALATVGVSAGLTPNLSLASHIVLMLLMFVGRIGPMTMALSLRRNRNNYDIRYAKTN ILIG
3.6E-58	207	26.9	2.5E-56	200.6	18.7	2.2	1	R5AYP9_9BACT	TrkH family potassium uptake protein	BN456_00564	Prevotella sp. CAG:1031	490	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:1031	1262917	>tr|R5AYP9|R5AYP9_9BACT TrkH family potassium uptake protein OS=Prevotella sp. CAG:1031 GN=BN456_00564 PE=4 SV=1MLTRLRNINFAIVARFIGWLVIIEGIFMLAPLLTALAWNESDVRAFLWPAAGCLTVGSLMAFGIRPRSLEMGTREGFLLTAMVWV AFSTFGMIPFLLIDNPLTVSEAFFEAMSGFTTTGASVIESVEGLSHGILLWRSEMNWIGGMGIILFTLAVLPMLNHSGGIQLFNAEVTGIT HDKIRPRISQTAKDLWSVYLMLTIVLIALLWAGPMNLFDAVCQAFSTVSTGGFSTRDDSIAAWDSTYVDIVITVFMFLGSINFTLIFMATR GRFDALLRNDVFLTFIKMIGFYYLLFVVCIIAEGEYTGVKSVTIDPLFQIMSCMSSTGMSVFNFERWGTFVLSMMFLMMFFGSCAGSTA GGAKIDRFLFLFKNLRNEIYRCVHPNSVTSVRINGKVMSNSVVQKVVAFLCLYVLIIAVGGTVLTACGLPLVDSYFSVFSCIGNTGFGAG VTGYGGGWDLVPPLGQWVLSLIMLTGRLEIFTVLILFTKGFWRK
3.7E-58	207	17.7	6.1E-28	107	4.4	2	2	D4MTE7_9FIRM	Trk-type K+ transport systems, membrane components	CL3_33340	butyrate-producing bacterium SM4/1	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, unclassified Clostridiales, unclassified Clostridiales (miscellaneous), butyrate-producing bacterium SM4/1	245012	>tr|D4MTE7|D4MTE7_9FIRM Trk-type K+ transport systems, membrane components OS=butyrate-producing bacterium SM4/1 GN=CL3_33340 PE=4 SV=1MNYSMISYIVGWILNFEGLFMLLPCLTAVIYGEKAGFAFVVTMALCFVIGVPLTIRKPKNMVFYTKEGFISVSLSWIVMSVMGSLP FLFSGATSNPVDALFETVSGFTTTGASIFSDVESLPYCILFWRSFTHWIGGMGVLVFILSLLPLTGGYHMNLMKAESPGPSVEKLVPKL QSTAKILYSIYIALTLLEILLLLAGGMPLFDTLTLSFGTAGTGGFGIKNDSMAGYSPYLQNVVTVFMILFGVNFSFYFLLLLRKPKKAFRM EEVRCYLGIIAAAIVIITINIKDFYPSVAQAFQQAAFQVGSIITTTGYATTDFNTWPQVSKTILVMLMFVGACAGSTGGGIKVSRFVILLKTI NKELHHFLHPKAVRKISMDGKVVEHEVVRSINVFMIAYVLIFSFSVLLVGFDNQDLVTNFTAVAATLNNIGPGLEMVGPAQNFGLFSNG AKCVLIFDMLAGRLEIFPLLILFVRDTWKKF
3.7E-58	207	17.7	6.1E-28	107	4.4	2	2	D6DIR1_CLOSC	Trk-type K+ transport systems, membrane components	CLS_21130	[Clostridium] cf. saccharolyticum K10	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, [Clostridium] cf. saccharolyticum K10	717608	>tr|D6DIR1|D6DIR1_CLOSC Trk-type K+ transport systems, membrane components OS=[Clostridium] cf. saccharolyticum K10 GN=CLS_21130 PE=4 SV=1MNYSMISYIVGWILNFEGLFMLLPCLTAVIYGEKAGFAFVVTMALCFVIGVPLTIRKPKNMVFYTKEGFISVSLSWIVMSVMGSLP FLFSGATSNPVDALFETVSGFTTTGASIFSDVESLPYCILFWRSFTHWIGGMGVLVFILSLLPLTGGYHMNLMKAESPGPSVEKLVPKL QSTAKILYSIYIALTLLEILLLLAGGMPLFDTLTLSFGTAGTGGFGIKNDSMAGYSPYLQNVVTVFMILFGVNFSFYFLLLLRKPKKAFRM EEVRCYLGIIAAAIVIITINIKDFYPSVAQAFQQAAFQVGSIITTTGYATTDFNTWPQVSKTILVMLMFVGACAGSTGGGIKVSRFVILLKTI NKELHHFLHPKAVRKISMDGKVVEHEVVRSINVFMIAYVLIFSFSVLLVGFDNQDLVTNFTAVAATLNNIGPGLEMVGPAQNFGLFSNG AKCVLIFDMLAGRLEIFPLLILFVRDTWKKF
3.8E-58	207	11	1.7E-30	115.4	0.5	2	2	Q3IMW3_NATPD	Trk-type transport system (Probable substrate potassium)	trkH1NP_4904A	Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) (Halobacterium pharaonis)	500	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Natronomonas, Natronomonas pharaonis (Natronobacterium pharaonis), Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) (Halobacterium pharaonis)	348780	>tr|Q3IMW3|Q3IMW3_NATPD Trk-type transport system (Probable substrate potassium) OS=Natronomonas pharaonis (strain ATCC 35678 / DSM 2160) GN=trkH1 PE=4 SV=1MVRIRVDWRASLDLTGRVLLYLAAPLCFPLVLAVWYGEALVPFLAAIAVTLALGASLRTLPGDPGNLGPREAFLAVALIWLLVAAV GAIPFIVAGVGTIAHPVNAMFESMSGLTTTGATVLQEFDHHSRSVLMWRQLIQWLGGLGILVLATAILSEIGVGGAQLMERESQTKNV SKLTPRISDTAKLIWGLYVGITLLAVGVYYGLHLAGVAPEMDLYNAIAHAFTSVATAGFSPEPLSIGAFEPIVQWAIIPFMIAGSTSFVLM YIAINGEPMRLLRNDEFHFYLGTLGLFSAIVVAVLVFDGTIDFSSEETIRHALFNVTSIVTTTGYASTDFELWSAAAKYVLFLSMFTGGM VGSTTCSVKSLRWLVALKSFRRNLFTSVHPEAVRPVRLSGSPVDEETIRDIYAYLLLVVVIFAVFAVFVAVDADRAGIGLSAFESMGAA ASTFLNIGPAFGEAGPYGTYDIFPMSTKVAMILLMWIGRIEIIPVLVLLTAAFWRS
4E-58	207	25.5	3.5E-57	203.4	17.7	1.9	1	R6YXQ5_9CLOT	Potassium uptake protein TrkH family	BN593_01059	Clostridium sp. CAG:299	448	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:299	1262792	>tr|R6YXQ5|R6YXQ5_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:299 GN=BN593_01059 PE=4 SV=1MLSNRVWALTPAKIILGGFFLIITAGALLLTLPISSKSGEMTPFIDAFFTATSATCVTGLVVHDTYTYWSVFGQSVILLLIQIGGMGV VTLAIAITILSGRKIGLKQRFVMQESISAPQVGGIVRMTNFIIKGTLLLELIGAFIMAVQFCPQFGVIKGIWFSIFHSISAFCNAGFDLMGGT SGLYSSLTSYHSNPLIVVPVMLLIVVGGIGFFVWDDIIQHRETRRAFRLQTKVVLTYTFFLILIPAVLFFLFEFTPQRWEGYSLADRLYAS FFQSVTPRTAGFNTVPLDGLSTQAQLLTIMLMIIGGSPGSTAGGIKTTTFAVALLCIRSVFQNQEGIHCYKRRIPYEILRNAIAILVLYLSLF LAASFLITWADGVTLMESSFEAASAIATVGLSLGITEDLSLFSKMILILLMYFGRVGGLTMLYALTNHKKFPFHLPEEKITVG
4E-58	207	22.6	1.1E-56	201.7	15.7	2	1	R6S1W3_9CLOT	Trk system potassium uptake protein TrkH	BN621_01499	Clostridium sp. CAG:352	487	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:352	1262798	>tr|R6S1W3|R6S1W3_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:352 GN=BN621_01499 PE=4 SV=1MNTSIIRYILGLVLKMEAALMILPCIVALVYGEYKGLLSYLSVLCICAIIGFISTHKKPESHVFYLKEGCVATSLSWIILSIMGCLPFVIT QEIPSFTDALFETISGFTTTGASILSDVESLSYCNIFWRSLTHWIGGMGVLVFLLAIIPLSGGSNFNLMRAESPGPSVGKLVPKIKTTARL LYIIYIGMTFIEIILLIAGQMPIFDAITTSFGTAGTGGFGIKNDSITSYSPYIQWVVTIFMILFGVNFNAYYFMLLKQWKKSLLMEEVRYYFIII GISTAIIFFNILNLFPNAFDALRHATFQVGSIITTTGFSSVDFDIWPETSKIILVLLMFIGACSGSTGGGIKVSRIMILIKTVVKELNSYIHPRS VRKIKIDGKPVEHDVVRATNVYFITFMVVFAFSVFAISFENIGLVTSFTAVAATINNIGPGLELVGPTQNFSVFGPFSKYVLMFDMLAGRL ELFPLLILFHPSALKDMVKKSNNY

4E-58	207	22	3.4E-57	203.5	15.3	1.9	1	A0A0F5ANQ6_9GAMM	Trk system potassium uptake protein	WN56_16095	Salinivibrio sp. KP-1	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Salinivibrio, Salinivibrio sp. KP-1	1406902	>tr|A0A0F5ANQ6|A0A0F5ANQ6_9GAMM Trk system potassium uptake protein OS=Salinivibrio sp. KP-1 GN=WN56_16095 PE=3 SV=1MINFKNTLRLLGMPILWMGVVQFVFGLLSLFIFRDGVSTDFFYPSLLMMISSLVISWLFRQSKLNQVTFRDALLFSTLTWILVGLLGGIPIELVTGVNFTDATFESISALSTAGATILSGLDNMPASFLLYRQFLQWMGGLGVVIFVVAVLPMLNVGGMRLLKAETPGPIKDEKLSPRISKTAHYLWGVYVVITIACALAYYVAGMSAYDAIAHSFSTVSTGGFSTHDASMWHFQSHLILMISNVFMLLGAINFGLHFRIFRIGWRGLKLYIDDEESRVFLIVVACLSLILGFYLYGEARYESLWMSLSFAAFHVVSFITSTGFGAADLSSWPAATALFLVFCAYLGGCSGSTAGGNKIIRDIVTFKIIRRQLHQLVHPSAIIPIRYQDKVVSNDVTQAVMAFMSLAALTTGVFTLLMMMTGLDFWSAFTAVVACINVLGPGFGEVGSNFQPVTDTGIWILNIAMILGRLEYFTVLALFMPHFWRW
4.1E-58	207	14.3	2.2E-55	197.5	9.9	2.1	1	C4ZHP6_EUBR3	Potassium uptake protein	EUBREC_2803	Eubacterium rectale (strain ATCC 33656 / VPI 0990)	499	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium rectale, Eubacterium rectale (strain ATCC 33656 / VPI 0990)	515619	>tr|C4ZHP6|C4ZHP6_EUBR3 Potassium uptake protein OS=Eubacterium rectale (strain ATCC 33656 / VPI 0990) GN=EUBREC_2803 PE=4 SV=1MNTSVIRYLLGYILKLEGFLLLLPCIVAGIYYEKSGIYFLIVALISIAIGFIFSAKKPRDFTFYLKEGCATTALGWVVLSIFGCLPFYISGEIPSFTDALFETISGFTTTGASILPEVESLSYCMNFWRCFTHWIGGMGVLVFLLAIIPLSGGSNINLMRAESPGPSVGKLVPKMKHTARLLYIIYFGLTTMEIIFLLFGKMPLYDAICTSLGTAGTGGFGIKNDSFCGYNVYLQWVVTIFMILFGVNFNAYYLLFFGHIRDALKVEEVRYYFGIIIASVVVISVNIAHMCTGVFDAVTKAAFQVGSIITTTGFSSTDFDRWPELSKTLLVLLMFIGACAGSTGGGIKVSRIVIAVKTILKELNGYIHPKSVKKLTFEHKPVDHDVIRSINVYFMTYAVIFVVSMLLVSVENYDFTTNFTAVAATFNNIGPGLSLVGPTCNFGFFNNFSKYILMFDMLAGRLELFPLLILFHPSIWKELFIQADKKVKGNRKEKQNVRM
4.1E-58	207	16.3	7.1E-56	199.1	11.3	2	1	R5WNQ1_9FIRM	Cation transport protein	BN568_00134	Blautia sp. CAG:257	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	1262756	>tr|R5WNQ1|R5WNQ1_9FIRM Cation transport protein OS=Blautia sp. CAG:257 GN=BN568_00134 PE=4 SV=1MNYRIIFYIVGWVFNLQAIFMVLPCLTAVIYGENDPGAFLVSIVICLAIGLPLTRKRPRNKVFYIKDGCIAVALSWIVLSITGAVPFVLSGSIPHPIDAIFETVSGFTTTGSSILTDVEILPKSILFWRSFTHWIGGMGVLVFLLSLLPLAGGYHMNLMRAESPGPSVSKLVPKVQSTAKILYSIYLGMTVLQIILLLLGGVPVFDSLCITFGSAGTGGFGIKNDSMASYSTYCQVITTIFIILFGVNFSAYYLILTKKFKQAFKLEEVRYYFGIILASVILIAVNTRHMFSGFAEAFQQSAFQVGSIITTTGYSSTDFNQWPALSKTILVLLMFVGACAGSTGGGIKVSRVVLLCKAARKEFQLYLHPNAVKKLKMDNKAVSHETLRSTNIFLSVYLLIFCGSILIISLDNFDLITNFTAVAATLNNIGPGLEIAGPMGNFSSFSYLSKSVMIFDMLAGRLEIFPLLLLFFKDTWKKF
4.1E-58	207	9.9	9.3E-58	205.3	6.9	1.4	1	K0I6F5_9BURK	Trk system potassium uptake protein	C380_22390	Acidovorax sp. KKS102	488	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax sp. KKS102	358220	>tr|K0I6F5|K0I6F5_9BURK Trk system potassium uptake protein OS=Acidovorax sp. KKS102 GN=C380_22390 PE=3 SV=1MTDMFPVLRVLGILLMIFSLSMGLPLAVSLWTRDGVWFVYPLSIAATMLAGAWLWWRLRLFRQELQPRHGVMLVSLVWALLPLSAALPLMLAGHHTGHPLSFTHAYFEAVSGLTTTGSTVLAGLDALPVSVNVWRTFLQWMGGMGILILAVAVLPLLGVGGSQLFKAEAAGPLKDTKLTPRMTGTAKGLWGVYALFSTLCGLAYWAGGMAPLDALMHMFTTVSLGGLSSHDLSFGYFQSPLLEAICIFFMLVASCNFALYFVAIRKGQWGGFWRDPELRATLVTLIGGGLLVALLLWAKGVYGPLDALRHGMFNLVSLATTTGYATVDYLAWPVFAPVFMLLLSGVATSAGSTGGGIKMVRMLILVKQARREMNRLVHPRAVQPVQLGGAAVDNRVIFSVLAFMLVYGGTVFGLSMVMLLTDLDPVTAFSVVLASVNCAGPGLGSVGPASNYAVLTDFQIWVCTLAMLLGRLEILSFMALLTPAFWRR
4.3E-58	206	24.2	6.3E-35	130	3.9	2	2	E6W3X7_DESIS	Cation transporter	Selin_1110	Desulfurispirillum indicum (strain ATCC BAA-1389 / S5)	481	cellular organisms, Bacteria, Chrysiogenetes, Chrysiogenales, Chrysiogenaceae, Desulfurispirillum, Desulfurispirillum indicum, Desulfurispirillum indicum (strain ATCC BAA-1389 / S5)	653733	>tr|E6W3X7|E6W3X7_DESIS Cation transporter OS=Desulfurispirillum indicum (strain ATCC BAA-1389 / S5) GN=Selin_1110 PE=4 SV=1MTLKNLLKSLSVITFVMGCSMIFPVITGIVYDEPFLPFLLLMLSVLAVCGAILWGLRHHNANLNVREGAFVVTSIWLILGVVGALPFVFYGATPSFSDAVFETISGFTTTGASIMSDIEALPKMLLMWRSAMHWFGGMGIIVFSIAVLPMVGNGALQLIKAEGIMDEKLTPHIRDTAMALWKVYLAFTIANALLLYWAGMLPFDAINHAFSTIATGGFSTKNDSFGHYAHNDAIMWITIFFMVISGINYLAHFKLLKKDFSGYRTSEPRLYLQLFFAISLLAGLMIFLHQPQQLGFYESMKHSFFTIASIMTTTGFASIDYVDWTNAFLIFTILVMVIGGCAGSTAGGVKVIRYVVLFKALAVEIKRMVHPRGVYVVMLMDNRKITSGILTAMLGFFALYFCTNAALTIYLSMRGLDLTTALSASLAMVGNVGPGLGLVGPMDNFSFMAWYDKLILSLAMVIGRLECYTFFLLLSRSFWKRF
4.4E-58	206	14.2	1.1E-35	132.6	0.1	2	2	Q82TP5_NITEU	Trk system potassium uptake protein	NE1835	Nitrosomonas europaea (strain ATCC 19718 / NBRC 14298)	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas europaea, Nitrosomonas europaea (strain ATCC 19718 / NBRC 14298)	228410	>tr|Q82TP5|Q82TP5_NITEU Trk system potassium uptake protein OS=Nitrosomonas europaea (strain ATCC 19718 / NBRC 14298) GN=NE1835 PE=3 SV=1MGHVLSHFLAVANILGRMVMMFGLVLLIPCGVAYWTLDGSLSVFLDALSVTLGCGATIWILTYRFKRELQIRDGFLLVVLVWLSLPLFGMLPLVWYLPELGIAKAYFEAASGLTSTGATILTRLDELPYAINLWRCLMAWLGGMGLIVLAVAILPMLGVGGRQLLSAEIPGPIKESRLTPRIAETAKRLWLIYVTLTLTCMIAYRLAGMTPFDAIAHALSTLGLGGFSTHDSSYGYWNSPLIEAIAILFMLIAGINFSSHFVAWRAKSFSPYRADPEAKLYILITLASCIGVAGFLWIKGIYTDPLVALRYAAFNVVSTATTAGYSNTDYALWPIFAPLWMLFLSGFCTSSGSTGGGIKMIRARILFQQFFREMIIIMHPRAVSLIKIGRSIITNEIIFAILGFFFVYLISIVLMTLALTLSGLDEITAFSAAVACLNNLGAGLGAVGPAMTYASLNDFQIWLCSFGMFLGRLEFYTLMIVFTPAFWRR
4.6E-58	206	31	1.3E-57	204.8	21.5	1.5	1	F8AD75_THEID	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Thein_0933	Thermodesulfatator indicus (strain DSM 15286 / JCM 11887 / CIR29812)	454	cellular organisms, Bacteria, Thermodesulfobacteria, Thermodesulfobacteria, Thermodesulfobacteriales, Thermodesulfobacteriaceae, Thermodesulfatator, Thermodesulfatator indicus, Thermodesulfatator indicus (strain DSM 15286 / JCM 11887 / CIR29812)	667014	>tr|F8AD75|F8AD75_THEID H(+)-transporting two-sector ATPase OS=Thermodesulfatator indicus (strain DSM 15286 / JCM 11887 / CIR29812) GN=Thein_0933 PE=4 SV=1MEWKRINRKLERHPARAVIYSFALADIIGAILLWCPFSHVKTLSFIDALFTSTSAICVTGLTVVNTAQDFTHLGQFIILVLMQLGGLGVMTFSVFIALGFKDSLSFSSRLSLQESFLPHFTPEPRKLLFTIFAYTFISEALIALGLFLCFLGHGLGIKVSLAQAIFHAVSAFCNAGFSTFNDGMIDFQKSYAVLALIALAILLGNTGFPIVYELLSFFKEKRHKLSLHFKLTVYTHVALIIFGTVAFLWFDSAGAMAGLSWPLKVVTAVFHSVSARTAGFNSIDIAHFSEHSIYVFLILMVIGACPGSTGGIKITTTFAVLSCTVWSRLRGFPQAVAFKRSIPVDQVGKAVTLVFIYLLAIMLFHFFLTFTEPNIPFYKSQHEFLGALFEVVSALGTVGLSTGVTSNLNLWGKICIILTMFVGRVGLLSLISFLSEVGHEPRPYRYPKERVMVG
4.8E-58	206	41.4	7.8E-58	205.6	28.7	1.2	1	F2F851_SOLSS	Trk-type K+ transport systems, membrane component	SSIL_3193	Solibacillus silvestris (strain StLB046) (Bacillus silvestris)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Planococcaceae, Solibacillus, Solibacillus silvestris, Solibacillus silvestris (strain StLB046) (Bacillus silvestris)	1002809	>tr|F2F851|F2F851_SOLSS Trk-type K+ transport systems, membrane component OS=Solibacillus silvestris (strain StLB046) GN=SSIL_3193 PE=4 SV=1MPFKKFEKRKITPFQILITYYSVAILISFLLLRLPGVHLEGVHVSFLDSLFTAVSAVSVTGLTTVTVAETYSSFGLAMILLILQFGAIGIMSIGTFLWLLFGKKIGMRERQLIMIDHNQYNLSGVVALIRQIAKLLFIIEFTGALILTVHFKRYFATWEESAINGLFASISATTNGGFDITGMSLQPFHHDYFIQFVCMILIFLGAIGFPVLIEVKAYLTKKDPAFRFSLFTKVTTFTYVALFVFGSVVIFIIESFQSFKGMRWHEAAFSAMFQSISTRSAGLTTYDVTSFNEATQLFMSALMFIGASPSSVGGGIRTTTFAIVILFLIAFSRGQSEIQIFNREIHLIDVYRSFAVLIFAIIMVLGAAMVLFITESSASMMEVIFEITSAFGTCGMSLGITGDLTAFGKMVIMVLMFVGRVGLISFLYSIGGSAKKKKYHYPKERIIIG

4.8E-58	206	25.3	1.7E-57	204.5	16.9	2	1	R7NV33_9BACE	TrkH family potassium uptake protein	BN821_01012	Bacteroides sp. CAG:98	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:98	1262754	>tr|R7NV33|R7NV33_9BACE TrkH family potassium uptake protein OS=Bacteroides sp. CAG:98 GN=BN821_01012 PE=4 SV=1MINSKMICKIMGSLFFIEAGFLILCALLAIYYKETDLTAFLSSAAITAGAGIVFSIFGKNAERKISRRDGYVVVSLAWIFFSLFGMLPFYLSGYIPSITDAFFETMSGFTTTGASILDNIESLPHGLLFWRSMTQWIGGLGIVFFTIAVLPIFGVGGVQLFAAEATGPTHDKVHPRIGVTAKWIWSIYLGLTIAEVFLLLLGGMDVFDSVCHSLTTTATGGYSTKQNSIAAFHSPYIEYVITLFMFLSGINFTLLFLFFLKGKFKRLIENTEFHWYLGTVGCFTLFTTVTLVLTSPMGIEESFRKAIFQVVSLQTTTGFISADYMTWVPVLWTLMCIIMLFGACAGSTSGGIKCIRIAIMSRVSRNEFKRIIHPNAVLPVRINRQVISSTTKSAILAFTFLYIAIVFIGWLLLMILGVGFEEAYSVVISSLGNVGPGIGKCGPSYSWSGLPDMAKWISALLMLIGRLELFTVLLLFTPGFWKKH
5E-58	206	31.9	8.6E-58	205.4	22.1	1.3	1	Q0SRT8_CLOPS	Potassium uptake protein, TrkH family	CPR_1855	Clostridium perfringens (strain SM101 / Type A)	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium perfringens, Clostridium perfringens (strain SM101 / Type A)	289380	>tr|Q0SRT8|Q0SRT8_CLOPS Potassium uptake protein, TrkH family OS=Clostridium perfringens (strain SM101 / Type A) GN=CPR_1855 PE=4 SV=1MYIKLTKKIKFSAVQILALGFSMVILLGAIILSLPISSKSGEFTPFLDSLFTSTSAVCVTGLITLNTAAHWNYFGKTLIIILIQIGGLGFMSFTTLFALMVKKKITLRERLLIQEAMNTFGIQGLVRMIRYILTFTFSVEMLGALLLSTQFIPKFGLLKGIYYSIWHSISAFCNAGFDLFGDNLVGYANNKTVILTIAALIVIGGLGFTVWSELYNYKGYKKLSLHSKVVIMITAILLIGGAILMFIFEYNNPNTLKYMSFGDKLTNAFFASATTRTAGFNSVSTADMTLAGKFLTILLMFVGGSPGSTAGGIKTATFGIVVLTLISIIRGREDTEVFKKRISKELVYKAFAVLFIGFGIVVLGTLILAVTEPGFSLEYILYEVTSAFATVGLTLGLTPYLSAIGKIIIIITMYLGRVGPMTVVLALANRKKPSAYKYPEDKILIG
5E-58	206	19.2	1.4E-56	201.5	13.3	2	1	R5DI45_9FIRM	Uncharacterized protein	BN457_00044	Dorea sp. CAG:105	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea sp. CAG:105	1262872	>tr|R5DI45|R5DI45_9FIRM Uncharacterized protein OS=Dorea sp. CAG:105 GN=BN457_00044 PE=4 SV=1MNRRMILYILAKMMGVEGVLLLLPAFVGLLYGEKSGACFLFPATILALIYIIFGIRKPNKTKIYAKEGMIIVASAWILWSMFGAIPFTLGGYIPNYLDAFFETVSGFTTTGSTILNDIESLSHCMHFWRCFTHWIGGMGVLVFVLVLTSLDKKNTMYLMRAEVPGPEKDKLVPKAMATARILYGMYFALTAVEIVLLLFGGMSPFDSIIHAFSTAGTGGFSNYANSIGQLDSAYIDGVITVFMILFGINFNLFYLLLLRQFKPVWKNEELRTYLAIIATAIALITWNITSIYGNPLKAFRYAAFQVASIITTTGFSTADYMKWPTMSQTIIIILMIIGACASSTGGGIKVSRFLIVVKSIKKELKQMVHPKSVNLIRINGKKMNPDIVQNVFVYLVAYAGIAGLSVLLVSIDDFDFATNLGSVMGTLNNIGPGLGVSGPAGNFAQFSPFSKLVFCMDMLIGRLEIFPFLMLFTSISWRKKF
5.2E-58	206	23.8	5.5E-56	199.5	16.5	2.1	1	R6VPJ2_9FIRM	Uncharacterized protein	BN546_00020	Firmicutes bacterium CAG:227	444	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:227	1263010	>tr|R6VPJ2|R6VPJ2_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:227 GN=BN546_00020 PE=4 SV=1MSKIIRKKHLTSFQLIILGFAGVILLGTILLMFPIATLENVPTPFSEALFTATSAVCVTGLVVKDTGSYWSVFGQTVILVLIQIGGLGVVTVAAAVSILSGKRISLMQRSTIQDAISAPKVGGIVRLTRFILKGTLLIETVGAMLLLPVFLSDYGLKGVWMAVFHSVSAFCNAGFDILGTTENTFPSLMRYSGNAIVNVVIMLLIIIGGIGFLTWDDIYMNKMNFKRYRMQSKIILVTTACLIFLPAVFFFVCDLKNLPAGQRLLAATFQSVTTRTAGFNTINISEMSEASSAVMILLMLIGGSPGSTAGGMKTTTFTVLLLNAIATFRSQENAGAFGRRLEYHAIKNAATISMLYFTLFFCGGLAISIYEDIPLLDCLYEAASAVGTVGLTLGITPKLHVFSQVVLIILMYLGRVGGLTLIYAVFSGRNRGNARLPLEKITVG
5.3E-58	206	12.3	8.3E-56	198.9	8.5	2	1	R5ATH4_9CLOT	Cation transport protein	BN454_01741	Clostridium sp. CAG:1024	486	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:1024	1262770	>tr|R5ATH4|R5ATH4_9CLOT Cation transport protein OS=Clostridium sp. CAG:1024 GN=BN454_01741 PE=4 SV=1MNYRMIGFVLGRILLVEAGLMAAPLIVTLLYGESAVAAFLIPIGLLLVLGLALGLRVPKDTTIYAREGLAVVALSWVTMSLFGALPFCLSQAIPSYIDSFFETVSGFTTTGASILSEVESMEHGLLFWRSFTHWVGGMGVLVFVMAVLPMADGRGMHLMRAEVPGPSVGKLSSKLSDTAKTLYAMYLVLTALEVVFLIAGGMPLFDALVNAFGTAGTGGFSHLNRSIGQYGNPYYEIVIGIFLLLFGINFNLYYFLLMRRFREVFRSEELLTYLSIVALATVGIAFNIRSICASLPEAFRQSFFQVATIITTAGFSSADFDLWPSFSKTVLVMLMFFGACAGSTAGGIKIARIVILFKSAARDVQRMIHPHAVATVRFEGKTLDDKTIRDTHLYLSAYLMLFVLSVLLISLEGNDLVTSFTSVAACLNNIGPGLGKVGPMGNFGFYSVPAKLLLSFDMLAGRLDIFPMLVLCAPAVWLKKLRREAR
5.4E-58	206	28.3	9.3E-58	205.3	19.6	1.3	1	S1QZB1_9ENTE	Trk system potassium uptake protein TrkH	OMO_01238	Enterococcus cecorum DSM 20682 = ATCC 43198	453	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus cecorum, Enterococcus cecorum DSM 20682 = ATCC 43198	1121864	>tr|S1QZB1|S1QZB1_9ENTE Trk system potassium uptake protein TrkH OS=Enterococcus cecorum DSM 20682 = ATCC 43198 GN=OMO_01238 PE=4 SV=1MLKKEKKSNIQKLGPVKFLSLGFAIIILTGGFLLSLPISSQSGQFTNFLDAVFTATSATCVTGLTTLNTAQHWSIFGQIIIMLLIELGGLGFMMLPIIFYTLAKKKVNLSTRIVLKEALNLDDMSGVMKLTLYVLKFSIAIQTTGMVLLAIDLVPRYGVIKGIWYALFHAISSFCNAGFDLFGDSLVPFQNDPYILLVISFLIVSGGLGFLVWRDLLQYKHTKRMSMHSKIALMMTGLLLLGGFVIFFFSEHNGRYLVQSDNFLVRLMNTLFMSVTPRTAGFYSVDYAAMSNPGLILTMFLMYIGGTSGSTAGGLKTTTFGVVLIQMISLLKGRQRAEFAGRSIKETAVFRAMTLFFITLSLCVISIMILSATEHLPRQNGIEYAAFEVFSAFGTVGLTMGLTPDLTEFGKLLIIGLMYIGRVGIMTVLFSLMSNNQKTTCRYQYPYESVLVG
5.5E-58	206	16.8	4.3E-32	120.7	2.8	2.3	2	S5ZRY8_9SPIO	Trk system potassium uptake protein TrkH	trkH TPE_0324	Treponema pedis str. T A4	486	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema pedis, Treponema pedis str. T A4	1291379	>tr|S5ZRY8|S5ZRY8_9SPIO Trk system potassium uptake protein TrkH OS=Treponema pedis str. T A4 GN=trkH PE=4 SV=1MIKIVQNKLFQYVRIIFMILAIIAISFVMPVLTAIYKNENYVIPAFIIPALSVCSIAALLFFIGKNKKIKLSTEGGIILVAAAWITACIFGALPLYFSKAIPGFIDSVFESVSGFSTTGGTVLTDAESCPISIHVWRCQMHWLGGMGIVALTVALFPLLGVGGFRLIKSETSGPDKGKVTAKITHTAKALWFIYLGMTVIQTALLMLAGLPFIEALCHTFATLGTGGFSTRNASIGSFNSPAVDFICAVFMLLAGVNFSLYFHLFTGHAEELFNNSELRAYLRIAFAATVLITVSIFPLYGFIGSLRHAFFQVASILTTTGFSTVNYDVWPEFSKLVLFALMFIGGCSGSTSGNIKVIRWLVLKKQAWIETERLLHPHGVFSIRLNKRPGRKDIVYSIAGFMFCYFFLGLVTAFVAVADGTDMLTGISAAFALIGNVGPGFGRVGPAGNFAFFSPAAKVFFSFVMLAGRLELYTMIIYFMPAFWKR
5.7E-58	206	21.5	3.6E-28	107.7	5.3	2.1	2	R7CPU5_9FIRM	Uncharacterized protein	BN806_00577	Ruminococcus sp. CAG:9	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:9	1262967	>tr|R7CPU5|R7CPU5_9FIRM Uncharacterized protein OS=Ruminococcus sp. CAG:9 GN=BN806_00577 PE=4 SV=1MNYSIIIYIIGMILEIEAVFMTLPAITALIYQETSGVAFLITIALCLVIGLPLTRKKPTRKAFYTKEGFVTVALSWIVLSIIGAIPFVISRSIPNPVDALFETVSGFTTTGASILSDVEALPHCMLMWRSFTHWIGGMGVLVFILSLLPLTGGYHMNLMKAESPGPSVSKLAPKVQSTAKILYSIYFVMTVIQILLLLVGGMPLFDSICTAFGTAGTGGFGIKNDSMASYSTYLQVVITVFMILFGVNFNAYFFIITKKFAQAFKMEEVRYYFGIIGIAILIIACNIYHIFGSAAKAFQQAAFQVGSIITTTGYATTDFNTWPEISRTILVLLMFIGACAGSTGGGIKVSRILILCKTVRKELHIFLHPNAVKKIKMDGKAIPHEVVRSTNIFFIVYMLIFASSIFLIAFDDFNLITNFTAVAATFNNIGPGLELVGPTGNFGMFSWFSKLILTFDMLAGRLEIFPLLILFVRDTWKKF
6.1E-58	206	22.4	1.2E-57	205	15.5	1.3	1	H5X363_9PSEU	Trk-type K+ transport system, membrane component	SacmaDRAFT_5095	Saccharomonospora marina XMU15	455	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharomonospora, Saccharomonospora marina, Saccharomonospora marina XMU15	882083	>tr|H5X363|H5X363_9PSEU Trk-type K+ transport system, membrane component OS=Saccharomonospora marina XMU15 GN=SacmaDRAFT_5095 PE=4 SV=1MLAWGRTGLRRLLPTWRHPARIVVTAFALVIVAGTALLMLPVATESGESSGFVTALFTATSAVCVTGLVVVDTPSYWSTFGELTILGMIQVGGIGIMTLATLLGILVVRRFGLRLQLTAQAETKTVQLGDVRRVVAGVVLISLAFEIVTFLLLFLRLRFGYGYESGTALYQAVFHSISAFNNAGFSLYSDSLMRYATDAAICLPIAFAVLAGGLGFPVWIELWRHRMRGVRRWSLHVKVTLLTTSTLLVVGSVLITAAEWNNPATLGQFGVGGKLLAGFFHGVMPRTAGFNSLDVSQFEPGTLLINNVLMFIGGGSAGTAGGIKVTTFALLAFVILAEIRGRPSVHVMGRRLDSTVQRQALTVALLSVGAVVSATLLLLALTPFSLDRVLFETVSAFGTVGLSTGITGRLPTSAELLVTGLMFLGRLGPITLASALALRERTRRYELPEERPIVG

6.1E-58	206	27.9	8E-58	205.5	19.4	1	1	U5L836_9BACI	ATP synthase	N288_08325	Bacillus infantis NRRL B-14911	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus infantis, Bacillus infantis NRRL B-14911	1367477	>tr|U5L836|U5L836_9BACI ATP synthase OS=Bacillus infantis NRRL B-14911 GN=N288_08325 PE=4 SV=1MWDEIKERLDKLSPAQVITGYYLLAVTISVLLLRIPAVHQPGVEVSWLDSAFTAVSAVSVTGLSVINISETYSTFGVFMLMFVLQF GGIGIMTLGTFFWILLGKKIGLRGRRLIMVDHNQSNLSGLVNLIREILKLILIIEAAGALILGVHFLSYYDTFQEAMLHGLFASVSATTNGG FDITGASLIPYADDYFVQLIHIILITLGAIGFPVLIEVKHYLFDRRDYKNFRFSLFTKLTSATFAVLLVVGTVLILLLEGRHYFSGMSWHKTF FYAFFQSATTRSGGLSTLNVNDFAESTQLLLSGLMFIGASPSSVGGGIRTTTFALNVLFLYQFAHGNRDIKVFKREVHQDDVLKSLVITI LAVGMCFFAVIVLSLTEAHSVTAIIFEVCSAFGTTGLSMGITPDLSAVGKCVIIILMFIGRIGLTSFLFIIGGKEKKSIYHYPKERVIIG
6.1E-58	206	30.9	1.9E-34	128.4	10.4	2.1	2	C4IM65_CLOBU	V-type sodium ATP synthase subunit J (EC 3.6.3.14)	CLP_0243	Clostridium butyricum E4 str. BoNT E BL5262	430	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	632245	>tr|C4IM65|C4IM65_CLOBU V-type sodium ATP synthase subunit J OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_0243 PE=4 SV=1MNKLKHISPGRLIVLGFFMVIMIGAFLLMSPFSRRSGVDVSFVDALFTSTSAVCVTGLIAIDTADTFNLFGKTVVAMLIQIGGLGVT SIGVGLILLIGRNVGIKQRMLVKEALNLTSMKGIVKLIKAVIIMTISFEIVGAILSYIVFSKDYKPWDAVGISIFHSIAAFNNSGFDVLGNFQN LSSYRDNILLNLVTCGLIIFGGLGFLTIKEIIEKHSFEKFSLHTKIVITMTGSLLIVGTVLLKFTENISWLTAFFYSTSARTAGFSTAPLSGFT SAGLFTLVILMFIGASPGSTGGGIKTTTFFAIIKNVYSASTNKHCVAFKRELSKNTIAKASIIATLSLTLVVVDTFILSIIEPEFSFMQILFEVT SAFGTVGLSTGITPSLSDLSKLIITLTMFIGRLGPLTMATIWTFKPTSHVHYLEEDITIG
6.4E-58	206	0.5	4.1E-52	186.7	0	2.8	2	A8NIY1_COPC7	Uncharacterized protein	CC1G_08729	Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) (Inky cap fungus) (Hormographiella aspergillata)	955	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Psathyrellaceae, Coprinopsis, Coprinopsis cinerea (Inky cap fungus) (Hormographiella aspergillata), Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) (Inky cap fungus) (Hormographiella aspergillata)	240176	>tr|A8NIY1|A8NIY1_COPC7 Uncharacterized protein OS=Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC MYA-4618 / FGSC 9003) GN=CC1G_08729 PE=4 SV=2MEKPKITINTFLRSPDAPNGGSDLTLSGTSEKHHHHHDDKLPTAGTVDVEDVDNHDPDSSEPPPETLLDRLLVHVNFYRIHLTAF TFIPLITSGVFYASNGRFRISYLDSLFLCYSAMTVTGLSTVNLSTLTPWQQVILYLLMIVGDITMVSWVMVLIRKRFFRTHCEWTVTMKK KKEKKKEEEKAKAKTQRLLQKSRSMFKMAISSPRDRRPQDPFVRSDPGPTPEEDVDPDLHPKNFGGSRASRSGHATSTTNGSSSRP SSRNVRDLSIVVSPATPKHTMQMALPTTIPEAEEPETGILVGSALSSSPEMQLQGLPPITHSPVQEEIDLSDNGSTRRSVKTVESGRGS GESESPVLDVTALSASPKSEAGSLPKDQQEPSPIEGLNLGPHTFGPDDVEYYGLSPATGAHSAGLGLHSQGHGHGVHSAGVDSSGG FSSGSGTDYGEVKSMVSGRTVRWEENTAQGNARYRRPAPKRSRTVIVPPRSRSNTLHSPLSVKDEGFGGFPGPVDLLTRFAQRAA PRKVTNALTRSATILSEREIRTEKTPWILMEVPAFIIGRNSDFRTETLTDEQVEAVGGAEYRALRLLSYLIPALFSYILFTPWLSTTTEYDE VFEAQARFVPKPWFALFQVMGAYTGGGLSLVDVLRFIMYALSTTLFVNLRRHLTNKPVYSWIGSRRSTPNSGLHVAFTFLLDHPRRT FHPFSSFSNVAHSATVPSTTLRLQKDIGIPVYEELPTGTKVIAGLFQGLAARASGFSIVPIASLAPALQFLYVVMMYIAVAMSIRSTNVYE ERSLGVFEAPPDDEDEEPDDLHKLGRKERVGKYIGWHLRRQMSIDIWWLVWGLALILVIERENIMDEDKKWFDVFRVIFELVSAFGGI GLTLGIPTDNYGFVGAMKPLSKLVVIVIMVRGRHRGLPVAVDRAIKLPREMVTGPHRKPSMNPQQMEEVKKEFNPV
6.5E-58	206	32.9	6.5E-58	205.8	22.8	2	1	Q3Y1H1_ENTFC	Trk family potassium (K+) transporter, membrane protein	trkG HMPREF0351_12304	Enterococcus faecium DO	466	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus faecium (Streptococcus faecium), Enterococcus faecium DO	333849	>tr|Q3Y1H1|Q3Y1H1_ENTFC Trk family potassium (K+) transporter, membrane protein OS=Enterococcus faecium DO GN=trkG PE=4 SV=1MHVDLFFRRLQRRGQKFAANHFSSIQIIVFYYILMTVLSLVLFYMPIFREPDSHVSFVDMLFMAISTVSVTGLSTFDINSVFNDNGII LLEILFQVGGLGIMMISTAFVIFSKRRITLKQRQLIMTDMNQPRLSGIVRLIRITFAILIWFQLLFGTFFSIYFYYRGYFDRWRDAVFYGFY QAISAVTNSGFDVTGDSIKPFAHDYFFLILIMFLIFVGGIGFPVLMECREWLLYKRSNAKLPFRFSLFTKLAVLAFVILFVSGTVLIYLLEK DHLFQDSNMSVKWINSMFYSITTRNAGLQIHDLGDFQITTLIIFSLLMFIGCSPSSVGGGIRTTTVAIIGLYLYSFLKSEDNINIFGRRIDQD DVRKSVVVFMLSLGMCFFCIVFLSATEEQTLISIIIEVTSAFGTTGLSLGITGDLSVVGKITIATLMFIGRIGMLYTLMLFVPKETRDLGYEY PSEKIIIG
6.6E-58	206	21	3.1E-57	203.6	14.6	1.9	1	R6ZRW5_9BACE	Uncharacterized protein	BN762_00920	Bacteroides sp. CAG:714	502	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:714	1262749	>tr|R6ZRW5|R6ZRW5_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:714 GN=BN762_00920 PE=4 SV=1MDDFLINDIHVTGNRNGNSLINRKMIFRILGVLLAIEAILLLISGCVSVIYDESDYIYFVYCALLNLGVGSVLVWLGRHADNTVTRRD GYCIVAFTWLLFTAFGMLPFYISGAIPSIPNAFFETMSGFTTTGATILDDIEALSHGMLFWRSFTQWIGGLGIIFFTIAVLPIFGVGNQVLF SAEATGVIHDKIHPKISVMAKWLWLIYLLITGSLIILLLIGGMDLFDAVCHAFATAATGGYSTKQASVAHWNSAYIEYVIAIYMLLSSINFSL YFMCLRGQVRHLFKDDETKAFLTSVMVVTLLITVSLVLHNGYGLERAFRSAFFQVASLHTSCGFGTDDYNLWAPFTWVLFLYTMVAG GCTGSTSGGVKLMRVVILLRNVKNEFNRLMHPRAVLPVKVNGQAVSQNTLATVATFVILYLICVFVGWTLLVFMGLNLEDALGIVLSSM GNTGPGLGSFGPAFSWNALPDAAKWVLSFMMLIGRLEVFGILLMFAPSFWEKH
6.6E-58	206	29.5	1.3E-57	204.8	20.4	1.4	1	F5LQN0_9BACL	Potassium uptake protein, TrkH family	HMPREF9413_1298	Paenibacillus sp. HGF7	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. HGF7	944559	>tr|F5LQN0|F5LQN0_9BACL Potassium uptake protein, TrkH family OS=Paenibacillus sp. HGF7 GN=HMPREF9413_1298 PE=4 SV=1MLKKSRFTPPQILVLGFALIILIGSGLLMLPVSSTDGLPLPFIDALFTATSATCVTGLVVVDTGSHFTMFGQIVIISLIQIGGLGFMSM ATLFAFILRKKISLRERLLLQEALNQGSMEGIVRLFRKVLIYSLSIEGIAAVLFTARWSMDLGFPKGLYYGIWHAVSFFNNAGFDLFGPIT GPFSSLTAYADDFITNVVTMALIVLGGIGFIVMSDVMDYRKTKRLTLHSKVVLSATSILIVTGALVIFIFEYSNSKTLGSLDFGGKILASFF QSVTPRTAGANTLDLASLRQATQFFMIILMFIGASPGSTGGGIKTTTFTFTMLVGAIVAMVRGKEDIVFFRNRLGKERILKAITLTMFALFLV IFVTMLLSTTEDHEFLMILYEVTSAFGTVGLTLGLTTKLTVFGKVMIALTMFAGRLGPLTLAYALQPKAEKELYRYPEGKITIG
7E-58	206	15.7	3.1E-57	203.6	10.9	1.7	1	F0RJT1_DEIPM	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Deipr_0387	Deinococcus proteolyticus (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703 / MRP)	459	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus proteolyticus, Deinococcus proteolyticus (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703 / MRP)	693977	>tr|F0RJT1|F0RJT1_DEIPM Potassium uptake protein, TrkH family OS=Deinococcus proteolyticus (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703 / MRP) GN=Deipr_0387 PE=4 SV=1MNSAFSLHFRRFGLSRFSPAQLIALTFGAAILGGTLLLWLPLSHEPGQTVSLLQALFMATSAVCVTGLGVVDIGTTFSPFGEAVM LLLVQFGGLGLITVGTMTALLLRRRVGVRSRLNAAQQVNASRLGEAPALVRTVVLSALAIELAGALLLAPDFIAREGLQRGLYYALFHSV SAFNNAGFSLYPTGLTGLVGNLAINIFIPLLIILGGMGFLVQVNVLAWLRDRRNQLSTNTRISLAMTFFLLLSAPVLFGLMEWNNPATLG GLPLRDKLLAAWFQGVTPRTAGFNTLDYAQMTFAGLFYSMLLMLIGGNSGSTAGGIKTNTVFVMVVSAWSLIRGRKDAVVFDRRLGT DIILRAMSVGLLSLVMLALGILLLLLLNSHGEGELSFIQLVFEAVSAFATVGLSMNATALLNPAQELVIIALMFLGRIGPLTLAVAFAQRELP PPVRYPQTSEVLIG
7.1E-58	206	21	2.2E-32	121.6	3.2	2.1	2	V5WM93_9SPIO	Potassium uptake protein TrkH	L21SP2_3425	Salinispira pacifica	483	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Salinispira, Salinispira pacifica	1307761	>tr|V5WM93|V5WM93_9SPIO Potassium uptake protein TrkH OS=Salinispira pacifica GN=L21SP2_3425 PE=4 SV=1MKGFAITRALAAILGIIGLFLLTPVIVAVFDSTPEFIMSFFLPSMASILISAVVLWLTWSYRGDINPRSGFLLVSLSWILVSAVGAVPF VLGDAIPSYTDAFFETMSGFTTTGASILTEIEAMPRPFLFWRSLTHWLGGMGIVVLAVALFPLLGIGGLQLMKAEAPGPDVDRLTSRIT GTAKILWMIYLGMTVLETLLLMLGGMSLFDSLTHTFGTLATGGFSPKNSSVGHYNSPYLQNVITIFMVLAGTNFIMHYRLLTGRFRLLW RNSELKAYLGIFIVTMLIMGFNLYREGVYPDLATSLRFSGFQTASILTTTGYATADFALWPGLSQALLFAMMFIGGSAGSTGGGVKVVR IISLLKQGFTEMKYLLHPRSVFTVKLNGSRLKKSVVYTITGFIILYMFFLILTTVVVAMDGKSLLTSFSTALATLGNIGPGFAGVGPTENYS SFSPAIKWFLSFIMMLGRLEIYTVLVLFSPQFWRR

7.2E-58	206	41.3	2E-33	125.1	10.4	2.8	2	L0RUR1_MYCC1	Cation transport protein	MCYN0561 MCYN_0561	Mycoplasma cynos (strain C142)	609	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma cynos, Mycoplasma cynos (strain C142)	1246955	>tr|L0RUR1|L0RUR1_MYCC1 Cation transport protein OS=Mycoplasma cynos (strain C142) GN=MCYN0561 PE=4 SV=1MKLLECLKKVLNKKTISKASDKWYIYLKSVSRVKYLLIVYFLIILFSSFLLWSPITQQKPPLNWNSSENYVNALFTTASAFSDTGLV VKNTYSHWNVLGQAIIAILILSGGIGIFSLKFFIINILFKKQVTTLYTLKMIQSERGHDDVNKVSSIIRSSVRFILTTSLISGFGMTIYFYFAEP SATYGIDKLINGEFINPRYDLAAAFRFGFFHTISAINNAGFDIISGNSLMPYYNNITLQIWFIILLIIGGLGYPTLYDIYRYIRHKVKRKKTKY HFSLFTKVSTITYFLVFLIGFLVLIGFETTSKSVDSLWNRVYVPDQLIHNYAKWVETFNEYGIKSDDKSIEVYNQILYLSKQIKENSYIDQN LLTTNVAKKLYSIVNQEIPNVGNLAQYLKQGTMYGNQWQKIFSLIFTSFSSRSAGFATVDVSHFSRGSIMLITLMMIIGAGPASTGGGIR TTTFAILILSMFSVILNTKKVRIFKRTIEPRTVFMSGQVFVIALIILIVSTLICFSSFDSHAGKIITHGVSSIDNYNIYGTEHVWFEVASAFGTT GLSVGITKEFNIVSKITLIFVMFIGQFGISSTLLVWRSKKSNKRNYEYVTADIVIG
7.3E-58	206	23.7	7.2E-57	202.4	16.4	2	1	R7A834_9FIRM	Uncharacterized protein	BN599_00235	Firmicutes bacterium CAG:308	498	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:308	1263016	>tr|R7A834|R7A834_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:308 GN=BN599_00235 PE=4 SV=1MMYSLNRTLQTFNWRVIFNIIGHVLMIEGCLLLFPLIVDLIYSQNVWSAYLKTIVICLVIGFPLSRMKEKHKSYFAKDGFVAVGLSW AILSFFGGLPFFFTQEIPSLVDCFFETVSGFTTTGSSILTDVEALSQASLLWRSFTHWVGGMGVLVFILAIIPRSNDRTMHIMRAEAPGP VIGKLVPRLKDSAAILYKIYFVLTIIMILFLLAGGMPLFDSLCTAFGTAGTGGFSIKNVGMAYYNSVYLEMVVTFFMLLFGINFNLFYFLLIK NVKAVWKNEELRTYLIIVAFSILMIMCNIVHLYDNSWFEAFRYASFQVASIISTTGFSSTDFNLWPQFSKMVLLLLMIIGACAGSTAGGIK VSRFLILLKKTKLDIQKLLHPQKVEAITMDQKIVDEQVVHQILSYFFCFMLILGSILLIVSLDDFDLETTLSACFTCIGNVGPGLGMAGPLS NFSMFSDLSKIVLSFAMLIGRLEIYPIIIFIVPLFATRKTKRHRD
7.5E-58	206	10.9	1.2E-57	204.9	7.6	1.3	1	I4MR51_9BURK	Trk system potassium uptake protein	Q5W_1265	Hydrogenophaga sp. PBC	487	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Hydrogenophaga, Hydrogenophaga sp. PBC	795665	>tr|I4MR51|I4MR51_9BURK Trk system potassium uptake protein OS=Hydrogenophaga sp. PBC GN=Q5W_1265 PE=3 SV=1MQSLWLPVLSVFSRVLLAFSPAFLVPMAWAWFLDQEHHVLIWAFGFAAAVLSGWLLSLATRHHRRELLPRDGFLLVNLVWLVL PAYAAAPLYYAVPELSLSKAYFEAMSALTATGATAISGLDLLPVSINVWRCFLQLIGGLGIMLLVVAVLPLLGLGGMQLYRAETPGPMK DTKFTPRIAETARGLWGVYAFFAGACMLAYRWAGMSWADAFMHMCTTMGLGGLSPYDASIGHFDSARVEWVATAFMTMAGISFLR YFVMIKRRSLRPIIGDREIRTYLMVLASAIAVVTLLLLVHGVYTDVGTALRSAAFHVVSVATTTGYASADYAQWPVFAPVLLIFLGCFASC AGSTGGGIKMVRMVLLIKQARRELVRIIHPRVVNPVTLAGGVVPPQVMNAVFGFMLIYGAATVGLTMALLLSGLDVVTAFSAVIATVNNI GPGLGLVGPSSNYGVLNDGQIWVLSFAMVLGRLEFLTVLVLFTGQFWRK
7.8E-58	206	33.3	1.1E-57	205.1	23.1	1.1	1	D3FWF9_BACPE	K+-transporter KtrD	ktrD BpOF4_03125	Bacillus pseudofirmus (strain OF4)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus pseudofirmus, Bacillus pseudofirmus (strain OF4)	398511	>tr|D3FWF9|D3FWF9_BACPE K+-transporter KtrD OS=Bacillus pseudofirmus (strain OF4) GN=ktrD PE=4 SV=1MKLGLSQFLSPFRVIIISYIVAMIVFSILLYLPISHKEGVDLTFSEALFTSVSAVSVTGLTVVNVSETYSYIGVFFLALAIQLGGIGIMT LGTFVWMLFGKKINLSQRMLIMVDQNQNKFSGLVNLMRGILFVALIIELIGALILGTYYIRYFDTVGEAFYQGAFASLSAFTNAGFDVTG QSLIPFANDYYVQLVVILLIFAGAIGFPVLMELKEYFSKDNPHFKFSLFTKITTTTYFAVFIIGVIGIWALETGSYYVGLEWHQQLFYSIFN SATTRSGGLATMDVSELNMATLLFMSALMIIGASPSSVGGGIRTTTIAVMFLTIKSFALGKDDVKVFGREIHPEDRQKAFIVLSVFLVML FAAVTLIVAFESQNDITLLAIIFETASAFGTCGLSMGITPDLSLPSQFVLMVLMFIGRVGLIAFLFSIRRRETKSHFKYPTERIIIG
8E-58	206	16.3	3.3E-57	203.5	11.3	1.8	1	I5B1U3_9DELT	Trk system potassium uptake protein	DespoDRAFT_01520	Desulfobacter postgatei 2ac9	483	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfobacter, Desulfobacter postgatei, Desulfobacter postgatei 2ac9	879212	>tr|I5B1U3|I5B1U3_9DELT Trk system potassium uptake protein OS=Desulfobacter postgatei 2ac9 GN=DespoDRAFT_01520 PE=3 SV=1MRWPFIIRIIGVLLFVLGLCMTLPLGCSLFFKDGAHQGHLTAMAVTTIMGAIMVVISKKAGNHDYINQREGIAVVALGWLGIGLFG ALPFFLAPDFSTYTDAFFESVSGFTTTGSSVMTNIEGAAPSLLLWRSLIQWLGGMGIIVLSLAILPFLGVGGIQLYKAEVPSPVPDKLTP RLSDSAKILWIVYAGMTLLLILFLYFGGMNLFESVCHALTTLPTGGFSPKNLSIAHYDSAYFDYTITIFMLLAGINFSLHYQILRGNGLAF WKDAECRFFLYTVLVGTLIITLNTWGPVYDNFSKAFRFAIFQVVSIVTTTGYATADYELFPGLSQVLLFFGMFIGASAGSTGGGMKCAR IMVCIKYCYRELFKLIHPRSVSHIKLNNALIPEELLRSILGFIALYILIFVMATTLLSALGVDLLTSLGAVASCIGNIGPGFGTVGPVENFAHL PQAGKWLLSWCMLAGRLEIYTVIIILLVPEFWKQ
8.2E-58	206	21.2	1E-57	205.2	14.7	1	1	R6XPC6_9FIRM	Uncharacterized protein	BN605_01566	Dorea sp. CAG:317	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea sp. CAG:317	1262873	>tr|R6XPC6|R6XPC6_9FIRM Uncharacterized protein OS=Dorea sp. CAG:317 GN=BN605_01566 PE=4 SV=1MVGQKKKNIRWNTMGILAGGFLGVILLGGVLLWMPFSNRQPIEFMDALFTSVSAVCVTGLVTITPAFQFTLAGQMILLVLIQIGGL GVIACVTAFFLLLRRKITLKERIVIQETYNMDKLSGMVLLVRGVLFGTFAVEGVGAALYAIQFIPEYGVAKGIWYSIFHAVSAFCNAGIDIL GDSSLTAYVTNPIVNLTTMILIILSGLGFTVWFDIIANGKKLIRREMPRRWWFTRLKLQSKLAIIMTILLISGAVFVFLAEYDNPETLGNLS LGNKVMASFFQSVTNRTAGFATISQNALHTESKLFHCILMFIGGSPGGTAGGVKTTTIAMLFLACLTFVRGGNDTECMGKKISVENFR TGFCVVMAAFSVFTVGTIAILIIEPDTVPLVNVLYETASAIGTVGLTADLTPHLARASQVVVLMLMMYAGRLGPMTLVLLFAGKMHPRDKI RKLPEERIMVG
8.5E-58	205	30.3	1.4E-57	204.8	21	1.3	1	A0A085L819_9FIRM	ATP synthase subunit J	DK28_00211935	Peptococcaceae bacterium SCADC1_2_3	456	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium SCADC1_2_3	1487582	>tr|A0A085L819|A0A085L819_9FIRM ATP synthase subunit J OS=Peptococcaceae bacterium SCADC1_2_3 GN=DK28_00211935 PE=4 SV=1MLRTGYKQFLLSKWKKIISLRLNPPQILVLGFAVLILAGALLLFLPHASRTGQYTSFLTALFTATSAVCVTGLVVVDTGTYWSTFG QVVILFLIQIGGLGFMTMATFFFILMGRYIGLRERLLIQESLNQLSLAGVVRLARAVLIFTFFTEGFFACILALRWVFDYGWSTGWWFGL FHAVSAFNNAGFDLFGHFRSLTAYTSDATVTFSVTTLIILGGIGFAVVAEIFKNNRKKYISVHTRLVFLSTVLLIGSGMFFFALLEWHGVL AELSWPGKLLASYFQAVTPRTAYGNTVEIGQLRAATQFFLILLMFIGASPGSTGGGIKTTTFSLLVLSVLSLVRGKEEVEVFRRRLPAQ QVYKALAILFLAAIIIITITLILSIIEKADFLALLFETTSAFGTVGLSTGITPHLSAAGRILIILTMFIGRLGPLTLTFALAQRRQKVSLRYPEEKI MIG
8.6E-58	205	10	3.2E-57	203.6	7	1.7	1	G2MHT9_9ARCH	Cation transporter	Halar_3295	halophilic archaeon DL31	515	cellular organisms, Archaea, unclassified Archaea, unclassified Archaea (miscellaneous), halophilic archaeon DL31	756883	>tr|G2MHT9|G2MHT9_9ARCH Cation transporter OS=halophilic archaeon DL31 GN=Halar_3295 PE=4 SV=1MARSLSTYVDYRTSLAYVGTTLKYIGVTTLFPLVLALYYGEALLPFVATGVVMGGGGALLERLRRGGELGNREGFLLVSLAWLV VPLAGTVPYLVAGTGTVAHPVNALFESMSGFTTTGATVLGEISVERHGHAMLMWRQLTQWLGGMGILVLMVAILPQLSIGGAQVIRE EAPSLQLEKLTPRIQETARVLWSVYAGFTVLAALVYYGLHLAGVAPTMDLYNAVAHALTTLPTGGFSPQARSAEAFAPSIQWAMMPF MLVAGTNFALFWHVLQGNPRRLTSNTEFRAYLLAITGLGAVISALLFLGVGLAEAPTAIDVIPGNLENSLRQGLFQVIAIVTTTGYASMD FNTWDQSTQTILLFAFFLGGSAGSAAGSIKIVRWVLVLKRAVGRSLFMSVHPEAVRPVRLADGIVDDDILRDVFVLVTVFFSLFALSTALL YLDSLWTPGLSLTGLEAMSVAAATLGNVGPGFGPVGPMNSFLAFSSPGKLYMVFLMWVGRLEVLSVLVVFTPAFWRR
8.7E-58	205	39.6	4E-56	199.9	27.5	2	1	A0A0B4S3K1_9FIRM	ATP synthase subunit J	NW74_01970	Parvimonas micra	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptoniphilaceae, Parvimonas, Parvimonas micra	33033	>tr|A0A0B4S3K1|A0A0B4S3K1_9FIRM ATP synthase subunit J OS=Parvimonas micra GN=NW74_01970 PE=4 SV=1MRQLKDKLETNPPAVLTLGFFLIITIGSILLFLPFSSKNLNFTNFLDCVFISTSSVCVTGLSTINITNEFNFFGKTVIMLLIQMGGLGF MTMATMVAMILGEKITLKDRLVIREQMGSTKLSGMVKLIRYVIFSTFLIEGLGAILLSFTFVPKFGLKGIFYSIFHSISAFCNAGFDILGENS LEGFNTNPYLLFVISFLIILGGLGFHVYIDINNFKFNFRKYSLHTKIVLVMTLGLLIFGTIAFFILEYSNAKTLKNFNFFDKITNSFFQSVTTR TAGFASINQTGFTESSTILTVFLMFIGGSPASTAGGIKTTTIFLLIVTTISFIQNNNEIEVFKRRISFSLVKRAIGIFVISLLLVNTVVFVLTLIE DVQFIDLLFETISAFATVGLSKDLTPHLKDITKVFIIILMFIGRVGPLTIIFSFYNKVNRKKFKYSNGNVIVG

8.8E-58	205	14.7	3.7E-57	203.4	10.2	1.7	1	Q11I12_CHESB	Trk system potassium uptake protein	Meso_1567	Chelativorans sp. (strain BNC1)	510	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Chelativorans, Chelativorans sp. (strain BNC1)	266779	>tr|Q11I12|Q11I12_CHESB Trk system potassium uptake protein OS=Chelativorans sp. (strain BNC1) GN=Meso_1567 PE=3 SV=1MLELKEHGERRELRPKPSINLETIQVHGAIIRAAAYVASIFSIYIAGAMLIPAAVDLYYGHSDWQVFAVCAFTTGAIALTVAAATRD RTPVRSTRLAFIVVVVLWSTLGIVGALPLYAASLKLDFADAVFESVSAITTTGSTVVVGLDTLPPGVLLWRSLLQWMGGLGVVVLGLFL LPMLNVGGFSYFRIESSDIEDRPFERLKSFLRALIGVYVFLTGVCAIAYAAAGMSTFDAINHAMTTLATGGISTHDASFGFFEDNNVLLW VSTIFMILGALPFSILILFVVQGRLDALRDPQIRVFLGYLVVIVLALAVQRRIADDVPFAEAVTTAAFNITSIVSTTGFASEDYTLWGPFAVT IAFFATFLGGCSGSTTGGIKAYRFFILGRMLRNELRILIYGSSVQPLRYGNRAVDAEMQRSIVLFFIAYIALWTAGTIALAASNLDLVTAA SSMLTAISNVGPGIGPIVGPAGNFLPLSDYAKWVLIVAMLLGRLEIFAVLVVFTPTFWRA
9E-58	205	33	1.2E-57	205	22.9	1	1	B3ET40_AMOA5	Uncharacterized protein	Aasi_1044	Amoebophilus asiaticus (strain 5a2)	447	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Amoebophilaceae, Candidatus Amoebophilus, Candidatus Amoebophilus asiaticus, Amoebophilus asiaticus (strain 5a2)	452471	>tr|B3ET40|B3ET40_AMOA5 Uncharacterized protein OS=Amoebophilus asiaticus (strain 5a2) GN=Aasi_1044 PE=4 SV=1MQLGLKNHSMTPQQVLIIGFSIVILSGTTLLFLPISSATQTSIGWINALFTATSAVSLTGLTVIDIGTNFSVFGQLIILLLIQLGGLGFM MFGVMFSLLLGKRITLKDRLLLQEATKSFSTQGIVKLAMHIILITFILEAFFAFILMLCWSSTLGWKTATYQAIFHAISAFNNSGMSLYPNS LQAYLGAPLVNICITTLSMIGGIGFTVLLDIYYNRSWRKLSLHSKLILLTSCILILVSFIVILSVEINNPATLEQLSWGKRIGAAWFQAIAPRS SGFSTLATPTLLPPSLFFIMLLMFIGAGTGSTGGGIKINTFAVAIMTIVNLLKGNKDVNILKRRIDNQVAMHSVAIILLACSSITLITWLLLFL EGTSKHNYMAVLFEVVAAFGTAGLSMGVTSALSTIGKILLIAAMFIGKVGPLTFAFALTAGAVERRIRYPEDKVLIG
9E-58	205	29	1.2E-57	204.9	20.1	1.1	1	A0A060LTC8_9BACI	Cation transporter	BleG1_0779	Bacillus lehensis G1	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus lehensis, Bacillus lehensis G1	1246626	>tr|A0A060LTC8|A0A060LTC8_9BACI Cation transporter OS=Bacillus lehensis G1 GN=BleG1_0779 PE=4 SV=1MNRKKSNPFRVILFAYLLSMFVFSVLFYLPMFHEPGVSLTYRDALFTSVSAVSVTGLVTINVVETFNWGGILILSLAIQLGGIGIMT LATFAWMMLGRRINLSQRLLIIVDQNRVQNQFSGLVRLMSSLIVIALCIEGAGALILGTYYLRFFDEPFEAYLQGAFASLSAFTNAGFDV TGQSLAPFVDDYFVQCITILLVFAGSIGFPVILECIEYIKSRKRTFKFSLFTKLTTTTYFLVFVIGAFGIWFLERDLAFATLSWHEQLAQAV FFSATTRSAGLSTVDLAAFHIPVLLFMSLLMMIGASPSSVGGGIRTTTLAVMALTLRSFAMGKKHVHVFGRRIHEEDQQKSFVVLSIFT GLLFLAILLIMTFEQDTPVTLLQVLVETASAFGTCGLSLGITSDLSLPSQVVLMVLMVIGRVGIIAVLFSFKGDRKGEQYQYSTERILIG
9.3E-58	205	19.3	2E-57	204.2	13.4	1.4	1	R7PAM1_9BACT	TrkH family potassium uptake protein	BN736_01119	Prevotella sp. CAG:617	486	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:617	1262933	>tr|R7PAM1|R7PAM1_9BACT TrkH family potassium uptake protein OS=Prevotella sp. CAG:617 GN=BN736_01119 PE=4 SV=1MINGRVICKVLAKLLFLEAFLLLISWGVGILYHENVHAVYGFPMLIAVGLGGLLRLIGLRSDNQVNRRDGYVIVLLTWLSFSLIGML PFLFGHYVNCGVVDACFEAISGFTTTGATILTNIDTLPRSILFWRSLTHWIGGLGIVIFTIAFLPSLGSNNLKLFTAESTGMSQDRIHPRV STTARWLWMVYLMLTAACTLSLWIAGMSFFDAINHAFSTLATGGFSTHQDSILYFKSPLIEYLIVFMFLGSINFTLFYLSLFKRQWKDL FRDEELRFYACLLGGVTLIITLILIFVQGQAVEMAFRHTLFTLLSFESTTGFITCDYMLWPPMVWILMLLLMAVGGCAGSTAGGLKCVRL LSFYKILQSEFKIMLHPKAVVPPCVNHTPLPLPVIQRLLAFVFAYMVIILVGTFFIASQGVPLLDALSIAMSTFSNAGPTVGHELGAYDSM AVLPDSVKWACCGIMLLGRLEIFSLILPLTPAFWRKD
9.3E-58	205	33.6	1E-56	201.9	23.3	1.9	1	C6RR33_ACIRA	Potassium uptake protein, TrkH family	ACIRA0001_1834	Acinetobacter radioresistens SK82	448	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter radioresistens, Acinetobacter radioresistens SK82	596318	>tr|C6RR33|C6RR33_ACIRA Potassium uptake protein, TrkH family OS=Acinetobacter radioresistens SK82 GN=ACIRA0001_1834 PE=4 SV=1MHFPNFRHLTQRTVNLSPPTLLALGFLSFILVGTLLLRLPISHHGHLSWMDALFTATSAVTITGLSTISVHDSLTGFGQTVLLLLIQS GGLGFMTFAILAALSLSPKVRLRQQMMAQTATGQTNLSKVTFVAKGVFFYTLFFELIGTVILTVLFTPEYGFPTSLHYAIFYSISSFNNA GFSIFGDSLMSFEGQYLVYLVISLLYIIGGIGFIVLMDIKRSKSWSKLSANSKLVLSSIAIINLLAFIVIWMLEATNYQTLGQLNLGEQAVHA WFQATAPRSSGLNTIDTGSMTSTSTLVVMLLMFIGGGSLSTAGGIKVGTFVVLLLSVISFLRRNEEVRAFNHSISQETTVKALAVAMITC ILIFGGFFLILLLEPRQNFLDLLFEIVSAACTVGLSRGITSELSPGSLMILIFLMYAGRLGPLTLAYLIATPKKSRLKHPPTDIQIG
9.3E-58	205	30.6	1.4E-57	204.7	21.2	1.2	1	A0A024P2C5_9BACI	Ktr system potassium uptake protein B	ktrB_1BN983_00632	Halobacillus karajensis	453	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Halobacillus, Halobacillus karajensis	195088	>tr|A0A024P2C5|A0A024P2C5_9BACI Ktr system potassium uptake protein B OS=Halobacillus karajensis GN=ktrB_1 PE=4 SV=1MWVRRKSLMWLNDLSPFQLIALYYMVAVTIASILIALPVAHRDGVDLAFIDVLFTAVSAVSVTGLTTVPTAETFSTTGYFIIAIVLQF GGIGIMTLGTMIWLMLGKKIGLKERRLIMTDQNQTTFQGMVRLVKQIILVVLMIEFIGFLVLGTYFLQYYEPGEAYLQGFFGTISAMTNG GFDITGESLIPFRDDYFVQFINIVLIAGAIGFPVLIEVKQYLWQNQEEKTIRFSLFAKLTTITFFALVLFGTLMIIILENNHFFAGRSWHEILF YALFQSVTTRSGGLATLDINQFTEQTQLFMSSLMFIGASPSSVGGGIRTTTFALVVIFVLTFARGGQNIRIFRREIHPEDLNKAVVVTMV ALFLCFIAVITLSIIEPFTLNEIVFEVCSAFGTVGLSMGITPGLSTFGKIILMLLMFLGRIGLLTFLFSFNKHDKARVNYHYPRERIIIG
9.4E-58	205	42	2.5E-57	203.9	29.1	1.6	1	D1AYP3_STRM9	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Smon_0953	Streptobacillus moniliformis (strain ATCC 14647 / DSM 12112 / NCTC 10651 / 9901)	442	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Leptotrichiaceae, Streptobacillus, Streptobacillus moniliformis, Streptobacillus moniliformis (strain ATCC 14647 / DSM 12112 / NCTC 10651 / 9901)	519441	>tr|D1AYP3|D1AYP3_STRM9 Potassium uptake protein, TrkH family OS=Streptobacillus moniliformis (strain ATCC 14647 / DSM 12112 / NCTC 10651 / 9901) GN=Smon_0953 PE=4 SV=1MEKKISPYILILISFIFIIVIGASLLTLSISLKSGVKISFFEALFTATSAVTVTGLTILDVSKTFNRFGNIIILILQLGGLGILTFSSLIVLIVS KKIGYYTKKIVKEDLNFEDKFDIYLYMKKVAMVVFGIELLGAIFLLSDFLKEYSIGEAIFYSIFHSISAFCNAGFSLFSNNFEGFVDNVYVNI IIAFLIFTGGVGFAAIIDIYEYIQGRGKRLTINTKFSLYITVSLLFIGAILFFTFEYTNSGSIGEMSFLKKILASFFQSVSLRTAGFNTVNLNNL RIPTVLVSCILMFIGASSGSTGGGIKTNTVGIIFLGIKASIKNREEIVFSRRRISFKAFNKAVALLFIALSYLFVIFLLMSIFESDKDLVKVLFE LISAMGTVGLSMGITSSLTIYSKMLIIITMFLGRVGLLTVVLALSRSGEKGKYIYPEGNILIG
9.8E-58	205	11.2	4.3E-57	203.1	7.8	1.8	1	F5XW81_RAMTT	Trk system potassium uptake protein	trkG Rta_05740	Ramlibacter tataouinensis (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310)	486	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Ramlibacter, Ramlibacter tataouinensis, Ramlibacter tataouinensis (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310)	365046	>tr|F5XW81|F5XW81_RAMTT Trk system potassium uptake protein OS=Ramlibacter tataouinensis (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310) GN=trkG PE=3 SV=1MHSLGPVLAVVARVLAGFSFAFLVPLAWAWVLDEPWLRPVWAGAFAGTLVAGLVLGWIVRHARRELQPKDGFLLVTLVWVAL PACSAIPLYLAVPGIDLAHSYFESMSALTATGATALSGLDALPVSVNVWRCFLQFVGGLGIILLVVAVLPLLGLGGVQLYRAEAPGPLKD AKLTPRIAETARGLWTVYFVLSAACFLAYRWAGMGWADAFMHMCSTMGLGGFSSHDASFGYWNSPLIEGVAIVFMALSGISFARYFI VWRNRSAATLVRDQEVRAYVTLLLLSIALLTWLLVDRAVYDGTAAALRAAAFQVVVSLATTTGYASTDYTQWPVFAPVLLIFLGCFVSC AGSTGGGIKLVRMILLVKQARRELVRIIHPRVVNPVTLGGATVPPQVIANVLAYMLIYGASIVGLTFLLLLSGLELVTAFSAVIVCVNNIGP GLGLVGPAGHFGVLTDFQLWVLSFAMLLGRLELMSVLVLFTVPFWRK
1E-57	205	16.9	3.1E-56	200.3	11.7	2	1	R7AHZ4_9CLOT	Trk-type K+ transport systems membrane components	BN593_01807	Clostridium sp. CAG:299	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:299	1262792	>tr|R7AHZ4|R7AHZ4_9CLOT Trk-type K+ transport systems membrane components OS=Clostridium sp. CAG:299 GN=BN593_01807 PE=4 SV=1MNYAMIAYVIGWILNCEGFLMLLPCLTAVIYQETAGFSFAAAMALCFLFGVPLTVRKPKNMVFYTKEGFVSVSLSWIVLSVMGSL PFLFSGSITNPVDALFETVSGFTTTGASILSDVEALPRCILFWRSFTHWIGGMGVLVFILSLLPLTGGYHMNLMKAESPGPSVEKLVPKI QSTAKILYSIYVAMTILEVLLLLAGNMPLFDALTTTFGTAGTGGFGIKNDSMASYSPYLQNVVTVFMILFGINFNFYFLLLMRKPKKAMK NKEVRCYLAIIAITISIITFNIRGLYPSIMEAFQQAAFQVGSIITTTGFATTDFNTWPQVSRTILVMLMFVGACAGSTGGGIKVSRFVILLKT VNKELHLFLHPKGVRKISMDGKVVEHEVVRSINVFMTAYVLVFAFSILLVGFDNHDLITNFTAVAATLNNIGPGLELVGPSQNFGLFSDP AKCVLIFDMLAGRLELFPLLLLFVKDTWKRF

1E-57	205	32.2	1.4E-57	204.7	22.3	1.1	1	Q4L531_STAHJ	Staphylococcus haemolyticus JCSC1435 DNA, complete genome	SH1935	Staphylococcus haemolyticus (strain JCSC1435)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus haemolyticus, Staphylococcus haemolyticus (strain JCSC1435)	279808	>tr|Q4L531|Q4L531_STAHJ Staphylococcus haemolyticus JCSC1435 DNA, complete genome OS=Staphylococcus haemolyticus (strain JCSC1435) GN=SH1935 PE=4 SV=1MSIFSKLLKKSSPQQGIVLYYLIAIVVAFLLLNLPFVHKHGVDVSPIDTLFVAVSGISVTGLSPVNIVDTYSTFGQIIILIILNIGGIGVM AIGTVLWVVLGKHIGIRERQLIMLDNNKDTMSGTVKLILEIIKTILTIEFIGALLLAFYFYRDNPDLKNALMQGLFVSVSATTNGGLDITGQS LIPYAKDYFVQTIVMFLIVLGSIGFPVLLEIRAYVRNRVSHFRFSLFTKITTCTYLFLFVFGVLAILALEHHHAFKGLSWHQSLFYSLFQSA TTRSAGLQTIDVTNFSDATNVIMSILMFIGSSPSSVGGGIRTTTFAILILFVINFNNNAEKTAIKVFNREIHVVDIQRSFAVFTMASILTFVS MIVILATEKTNLTFLQVFFEVMSAFGTCGLSLGVTDDISGLTKVILMILMFIGRVGLISFIIMIAGRKEPDKYHYPKERVQIG
1E-57	205	21.4	1E-56	201.9	14.8	2	1	R6FDY5_9BACE	TrkH family potassium uptake protein	BN744_02591	Bacteroides sp. CAG:633	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:633	1262744	>tr|R6FDY5|R6FDY5_9BACE TrkH family potassium uptake protein OS=Bacteroides sp. CAG:633 GN=BN744_02591 PE=4 SV=1MVNFKTITRIIGILLLLETAMLLACSGISLYYQDEALTDFWKSAGIAAGVGILMVLLGKGSDGVLTRRDGYVLVSLAWIAFSFFGML PFYISGYIPDITNAFFETMSGFTSTGATILDNIESLPHGLLFWRSMTQWIGGLGIIMFTIAVLPIFGVSGLQVFAAEASGPTHDKVHPRIGI TAKWIWSVVTGITATLVGLLMLGGMSWFDSICHAFATTGTGGFSTKQASIAYYHSPYIEYVISTFMFISGINFTLLLLLVNRKFKKAFHD VELKWYFWSVILFTGIIATILYYTSPMDAEEAFRKSLFQVTSLHTSTGFATDDYMLWPSVTWGLLTIVMVIGACAGSTTGGLKCIRLVIL SKVSKNEFKHILHPNAVLPVRINKQVLSTSIVSTVLAFSFLYLVIIIISILLMMAMGVGFEESIGCVISSIGNMGPGLGDTGPAYSWNALPD AAKWLLSLLMLLGRLELFTVLLLFTPDFWKKN
1.1E-57	205	28.4	1.6E-57	204.6	19.7	1.1	1	Q831F3_ENTFA	Cation transporter	EF_2558	Enterococcus faecalis (strain ATCC 700802 / V583)	471	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus faecalis (Streptococcus faecalis), Enterococcus faecalis (strain ATCC 700802 / V583)	226185	>tr|Q831F3|Q831F3_ENTFA Cation transporter OS=Enterococcus faecalis (strain ATCC 700802 / V583) GN=EF_2558 PE=4 SV=1MNHTRLLWLAQRKSDRFIRKNFSSIQIIVAYYILMTVISYLLFCLPIFREPDSHVPFIDLFFLAISTVSVTGLTTVDINSVFNDRGIVLL EVLFQVGGLGIMMISTVFFILSKRRITLKQRQLIMTDMNQPRLSGIVRLIRTTFLILIWFQVIFGSLFSLYFYISGYYTNWRDAIFYGFYQAI SAVTNSGFDISGDSIIPFAHDYLFLLAIMFLIFIGGIGFPVLLEIHEWLHFKKKNFRKKKRGLPFRFSLFSKIALLAFIVLFIGGTILIYLLEKD HLFLTMNESGRWVSSMFYSMTTRNAGLQINDLGDFQITTLIIFSVLMFIGCSPSSVGGGVRTTTVAIIGLYLLAFLKSEDDISVFSRKIDD DDVKKSIVVFMLSLIMCFFAVVFLSATENLPLISIIVEVASAFGTTGLSLGITDDLTTVGKLMIALLMFIGRIGMLYTLMIFVPKETRDLGYE YPSEKIIIG
1.1E-57	205	12	2.2E-40	148	3	3.4	3	D8SAE4_SELML	Sodium transporter	HKT1 SELMODRAFT_449866	Selaginella moellendorffii (Spikemoss)	533	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8SAE4|D8SAE4_SELML Sodium transporter OS=Selaginella moellendorffii GN=HKT1 PE=4 SV=1MDVSAVLRRLAKKRPSYYHLHVLYFVGLSLLGALLLRSFGTRKGSTHNHFSFLDCFYTAVSAMCLSGLSSIQIEDIPASGQVLVM VLMVLGGQVLLSVVPLLVKKHRYCKIARMALRPRVKSNSLFKSLYRTLCLRSNDDLWMESLASRPNLPEPFKVVFLEHQAICHLADIVV WYLLAVHLLGFVVAWISIQCSLNTKSVLESKTINPGFFALFATISAFNNIGFVLTNENLVAFNTNSVLLLDLGLVILLGNTLFPVALRGILW LLYRYTTGTKKEVYTLLLEHPRKYYLHLFPKTATLWLLLAVTGSNALGGLIFCALDWNNEALDGLRPGEKLVNGLFQSFSTRSGGMNS LNLVELSQATLFFYCVMMYIKPYPVSLREEQSREDDTTLLTQSRRNLANDNTFLFLLVIFSSISLNSQMEKDPRNFNLFAILFEVASAYG CVGLTLGYSCNLRLQPGHCKDTTLSFSGTWNAPGKMFIIAVMFIGRHRDLPYHIDSTTDMEKITRLSRRPSFIALTQPPVVVPESTPPV
1.1E-57	205	9.9	4.2E-56	199.8	6.9	2.1	1	Q5P4Q3_AROAE	Trk system potassium uptake protein	ebA2824	Aromatoleum aromaticum (strain EbN1) (Azoarcus sp. (strain EbN1))	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Aromatoleum, Aromatoleum aromaticum, Aromatoleum aromaticum (strain EbN1) (Azoarcus sp. (strain EbN1))	76114	>tr|Q5P4Q3|Q5P4Q3_AROAE Trk system potassium uptake protein OS=Aromatoleum aromaticum (strain EbN1) GN=ebA2824 PE=3 SV=1MRSYFPVLSALGLIVTMFGVLMGFPLAVSFFLDDGATRAFDHAVLLTCAVGVVLLALTRRVKRDLKPSDGFLLVALTWVVTPVF GAIPLFGYVPGLSVIDAYFEAVSGLTATGATILSGLDRMPISINLWRTFMHWIGGMGVIVLVVAILPLLGIGGRQLFRAEVPTPMKESSL TPRITETAKGLWTAYILLTAACGLSLWLAGLDGWEALIHAFSVTGLGGFSSKDASLGHFNSVPVEMVAITFALLAGLNYATHYLALVRR SARPYLSDPELPFYFGVLLASVAVLTAYLMSVEAHAGFLNTLRYVAFHVVSMSTSLGLTIYDYTLWPMFAQMWILFLGSFIACSGSAG GGMKMMRAIILYKQVYREIVRSLHPNAVHPVRLGSQPVSEDILHAVLGFSFMYMVSIVALTLVLTATGLDIITAFSGVVACLNNTGPGLG AIGPASNYAGLNDFQTATLAFTMILGRLEIFTLLVVLTPVFWRR
1.2E-57	205	30.5	1.5E-57	204.6	21.1	1.1	1	K9YGT5_HALP7	Potassium uptake protein, TrkH family (EC 3.6.3.14)	PCC7418_3572	Halothece sp. (strain PCC 7418) (Synechococcus sp. (strain PCC 7418))	446	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Halothece cluster, Halothece, Halothece sp. (strain PCC 7418) (Synechococcus sp. (strain PCC 7418))	65093	>tr|K9YGT5|K9YGT5_HALP7 Potassium uptake protein, TrkH family OS=Halothece sp. (strain PCC 7418) GN=PCC7418_3572 PE=4 SV=1MSIARTICLGFIAVILIGTLLLILPFTTADGSWNDPITALFTATSAVCVTGLAVVDTGTYFSFWGQLTILLLIQVGGLGYMTTNTFLLF LIRKKFDFRQKVAIQESFDRPFLQGSTNLLISIVATTLLFELTGFFFLLPLFSDQPNPTWLALFHSISAWNNAGFSLFSNSLMDYQSSISM NIIIPFLVIFGGLGYQAIFEIFLWIRQQFNQLILRKNAEAFDFSLNSKIVIDTTIILILGTIAFFFTDFSNNNIFGYFSFKDRLLGAWFQSVTT RTAGFNTVPLETMTDAGLFITIAFMVIGASPSGTGGGLKTTTLRILINGTISTLQGKTDVIIYKRRVPVNLILKALGVLCASVTLLSLVTALIA ITDPALSFIQIFFEVCSAFATVGLSTGITSSLSPLGKLIIVVTMYIGRVGVLIVINTLVRESRPSAIQYPEENLLVG
1.2E-57	205	28.9	1.8E-57	204.3	20	1.3	1	K9WXC6_9NOST	Potassium uptake protein, TrkH family	Cylst_2831	Cylindrospermum stagnale PCC 7417	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Cylindrospermum, Cylindrospermum stagnale, Cylindrospermum stagnale PCC 7417	56107	>tr|K9WXC6|K9WXC6_9NOST Potassium uptake protein, TrkH family OS=Cylindrospermum stagnale PCC 7417 GN=Cylst_2831 PE=4 SV=1MTAARTIILGFLAVILAGTILLMMPFSTSEGTWNDPIVALFTSTSAVCVTGLSVVDPGTYFSFWGQFFIALLAQVGGLGYMTTTTF LILLIGRKFDMRQKIAIQQALDRPGMSGSTQVIRSIIATTVIFEITGVLLLLPAFVPDYGWSQGLWLAIFHSVNAWNNAGFSLFKDNLIGY QSSALVVFTITGLIIFGGIGYQVILEMYLWLRDRFLKKSSCVILSLNFKVGVSTTILLLFIGTIAFFCIERRNPETFGNLSLRDQWLVAWFQ SVTPRTAGFNTIDNGKMTTAGLFITIALMFIGANPGGTGGGIKTTTLRVLTSCTKAILQGKEEVLLYDRKIAISLILKAVGVLVGSIATVILS TILIALTDPELDFIQILFEVMSAFATVGLSTGITASISTAAKLILIATMYIGRVGVLLLMSSLLGDPRPTRIHYPEENLLVG
1.2E-57	205	15.1	8.5E-57	202.2	10.4	1.8	1	I0HDJ1_ACTM4	Putative cation transporter	AMIS_58580	Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes missouriensis, Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	512565	>tr|I0HDJ1|I0HDJ1_ACTM4 Putative cation transporter OS=Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431) GN=AMIS_58580 PE=4 SV=1MRSPWQHPARIVPLAFLGAIAVGTALMMLPAARAEPGHAPLVTALFTAASAVCVTGLSVVDTPTYWSTFGHVLLTVLSQIGGFG IMTLATLLSLLVSRRLGLRGRLMAQAESAGLSGGNIAAVLRRVALVMVICEGAIAVVLTLRFWLGYGYPPGRALWYAVFHAVQAFNNA GFALYPDSLVRFVTDPWICLPLAFGVLAGSIGFPVLFELAREWRTPKCWSTHTFLTVAGSLLLTVFGFLTFLIFEWRNPGTLGPLGTPA KVLTAFTQDIMTRSGGFNTVDLGQLNSETIATTTGLMFIGGGSASTAGGIKLTTFLLLAYVIWAEIRGEPDVVVRNRRIAEETQRQAITV ALMGVALVATGTVVLDALTEDIPFDRVLFEVTSAFATVGLSTGVTGSLPASAQVVLVVLMFVGRVGTIAVGTAIALNTRRRLYRYPEER PLVG

1.2E-57	205	34.6	1.9E-57	204.3	24	1.3	1	Q81G88_BACCR	Potassium uptake protein KtrB	BC_1320	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	226900	>tr|Q81G88|Q81G88_BACCR Potassium uptake protein KtrB OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) GN=BC_1320 PE=4 SV=1MRDIKKFLQKLRPVQLIVLFYLLAVVVSVILLSLPFVTKPGVKWTFIDALFTSVSAVSVTGLSVITISDTFTTAGIIVLALILQLGGLGI MALGTFVWIITGKKIGLQRRRLIMADHNQGNLSGLVELMRSILIVIISIELIGAILLGTRFLLYFPTWQEAYFHGFFAAVSATTNGGFDLTG QSLIPYKKDYIVQMIHMLLIILGAIGFPVLMEVKQFLSKRRQQLFRFSLFTKLTTTTFFALVVVGTIMIFLLERNHFLVGKSWHETVFYTLF QSVTTRSGGLATMDIRELSQPTLLFMSILMFIGASPSSVGGGIRTTTFAVSILSLYTFARGGRTVRVFKRQLHEEDVLKASVVMTMGILL CATALFILSITENVPLMSLIVEVCSAFGTTGLSTGVTPDLTTVGKLVLIVLMFIGRVGILTFILASGGREQPPRYKYPKERIIIG
1.2E-57	205	24.2	1.8E-57	204.4	16.7	1.1	1	B0TEV5_HELMI	K+ uptake transporter trkh family protein	trkH HM1_1792	Heliobacterium modesticaldum (strain ATCC 51547 / Ice1)	459	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Heliobacteriaceae, Heliobacterium, Heliobacterium modesticaldum, Heliobacterium modesticaldum (strain ATCC 51547 / Ice1)	498761	>tr|B0TEV5|B0TEV5_HELMI K+ uptake transporter trkH family protein OS=Heliobacterium modesticaldum (strain ATCC 51547 / Ice1) GN=trkH PE=4 SV=1MYRYEPPRPIFAPYVQGKRPAHGLSPARVLVAGFALIILIGGFLLSTPMASRSGLGTRFVDALFTATSAVCVTGLVVVDTHDNFS LFGQLIIITLIQVGGIGFMTMATLIYLLMGKRINLKERLLMQEALNSLSVQGVVRLARHVLLATFLIEGIGGVILSMRFIPEMGLAKGLYYGF FHAISAFCNAGFDLFGGFRGITGYVDDPIVNVTVSILIIIGGLGFTVIAETFRYREIRRFLSLHTKLVWMMTVILILLAATAIFFLEFNNPKTLG ALGWEGKLLAAYFQGVTPRTAGYNTVSIADLKPATQFFLIILMFIGASPGSTGGGIKTTTLASLLAAVWSMRQGKIDVGFFERRIPPDTI YKAVGITVMAVLLVVTVTMLLTITENADFLALLFEATSAFGTVGLTMAVTPNLSDFGRMLIALTMFIGRLGPLTLAVALSSNVPAKLRYPE EKIMVG
1.3E-57	205	29.9	1.3E-57	204.9	20.7	1.5	1	V5XTF0_ENTMU	Trk family potassium (K+) transporter, membraneprotein	trkG EMQU_2362	Enterococcus mundtii QU 25	466	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus mundtii, Enterococcus mundtii QU 25	1300150	>tr|V5XTF0|V5XTF0_ENTMU Trk family potassium (K+) transporter, membraneprotein OS=Enterococcus mundtii QU 25 GN=trkG PE=4 SV=1MQLNLFFRKWRRRSARYVSSHFSSIQIIVFYYILMTMISLGLFYIPFFRNPGSHASFIDMLFMAISTISVTGLSTFDIHAIFNNNGIILL EVLFQVGGLGIMMISTAFIIFSKRRITLRQRQLIMTDMNQPRLSGIVRLIRITFVILLWFQLLFGALFSVYFYIRGYFDHWHEAIFHGFYQA ISAVTNSGFDITGESIKPFEHDYPFLFMIMFLIFIGGIGFPVLMEFREWRLYRKTKAKIPFRFSLFTKLAVLAFVILFVSGTVLIFLLEKNHLF KDLHPSVQWINSMFYSMTTRNAGLQIHDLGDFQITTLIVFSLLMFIGCSPSSVGGGIRTTTVAIIGLYLYSFLKSEDNINIFGRRIDEDDVR KSVVVFMLSLGMCFFCILFLSATEKQPLISIIVEVTSAFGTTGLSLGITGDLSTVGKITIGALMFIGRIGMLYTLMLFVPKETRDLGYEYPT EKIIIG
1.4E-57	205	31.2	2E-57	204.2	21.7	1.1	1	Q8RD51_CALS4	Trk-type K+ transport systems, membrane components	TrkG TTE0196	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	273068	>tr|Q8RD51|Q8RD51_CALS4 Trk-type K+ transport systems, membrane components OS=Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) GN=TrkG PE=4 SV=1MIKIKLTPTQVLALGFATIILIGTLLLMLPVATKSGEGADFITALFTATSATCVTGLVVVDTETYWSTFGQIVIMLLIQVGGLGIMTMS TLFALILGRRITFKERLVMQEAFNTNSLGGIVKFAKYILMVSFLFESIGAIILTLRFLPQMGLKKAVYYGLFHSISAFNNAGFDLMGNFRSL TGYVSDWVVNLVIMSLIIFGGLGFYVLLDIYEHRHFSKLTLHSKAVITITLFLIAGGALLIFLFEYNNPKTLKPLDFPTKILASLFQAVTPRTA GFNTLSLSDMTIASKFLTIILMFIGASPAGTGGGIKTTTFGVILYTVLSVIKGEEETVLYKRTISRNIVYKAVAISFISVFIIFSVTMVLSITETS DFLTLLYETTSAFGTVGLSLGLTPELTTVGRIIIIFTMYTGRVGPLTLALALAQRQKKPKPIMKYVEEKIMVG
1.4E-57	205	16.1	5.9E-31	116.9	1.8	2.1	2	Q7CZR7_AGRFC	Trk system potassium uptake protein	trkH Atu1204	Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	445	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Agrobacterium fabrum, Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	176299	>tr|Q7CZR7|Q7CZR7_AGRFC Trk system potassium uptake protein OS=Agrobacterium fabrum (strain C58 / ATCC 33970) GN=trkH PE=3 SV=2MFALSGFMCGGFSLACALATRGPITSFNKRFGFLLVNLLWLVFSIVGAVPLYLSELGLTPGQALFESVSAITTTGSTAISGLDHAP QGILLWRSLLCWLGGIGIVALGLFILPLLRVGGMTFFRMESSDTGNDRPFARLASFTRAFVAIYIIMTLACTMAYDFAGMSHFDALNHA MSTVATGGFSTHDASFAYFNNTALLWIATIFLIFGSLPFSVMILLAVRRRLETLRDPQIAVFLGYLCAISIAVGVYHHFRNGVPLDDALSH SFFNMTSILSTGGFASDDYTLWGPFVVVVAFFATFMGGCSGSTAGGIKAYRFLIMFNVVRAGLKKLIYPNAVYSVRYGQQVVDPDTIR TIFLFVSCFIALWIAGSLAMSLMGYDFLTATSAVATSLANVGPGIGPIIGPAGNFSTISEPALYLLSVLMLLGRLEILTVLVLLMPIFWRS
1.4E-57	205	12.8	4.3E-56	199.8	8.9	2	1	K9WE19_9CYAN	Trk-type K+ transport system, membrane component	Mic7113_2194	Microcoleus sp. PCC 7113	475	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	1173027	>tr|K9WE19|K9WE19_9CYAN Trk-type K+ transport system, membrane component OS=Microcoleus sp. PCC 7113 GN=Mic7113_2194 PE=4 SV=1MRAYTKTILRDVGLLLHVPGVMALISLPVGFIFNEHYAISSFLWTAFISLGMGQLLYRLFRNASEEAHLRHAMLTVALSWGLIPLL GAIPFVLIASHLSVFPLTPQTVLEFQNPWNAVFESFSGFTSTGLSMALRSSELPRSLQWWRSFIEWIGSVGMIVLVLSVLEPSMDAYQ LYYAEGRSKKIALTVKATVRKIWKIYLLYTVLSILLLCLVGMPWWEALNHAMTGIATGGFAVTDDSIGAYSPIVQLAVVPIMIVGSISFSA HYQLLAKRRLSALWRDAQHRALWLLLGLGTIVLLLENYWFQGSFLWVDTWFQWVSALGTCGFSTVKLQDWSPSAKLLLSVAMVFG AASGSTVGGLKLNRVVALYKGVLWHFRHMSLRSHQLMRYQLDGEVLQEAQARRRVGSAAVLAILWVGWLGLGVLVLLHVVQPQYT LIDVIFEAASALGSVGLSIGISEPDLPWVGKLILILFRAC
1.5E-57	205	27.9	5.1E-56	199.6	19.3	2	1	R7A3U4_9BACE	Uncharacterized protein	BN656_00297	Bacteroides pectinophilus CAG:437	442	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides pectinophilus CAG:437	1263051	>tr|R7A3U4|R7A3U4_9BACE Uncharacterized protein OS=Bacteroides pectinophilus CAG:437 GN=BN656_00297 PE=4 SV=1MRHLTKHFSSAQIIIIGFAGVILLGSLLLMLPFATRDGQGAGFADALFTATSAVCVTGLIVRDTATYWSEFGQAVILALIQIGGMGVI TVAVAVTLISGKRISLKQRSTMQDAISAPQVGGIVRLTGFIVKASAAIEIIAALIMTPCFVREFGMAKGLWYGIFHSVSAFCNAGFDLMGV REQFSSITYYVDNPIVNITVILLIIVGGIGFITWEDIKNNRLHFASYRMQSKVILVATALLIFIPSVYFFFCEFTDGSVWHRVISSVFQSVTT RTAGFNTVDLTSLSDDGVAVMIILMLTGGAPGSTAGGMKITTLAVLAGTMISVFARREHTHFFARRIDSDIIRNAVAVFMMYIILFLLGGLI ISRVEAIPLLTCLFETASAVGTVGLTLGITPGLGMLSRTILVLLMYIGRVGGLTLIFAAVSPRKGNTARLPQEKMTVG
1.6E-57	205	17.5	9.1E-57	202	12.1	1.8	1	D7CY22_TRURR	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Trad_0242	Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24)	452	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Trueperaceae, Truepera, Truepera radiovictrix, Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24)	649638	>tr|D7CY22|D7CY22_TRURR Potassium uptake protein, TrkH family OS=Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24) GN=Trad_0242 PE=4 SV=1MVDRGSIRPPRRAAPSPAKIIALYFVSAIAVGTLLLWLPISHAPGAEIGLLEALFTATSALCVTGLVVVDTATAWSIFGKVVIMLLIQ VGGLGIVTLGTLVALLLGRRVGFRERLRAAAQVNALQTGGIVKLVRTIFLISLGFEAVGALLLYPTFAALHGPGMGAFYAFFHAVSAFN NAGFALYSENLTGFVRDPTVNLVLAALFITGGLGFLVHLNLWARLRHGSHFQLTLQSRFVLLTSLGLGLLGWVAVCLFEWTNPQTLGA LPWPSRLLAGFFQGVTPRTAGFNTLDYAQVREPTLLVTMALMFIGGSPGSTAGGIKTVTFAVLAASAWSMVRGRGELTAFGRRVTTE TVVKAGSVALLSLGIVFGAMLLLSISETVPLVPLMFEAFSAFGTVGLSLNLTPELSAPGQLIVTLLMYLGRIGPLTFAVALVQEPRDSPIT YPDEGVMIG

1.6E-57	205	13.4	1.5E-29	112.3	4.3	3	2	F4BYP2_METCG	Cation transport protein	MCON_0896	Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) (Methanothrix concilii)	533	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosaetaceae, Methanosaeta, Methanosaeta concilii (Methanothrix soehngenii), Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) (Methanothrix concilii)	990316	>tr|F4BYP2|F4BYP2_METCG Cation transport protein OS=Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) GN=MCON_0896 PE=4 SV=1MPSAILVRHCLMKFRVFLRLLAQLLKLLAILLLVPGAVAAVYAETGGVIAFAATSLISLATGIALGRLSSEEEPGLREAFALVALGWI AVAFFGAFPYVFLGMSLIDGLFESMSAFTTTGSSVFTEINHLGYWKMNQTLADSSLVAEMQMQLVRMTGNSILLRMRSGPDDTIMGL LFWRSFAQWLGGMGIILLFVAILPRLGVAGRQLYRAEVPGPDKESIKPRIKQTARMLWMVYILLTLVEVALLLLAGMPPFDSFCHAFSS MATGGFSPRGLSIMAYNSWIIDAIIVLFCFLAGANFALHYRMITSDRKALISDTEFRAYALIILLATSIIILWGGLEGDIYQKIQLAGFQVVSI LTTTGFATADFNQWTATARITLLLLMIIGACAGSTAGAIKVVRLILIFKSAYRELIRTLHPKAVQSVRLGDMVVKEEILRASNIFVSMYIIIFA IASLLLAMISYSDPKMDMESVLSAVATTLGNVGPGFGVVGPMFSFADIHPAGKMLLILCMWIGRLEVVTAMVLFLPEFWKK
1.7E-57	205	22.1	6.4E-56	199.3	15.3	2	1	E8T4R6_THEA1	Cation transporter	Theam_0355	Thermovibrio ammonificans (strain DSM 15698 / JCM 12110 / HB-1)	480	cellular organisms, Bacteria, Aquificae, Aquificae, Desulfurobacteriales, Desulfurobacteriaceae, Thermovibrio, Thermovibrio ammonificans, Thermovibrio ammonificans (strain DSM 15698 / JCM 12110 / HB-1)	648996	>tr|E8T4R6|E8T4R6_THEA1 Cation transporter OS=Thermovibrio ammonificans (strain DSM 15698 / JCM 12110 / HB-1) GN=Theam_0355 PE=4 SV=1MRFQLVFKYVATLLFFLSLSYFIPFFYSLWCKDGLFHYYLYPVALTGALFLIALQIEGGELNIKEALLTVSLTWFLFPAISALVYQET GAIKNFIDAYFESVSGFTTTGASILTNIEALPKSVLLWRSTTHWIGGVGFVVFSLSVLPAFGAGGAQLMRFEASKAVEERLVPKVKEMA RVILAVYVALTAAEVIALVAAGMPLYDAVNHAFATIATGGFSTKNGSIGEYHSPLIEVIVSFFMLAGATNLLTYYLALKNRSLKAIYSYYEF RSFMAIVAFAVAFTTLVLYFKGTYHSLLEALRFGSFAVISAITTTGFGVADYTKWPPVTQALMMLLEIMGGSSGSTAGGLKQFRIVTMA KTTYYEMKKTLHPRMVYRIVLGKKVVDYSLMNNIWAFISIFFSTTLLFGFLISLSGHDIITSFSASVACITGSGPGLEKVGPAGNFAFFSPI DKLLLSIEMVLGRLEVMSVLTLLLPSFWKE
1.7E-57	205	25.8	4.5E-56	199.8	17.7	2.3	1	S1NE53_9ENTE	Trk system potassium uptake protein TrkH	I568_01360	Enterococcus columbae DSM 7374 = ATCC 51263	460	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus columbae, Enterococcus columbae DSM 7374 = ATCC 51263	1121865	>tr|S1NE53|S1NE53_9ENTE Trk system potassium uptake protein TrkH OS=Enterococcus columbae DSM 7374 = ATCC 51263 GN=I568_01360 PE=4 SV=1MKDEGVKMLKKEKKSNLQKLGPVKFLSLGFLGIILFGGFLLSLPISSQSGKFTNFLDAVFTATSATCVTGLTTLNTAEHWSLFGQI VIMVLIELGGLGFMMLPIIFFTLAKKKVNLSTRIVLKEALNLEEMSGVMKLTLYVLKLSIAIQGVGMLLLSFDLVPRYGVIKGLWYALFHAI SSFCNAGFDLFGDSLVPFQNDPYMLLVISCLIVSGGLGFLVWRDLLNYRQTKRMTIHSKLALSMTACLLIGGLVLFFLSERNGRYLVQS DNFFTRLVNTLFMSVTPRTAGFYSVDYAAMSNPGLIVTMFLMYIGGTSGSTAGGLKTTTFGVLLVQIISLLKGRTRAEFAGRSIKETAVF RAMTLFFITLSLCVVSVMILSATEHLPRTDGIEYVAFEVFSAFGTVGLTMGLTPDLTEFGKLLIIALMYIGRVGIMTVLFALMSNNQKQEA RFQYPYESVLVG
1.7E-57	204	26	6.7E-57	202.5	18	1.7	1	A0KQB7_AERHH	KtrB	AHA_4043	Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	451	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Aeromonas, Aeromonas hydrophila, Aeromonas hydrophila subsp. hydrophila, Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	380703	>tr|A0KQB7|A0KQB7_AERHH KtrB OS=Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240) GN=AHA_4043 PE=4 SV=1MTRWRSNYAFALHRDDESRWSEAKLILGSFLIILLVGTLFLVQPSSHNGEVSFINALFTATSAISVTGLGVVDTGTAFTLQGQIFLL MLMEIGGLGQMTMTLLLIAMFSKRVGLRQQVLAKEALGQEGSVNIIQLVKRIVLFAFIAQLIGTGLMAIRWVPELGWERGLYVSFFHAV SAFNNAGFSLFANNLMDYRDDPIISLTIAALIILGGIGFTVIVDLVRNRRWRKLKLHSKLMLIMTPGLLLLGTLMFWLLEHNNPGTLGKAS FGGQWLAAFFQSTSARTAGFNSIDIGQMVPASLLFMMMLMFVGAGATSTGGGIKVTTFAVVLLATKAFLTKRPHVTAFGRTLSPQIVT RSLAIIIVSTMVLMLAMFLLMLTEQQSFDKIMFETISAFATVGLSTGITAGLSEPGKLILVLVMICGRLGPLTLAFMLARPSETRIKYPEEA VYTG
1.7E-57	204	24.9	2.6E-57	203.8	17.3	1.2	1	D3H69_STRM6	Potassium uptake protein	trkG1 smi_0088	Streptococcus mitis (strain B6)	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus mitis, Streptococcus mitis (strain B6)	365659	>tr|D3H699|D3H699_STRM6 Potassium uptake protein OS=Streptococcus mitis (strain B6) GN=trkG1 PE=4 SV=1MLFKLFVKKIERALGGLSPARRIFLSFAGVIFIGSLLLSLPFVQANGSQATYFDHLFTTVSMVCVTGLFTQPVATTYNVWGQLICM FLIQIGGLGLMTFIGVFYIQGKQKLSLRSRETIQESFSYGETRSLKAFMRSIFLTTFLVEGLGAFLLSFRFIPEFGWGRGIFTSIFLAISAF CNAGFDNFGSNSLVSFQTDPLINLVIAGLIITGGLGFMVWFDLATQFDKKKKRRLRFHTKLVLFLTAGILLFGTVSTLFTEWHNPGTIGN LSVPEKVLVSFFQTVSMRTAGFASIDYTQARPVTLFIYILQMFLGGAPGGTAGGLKITTFFVLLVFARSELLGLPHANVAQRTIEARTVQ KSFSVFIIFLMTFLLGLVLLGITAEGTPRFIYLMFETISALATVGVTANLTPELGKLALSIVMVVLMFIGRIGPLTLLVSLADYQPDKKDLIQY MKADISIG
1.9E-57	204	35.7	3.4E-57	203.5	24.8	1.3	1	H6LK13_ACEWD	Potassium uptake protein TrkH2	trkH2 Awo_c19890	Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	474	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Acetobacterium, Acetobacterium woodii, Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	931626	>tr|H6LK13|H6LK13_ACEWD Potassium uptake protein TrkH2 OS=Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655) GN=trkH2 PE=4 SV=1MLKYVWLLNILIGDSVVAKKIRWNFNKFVGQRSPAEMLIYGFALVILLGAILLSLPIAAQSGKSGGFINALFTSTSAVCVTGLVVVD TGTFWSAFGKTVIILLIQIGGLGFMSLTTMFFVLAGKRITIKDRLLIQSSVNMDSISGIVKFTKYIFFSSIIEGIGAVLLALVFIPEYGFLKGT AYSFFHAISAFCNAGFDLFGHYSSLTKYVDNFVVNFVMCGLIILGGLGFAVTSDLINIRKFERMSMHTKLVLVTVSGVLLISGFVLFFIFEY NNPKTMGNLSLPGKMMAAFFQSVTPRTAGYNTINISALTKPSLFLTMLFMFIGASPGSTGGGVKTTTFAIIVMTVASVLNGKKDVTAFK RSILGPAIRRAISVLVIAFAIVIFMIFVLLCTEPDASFETVIFEVISAFGTVGLTTGLTPHLSIAGKIAISITMFVGRLGPLTVAYAISRSEKRSR ENVGNFKLPEGNIMIG
1.9E-57	204	24	2.4E-28	108.3	5.9	2.1	2	U6ED88_9EURY	TrkH family potassium uptake protein	MBMB1_1836	Methanobacterium sp. MB1	467	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium sp. MB1	1379702	>tr|U6ED88|U6ED88_9EURY TrkH family potassium uptake protein OS=Methanobacterium sp. MB1 GN=MBMB1_1836 PE=4 SV=1MLLITNPLGIIMQGIGAVILIPIIIALIYGEHDYIGFLAFGAFSIGLGSILRRLPADYNRLQLKHGMIIVSLAWLWAALIGSFCLMYSTNI DFLNAYFESMSAWSGSGLTIYPNVEILPKSILFLRSLEQWVGGLGVVIVVIGVLIRPGTAASRLYKSEAREEKIKPSITSTVKTIWWIYLL YTIVGIALYVVVGMNLFDAINNTFTNLSTGGMSIKNDNIGAYGSTAIYIVTMILMILGGTSFLVHYKALKGRAIDVFHDIQFQAMIIILSVFYI LLVVNANFTSIDSAFFVISALSCTGSSIQPLSTMIQWSDYAKVIILVAMIIGMSAGSTTGAIKLIRIVTLIKGFYWEIKRILSPQGSIIPRKISG KPVGDVEIREAGSYTFIYLFFIFVSWIVLTSYGYGGLNSLFEVASAQGNVGLTMGIVSPTMPDLAELFLIFNMWIGRIEIIPALVLLKGLW DAIKG
1.9E-57	204	14.6	1.7E-29	112.1	1.1	2	2	F8D973_HALXS	Cation transporter	Halxa_1047	Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6)	505	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halopiger, Halopiger xanaduensis, Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6)	797210	>tr|F8D973|F8D973_HALXS Cation transporter OS=Halopiger xanaduensis (strain DSM 18323 / JCM 14033 / SH-6) GN=Halxa_1047 PE=4 SV=1MRIRVDWRSSCSLSGTVLKWIAVPLAVPLLLAVVDGDDVLPFAAAVVVTVVLGAALELLSDDRELGQREGFLMVAFTWLSVGLV GAIPFYLAGLAAGPDSAFYSLVNAAFESMSGLTTTGATIMNGWDFANQSRAILLWRQILQWLGGLGILIVAIGLLSNLMVGGAQLMETE TQTKNVTKLTPQIESTARLIWGLYVGLTVLAAATFYALQLLGLAENMHLFNAVAHALTSVSTAGFSPEAESIAAFEPIVQWAITPFMLLG ATNFVLLYYVVQGDFERPLESEELRFYLGLVVGISAIVAFIIGIDPEMDFGLEATIRHGVFNVVSMVTTTGYASANFDLWTAGAKHVLFL CMFLGGMAGSTTCSIKTLRWLVIVKGLYRNFFTSIHPEAVRPVRLGDGVVDEETITDIFAYVMLAIVIFFLLTVLIVVDAARSGTTVTEFE ALGAAASIFLNIGPAFGMAGPMDNYAGFPATTRAVMVIMMWIGRIEIIPVLVLLLPAYWQS

2.1E-57	204	26	1.2E-56	201.6	15.7	2.4	2	C4LWU8_ENTHI	High-affinity potassium uptake transporter, putative	EHI_199020	Entamoeba histolytica	733	cellular organisms, Eukaryota, Amoebozoa, Archamoebae, Entamoebidae, Entamoeba, Entamoeba histolytica	5759	>tr|C4LWU8|C4LWU8_ENTHI High-affinity potassium uptake transporter, putative OS=Entamoeba histolytica GN=EHI_199020 PE=4 SV=1MSNKHSELNETQEAVQSSMQKPEEKVVSERGNTESNKVNDESVNPVIPSLNKHPDKQEFVEIEMDNQVGDSKSYGQSQSDKESVVAQPTRWYSHNVSPSLISDSCEWGQIKPESCQSEMIKGTNSEDSSETSIASVSNQISKRVRPVVAFKDGSNEDDEQGRSDDNFEDENEIKEDKTLPCHDLGHYVARLRTIIYPNFLNYYLMHFLFFTALCFVGAIIMILIDSNINYIDALYTAVSSYTGSGLTVFDLTKVKFGIQFISYLLTFIGSIVLDSSYYILIKLFRMGTKKQTKSLEGTAPQVVIDAAIAQARHINSTETKTSIILLAVIWLYNIIVQIIGFLLLLIAFAKDKDKIEATGVNWVWFTLYQTNSAFNNCGIVLSSNSLVSFSNNAGVSIVTSILTVLGNTCYPIVLRGIIELLGIVLKCTRYNKIVQYILRYPRRCSTHIYPRKATIWLVIVFLMITFSEFIIQMSLDFKNFEDIPVGYRTIDIFAQSISTRTAGFAFLDFSKISSGCYVMMIGFMYLSSYPITVTLRETNPYLRHKENSNQDSGIVYQAKNMLAWDVVCFYSFYFLICCCEQDALRKDYTYTEFMILFEVISAYGTVGYSLPMTNGAYSVSGGFRPICKLFICCVMMFGKHRGFPERVDRGFTPYQIVINRKENEDSSLECQVNDRDEKKIRKEEKAKVQSENNKEVNTSTSIISAVDTPLNLPQRSQIGSRNYDEITFRNNDL
2.1E-57	204	30.3	6.6E-56	199.2	21	2	1	F9Z6Y9_ODOSD	Cation transporter	Odosp_1851	Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) (Bacteroides splanchnicus)	482	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, Odoribacter splanchnicus, Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) (Bacteroides splanchnicus)	709991	>tr|F9Z6Y9|F9Z6Y9_ODOSD Cation transporter OS=Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) GN=Odosp_1851 PE=4 SV=1MINFRFIANLMGRLLLIESAFLLLCVLIALIYGEHDASAFFYTSLITMSAGFLLSKLIKIKDRVLAKKDGYFMVTMVWIIFSLFGSLPYMIGNTIPSFADAFFETMSGFTTTGSSILNHVEALPHATLFWRSLTQWLGGLGIIMLFIAILPSLGIEGRDLYVAEVPGPTHNKTSFTFTSSARQMWILYTILTLLQTLLLFGGMNLFDGICHAFTTMATGGFSTKQNSIAYWDSAYIQYVIIIFTFMAGTNFGLLHTAIRGNWRKLIQDNEFQLYFTIVLLASVVIGVGLYVIGWADFEKSMRDATFQVVTLITTTGFATADYLLWPPLLGLILFLLLFVGASAGSTAGGMKVVRVYLLFKNSFVELKRIIHPNGIINVKYNNKSVHPNIMTGIMAFAILFMIVFTIGSLIMTIFTEDIITACSAVVSSMSNVGPGFGSVGPMFSYAHLNDFAKLFLAFLMLVGRLEIFTVMVLFTKAFWRK
2.2E-57	204	27.4	1.3E-55	198.3	19	2	1	R6GX17_9FIRM	Potassium uptake protein TrkH family	BN490_00087	Firmicutes bacterium CAG:137	447	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:137	1263004	>tr|R6GX17|R6GX17_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:137 GN=BN490_00087 PE=4 SV=1MNERVFLPHKKKKLTSFQIIILGFLGVILLGTVFLMLPVSTRAGTATPFSDALFTSTSAVCVTGLVMHDTATYWSFFGQVVILFLIQIGGLGVITVAASFAMISGKKISLMQRSTMQEAIAAPKVGGIVRLTNFMIRTTLAIELLGTIIMAPVFCRDFGVKGLWVALFHSVSAFCNAGFDLMGTTEAFSSLTGYASEPVVNLTIMSLIIIGGIGFLTWDDLRANRLHWQKYRMQSKVILCTTAVLLIVPAIYFFFFEFSALEPGKRILCSLFQSVTPRTAGFNTVDLTSLRESGQAIIILLMLIGGSPGSTAGGMKTTTVAVLFATALSTFRRKEDTHFFGRRIEDGVVKNAATIGFLYVALFLFGGLAISMAEGLPMLTCLFETASAVGTVGLSLGITPGLGILSRVILILLMFFGRVGGLTLIFAALSGTQKQVAKLPLEKITVG
2.2E-57	204	28.7	8.2E-57	202.2	19.9	1.7	1	R5XCF6_9CLOT	Potassium uptake protein TrkH family	BN488_01097	Clostridium bartlettii CAG:1329	490	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bartlettii CAG:1329	1263063	>tr|R5XCF6|R5XCF6_9CLOT Potassium uptake protein TrkH family OS=Clostridium bartlettii CAG:1329 GN=BN488_01097 PE=4 SV=1MNRKMIFRILGNIIMFEGAIMLLPFLVSLIYKEHTAIYFIITAAVAIAIGYILSNLKTENRHIYAKEGFIIVALSWVVVSLVGALPFYISGEIPNYIDAFFETVSGFTTTGSTILNDIEVLSRGMLFWRCFTHWIGGMGVLVFVLALIPKSEGQDMFLMKAEVPGPVVGKLVSKVHMTARILYGIYAFLTVIEIIFLLFGGMPLFDSIVHAFSTAGTGGYAIKNSSIAFYNSYYIDMVVTVFMLLFGINFNLYYLLLLKDFKQIFKSEELRWYILIIAVFTGIITVNTLGIYGNSISESFRYSIFQVASIITTTGFATTDFGMWPTLSQILLLLLMVVGACAGSTGGGMKISRIMILIKSAKCSMKKMVSPRSVTTINVEGKSVDKQVLDFAYSYFVVYALIFFASVLLISFENLDILTTLTAPLTCLGNVGPGFGDLIGPVGNFSSLSSFSKIVLSFDMLAGRLELFPMILLFYSLKDCINVAREKVLKR
2.4E-57	204	28.7	1.3E-55	198.2	19.9	2	1	R5CQ72_9FIRM	Potassium uptake protein TrkH family	BN785_00580	Firmicutes bacterium CAG:791	449	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:791	1262993	>tr|R5CQ72|R5CQ72_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:791 GN=BN785_00580 PE=4 SV=1MNNETKRVFRRRPELTSSQIIFFGFLGVILIGTLLLMLPIATRDRQGASFADALFTVTSATCVTGLVVKDTVTYWSLFGQVILMLLLQIGGMGIVTASLAVFLFSGKRISLRQRSTMQESISAAQVGGIVRLTGFILKTSLLLELVGAAFLTPVFVRDFGLARGIWYGLFHSVSAFCNGGFDLMGHLEPYSSLCWYVANPVVNVTIMLLIVIGGLGFSVWDDLRKNRFRFRFCTMQTKTVLTVTGILIFLPALYFFFFELAEMPLPQRFWGSLFQSVTMRTAGFNTVDYAQISEGGLLVMIFLMLIGGSPGSTAGGMKTTTFAVLAATAFAVFRRKDATQMFHRRVPSAVIRNAVAILFLYLTVFVTGGIIISRLEGLPLISCLFETASAIGTVGVSLGITRELGTVSRLILVLMMFCGRVGGLTVVFATISPRAGSELHYPQENLIVG
2.4E-57	204	25.2	5.9E-55	196.1	17.4	2.1	1	A0A0F2NQK2_9FLAO	Potassium transporter	VR77_12225	Flavobacteriales bacterium BRH_c54	486	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, unclassified Flavobacteriales, unclassified Flavobacteriales (miscellaneous), Flavobacteriales bacterium BRH_c54	1629721	>tr|A0A0F2NQK2|A0A0F2NQK2_9FLAO Potassium transporter OS=Flavobacteriales bacterium BRH_c54 GN=VR77_12225 PE=4 SV=1MINIKVVFNVIGNLIIITGLLMATAIPFSLYYDEGDLYPLILSSLTTLFFGLIVKLRTQKHKNDEVKKREGYLIVAFGWLAMTIFGSLPYVFSNAIPDYTNAFFETISGLTTTGATILNDIESVPKGILFWRSMTQWIGGMGIIVLTIAILPLLGVGGMELFASESPGPTKDKIHPRIKETAKRLWLIYFSLTAIQCVLLLFGGMDFYDAINHSLTTMSTGGFSTKQASIGHFDSAYIQYVVILFMFLAGTNFTLLYFGFKLNFKKFWINDEFKWYIAAIIVLCFVIFPTVYFVYGRADGVEASFRAVLFQVTSIITTTGYATSDYTLWGSFVTFLFFLLLFTGASAGSTSGGMKLVRIVLLMKNGFLEFKRRLHPNAVIPVHLNGIGVSQKIIYNLLAFVFFYLFLFVTGSIVVTFFGVDFIDALSAVATSISNVGPGIGSIGPSFSFSHLPDGVKWVLSFLMLVGRLELFTITILFTPYFWRLK
2.4E-57	204	22.8	7.5E-57	202.3	15.8	1.7	1	Q5QUZ1_IDILO	Trk system potassium uptake protein	IL0919	Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	495	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Idiomarinaceae, Idiomarina, Idiomarina loihiensis, Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	283942	>tr|Q5QUZ1|Q5QUZ1_IDILO Trk system potassium uptake protein OS=Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) GN=IL0919 PE=3 SV=1MQASQSLRQTPLDKRQAIKLLLKAIGGLIALLSIALLAPFVMAVVSGEKEQWTYLTLSSLGLVFGLLLFLQPAGEAKLRARQVFLLTSLCWVSASLFATLPFIFARPYLDFSSAWFEAMSAITTTGATVISGLDDLPASVLLWRAMLQWLGGIGIIVMAMAILPFLQVGGMRLFQAESSDMSGKFMPRSSHMVLAIGRVYLILTAAVISLYLIGGMGSFDAFVHGMTTIATAGFSNYDASFGHFSNTPFLVITGTIFMVAGALPFVLYIRFVKGDFGPLWKDSQVRAFVTFLLIAIALITLVQIVKGRELGDALMHTAFNVVSVVTTTGYATEDYGNWGSWSLMAFFYLMFIGGCTGSTSGGMKIFRFQLSQLLLRKQFSQLIHPNLVSVQTYQERRVNDSLLGSMVAFCFMYFLLIAVIALGLSLFDLDFMTAISGAASAVGNVGPGLGDIIGPAGNFASLDGGAKLLLVFAMLAGRLEIMTVLILFHRHYWRH
2.4E-57	204	41	3.5E-56	200.1	28.4	1.9	1	Q81G98_BACCR	Potassium uptake protein KtrB	BC_1310	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	439	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	226900	>tr|Q81G98|Q81G98_BACCR Potassium uptake protein KtrB OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) GN=BC_1310 PE=4 SV=1MKRINISMSPPRVLTLSFLVLSVVGTCLLKLPIATTTSISWLDALFTTVSACTVTGLGVVDTGKVFTLFGQCVILTLIQVGGLGIMSFAVLIAIMLGRKIGLQNRILLQQALNQTNIGGIIRLAKALFLFSFTVECIATIILSFEWVPKYGVMKGIYYSFFHSISAFNNAGFSVWSDNLMSHSHSILVNLVISSLIILGGIGFTVIVDIKRKKNFKNLTLHSKLMLSSTLIVNIIATLFIFIFEFHNSLSMRGFTPFEEGLASYFQAISTRTAGFNTVDISTLSKPSLLLMMLLMFIGAGSASTGGGIKLTTFLIIFFGVFKFLQQQEDIVVFKKSIKDTLIVKSLTITIIISISFIFFAILILSITERVPLLMSAFEVFSAFGTVGLSMNLTPHLTIIGKAIIIFMMFFGKMGPLTLAFSFARKKNLKIKYPNEDILTG

2.5E-57	204	10.4	8.2E-57	202.2	7.2	1.6	1	A9C1G3_DELAS	Trk system potassium uptake protein	Daci_5998	Delftia acidovorans (strain DSM 14801 / SPH-1)	488	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Delftia, Delftia acidovorans (Pseudomonas acidovorans) (Comamonas acidovorans), Delftia acidovorans (strain DSM 14801 / SPH-1)	398578	>tr|A9C1G3|A9C1G3_DELAS Trk system potassium uptake protein OS=Delftia acidovorans (strain DSM 14801 / SPH-1) GN=Daci_5998 PE=3 SV=1MRDLFPVLRVLGMLMVMFALSMLLPFAVSWFADDGIWRIYPWAIGITAAVGLSLWVGLDHFRRELQPRHGVILVTLVWVVLPLC AMLPLVLGLGHVGLSISFTHAYFEAVSGLTTTGATVLTGLDALPVSINVWRTFLQWLGGMGILILAVAILPLLGVGGAQLFRAEAAGPIK DTKLTPRMTETAKGLWGVYGVFSLACALAFWAAGMEPLDALMHMFATVSLGGLSSHDASFAYFDSPLIELIALVFMLLASCNFALYFV AMRKGRWDGFWRDPEMRATLAVLLGGGLIVALLLWAKGVYGPVEALRYGIFHVVVSVATTTGFTTVDYLSWPVFAPVLMLLLSGVAT SAGSTGGGIKMVRMLILLKQARRELTRLVHPRAMQPVRLGNGVVDDRMIFSVLAFMLVYGATVITLSMVLLLTDLDPVTAFSAVLASVH CTGPGLGALGPSSNYAVLTDFQTWICTLAMLLGRLEILSFMALLSPAFWRR
2.5E-57	204	19.7	3.3E-57	203.5	13.7	1	1	K1LZ68_9LACT	TrkH family potassium uptake protein	HMPREF9706_00516	Facklamia hominis CCUG 36813	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Aerococcaceae, Facklamia, Facklamia hominis, Facklamia hominis CCUG 36813	883111	>tr|K1LZ68|K1LZ68_9LACT TrkH family potassium uptake protein OS=Facklamia hominis CCUG 36813 GN=HMPREF9706_00516 PE=4 SV=1MKHALIKLTPPQKIALSFLLVILSGSLLLSLPISQLASSQANYLDHLFIAVSAVCVTGLWTQSIHDSYNILGQVIMMILIQIGGLGLMTI IGSIYHGLGQRIELKDQITTSQALNRSSQQNLGEFLGRIIRYTAVIEGTGALLLAGFFVPHLGWGRGLFNAIFTAISAFCNAGFDLMSND SLTYYNDNPLLLITIMVLIVLGGIGFAVWFDVADQFQAYRQAKRGKKIGYYLRHLKTHTKLMIRATLALILLGTLFISLLEWHNPDTLGPLS SGHKLLVAFFESITMRTAGFSSIDYTKAHPVTLLYFIANMFIGGGSGGTAGGLKVTTFVLTLMLAMQEIRQSRYVSYDYHTIPTSTVRSA FVLFLIYISLLLSGSALLLAFEPDINYLYLLFESMSALATVGVSASLTPGLSTASHLVLIVLMYAGRIGPMTLLLSLHGRQRNKYDVEYSRT EIIIG
2.7E-57	204	22.6	1.5E-56	201.4	15.7	1.8	1	Q0W7J1_METAR	Putative K(+) uptake system, membrane component	RCIX163	Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	485	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanocellales, Methanocellaceae, Methanocella, Methanocella arvoryzae, Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	351160	>tr|Q0W7J1|Q0W7J1_METAR Putative K(+) uptake system, membrane component OS=Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50) GN=RCIX163 PE=4 SV=1MPRNNDLNIILGDLKSLFSIAAVLMSAMVVSSLLFWELRSAAGFIAGMLVSLIIAAAIHSITPRSEALELKHAIIIAALAYLLIPAVSAIP YMISTGMSPVDAYFESISGWTSSGFTMLPAPDSIGHSMQLWRSVTQWIGAVGVILLMVTVLIRPGTSAYILYQSEARKERIRPSIRSTV RTIWKVYLALTIISFFILLLAGMPAWDALNVSMTAIGGGFTLYSDSIGHYDSLPIEIVLLPVMIAGAIPFAVLFMMFKLKLHTMIYDIQVRTF AGLIATGCLLLVAQNYFYFYNDLFSATRYSVFQLVSAITSTGLQTTDISGWSPTALLIMSIAMIIGGCAGSTSGGIKVAREIFLVNQIKLWL KKTLLSKKAVIVIRLGQHKVVEKTITEELNEATLISFLWILNILVSIMLLANILGPEVSLSNLIFEVCSAQGNCGLTTGIINPAISPLAKLIFIAD MWMGRLEIVPVILLLRTVFRGFGR
2.7E-57	204	28.6	5.1E-57	202.9	19.8	1.3	1	X2GYU3_9BACI	V-type sodium ATP synthase subunit J	T479_15285	Lysinibacillus varians	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus varians	1145276	>tr|X2GYU3|X2GYU3_9BACI V-type sodium ATP synthase subunit J OS=Lysinibacillus varians GN=T479_15285 PE=4 SV=1MKKLIHYLSPPKILVLGFAIIIFIGACLLTLPIATEDGNGLPFLNALFTATSATCVTGLIVVDTGDTFTMFGEIVILALIQIGGLGFMTFA TLLFLLLGKKISLKERLLLKEAFNNISMAGLVKLVKRILLFTALIELIGGLILSIRFSFDMPIGKAIYFGFFHSISNFNNAGFDLMGGFQGLTA YVADPFVVLTICALITIGGLGFIVMNELYEYRETKRLSVHSKIVLSATVILTVGSTLLIFLFEYTNSKTIGDLTGMGKILGSFYQAVTPRTAG SNTLPIGDLTHSTLFLTILLMFIGAGSGSTAGGIKITTFAVLAATLWAQIRGKEDVVLFRRRIVIETILKALTVAMCGMVIVVFVTIFLSITEQ KHSFMMYLFEATSAFGTVGLSMGLTPELTPAGRILIILTMFAGRLGPLTIAFAITKRRKPEAFHHPKGNIMIG
2.8E-57	204	22.7	5.7E-55	196.1	15.7	2	1	F0LK83_THEBM	TrkH-like system potassium uptake protein	TERMP_01820	Thermococcus barophilus (strain DSM 11836 / MP)	489	cellular organisms, Archaea, Euryarchaeota, Thermococci, Thermococcales, Thermococcaceae, Thermococcus, Thermococcus barophilus, Thermococcus barophilus (strain DSM 11836 / MP)	391623	>tr|F0LK83|F0LK83_THEBM TrkH-like system potassium uptake protein OS=Thermococcus barophilus (strain DSM 11836 / MP) GN=TERMP_01820 PE=4 SV=1MKLKETLALLGEIMLLFSISFLAPLTVALYYKTPISPFLIPMVMSLIIGGFLRSLGAGEEIGIREAFLLVSLAWLSIAVLGALPYILAGE GSIANPLNALFESMSGFTTTGATVVVDFSIHSKAILFWRQLTQWLGGMGIVVLAIAILPRLSVGGSELMSLEAPGPQLEKLTPHIKNTAR IFWGIYVGLTAMETLILITLHYIGIAPKMTPYMALVHSFTTMSTGGFSPLSQSIKAFSPAVQWIITIFMILAGANFALFWYLMRKDYRIIRN EEFRWYIFAILGLSLLTVPYLEHQFNLNFITAFRYSIFQVASIVTTTGYATMNFSRWVFPAQFILFFAMFLGGSSGSTAGSIKIVRWVTAL KAIKRELSLSFHPKSLMNVKLGGIVVGERSIRSALAFIALYFIIFSVSSLFVILNGASVNLNPTDAMSAVAATLGNIGPGIGKIGPMANYLIF PPQTRALMIVLMWFGRLEIVTVLVLFTRSYWRW
2.8E-57	204	1.8	8.4E-43	156	0.6	3.1	3	L8WS18_THACA	Potassium ion transporter (Trk1), putative	AG1IA_06785	Thanatephorus cucumeris (strain AG1-IA) (Rice sheath blight fungus) (Rhizoctonia solani)	1149	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Cantharellales, Ceratobasidiaceae, mitosporic Ceratobasidiaceae, Rhizoctonia, Rhizoctonia solani, Thanatephorus cucumeris (strain AG1-IA) (Rice sheath blight fungus) (Rhizoctonia solani)	983506	>tr|L8WS18|L8WS18_THACA Potassium ion transporter (Trk1), putative OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_06785 PE=4 SV=1MDRGSLGAVHVPPTFVRSTTVYLTIPPPGAHRQPYLQAHGVLSLTAWPTYCLIILPHRRLDRKSLIRIIYLHKYIHLEPCVLISFYHP YSFIDALFNCVSAMTVTGLATIDLSQLTGFQQSILFVLMCIGNPVIISWFIVYTRRRFFRNKLSHIIAEELKRERQGGIIAAMRERTMSISR SLSRDHQAQAGGASPTDIHGKHYSRPGLLGRFANWAFPAASPGKSPSSTMSGAATPSSDRTKRKTGLAQRLRTDMIRRTEAEPQRV DPMGGIGGLMVDDIGGKGKARELSGQQFPEKGDQFNHGGEVHHVITGSSGSQTRYGGDNSSNPSLHRTNSLRSTEAERMADDDTS LAQTLAMPSRHSNGTIPTPHRPEYDMAPNPANLSPPVTDELHLGPLMGSPSHIDDRDGILLHPDADRNMDIIEGDSEGLDRATSADRS HSRGRPTSEARDSDSRTRVSSSPVRFRPPPIRVNPSTIGEERLSPSQGREADLMSVSFSGHERHPSEAVTQREPGTGIGEFPRNQTI EFVNTPHVRGRATARRQSAGVNSERERARFRNFSLGGSSNAAPAGSDAEDTSSANIGVGTSSIGHGNYGRGRASRQRMGSVSTAY FPRTATGRSHGTTRMNPSAQLPSHQSGYGGFPMPHELIGQGIKRFFPRTMTITRTLTMGSGGGEPRQVPYITFDAVVGRNSQFHDL TQEEQEELGGVEYRALGALLWIVPVYHFGIQLFGFVVFAPYSSMSKWAPIFREQQHRYVPPTCEATVTYGKILANFVSTFKARGKLSP NHPQFKSSLRFFIWLLSKVVGKRTHETLSFLLDHPRRCFIYLFPSHQTWFLLIVLVTMVLTDWISFMVLDIGNDVFESIPVGTRIALGLLQ AGAVRAAGFASVSISALAPAVKYVAVYPIALSVRATNVYEEQSLGIYLDGDEEEPNNPSNAYSWGSYLAWHARRQLSFGPSILQPFTF RAQLIILPTQLLDMWWLAVALWLLCIIERAEIMNPNSEHWFDIFTIIFELVSAYGTVGLSLGLPTVRMINERAVPFGLVTAPIACFQLTLIV LVVVLPWELMGRQGQNRSFNGLDTLGNRQSMTAEPGSFEGHSTSRAPTTAHGGVDLKHRGNTILSPVREVLTPVTSVTGTPRATFS ALGSGGN
2.9E-57	204	12.1	1.6E-55	198	8.4	2	1	B9L3I1_THERP	V-type sodium ATP synthase subunit J (Na(+)-translocating ATPase subunit J) (EC 3.6.3.14)	trd_A0345	Thermomicrobium roseum (strain ATCC 27502 / DSM 5159 / P-2)	481	cellular organisms, Bacteria, Chloroflexi, Thermomicrobia, Thermomicrobiales, Thermomicrobiaceae, Thermomicrobium, Thermomicrobium roseum, Thermomicrobium roseum (strain ATCC 27502 / DSM 5159 / P-2)	309801	>tr|B9L3I1|B9L3I1_THERP V-type sodium ATP synthase subunit J (Na(+)-translocating ATPase subunit J) OS=Thermomicrobium roseum (strain ATCC 27502 / DSM 5159 / P-2) GN=trd_A0345 PE=4 SV=1MDRVRHPSRPQEQVRRPGDRVVRRAVAPREAVRLPKPRQPRRPRPIAFRLVLGFAGLILTGTLLLSLPFAAADGQRAGVIDALF TATSAVCVTGLVVRDTATNWSGFGQAVILLLIQLGGFGFATSATLLLALLGVRPTLRDRLACGMSLGEAGPGGVVRLLRRLAGLTLAIE VAGAIALLPAALAATGSLGSGLWWAVFHSVSAFNNAGFDVVGGFRSLTPYQREPLVLVPVAILVILGGLSFAVISDVVRERRWGRLTL DSKLVLVTTASLLITGTLLFLAFEWSNPRTLGPLPWPDKVLNAFFHAVVPRTAGFNSLDVAHLNDESLFVTIGLMFVGGASGSFAGGIK VQSFAVLLLAVWAVLRGRPHVAAFGREVASEFVFRAMAIALLAVALVFLASFVISLIEPFGLLAIWFETTSAFGTVGLSTGITPQLHDAS KVVLVATMFAGRLGPLTLALALAERARPEPIRYARTAIALG

3.1E-57	204	40.5	9.5E-57	202	28.1	1.6	1	S0KVC7_9ENTE	Cation transporter	I573_00693	Enterococcus sulfureus ATCC 49903	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sulfureus, Enterococcus sulfureus ATCC 49903	1140003	>tr|S0KVC7|S0KVC7_9ENTE Cation transporter OS=Enterococcus sulfureus ATCC 49903 GN=I573_00693 PE=4 SV=1MTWWVFRHLIMNISRLSQLTLRKSQNFFAKNISSIQLIVFYYLVMTAIALILFYLPFFRIPDQHIRFIDLFFLAISTVSVTGLTTIPLTEVFNHNGVVLLEIFFQVGGLGIMMITTFFAIISKRKISLKQRQLIMTDMNQPKLSGIVRMIRITFTMILIIQLIAGTSFALYFKFAHYYDDWYHSIFYGFYQAISAVTNSGFDITGNSILPFANDPIFLLSIMFLIFVGGIGFPVLMDIREFTTYRFSKKTSHTLPYRFSLFTKIALLAFVVLFVGGTLIIYFLEKDHLFLNMNMGNQWLNSAFYSMTTRNAGLQIHDLNQFQITTLIVFSFLMFIGCSPSSVGGGIRTTTIAIIALYLFSFLKGESNVNVFGRRIDNDDVQKSITVFMLSMMMCFFCVLFLSATEDLPLIAIIVEVSSAFGTTGLSLGITPDLTDVGKLIIALLMFIGRIGMLYTLLLFVPKETRDLNYKYPTEKIIIG
3.2E-57	204	16.9	8.8E-55	195.5	11.7	2.1	1	R7DBM4_9FIRM	Cation transport protein	BN639_01693	Ruminococcus obeum CAG:39	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus obeum CAG:39	1263107	>tr|R7DBM4|R7DBM4_9FIRM Cation transport protein OS=Ruminococcus obeum CAG:39 GN=BN639_01693 PE=4 SV=1MNFRIIAYIVGWVCNFQAMFMVLPCITALIYQEHEFFAFLISMIVCLIVGLPLTIRKPKNKVFYTKDGCVAVALSWFALCISGAVPFVLSGAIPHPIDAFFETVSGFTTTGSSILTDVEVLPHCILIWRSFTHWIGGMGVLVFLLSLLPLAGGYHMNLMKAESPGPSVGKLVPKVQQTAKILYTIYIGMTLFQIILLIGRIPLFDTLCISFGTAGTGGFGIVNDSMGSYSTYCQVVTTIFMILFGVNFSAYYLLLTKKFVQAFKFEEVRYYFGIILAAILVIGLNTAHLFRNLGEAFQQAAFQVGSIITTTGFSSTDFSQWPSLSKTILVLLMFVGACAGSTGGGIKVSRILILCKAAKKEFQLYLHPNAVKKIKMDEKTIGHDIIRSTNIYLSVYLLILAASVLIISLDNFDLITNFTAVTATLNNIGPGLEIVGPMGNFSSFSYLSKCVLIFDMLAGRLEIFPLMLLFFKGTWKKF
3.2E-57	204	29.2	5.8E-57	202.7	20.2	1.3	1	K9ZMZ8_ANACC	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Anacy_5287	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	272123	>tr|K9ZMZ8|K9ZMZ8_ANACC Potassium uptake protein, TrkH family OS=Anabaena cylindrica (strain ATCC 27899 / PCC 7122) GN=Anacy_5287 PE=4 SV=1MTVARTICLGFMAVILLGAILLMMPFSTSNGMWNDPIVALFTSTSAVCVTGLSVVDPGTFFSFWGQLFITLLAQIGGLGYMTTTTFLILLIGRRFDLRQKVAIQQALDRPGISGSTQIIRSIIATTMIFEITGILLLLPAFVPDYGWNQGLWLAIFHSVNAWNNAGFSLFKDNLIGYQSSGLVVFTITGLIIFGGIGYQVILDIYLWLRDRILKKPNAILFSLDFKVATSTTLILLVLGTVAFFCIEIRNPQTFGNLSFTNQLLSAWFQSVTPRTAGFNTIDIGQMTDSGLFITIALMFIGASPGGTGGGIKTTTLRVLTSCTKSILQGKEEVLLYDRKIASLILLKAVGVVFGSLATVIGATILISLTDPNLEFIKILFEVVSAFATVGLSTGITGGISTAAKLILIVTMYIGRVGVLLLMSALLGDPRPSRVHYPEENLLVG
3.3E-57	204	35.3	2.8E-56	200.4	24.5	1.9	1	Q189P3_PEPD6	Putative cation transport protein, Trk family	CD630_06960	Peptoclostridium difficile (strain 630) (Clostridium difficile)	458	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptoclostridium, Peptoclostridium difficile (Clostridium difficile), Peptoclostridium difficile (strain 630) (Clostridium difficile)	272563	>tr|Q189P3|Q189P3_PEPD6 Putative cation transport protein, Trk family OS=Peptoclostridium difficile (strain 630) GN=CD630_06960 PE=4 SV=1MKTIVRRLILYADGMRPTQIMVSGFAAIIVIGALLLTLPIASQSGESIGLLNALFTATSAVCVTGLVMVDTATYWSLFGQIVIITLIQIGGLGFMTVATMFSLMARKKIQLRERLLIQESLNQADLSGLVRLTRFVLIITITIEGIGALVLSTVFIPQFGLSKGIWYSVFHAISAFCNAGFDLMGSVSGPFTSLNSYVNNFTVSMTVCALIVLGGLGFPVVLDIVRKRRFSKLNVHSKVVLFSTATLIFVGALFIFLIEFNQKATMADLPLKGKVLSAIFQSVTARTAGFNTLDLATLRESSVFVMIILMFIGASPASTGGGIKTTTLAVLIITVRSFLSGKSDIEAFERRLAPSTIKKSLGIFVISISAVIFGTLIISITQPNFTLVQSAFEVTSALATVGSSLAGTPNLNALGKIIIIIFMFMGRVGSLTLFMAILSGGRRKSQPIRYAEGKIMVG
3.4E-57	204	33.4	3.4E-57	203.5	23.1	1.9	1	S0JNI2_9ENTE	Cation transporter	I571_00506	Enterococcus durans ATCC 6056	466	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus durans, Enterococcus durans ATCC 6056	1140001	>tr|S0JNI2|S0JNI2_9ENTE Cation transporter OS=Enterococcus durans ATCC 6056 GN=I571_00506 PE=4 SV=1MQLNLFYRKLKRRSQRYATTHFSSIQIIVFYYVLMTIVSLGLFYIPIFRQPDSHVPFVDMLFMAISTVSVTGLTTFDISSVFNDNGVILLEVLFQVGGLGIMMISTAFIIFSKRRITLRQRKLIMTDMNQPRLSGIVRLIRITFTILLWFQIIFGTFFSIYFYYRGYFDHWRDAIFYGFYQSISAVTNSGFDVTGQSIEPFAHDYLFLILMFLIFIGGIGFPVLMEFREWLLYKRSKAKLPFRFSLFTKLAVLAFVILFIGGTILIYLLEKDHLFQDASLSVQWINSMFYSMTTRNAGLQIHDLGNFQITTLIVFSLLMFIGCSPSSVGGGIRTTTVAIIGLYLYSFLKSEDNINIFGRKIDEDDVRKSVVVFMLSLGMCFFCIVFLSATENQTLISIIVEVTSAFGTTGLSLGITGDLSIVGKITIAALMFIGRIGMLYTLMLFVPKETRDLGYEYPTEKIIIG
3.6E-57	203	45.6	5.9E-57	202.7	31.6	1.3	1	C0QVY2_BRAHW	Cation transport protein TrkH	trkH BHWA1_00057	Brachyspira hyodysenteriae (strain ATCC 49526 / WA1)	585	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Brachyspirales, Brachyspiraceae, Brachyspira, Brachyspira hyodysenteriae (Treponema hyodysenteriae), Brachyspira hyodysenteriae (strain ATCC 49526 / WA1)	565034	>tr|C0QVY2|C0QVY2_BRAHW Cation transport protein TrkH OS=Brachyspira hyodysenteriae (strain ATCC 49526 / WA1) GN=trkH PE=4 SV=1MKNIFNNKLNNPSNPNKTFIQAIDEFLRRISNLIAIAGSIFAIFVLLMQVRQINVYNFYIYNYDKIINIITICFVFILIDQIRIAPRKLYIVVPIIQLIGLLLLNFFSRKYYDVYANRIIWTIAGSILFFLVIVINWLRLSYSKFTLYQMIIASFIFVITLGSLLLYLPLSTVTGKLSFVDALFTATSAVCVTGLSVIDISKEFTLFGQIVLITLIQIGGLGIMSISAIVLLFSISKGSVQDRVRTLEMFNTQNKDIIQSTIKVIFLSTFLIELLGAVSLFTVIDTNDRLGMRIFSSSVFHSISAFCNAGFSLYTDNLHQYSANVVVNVTIMLLITLGGIGYPVMLTVTRAIINKFKGKRYYVFDVQARIVIFTSILLIILGSAFIFFNEYSNSLKDLPLKEKILVSLFQSVSPRTAGFETIAYSSMSSVTIGVVIFLMFVGASPNSTGGGVKTTTLFVFMFSVITAIFNRPYIVVNGRKIKDDTVNKSVAIVTLAIAISVLASFIMFYIEKSNSMMPILFEAVSAISTVGLSLGITPTVTIWSKLILIVLMFIGRVGYLTLFMSIGSINQGKYGIIDLPTGEVTIG
3.6E-57	203	7.4	4.5E-57	203	5.1	1	1	I1CVG7_RHIO9	Uncharacterized protein	RO3G_16969	Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) (Mucormycosis agent) (Rhizopus arrhizus var. delemar)	269	cellular organisms, Eukaryota, Opisthokonta, Fungi, Fungi incertae sedis, Mucoromycotina, Mucorales (pin moulds), Mucorineae, Rhizopodaceae, Rhizopus, Rhizopus delemar, Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) (Mucormycosis agent) (Rhizopus arrhizus var. delemar)	246409	>tr|I1CVG7|I1CVG7_RHIO9 Uncharacterized protein OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_16969 PE=4 SV=1MSRPVAKSELTRHERYRIGGTEYRALEMLARIVPLYYLGFIISFGFFFRIYIACSTYAQTVLQTSNDNGPIEPWFFSFFISLSSFTNLGLNHLDASMVPFQNAPCPLIFCIILILVGNTAYAIMLRFIIWICYKMTPSSKEMERETFRYLLDHPRRCYTTLFPATQTWWLFIILIIITLVELISFLALNYWLPILSGISGGSRFLDGLFQSVATRNAGFSVVSLADLNPGSQLVYIVAMYISVYPVAISMRNSNVYQVSANRSMVCFLV
3.6E-57	203	17.3	6.7E-56	199.2	12	2	1	S6AU46_PSERE	Trk system potassium uptake protein	trkH PCA10_39410	Pseudomonas resinovorans NBRC 106553	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas resinovorans, Pseudomonas resinovorans NBRC 106553	1245471	>tr|S6AU46|S6AU46_PSERE Trk system potassium uptake protein OS=Pseudomonas resinovorans NBRC 106553 GN=trkH PE=3 SV=1MALPTLRIIGFLNGIFLITLAVSMAVPVLTLVVYDRTSDINSFVWSSLITFVAGLALVIPGRPEHVHLRPRDMYLLTVSSWLIVCVFAALPFLLTQHISYTDAWFESMSGITATGATVLSGLDNMSPGILIWRSLLHWLGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSDKVMPRSHMVAKYIVVIYVGFTLLGSLAFWAAGMSLFDAVNHAMSAISTGGFSTSDSSLAKWQQPAVHWVAVVVMILGSLPFMLYVSVLRGHRMALLKDEQVRGFLGLLLVIWLVLGTWYWWTTSLHWLEALRHVAVNTTSILTTTGFALGDYSLWGNFSLMLFFYLGFVGGCSGSTAGGIKIFRFQVAYILLKANLKQLVHPRAVINQSYNGHRLDEDIVRSILTFSFFFTIIICAIALGLSLMGLDWITSLTGAAATVSGVGPGLGEIIGPAGNFSSLPDGAKLLLTLGMLLGRLEILTVLVLLTPYFWRH

3.7E-57	203	28.8	5E-28	107.2	7.8	2	2	A6Q5T7_NITSB	Trk system potassium uptake protein	NIS_1741	Nitratiruptor sp. (strain SB155-2)	484	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, unclassified Epsilonproteobacteria, Nitratiruptor, Nitratiruptor sp. (strain SB155-2)	387092	>tr|A6Q5T7|A6Q5T7_NITSB Trk system potassium uptake protein OS=Nitratiruptor sp. (strain SB155-2) GN=NIS_1741 PE=3 SV=1MDLHSIKNIAKFLSTIGLVLSLFLTIPSLTGLVYHEPIKPYLIFNLIFFLFHYLLFSLLWKHPAQMSIKEGIFAVNLVWILLGIGGGIGLYLTSNVTFAQAFFEAISGFTTTGATIYGDIESLSHTTLMLRSLYHWLGGMGIIVLGVGLLTIINPTGSLTLFKAESTGVTLEKLTPKIKDTAKRLWAVYIALTLFDALLLYAGGMNLFDAVNHAFSTISTGGFSTKNASLGYWENNTFILWVTTLFMFLSGINFIAHLKALSKDFSGYRSEEVLWYTAVFLFLSFALSVIHIYIGHDTFFNAVTHSFFTISSIITTTGFASTDYGQWSPIAIALIFIPMFIGANAGSTAGGVKVIRYVVVLLKNLGAQIKQILHPNAVIGVYIDQKRIGSKILGSVSGFFFIYILTTLLLSFYLYAKGYDYLTAMSASIAVIGNIGPGFGHVGPADNFTIFSEFDKVVLAIFMIIGRLEFYTFIILFSREFWKKF
3.8E-57	203	19.6	4.4E-56	199.8	13.6	1.9	1	Q8PU48_METMA	Trk system potassium uptake protein	trkG MM_2502	Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) (Methanosarcina frisia)	476	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina mazei (Methanosarcina frisia), Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) (Methanosarcina frisia)	192952	>tr|Q8PU48|Q8PU48_METMA Trk system potassium uptake protein OS=Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) GN=trkG PE=4 SV=1MNKKAIYNALGKILILLAFTMLVPLLVAFYYGEPLKPFTVSILITFLAGLLLTRIKSSAEWQQKEALAIVALTWLSAAIFGGIPFLFEGVSFIDAVFETMSGFTSTGSTIFVDIESYSRSLLFWRSFTQWLGGMGIIVLFIAILPKLGVAGRQLFRAEAPGPTEDKLKPRIKDTAKILWALYVLISAVEVVALMLAGMSLYDALTHTFAGMACGGYSPYGLGIEAFNSPLIEFILTFFMFAAGANFALYYRAIFIDSNFLLKDEEFRAYTFILLGFSGLLTLVLYKDMDFSLFNSFRYAIFQITSIMTATGFASTDFNLWTDSAKVLVFAVMFIGGCAGSTGGGMKVVRFLLMLKYARRELFKFVHPRLIRPIRFNNKAVPDDVLQSILSFVVIYILVFIFSAMFLTLLGVDMISSATASIATLGNIGPGFNVVGPMANFSALPPLGKIILINNMWVGRLEVYTVLVLFTSDFWHS
3.9E-57	203	15.9	4.2E-31	117.4	2.7	2.2	2	R5EKS2_9CLOT	Trk system potassium uptake protein TrkH	BN724_00463	Clostridium sp. CAG:590	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:590	1262825	>tr|R5EKS2|R5EKS2_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:590 GN=BN724_00463 PE=4 SV=1MNITMIFYLLGWLLNTVAALMILPFTVSIYYGEDCGKYFLLCSLVMFMVGLFLTRKRPKYTKFYAKEGFVITAISWILLSITGCLPFFLSKSIPSFTNALFECISGFTTTGASILHEVESLPRCMNFWRCFIQWIGGMGVIVFMLALIPLSGGQDLYLMKAESPGPNVGKLVPKIQKTAYYLYAIYFALTMLQIISLVIAGMPFFDSVCTSFATTSTGGFGVKNDSICGYSPAIQYVTTLFLFLSGFNYNFYFFVWIKRFRDAISMQEIKLYIAVFFGSIAIITANIFQTGYTLEESFRHASFQVGSIMTTAGFSSANFDVWPGLSKSILVLLMFIGGCAGSTCGGIKVSRILIYLKTVKKEIAQLCHPRNVKVIKIDGKPLAHNVLRSANIFLIVYMMIFVCSTLLISVDEFDLVTNFTAVASALGNIGPGLSLVGPTRNFDLYSGFSKYVLMFDMLAGRLELFPLLVCLSPSTWKKN
4E-57	203	18.2	1.4E-55	198.2	12.6	2.1	1	R7IRN4_9FIRM	Trk-type K+ transport systems membrane components	BN596_00103	Roseburia sp. CAG:303	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:303	1262944	>tr|R7IRN4|R7IRN4_9FIRM Trk-type K+ transport systems membrane components OS=Roseburia sp. CAG:303 GN=BN596_00103 PE=4 SV=1MNYAIIIYVLGYIFNFSAGFMLLPGIVAIIYREQEGWWFLLSALIIGIILLLTRKKPENKNFYAREGMVVVALGWVGISILGAVPYVATGSIPNVVNALFESVSGFSTTGASILADVESLPHCVLFWRCFTNWIGGMGILVFIMAVLPYLGANNMYLMRAESTGPAVGKLVPKIQKTAFWLYSMYIGLTVLQMILFLIGKMPVFDAVCDSLATAGTGGFAVRNDSIAGYSTYIQVVTTIFMFLFGINFKFYFLIISRKIREAFRMEEVRWYFIIYAVITILITLDLTHMAGGLLANLKDSSFQVATIMTTTGFATADFNNWPAFSQTILVLLMFVGACAGSTSGGIKVSRFIIYAKSIRKELEYQLHPRSIRKIKSDGKTMEHEVLRSTKAYLIMVLALLIVSVLIISLDGFDLVTNFTAVTSCMNDIGPGLSMVGPTGNYAAFSPLSKVVLMFDMLAGRLEMIPMLLLFTPATWRKQ
4E-57	203	21.7	6.2E-57	202.6	15.1	1.2	1	Q9RTT8_DEIRA	Potassium uptake protein KtrB	DR_1668	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	512	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus radiodurans, Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	243230	>tr|Q9RTT8|Q9RTT8_DEIRA Potassium uptake protein KtrB OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) GN=DR_1668 PE=4 SV=1MLLERGRGIAEQYSPVGPCEPRGPGPARCYNPPRSMTRPGPAPRDLASQSASQRGPGRPAETRRPWTSRLRPPQLIALTFAAAILIGAVLLWLPFAHEAGKSITFIQALFMATSCVCVTGLAVVDPGSTFNVFGESVMLLLIQVGGLGIITLGTLFALALRRRLGVIGRINAQQQVSATSLGSATSLVRSIVLTSLLFEGLGALLLLPAFIPREGVLRGIYYAIFHSISSFNNAGFSLYSTNLTGFVSDPLINMVVTLLIIFGGMGFLVQLNLLGWLRDRRRNRLSTNTRLSLTMTGVLLVVGTVFFALTEWNNPGTLAPLPLHGKLLASWFQSVTPRTAGFNTLDYGLMGFPALFMTIVWMFIGANPGSTGGGIKTNTFYVIVASAWSMVRGRRDTTLFDRRIDTETLLRAMTVGLLSMGLVTAGFMLMLLLNTNKKVLFLQLFFETVSAFGTAGLSMNTTPLLNTAQEAVLIALMFLGRIGPLTFAVAFSRPASEKMLTRYPADRDILIG
4.1E-57	203	33.8	5.6E-57	202.8	23.4	1.2	1	B1WN99_CYAA5	Probable K+ transporter	trkcce_0390	Cyanothece sp. (strain ATCC 51142)	454	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain ATCC 51142)	43989	>tr|B1WN99|B1WN99_CYAA5 Probable K+ transporter OS=Cyanothece sp. (strain ATCC 51142) GN=trk PE=4 SV=1MTIARTICVGFLAVIAVGTLLLMLPFATNDGSWNNPLVALFTSTSAVCVTGLIVVDTGSYFSFWGQLIILLLIQVGGLGYMTTTTFLILLLGRRFDLRQKLAIQESFDRPFLHGNSQTLIRSIIATTLIFEILGILLMFNVFAEKYGNLEGLWLAIFHSISAWNNAGFSLFTDSLMGFYDSWTINLVIPLLIIFGGIGYQVIMELYMAVVHRITNKRERLMFSLNFKVVISTTIILLVAGTIIFFIIEYSNPDTFGQLNFNSKLLTAWFQSVTTRTAGFNSIDIGQMTFAGLFLTMGLMFIGASPSGTGGGIKTTTLRILTNCTRSVLRGNDEVVMFRREIAVPLILKAVAVVFGSTNMVVLMTFLISLNEGIVNPSFFDSGVSSLQVLFEVISAFATVGLSTGITASLSPISQLLLILTMYTGRVGILLFMAAIVGETQPRVVQYPEETLLVG
4.2E-57	203	20.6	1.1E-56	201.7	14.3	1.5	1	C5D5C4_GEOSW	Potassium uptake protein, TrkH family (EC 3.6.3.14)	GWCH70_0431	Geobacillus sp. (strain WCH70)	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Geobacillus, Geobacillus sp. (strain WCH70)	471223	>tr|C5D5C4|C5D5C4_GEOSW Potassium uptake protein, TrkH family OS=Geobacillus sp. (strain WCH70) GN=GWCH70_0431 PE=4 SV=1MNKKRMFYLDPPKILVLGFSFIILIGAFLLTLPAATVDGKGLPWLDALFTATSATCVTGLVVVDTGTTFTLFGQLVILALIQIGGLGFMAFATLFALILGKRISLKERLLIKESLNNLSIDGVVRLVKRILIFTAVIELIGGILLAIRFSFDMPLPKAIYFGFFHAISNFNNAGFDLMGDFRSLTGYVDDPLVTLVVCTLITLGGIGFIVMNEVYEYRQTRRFSLHTKIVFVMSSILVVFGTILIFILEYHNPKTLQPLSPLGKFLASLYQAVTPRTAGSNTLNIPDLTQPTLFLIIFLMFIGASPSGTGGGIKTTTFATLLGAVWSNIKGKEDVIFFRNRILYDTIYKALTVTVSGLFVVMMITMLLTITEPNKDFLMILFEATSAFATVGLSMGLTPELSPVGKILIILTMFAGRVGPLTIAYAVTLHRKPDPFKFPKGKIMIG
4.2E-57	203	18.4	5.5E-57	202.8	12.7	1.1	1	R6SEM1_9FIRM	Potassium uptake protein TrkH family	BN586_00909	Dorea formicigenerans CAG:28	461	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea formicigenerans CAG:28	1263073	>tr|R6SEM1|R6SEM1_9FIRM Potassium uptake protein TrkH family OS=Dorea formicigenerans CAG:28 GN=BN586_00909 PE=4 SV=1MKRYNRKKNIRWNTMKILAAGFLFVIVAGAVLLWLPVSNQKPIEFFDALFTSASAVCVTGLVTIIPQTQFTLFGKVILILIQIGGLGIIACVTAFFLLLRRQITVRERMVIQETYNADSIGGIVGMVRRILIGTFTVEGVGALFYAVQFVPEYGLLRGIGYSIFHSVSAFCNAGIDILGSDSLAKYICNPLINITTMLLIILSGIGFGVWYDVLGNIKKIRKKEIPGKWWFTRLRLHSKLAIVTTLILLAVGTLLTFLLEYHNPDTIGHLSFGEKWMASAFQSVTTRTAGYSTFSQAGMHEETRFLNILLMFIGGSPGGTAGGVKTTTIAMLMLTCIAFVRGGQDTECFGRRISAQNVRMGFVTVVLALICYLTGTTLIAVFEADRLSFLNIMYETASALGTVGLTADLTSHLCRESQAVIIALMYIGRVGPVTIALLFAGKKNQKDRMRTLPTNNILVG

4.3E-57	203	22.2	3E-31	117.9	4.6	2.1	2	Q8REU6_FUSNN	Trk system potassium uptake protein trkG	FN0993	Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131)	483	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Fusobacterium, Fusobacterium nucleatum, Fusobacterium nucleatum subsp. nucleatum, Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131)	190304	>tr|Q8REU6|Q8REU6_FUSNN Trk system potassium uptake protein trkG OS=Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131) GN=FN0993 PE=4 SV=1MNTKIISYVISNLFKLMMVLFLFPLATSIYYKEGLKLSMAYIIPIIILCILSYFLSDKSPENQSFFSKEGLVIVSLSWLLISFFGALPFVIS GSISNIVDAFFESVSGFTTTGASILPEVESLSRSILFWRSFTHVVGGMGVLVLVLAILPKGNNQALHIMRAEVPGPTVGKIVAKMNYNSR ILYIIYISMIIILIFLLLGGMPLFDACIHAFGTAGTGGFSCKNTSIGFYNSAYIDYVTSIGMIAFGLNFNLFYLLILGNIKQVFKSEEAKYYLGII FIATTLICINIYPIYSSISRMIRDVFFTVSSIITTTGFSTVDFDKWPTFSKTILMFLMFCGACAGSTAGGFKVSRLAILIKKFVREFKKIGHPN KVLNIKLEGKTLDKEMLEGVDSYFILYSVILFILLLITAWDSDTFITALSAVLATFNNIGPGLGAVGPTSNFASYSAFTKIVLSLGMLLGRLE IIPLLILVSPRIYRKRD
4.4E-57	203	30.2	8.3E-56	198.9	20.9	2	1	R5W4L3_9DELT	Potassium uptake protein TrkH family	BN495_00326	Corallococcus sp. CAG:1435	452	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, environmental samples, Corallococcus sp. CAG:1435	1262867	>tr|R5W4L3|R5W4L3_9DELT Potassium uptake protein TrkH family OS=Corallococcus sp. CAG:1435 GN=BN495_00326 PE=4 SV=1MKSKRSFKLSGWQLLAVGYLTVILCGSALLSLPSATADGTTTYINALFVSTSATCVTGLVPYDTGTHWTFFGQIVILALIQTGGLG FMTFVSLAVSMFGKKMGLYGRKVLMLSAGGSDLASLRHMIKRIFLGTFLFEGIGAILLSIRFIPTFGTLYGLYFAIFHSVSAFCNAGFDIL GAEYGEFASLTYYAKDPLVVLTIAFLIIIGGLGFCVWSDIWDTKFRWKKFRLHTKIVLSVTASLLVVSTLLFVVFERNNVETADFTFGEKV LVAFFNATTTRTAGFNTVDMSGLSDSGYLLAVMLMFIGGSSASTAGGVKTNTMAVIVMGMFAAFRGKKDIEAGKRRIDHALLGQALAI FVSCLFLVIVATLAICTIEMDSVAPFKAVLFETVSALGTVGLSMSLTTKLGSISKLILILLMYAGRVGILTLALAFGENRSVSNIRKPLDDTIL VG
4.4E-57	203	12.9	1.1E-55	198.5	9	2	1	A0LD79_MAGMM	Trk system potassium uptake protein	Mmc1_3436	Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1)	478	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Magnetococcales, Magnetococcaceae, Magnetococcus, Magnetococcus marinus, Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1)	156889	>tr|A0LD79|A0LD79_MAGMM Trk system potassium uptake protein OS=Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1) GN=Mmc1_3436 PE=3 SV=1MNYRMNVRLLSVLALLLGTLQLMPLFYAWYAKLSLWPWQLSLMISMGGGGIGLLLTRGAASALCPRDGFFVTTAGWSLAIVLG AIPYVASHELGWAAAIFESSSGFTTTGSSILPHPEGLPASLQLWRSQTQWVGGMGMLLLTIAILPFLGVGGMQLMKAEVPGPSKERL TPRLMTTARVLWGFYLGLTVLAGLAYYFAGLSPFDALNHAFTTVATGGFSTKDQSFLAFSPAAQWWCILFMALAGTNFLLHYRLVMH RDLSIFKDDELRLYLAIMLGVGGAVALLLMHDMQMDAMHALRESLFQTVSLMTTTGFASTDWEQWPALPIFLLFLLMGVGGMAGSTS GGPKVVRVAVVMKLLSMVTRRLVQPNRVVVLQLGHRAVTTAVVEGCVGLLVATVILVVVSGCLLHLLGMDLTSALSAALTCVANVGP GYGSVGAMDNFSQVSELGKLLLAFDMLAGRLEIFTVLMLFTPGFWRR
4.7E-57	203	21.1	6.4E-57	202.5	14.6	1.1	1	C4LII3_CORK4	Potassium uptake protein, TrkH family	ckrop_0884	Corynebacterium kroppenstedtii (strain DSM 44385 / CCUG 35717)	461	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium kroppenstedtii, Corynebacterium kroppenstedtii (strain DSM 44385 / CCUG 35717)	645127	>tr|C4LII3|C4LII3_CORK4 Potassium uptake protein, TrkH family OS=Corynebacterium kroppenstedtii (strain DSM 44385 / CCUG 35717) GN=ckrop_0884 PE=4 SV=1MAKRGIGGRSLNPTQLVSIGFFGLIVIGALALMMPFSSVTHTVTDPLTAIFTSTSAVSLTGLTVVDTGGHWSTTGKIIIATLIQLSGL GIMSLTSLAGMILTGRFGLRLRMNAAAEGRTLSIGDVKSTLIATLGFTALVEGAVTLMLASRFANKYGMSVDRAMGEGLFHAISSFNNA GFGLRKDNLVPYAADAWILLPLAGSIIIGGLGFPVLRELVTRLRIRLSRGWNWSNRDKRLGHLSVTSRLTLIGTAALLLGGWLVIGVLE WNKAMSGMPIGEKILTAFFQSVTPRTAGFNSVDYGQFHPSTLFITDIFMFIGGGSAGTAGGIKISTLLVLVAAMIAEFRGETDTVIGHRK ISYSVVRQAMTVFALGIMLVAVGVISLMLIENKFTGSQILFEVTSAFGTVGLTTGITPSLQGSSQIILCFIMYLGRIGPITLVTALAGQDKA RRFSYPEERPFIG
4.7E-57	203	30.1	7.5E-57	202.3	20.9	1.3	1	A0RRD6_CAMFF	Cation transport protein, putative	CFF8240_1641	Campylobacter fetus subsp. fetus (strain 82-40)	442	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Campylobacter, Campylobacter fetus, Campylobacter fetus subsp. fetus, Campylobacter fetus subsp. fetus (strain 82-40)	360106	>tr|A0RRD6|A0RRD6_CAMFF Cation transport protein, putative OS=Campylobacter fetus subsp. fetus (strain 82-40) GN=CFF8240_1641 PE=4 SV=1MNKIFSTILASYILLAFIGAIILSFDIMRLKPISFIDLLFTATSAVCVTGLITANTATDFSGYGQGIILALIQAGGFGYMSLAGFLFLLIGK KVDFKGKMLLKESLDYPNMQGIIKYLKKIFVFTACIEIIGAVILTLNFMLDMPFKKAVWAGVFHSISAFNNAGFSIFEYNLAEYRDNFVLNI TICFLVILGGLGFLVLSECFNYYKKSSRISIHTRIVLIATIICILLGMAVLLIFEWENSKSIGSLNWFHKLLSSFFVSVNLRTSGFNTIDLGSL HDQSLFFSSLLMIIGAAPGGTAGGIKITTVAVLLIYAYCSLRDKETVIFQRTIPENIVKKSFLIFIIAVFYIISTIILSTTDDKENRYFLPLLFEIC SAFGTVGVSTGDGESLSLSAKFSDFGKFYIIVLMFMGRVGVLVFSMALFRKSKNNSIKYPEEGVVL
4.8E-57	203	37.9	6.4E-57	202.5	26.3	1.1	1	Q7VGW5_HELHP	Uncharacterized protein	ktrB HH_1205	Helicobacter hepaticus (strain ATCC 51449 / 3B1)	466	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter, Helicobacter hepaticus, Helicobacter hepaticus (strain ATCC 51449 / 3B1)	235279	>tr|Q7VGW5|Q7VGW5_HELHP Uncharacterized protein OS=Helicobacter hepaticus (strain ATCC 51449 / 3B1) GN=ktrB PE=4 SV=1MTNLKSMQILIIGYVGIIILGALLLFLPCMHSSSLSFIEALFTSTSAFTCTGLIIKDTALDFTPFGQAVILALIWLGGLGYMSMLGIVYV FLRKRLSNRERNMIKESLNYPSYDGMMSFLKKVLFFVILIESFGALALFIYFYFVQDFSVFTALWAGIFHAISAFNNAGFSIFSTNLMAYR QSVFVNSVICFLIIAGGMGYIVLIELHTFIKSRLYIFWNICLAFMRNKPLSNLHTIRLSLHSKIVVSYTFVLLTLGFSFIFVLEYHNPKSMGNF EFFDKILSSFFMSVNYRTSGFNSIDLGGLKDSTMFFSSLLMIIGGAPGGTAGGIKVTTLATLFAFCAALFYDTQPRLFKRRIMEKSVKKAI GVGIIAMICITLANFIIAALQEDTRFMLIMFEVSSAFATTGVSAGNGGTLSLSANFSPLSQIVIIGLMLMGKVGILAFWLAFVGKRKQSYIT LQEERVII
4.8E-57	203	20.4	6.9E-55	195.8	14.1	2	1	R6KG52_9FIRM	Trk-type K+ transport systems membrane components	BN564_00453	Eubacterium sp. CAG:252	493	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:252	1262887	>tr|R6KG52|R6KG52_9FIRM Trk-type K+ transport systems membrane components OS=Eubacterium sp. CAG:252 GN=BN564_00453 PE=4 SV=1MNRSIVIYVLGYILKTEGVLMSLPCLVALIYQEKEGFAYLIVGVISILLGQLLTMRKPKDYVIYLKEGCVATSLSWILMGVVGAIPFMI TGEIPSFINALFEMVSGFTTTGASILSDVEVVSRCSTTWRCFSHWIGGMGVLVFIIAIVPLSGGSNINLMRAESPGPSVGKLVPKVKHT ARILYIIYLGLSLIEFIILLLAKMPVFDAMNTTFGTAGTGGFGIKNSSLGGYSVTIQWIVTVFMILFGVNFNAYYLMLFGSIKKALTMEEVRA YFGIILTSIVIITINIYSMCSSVWDAITKSAFQVGSIITTTGFSTIDFNLWPQTSKTILVLLMFVGACAGSTGGGIKVSRFVILIKTMVKELNS YIHPRSVRKIKVEGKPVEHEVIRSVNVYLITYVLVFVASVFLVSFEGKDLTTNFTAVAATFNNIGPGLELVGPTQNFAHFNVLSKLVMIFD MLAGRLELFPLLLLFHPVIIKEMFEDKRRYKKAKKMS
5E-57	203	29.4	1.7E-55	197.9	20.3	2	1	R6T3N8_9FIRM	Potassium uptake protein TrkH family	BN714_02178	Ruminococcus sp. CAG:57	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:57	1262962	>tr|R6T3N8|R6T3N8_9FIRM Potassium uptake protein TrkH family OS=Ruminococcus sp. CAG:57 GN=BN714_02178 PE=4 SV=1MLHKNRVKNRTHMTSFRVIISFFCLILVGTLLLMLPISSRQRCVTSFPDAMFTAVSATCVTGLVVKDTATYWSMFGQVVILMLIQI GGMGVITVGLAIIRASGRKIGLWQRSTMQESISAPQVGGIVKLTGFILKTSLIIEMIGAALLAPVFCNDLGIAKGLWYSLFHSISAFCNAG FDLLGIKEPFSSLTFYHSNIYLNIIIMLLIITGGIGFLVWGDIGTHKHRIRRYSLQSKVVLMTSAVLIVLPALYFFFEYDHGTIHDRTIHSLF QSVTTRTAGFNTTDLAAMDESGTAIMIILMLIGGSPGSTAGGMKTATFAVLFLSAITVFSRRNDVQCFKRRISDETVRSAGAVLFMYLV LFFTSGVIISRVENLPLLTCLFETSSAIGTVGLSLGITSGLSAVSRVILMILMFFGRVGGLTLIYAALPSADSQNSRLPLEKISVG

5.3E-57	203	22.6	1.1E-56	201.8	15.7	1.4	1	D2RLA5_ACIFV	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Acfer_1498	Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4)	442	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Acidaminococcaceae, Acidaminococcus, Acidaminococcus fermentans, Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4)	591001	>tr|D2RLA5|D2RLA5_ACIFV Potassium uptake protein, TrkH family OS=Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4) GN=Acfer_1498 PE=4 SV=1MNQIKRFSPSQLIALTFVGLILAGALLLMLPCASADGSSLSFVDALFTATSASCVTGLVVVDTGTYFSLFGQLVIIALIQLGGLGLVL FATLFSVIMRKRIDLQSRLNIQASLNQNELDGVVRMSLRIAKYTAVIEGVFGTLLAIRFYPQYGIRGIVYGYWHSVSAFCNAGFDLFGHY QSLTAYVGDPVVNLCICLLIILGGLGFAVMRDVMEKRNFRQLKLHSKMVLVSTVVLIAGGTAVIGLLERDNPGTLGSLTGSEAFWASFM QSVSPRTAGFNTLDLNSLRVPTMIFVIMLMFIGASPASTGGGIKTTTFSLLLLNIWQVVRGKEECEIFGRRITGETMFQAFAIASMSLLW VFFATLMLTCLEDTSFLYAAFEVVSAYATVGLSTGLSQHICTASKIILMLSMYAGRVGFMTFALALAANKPSGHIHYPKENIIIG
5.3E-57	203	29.7	7.4E-57	202.4	20.6	1.1	1	J7M6Y9_STRP1	Potassium uptake protein	ktrB M1GAS476_0341	Streptococcus pyogenes M1 476	463	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pyogenes, Streptococcus pyogenes serotype M1, Streptococcus pyogenes M1 476	1207470	>tr|J7M6Y9|J7M6Y9_STRP1 Potassium uptake protein OS=Streptococcus pyogenes M1 476 GN=ktrB PE=4 SV=2MSGGNMKRSFIKSLSVTQRLTFSFAIVILIGTLLLSMPFTHYQNGPNTVYLDHFFNVVSMVCVTGLSVVPVAEVYNGIGQTIAMAL MQIGGLGLVTLIAVSTFALKRKMRLSDQTLLQSALNRGDSKDLKHYLFFAYKVTFSLEAFAAIVIMIDFIPRFGWKNGIFNSIFLAVSAFC NAGFDNLGSSSLKDFMLNPTLNVIITFLIISGGLGFAVWVDLGVAFKKYFFEKPHCYGATFRKLSNQSRLVLQTTAVILFLGTFLTWFLE KDNSKTIANFSLHQQLMVSFFQTVTMRTAGFATISYNDTLAPTNILYMIQMVIGGAPGGTAGGIKVTTAAITFLLFKAELSGQSEVTFRN RIIANKTIKQTMTVLIFFFAVLMIGFILLLSVEPHIAPIPLLFESISAIATVGVSMDLTPQLSTAGRLIVIVLMFVGRVGPITVLISLIQRKEKTIQ YATTDILVG
5.5E-57	203	29.2	1.9E-55	197.7	20.3	2	1	R6CEU5_9FIRM	Potassium uptake protein TrkH family	BN718_00146	Ruminococcus sp. CAG:579	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:579	1262963	>tr|R6CEU5|R6CEU5_9FIRM Potassium uptake protein TrkH family OS=Ruminococcus sp. CAG:579 GN=BN718_00146 PE=4 SV=1MLHKNRVKNKTHMTSFQVIIISFFCLILVGTLLLMLPISSRQRCVTSFPDAMFTAVSATCVTGLVVKDTATYWSLFGQAVILMLIQI GGMGVITVGLAIIRASGRKIGLWQRSTMQESISAPQVGGIVKLTGFILKTSLIIEMIGAALLAPVFCNDLGIAKGLWYSLFHSISAFCNAG FDLFGIKEPFSSLTFYHSNIYLNIIIILLIITGGIGFLVWGDIGTHKYRIRRFSLQSKVVLMTSAVLIVLPALYFFFYEYNRETIHDRTIHSLFQ SVTTRTAGFNTTDLAAMDESGTAIMIILMLIGGSPGSTAGGMKTTTFAVLFLSAITVLSRRNDVQCFKRRISDEAVRSAGAVLFMYLVLF FTSGIIISRVENLPLLTCLFETSSAIGTVGLSLGITSGLSAVSRVILMILMFFGRVGGLTLIYAALPSTDSKNSRLPLEKISVG
5.8E-57	203	36.4	8.2E-57	202.2	25.2	1.1	1	A0A088T0Q1_9MOLU	Ktr system potassium uptake protein B	ktrB KQ51_00611	Mollicutes bacterium HR1	449	cellular organisms, Bacteria, Tenericutes, Mollicutes, unclassified Mollicutes, unclassified Mollicutes (miscellaneous), Mollicutes bacterium HR1	1541959	>tr|A0A088T0Q1|A0A088T0Q1_9MOLU Ktr system potassium uptake protein B OS=Mollicutes bacterium HR1 GN=ktrB PE=4 SV=1MDRIRKKRRIHFNAAEIIAIGFAAVIFIGAILLVLPFASKSGVSVGFVDALFTAASAVAVTGLVVVDTATHWSTFGQVVILMLIQIGGL GFITMGTLFALLLGRKITFGRRVIMKEAMNKITANGVVRLAKSILILTFIVEGIGAVILSSRFIPIYGLGKGIWFSVFHSISAFCNAGFDLIGN FQSLTPFVQDPIIVLTVALLVIVGGLGFVVIFELLEKKNLKRLSLHSKITLSLTAFLLVFGFIVVMALEFNNPDTMGNLSFGGKLLSGFFHS VTPRTAGFNTLPMNQLMMGTIVITILFMFIGAGSAGTAGGVKITTVGVIIATIVSTLKGRKETESFKRKIPRGLVNKALAILSIAAMWVIMV TFILSITENADFMTILFEVVSAFGTVGLSLGITTQLSTIGRIVLTITMFVGRIGPLTLFMALAQRHQMPTNLAYPDEEIMIG
5.8E-57	203	22.6	1E-55	198.6	15.7	2	1	C9LRI3_SELS3	H(+)-transporting two-sector ATPase (EC 3.6.3.14) (Potassium uptake protein, TrkH family)	Selsp_1944 SELSPUOL_00049	Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	440	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Selenomonas, Selenomonas sputigena, Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	546271	>tr|C9LRI3|C9LRI3_SELS3 H(+)-transporting two-sector ATPase OS=Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28) GN=Selsp_1944 PE=4 SV=1MNIIGLLRRLSPFRIIILSFLVLILCGTGLLMLPWATANGEGASLSDALFTAVSASCVTGLTAVDTASYWTLFGQLVILAMIQVGGF GVITVAVSLAALSGQRIGLMQRSLSKEAVSAPQLGGIVPLLYFILRLTFFIEFLGALFLAPSFCQKVGLVRGIYFAVFHSISSFCNAGFDLF GNSLMDFAADPVVNITVMLLIIAGGLGFTTWADIRLNRRNFRAYSLQSKIALTMTAVLILVPALFFFFFELDPGVSTGEHFLISLFQSVTT RTAGYNTIDIKDFSETGRAALIVLMLIGGSPGSTAGGIKTTTAFTLFAIMIATFQLKENPTCFSRRLSPETQRHAVTILMMYLLLFASGSVL LNLIDDIRLIDSAFETASALGTVGLSIGVTEDLGPLSKCVMMILMFFGRIGGLTVIFAAHARGRHESGRRPEERITIG
6E-57	203	22	1.7E-55	197.9	15.3	2	1	R5BRW7_9FIRM	Uncharacterized protein	BN499_01701	Blautia hydrogenotrophica CAG:147	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	1263061	>tr|R5BRW7|R5BRW7_9FIRM Uncharacterized protein OS=Blautia hydrogenotrophica CAG:147 GN=BN499_01701 PE=4 SV=1MFFNKIKIQPGQIIIVGFAGTILIGALLLMLPFATKDGRGAEFIDALFTATSATCVTGLVVFDTFTYWSVFGQVIILLLIQVGGMGVVT MAITIFIVTGRKIGLNQRFLMQESISAPQMGGIVRLTGFIIKSTILMESVGAILLAIRFCPQMGLGKGLWFAVFHSITAFCNAGFDLMGEK GEFSSLTHYEADPIVNLTIMLLIIIGGIGFFVWDDLRKNKLRFRYYRLQTKLVLVTTACLLILPAVYFFFAEFGKSVWGFSSLSERIWASV FQSVTPRTAGFNTVDLTLAAEPTVFLIIVLMVIGGSPGSTAGGFKTTTLATAILCIRSVFRKQDHIQCFGRRLPSEIIRHTTALCTLYLILFL TGGVLICSLEDIPLLTALFETASAIGTVGLTLGITPELGDASHIILILLMYFGRVGGLTMIYALHGDQVPVMAQMPKEKITVG
6.1E-57	203	14.2	6.2E-29	110.2	2	2.1	2	D9R130_CLOSW	Cation transporter	Closa_1998	Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	610130	>tr|D9R130|D9R130_CLOSW Cation transporter OS=Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1) GN=Closa_1998 PE=4 SV=1MNKKVIIYVMGWILNIEAIFMLLPCIAALIYKETSGYWFLVVMAACGAIGLIFTHRKPENMVFYAKEGFVSVALSWIVLSFFGALPF YLSGEIPEFEDAMFEVISGFTTTGASVLPDVESLSKCMIMWRSFTHWIGGMGVLVFILSILPLAGGYNMYIMKAESPGPSVGKLVPKVR ATAKILYKIYLFMTALEVILLMLGGMPFFDSLAISFGTAGTGGFGIKNNSMAFYESYYLQGIVTVFMVLFGINFNVYHLFLTRHPKEALHS EEARAYLGIIAASVLLITINIRGGFGSLFSAFHHAAFQVASIITTTGYSTVDFDLWPEFSKGILVALMFVGACAGSTGGGFKVSRIVILLKA LKKELGTLIHPRSVKILKLEGKPIEHHVLRSINTFLGAYIAIFTASVLLVSLDNFDFTTNFTAVAATFNNIGPGLAGAGPSQNFSHFSPFSK YVMMFDMLAGRLEVFPMLLIFAPSTWKDS
6.2E-57	203	20.3	2.4E-29	111.6	5.7	2.2	2	Q3ZAG5_DEHM1	Trk system potassium uptake protein, putative	DET0029	Dehalococcoides mccartyi (strain ATCC BAA-2266 / KCTC 15142 / 195) (Dehalococcoides ethenogenes (strain 195))	481	cellular organisms, Bacteria, Chloroflexi, Dehalococcoidia, Dehalococcoidales, Dehalococcoidaceae, Dehalococcoides, Dehalococcoides mccartyi, Dehalococcoides mccartyi (strain ATCC BAA-2266 / KCTC 15142 / 195) (Dehalococcoides ethenogenes (strain 195))	243164	>tr|Q3ZAG5|Q3ZAG5_DEHM1 Trk system potassium uptake protein, putative OS=Dehalococcoides mccartyi (strain ATCC BAA-2266 / KCTC 15142 / 195) GN=DET0029 PE=4 SV=1MKINNVLHYLGLVIAILGGFMFIPFVFSLINAEPDQLAFGVSIVITLSAGFLLWRFTPITERRISLRESLAIVAGSWIMAALFGSLPFII SGVLPSVIDCIFEAMSGLTTTGASVFSSVENLPHGILVWRSLTQWIGGLGIIMLFVTILPMLGIGASQLMEAETPGQQERLTSRIRDTAR TLWLLYLGFTVAGFIALMLAGLPGFDAFNIILTTTPTGGFAPVSSIGVYNNLAVELILIFFMVASGVNFGLYYYLLWKGRPAKFFGNAEF KLYIGILIGCILLINWDLVANAGMGIFEGLRQASFQTASVMTTTGFATADFAQWPHFSQAILLVLMVVGASAGSTGGGLKVIRLLVLFKY TYRRIQLTFNPNAVIPIKIGGYVISDKLISRSVGLTILYFATLWAGFLVMSAIGLDFVTALSSITSCLGNVGPALGTVGPMASYADIPGIGK LVLLTAMLVGRIELFTLLVLFIPAFWRWR

6.2E-57	203	25.7	1.4E-55	198.1	17.8	2	1	D9R4D5_CLOSW	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Closa_2435	Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	453	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	610130	>tr|D9R4D5|D9R4D5_CLOSW Potassium uptake protein, TrkH family OS=Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1) GN=Closa_2435 PE=4 SV=1MNLEEKQSKRVKRHVSQTQFIAYGFFCLIITGALLLMLPISSRDGQSEDFLSCLFTATSASCVTGLVVRDTWTQWSLFGQMVILT MIQIGGLGFVTVGVFISIVLRRKIGLKERGLLQESVNTLQIGGVVRLAKGIIKGTCLFEGVGAILLAIRFIPKYGFWRGMFYGIFHSISAFC NAGFDLMGNQTPYSSFVSYYDDWLVNLVIMSLIIIGGIGFIVWEDLYRNKLHFKKYMLHTKMVLVITSVLVFGGGLLFYLLERNNLLVGM NVSGQILTSLFSSVTARTAGFNTTDTAALTDGSKLLTIILMFIGGSPGSTAGGIKTTTMFVLLMCVHSNIKQTYGVNIFGRRLEDNVIKRA GAILTINLFLALSASLAIMAIQPLGFSDILFETTSAIGTVGMTTGITRDLYSVSRVIIIILMYSGRIGSLSFALAFAQSHRKAHVEQVTETINV G
6.2E-57	203	24.7	4.1E-56	199.9	17.1	1.8	1	R6R1R6_9FIRM	Uncharacterized protein	BN652_02652	Firmicutes bacterium CAG:424	445	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	1263022	>tr|R6R1R6|R6R1R6_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:424 GN=BN652_02652 PE=4 SV=1MKKRKWTTTKVIAVGYVLVIAIGTILLMLPISGRSHEPTPFMDAWFTATSATCVTGLVTHDTYTYWSSFGQGVLLVLIQIGGMGF MTIAISALTFTRKKIGLSQRLMMQESVAAPQVAGVVRMSRLILVGTVLCEGLGAVLLSFYYVPRLGLGKGIYFSVFHSVSAFCNAGIDL MGYYEPSSSLITASDSYLVGITIASLILVGGIGFLVWEDIKHWKWHISRYRLHSKVVLTSALILVVGGTLFMFLFEYGKPSMEGKNLGEQ ILCSFFQAVTPRTAGFNTMDLNQLTDSSQMLMVCLMFVGGAPGSTAGGIKTTTMAILLLTIWTEFKKRKDVEMFKRRVEGEVIRHAVCI LMLYGSLILISSMAICAVEGIGAKEVIFEVVSALCTVGLSLGITPEVGTLSHIILILLMFIGRVGGITILIAFSNRISSIPSKLPAEKIAVG
6.3E-57	203	34	3.9E-55	196.7	23.5	2	1	C4IIX4_CLOBU	V-type sodium ATP synthase, J subunit (EC 3.6.3.14)	CLP_2360	Clostridium butyricum E4 str. BoNT E BL5262	448	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	632245	>tr|C4IIX4|C4IIX4_CLOBU V-type sodium ATP synthase, J subunit OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_2360 PE=4 SV=1MEKVITKKNRLSEVRILALGFAVVILLGGVILSLPISSKSGRYTSLVDSIFTATSAVCVTGLVTLDTGTYWNTFGQCIIMILIEIGGLG FMSVTTFIAMILGRKITLRDRLIMQEAMNTFNIQGLVKMLRYVLGLTFTVQIAGAFLLSFVFVPKFGISTGVFYSIFHSVSAFCNAGFDLF GNFSSLTSFSGNYLVIIVISLLIIIGGIGFTVLIEILNYKKMKKLSVHSKIVICITASLIFGGAAFIFLVEYKNTATLGNLNLGEKILNSMFSSITP RTAGFNSISTGDMTMSGKLMTIILMFIGGSPGSTAGGLKTATFGVLVLTVISVLRGRNDTEAFGRRFSKETVYKAFTVFALGMAIVLVV TTILSIAEPNQQFIDLLYEASSAFGTAGLTTGVTQEIGTLSKIVLMFTMYCGRVGPITVFLALIKRNNKSGIKYPEGKILIG
6.4E-57	203	32.9	1.1E-56	201.8	22.8	1.3	1	Q8XJ70_CLOPE	Probable potassium uptake protein	trkB	Clostridium perfringens (strain 13 / Type A)	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium perfringens, Clostridium perfringens (strain 13 / Type A)	195102	>tr|Q8XJ70|Q8XJ70_CLOPE Probable potassium uptake protein OS=Clostridium perfringens (strain 13 / Type A) GN=trkB PE=4 SV=1MYIKLTKKIKFSAVQILALGFSMVILLGAIILSLPISSKSGEFTPFLDSLFTSTSAVCVTGLITLNTAAHWNYFGKTVIIILIQIGGLGFM SFTTLFALMVKKKITLRERLLIQEAMNTFGIQGLVRMIRYILAFTFSVEMLGALLLSTQFIPKFGFLKGIYYSIWYSISAFCNAGFDLFGDN LVGYANNKTVILTIAALIVIGGLGFTVWSELYNYKGYKKLSLHSKVVIMITAILLIGGAILMFIFEYNNPNTLKYMSFGDKLTNAFFASATTR TAGFNSVSTADMTLAGKFLTILLMFVGGSPGSTAGGIKTATFGIVVLTLISIIRGREDTEVFKKRISKELVYKAFAVLFIGFGIVVLGTLILA VTEPGFSLEYILYEVTSAFATVGLTLGLTPYLSVIGKIIIIITMYLGRVGPMTVVLALANRKKPSAYKYPEDKILIG
6.8E-57	203	18.7	1.8E-56	201.1	12.9	1.6	1	D5BK20_ZUNPS	Cation transporter	ZPR_1364	Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87)	519	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Zunongwangia, Zunongwangia profunda, Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87)	655815	>tr|D5BK20|D5BK20_ZUNPS Cation transporter OS=Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87) GN=ZPR_1364 PE=4 SV=1MFKTILQQIAILQLILGGVILVPGVVAVIYGEWYSLLGFCISSLMISGIAYGIYKSLKNVEDPQYQQSLMIAALGWLMIIVMGSIPYYM IAQFTPLEVMQSFVPSGLEYESSLLNFRNPLHCLFESTSAFTTTGLTMSYHEPSIGKSLMFYRCFSQWIGGAGFIVMALAIFKQIPGQS ALLLYGSEASGTKLKTNVIQTARSIWKIYVFITFLMAVYLFIGTYFILPDYPIAENIFDAVNHAMAGQSTGGFSTLDDSIAGYQSAKMEILF LLPMLVGGFSIPFLYRFTILQNYKLLWHDIQTRAFIIASVIGGILLSVLLMNSNGVSDPVREGIFQFVSGLSTTGWQTANIGAWDDLPVLF MVAGAMIIGGSAGGTVGGIKIIRALLLQKGLRWHINKIFASEHTIKKVKFNNRYLLPAEMNEELARAGLFTLIYLLFVFFSTCFTVYFMQD GYTLADAIFESASAQGTVGLSTGISDPSMNPVLELIYIIQMWAGRIEIIPILVLVRVLLYGTKIRNI
6.8E-57	203	11.7	6.1E-55	196	8.1	2	1	R6DWC5_9FIRM	Trk-type K+ transport systems membrane components	BN516_00822	Firmicutes bacterium CAG:176	446	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:176	1263007	>tr|R6DWC5|R6DWC5_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:176 GN=BN516_00822 PE=4 SV=1MTESGFHLKHHLTSFQIMILGFAGVILLGALVLMLPIATASHTWTPFHEALFTSTSAVCVTGLVVQDTGSYWSGFGQTVILLLIQI GGLGVITAAVTFLMLSGKNISLKERSAMQDAISAPVVGGIVRLTRFILKGTFFVELVGALALLPAFCRDYGLRGVWMAIFHSVSAFCNA GFDILGRADTLYPSLTAYISDPLVNIVIMLLIIVGGIGFLTWDDVCTHRLHLRRYRMQSKVILSVTAILIALPALLFFLTDFAEFPTGQRVLA SLFQAVTPRTAGYNTADLTKMSDTSQAVTILLMLTGGAPGSTAGGMKVTTLAVLAANAVAAFRRREDPQLFKRRLEPSAVRNAAAILL LYLGLTFAGAAVISAAENLPLGACLYETASAAGTVGLTLGLTPQLGTLSQGILILLMFFGRVGGLTLIYAAFSGHDLTYARYPKEMITVG
7E-57	202	32.8	9.4E-57	202	22.7	1.1	1	B9DQA3_STACT	Putative sodium transport protein	Sca_0626	Staphylococcus carnosus (strain TM300)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus carnosus, Staphylococcus carnosus subsp. carnosus, Staphylococcus carnosus (strain TM300)	396513	>tr|B9DQA3|B9DQA3_STACT Putative sodium transport protein OS=Staphylococcus carnosus (strain TM300) GN=Sca_0626 PE=4 SV=1MSIFNQLFKKTSPQQGIVMYYLIAIVAAFLMLNLPYVHKPGVHVNPIDTLFVAVSGISVTGLTSISIVDTYSTFGQIIILIILNIGGVGV MAMGTVLWLVLRKRIGLRERQLIMLDNNRNTMSGAVKLIIEIVRAILLIELVGALLAFYFYRDSSDIQYALMQGFFVAISSTTNAGLDITG NSLIPYADDYFVQTIVMFLITLGSIGFPVLLEVKAYIKNRIPNFRFSLFAKITTITYFALFAFGTIVILLLEANHAFQGASWHKALFYAMFQS TTTRSAGLETIDITHFSDATNILMGLLMFIGSSPSSVGGGIRTTTFAIILIFIINFRNDTNSTTIKVFNREIQPSDIQKTFTVFGVATILTSVAII LTSAFEGTKLSFLQVFFEIMSAFGTCGLSLGASGDGNDFTKVILMLLMFIGRVGLISFIIMIGGRKDPVMYHYPKEKIQIG
7.7E-57	202	17.4	5.6E-28	107.1	6.7	2.1	2	R6SJ63_9CLOT	Trk-type K+ transport systems membrane components	BN719_01307	Clostridium sp. CAG:58	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	1262824	>tr|R6SJ63|R6SJ63_9CLOT Trk-type K+ transport systems membrane components OS=Clostridium sp. CAG:58 GN=BN719_01307 PE=4 SV=1MNYSMIFFIIGWVFIIEAALMAPSALVAVLYSERSIWAFAAAIGLCLLLGVPLVRKQPANKVFYAKEGCVTVALSWIVMSLMGALP FVFSGVIPSIVDAMFETVSGFTTTGASILKDVEVLPRCMLFWRSFTHWIGGMGVLVFLLCLLPMSGGGYSMNLMKAESPGPSVSKLV PKVRSTAKLLYGLYVALSLLELALLLLGSMPLFDALCTTFGTAGTGGFGIKNSSIGEYSAYIQSIVTIFMILFGINFNVYFLLYMRKPKEAL RCEEAGWYLAIIAVSTLIITVFIRNSFPDLVTAFRHAAFQVGSIITTTGFSTVDFNVWPAVPRAILVLLMFIGACAGSTGGGIKVSRIVLLF RTMTREIGQIIHPHMVKKLKFEGRVVGQEVLRSVNAFMVAYVLIFAVSTLFVCLDGFDLVTSFTAVAATLNNIGPGLEMVGPIGNFSCF SDLSKIVLIFDMLAGRLEIFPLLVLFFRDTWKKF

7.7E-57	202	25.3	1.2E-28	109.3	6.6	2	2	E5BGP1_9FUSO	Potassium uptake protein, TrkH family	FSBG_01161	Fusobacterium gonidiaformans 3-1-5R	494	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Fusobacterium, Fusobacterium gonidiaformans, Fusobacterium gonidiaformans 3-1-5R	469605	>tr|E5BGP1|E5BGP1_9FUSO Potassium uptake protein, TrkH family OS=Fusobacterium gonidiaformans 3-1-5R GN=FSBG_01161 PE=4 SV=1MNNKMIRYVLSNILKLEAVFMIVPLILSIYYQEKTLVSLAHLFTILLLIGTAYLLSKKQPENVQIFAKEGLFIVAFSWLALSFFGALPFVISREIPSFVDAFFEVVSGFTTTGASILSNVEALSHSLLYWRSFTHFVGGMGVLVLALAILPKNNNQSLHIMKAEVPGPTVGKLVSKMTYNSRILYMIYIFLTLLITLFLYLGGMPLFDSVLHTFGTVGTGGFGIKNTSVAYYHSAYIEYVLAIGMLLSGMNFNLFYALLLRNFKQVLHNEELKYYLSIVAFAILAICIDNYNQYDNIEQLFRDSLFTVSSIMTTTGFSTINFDTWSVFSKTILLLLMMIGGCAGSTAGGMKVSRFIVLFKTFIYEFKKTYSPNRVFRLKMDGRALSQELIMSIRTYLILYLSLFFLLLCVAPESPDFISACSAVAATFNNIGPGFGTVGPTMNYSHFSNFNKIVLSISMLLGRLEIFPILLIFSPEIFTPFFKKIKSLFQTEK
7.7E-57	202	29.6	1.1E-56	201.8	20.5	1.1	1	Q9A1D8_STRP1	Putative V-type Na+-ATPase subunit J	ntpJ SPy_0327	Streptococcus pyogenes serotype M1	463	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pyogenes, Streptococcus pyogenes serotype M1	301447	>tr|Q9A1D8|Q9A1D8_STRP1 Putative V-type Na+-ATPase subunit J OS=Streptococcus pyogenes serotype M1 GN=ntpJ PE=4 SV=2MSGGNMKRSFIKSLSVTQRLTFSFAIVILIGTLLLSMPFTHYQNGPNTVYLDHFFNVVSMVCVTGLSVVPVAEVYNGIGQTIAMALMQIGGLGLVTLIAVSTFALKRKMRLSDQTLLQSALNRGDSKDLKHYLFFAYKVTFSLEAFAAIVIMIDFIPRFGWKNGIFNSIFLAVSAFCNAGFDNLGSSSLKDFMLNPTLNVIITFLIISGGLGFAVWVDLGVAFKKYFFERPHCYGATFRKLSNQSRLVLQTTAVILFLGTFLTWFLEKDNSKTIANFSLHQQLMVSFFQTVTMRTAGFATISYNDTLAPTNILYMIQMVIGGAPGGTAGGIKVTTAAITFLLFKAELSGQSEVTFRNRIIANKTIKQTMTVLIFFFAVLMIGFILLLSVEPHIAPIPLLFESISAIATVGVSMDLTPQLSTAGRLIVIVLMFVGRVGPITVLISLIQRKEKTIQYATTDILVG
7.8E-57	202	29.1	1E-56	201.9	20.2	1.1	1	T1ZFX4_STRIT	Potassium uptake protein, TrkH family (EC 3.6.3.14)	trkH SIR_1394	Streptococcus intermedius B196	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus anginosus group, Streptococcus intermedius, Streptococcus intermedius B196	862967	>tr|T1ZFX4|T1ZFX4_STRIT Potassium uptake protein, TrkH family OS=Streptococcus intermedius B196 GN=trkH PE=4 SV=1MSHFLSRLSPARRILLSFALVIVVGSLLLNLPFMQIATSKANYFDHLFTSVSMVCVTGLFTQAVADTYNIWGQIICMLLIQIGGLGLISFIGLIYVRSNQKLSFSNRTTLQESLSRDETNSIRDFLRSIFLITFSIELLGALILSFRFVPLLGWGKGLLTSIFLAISAFCNAGFDNLGSTSLLSYKTDTLVNLTIAALIIMGGLGFSVWFDLKTNIQAKGRKRKLRFHTKLVLALTAIILISGTCLTFLTEFQNTATIGQLPFGKKVLVSFFQTVTMRTAGFATIDYTQARPVTLLLYIIQMFLGGAPGGTAGGLKITTFLVVLAFARTEILGLPHTNFGHHTFSPSTIQKAFSVLIVFTTTFILGLTFLTMVADKGHRFIYLMFEAMSALGTVGVTANLTPTLNHAALTVIMFLMFIGRIGPLTLIVSLSNRKPKKNDTIKFANANTIIG
8.1E-57	202	20.6	3.5E-55	196.8	14.3	2	1	D5ELK5_CORAD	Cation transporter	Caka_2123	Coraliomargarita akajimensis (strain DSM 45221 / IAM 15411 / JCM 23193 / KCTC 12865)	491	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Opitutae, Puniceicoccales, Puniceicoccaceae, Coraliomargarita, Coraliomargarita akajimensis, Coraliomargarita akajimensis (strain DSM 45221 / IAM 15411 / JCM 23193 / KCTC 12865)	583355	>tr|D5ELK5|D5ELK5_CORAD Cation transporter OS=Coraliomargarita akajimensis (strain DSM 45221 / IAM 15411 / JCM 23193 / KCTC 12865) GN=Caka_2123 PE=4 SV=1MNTAIIYKLLSKVLLALAGAFVVCLGVGLINGEHLTEDHSLKAFLITIAISLVLSGVFHWKGRKGPNRMFRREALCLIGLSWVLATLIGAIPYILIVENCDYADAIFESSSGLTTTGATAFDNFYEFPPSLLFWRSLSQWIGGLGVVVFFVALLSSLGAGAKILFSNESSGSAADFDQGRIQQGAVLLMIYYLGITALCTVAYKIAGMNWFKAVNHGMTTIATGGFSTEPNSLGDFNSPAIEWIAIFFMALSGTTFVFVIRLFMRKWNVLRHTQEVAWFYAILGGATLLLTMYLVEMTGELPSADSFRTAAFQTVSIMTTTGYASADFESWLPPAKMLLIILMFIGGCSGSTAGGTKVVRIIILARASMRSIAHSFRPNLTISMRMGGKPLNERAIQSVIVFIILMVSLQIASMLFVSANEPELTFLSTFSCVQATLFNIGPGFDQVGPMDNFHFLRSSTKLFLSLLMTFGRLELYAVLVLFMPMAWRRFS
8.1E-57	202	29.8	1E-55	198.6	20.6	1.9	1	Q3Y1T6_ENTFC	Proton (H+) or sodium (Na+) translocating V-type ATPase (V-ATPase), subunit J (EC 3.6.3.14)	ntpJ HMPREF0351_12087	Enterococcus faecium DO	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus faecium (Streptococcus faecium), Enterococcus faecium DO	333849	>tr|Q3Y1T6|Q3Y1T6_ENTFC Proton (H+) or sodium (Na+) translocating V-type ATPase (V-ATPase), subunit J OS=Enterococcus faecium DO GN=ntpJ PE=4 SV=1MIKQSKQIKKRLPAVQLLALGFFLLILVGGGLLTLPFFSNSGHGTNFIDALFTATSAVCVTGLTTLNTAEHWNSAGQFLIMLLIEIGGLGFMMVPILCFALIKKKVSLSTRIILKEALNLEEVSGVMKLMLYILKLAFVIQLIGTVALSFVFVPEFGWLKGIWYSLFHAISSFCNAGFDLLGDSLANHQQNVYLIMVVSALIISGGLGFIVWRDLLEYHQKKKITIHSKIALTVTGTLLLGGFVVFFFTERNGETLVEGNMFQRLANTFFMSVTPRTAGYYSVDYLHMSHAGLILTMFLMYIGGTSGSTAGGLKITTLGVLLIQMRSMLKGRTRAEAFGRTIRQGAVLRALTLFFVTLTLCVVAIMILSVTETIPKTSGIEYIAFEVFSAFGTVGLTMGLTPDLTAIGKLIIIALMYIGRVGVLTVVFSLMTKAQRTQSKYKYPEESVMIG
8.2E-57	202	20.4	3.1E-32	121.1	3.7	2.1	2	Q73RK0_TREDE	Trk system potassium uptake protein TrkH	trkH TDE_0088	Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222)	480	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema denticola, Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222)	243275	>tr|Q73RK0|Q73RK0_TREDE Trk system potassium uptake protein TrkH OS=Treponema denticola (strain ATCC 35405 / CIP 103919 / DSM 14222) GN=trkH PE=4 SV=1MKALQYVRIIFMILAIISFSIIPIGTALYENEAYLIPSFLIPTAFVFAVAAAFFFFLRNKKVRLSVSGGIILVAAAWIAAGILGAIPLCISGVIPNFADAIFESVSGFTTTGATILTNVEACPMTMHVWRTQMHWLGGMGIVALTVALFPLLGVGGFHLIKSETTGPDKGKVTAKITHTAKALWFIYLGMTIVQIILLMLAGLPFLEALCHTFASLGTGGFSTRNASVGAFNSPSVEIICAVFMILAGVNFSLYFHLFTGNPEEFFHNSELKAYLKIVFVSTVLIALSIYPIYGIGGGLRQSFFQVASVITTTGFSTADYNAWPEFAKMVLFFLMFVGGCSGSTAGSIKVIRWLILQKQAGMEAKRLLSPHGVFGIQLNNRPGRKDIVYSVAGFMFCYFLLTLITALVAAADGADLLSGFTASLALIGNIGPGFGRVGPAGNFAFFSSPVKIFFSFIMLAGRLELYTMIIYFMPAFWKR
8.4E-57	202	14.1	4.4E-54	193.2	9.8	2	1	D3SUP8_NATMM	Cation transporter	Nmag_1730	Natrialba magadii (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) (Natronobacterium magadii)	509	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natrialba, Natrialba magadii, Natrialba magadii (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) (Natronobacterium magadii)	547559	>tr|D3SUP8|D3SUP8_NATMM Cation transporter OS=Natrialba magadii (strain ATCC 43099 / DSM 3394 / NCIMB 2190 / MS3) GN=Nmag_1730 PE=4 SV=1MRIRVDWRSSCSLTGTVLRWLSIPLAAPALLAVLDGNDPVPFLVAIAVAIASGLALEQLSADRELGQRESFLMVALTWLGVASVGAIPFLFAGAGSAGESAFTGLINTPINAFFESMSGLTTTGATVMEEWDFNNQPRSILLWRQLIQWLGGLGILIVAIGLLSHLMVGGAQLMETESQTRNVRKLRPHISETARLIWGLYVGLTLLAVAVFYGLHLLGFADGMDLFNAVSHALTSVATAGFSPEGDSIAAFSPIVQWSIIPFMILGSTNFVLLYYITQGEFERPLQSEELRFYLGVLALFSALVVGILAFDADLDLGIEPTIRHGVFNVVVSLVTTTGYASMDFNQWSPGAKHMLFLSMFIGGMAGSTTCSIKSLRWLVVLKAFKRNLFTAIHPEAVRPLRVSGSVVDEETVNDIFGYVLLAIVIFFGLTVLLVVDAARAGTDVSEFGALGAAASIFMNIGPAFELAGPMENYNDFSAFSRSVMVIMMWIGRIEIVPVLVLLLPAYWRS

8.4E-57	202	22.8	3.1E-56	200.3	15.8	1.7	1	A6LFB7_PARD8	Potassium uptake protein TrkH	BDI_2662	Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides distasonis, Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	435591	>tr|A6LFB7|A6LFB7_PARD8 Potassium uptake protein TrkH OS=Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152) GN=BDI_2662 PE=4 SV=1MLNVRFIVKMLGVMFILETFFMLAATVVAFLYRGSDVYPLLISSGILFGTGFLFYSMGFKANEHSAGRREGMLIVTLTWILFSLFG MLPFYIGGYIDNVTDAFFETMSGFTTTGSTILTNIEALPKGILFWRSLTQWQGGIGMVVFTVALMPIFGGGASQMFDAETPGITHERFR PRITQVAKRLWGVYVFLTLFLVGLLWAGPMNLYDAVNHAFTAISTGGYSTKNASIAYWNSSYIEYVITIFMFIGATNMTLVYFCFNGNV KKLIKDEEFRWFFFFVLGAIIVVMVWILYLGFASDVENAFRKAAFQVVTLVSTCGFATDDYIPWGPFFWFIALILMFICGCAGSTCGGLK MGRFVILTKNLSNEFKKQTHPHAVIPVRMNGHVVSGDIVHRVLAFVFAYITLIVVSCLALSLDGMGFSEAIGAAVSAISNVGPGLGTLGP VSNFADVPTVSKWFLSFLMLTGRLEIFTVLTILVPGFWKQ
8.6E-57	202	37.1	1.1E-56	201.7	25.7	1	1	A0A077JDX4_9CYAN	K+ transporter	trk ETSB_0172	cyanobacterium endosymbiont of Epithemia turgida isolate EtSB Lake Yunoko	454	cellular organisms, Bacteria, Cyanobacteria, unclassified Cyanobacteria, cyanobacterium endosymbiont of Epithemia turgida, cyanobacterium endosymbiont of Epithemia turgida isolate EtSB Lake Yunoko	1228987	>tr|A0A077JDX4|A0A077JDX4_9CYAN K+ transporter OS=cyanobacterium endosymbiont of Epithemia turgida isolate EtSB Lake Yunoko GN=trk PE=4 SV=1MTIARTICLGFLAVISVGTLLLILPFSTYDYHWNNPIIALFTATSAVCVTGLIVVDTGSYFSFWGQLIILLLIQIGGLGYMTTTTFLILLT GRRFDLRQKLAIQESLDRPLRQENSKTIIRSIIGMTLVFEIVGALLLFNFFKEKYGKISALWISIFHSISAWNNAGFSLFLDSLVGFQDSLTI NLVVAFLIILGGIGYSVIIELYLWILHKITKRRERVFLSLNFKVVISTTAFLLILGTIMFLLVEYKNQNTLASLNFKSKLLGAWFQSVTTRTAG FNSIDIGGMTISGLFLTMGFMFIGASPSGTGGGIKTTTLRILTNCTRSVLRGNDQVVMYKREIPVSLILKAVAVVFGSTITVISITFLISFIEI SFHPAFFDTEVSSFQVLFEVISAFTTVGLSTGITASLSSLSQLLIILAMYTGRVGILVFMAAIVGEINPRVVQYPEERLLVG
8.7E-57	202	8.8	4.8E-55	196.4	6.1	2.1	1	K9TQN7_9CYAN	Trk-type K+ transport system, membrane component	Oscil6304_4784	Oscillatoria acuminata PCC 6304	487	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria acuminata, Oscillatoria acuminata PCC 6304	56110	>tr|K9TQN7|K9TQN7_9CYAN Trk-type K+ transport system, membrane component OS=Oscillatoria acuminata PCC 6304 GN=Oscil6304_4784 PE=4 SV=1MLHIPGGMALVSLWVCVAFREFYAIAPFLLTSLVSFGIGQLLYRSVHQYSEEAHLRHAMITVALSWGLIPLVGAIPFLVIASHLAPL PDASETVILFQNPWNAVFESFSGFTSTGLTMAFNPRELPYCLQWWRSFMEWVGGVGTIVLMLSVLDPSTEPFQLYNAEGRSRRIAL TVRGTVRQLWKIYLVYTAVCISIFGVLGMPWWDALNYGLTTSSMGGFDLTPDGIGSYSRMIQLALVPLMIIGAISFAIHVRLIRDRQFSL LWNREEYRALWLLLGVGVVLLFLENYWFQGSFLWIDSLFQWVSALTTCGFNTVKVETWSASAKLLLSVAMAVGGAAGSTVGGLKIK RVLVLYKGVLWHFRRISLRPHQLMRYQLDGKSLGEAEAYRRIEGAAVLAVLWISWLAIGVMVLNRLVPEKYQLSDTIFEAASALSGVG LSTGISHPNLHWDGKLVLILLMWMGRLEIIPVMLLLSALMRKMKARIFKI
8.7E-57	202	31.8	1.3E-56	201.6	22	1.1	1	A0A037UQK3_SPIME	K+, Na+ uptake protein bound cytoplasmic subunit	SPM_001895	Spiroplasma melliferum KC3	530	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma melliferum, Spiroplasma melliferum KC3	570509	>tr|A0A037UQK3|A0A037UQK3_SPIME K+, Na+ uptake protein bound cytoplasmic subunit OS=Spiroplasma melliferum KC3 GN=SPM_001895 PE=4 SV=1MVFFQLYFKNIFKRKNDNKRQRNNDPTAPLTRRRHWLPFSKISGRLFLVYILIVLLGGLLLSIPGFVHSGERMVLDGKGKILDHSV TFAWNYLIGLFTASSAFSDTGITISNPAADYTFWGQLVILILIQTGGFGIVTFKIMIFVWLGRRISIKDKMLVQGERGSSNFGHTMDLIKN SFIFLIILECFGAILLFCNFYFSELSVEGKFMIDNVTYHNFWRSLWSGVFHSISSINNAGFDIIGNSSLMPYNTNYFIQFVFLFQFIIGGLGF PTFYDLKRKFVAWRRKEHVKFTLFTKINLITYIGLSIVGVFSVWLIEFTNINTIMPETGQYVESILRNSKSNWNGFMNIFFNTMSTRNAG YSTVEMSNFLPGSRIVMSIMMFIGSAPSSTAGGIRTTTLAVIIITIWSIIRNNNSVNAFKRKIPNETVKRALGVTVISGALIAIAIICISAENPH LDVLNTFFTICSAFGTTGLSTLNFTELYNIGILSTLILILLMFIGQLGVSSTLLVSIRGSGEKEYSYVEENILIG
8.8E-57	202	29.9	7.6E-55	195.7	18.9	2.3	1	A8F5M4_PSELT	Cation transporter	Tlet_0892	Pseudothermotoga lettingae (strain ATCC BAA-301 / DSM 14385 / NBRC 107922 / TMO) (Thermotoga lettingae)	496	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Thermotogaceae, Pseudothermotoga, Pseudothermotoga lettingae, Pseudothermotoga lettingae (strain ATCC BAA-301 / DSM 14385 / NBRC 107922 / TMO) (Thermotoga lettingae)	416591	>tr|A8F5M4|A8F5M4_PSELT Cation transporter OS=Pseudothermotoga lettingae (strain ATCC BAA-301 / DSM 14385 / NBRC 107922 / TMO) GN=Tlet_0892 PE=4 SV=1MNIYSKKSYAIVFRVLSSLIFFSVILLVPLIFSIFYGEFFRIAYAFFIASAISILLAYIFRIPKREKTEAITSKEGALIVLMSWIIVIFLSSLP YYLSNTLTMSQAIFEATSGWTTTGLTMITDVENTSKSLLAWRSITQFLGGAGFAIIVMGAIIGPTGLGLYQAEGRIDNIVPNIRYSARIIMI AYTAYAIAGMIALVIAGMNFFDAFNHSLTALATGGFSTKNSSIGYYNSEIIEIIIMILMWWLGATGFGIHYVFWLRNWKALRKNYEPKQMAF FTILGVTIVSLTGINKVFPDTSQALRHASFQVISALTGTGFSTVDLSKWSNFPTGMFVLTILMLLGGCMDSTSGGIKQYRITVLIKAIYLAV KKFLLPRDAIIQVEIWKGHTKKYLDDTLIREAFIIIGLYMVSYLTGVLVLTSHNYTLQQSMFEVASAIAGVGLSCGITTPVMPAGALWTLIV EMFLGRLEFLVVIYAIARIIRDLSSRRFCKKTAV
8.8E-57	202	25.2	1.1E-56	201.8	17.5	1	1	V4QQ23_STRIN	V-type Na+-ATPase subunit J	IUSA1_06850	Streptococcus iniae IUSA1	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus iniae, Streptococcus iniae IUSA1	1273539	>tr|V4QQ23|V4QQ23_STRIN V-type Na+-ATPase subunit J OS=Streptococcus iniae IUSA1 GN=IUSA1_06850 PE=4 SV=1MDGNFLMRTWSVTQRLTLSFALVIFIGSILLSLPFSQYPNGPDSTFLDHLFNVVSMVCVTGLSVLPISEAYNGFGQSISIILMQIGG LGLITLIAISTFALKRKMDFAGHTLLQSALNKEDSKGLKDYLFFAYKVTFCIEFIGFVLIATDFVPRFGWKNGLFNSLFLTVSGFCNAGFD NFGSSSLKDFVLNPTINFVIIALIISGGIGFAVWSDIADNVKRVAIEKPRWHGNFYRKLSNQTKLVLQTTAVILVIGTLISWFLEKDNPKTIA NYSLFQQLMVSFFQTVTMRTAGFATISYNDSLAPTNLLYMIQMIIGGAPGGTAGGVKVTTVAILFLLFKSELSGQTEVTFRNRIIASKTIK QTMTVLIFFFSILISGYILLLSFEPHLDPVALLFEAISAIDTVGVSMDITPQLSTAGRIVIMFLMFIGRVGPITVLISLIQRKEKTVHYATTNILV G
8.9E-57	202	32.1	1.2E-56	201.7	22.2	1	1	A0A089LUY5_9BACL	ATP synthase subunit J	PSTEL_21700	Paenibacillus stellifer	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus stellifer	169760	>tr|A0A089LUY5|A0A089LUY5_9BACL ATP synthase subunit J OS=Paenibacillus stellifer GN=PSTEL_21700 PE=4 SV=1MALPIPKISEFRWLKLSPPQILVIGFALIIMIGALLLMLPVSHTQGQGISFLDAVFTATSAVCVTGLVVVHDTGTFFSVFGQVVIMVLI QIGGLGFMTMATLFALVFRRRISLRERLVLQEAMNQSSMEGIVRLIRSVLIYSLVIEGGAAILLTIRWAFDMPFGRAMFFGLFHAVSMFN NAGFDLFGNYRSLTGYTSDPVVNVVVMFLIVSGGIGFIVMSDLIGYRRGRRLSLHTKVVLTSTAALIGIGALVLFVFEFTNTRTLGSLNF GGKVWGALFQSVTPRTAGANTLDLTGLRQASQFFIIILMFIGASPGSTGGGIKTTTFTIMLGAVIAMLRGRDDIVLFRYRLSQERVFKAL TITVLALLLIGTVTMLLSTTEEMPFLDLLFETTSAFATVGLSLGVTPELSGAGKVLIALTMFAGRLGVLTLAYALGPKQGKPLYRYPEGK MIIG
9.1E-57	202	31.5	1.4E-56	201.5	21.8	1.2	1	B3QYA4_CHLT3	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Ctha_2621	Chloroherpeton thalassium (strain ATCC 35110 / GB-78)	611	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Chlorobi, Chlorobia, Chlorobiales, Chlorobiaceae, Chloroherpeton, Chloroherpeton thalassium, Chloroherpeton thalassium (strain ATCC 35110 / GB-78)	517418	>tr|B3QYA4|B3QYA4_CHLT3 H(+)-transporting two-sector ATPase OS=Chloroherpeton thalassium (strain ATCC 35110 / GB-78) GN=Ctha_2621 PE=4 SV=1MAKRLLFIKSSTQKDSTVAPRFIEQNQERLLKWIRSSLLLLAILAVVSIITDYGFPHDTETTYWLQRLDFFILTGFLGLGCARLILEE DKLQYAKDHWIDLVILVLILLHLILPLPISNLLPTHDGLLNLESLTRFYIILTQFFVLLPLIPPFLRYSQKLMTYNIQPTMLILVSFAILILIGALLL LLPRATVSQPLSFVDALFMSTSAVCVTGLIVVDTATYFTTLGHTILLVLMQIGGLGIMTLTTFFAYILGSDAKLKEYSAMKDLLGEENLGK IRQTVIQIALTTFVIEFLGAISLYGFLPPHSFDSHKEKLFFSIFHAISAFCNAGFALKTDNLMDTTFRYNEGALLTVMSLIVLGGIGFPVLSN MGSVLYAKVFNQKGSWASKRLTVHSKLVLITTGLLLLVGTLGFYLLETNKTLAELPFHQKFLAALFHSVSARTAGFNTVDIGKLATPTLF FMSLLMWIGASPGSTGGGVKTTTAALSLLNIIAIVSGKNRIEVFRKQVSTVAVIKAFSTMLLSIIYIATVLFILLITEHLPLESIAFEIVSALGT VGLSTGITSQLSTFGKIVITITMFFGRIGLLSTLIALTKKRSIARYRYTEENVLVN

9.4E-57	202	30.7	6.8E-31	116.7	9.7	2	2	G4SW E6_ME TA2	Putative Ktr system potassium uptake protein B	ktrB MEALZ _2479	Methylomicrobium alcaliphilum (strain DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z)	456	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomicrobium, Methylomicrobium alcaliphilum (Methylobacter alcaliphilus), Methylomicrobium alcaliphilum (strain DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z)	1091494	>tr|G4SWE6|G4SWE6_METAZ Putative Ktr system potassium uptake protein B OS=Methylomicrobium alcaliphilum (strain DSM 19304 / NCIMB 14124 / VKM B-2133 / 20Z) GN=ktrB PE=4 SV=1MRTKLTLQRHFKKHRLKFSHAVLKASPPAILVAGYLGLITAGTLLLKLEIATNKAIGWLDALFTATSAVTVTGLVVLDTGTDFSLFG QIIIALLIQSGGLGFMTFSILTAMNLGKRIGIKHQLLALEALNQTSMNKIWEVAVAVIYFAFVIEAVGLILLTVLWSTDYGWVKALYEAFFY TVSAFNNAGFALSADSLTRYVDNIPVNLVVSGLFITGGLGFVVLLDLWQIRGWKKLQIYSKAMIGGTLMINLVSWLMVWLFERHNPATI GNFHLSSQLIASWFQAVTPRTAGFNALPIESLSDSTTLLTLLLMFVGGGSLSTASGIKLGTFIVIFMAIYAFLGRRDEVTLMQRSISQNIV MKAFAITLISIVLVFIGTLLLSVSEQAPLVDVLFEVVSALGTVGLSRGLTGELSVTGQWIIMILMFVGRLGPLTFVYVIATPRPPRRINYPSL DIQVG
9.4E-57	202	36.6	1.6E-56	201.3	25.4	1.2	1	J9R4E 7_RIEA N	Uncharacterized protein	B739_2 177	Riemerella anatipestifer RA-CH-1	582	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Riemerella, Riemerella anatipestifer (Moraxella anatipestifer), Riemerella anatipestifer RA-CH-1	1228997	>tr|J9R4E7|J9R4E7_RIEAN Uncharacterized protein OS=Riemerella anatipestifer RA-CH-1 GN=B739_2177 PE=4 SV=1MIINFKLLYIFSFIISTLGIVAFFGDFGFNQSKDSRMMFDGYYHFAIAIGLISTAARYYEKRTSVNRKAFIFDLATVIFTVVIFYFHFLS PLYGSLDRFFESRYWVIMAVVFTFIREFSDLKINFKRTILNPAQLFISSFIVIILMGAFLLTLPKATTHGISFLDALFTSTSAVCVTGLSVLN TGSDFTTFGKLIIIILIQIGGLGILTFASYFSYFFKGGTSYENQLALSDMTSSKKLGDVFSTLKNIILITFGIELFSGILIYTSVSSTLFTSEFQ HIFFSIFHSVSAFCNAGFSTLDANLYDSAYKYNYYLHLVVIFTFVFGGLGFPIVVNIINYIKYKIAHISPFSEQKRRYRPWVLTLDSRITLVT TVSLTIVGTIIFIYILEYHNTLAEHEGFGKFVTALFGATTPRTAGFNTINNASMSFPTIMVIFLLMWVGASPQSTGGGIKTNTFAIAFLNVLS LAKGKSKVEIFRREIADISIRRAFAIMTLSLMAIGLGVMLITFFDPDKNLLDISFECFSAYSTVGLSLGITASLSEASKMVLIGIMFVGRISML SLAIAIVKKSKYKNYSYPKEEITIN
9.5E-57	202	17.5	1.1E-56	201.7	12.2	1.1	1	W5XR F3_9C ORY	Potassium uptake protein, TrkH family	CCASE I_04665	Corynebacterium casei LMG S-19264	407	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium casei, Corynebacterium casei LMG S-19264	1285583	>tr|W5XRF3|W5XRF3_9CORY Potassium uptake protein, TrkH family OS=Corynebacterium casei LMG S-19264 GN=CCASEI_04665 PE=4 SV=1MFTVTSAVTVTGLAVVDTGTHWSGLGQATVLTLIQIGGFGIMSVSSLAGMLLTGRIGLRSRRYNQAENRTLGTGDVARTVIAALA ITVICEFVVALVTAIRFATFYDMPALRAAWEGLFHAISAFNNAGFGLRSDSLVPYVGDGWIILPLACALIIGGLGYPVVAEMWDKLRFRL THGNLGHPRKFSVSTKITLVGTAMLIAAGVLVVGALEWNNTLAGQPLGTKLLGAFFQGVTPRTAGFNSVDFGEVQPVTLMATGLLMFI GGGSAGTAGGIKITTAAVLLAAIIAEIRGHNHVTIAHRTINSSVVRQALTVASISVVLVVSCVVIIRLLEPGFSGEAITFEVISAFATVGLST GITADLSAPSQIVLCFLMYIGRIGPVTLVVALAAQHSARRFEYPEERPFIG
9.6E-57	202	20.6	2E-55	197.6	14.3	2	1	R5K3N 0_9CL OT	Potassium uptake protein TrkH family	BN572_ 00085	Clostridium sp. CAG:264	486	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:264	1262786	>tr|R5K3N0|R5K3N0_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:264 GN=BN572_00085 PE=4 SV=1MNRSMILYVVGHVVMLEGVMLLLPCLVSLIYQESEGIDYLVMAVICMLIGAIIVKHKPKVNVFYLKEGCIATALSWIALSIFGALPMC ISGDIPSFTDALFETISGFTTTGASILNDVEALSRTTLFWRSFTHWIGGMGVLVFLLAVLPLSGGSNINLMKAESPGPSVGKLVPKIKYT ARILYVIYIVLTAIEIILLIAGKMPVFHAFCTGFGTAGTGGFGTKNDSFASFSPYLQWVVTIFMILFGVNFNAYYLILFGNIKKALKMEEVRT YFLIIVAAIAVLVLNLIHTMDGFWTVLRHASFQVASIITTTGFSSVDFDLWNQTCRTILVILMFIGACAGSTGGGIKVSRFIIVVKSVVKELN SYLHPKSIKKIKMDGKPVEHEVVRAVNVYFITFIILFTTSVLLISFEGKDMTSNFTAVAATINNIGPGLELVGPTKNFNVYGTFSKYVLMFD MLAGRLELFPLLLLFYPPAWKELLAVRRRK
9.9E-57	202	21.7	4.4E-55	196.5	15	2.2	1	D7A3 W7_ST AND	Trk system potassium uptake protein	Snov_4 488	Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	483	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Starkeya, Starkeya novella (Thiobacillus novellus), Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	639283	>tr|D7A3W7|D7A3W7_STAND Trk system potassium uptake protein OS=Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113) GN=Snov_4488 PE=3 SV=1MIDFRPIAAILGVLLAILGTTMMIPALVDLIAGEPDFVVYAAAGVITAFVGLSLWLAGRSSEVEKLDLRQAFVLTTASWLLLSAFAAI PFMWAQTDLSFTDAYFEAMSGLTTTGATVVTDLDNRPPGVLIWRAFLHWYGGIGIIVMAMALLPMMQIGGMQLFRAESSDKSEKML PRAAQMAKSILGTYLLLSFACAVTYAFLGMSVFDAIAHAMSTISTGGFSTHDASIGYFKSSAIDYAAIFFMLSGSLPFVLYLRVLAGDFS RLFANTEVRLFLSLVMLFTLISTVEQVRGGIAVGETALRQALFNVVSIMSTTGFVAVDFTHWGPPTDALYFILLFLGACTGSTAGGMKS FRIAILGSALGQHLKRIIYPSGVFPVLYGGKPISDEVVASVLSFAFLYLAAFMVIGMAINAVGPGLGPVVGPAQ NFSALPEHVIWMLSFGMVVGRLELFTVLVLFLPSFWRR
1E-56	202	20.7	2.1E-55	197.5	14.3	2	1	R7AZ2 1_9CL OT	Trk system potassium uptake protein TrkH	BN653_ 00686	Clostridium sp. CAG:43	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:43	1262805	>tr|R7AZ21|R7AZ21_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:43 GN=BN653_00686 PE=4 SV=1MNYSIVFYIIGWILNFEAAFMALPTAVALIYRESEVWCFLATMAVCLMVGMLLVRRKPKNQIFYVAESFVAVSLSWVLLSVMGAA PFVLSGYIPNPIDALFETVSGFTTTGASILSSVEQLPNCLLFWRSFTHWIGGMGVLVFLLSILPMVGGSHMNLMKAESPGPIVSRLVPK VQMTAKLLYQIYLGMTILEAVILILGKMPIFDAITITVGTAGTGGFAIRNDSLASYTAFQKNVVTVFMILFGVNFNFYFFLLMRKIGQAFKM QEVRAYFLIIASAVGIITVNTVSLCGNALQAFQDAAFQVGSVITTTGYATVDFDKWPQLSRTIMVLLMFIGACAGSTGGGIKVSRVLILLK SVKKELKQYLHPSVVEKIKMDGKIVEHEVVRSTNVFMVAYVLIFAVSVLLISLDEYDLVTNFTAVTATFNNIGPGLALVGPTGNFGFFSN FSKVVLIFDMLAGRLEIFPLLLLFSRETWKRF
1E-56	202	28.4	1.5E-56	201.3	19.7	1.1	1	X5A35 9_9BA CL	TrkH family potassium uptake protein	PSAB_ 19300	Paenibacillus sabinae T27	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	1268072	>tr|X5A359|X5A359_9BACL TrkH family potassium uptake protein OS=Paenibacillus sabinae T27 GN=PSAB_19300 PE=4 SV=1MDGGMDMALQLSKVSEFRWLKLSPPQILVIGFAVIILIGALLLMLPVSHAAGEPIGFLDALFTSTSATCVTGLVVKDTGTFFTTFG QIVIMLLIQVGGLGFMSMATLFALVFRRRISLRERLVLQEAMNQSSMEGIVRLIRSVLIYSLVIEACGALLLTIRWAFDMPLGRAVFFGIF HAVSMFNNAGFDLFGGYRSLTGYAGDPVVNIVVMFLIVSGGIGFIVMSDIMDYRRKRKLSLHSKVVLSMTAALIVIGAVVLFVFEFTNPR TLGSLGWGGKIWSSLFQSVTPRTAGANTLDMTGLRQASQFFIVILMFIGASPGSTGGGIKTTTFTIMIGAVIAMLRGREDIVLFRCRLA QERVFKALTITLLALLLIVAVSMVLSTTEDTSFLKVLFETTSAFATVGLSLGLTPELSAAGKILICLTMFAGRLGVLTLAYALGPKKGKELY RYPEGKMIIG
1.1E-56	202	26.3	1.2E-54	195.1	18.2	2.1	1	D7GR W1_9F IRM	Trk-type K+ transport systems, membrane components	CK3_07 650	butyrate-producing bacterium SS3/4	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, unclassified Clostridiales, unclassified Clostridiales (miscellaneous), butyrate-producing bacterium SS3/4	245014	>tr|D7GRW1|D7GRW1_9FIRM Trk-type K+ transport systems, membrane components OS=butyrate-producing bacterium SS3/4 GN=CK3_07650 PE=4 SV=1MFRILSAFRRLNSFQIIVLGFAFVILLGAGILMLPVSSADGSWTPFVNALFTSVTSVCVTGLVVCDTGTYWSSFGHAVILLLIQTGG LGVVTISASFTILSGKKIGLSQRSIMAESVAAPQLSGVVRLTGFIVRVTLGIELIGALLMAPVFCRDFGLFRGLWMSLFHSVSAFCNAGID LLGVRGAYSSLTSYAYDPLINLVIILLIVIGGIGFLTWDDIYRNRHHISRYRMQSKVILSYSLALIFIPAILFFFLEFQDIPAGKRILVSLFQSV TTRTAGFNTADLSSMRESGQFLMILLMLVGGSPGSTAGGIKTTTFLAVLISCATAVFARKDSPEMFKRRIIPDIVATAIAILFMYTSLGILCA MTLSILESLPLMPCLFEAFSALATVGLSFGITPTLSVPSKLILIAFMFIGRVVGGLTIIYATMSGYKIQCGKFPQEKISVG
1.1E-56	202	16.7	5E-54	193	11.6	2.1	1	R5UBS 8_9FIR M	Uncharacterized protein	BN481_ 00058	Ruminococcus gnavus CAG:126	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	1263106	>tr|R5UBS8|R5UBS8_9FIRM Uncharacterized protein OS=Ruminococcus gnavus CAG:126 GN=BN481_00058 PE=4 SV=1MNNRMIVYMIGRMLGVEGLLLLVPAFVSFLYGEQSGIAFLLTAAILLIFLLAGRKKPKDTSIYGKEGLALVGIAWILWSLFGALPFFI SGSIPDYLDAFFETVSGFTTTGSTILTDIEALPQGMLFWRALTHWIGGMGVLVFVMVLLSLDDDGSMYLMRAEVPGPEADKLVPKARS TARILYLMYLILTMAEVIFLLFGGMNLYDALIHSFSTAGTGGFSNRNASVSYYDSAYIDGVITVFMILFGINFNIYFAIYIKNWKSALKNEEA RTYLGVIAAAILMITVNIYHIYGNVASAFRYSSFQVAAVITTTGFYTADFNLWPEFSKTILLVTMIIGACAGSTGGGMKVSRILILCKSVKQ EIKRILHPKAVTVVTVNGQKVGRETLHGVYVYSICYALILVSSVLIVSIDNYDFATSVSAVLTTLNNVGPGISQVGPVENFFEFSWLSKLV FCADMLLGRLEIFPCLVLLAPELWKRKF

1.1E-56	202	20.1	1.5E-56	201.4	14	1.1	1	A5GNT9_SYNPW	Sodium transporter, Trk family	ktrB ntpJ SynWH7803_2178	Synechococcus sp. (strain WH7803)	470	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain WH7803)	32051	>tr|A5GNT9|A5GNT9_SYNPW Sodium transporter, Trk family OS=Synechococcus sp. (strain WH7803) GN=ktrB PE=4 SV=1MKPMPLPKAIHRTQAWYRRLTVPQFTVVTGLLVITTGTFLLASPMCSDSTVGLWEALFTATSAVTVTGLTVIDVGRDLTPFGQGVLAFMILVGGLGLMAITTFLQGFVVRGASLRRRLDRGQTLDQFGVGGIGSTFRSIALTATVLILMGALVLYTFGFSDLPAGGSRAWASLFHSISAYNNAGFGLWSDSLEGYRTNRVVNAVIMLLIVLGGLGWRVTNDLWSNRQRLKRRNLSLHTRLVLRTSALLILIGMLGLMLTESLSKGHVLTTMGWQERVMSTLFGSVSARTAGFTTVPLSIQSISDSGLLLLLMTLMFIGASPGGTGGGIKTTTVAALMATTRSTLRGHDDVVIRHRQIPDKVVLRAVSITVASLLFVLMMALLLALISDPTADDPLSFLELMFTCISAFATVGLDLGVTEQLGHLGQLILVVGMFVGRLGILLLSAIWESFERDQIQRQNRVGYPREDLYV
1.1E-56	202	20	1.9E-56	201	13.8	1.2	1	D4K4R9_9FIRM	Trk-type K+ transport systems, membrane components	FP2_09510	Faecalibacterium prausnitzii L2-6	461	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii L2-6	718252	>tr|D4K4R9|D4K4R9_9FIRM Trk-type K+ transport systems, membrane components OS=Faecalibacterium prausnitzii L2-6 GN=FP2_09510 PE=4 SV=1MGKNKTKKRTRRPNKGWLAGSSATQTICGSFLLVIAVGTLLLTLPISSRTGRLGVIDAMFTATSATCVTGLVVVRDTWSQFSLFGQVVILMLIQVGGLGLVTLTSFFALAARRRMGFRDLRLLGESVSADGLSKATEVLKIVIKLAAAFEAVGIVLLLFAFVPQFGAEGVWVSVFTAISAFCNAGFDLFGRFGAYSSLVPYVNNYYVQAVIMFMIMAGGLGFMVWVELAEHRKKRRLSLHAKVVLQFSVIFWVGGAALLALLEWSNPRTMGGLSVPGKIMAALFQSVSTRTAGMNTIDLAACSPISKLLMSVLQFIGAAPGSTGGGVKVTTFAVLILTIRSVAQGRDDCVIGGHHIESKTVYYRALTIIVIGAVAAFGSAVVVYYYNTAETVSVIDCIFESCSAFGTVGLSVGVTGQLNTGAKLLYMACMFMGRVGPVSLAISLTAKPDDNKRKVLPVGHINVG
1.2E-56	202	18.4	8.4E-55	195.6	12.7	2	1	R6RZU1_9FIRM	Trk system potassium uptake protein TrkH	BN652_02233	Firmicutes bacterium CAG:424	480	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	1263022	>tr|R6RZU1|R6RZU1_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:424 GN=BN652_02233 PE=4 SV=1MNYSIVRYIIGKVLYFEAAFMGLPCVTAIIYQEHSGWAFFFTALLCILLAYLLTRKRPANDTFYVKEGFVTVALSWIVLSIMGALPFLFCGSITNPVDALFETVSGFTTTGASILKDVEILPKCVLMWRSFTHWIGGMGVLVFLLTFIQGHGSGSHMNLMKAESPGPSVSKLTPTVQSTAKILYLIYVVLTVIEIILLLLGGMPLFDSLTTSFGTAGTGGFGIKNDSIGGYSPYIQIVVTIFMILFGINFNAYFFILCKKFRQAFLMTEVRCYLGIIAAAILMIAWDIRHLFPTIGEVFRHASFQVASIITTTGFATTDFDCWPQVAKTTLIMLMFIGACAGSTGGGIKVSRFVILIKTIQKELHTLLHPRMVKKLKIDGHTLEHEVVRSTNVFLIAYVLIFSLSVLLLGFNDFDLITNFTGVAATLNNIGPGLELVGPTQNFSIFSDGSKLVLIFDMLAGRLELFPMLLIFVPDTWRKY
1.2E-56	202	29.9	4.4E-55	196.5	20.7	2	1	F2F850_SOLSS	Trk-type K+ transport systems, membrane component	SSIL_3192	Solibacillus silvestris (strain StLB046) (Bacillus silvestris)	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Planococcaceae, Solibacillus, Solibacillus silvestris, Solibacillus silvestris (strain StLB046) (Bacillus silvestris)	1002809	>tr|F2F850|F2F850_SOLSS Trk-type K+ transport systems, membrane component OS=Solibacillus silvestris (strain StLB046) GN=SSIL_3192 PE=4 SV=1MKIFKESLNPSKILVMGFAILILVGAFLLTFPVATADGKGLPFLDALFTATSATCVTGLVVVDTEEAFSLFGELVILSLIQIGGLGFMTFATFLFTLLGKKISLKERILLKEAFNAASTLDIVKIVKRILIFTVIVEGIGAIILSIRFSFDMTIGKAIYFGFFHSISIFNNAGFDLMGGFKSLTEYVDDPFVVLTVCSLIVIGGLGFIVIHELYEYPVTHKISLHSKVVLFTTLMLIVGASILIFLFEYSNDKTLGPLSSTGKALGALFHSITPRTAGANTLPMADLTHATLFLTIFLMFIGGGSGSTAGGIKVSTFAVLMATAFSQLKGREDVVLFKRRIVMQSILKALTVAMSGIMIVVIVTFLLSITEPGHDFILYLFEATSAFGTVGLSMGLTPELSPFGRVLIILTMFVGRLGPLTLGFAISKRRKKEAYHYIKGNIMIG
1.2E-56	202	14.2	2.2E-56	200.8	9.8	1.4	1	Q0ASF4_MARMM	Trk system potassium uptake protein	Mmar10_0490	Maricaulis maris (strain MCS10)	485	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Maricaulis, Maricaulis maris, Maricaulis maris (strain MCS10)	394221	>tr|Q0ASF4|Q0ASF4_MARMM Trk system potassium uptake protein OS=Maricaulis maris (strain MCS10) GN=Mmar10_0490 PE=3 SV=1MTQALRQVLFMIGMMVTVLAVTMLAPAVVDFASGQQESATAFILSSIIGVFVGGAVTLSTRGPVGDMPARGAFVLIVGAWLGLALCAALPLRLSGQGLDWTDAIFESISGLTTTGATVITGLDMRPPGLLLWRAILQWIGGIGIIVTAMAFWPMLGIGGMQLFQLETGDTSEKVLPRATQIAAGIAAIYLALTIVCFLAYVGTGMAWLPALCHSMSTVSTGGFSTSDNSMGEYVHLGSDMITVVFMILASLPFGLFLLASRGKFSGLYKDSQVRGFLLVVAVATLGLTALIMAQDLPAGDVAAWRHASFNAISIITGTGFATTDYGQWGPLAQAGFFVFMFIGGCAGSTTCSVKIFRYQIAGTAMRRYLARLLRPNAIIPMHYNGRPVSESILHSVLGFFFVFFAVYAASASILSAMGLDLVTALSGAAATLTNVGPGLGSIIGPAGTFEPLSDPVKWVLTANMFIGRLEVLAVLILLSPRFWRP
1.2E-56	202	32.1	1.7E-56	201.2	22.2	1.1	1	A0A024P9F3_9BACI	Ktr system potassium uptake protein B	ktrB_2 BN983_03357	Halobacillus karajensis	455	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Halobacillus, Halobacillus karajensis	195088	>tr|A0A024P9F3|A0A024P9F3_9BACI Ktr system potassium uptake protein B OS=Halobacillus karajensis GN=ktrB_2 PE=4 SV=1MAHSIQKNGSNFFDRLTPFQIIVLFYASAVIISTVLVSLPFLHKEGVQLSFIDALFTAVSAVSVTGLTVVSTADTFNTPGYFVLMFVLQFGGIGVMTLGTFIWLMLGKKIGLKRRELIKTDQNRSTFAGMVKLIKQILLIIIILIECIGAIILSIYFTQYFPTVGEAIVQGMFASVSATTNAGFDITGVSLVMFENDYFVQFINILLLTLGAIGFPVLIEIKDYLTHKQTSFHNFSLFAKLTSITFGALVVVGTVLIYILDRNHFFADKSWHEAFFFALFQSVTTRNGGLATMDVAEFSAPTLLVICVLMFIGASPSSVGGGIRTTTFAITLLSVIAYARGKSNVRIFRREIDPDDIFRSFIVINTAITITATAVILLNYFEPQFSFMEILFEACSAFGTTGLSMGITPELHLSGKLIIITLMFIGRIGIFSFLFIIRGKVIKDKYHYPKEPMIIG
1.2E-56	202	11.7	3.6E-56	200.1	8.1	1.6	1	A1WCP2_ACISJ	Trk system potassium uptake protein	Ajs_3911	Acidovorax sp. (strain JS42)	488	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax sp. (strain JS42)	232721	>tr|A1WCP2|A1WCP2_ACISJ Trk system potassium uptake protein OS=Acidovorax sp. (strain JS42) GN=Ajs_3911 PE=3 SV=1MSDVLPVMRVLGALLALFAVSMGVPLAASLWAREGLWQHYATAIAVTSMASALLWGGLRAHKRELLPRHGVMLVSVVWGILPLFAALPLLLVMHAIGRPLSFTHAYFESVSGLTTTGATVLAELDRLPLSVNMWRTFMQWIGGMGILILAVAVLPLLGVGGSQLFKAEAAGPVKDTKLTPRMTETAKGLWGVYVVFSLVCALAFWLGGMTPPDAIMHMFATVSLGGLSPHDASFAYFESPLLETIALVFMLCASCNFALYFIALRKGNWRGFWRDPEMRATITALLGGGLLVALLLWVKGVYDPLQALRHGMFNVVSVATTTGFATTDYLGWPVFAPVFMLLLSGVATSAGSTGGGIKMVRMLILLKQARREMTRIVHPRAVQPVRLGDRVVDNRMIFSVLAFMLVYGATVITLSMVLLLTDLDMVTAFSAVLASVHCMGPGLGMLGPASNFAVLTDFQLWVCTLAMLLGRLEILSFMALLTPAFWRR
1.3E-56	202	37.8	3.2E-56	200.3	26.2	1.5	1	S0KL66_9ENTE	Cation transporter	OMK_01704	Enterococcus dispar ATCC 51266	468	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus dispar, Enterococcus dispar ATCC 51266	1139219	>tr|S0KL66|S0KL66_9ENTE Cation transporter OS=Enterococcus dispar ATCC 51266 GN=OMK_01704 PE=4 SV=1MHIMRVLRQKSRRARFFIASNVSSIQVIVSYYLIMTVISLLLFYLPFFRQPNVHVPFLDMVFMAISTVSVTGLTTFNINHVFNDNGVILLEVLFQIGGLGIMMISTFFFIISRRKISLKQRQLIMTDMNQPRLSGIVRLIRITFTMILVFQVSFGLLFAGYFLWQGYYHKLGDALFYGFYQAISAVTNSGFDVTGDSIMPFAHDYPFLLVIMFLIFIGGIGFPVLMDFYEWVLYRRKKIQRRLPFRFSLFTKIAVLAFVILFIGGTLLIYLLERDHLFAAIDPFGRWVNSMFYSMTTRNAGLQIHDLGEFQVTTLIIFSLLMFIGCSPSSVGGGVRTTTIAIIGLYMTSFLKSEDNINIFGRRISDADVRKSVVVFMLSLAMCFFSVLLLSATEEQSLIAIIVEVTSAFGTTGLSLGITADLSVVGKIVIALLMFIGRIGMLYTLLLFIPKETRDQGYEYPTEQIIIG

1.3E-56	202	42.6	5.3E-56	199.5	29.5	1.9	1	D5E5E6_MYCCM	Potassium uptake protein B	trkB MCRO_0351	Mycoplasma crocodyli (strain ATCC 51981 / MP145)	553	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma crocodyli, Mycoplasma crocodyli (strain ATCC 51981 / MP145)	512564	>tr|D5E5E6|D5E5E6_MYCCM Potassium uptake protein B OS=Mycoplasma crocodyli (strain ATCC 51981 / MP145) GN=trkB PE=4 SV=1MKRKLRDSFIYKIYYKMKNWRQNVSKIKYILLIYFIVVIISSLFLWSPWTQNTTFEMNGSIEKIDRISYIGALFTTSSAFSDTGLVVVD TFKHWNMFGQAIIAILLLGGIGIFTIKIFIINWILRKKSISLSEINLVNTERGGIKINETAKLVITSVKFLLFCILLFGLLLSFYFYVPPQTTEGI KEYINNNYISPYNNWSLSFRYGFFHVISAINNAGFDIIGGNSLMPYYLNYGIQIIFILLLVIGGLGFPTLYDISNFIIHKITRKKTKYHFSLFTK MSLICYIGVLIFIFLFSFIFEITSTNQESFWNLVYIPKDDRLLNTFDLNNPVLKPYVDLGQMYGSTGSKLFALLFSSFSTRSAGFTTIDMW NLSPGTIATFTMAMFIGAAPSSTGGGIRTTTFAIIIMSLVNRMLGRKEVVAFKRTINKNTVKMAFQVTLISISLLMIISLISVSSFDIHGGSIN SYYSVDKYIGMRNYGIEHIMFEVSSAFGTTGLSTGLTKELNTASIIVILLLMFIGQFGVSSTLLVWGRKKNYFNRYSYIEDDLVIG
1.4E-56	202	31.1	2.5E-56	200.6	21.5	1.3	1	V5WJQ2_9SPIO	Potassium uptake protein, integral membrane component, KtrB	L21SP2_2456	Salinispira pacifica	618	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Salinispira, Salinispira pacifica	1307761	>tr|V5WJQ2|V5WJQ2_9SPIO Potassium uptake protein, integral membrane component, KtrB OS=Salinispira pacifica GN=L21SP2_2456 PE=4 SV=1MLPDGLFISVGHALLAAAIYTIIRTMETPARSRRIENIRKILTPVIIFTFVLSIISLFLEQAEIDSPFIGVFTNAVDFTLAFFILLELIFELIS APYKGIWLKNNLASTLFSAAFLILFTYNKYVEFVIQPDLESGFQIAGLIVVRNFFMLFKVFGRIRRISALLNNLTIHPAQTLVLSFLMVILVG TFFLMLPVTTVDGSGLNFIDALFTTTSAVCVTGLIVVDTATHFTLLGQAGILILIQIGGLGIMILSYSAAWALRRSFSLQDKLLISYMTNED DLNRVSRSLLQIITLTFSIEALGALWLFFSFFSEGMALGKSAWFAVFHSVSAFCNAGFALFSDSLEGFAGNIPVNLGVAFLIICGGLSFA VMMDLMKIPGKLRPFSGRAGISGKRGLQLQLNTRVVLLVNLILLTAGVLIFYGLEYRNSLSAEPVGRQYLLAFFQTVTLRTAGFNTMNF ASLGSAALMLSLFLMIIGGASGSTAGGMKVNTVAVVFSYLKSRLTGRDRVRIFEYTLTRNTSSNALVLFIFAVSTIFAGVFFLSISEEQPF QDIVFEVVSAFATVGVSRGITSGLSTPGRLIISILMFMGRIGPLTLLTALAGRRVNDGVYYPETDILIG
1.5E-56	201	18	2.3E-55	197.4	12.5	2	1	A0A0F7GC20_9CHLR	TrkH	trkH DGWBC_0231	Dehalogenimonas sp. WBC-2	483	cellular organisms, Bacteria, Chloroflexi, Dehalococcoidia, Dehalogenimonas, Dehalogenimonas sp. WBC-2	943347	>tr|A0A0F7GC20|A0A0F7GC20_9CHLR TrkH OS=Dehalogenimonas sp. WBC-2 GN=trkH PE=4 SV=1MNLIAIAHYVGLVTGLVGAAMAVPSLLSIIGGEPAAGALAAAAVITVVCGAVMFLLTRNGRKAPSQREVFVIVIGAWFSVTIFGALP YYFSGALPTYLDALFETMSGFTTTGATVMNNIGAQDHGILLWRSLTQWLGGMGIIMLFVALFPLLGIGAAQMADAEMTGDKGERMTS RIRETAKVLWLIYVIFTLLCFVSLVLAGLPIFDSINISLTTVPTGGFAPVDFSIEEYGHIPAQLIVNFFMFLSGINYALFYYLVMKRRPGKLF KNPEFQLYAGLMAVASLVITLNLVTNNVLPFADALREGTFSATTIMTTTGYTGANFNDWPTFSRALLLMLMVVGGSAGSTAGGLKVIR VLVLFKYSYRRVIQAFNPSAVIPLKVGDMVLQETTVSRTISLTVIYFAILWGGFLIMSALGLDIETALSSVVSALSNIGPGLGGVGPYENF AWIPSLGKGVLIVLMLAGRLELFTLMVIFVPSFWRRY
1.5E-56	201	32.7	2.1E-56	200.9	22.7	1.1	1	F4A083_MAHA5	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Mahau_1736	Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	442	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family IV. Incertae Sedis, Mahella, Mahella australiensis, Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	697281	>tr|F4A083|F4A083_MAHA5 Potassium uptake protein, TrkH family OS=Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON) GN=Mahau_1736 PE=4 SV=1MTRFTPTQILVMGFAAIILTGTLLLMLPISSAAGQNTDFITSLFTATSAVCVTGLVVVDTGTYWSLFGQIVIMLLIQAGGLGFMTMA TLASMLLGRRIGLKERLVIQEALNEFSLQGLVKLTQRILITTALFELSGMALLSTRFIPIYGIGKGLYFSLFHAVSAFNNAGFDIIGDFVSFT PFVGDIIINFTVMGLIIIGGIGFAVIMDVFYNWHVKRLSLHTKLVLTTTTVLIVAGFLFFFVEYNNPKTLGPLSVPVKAMAALFQSITPRTA GFNTISEGDLTDASKFVTILLMYTGASPASTGGGIKTTTLSTIILAVAAVLRGRENVNIYGKRLSWTLVMRSLSIAVLALGLISAVTIILSLA ENQAFIKVLFETVSAFGTVGLSTGITPTLSAVSKIALAFTMFAGRVGPLTIAVALLQRQHGMKDLCRYPEEKIMVG
1.7E-56	201	16.3	1.7E-32	122	2.1	2.1	2	Q4KGB8_PSEF5	Trk system potassium uptake protein	trkH PFL_1589	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	220664	>tr|Q4KGB8|Q4KGB8_PSEF5 Trk system potassium uptake protein OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=trkH PE=3 SV=1MALPTLRIIGFIIGIFLITLAIAMVVPMATLVVFERTGDLPSFLWASMITFIAGLALVIPGRPEHVHLRPRDMYLLTVSSWLVVCIFAA LPFLLTQHISYTDSFFESMSGITATGATVLSGLDSMSPGILIWRSMLHWLGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSEKVMPRS HMVARLIVATYVGITIFGSLAFWWAGMNVFDAINHAMSAISTGGFSTSDDSLAHWKQPAVHWVAVVVMILGSLPFTLYVATLRGNRR ALIKDQQVQGLLGLLLVTWLVLGTWYWWTTNLHWLEALRHVALNVTSVVTTTGFALGDYSLWGNFSLMLFFYLGFVGGCSGSTAG GIKIFRFQVAYILLKANLNQLIHPRAVIKQKYNGHRLDEEIVRSILTFSFFFAITICMIALALSLLGLDWMTALTGAASTVSGVGPGLGETIG PAGNFSTLPDAAKWILSLGMLLGRLEIITVFVLCIPAFWRH
1.7E-56	201	18.2	2.3E-56	200.7	12.6	1.1	1	A5GUB4_SYNR3	Trk-type K+ transport systems, membrane component	trkG SynRCC307_1570	Synechococcus sp. (strain RCC307)	456	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain RCC307)	316278	>tr|A5GUB4|A5GUB4_SYNR3 Trk-type K+ transport systems, membrane component OS=Synechococcus sp. (strain RCC307) GN=trkG PE=4 SV=1MSAWQRQLTVPQFTVVSGLLVIALGTLLLATPLCSGPSVDLWEALFTATSAITVTGLSIIDVGTELTFFGQLVLAVLIITGGLGLMAI STFLQGFVQGRTGLRQRIDQGRTLDQFGVGGVGSTFRAIVISGGVLMLIGTVLLYAFGFTDISNPAERLWAAMFHSISAFNNAGFSLW SGSLEAYQSNAVVCAVVAALVIAGGIGWRVLSDLWIHRRNPLEWRRLSLQSRVVLRSSVLLIAAGTLGLLFTERLAPAGVVGGLPLLQ KVGVSLFQVISARTAGFVSVPLSLDTISHAGLFLLILLMFIGASPGGTGGGIKTTTFAVLLCTTRSTLEDRTEVVINRRRIPGKQVLRAVGI TLASAGVVVLMTMLLGLGDTEAGVLGDEDFTFLEKLFTCVSAFASVGFDLGITARLDRWGQLVLLVGMFIGRLGILLLLSALFGRRPPS RVRYPQEELIL
1.7E-56	201	25.7	1E-54	195.3	17.8	2	1	A0A089KYU8_9BACL	ATP synthase subunit J	R70331_16540	Paenibacillus sp. FSL R7-0331	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. FSL R7-0331	1536773	>tr|A0A089KYU8|A0A089KYU8_9BACL ATP synthase subunit J OS=Paenibacillus sp. FSL R7-0331 GN=R70331_16540 PE=4 SV=1MANISLGHLKLTPPKILSLGFIALIAIGTLLLCLPAASTSGQISFIDALFMATSATCVTGLAVIDTGTQLTVFGQIVLLVLFQFGGLGF VTMATLITLVLNKKISLKERLLLQESMNQSSMQGIVKLIRRVLIYSLVIQLIGALLFTVRFLMDMPAGKAVYYGLFHSVSIFNNAGFDLFGD LHGPFSGLTRYAEDPIVNITSMLLIFLGGIGFIVLSDIVDFPKRKRLTLHSKVVLAASAALILIGAVIFFWLELNQSLKPLHAGGKIMASFLQ AITPRSGGVTTIDIPLLRESTQFMMILLMFIGAAPGSTGGGIKITTFAILVVTAYSKIRGKEDIVMFRHRISKDNVYRAITMTLLSLMLVVIAT MLLSVTESADFLTVLFEAVSAFGTSGITMGLTPELTTPGKILVIILMFVGRTGPLTLAYAIKPKKNKELFRYPEGNITIG
1.8E-56	201	15.1	3.9E-55	196.7	10.4	2	1	R5YC55_9FIRM	Cation transport protein	BN528_01901	Roseburia sp. CAG:197	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:197	1262943	>tr|R5YC55|R5YC55_9FIRM Cation transport protein OS=Roseburia sp. CAG:197 GN=BN528_01901 PE=4 SV=1MNYKMMGKFISQILFVEAAFMLPALLLSIVYGEQSAVRGFIGAIIITLIVAAIMYVLCRNAVKRFYAREGLVCVGMSWIALSIMGCLP FFISREIPDFLDALFEIVSGFTTTGSSILTDVEALSHGLLYWRSFSHWLGGMGVLVFLLAVVPRDRGGSGFTLHILRAESPGPNVGKLV PKMHTTARILYVIYVLLTIINIVFLLFGGMPVFEAVCTAMGTAGTGGFGIKNDSMASYSPYIQNVCTVFMLLFGVNFSCYYLLLVRHFKTV FKDQELRMYIAIVLGSIVLITWNLHGFYSTLGETVRHAAFQVATVITTTGFATTDFDLWPSFSKGILLALMFLGACAGSTGGGLKIGRTL LLLKNLRRKTRRILNPKRVEVVRVNGQKVSESVLENTNTYLIAYVVIVLGSFLLISIDNLSMMTNFSAVVACFNNIGPGFDAVGPTCNFS VFSGFSKVVLIFDMLAGRLEIFPILILASKSTWSRK

1.8E-56	201	22.7	2.4E-54	194.1	15.8	2	1	R6G1H4_9FIRM	Cation transport protein	BN476_00054	Eubacterium hallii CAG:12	492	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium hallii CAG:12	1263078	>tr|R6G1H4|R6G1H4_9FIRM Cation transport protein OS=Eubacterium hallii CAG:12 GN=BN476_00054 PE=4 SV=1MNSSIIRFVLGYVLKMEAVLMLLPCIVAVLYREQTGFAYLLVAAVSMAFGTLMTIKKPKSHVFYLKEGCVATALSWIFLSFFGALP FWISGEIPSLIDALFETVSGFTTTGSSILADVEALSHCALFWRSFTHWIGGMGVLVFLLAVIPLSGGSHINLMRAESPGPSVGKLVPKIK YTAQILYIIYFGMTIVEIVLLLISRMPAFDAITLSFGTAGTGGFGIKGDSLASYTALQQWIVTIFMILFGVNFNAYYLILFRKFKKALQMEEV RAYFAIIFVATAIITGSLVGGNMQFFDALRHAAFQVGSIITTTGYATVNFDAWSQTCRAILVLLMFVGACAGSTGGGIKVSRFIVMVKTMI KELNSYIHPKSVKKIKMDDKPIEHEVVRSINVYFITFMIIFVASVIAISFEGHDLVTNFTAIAATINNIGPGLSMVGPDCNFGFFSDFSKLVII FDMLAGRLELFPLLILFHPAIWKELFTQKITMRRKKKF
1.9E-56	201	23.3	6.2E-56	199.3	16.2	1.6	1	Q24QY9_DESHY	Putative uncharacterized protein	DSY3764	Desulfitobacterium hafniense (strain Y51)	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium hafniense (Desulfitobacterium frappieri), Desulfitobacterium hafniense (strain Y51)	138119	>tr|Q24QY9|Q24QY9_DESHY Putative uncharacterized protein OS=Desulfitobacterium hafniense (strain Y51) GN=DSY3764 PE=4 SV=1MMFLGKFRANSIQMIALGFAGIILIGTLLLSLPAASRDGASLPFIDALFTSASATCVTGLVVHDTYTQFSLFGQIVILCLIQIGGLGFM TVATLFLMMARRKIGLAERGVLTESVSAFQIGGIVRLIRRIIICTAIVEGMGAILLAIRFCPQMGVATGVYYAVFHSISAFCNAGFDLMGR FAPYTSLIPYQSDVLVNLTIMTLIVIGGLGFVVWDDIMEHKLRYVRYKLHTKIVLLSTAFLIGGAILFYAMEQGNVLAAMHPIDKLLASLFQ SITPRTAGFNTVDTAALTEGGTVLSMLLMLIGASPGSTGGGIKTTTIMVILLATISYIRNTDDINIFHRRLENNTIKRAYCSTTIYIMLSILGIF LLITTQGLPAKDAAFETLSALGTVGLSTGITRELDTLSRMVIILLMYSGRVGSLTLLMAVMMGTKSKLRNPEEKIIIG
1.9E-56	201	31.8	1.8E-54	194.5	22.1	2	1	R7CR26_9FIRM	Potassium uptake protein TrkH family	BN625_01631	Dialister sp. CAG:357	443	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Dialister, environmental samples, Dialister sp. CAG:357	1262869	>tr|R7CR26|R7CR26_9FIRM Potassium uptake protein TrkH family OS=Dialister sp. CAG:357 GN=BN625_01631 PE=4 SV=1MDVLKYGRSLSPAQIIVYSFALFILAGTALLMLPAATVDGAGATFTDALFTIVSAVCVTGLSVQDTGTYWTFFGQAVILFAIQVGG LGVVTAAISLTVFSGCKIGLMQRNTMQEALAAPQLKGIVQLVLFILKYVAIIELVGTLLLYTVFAPQYGWVTGWWYAMFHAISAFCNAG FDIMGPAGGGSLTTYEFNPVVNTVIMLLIIIGGLGFMTWADVRTHGFHIRAYRLQSKIILIMTAVLIIVPTLIFYATEFGQNHDTMYLFPAM FQAVTTRTAGFNSVDLMTLSESNRAILILLMLVGGAPGSTAGGIKTTTAFALLASVWAMMRRSSDISCFGRRISEDTLHKATVLFMMYL LLIIFSTIFISALDDFSILDSCFETVSAIATVGLSIGITDQLSTLSKYILIFLMFFGRVGALTFVFAVHSKFDGTRSHYVKEDVVIG
1.9E-56	201	13.5	2.7E-56	200.5	9.4	1.1	1	Q67QG3_SYMTH	Potassium uptake system protein	STH1095	Symbiobacterium thermophilum (strain T / IAM 14863)	456	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Symbiobacteriaceae, Symbiobacterium, Symbiobacterium thermophilum, Symbiobacterium thermophilum (strain T / IAM 14863)	292459	>tr|Q67QG3|Q67QG3_SYMTH Potassium uptake system protein OS=Symbiobacterium thermophilum (strain T / IAM 14863) GN=STH1095 PE=4 SV=1MALQHRRRGPTFTPPQALAAGFALLILIGTVLLALPVAHEPGHRLSLTDALFMATSAVCVTGLAVVDVSTTFSAFGEVVLLLLVQA GGLGIMSLSALMFLLTGRRIGLHERLMMQEALGSLSIAGVVRLTRTIIAGTLAVEAIGAALLSLRFLAYYPPAQALYFGIFHSITAFNNAG FDLTSRSLRPFQHDPAVLLVMAGLILMGGMGFVVLQDVWHHRRWERFSLQTKLVLAVTGVLVGAATLLVLALEWGNPATLGGLPVP EKLLNAFFTAVTFRTAGFESIPTAGMASAALLLAMVLMFIGGSPGGTGGGIRTTTFAVIALAVRATVRGTEDIQAMGRRLPRELLDRAIA IVAMSMAVIVAVGGLLLVTEGHLVTAPGNPFGAADVLFESTSAFTTMGLSTGVTPHLSMAGRLLLTVTMYVGRIGPLTAAVALAQRRR ERVNIDYPEERVMIG
1.9E-56	201	17.1	2.7E-54	193.9	11.9	2	1	D7GRH9_9FIRM	Trk-type K+ transport systems, membrane components	CK3_06060	butyrate-producing bacterium SS3/4	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, unclassified Clostridiales, unclassified Clostridiales (miscellaneous), butyrate-producing bacterium SS3/4	245014	>tr|D7GRH9|D7GRH9_9FIRM Trk-type K+ transport systems, membrane components OS=butyrate-producing bacterium SS3/4 GN=CK3_06060 PE=4 SV=1MNYSMIFYIIGWILDVEAALLVPSLAVSLIYHESCALAFFITIVLCLIPGVILVRKQPKNKVFYAREGSVTVALSWIVMSIMGSIPFLLS GSITNPVDALFETVSGFTTTGASILPAVEPLQHGILFWRSFTHWIGGMGVLVFLLCLLPLTGSGYHMNLMKAESPGPSVTKLVPKVQS TAKILYGLYLFLTVMEFVLLLVGQMPVFDSLCTVFGTAGTGGFGIKNDSFGSYSTYLQGVVTVFMILFGINFNVYFLFYMKKPKEALRC EEARWYLGIIAASILVITFFVRDFFDSLFLAFHHVAFQVASIITTTGFATVDFNLWPTIPKTILVLLMFIGACAGSTGGGIKVSRVVLLFRSL TKELSQSLHPNQVRKIHFEGRAVDHVVLRSVNVFMAAYILIFAISVLLIGIDNFDLVTNFTAVAATLNNIGPGLELVGPAQNFGLFSNFSK LVLTFDMLAGRLELFPLLLLFYRGTWKRF
2E-56	201	21.9	8.1E-55	195.6	15.2	2	1	A0A0F2NDU7_9FIRM	Potassium transporter	VR68_09540	Peptococcaceae bacterium BRH_c4a	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c4a	1629716	>tr|A0A0F2NDU7|A0A0F2NDU7_9FIRM Potassium transporter OS=Peptococcaceae bacterium BRH_c4a GN=VR68_09540 PE=4 SV=1MNTKLILKALGLVLLCEGVSMGPSLLMTFYYANGDFEAFLISMVITVFAGGALFLMGAGAGGSVGYREGFAVAAFGWILLAGFG SMPYVLSGVLPSPVDAYFETMSGFTTTGASVIVDVEILSRGMLFWRSLTHWLGGMGIIVLTVALIPSLKIAGLQMFKAEVPGPTKSKVL PRIAQTSRELYKIYLVITVVEIFMLKLAGMDWFDSFIHTFGTVATGGFSSKNTSIAAYDSVLIELIIVVFMIISGINFALHYYSLRGNFRPTL KDPEARLYMGIILVSVCLITFDLVNSANYGADKAARDSLFQVASIVTTTGYASADYDQWPSMSKAVILLLMFIGGCAGSTGGGIKVSRY LIMFKGISRQIMKLIHPQAVIPLRIGKGVISQEVLDNVQTFFFLYMLILGASVVFLTALGVDLVSSISAVAATMGNVGPGFNLVGPMTNYF TLPMAAKAALSFCMLIGRLELYTVLVILSSRFWRN
2E-56	201	28.6	3E-56	200.4	19.8	1.1	1	Q2LUG2_SYNAS	Potassium uptake protein	SYN_01091	Syntrophus aciditrophicus (strain SB)	456	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Syntrophus, Syntrophus aciditrophicus, Syntrophus aciditrophicus (strain SB)	56780	>tr|Q2LUG2|Q2LUG2_SYNAS Potassium uptake protein OS=Syntrophus aciditrophicus (strain SB) GN=SYN_01091 PE=4 SV=1MRLTALQLKMSISGYLTPARSFILSFAAVILAGTLLLWSPFSSSGKPLSFIDALFTSASAVCVTGLAVVDIGRDLSLPGQLITLLLFQI GGLGIITFSVLFFGIMGRGISFRGREIVQSTFLHTPRRDFFMILKWVLLMTLIIESIGTLLLFSRFIQDFPLPRALYLSVYHAVSAFNNCGY SLFSNSLMDYRSDWIVNLTIMSLIVLGGIGFIVLYEIISRVRGNQKKLSLHSRIALLMTGFLILLGAVLFYFFEMHHVLRGASWQENLLVSL FQSVTSRTSGFNTVDIGQLTNATILLLMGLMFIGASPGSTGGGIKTTSFTLLLMMIWNRIQGSEQVTIFNRSIPEEITTRTISIVFASAFSV ALISSILLFGSPDSLPPASSRHLFVEYVFETVSAYGTVGLSMGITAKLSELQKLAIILMMFAGRVGPLTLAFAWSKSKRKIIYAEESVMVG
2E-56	201	15.1	5.7E-32	120.2	1.7	2.1	2	C3JZ90_PSEFS	Trk system potassium uptake protein	PFLU_4861	Pseudomonas fluorescens (strain SBW25)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens (strain SBW25)	216595	>tr|C3JZ90|C3JZ90_PSEFS Trk system potassium uptake protein OS=Pseudomonas fluorescens (strain SBW25) GN=PFLU_4861 PE=3 SV=1MALPTLRIIGFIIGIFLITLAIAMVVPMATLVIFERTSDLPSFLWASMITFIAGLALVIPGRPEHVHLRPRDMYLLTVTSWVVVCIFAAL PFLLTQHISYTDSFFESMSGITATGSTVLSGLDTMSPGILMWRSLLHWLGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSEKVMPRSH MVARLIVAAYVGITILGSLAFWWAGMGLFDAINHAMSAISTGGFSTSDESLAHWKQPAVHWVAVVVMILGSLPFTLYVATLRGNRKAL IKDQQVQGLLGLLLVTWLVLGTWYWWTTNLHWLEALRHVALNVTSVVTTTGFALGDYSLWGNFSLMLFFYLGFIGGCSGSTAGGIKI FRFQVAYILLKANLNQLIHPRAVIKQKYNGHRLDEEIVRSILTFSFFFAITICAIALALSLLGLDWMTALTGAASTVSGVGPGLGETIGPAG NFASLPDAAKWILSLGMLLGRLEIITVFVLCIPAFWRH

2E-56	201	25.6	3E-56	200.4	17.8	1.1	1	Q3A8E3_PELCD	Ktr system potassium transporter, membrane protein	ktrB Pcar_0086	Pelobacter carbinolicus (strain DSM 2380 / Gra Bd 1)	457	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Pelobacteraceae, Pelobacter, Pelobacter carbinolicus, Pelobacter carbinolicus (strain DSM 2380 / Gra Bd 1)	338963	>tr|Q3A8E3|Q3A8E3_PELCD Ktr system potassium transporter, membrane protein OS=Pelobacter carbinolicus (strain DSM 2380 / Gra Bd 1) GN=ktrB PE=4 SV=1MTRPFLQIKNLDPGWMLILYYGFAILIGAALLTLPFAAQGAPLSFLDALFTATSAQCVTGLIVVDTGTKLTLFGQLVVLLLIQIGGLGITTFSVYLFFYLGMGVGIRDRWVIQETLLHTPVDSLRDLVRSIFRYTLVIEGVGAALLATAFVPQMGWSKGLYSAVFHSISAFCNAGFSLNADSMIGYRANPLVNITLMALIILGGIGFLVIKEIFDLSKQHNRRRRRRLSLHSRLVFMTTAVLIIGGALLIGVLEAPSALASMNTAESIWVTLFQSITARTAGFNSIDLNLFEVPTLFLMMFLMFVGASPGSCGGGIKTTSLALFVAIMHSRLKGNPHTNVFRRTLPEAAVTKTLTLVMTALLFVAFAVFSLLAVQMQGMPAMASRGVFLEYTFEAVSAFATVGLSLGATAKLVPAGKLIIVIVLMFIGRVGLLTVAFTMIRRSREGAVHYAEENIMIG
2E-56	201	34.8	6.4E-55	196	24.1	2.1	1	F2I3B3_PELSM	Trk system potassium uptake protein	SAR11G3_00167	Pelagibacter sp. (strain IMCC9063)	481	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Pelagibacterales, Pelagibacteraceae, Candidatus Pelagibacter, Pelagibacter sp. (strain IMCC9063)	1002672	>tr|F2I3B3|F2I3B3_PELSM Trk system potassium uptake protein OS=Pelagibacter sp. (strain IMCC9063) GN=SAR11G3_00167 PE=3 SV=1MKDGTKTVFLVIGALLIILGLFMLIPYLIEITIGDKSHNFLFWSFFSIFIGFLLLITNQTEEKSLNIKQAFMMTSFSWIAITLFASFPLMYSSLQLSFTDAFFESMSGITTTGSTILDDIESSSKGVLIWRAILQWLGGIGIVVMAITVLPLLNIGGMSLFKSEGAEFEKILPSSKEIAMVCTKIYFILTAICALCFYFFGMNAFDAVAHSLTTISTGGFSTYSGSIGQFNSVSIEIITMIFIICGSVPFLTYLKFLKGEKAAFFKDTQIKGFLYFVSLSTVIVTIYCYFFVKDFLPDNIRESTFNVISIVSGTGFTTQDFGTWGNFSLFFFLILMFVGGCAASTTCGIKIFRFQILNLFIKKQIKQIIYPNGVFPIKYRGEVIGDTFLTSVLTFVFLYIFIFFLLTALLSLSNLDFTTAISAAATSLSNVGPGLGEIIGPNGSFKYLPDLTKWYLSIAMLLGRLEFFTVLVLFLPSFWRD
2E-56	201	13.7	9E-55	195.5	9.5	2	1	M4ZVL0_9ACTN	Trk system potassium uptake protein	trkH YM304_03940	Ilumatobacter coccineus YM16-304	502	cellular organisms, Bacteria, Actinobacteria, Acidimicrobiia, Acidimicrobiales, Acidimicrobiaceae, Ilumatobacter, Ilumatobacter coccineus, Ilumatobacter coccineus YM16-304	1313172	>tr|M4ZVL0|M4ZVL0_9ACTN Trk system potassium uptake protein TrkH OS=Ilumatobacter coccineus YM16-304 GN=trkH PE=4 SV=1MLGRRGERLLREDRRPTLTGHIVGLSTAVVGLGIFLAGLVDVVDGGPDIVVLLVTGLVMAIVGAVAWRSTITPKQIRVLDVFTAVTVTWVVIAVLGAIPYVLTGHFGRVDDALFESISGFTTTGATVTSDIEATSKGLLFWRSTTQWMGGMGVIVLVVAVLPTVGSGGMNLLEAEAPGPTGERLTPRVRETARRLWAVYLGFTAVLAALYCLAGMSIYDGVSHSFTTVSTGGFSPYQASMGHFESDVIQWLAIFGMFFAGGSFTLYWRAIRRNPKPLLMSTEFRVYALFALAITLWAFVTSGNGGGQSAGFRDSLFTTLSTVTTTGYVTTEYGLWSETAQSLLLIALPIGAMAGSTAGGIKIVRVMAVASFAHREALKHLHPKLVRPIRVGSGMLSDDVAGKVVGFLLLTLVIFGGGSFFIAATGPDLITAFSASATALGNVGPGLGDLDHTGDFTAIPSLGRAIAMVQMLLGRLEIYPVILALSVVTLRAPRLGRAVRNNN
2.1E-56	201	20.1	1.5E-54	194.7	13.9	2	1	R7FDV1_9FIRM	Potassium uptake protein KtrB	BN611_00157	Ruminococcus sp. CAG:330	442	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:330	1262954	>tr|R7FDV1|R7FDV1_9FIRM Potassium uptake protein KtrB OS=Ruminococcus sp. CAG:330 GN=BN611_00157 PE=4 SV=1MRAFWKQISTFQVILLGFLAVILLGSLLLMLPVSASAGTVTSFPNALFTATSAVCVTGLIVQDTATYWSEFGQAVILLLIQIGGLGVISAASAISLLAGRRIRLRQRSTIQEAISAPQVGGVVRFTRFILKFTFCAELLGALCMLPVFAKDFGLGKGIWYAVFHAVSAFCNAGFDLMGVREPYSSLTSFVGEPLINLPIMLLILSGGLGFYTWDDIFTHRFRFSRYHMQSKIILVMTAVLVVLPAAYFFFAEFSAWQPAQRIFASLFQAITPRTAGFNTASFSAMKDSSIAVLIVLMLIGGAPGSTAGGLKTTTAAVLVSSAVSVFRRNKETHFFGRRIPEDTIAKASALLLLYLALFLTGGVSISLAEGLPLQDCLFETASAVATVGLTVGITPTLGLFSKIVLILLMFFGRVGGLTFLYAAVFPKQENFSKLPLEKINIG
2.1E-56	201	26.8	1.1E-54	195.2	18.6	2.1	1	R6FT03_9CLOT	Trk system potassium uptake protein	BN542_00466	Clostridium sp. CAG:221	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:221	1262780	>tr|R6FT03|R6FT03_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:221 GN=BN542_00466 PE=4 SV=1MNYRVVLKLLGNVLKYEIFLLMIPFLVALYYGDGDALSFFITMVLMLPIMIFLCNIRTDKEEIYAKEGFLTVGLAWILISVVGALPFVISGAIPSFIDAFFETSSGFTTTGASILTEIESLPRGILFWRSFTHWIGGMGFLIFILALIPSLSTNTIFLLKAESPGPNPGKIVPKIKETAKILYMIYFIMTVIETILLMMAGLSLYDALIHALGTAGTGGFSNMNSSVASFNNPAVEWIITIFMLLFGVNFVLYFQMFKGDFKSVFKSEELKYYILMVVVSIVLITINIIDFNGGNIGLSIRESSFQVASVITTTGYATTDFNLWPTFSKIILTLLMFAGGAMAGSTGGGIKTVRIVLILKAIKREIDKILHPKRIQRVKMDGKVVEEEVVSGVLLFIGSYIVISLIAIFIVALDGFDLVTTTTSVIATISNIGPGFEMVGATGNFAAFSPLSKIVLSFCMLAGRLEIYPMLILFSPSIWRKKY
2.3E-56	201	20.5	2.9E-56	200.4	14.2	1	1	R6GF74_9FIRM	Potassium uptake protein TrkH family	BN690_01614	Blautia sp. CAG:52	461	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:52	1262758	>tr|R6GF74|R6GF74_9FIRM Potassium uptake protein TrkH family OS=Blautia sp. CAG:52 GN=BN690_01614 PE=4 SV=1MSEKQKKRQWHTPTERIMMTGFGVVIILGTLLLCLPVSSASGKGVYWLDALFTATTSVCVTGLVTVPTATTWSVFGKIVILGLIQFGGLGIMACMIMIFLVLRRKISLQSRKLIQDTYNLPVLKGSVGIVRRLLIGTAVVEIAGAICYSFWFVPHYGLWRGIWYSIFHSISAFCNAGIDLVGESSFAPFVTNPLINVTTMGLIILSGLGFPVWWEVIEHVQDLLKGKRTRKNFIRGFTLHTKLVLTTTVILITGGALLILLDWNHTGSLGDLKPGEKVMAAFFQSITTRTAGFETIPQKNFTDGSAMVSIILMFIGGSPMGTAGGVKTITVALLIVLVTSYIRGNHDTVVWGRKVVEENIRSAVVIFFFALTTALTATILLVAVSGHPLLDCAYEVVSAVATVGLTRSLTSQLPAAGKIIVILVMYMGRIGPITLAVALGRRTRHVDADIQRPEQRILIG
2.3E-56	201	22.6	5.5E-56	199.5	15.7	1.5	1	A0A0A2FKI1_9PORP	Potassium transporter	HQ45_08950	Porphyromonas crevioricanis	487	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, Porphyromonas crevioricanis	393921	>tr|A0A0A2FKI1|A0A0A2FKI1_9PORP Potassium transporter OS=Porphyromonas crevioricanis GN=HQ45_08950 PE=4 SV=1MVRHINFRFVLKTVGLACIMESGFLFLAIVIAFLYREEDLMPLIYTTLFMLGVGLVGWLSGFRTRLARLSRREGMLIVTLIWVVLSSIGMLPFWLGGYVGSISDAFFETMSGYTTTGATIFPSVEHLPHGILFWRSLLQWQGGIGIVVFTLALLPVITGDRGASTIYNAETTGIMHDRFLPRISTVSKRLALVYVVMTTLLFFLLWIGPMNSFDAVCHALTCISTGGYSTKDSSVAYYNSAYVEYVLSAFMFIASLSLTLIYFCFVGKPTKLLRDEEFRWYSILVLAAILITSLWLWAHWQNDSVEETIRTALFQVTSLISTTGYLTSDITQWQPFFWVIMLLLMFICGCSGSTSGGLKVSRFMVLVKNLRNEFKKRIHPNAVVPVKANGIVIPGALVSQVLAFFFAYLGLICVGVLLLTFDGIPFIESISASVSATGNVGPALGSLRSNFAEISPFSKWVLSFLMLAGRLEIFTVLSILRPAFWKE
2.4E-56	201	28.3	6.2E-56	199.3	19.6	1.6	1	R5I621_9PORP	TrkH family potassium uptake protein	BN472_01136	Tannerella sp. CAG:118	491	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:118	1262978	>tr|R5I621|R5I621_9PORP TrkH family potassium uptake protein OS=Tannerella sp. CAG:118 GN=BN472_01136 PE=4 SV=1MHKNDIQQINFKIVFRVIGMLLCMEAFFMIVPFLVSLWYDESDAFALFTTIGITIVAGVIMIMTTRNHSKHLAKREGFLIVATTWIFFSIFGMLPFIIHGCIPNVADAFFETISGFTTTGATIVLTDIDSLPHGILFWRCFTQWLGGMGIILFTLAILPMLNSGGIQLFNAETTGITHNKLRPRIGQTAKRLWGMYVAITTVLVICLVLGPMDLFDAICHAMSTTATGGYSTKQASIAYWNSAYIDYVIIFFMYISGINFSIVYFAVAKGDYKSLFKDEEVRWYTYVLILATAIAIAAGLFMSGQIQGSAEGTIRSSLFQVVTNITTTGFTTANFNDWGPFYAVILFLVMFFGACAGSTSGGAKTIRLVVLIKNTVNELYRHIHPNAVVPVRVNNKVISYELVSKILAFIFVYLLVFVISSVLLSAMGLTFEEAFGCTLSCLSNIGPGFGRMGSDFALIPDAGIWLLSFVMLVGRLELFTILIIFTPYFWKK
2.4E-56	201	26.5	1.4E-27	105.8	8.2	2.1	2	C7RE08_ANAPD	Cation transporter	Apre_1398	Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) (Peptostreptococcus prevotii) (Peptococcus prevotii)	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptoniphilaceae, Anaerococcus, Anaerococcus prevotii, Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) (Peptostreptococcus prevotii) (Peptococcus prevotii)	525919	>tr|C7RE08|C7RE08_ANAPD Cation transporter OS=Anaerococcus prevotii (strain ATCC 9321 / DSM 20548 / JCM 6508 / PC1) GN=Apre_1398 PE=4 SV=1MNGSVVKYTIGRLMQVLAMLMLIPLLVGLIYRESLIDIRNFVIPIVLAFLLGFILMRSGSAKGHIFTKEAMFITASCWIIFSIIGAIPLYLTASNYPSFVDAFFEMMSGFTTCGASVASNVELLPNSIIFWRSFSHFIGGMGILVFTLAIMPKANKESSSLMQAEVPGPTFGKITPKLSQTARVLYLMYIALTVIVIILLLFGGMNLFDAIIHAMGTAGTGGFSNKAASIGYYNSRYIEIVLSIAMLAFGINFNIYYFSLIRSARQAFKSEELYWYLGIVATTALLIFFNIRSMYDSSFFTGVTSLFTVSSIITTTGYVSLDYGAWPLFSRHILIFLMFVGGCAGSTAGGIKVSRFVVLFKSALNQIRKALNPLRVSVNKMDGKRVDKEVEESINRYILVYIFLFIIFMLVITLETNNFESAFSAVATTFNNVGPGLIDFGPVTSFEAMSKLSKLTLTFAMLFGRLELYPMILLFSAGTYRNIRK

2.4E-56	201	38.6	3.9E-56	200	26.7	1.3	1	B0VFH6_CLOAI	Trk-type K+ transport systems, membrane components (Modular protein) (EC 3.6.3.14)	CLOAM1457	Cloacimonas acidaminovorans (strain Evry)	564	cellular organisms, Bacteria, unclassified Bacteria, Cloacimonetes, Candidatus Cloacimonas, Candidatus Cloacimonas acidaminovorans, Cloacimonas acidaminovorans (strain Evry)	459349	>tr|B0VFH6|B0VFH6_CLOAI Trk-type K+ transport systems, membrane components (Modular protein) OS=Cloacimonas acidaminovorans (strain Evry) GN=CLOAM1457 PE=4 SV=1MPAEKKSGTFKHIELIAYILAFWSFFVLFLEPIFEYYTSSYPTIEFITALANLVLLVLTILSRVLSREVKENKTVVYFDLVMLILGSLLLTYQAKFVIFFLLIRQTWFIVQFILFRAFEGKIYKLLMRNPPVSLMVSFASVILIGTILLMLPASSTEGYITNFVDALFTATSATCVTGLTVLDTGTYYSLFGQIVILLLIQVGGLGIMTISTAFALMLGQRISLNVANLMHKVVGETPVIDVLKLLRSTVLVTLIIEITGALFLFTAFAKLMPAGQAIYYSLFHSISAFCNAGFSLWSNNLAGFVESPLVNFSITFLIILGGLGFAVLIDIYHYFFSSRRVRKLALHSKIVLSTTAILIVTGFLGLYISEYNSSMKGFSVAGRVLSSWFQSVTARTAGFNTINIGLYSSASVLLTVLLMFIGASPGSTGGGIKTTTFSTLMLSVLSMLTGKSDLVVFKRKIPLANAREATTLATLALVIILTIIFILMLIEPFPFEKILFEAFSAFGTVGLSMGITSQLSYAGKLLITLLMYIGRIGPLTLVYAISIRKRQPHISYAEERISIG
2.4E-56	201	31.8	1.3E-54	195	22	2	1	R5QKI6_9FIRM	Trk-type K+ transport systems membrane components	BN526_00099	Firmicutes bacterium CAG:194	445	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:194	1263008	>tr|R5QKI6|R5QKI6_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:194 GN=BN526_00099 PE=4 SV=1MSKHIGFQNKLSSFQIIILGFAGVIVLGALLLMLPISTQNGAVTPFSKTLFTATSAVCVTGLVVFDTASYWSGFGQLIILIMIQIGGLGVISVASFLSMLAGRKISLMQRQTMQNALSAPQMGGIVKLTRFIFLVSFAIEGIGALLLMPVFMTKYGIRGIWMAVFHSVSAFCNAGFDLMGNQTGQYSSLTSFAGSGYVTLVICLLIMIGGIGFLTWKDIAVKKTRFKEYSMQTKVILVTTAILIVIPAVFFFFSDFANEPLKDRICMSVFQAVTPRTAGFNTADLNKMSDAGRSVMMLLMLIGGSPGSTAGGMKTTTIAVLFANAIAVFRKRQNANCYGRRIDDSTVKNASAILFMYVFFSMLSAIIISITDGISMQMGMFETFSAIGTVGLTLGITPTLSAVSRFVLILLMFFGRVGGLTIIYAAFSQKDASTLKYPMENITVG
2.4E-56	201	30.6	4E-56	199.9	21.2	1.2	1	A0A089MSR3_9BACL	ATP synthase subunit J	PODO_25660	Paenibacillus odorifer	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus odorifer	189426	>tr|A0A089MSR3|A0A089MSR3_9BACL ATP synthase subunit J OS=Paenibacillus odorifer GN=PODO_25660 PE=4 SV=1MSEFKFLKLSPPQILVLGFASIILIGALLLMLPISSTGSNSVEFIDALFTSTSATCVTGLVVLDTGTSFTIFGKTVIMILIQIGGLGFMTMATLFSLVLKRKISLRDRLILQEAMNQGSMEGIVRLIRRVLIYSLVIEGCAALLLSIRWAFDMPLGKAIYYGIFHAVSMFNNAGFDIFGDFRSLTDYVYDPLVNIIVMFLIVSGGIGFIVMSDLVEFRVTRRLSLHSKVVLSTSTGLILIGALVIFIFEFTNTRTLGSLNFGGKILSAFFQSVSPRTAGANTVDIAGLRQATQFFIVILMFIGASPGSTGGGIKTTTFTMMIGAVIAMLRGREDVVLFRYRLAQERIYKALTITLLALLLIASVSMILSTTEDSNFLAILFETTSAFATVGLTMGLTPELSAIGKILLCLTMFAGRLGPLTLAYALGPKQGKPLYKYPEGKIIIG
2.4E-56	201	15.2	1.9E-54	194.4	10.5	2	1	R6NGR1_9CLOT	Cation transport protein	BN578_00929	Clostridium leptum CAG:27	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium leptum CAG:27	1263068	>tr|R6NGR1|R6NGR1_9CLOT Cation transport protein OS=Clostridium leptum CAG:27 GN=BN578_00929 PE=4 SV=1MNRRMILYLICQILRIEAVTMIPAAVIAIVQKEYPSLIGFIFAMLAMGGVSLLSAAFRVRKKEIYARDGFLTVSLAWIAVSLFGALPFWISGEIPNFIDCIFETVSGFTTTGASVVQNVEALPMSLLYWRSFTHWLGGMGVLVFLLAIIPIMKGKSTLVHLLRAESPGPSVEKLAPKLHQTAKILYGIYIALTMVQILILLAGGMPLFDSVTTSFATAGTGGFAIKNDSMAGYSPFQQGVVTVFMALFGVNFNIFYLLLLRQFSRVFRNQELRLYLGTMIGAILLITWNVLPQFDWNPGTAAHHVAFTVSSVMTTTGFATVDFNQWPMFSKTILVILMIFGACAGSTGGGIKSIRVLILFKEAKRNIRKMLRPRSVSAIHVDGAKVDDEVVHGVHDYLTVYTIISIASLLLIAIDNFSMETSLTAVLACLNNIGPGLDLVGPMGNYACFSAGSKLILSLDMLIGRLEIFPMLMLAVPAAWKR
2.4E-56	201	35.3	6.5E-55	195.9	24.5	2	1	E6TQV8_BACCJ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Bcell_3491	Bacillus cellulosilyticus (strain ATCC 21833 / DSM 2522 / FERM P-1141 / JCM 9156 / N-4)	444	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cellulosilyticus, Bacillus cellulosilyticus (strain ATCC 21833 / DSM 2522 / FERM P-1141 / JCM 9156 / N-4)	649639	>tr|E6TQV8|E6TQV8_BACCJ Potassium uptake protein, TrkH family OS=Bacillus cellulosilyticus (strain ATCC 21833 / DSM 2522 / FERM P-1141 / JCM 9156 / N-4) GN=Bcell_3491 PE=4 SV=1MMKLINLFPHWRMSPPQILALGFICTIIVGMLILKLPVSTVHGITWLDALFTATSATTVTGLVVLNTGSDFTIVGQIVIMVLIQIGGLGLMTFAIITVLVLGKRIGLRERVLIQEALNQHSIGGVVKLVKILFLFSITIEFIAALLLSFRWVPEYGWKDGVFTSIFHSISAFNNAGFSLWSDSLTGYRGDPTINIVITVLFIIGGIGFTVLYDVMTTKRFRLFSLHTKIMLTGTVVVNIIAMIVIFLLEYGNPLTLGALPLSDQLWTSYFQAVTPRTAGFNTLEIGDMNPGTIVFMLLLMFIGAGSASTGSGVKLTTFLIIILAVITYLRGKQETVIFHRTIHHDIIIRALAIVVISLSIIFLVILGLSVTENAPFIHIVFEAFSAFGTVGLSMGLTDQLSIYGKQMIIVLMFIGRIGPLTLAFALAKSAKRTVSYPKGEVFTG
2.5E-56	201	13.7	2E-55	197.6	9.5	1.9	1	D4DNI7_NEIEG	Trk system potassium uptake protein	NEIELOOT_00619 NELON_05845	Neisseria elongata subsp. glycolytica ATCC 29315	484	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Neisseriaceae, Neisseria, Neisseria elongata, Neisseria elongata subsp. glycolytica, Neisseria elongata subsp. glycolytica ATCC 29315	546263	>tr|D4DNI7|D4DNI7_NEIEG Trk system potassium uptake protein OS=Neisseria elongata subsp. glycolytica ATCC 29315 GN=NEIELOOT_00619 PE=3 SV=1MYKIAPIVHVLSKLAVLYAVLLLVPTLVSYLYHDSAFNAFAGTTLATLAGSTAVWAATRKHDRELRPRDGFTLVFLLWLGFAAISALPFYLYFPNIGYTDAFFEAVSGLTTTGATVMSSLDTLAPSLNFWRHMMNWLGGMGIIVLAVAILPMLGVGGTQLFKAEIPGIDKDSKMAPRISQTAKRLWLVYLTFTLLTCMGLKWAGMGWFDAVCHAMSAFSLGGFSTHDASIAFFDSPAIEAVLIAATLLGAVNFASHFAMAREKSPKPYWRDEEARAMLTILAASIAAASVYMWQQGYYTPLEALRYVGFNFVSIGLANGFANADFATWPLLVTLWMFFLSNVLANTGSMGGGIKMARALVLAKFSLREVSLLLHPNAVRTVKLNRRSISDRTAMAVMAFIFVYFMTVVIFTLGLLASGMDFITALSATIACITNAGPGLGAVGPADNYAALSGLQKWMCAAVMLLGRLEIFTVFILFTPDYWKK
2.5E-56	201	38.1	3.6E-56	200.1	26.4	1.1	1	D1ARA4_SEBTE	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Sterm_3556	Sebaldella termitidis (strain ATCC 33386 / NCTC 11300)	453	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Leptotrichiaceae, Sebaldella, Sebaldella termitidis, Sebaldella termitidis (strain ATCC 33386 / NCTC 11300)	526218	>tr|D1ARA4|D1ARA4_SEBTE H(+)-transporting two-sector ATPase OS=Sebaldella termitidis (strain ATCC 33386 / NCTC 11300) GN=Sterm_3556 PE=4 SV=1MAEKKKRMSPYSVLILSFLLIIIIGTTLLSLPVSSFPGKKLSMVDALFIATSAVTVTGLVITDINYTFTLFGKTVLIILVQLGGLGVMTFSSVIVLLLTRKIDYTAKKIIQKDLNYNTLFNIQAYIKNLIKIVFLIEFIGAFCLFFVFIKKFSFLKAVYYAAFHSISAFCNTGFSLFPDSLSAYRTNVPVNLIIPLLITLGSLGFTTLNSIYISLFPKFRSDNKRMHFTLTARLSVIVSLILIISGTVLTLLIEMSNPETLKNFVFHDKLLLSFFQSVSIRTAGFQTLNLIHMKNSTLILYMILMFIGASPGSTGGGIKTTTIAVITLGVFTTLSHRKNIEFHKREISWRIFNKAIALVFISVMYIFFTVFILSYIEKEQKFILLLFEVISAFGTAGLSLDITPVLSSFSKILISLTMFLGRVGPLTVAMALTMKRRKKGRYSYPVDKIQIGC

2.8E-56	201	33.1	5.7E-55	196.1	22.9	2	1	S0JIZ0_9ENTE	V-type sodium ATP synthase subunit J	I571_01462	Enterococcus durans ATCC 6056	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus durans, Enterococcus durans ATCC 6056	1140001	>tr|S0JIZ0|S0JIZ0_9ENTE V-type sodium ATP synthase subunit J OS=Enterococcus durans ATCC 6056 GN=I571_01462 PE=4 SV=1MKKKRNKKISPVQLIAAGFFVLILIGGGLLSLPMFSQNGQQTNFLDALFTATSAICVTGLTTLNTAEHWNSAGQLLIMMLIEIGGLG FMMIPILFFALAKKKVSFSMRIVLKEALNLEEISGVMSLMLYILKFAVVIQLLGALALSFAFVPKFGWGKGIWFSIFHAVSSFCNAGFDLL GDSLHDYQTNAYLIMVISVLIIAGGLGFIVWRDLLSYHKVKRITLHSKIALTVTASLLIGGFILFFFTERNGLKLVDGTFWEKLANTFFMSV TPRTAGYYSIDYLRMSHAGLIVTMFLMYIGGTSGSTAGGLKTTTLGILFIQMRAMFKGKTRAEAFGRTIRQAAVLRALTLFFVTLTLCVV AIMILSVTETFPSTSGIEYIAFEVFSAFGTVGLTMGLTPDLSVVGKLVIISLMYIGRVGVMTVIFSLLVKANKAEPNYKLPEESVMIG
2.8E-56	200	12.3	2.8E-56	200.4	8.5	2	1	D2R3J1_PIRSD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Psta_2275	Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	608	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Pirellula, Pirellula staleyi, Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	530564	>tr|D2R3J1|D2R3J1_PIRSD H(+)-transporting two-sector ATPase OS=Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) GN=Psta_2275 PE=4 SV=1MNPTLPETFIARKRAASRLRLADGVLLVFAIATLLLGHGVERFESAVGTEVQIFVSVSMALLFIGQAWRLYIEYEADGFSWNSLTS ERKLVLGVHVLWFVMLPLVALTPIRPIVTQPSTFERLLFWSEFMLTVRLFATLFAIIRLVIQERSNPAFVFVVSFFLLIATGTLLLMLPVCW IQKEGNLTEESAPALVALFTATSASCVTGLVVVDTGTSWTRTGQGVILALIQAGGLGVMTFGGFFALGQRRSFLVRESVFLGKLLDAD DATAVRSLIRSIFVFTFISEALGAIALYTMAPAGPTGDRVWFGVFHSVSAFCNAGFGLLPKNLEGYGHTWQVWGGVASLIIVGGLGFD VLRNTTTYIASQLGTKFAPDLARRYIPMTRLTATSRLVLWTTGILLAAGTISLLVLELNNDVNNDKPIGAQIADAWFQSVSCRTAGFNTID FAKITPGSKLFCIGLMFIGASPGSTGGGIKTVVFAVTVLATATVVTSRERLEVGGRTIPDMTIKRAIAMLGLAISVVLIASLLIVILEDKPELF LDHLFEVTSAFGTVGLSTGVTAALKPASQLVLVLTMFLGRVGPLTMLVALARQRPAPNYEYPTERVTLG
2.8E-56	200	17.4	6.7E-56	199.2	12.1	1.5	1	R7XU01_9ACTN	Cation transporter	CF8_3203	Nocardioides sp. CF8	455	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Nocardioides, Nocardioides sp. CF8	110319	>tr|R7XU01|R7XU01_9ACTN Cation transporter OS=Nocardioides sp. CF8 GN=CF8_3203 PE=4 SV=1MAASISRVLRRGDRPWLRHPAQVVVVAFAVTILVGAALLMLPVARTDAASAPFIVALFTSTSAVCVTGLVVVDTPSYWSTFGEV VILGLIQIGGFGIMTLASLLGLLIFRRLGLRSRLTAATETKATGLGEVQTVVKGVVAISLLFETVTATLLTLRFAWGYDEEWGHAAYLGVF HAVSAFNNAGFALYSDSLMGFVSDPWICLPIAFAVIAGGLGFPVWLELYRRFHPTWAWSMHTRMTLIFTGVLLIGTVFVTASEWNNP ATLGALGAPDRLLAGFFQAVMPRTAGFNSLDYGQMRDGTLLGTEILMFIGGGSAGTAGGIKVTTFILLFFVIFAEVRGESDVTAFGRRI DPRAIRQALTVALLALGAVVASTLVILQLSDVATEDALFEVTSAFATVGLSTGITAGLPPSAHLVLVLLMFVGRLGPITLVSALAMREHSH LHRLPEGRPLIG
2.8E-56	200	12	5.6E-54	192.8	8.3	2.1	1	D4KC08_9FIRM	Trk-type K+ transport systems, membrane components	FPR_21780	Faecalibacterium prausnitzii SL3/3	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii SL3/3	657322	>tr|D4KC08|D4KC08_9FIRM Trk-type K+ transport systems, membrane components OS=Faecalibacterium prausnitzii SL3/3 GN=FPR_21780 PE=4 SV=1MNYAIVFRLLGYVLMIEGALLLLPAAASLVYGEWMVLGVFLLTAAVSAGIGYALHTIKPRSKVFYMREGFAATSLCWVFISVIGAV PFVLTGCIPNPVDALFETVSGFTTTGASILPAVEGLPNGILFWRSFTHWIGGMGVLVFLLSLLPLTGGSHVNLMKAESPGPQVDKLVPK VQSTAKILYGIYFALTMLELVFLLIGRMPLFEALLTAFGTAGTGGFGFRNDSFGSFSPYIQWVVTIFMILFGVNFNAYFLLLMRKFRRAA ASEEVRGYFVVIAVAVGIITANIYSMYNSFGEALRQAAFQVGSIITTTGFSSCDFDLWPTLSKEILVLMLMFIGACAGSTGGGIKVSRFLIL GKTLAKELKTALHPQVVAPARMDGKLLNHETIRTTNVFIAAYIFIFAASFFLISLNGFDMVTNFTAVAATLNNIGPGLEMAGPMQNFGCF ADPAKLVLIFDMLAGRLEIFPMLVLFMPDTWRRF
2.8E-56	200	21.9	1.3E-54	194.9	15.2	2.2	1	Q0W0D6_METAR	Putative K(+) uptake system, membrane component	RRC457	Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	485	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanocellales, Methanocellaceae, Methanocella, Methanocella arvoryzae, Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	351160	>tr|Q0W0D6|Q0W0D6_METAR Putative K(+) uptake system, membrane component OS=Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50) GN=RRC457 PE=4 SV=1MVSHKHLRIILSNLTGLFAVTAVIMAVMAVLCVLLNEAYAAPGFLVAMALSGGLAIVLKLLFPRAEDLELRHAMLVAAIAYLAVPAV SVFPFLMVEQMTVIDAFFESISGWTCTGMTMIQFPEHSSRSIQLYRSTMEWIGGIGVILLMVTILIRPGTSTYLMYKSETRKDRIMPSIQ STLKMIWFLYFLLTVGGVLLLIAGMPVWDSINHSMVAIGTGGFSIYSDSIAHYNSFPIEIVTMALMIIGALPFIFIFKVIKNPETVFRMDSE VKAFFFILLLGAALVTAENYLHFGNLLGTFRHSVYLFVSCLTTCGLQTSNLTGWSYTSLLIMSIAAIIGGCAGSTTGGLKVARAMFLYTE FRLWLKRTLLPRNAIVTIKIGNKRLEDDVVTKELSEAALILFLYLITILISVMVLSHLVDPKYDLCQIIFSICSAQGNVGIQNDLINPAMSSIG KVLLMINMWLGRLEIIPVLLLLRALLKGFKV
2.8E-56	200	29.3	4.8E-56	199.7	20.3	1.3	1	D7E321_NOSA0	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Aazo_3464	Nostoc azollae (strain 0708) (Anabaena azollae (strain 0708))	444	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Trichormus, Trichormus azollae (Anabaena azollae), Nostoc azollae (strain 0708) (Anabaena azollae (strain 0708))	551115	>tr|D7E321|D7E321_NOSA0 Potassium uptake protein, TrkH family OS=Nostoc azollae (strain 0708) GN=Aazo_3464 PE=4 SV=1MTVARTICLGFLAVILVGTILLMMPLSTSNGMWNNPIVALFTSTSAVCVTGLSVVEPGIFFSFWGQLFITLLAQIGGLGYMTTTTFL ILLIGRRFDLRQKVAIQQALDRPGISGSTQIIRSIIATTMVFEITGILLLLPAFVPDYGWNKGLWLAIFHSINAWNNAGFSLFKDNLIGYQS SGLVVFTITGLIIFGGIGYQVILDIYLWMRDRFLKKPNAIVFSLDFKVATSTTLLLLILGTIAFFCIEVRNPKTLGDLSFTNQLLSAWFQSVT PRTAGFHTIDIGQMTDAGLFITIAMMFIGASPGGTGGGIKTTTLRVLTSCTKAILQGKEEVLLYDRKIAISILKAIGVVFGSLATVIGGTILI SITDPKLEFIQILFEVVSAFGTVGLSTGITGGVSTTAKIILILTMYIGRVGVLLLMSAILGDPRPSRIHYPEENLLVG
2.9E-56	200	34.9	2.9E-56	200.4	24.2	1.4	1	S0JDW8_9ENTE	Cation transporter	OMQ_00170	Enterococcus saccharolyticus ATCC 43076	468	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus saccharolyticus, Enterococcus saccharolyticus ATCC 43076	1139996	>tr|S0JDW8|S0JDW8_9ENTE Cation transporter OS=Enterococcus saccharolyticus ATCC 43076 GN=OMQ_00170 PE=4 SV=1MNFGRFTRLTVRRGKNFFSKNISSIQLIVTYYILMTLFALILFYLPIFRKPDVYVSFIDMFFMAISTISVTGLSTFPIDEVFNERGVILL EILFQIGGLGVMMISTFFFIVSRRKISLKQRQLIMADMNQPRLSGIVRMIRTTFTIILVCQLIGGTVFGIYFKTMGYYEHWTDAIFYGLYQA ISAVTNSGFDVTGESIVPYANDTLFLVSIMFLIFIGGIGFPVIMDFREWLVYQVFKKKRQLPFRFTLFTKIAFLAFVVLFIGGTLTIFFLEKD HLFKNMTAVGQWVNSMFYSMTTRNAGLQIHDLNEFQTTTLMIFSVLMFIGCSPSSVGGGVRTTTVAIIGLYLISFLKSESHINIFGRKID NEDVRKSVVVFMLSLLMCFGCVIFLTATEDVSLIAIIVEVTSAFGTTGLSLGITPELSVIGKLIIALLMFIGRIGMLYTLLLFIPKETRDLGYE YPTEKIIG
3.1E-56	200	18.1	5.8E-56	199.4	12.5	1.3	1	Q4JXF8_CORJK	Potassium uptake protein, TrkH family	trkH jk0347	Corynebacterium jeikeium (strain K411)	454	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium jeikeium, Corynebacterium jeikeium (strain K411)	306537	>tr|Q4JXF8|Q4JXF8_CORJK Potassium uptake protein, TrkH family OS=Corynebacterium jeikeium (strain K411) GN=trkH PE=4 SV=1MIAHPGENRRRDWQGFSPAQLVSVSFLLLIAGTALLLLPISRSGPESPEFTTALFTATSATCLTGLTVVDTATYWSHFGQVVIM LLIQVGGLGIMTLATVVSFVLAGQMGVKGRLRAAAEQRGRNLGEIRTIIFGTIGFSLATELVIAIVLTFRFASGYGYGFLPAVWEGTFHAI SAFNNAGFGLRSDNLMPYVNDAGIILPIAAGIVIGGLGFPVLLELRARWRSKVKHPPSLTLIFTLTGTAILLLVGTVGFALMEWTNALRDL TPLSALQAAFFHSVSSRTAGFNSVDLTELRPSSLMLTDFLMFIGGGSGGTAGGVKVTTAAVLVAVLIAEVRGDEQLLVTGRRIPSRIVR QAMAVFMMAFLVVGVSIMALQLLLPQYDSHQITFETISAFATVGLTTGITPELPDFARIWLVVLMYLGRIGPITVVAALAARTNQRLYSY PVERPFIG

3.3E-56	200	14.8	1.1E-55	198.4	10.3	1.7	1	V9TTJ6_9PROT	Trk system potassium uptake protein	P856_722	Candidatus Endolissoclinum faulkneri L5	483	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Candidatus Endolissoclinum, Candidatus Endolissoclinum faulkneri, Candidatus Endolissoclinum faulkneri L5	1401328	>tr|V9TTJ6|V9TTJ6_9PROT Trk system potassium uptake protein OS=Candidatus Endolissoclinum faulkneri L5 GN=P856_722 PE=3 SV=1 MIYFGPVLFNLGILLTSLALSMSVPAAIDLVNDYSDWQVFLDAAGMTLFVGVIVILVTRKLRQSKLNLHQAFLLTTLSWLATASVG ALPFVFSDLDMTLADSFFESMSGVTTTGATVISDLGRASPGLLMWRALLQWLGGLGIIVIALAVLPTVRVGGMQLFAAEAFELAHKALP RASDLAAGLGIMYFIVTFVCALALFAAGMDMFDAVAHAMSTISTGGYSTKDDSIGYFKVPAIDWIVTFGMIAGSLPFIHYVGIARGDIRSI LRDRQVQWFLTLVLISVALIAIWIKHYIDLNSYDAIRLAAFNVVSIITGTGYLTADFSNWGGFAITLILLMFVGGCSGSTTCGIKIFRFQIL YAIAKVRFARLLQPHGVFIPYYNRKPIPQSVLESVIGFVFLYILFFGIVAIGLAAMGLDPITALSGAATTISNVGPGLGPIIGPAENFDKLPE AAKWLLCFAMLLGRLEIFTVLLLFTPKFWSK
3.3E-56	200	53.2	1E-23	93	11.4	7	4	A0A0E0LFA8_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	928	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0LFA8|A0A0E0LFA8_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1 MQKSSMLSYFLLISILGSVLLMFLKPSNPEFRPGYIDMLFLSTSALTVSGLSTIEMEVLSSSQIVVLTLLMLVGGEVFVSFLGLMLR LNISEDKVSSVPIELDTIESASTVMSHEELQMEEAIPANPSSTIKDLKRSKRQRWFLGFVVFSYFAVIHVVGFLLVLWYISRVSSANAPL KNKGINIALFSFSVTVSSFANGGLVPTNENMVIFSKNPGLLLLFIGQILAGNTLYPLFLRILIWFLGKVTKLKDLKLMIKNSEELQYDYLLP KLPTAFVASTVIGLMASLVTLFGVVDWKSSVFDGLSSYQKIINALFMAVNARHSGENSIDCSLIAPAVLVLFIILMYLPPSTTFALSNGDE KTANKKAKRKLSLVVQNVAFSQLACNAVFVIVALITERSRLRNDPLNFSALNMIFEVISAYGNVGLSTGYSCSRLQKLHPGSICQDKPY SLSGWWSNEGKLLLVFVMLYGRLKAFTKGTVITLHKNSEMISSRVTVTGLATIQMEDLSSSQIVVLTLLMFLGSELFISFLGLVLESSKQ NKHDPENRRVSSVTVCEQSQLEEAIPQTPSMNSTDIKKSCLKYLVFVMLAYMIIILVTGSLMVFMYIAHVSSARDVLTRKSINKALFSISV TVSSFTNGGLLPTNESMAVFSSNNGLLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKAEEPGFMINNSSTVGFSHLLPNLQTTFLAAV EIALVAMTVILFCCLNWDSAVFAGLTLSLQKIINALFMAVNARQAGENSIDCSLVAPAALVLFMVMMYTPSLTKLFSACQDHKRISLESDN RTSNGKPFLKMMAFSPLAFNTTVIMLVCITERRSIFTDPLNFSTFNIIFEVISAYGNIGLSTGYSCSRQLQHQEEKKGIACHEKPYSFSG WWSEPGKLILVLAMLYGRLKGFHKRTTN
3.3E-56	200	31.2	1E-55	198.6	21.6	1.7	1	A0A075LHT7_9BACI	Uncharacterized protein	GZ22_06025	Terribacillus aidingensis	454	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Terribacillus, Terribacillus aidingensis	586416	>tr|A0A075LHT7|A0A075LHT7_9BACI Uncharacterized protein OS=Terribacillus aidingensis GN=GZ22_06025 PE=4 SV=1 MRTYDPRWRWLNNISPTRLIILFYLAAVVISTCLLALPVAHKEGTDLSFVDVVFTAVSSISVTGLASVPIHEYFNTTGIIFIAFTMQL GGIGVMTLGTFVWLLFGKKIGFKERRLIMVDQNQVSFRGAVNLMRQILIVVLSIELIGFLVLGTYYLQYFPTAGEAYFQGLFAAISATTN GGFDITGQSLIPFRHDYFVQFVHMLLIVLGAIGFPVLIEVKQYIFASKDERTFIRFSLFAKLTSITFMVLIFVGAIIIALLDSRNFFVGKSWHE VLFYSLFQSVTTRSGGLATMDIAQLTEQNQLFMSALMFVGASPSSAGGGIRTTTLALVVIALYHFARGNKQITVLRREIHPEDLFKAINV TIFGMILVFTSAVILVSIEPFSLTEVIFEVCSAFGTVGLSLGITPELSDASKIVLMLLMFLGRVGILTFLYSLQRNSQTANFHYPKERIIIG
3.4E-56	200	40.9	4.4E-56	199.8	28.4	1.1	1	X2GI16_9BACI	ATP synthase	T479_03815	Lysinibacillus varians	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus varians	1145276	>tr|X2GI16|X2GI16_9BACI ATP synthase OS=Lysinibacillus varians GN=T479_03815 PE=4 SV=1 MPWKKSSNRQITPFQALVSYYFIAIAISFLLLRLPGVHRAGVEVSFLDSLFTAVSAVSVTGLTTFNISETYTTFGLVMVLVILQLGAI GIMSLGTFVWLLVGKKIGMRERQLIMIDHNQYNLSGVVQLIREILKILIGIELAGAIILTAHFMNYFDTFEEALIHGVFAAVSATTNGGFDIT GMSLLPFHNDYFVQLITMVLIVLGAIGFPVLIEVKSFLLNRHANFRFSLFTKITTTTYAILFIVGALVILLLESFHSFKGMVWHEAIFSAMFH SISTRSAGLTTYDVTSFSEATDIFMSFLMFIGSSPSSVGGGIRTTTFAIAILFLIMFARGKEDIQIFGREIHLIDVFRSFVVILLACFMVLIATII LLITEPHATLIQIIFEITSAFGTCGMSLGITSDLSVVGKIIIIILMFIGRVGLISFLYSVGGGGRGKKSKYHYPKERVIIG
3.5E-56	200	26.3	5.1E-56	199.6	18.2	1.2	1	D4ZEW6_SHEVD	Potassium uptake protein KtrB	ktrB SVI_0375	Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella violacea, Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)	637905	>tr|D4ZEW6|D4ZEW6_SHEVD Potassium uptake protein KtrB OS=Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12) GN=ktrB PE=4 SV=1 MRFIAHRNTFFPIKAEKSGVKWSEPKIILCSFFAILFPSALLLTLPVFSVTGLSFTDALFTATSAISVTGLGVVDTGTHFRASGKILLL FLMQIGGLGQMTLSAILLYMFGQRLSLRQQALTKEALGQDKSINIKRLVEHIIVFAIIAELLGFIFLAIRWVPEMGWKQGLFAALFHAVSA FNNAGFSLFSDSLSSYATDPMITFTIAGLIISGGLGFTVISDIRRNFSNGFHHLQLHTKLMLLATPCLLIFGTLMFWLLEHNNPNTLGQLD LGQQWLVAFFQSVTARTAGFNSVDISMFTQGAFFIMIILMLIGAGSTSTGGGIKVSTFVVVAVATWSFLRQRPHVILFKRTVPSRTVTK CLAIIVISGIILALAMFALMLTENAPFEQIMFETISAFATVGLTAGLTANLSEAGKYIMIVVMVIGRIGPLTLAYLLAKPKPTLLKYPEDNVLA G
3.7E-56	200	16	8.9E-56	198.8	11.1	1.5	1	C1D483_DEIDV	Putative K+ uptake transporter (Trk family) putative membrane protein	Deide_3p00460	Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	451	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus deserti, Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	546414	>tr|C1D483|C1D483_DEIDV Putative K+ uptake transporter (Trk family) putative membrane protein OS=Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923) GN=Deide_3p00460 PE=4 SV=1 MTSPNRRLLLNRLTPPQLIALSFAVAILVGTLLLYSPVTHAPGKNVTLLQALFTATSATCVTGLNVLDPGSTFNRLGEVILMVLIQV GGLGIITFGTLFASLRGQRVGVQERLRTAQQANLNEFGDVTRVIKGIFIYTLLTELIGALLLMVHFVPLEGWDRGIHLSVFHSVSAFNNA GFGLYPDNMIRFAEDPLVLLTTSTLVILGGLGYLAVLGVALYLRDPRRNRLSLNTIIILVTSAFLIVLGTVVVTVLEWNNPGTLGPLSTGG KLLSGYYQGVAPRTAGFNSVDYGAMHGATLFITMLLMFVGGSPGSTAGGIKTTTFYVLVSSIVSHAKGEHENVSFHRRIETEDLLRAS VVTALSLVVVTSGMFLLLATNPKLPFVNVAFEAFSAFATVGLSMNTTPLFNAPGQLVLIGLMFLGRIGPLTFAIAFARQQRHRVRYPVD KSIVVG
3.8E-56	200	14.5	6E-56	199.3	10	1.2	1	D0L5D7_GORB4	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Gbro_4248	Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	443	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia bronchialis, Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	526226	>tr|D0L5D7|D0L5D7_GORB4 H(+)-transporting two-sector ATPase OS=Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) GN=Gbro_4248 PE=4 SV=1 MLTPVRMVALGFAAAIVVGTILLMLPLASQQGGTGPGLVDALFTSTSATCLTGLIVVDTPTYWSGFGQGVILALIQIGGLGIMTMAS LVGLLLANRIGLKAKLNTVAEAKSSGLGDVRSVVFGVVRVSLVFEAVTAAILALRFAIGYDENPLRALWLGTFHSISAFNNAGFALFSDN MIGFAEDPWICVPLMIAVICGGLGFPVLFEIGRRVRRDRTRQRSRRWSLHTRLTVSVTAILLAAGFGSVLALEWFGTLQHHGLGSKLLI AAFQGVMPRTAGFNSVDYAQMDDATLLVTDILMFIGGGSGGTAGGIKVTTFAILLYVIIAEVRGDKSVTVFDRRIEPRLQRQALTVSAIG IALVVVPTVVLLAGTSFDLNVLLFEVTSAFATVGLSTGITAALPVWGQLILVALMYLGRVGPITLVSALAARQRQRRYELPTERPFIG
3.8E-56	200	30.7	2.3E-54	194.1	21.3	2.2	1	R6RHG0_9FIRM	Potassium uptake protein KtrB	BN652_02433	Firmicutes bacterium CAG:424	451	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	1263022	>tr|R6RHG0|R6RHG0_9FIRM Potassium uptake protein KtrB OS=Firmicutes bacterium CAG:424 GN=BN652_02433 PE=4 SV=1 MIQSGKKIKSHFSSFRIISFGFVMVILIGCFLLMLPISTAGSGGASFLDALFTSTSAVCVTGLVLHDTATYWSTFGQVVIMLLIQIGG MGVVTVAISIAMVSGRKIGLMQRSTMQEAIAAPHVGGIVRLTGFILKTAMLIEAVGVAVMAPVFCKEFGFFRGIWYALFHSVSAFCNAG FDLMGINSPFSSLTAYAGHPVINLAIMFLIVSGGIGFLTWDDIRSHTWHLKKYRMQSKVILSVTGALIVVPALYFYFMEFSGSQWEEFST GERILASFFQSVTPRTAGFNTVDLTKLTEAGLAIMIVLMLTGGSPGSTAGGMKTTTVAVMISSAISVFQRRESAHMYGRRIPQEAVRNA ATILMMYLSLFFMGGLAISCIEKLPMLPCLFETASAIGTVGLSLGITPQLGIISRIILILLMFFGRVGGLTLVFAAFSITHKNVSKLPQEKITV G

3.9E-56	200	21.1	1.8E-53	191.2	14.6	2	1	G2T5N7_ROSHA	Cation transporter	RHOM_14635	Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, Roseburia hominis, Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	585394	>tr|G2T5N7|G2T5N7_ROSHA Cation transporter OS=Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183) GN=RHOM_14635 PE=4 SV=1MNYSMVLYILGYILQFESAFLMLPALVSLIYQEEAGIPFVITAAICLVLGIVFTHKKPSSSTVYTREGFVTVALSWIVMSIFGAIPFVWNGDIPYYVDALFETVSGFTTTGSSILSDVESLSHASLFWRSFSHWIGGMGVFVFIMSILPLMGGSTINLMKAESPGPSVSRLVPHIKDTAKILYGIYLAITLLEIVILCALGMPLFESLLTSFGTTGTGGFGFRNDSFASFSPAIQNTVTTFMILSGINYTFYFCILSRRIKDAFRIEEVRWYLFLIFASVGMITYNIRPLYANTRDALRNAFFQVGAIITTTGYSTADFDMWPALSQTILVLTMLFVGACAGSTGGGMKVSRLVILFKTIRKELSLIIHPREIRKIRMDGHVVEHSTLRSTNVFLVIYFILLMLSTLIISLDEFDFTTNFTAVVSCLNNIGPGLNRVGPAQNFSIFSPLSKVVLIFDMLAGRLELFPLMILFMPSTWRKK	
3.9E-56	200	22.6	5.2E-56	199.5	15.6	1	1	R5BWV5_9FIRM	Uncharacterized protein	BN499_02018	Blautia hydrogenotrophica CAG:147	462	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	1263061	>tr|R5BWV5|R5BWV5_9FIRM Uncharacterized protein OS=Blautia hydrogenotrophica CAG:147 GN=BN499_02018 PE=4 SV=1MDGKRFKSKIKLSTPQIITLGFAGVIFVGGLLLWLPWATVEGEYTSFTDAMFTSTTSVCVTGLVTQVTATHWTLFGKIVILGLIQVGGLGIVSLVSLVFITVRKKINLKSRRIIQETYNQDHLSGMVVMVKRIAKGVFIAEGLGAVLYAFTFVPRYGVARGIWYSVFHSVSAFCNAGIDILGPDSLSSYVENVPVNLITMLLIITGGIGFIVWWDLGKNIRKVYRREITLRNLWKNLQLHSKLVLNMTAILLVAGMVFILIFEYDNPETIGTLTPGGKVLASAFQSVTTRTAGFLTIDQAGLRDQSVLVSLLLMFIGGSPMGTAGGIKTTTIAVLILTVNAYLRGKQDVEVYHRKLRELQVRAAIAVSMISFAVLIIVVIVLSVMMPHADFVDITYELTSALGTVGLSRGMTPALNTAGKWLGIFSMYFGRIGPITLVTAMFLKSNKRPGNVRLAEGRVLIG	
4E-56	200	20.3	5.2E-30	113.8	4.6	2.1	2	Q92PU8_RHIME	Trk system potassium uptake protein	trkH SMc00937	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Rhizobium meliloti (Ensifer meliloti) (Sinorhizobium meliloti), Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	266834	>tr|Q92PU8|Q92PU8_RHIME Trk system potassium uptake protein OS=Rhizobium meliloti (strain 1021) GN=trkH PE=3 SV=1MNANLIRHAVHLAAILGLYLSGAMLIPALVDLYYGHPDWQVFAVTAFMSGAISSTTFMATRAGPPPFSKKFGFLVVNVLWIVFSIVGAIPLWLSSVKLDFAQALFESVSAVTTTGSTVIVGLDDAPPGLLLWRSLLSWFGGIGIVVLGLFIIPYLRVGGMSFFKMESSDTSDKPFARLASFGRAFLVVYVSITLLCAISYAMLGMNRFDAINHAMTTVATGGFSTHDASFGYFSSIPLLWASTFFMTVCSLPFSILIVLVVRGRLDALRDPQIIVFLGYLTAFSVAVAAYHRLANGVEFHLALTYAFFNITSILSTTGYASEDYSLWGPFVVMVAFICTFIGGCSGSTAGGMKAYRFVVLFNAIRSALNKLVYPNAIYAVRYGKNTVDADVQRAILLFFITYILLWVFGSLVMGALGYDLVTAVSAVITCLSNVGPGLGSLIGPAGNFSTLQDPELYLLSLMMLLGRLEVLTVLVVLTPIFWKQ	
4.1E-56	200	36.8	6.3E-56	199.3	25.5	1.2	1	Q81TE6_BACAN	Ktr system potassium uptake protein D (Sodium transporter family protein)	ktrD GBAA_1333 BASH2_04528	Bacillus anthracis	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus anthracis	1392	>tr|Q81TE6|Q81TE6_BACAN Ktr system potassium uptake protein D OS=Bacillus anthracis GN=ktrD PE=4 SV=1MRDIKKFLQKLRPVQLIVLFYLLAVVSVILLSLPFVTKSGVKWTFIDALFTSVSVVSVTGLSVVTISDTFTTAGIIILALILQLGGLGIMALGTFVWIITGKKIGLQRRRLIMADHNQGNLSGLVELMRSILIVIISIELIGAILLGTRFLLYFPTWQEAYFHGFFAAVSATTNGGFDLTGQSLIPYKKDYIVQMIHMLLIILGAIGFPVLMEVKQFLSKRGQQLFRFSLFTKLTTTTFFALVVVGTIMIFLLERNHFLVGKSWHETVFYTLFQSVTTRSGGLATMDIVELSQPTLLFMSILMFIGASPSSVGGGIRTTTFAITLLAIFAYARGRSHVRIFHREIDQEDIFRSFIVISTAIMITSGAVILLSLFEPEFSLLEVMFEACSAFGTTGLSMGITSDLHSIGKIIIIGLMFIGRIGIFSFLFILRGRVTPENYRYPREPMIIG	
4.2E-56	200	34.2	5.8E-56	199.4	23.7	1.1	1	I0JRW5_HALH3	Cation transporter	HBHAL_4548	Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	453	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Halobacillus, Halobacillus halophilus (Sporosarcina halophila), Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	866895	>tr|I0JRW5|I0JRW5_HALH3 Cation transporter OS=Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) GN=HBHAL_4548 PE=4 SV=1MAHAFKTPHFFDKLSPFQIIVLFYISAALLSTLLISLPFLHREGVHLSFIDSLFTAVSAISVTGLTVVSTADTFNTPGYFVLMFILQFGGIGVMTLGTFIWLLLGQKIGLKRRQLIKTDQNRSTFAGMVQLIRQILLIIVIIEIIGALILGVYFTQYFPTTSEAFIQGAFASVSATTNAGFDITGSSLVMFESDYFVQFINILLLTLGAIGFPVLIEVKDYLTRRNEDFFNFSLFTKLTSVTFGLLVLIGTVLIYLFDRTHFFQNKSWHESFFYAFFQSVTTRSGGLATMDIVESEFTPSTLLVICVLMFIGASPSSVGGGIRTTTFAITLLAIFAYARGRSHVRIFHREIDQEDIFRSFIVISTAIMITSGAVILLSLFEPEFSLLEVMFEACSAFGTTGLSMGITSDLHSIGKIIIIGLMFIGRIGIFSFLFILRGRVTPENYRYPREPMIIG	
4.5E-56	200	19.5	1.3E-55	198.3	13.5	1.6	1	Q8TQQ9_METAC	Sodium transport protein	trkH MA_14 81	Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A)	476	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina acetivorans, Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A)	188937	>tr|Q8TQQ9|Q8TQQ9_METAC Sodium transport protein OS=Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A) GN=trkH PE=4 SV=1MNDKAIFNALGKILVLLAFTMLVPLFVALYYREPLEPFLVSTLVTFLAGLILARINENADWQQKEALAIVALSWLAAAIFGAIPFLFEGISFLDAVFETMSGFTSTGSTILVNIESYSRSLLFWRSFTQWLGGMGIIVLFIAILPKLGVAGRQLFRAEAPGPTEDKLKPRIKDTAKILWALYVLISALEVLALMLAGISLYDSLTHTFACMACGGFSSYGAGIEAFGSPLIEFILTFFMFAAGANFALYYRAVRIDKNLLFRDEEFRAYASFLLGFTGLLTLVLYKDMGLSLFNSIRYASFQITSVMTATGFASVDFNRWKDSAKVLVLAVMFIGGCAGSTGGGMKVVRFLLMLKYARRELFKFIHPKVVRPIRFNGRAVSDDVLQSILSFVVIYISVFVFSSMLLTLLGVELISSITASITTLGNIGPGFNLFGPMENFESLLPLGKIILITNMWIGRLELYTVLVLFTSDFWHS	
4.5E-56	200	33.1	2.6E-54	193.9	23	2	1	R7BUI0_9FIRM	Potassium uptake protein TrkH family	BN674_00882	Firmicutes bacterium CAG:475	442	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:475	1263026	>tr|R7BUI0|R7BUI0_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:475 GN=BN674_00882 PE=4 SV=1MKTPKKKLSSFQIILLGFAGVVLLGAFLLSLPISSKNHEWTPFIDALFTSTSAVCVTGLIVFDTATYWTIFGQIVILLLIQIGGMGVVTIAVSLAVISGKKIGLFSRETMKNAISAPNVSGIVRLTGFIIKGIFLIELIGALVMMPVFCIDYGAEGIWLSIFHSVSAFCNAGFDIMGTKSGEFTSITHYSAQPVINITIMLLIIIGGIGFLVWEDVCKHKWRIKEYRTQSKVVLIVTAVLIVLPAIYFFFFEFSDMPVGKRILASLFQSVTPRTAGFNTVDLTAISDTGLYLMIILMLIGGSPGSTAGGMKTTTIAVLFSSAFSVFRKKDNAELMKRSVDDGTVKTASAIFMMYITLFLFGGMAISAIENLPITSCLFETASAVGTVGLTLGITPTLGIASKLILILIILMFFGRVGGLTLIYAAFGTNKKQVAKLPTDTIAVG	
4.6E-56	200	36.7	6.2E-55	196	25.4	1.9	1	C4L0Y0_EXISA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	EAT1b_2019	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	360911	>tr|C4L0Y0|C4L0Y0_EXISA H(+)-transporting two-sector ATPase OS=Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b) GN=EAT1b_2019 PE=4 SV=1MRHRLSARELRLKRIEVLYRVVFEKPARFIAGGFLLAIFIGATLLYMPFAQEESVSWIDCLFIATSAGTVTGLSTVDIGSSFTLFGELVIVALIQIGGLGFMTIALMLLSVLGKKIGLKQRILLQESLNLAGPGGTVRLVRNIVFTTVIVQFIGMLFLTFELFSTENYSFGTALYYGFFHAVSAFNNAGFALFPDSLMSFEQNTAIIVTIAIMIMIGGLGFTTIADATEVRGWKRLALHSKIMILSLLVINGVAWFALMMFEWVSNEGVLYGRSLGEALHVTFFQAVTTRTAGFNSIDIATMAPASIGLILILMYIGAGAASTGSGIKVTTLAVIFADMWAFIAGKKETVIMERTIDAFQIKKAYVVAISSFLFIMMITTLVILSNGHIPATAILFETVSAFGTVGLSLGITAELNDAGKGLIMFMMLLGRVGSLTILFTVARQADRKIRYPKEKILIG	

4.6E-56	200	31.8	4.3E-54	193.2	22	2	1	B0VQK9_ACIBS	Putative potassium uptake protein (TrkH)	ABSDF2058	Acinetobacter baumannii (strain SDF)	445	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter calcoaceticus/baumannii complex, Acinetobacter baumannii, Acinetobacter baumannii (strain SDF)	509170	>tr|B0VQK9|B0VQK9_ACIBS Putative potassium uptake protein (TrkH) OS=Acinetobacter baumannii (strain SDF) GN=ABSDF2058 PE=4 SV=1MSLKPKPHKTLNLSPPSLLALGFLGFIVFGTLLLKLPIANNGHVSWMDALFTATSAVTITGLSVLNIHESFTLFGQAIILLLIQSGGLGFMTFAILAALSLSPKVGLKQQMMAQDSLGQTSLSKVTFVAKGVVTYTLLFELIGTVILTTAFTPIYGFARGLYYAVFYSISSFNNAGFSLFSNSLVNFQSNYLICITISLLYTLGGLGFLVLMDIKQNKKWKKLSPNSKLILTTIAIINLVAFVLIWVLEAQNPHTLGLLNVGDQALNAWFQATVPRSSGFNTIDTGAMTNSSSLLMMLLMFIGGGSLSTAGGIKVGTFVILVLSVLSFLRRTDEIRVFNHSVSHETTYKALAVTAITSILIFIGFFILLLLEPKADFMNLLFEVVSAACTVGLSRGITPDLHNGSLFILSLLMFAGRLGPLTLAYLIATPKKSRLKHPQANIQIG
4.7E-56	200	31.6	1E-54	195.3	21.9	2	1	A0A062XN05_LEUPS	Potassium uptake protein, integral membrane component, KtrB	L965_1094	Leuconostoc pseudomesenteroides PS12	455	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Leuconostocaceae, Leuconostoc, Leuconostoc pseudomesenteroides, Leuconostoc pseudomesenteroides PS12	1339247	>tr|A0A062XN05|A0A062XN05_LEUPS Potassium uptake protein, integral membrane component, KtrB OS=Leuconostoc pseudomesenteroides PS12 GN=L965_1094 PE=4 SV=1MRKFHDYSQRRFFWSRISMPQRLSLGFLTVITVGALLLMLPISYVGGRDHTFMDALFTATSAASVTGLTVVDTATHWTTFGQTIIMILIEIGALGFMSFSVLLFTATRRQMDLRSKMMVQEVYNLQSLYDTRAVFGYVIKLSIAIQLIGTILLAPFFIHDFGWGRGAFYAIFHAISAFGNSGFSILPKNTAEYVNQPFVLAIIAALVIAGSLGFLVWRDVLLYQKTHRLTLHSKLALVMTGVLIIGGWLLFELTERNLAFASGLSPVMRVFDTLFMSISYRTAGFTQFDVGGLGSATILLTMMLMYIGGTPGSTAGGIKTTTLGVLILQTHAALRGKKDVTFAHRRLTQENIMRALLLVCVSLVFLGILSFMLMLTQSHAANHGLEYVIFEVVSAFATAGLTLGLTPHLTTFGQLVIMLAMFIGRVGIYTVMFSILNVHDEAAPYRYPEESVIIG
4.8E-56	200	30.5	2.8E-54	193.8	21.1	2	1	Q0C2K2_HYPNA	Potassium uptake protein, TrkH family	HNE_1323	Hyphomonas neptunium (strain ATCC 15444)	457	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hyphomonas, Hyphomonas neptunium, Hyphomonas neptunium (strain ATCC 15444)	228405	>tr|Q0C2K2|Q0C2K2_HYPNA Potassium uptake protein, TrkH family OS=Hyphomonas neptunium (strain ATCC 15444) GN=HNE_1323 PE=4 SV=1MRAPRMIGAIRKPLAVASLYAHRLMRRVHPAKLIFAGYAFYMALGCALLCLPFSQSVPVHLLDNLFTAVSAVSTTGLVTVDPGTSYTFMGELVILLLIQAGGIGYMTVSSFVMMATVQHLSPLRERLARAAFILPEDVSIGIFIRTVVIYTFSVEIMGAILLFIQFSASGVDNAIWNAIFHSVSAFCTAGFSLNPNSLEDFRGDVGVNATISALSILGAMGFLIAWDVWRSLTRRSFVLSFTSKVILKLTGAFLLAGTAIFFVADPGISALPSGERLMASFFQTMTATTTVGFNTHPISALTPAVIVLLFFLMAIGASPSGTGGGLKTTTFAAMIGLVRSTVRRRPEITFFNRVIAPARLQLAMASSAYFVMLMTPAVFVLCLTEPGKEFQMLLFEAISAIGTVGLSMGITGSLSDIGKLTIILLMFAGRVGILTFGIALASKDEETEVRRQEDLLV
4.8E-56	200	37.6	8.9E-55	195.5	26.1	2	1	A0A024QFE0_9BACI	Ktr system potassium uptake protein B	ktrB_2BN990_03570	Virgibacillus sp. Vm-5	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Virgibacillus, Virgibacillus sp. Vm-5	1462526	>tr|A0A024QFE0|A0A024QFE0_9BACI Ktr system potassium uptake protein B OS=Virgibacillus sp. Vm-5 GN=ktrB_2 PE=4 SV=1MIKIISLHPLRGKTIRLSPPQILALGFLVFIIVGTLLLKLPFATTVSVSWLDALFTATSAITVTGLVVVDTGSAYSLFGEIVIMSLMQLGGLGLMTFSVLLLMMLRRKVGLHQRILTQESLNLNEASIGGLLRLVKLLFVFSIAIEAIAFVLLSIRWIPEYGWSEGIHQSVFHSISAFNNAGFSLWSDSLSGYVGDPLVNIVITGLFITGGLGFTVLVDIWDKKSFRKLSLHSKLMLVGTFIINITALLTLFILEFSNPETIGSFSFSFTDKLWGSYFQAVTPRTAGFNSLPIAEMTVPSILFLMLLMFIGAGSGSTGSGIKVTTFIVMLLATVSFLRGKSETTVFNRMIKVHTIVRALSIMIISILAIFIAVFILSITEAAPIMEIIFEVISAFGTVGLSMGLTTDLTSFGKCIIMVMMFIGRLGPLTLAFVFARQKQSSIRHPEEEVFTG
5E-56	200	34.7	1.5E-55	198.1	24	1.6	1	A8MES8_ALKOO	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Clos_0858	Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus oremlandii, Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	350688	>tr|A8MES8|A8MES8_ALKOO H(+)-transporting two-sector ATPase OS=Alkaliphilus oremlandii (strain OhILAs) GN=Clos_0858 PE=4 SV=1METRIRTKFKLTYAQLSAITFFTIILIGAGLLSLPIASRSGEFTPFINSLFTATSAVCVTGLVVYDTYSYFSVFGQSVILMLIQIGGLGFMIIATMFLLMLRKKIGVKERDFLRESVNSIHIGGIVRLAKHILLGTFLLEGMGAIILSIKFSSEMGIASGILNGIFHSISAFCNAGFDLMGRYEQYSSLTRYSGDTAVNLTIMALIVIGGIGFLVWEDVYKNKLAFKKYQLHSKIVLYTTFLLILCSAIIFYIIEKNNLLADMNMKERVLSSLFQAITPRTAGFNTIDTASLLESSKLFTMFLMIIGGSSGSTAGGIKITTFVITLTVISSVRNSADLNIFGRRLENGVLKRAYSIVTIYILGALLAMLSISFIQPELMLSDIGFEVLSAIGTVGMSTGITRQLVGMSKFIIVVLMFCGRIGSLAVLMAVAENKNNVLVKNPVEKIIIG
5.1E-56	200	36.4	8.9E-56	198.8	25.2	1.3	1	A7GML3_BACCN	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Bcer98_1045	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cytotoxicus, Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	315749	>tr|A7GML3|A7GML3_BACCN H(+)-transporting two-sector ATPase OS=Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98) GN=Bcer98_1045 PE=4 SV=1MKGIKKFLQKLRPVQLIVFFYFIAVIVSVILLSMPFVIKPGVKWTFIDALFTSVSAVSVTGLSVVSIPDTFNTVGIIVLAFVLQLGGLGIMALGTFLWILTGKKIGLQRRRLIMADHNQGNLSGLVELMRSILIVIISIELVGALLLGTRFLNYFSTWQEAYFHGFFAAISATTNGGFDLTGQSLIPYQKDYIVQIIHMLLIILGAIGFPVLMEIKQYISKRKHQLFRFSLFTKLTTTTFFALIVVGTIVIILLEQDRFFTGKSWHETLFYALFQSVTTRSGGLATMDIRDLSQPTLLFMSVLMFIGASPSSVGGGIRTTTFAVNILSLYSFAKGGRTVRIFKRQLHEEDILKASVVMTMGILLCASALFILSITETAPLMKLIVEVCSAFGTTGLSTGITSDLTTVGKCVLIVLMFIGRVGILTFILASGGREQPPRYKYPKERIIIG
5.2E-56	200	31.3	1.5E-32	122.1	8.6	2	2	A5WDG0_PSYWF	Potassium uptake protein, TrkH family (EC 3.6.3.14)	PsycPRwf_0749	Psychrobacter sp. (strain PRwf-1)	441	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Psychrobacter, Psychrobacter sp. (strain PRwf-1)	349106	>tr|A5WDG0|A5WDG0_PSYWF Potassium uptake protein, TrkH family OS=Psychrobacter sp. (strain PRwf-1) GN=PsycPRwf_0749 PE=4 SV=1MPSTPTKLLSSPPAILATGFLLLITLGTCLLKLPAATINSVSWLQAAFTATSAVTVTGLSIVDTANYTHLGQVVIAILIQLGGLGFMTFAVFAFLSLQRRLNLVGQKIAREAFAETSFGNITTTAKSVITIALSVELLGFIALSIAFVQEMPLSDALYHGFFYTVSAFNNAGFALTSDNLTGYVDNKAINFIITSLIIIGGLGFIVIKDLIDHRSWHKISVNTKVVVGTTIGLNLVAFVLFWLLEHNNPNTFGHLSLSDQLTAAWFQAITPRTAGFNTIPIEQLTDASTLLTMFLMFIGGGSLSTASGIKIGTFVILILTTWAFLRQRDHVIIFKRRIPDRLVRKSLALISITMMLIFMSVFILSVVEAEHSLEDVLFEVVSALSTVGLTRGLTTQLSHTGEVVIMFMMFAGRVGPLTLAYLIAMPKSSRIHYPETNVLVG
5.2E-56	200	31.4	6.4E-56	199.3	21.7	1.1	1	B7K8N8_CYAP7	Potassium uptake protein, TrkH family (EC 3.6.3.14)	PCC7424_2829	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	453	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	65393	>tr|B7K8N8|B7K8N8_CYAP7 Potassium uptake protein, TrkH family OS=Cyanothece sp. (strain PCC 7424) GN=PCC7424_2829 PE=4 SV=1MTVARTICLGFIAVITVGTVLLLMPFSTSDGSWNDPIVALFTSTSAVCVTGLVVVDTGTHFSFLGQFIIALLIQIGGLGYMLTTTFLMLLIGRRFDLRQKFAIRESFDRPFLHGSQNIVRSVIATTLVFELVGSILLYIRFSIDFGAILGLWMAIFHSISAWNNAGFGLLKDNLISYQSSYIINFTIPLLIIFGGIGYQVILEIYLWFTDRVKKERFDFSLNYKVAVHTTIFLLIIGTLGFLFIEFTNPETFGGMSLKDKLLAAWFQSVVTRTAGFNSIDFGKLTIAALFLTMGLMFIGASPSGTGGGIKTTTLRILTSSTRSVLRGREQVVLYEREVSFPLVLKAVAVVFGSVMVVLLITFAISLIEFSVIQNPLFIDGTYNSIHIFFEVISAFCTVGLSTGITAGLGAVSKLLLVLSMYTGRVGVLLFMAAIIGDPRPRSIQYPEENLLVG

5.2E-56	200	24.6	4E-55	196.6	17.1	1.8	1	K0AZZ5_CLOA9	Ktr system potassium uptake protein B	ktrB Curi_c08560	Clostridium aciduricii (strain ATCC 7906 / DSM 604 / KCTC 5404 / 9a)	441	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, unclassified Clostridiales, Gottschalkia, Clostridium aciduricii (Gottschalkia aciduricii), Clostridium aciduricii (strain ATCC 7906 / DSM 604 / KCTC 5404 / 9a)	1128398	>tr|K0AZZ5|K0AZZ5_CLOA9 Ktr system potassium uptake protein B OS=Clostridium aciduricii (strain ATCC 7906 / DSM 604 / KCTC 5404 / 9a) GN=ktrB PE=4 SV=1MQKPALVLSLGIAAIMLIGAILLNLPISSNNGQSIGFLNALLTATSAVSVTGLVVVNTAEHWTIFGKVVIILLIQAGGLGFMTLATLVALITGKRIGLKERLIMQEQLNQDSLSGIVKLTRFAILATLAIEGIGALLLSTRLIPIYGPIKGIGYSVFHAISAFCNAGFDLFGDSLVPFVGDTVMNLTIGGLIILGGLGYTVYIDIKQRKSYRMLSLHSKIVLIVSALLIVVGGVVIFISEHNNPNTMGNLTLYEKVLASFFQSVVARTAGFYSIDLNGMVNSSVFFLIILMFIGGSPGSTAGGIKTTTFATIVLTLISVIRGKEDVEVFKKRIPQWHISKAFILLSAGLTLVLVVAFLLTMTEPTKPFIDLLFETMSAFATVGSTRNITPELSDMGKLLITFTMYSGKVGFLTLALALTNRGKGTPNKKNYKYPEGKIIIG
5.3E-56	200	22.3	1.4E-54	194.9	15.4	2	1	R7CAM9_9CLOT	Cation transport protein	BN737_01001	Clostridium sp. CAG:62	489	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:62	1262828	>tr|R7CAM9|R7CAM9_9CLOT Cation transport protein OS=Clostridium sp. CAG:62 GN=BN737_01001 PE=4 SV=1MNTSIIRYIVGYILKIEAALLLIPSIVAAIYREPEGLCYLSVSALCIFLGVLLSFRKPKNHVFYLKEGCVATSLSWIVLSFFGSIPFLLTGEITSVPDALFETISGFTTTGASVLNNVEALSHCSLFWRSFTHWVGGMGVLVFLLAVIPLSGGSHINLMRAESPGPSVEKLVPKVRSTARILYVIYLTLTIIEIVLLLLGNMPLFDSLTISFGTAGTGGFGIKNDSMGSYSAYLQWVVTIFMILFGVNFNAFYLILYRKFKKAFRMEEVRYYFLIIFASIAIITMQILHTSAGIFDALRHASFQVASIITTTGYSTIDFNLWSQTCKTILILLMFVGACAGSTGGGIKVSRFVILCKTVKKELNAYIHPKSIKKINFEHKTVEHEVVRATNVYFITFMILFAFSVFAISFDGNDLITNFTAVAATINNIGPGLELVGPTQNFGLFSGFSKFVLMFDMLAGRLELFPLLLLFHPTLWKEIASGKIRKLKK
5.4E-56	200	36.1	2.2E-55	197.5	25	1.7	1	NTPJ_ENTHA	Potassium/sodium uptake protein NtpJ (K(+):Na(+) symporter)	ntpJ EHR_08275	Enterococcus hirae (strain ATCC 9790 / DSM 20160 / JCM 8729 / LMG 6399 / NBRC 3181 / NCIMB 6459 / NCDO 1258)	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus hirae, Enterococcus hirae (strain ATCC 9790 / DSM 20160 / JCM 8729 / LMG 6399 / NBRC 3181 / NCIMB 6459 / NCDO 1258)	768486	>sp|P43440|NTPJ_ENTHA Potassium/sodium uptake protein NtpJ OS=Enterococcus hirae (strain ATCC 9790 / DSM 20160 / JCM 8729 / LMG 6399 / NBRC 3181 / NCIMB 6459 / NCDO 1258) GN=ntpJ PE=1 SV=2MTIMKKRVRKRLSPVQLIAAGFFILILFGGSLLTLPFFSRSGESTHFIDALFTATSAVCVTGLTTLNTAEHWNSAGQFLIMTLIEIGGLGFMMIPILFFAIAKKKISFSMRIVLKEALNLEEMSGVIKLMIYILKFAVVIQVIGAVALSVVFIPEFGWAKGIWFSIFHAVSSFCNAGFDLLGDSLLADQTNVYLIMVVSALIIAGGLGFIVWRDILSYHRVKKITLHSKVALSVTALLLIGGFILFLITERNGLTLVKGTFTERLANTFFMSVTPRTAGYYSIDYLQMSHAGLILTMFLMYIGGTSGSTAGGLKTTTLGILLIQMHAMFKGKTRAEAFGRTIRQAAVLRALTLFFVTLSLCVVAIMVLSVTETIPKTSGIEYIAFEVFSAFGTVGLTMGLTPDLTLIGKLVIISLMYIGRVGIMTVVFSLLVKANRAEANYKYPEESIMLG
5.4E-56	200	26	3.1E-55	197	18	1.8	1	I4C3U0_DESTA	Trk-type K+ transport system, membrane component	Desti_1519	Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	460	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfomonile, Desulfomonile tiedjei, Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	706587	>tr|I4C3U0|I4C3U0_DESTA Trk-type K+ transport system, membrane component OS=Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1) GN=Desti_1519 PE=4 SV=1MAFFSKMNNPFLRFLGSPQTILVGSFAGVILIGALFLMLPWAQTQNKIGFVDALFTATSAVCVTGLIVVDTATDYTFFGQAVILFLIQIGGLGVMTFASLAFQILGRRLSLQTQAVVHDSFFQQDVGAEFKRTFATILLLTFGIEALGAFFLFIRFIPNMDFGEALWSSVFHSISAFCNAGFSIRSDSLIGLRHDFVVLFVIMALIVLGGLGYMVLHELWIAGGRRFGFFPVMRYRERRFSFHSRVVMYVTSILLVGGTFMLMASGLTPEETTWYDKGMNAVFQSVTSRTAGFNTVDIGLLPSGSLFILIVLMFVGGSPGSCAGGIKTTTSVAIWLARLRSGVYGDTDVHLMDRRLSQELVGRTDLLIAVATVWNVIGILLLYQTETHLRVDSLHLFFEQISAFGTVGLSTGVTPNLSIAGKLWIISATMFMGRLGPLTITLWMFPRSPVQVSYPKGRVMIG
5.5E-56	200	37.6	5.5E-56	199.5	26.1	1.8	1	Q98R66_MYCPU	POTASSIUM UPTAKE PROTEIN KTRB	MYPU_1440	Mycoplasma pulmonis (strain UAB CTIP)	523	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma pulmonis, Mycoplasma pulmonis (strain UAB CTIP)	272635	>tr|Q98R66|Q98R66_MYCPU POTASSIUM UPTAKE PROTEIN KTRB OS=Mycoplasma pulmonis (strain UAB CTIP) GN=MYPU_1440 PE=4 SV=1MSFIFDEKSNNINEVYVYFKYWLRQILEKSKIPYLYSRYGVFKQNISKARYILFTYFIITMLGSIFLYQGFSQNPNAKISFFESVFTAASAFSDTGLVLKPTYSSWNMVGQAIIAILILVGGLGYFTLKMFFISWIFKLNSNINQRELVSIERGAKEVGKTTRVIVVSIFTMFVFMIISSIILTLYFYYVAPSSTYSRKSYTFDSPIRDWKKSIRYGIFHSITALNNAGFDIISDKSILPYNQNYSLQIIFIILFIVGGIGYPTVYDIVQNLYIKLFRKNEPIIWSLFTKVSVLFYFLVTIFSIALVFIFETTSKSASSIWNNKENGSNFDKSMAIIFNTLSTRSAGFSSVDLYNLTPGSLLIFSIAMFIGASPSSTGGGIRTTTFAIILLGIAAKLSNKPSLRMFKRKIESSTVSMSYLVFTLSMTIVLANTFILLTSHRLFDGTQEREYDLSHIIFEVTSSFGTTGLSTGLTHLLNTFSLVSLSLLMFIGQLGISSTILSWKNKRKKPWLYDYVETDISIG
5.6E-56	199	9.2	6.7E-27	103.5	0.8	2.1	2	R5MPD6_9FIRM	Trk system potassium uptake protein TrkH	BN519_00998	Eubacterium sp. CAG:180	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:180	1262882	>tr|R5MPD6|R5MPD6_9FIRM Trk system potassium uptake protein TrkH OS=Eubacterium sp. CAG:180 GN=BN519_00998 PE=4 SV=1MNYKMMGRIFAEILALEAFFMLPPLFISIYDGVDGAAKAFLYTIGILIAVSAFLWLICRKAKRGFYAQEGIVCVGLGWIFLSLFGALPFFISGEIPFYIDAFFEMVSGFTTTGASIVPVVEDLSRGILYWRSFSHWLGGMGVLVFLLAIVPSNSKSGGSRLHLLKAESPGPDVGKLVPKMRDTAMILYVLYIALTLLNILFLLAGKMPLFDALCTAFGTAGTGGFGIKNDSIAGYSIYIQWVCTVFMMLFGVNFNCYYLLIMRQFKALFKNEEVRCYFGISIMSAALIAIDIRKIYPTIHETIRHACFQVASIMTTTGFATTDFDTWPSFSKTILLTLMVIGACAGSTGGGLKCARVLLLFKNLRRNIHKILHPRRVQVVHVDGTPVDEKIINGTSVYLAAYFILVVLSILLISVDNKPLVTNLSAVLSCFNNIGPGLEIVGPTGNFSSYSAFSKLVLIFDMLAGRLEIFPILALISRGAWKKA
5.9E-56	199	25.8	7.8E-52	185.8	14.4	3.2	2	F0Z9F5_DICPU	Putative uncharacterized protein	DICPUDRAFT_75029	Dictyostelium purpureum (Slime mold)	674	cellular organisms, Eukaryota, Amoebozoa, Mycetozoa, Dictyosteliida (dictyostelid cellular slime molds), Dictyostelium, Dictyostelium purpureum (Slime mold)	5786	>tr|F0Z9F5|F0Z9F5_DICPU Putative uncharacterized protein OS=Dictyostelium purpureum GN=DICPUDRAFT_75029 PE=4 SV=1MIKFKNISKYFKIKFRKALVWFVGYLDQNYFFRFHLLYFVTLSLVGALIIFLIEIKSKVSFIDCLYISASAITTTGLVSVDISQWSNAALFVVMVWVQLGSTVLLTLPIVLLRRYFIRNSYNNPKSLGDSSNTSSLKESHSTPNLLSSFIDPFHTMTESLHLDQPLEFSDDDDEENEDNSDHSKGDEENQYEDDHSDNPKYQHDDEIGAHHEDDIEIGGVLTMDTPIGIDDHSDEESHHDYKTPIMKSKTSPNTLTTVNTSSSSSSSIKTNNTNNNNNTNNDNNNNNNNNNNNNSNNNGNTNSIVINKSSPKVVSTTHVHSYVDNMEYRSLGKLLVIIPLYIVVIYFIAFFSLAIYIQANSNSQEIMKKNNVNGWWWTLFHVISAFNNAGLGLFPDSLIQVNHKYFILLVLSTLIIVGNTLFPFFLRGILRIISKFTKDPDPYNNLLDNPRSIFTHLFPYKETIKLFLVWIIFNVSQISLMALFDTNDIAFTNMNAGETLLNYYFSSISTRTCGFNSIDISLLSESVLLLFLGLMFVSSYPFIISLRSSAVNNKYSNQRDVMKDILIRDIFIPYVCILSIAIFENQLLESGRASVFQLIFEIVSAFGNVGLTMSPGGHAISTLLRPISKLIVVITMLAGRHRNLPESIDQSINPATLKKNSIISKIITRYKRRKL
6E-56	199	28.8	1.2E-54	195.1	20	2	1	A0A090IAT0_9GAMM	Ktr system potassium uptake protein B	ktrB MVIS_1132	Moritella viscosa	454	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Moritellaceae, Moritella, Moritella viscosa	80854	>tr|A0A090IAT0|A0A090IAT0_9GAMM Ktr system potassium uptake protein B OS=Moritella viscosa GN=ktrB PE=4 SV=1MVLWHPSISPIERKPKAGKKLLGAPPLILSGSFALLILLGTCLLKLPIATLEPISWLQSFFTATSAVTVTGLVVVDTGTAFTPFGQTIIALLIQCGGLGLMTFAIVTLIALGGKIGFLQCTVAREAFNQTNTSTLASTAKSVLVFSLFVELIGMVILSVYWSGELGWTTSLFHGFFYTISAFNNAGFALSADSLMPYVADPVVNLTITGLLIIGGLGFSVWTDLRRNRRWSRLTVYSRMMITGTIFINAVAVITIYLIEYNNPNTLAPLSEQGKWLASWFQAVSPRTAGFNTLAIDQLEDATTAIMLVLMFIGGGSSSTASSIKVVTFMLLIMATYSYLRRDESVYVFKREIAKDTVSKALALTMISVGITWFAIFSLLLSENAPMIDIVFEAVSALGTVGLSRGLTGSLSESGEFIIIFMMFMGRLGPLTLAYFLASPRTKKLRYAETKLAIG

6.1E-56	199	41.3	1E-55	198.6	28.6	1.3	1	A0A088F4B9_9SPHI	ATPase	KO02_23310	Sphingobacterium sp. ML3W	592	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. ML3W	1538644	>tr|A0A088F4B9|A0A088F4B9_9SPHI ATPase OS=Sphingobacterium sp. ML3W GN=KO02_23310 PE=4 SV=1MLSFLKFVFKYKNGIVDQVMFYVSMICALAVIFNVGYVRDPELAQILDHIILAMFYVLFIMTGLRTASSIFALKKIEVEHYSGLVIFAYFILIIIARLASVPTVDLFGKDQWIYLGIYIVFIAELSKSTLFFDNFYFNPTILFVISFFALILIGTVLLMLPRTTIEAPLSFIDALFMATSAVCITGLSVTDISTNFSLFGQTIILVLIQIGGLGIMTFTGFFGYFFSGGFSFKNQLMFGEILGENKVGSVVKTLLTIIFITLLFEFLGAVLIFGTLEAQNFPSVGHQIFFAVFHSISSFCNAGFSILTDGITNNAYKFNYNFQLALSSLFILGGLGFGIVLNIYSYVKESAIYWYHRFITKKNYKHHKAWSFSFNSKLVLVCNAVVIVVATVFFFLLEKEKTLSLEQGKVGEWVTSFFMANASRSAGFNSVDLSFVSMPTVLLIILLMWVGSSPGSTGGGVKVTTIAVAMMNIIALARGKEHIELFKRRIAGESVHKAFAIILLSLFTIGVSFMLLVFSDPDKSFKALLFESVSAYTTCGLSLGITPSLSVAGKFIVMMTMFVGRVGTLTLLVAFIKNITRKNYIYPEEKILY	>tr|A0A0A3VYG7|A0A0A3VYG7_9GAMM Uncharacterized protein OS=Acinetobacter sp. HR7 GN=GW12_27860 PE=4 SV=1MKMTAHKNRTINLSPPSIIALGFVGLIIIGSLLLMLPIAHHGEVTWFQAVFTATSAVTITGLSVVNVGAAYTVFGKVVIMILLQCGGLGFMTFAILAAMSLAPKMGLRQQVMAQESIGQTSLKKISTTIKAVFLYSICIEAIGTVILTIAWLQDYNFSQAFFYALFYSISAFNNGGFSLFPNSLMSFSDQYFITFTISMLYIIGGIGFLVLMDVRQHKRWSKLTTNSKLILSTIAGLNLSAFILIWILEASNPQTLALMSVGDQAVNAWFHATVPRSSGFHSLPLDQMTNASTLVTMFLMFIGGGSLSTAGGIKVGTFFIIVVISVISFLRREDEIRLFRHSIPEKTTFKALAVVCITALLIAGGFMSLLILEPDQDFLDLLFETVSAACTVGLSRGITHELQPASLFVLMLLMFAGRLGPLTLAYFIATPKKSRLKHPPSEIQVG	1509403
6.2E-56	199	31.1	6.4E-27	103.6	10.5	2	2	A0A0A3VYG7_9GAMM	Uncharacterized protein	GW12_27860	Acinetobacter sp. HR7	445	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter sp. HR7	1509403	
6.4E-56	199	26.5	1E-55	198.6	18.3	1.2	1	E3E6P4_PAEPS	ATP synthase subunit J	ktrB3 PPSC2_20340	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus polymyxa (Bacillus polymyxa), Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	886882	>tr|E3E6P4|E3E6P4_PAEPS ATP synthase subunit J OS=Paenibacillus polymyxa (strain SC2) GN=ktrB3 PE=4 SV=1MNPNARWLRLSPPQIFVAGFAIIILIGSLLLMLPISNTTGKPLAFIDALFTAASATCVTGLVVKDTGLFFTTFGQIVIVALIQIGGLGFMTMATLIALVFKRRISLRERLILQEAMNQTSVEGIVGLIRKVLWYSLMIEGVCAAIFSIRWSFDMPVGRAIYFGIWHAISMFNNAGFDLFGEFRSLTGYVYDPIVNFTAMFLIISGGIGFVVMSDLADYRKRKRLSLHTKVVLSMTAALIVVGTLVIFVFFETNPKTLGSLDWGGKLLGSLFQSVTPRTAGANTLDIAGLRQATQFFIIILMFIGASPGSTGGGIKTTTFALLIGAVFSMLRGREDIVLFRYRLAQARIYKALTITLLGLLFVIGVTMILSATEDHHFLMILFETVSAFGTVGLSMGLTPDLSVVGKLVITLTMFAGRLGPLTLAYALGPKKGKELYRHPEGKIIIG	886882
6.6E-56	199	25.1	1.1E-32	122.6	8.7	2	2	F4GL48_SPHCD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Spico_1175	Sphaerochaeta coccoides (strain ATCC BAA-1237 / DSM 17374 / SPN1) (Spirochaeta coccoides)	430	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Sphaerochaeta, Sphaerochaeta coccoides, Sphaerochaeta coccoides (strain ATCC BAA-1237 / DSM 17374 / SPN1) (Spirochaeta coccoides)	760011	>tr|F4GL48|F4GL48_SPHCD H(+)-transporting two-sector ATPase OS=Sphaerochaeta coccoides (strain ATCC BAA-1237 / DSM 17374 / SPN1) GN=Spico_1175 PE=4 SV=1MLGKRRMRISPGSTLLIGFLAIIVLGSILLMVPFSLKDGMKLKYVDSLFISTSSVCVTGLVTVSPGDTFTVFGRTVIALLIQTGGLGFSVFVVFFLVMLGRPVGFAERGPVREALGVSPRGLVNLVKFVMLSALVVETIGAVGFYHVFSRMYPFWESVGYAVFHAVSSFNNAGLDIFPGFESLIPYRADVLLNIMTSALVIIGGLGFSVLREIVSWRKIRRLSTHARIVLLTSACLLVAGTVLLRVAGVPWFEAFFQSVSARTAGFSTIDIGAISSGALLVLNVLMFIGASPGSTGGGIKTTTFFAIIKTIQQVFTRQEPVAFKRRMSADSMRKAFMVLLLALCVVLIGSCLIAVMEGSGYSLDHIVFESISAFATVGLSMGITPALSGFSKVVLIVLMYIGRVGPLTVAGSWMIRHRQTDFIEEQILIG	760011
6.6E-56	199	20.1	1.3E-29	112.5	5.8	2.1	2	R6EII8_9FIRM	Uncharacterized protein	BN538_02192	Lachnospiraceae bacterium CAG:215	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	1262985	>tr|R6EII8|R6EII8_9FIRM Uncharacterized protein OS=Lachnospiraceae bacterium CAG:215 GN=BN538_02192 PE=4 SV=1MNNKMIVYIIAKMLGVEGAVLLIPAFVAFLYGESDVIQFLIVSAVLGAIFFIFGRKRPENKVIYAKEGLVIVGLAWILWSLFGALPFVLTGSIPSYVDAFFETVSGFTTTGSTILTNIEALPKGVAFWRSLTHWIGGMGVLVFVMMLTSLDDEHSMHLMRAEVPGPEADKLVPKARATARILYLMYFVLTAAEVVFLMFGGMSFYDALLHSFSTAGTGGFSNRNASVAYYDSAYIDGVITVFMILFGVNFNLYFLIRLKNWKDALKNEELHAYLGIIAGAVAIVTVNILGIYGNLVHAFRYASFQVASVITTTGFCTADFNLWPELSKVVLLGIMVIGACAGSTGGGIKVSRFLILVKSIKQEVRRMLHPKAVTIVKINGKRVGNDTIRSVYIYFISYILVMMVSILLVSINNFDFATTFSSVLTTLNNVGPGISMVGPVENFHMFSPLSKLVFCMDMLLGRLEIFPYLLLMSPELWRRRF	1262985
6.7E-56	199	15.7	5.4E-54	192.9	10.9	2	1	A0A089ZQ37_9PSED	Trk system potassium uptake protein	LT40_05820	Pseudomonas rhizosphaerae	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas rhizosphaerae	216142	>tr|A0A089ZQ37|A0A089ZQ37_9PSED Trk system potassium uptake protein OS=Pseudomonas rhizosphaerae GN=LT40_05820 PE=3 SV=1MALPTLRIIGFIIGIFLITLAMSMVVPMGTLVVFERSQDIQSFLWASLITFVAGLVLVLPGRPDNVNLRPRDMYLLTVSSWVVVCVFAALPFLLTQHISYTDAFFESMSGITATGSTVLSHLDEMSPGILMWRSMLHWLGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSEKVMPRSHMVAKFIVLVYVGFTALGTLGFWWAGMSPFDAVNHAMSAISTGGFSTSDLSLGKWQQPAVHWVAIVVMILGSLPFALYVSTLRGNRQALLRDQQVQGMLMLLVVTWLVLGTWYWATFRHVALNVTSVVTTTGFALGDYSLWGNFSLMLFFYLGFIGGCSGSTAGGIKIFRFQVAYILLKSNLNQLIHPRAVIKQKYNGHRLDEEIVRSILTFSFFFGFTVGIIALALSLLGLDWMTALTGAASTVSGVGPGLGEVIGPAGNFATLPDAAKWILALGMLLGRLEIITVLILCMPAFWRH	216142
7E-56	199	28.1	6.4E-55	196	19.5	1.9	1	W6RXB7_9CLOT	Trk system potassium uptake protein TrkH	CM240_1110	Clostridium bornimense	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium bornimense	1216932	>tr|W6RXB7|W6RXB7_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium bornimense GN=CM240_1110 PE=4 SV=1MNLKLVLRNLGILLVCEAISLIPSLIISAIYRDGDFSSFLITIIIISILSLILLSIKPDSKNIYPRDGFAIVAFGWILISLLGALPFYLSKSIPSFVDAFFESSSGFTTTGASILSQIEGLPHGILFWRSFTHWVGGMGILVLTIALLPSMGIGSMQIMKAESPGPVVDKLVPRLGKTAKILYSIYFCMTMLEIFLLCIAGMPLYDSIVHSLGTVGTGGFSIMNSSIAHYDSVSIDIIITIFMILSGINFSLYYLILKGKFKSFWKNEEFRLYISILSIAILLITFDLLMKNTYKSFGTALRYSSFQVASIMSSTGYATADYNTWSIFSKVILLLLMFIGGCAGSTGGGIKNIRFLIFFKSMKNSLLRIIHPRGVYTVRINDKPMDGKTVSDVLVYFYIYMTVFTIGVIIISFNGMDIGTTVSSVLATLSNIGPGIELVGPAGNYAAFSSLSKITFSIIMIIGRIEIYPIIILLLPQFWKNN	1216932
7.1E-56	199	31.9	1E-55	198.6	22.1	1.1	1	A0A0A2TRU3_9BACL	ATP synthase subunit J	P364_0129215	Paenibacillus sp. MAEPY2	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. MAEPY2	1395587	>tr|A0A0A2TRU3|A0A0A2TRU3_9BACL ATP synthase subunit J OS=Paenibacillus sp. MAEPY2 GN=P364_0129215 PE=4 SV=1MKFRLHIAKFLSPPLILVGGFMLIITIGTILLMLPISNQSGQHLAFIDALFTSTSAACVTGLVVVDVRTTFNLFGQIVIMVLMQLGGLGFMTIATLFALVLGKRISLKDRLLLKEAINADSMEGIVRIIRKVLIFSFTIEGVAAVILALRWATEMPFWQAVYYGAFHSVSLFNNGGFDLFGNSFQHYTGDWLFNVTASVLVISGGLGFVVLNDLFEYRKRRRLSLHSKLVLSVSGALIGVGAIVLFVFEFTNGHTLASLSWSEKIYASFFQSVSTRSSGTSTIDIAQMRQATQFFFILLMFIGASPGSTGGGIKTTTFLIMIGAVYAMIRGNKDIVFFRQRVPKELLMRALTIIMVSLIIFMVVVMLLLTTEDAPFLSLMFEAASAIGTVGLSVGVTHELTVWGKVIIAFTMFIGRIGPLTIAYALRPRKEKKLYRHPEGRIIIG	1395587
7.3E-56	199	6.4	5E-55	196.3	4.4	2.2	1	I1CPE2_RHIO9	Uncharacterized protein	RO3G_15033	Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) (Mucormycosis agent) (Rhizopus arrhizus var. delemar)	458	cellular organisms, Eukaryota, Opisthokonta, Fungi, Fungi incertae sedis, Mucoromycotina, Mucorales (pin moulds), Mucorineae, Rhizopodaceae, Rhizopus, Rhizopus delemar, Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) (Mucormycosis agent) (Rhizopus arrhizus var. delemar)	246409	>tr|I1CPE2|I1CPE2_RHIO9 Uncharacterized protein OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_15033 PE=4 SV=1MFACNIEQQREIARRQFEKGKRLEDMPPGPSTKEAVIELENDEVVPREPTQKSELTRQQRYRLGGAEYRALDLLSRLVPAYYFFFLFGFGFIIRAYIAMSPFVQDLLKNGRSVINPWHFSFFTSLSAFNNLGLSQVDESMEPFRQEPVMLTLVMILVLAGNTAYAILLRLVIHVLYKLTPHSFGMRRETLRYVLDHPRRCYTTLFPSAQTRWLLVVLVGITLIEFICFMALNYWLPVLEKMDIGTCILAGLFQSVSTRSAGYSVVDIMNLNPVTIMMRNSNVYQERALGIYKGINESYGYDIELNNSETFHHLKRSNTISSVVTASRRALRGPDFFVRTQIQQQLTSEIFWLIACIFAICVIETSVVMSPSPITMFTIIYECVSAFGNIGASTGYPNTSTSQSAQYHRLRLPAAIDRAVLLPSEQLEQKEEEDVLFRRRTASFGDGMPQEIYSRCRTL

7.9E-56	199	30.9	4.6E-54	193.1	21.4	2	1	R6Z01 1_9FIR M	Potassium uptake protein TrkH family	BN617_ 00115	Firmicutes bacterium CAG:345	442	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:345	1263020	>tr|R6Z011|R6Z011_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:345 GN=BN617_00115 PE=4 SV=1MGILKRKLSSFQIILIEFAGVILLGAFLLTLPISSKTHEWTSFIDALFTSTSAVCVTGLIVFDTATHWTIFGQIVILLLIQIGGMGIVTIAV SLAVISGKKIGLFSRETMKNAISAPNVSGIVRLTGFIIKGIFLIELIGALVMMPVFCIDYGAEGIWLSIFHSVSAFCNAGFDIMGTKSGEFTS ITRYSAQPVINITIMLLIIIGIGIFLVWEDVCKHKWRIKEYRTQSKVVLIVTAALIVLPTIYFFFFEFSDLPVGKRILASLFQSVTPRTAGFNT VDLTAISDTGLYLMIILMLIGGSPGSTAGGMKTTTVAVLFSSAFSVFRKKDNAELMKRRVDDETVKTASAIFIMYITLFLLGGMAISAIENL PVTSCLYETASAVGTVGLTLGITPTLGIASKLILILSMFFGRVGGLTLIYAAFGTHKKQAAKLPTDTIAVG
8E-56	199	18.1	1.4E-27	105.8	4.1	2	2	R5HX8 5_9FIR M	Cation transport protein	BN729_ 00067	Ruminococcus sp. CAG:60	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:60	1262964	>tr|R5HX85|R5HX85_9FIRM Cation transport protein OS=Ruminococcus sp. CAG:60 GN=BN729_00067 PE=4 SV=1MNYSMISYILGWIFNFEAAFMLLPGITAIIYREKDGLAFLVTMIICLAIGIPLTRTKRKNKVFHAKEGAVTVALSWLVLSIAGALPFVI SGSIPHPVDALFETVSGFTTTGASILSDVESLSHCILLWRSFTHWIGGMGVLVFILCLLPLTGGYHMNLMKAESPGPSVSKLVPKVQST AKILYTIYILMTVVEMVFLLLGGMPLFDTLCLSFGTAGTGGFGIKNDSIASYSTYNQIVITVFMILFGVNFNAYYLLLSKKVMQAAKNEEV RYYLGIIGLAIVAIAVNTRGMFTSFGRAFQQAAFQVGSVITTTGYATTDFNVWPVFSKTILVILMFVGACAGSTGGGIKVSRLLILCKSAR KELQLYLHPNAVKKIKMDEKAIPHEVVRATNMFLFVYIMIFVTSLLVISLDNLDMISNFTAITATLNNIGPGLGAVGPTGNFGCYSYISKLV MIFDMLAGRLEVFPLLLLFKRDTWRKF
8.1E-56	199	28.3	1.1E-33	125.9	11.9	2	2	R6PTA 2_9CL OT	Uncharacterized protein	BN618_ 01591	Clostridium nexile CAG:348	434	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	1263069	>tr|R6PTA2|R6PTA2_9CLOT Uncharacterized protein OS=Clostridium nexile CAG:348 GN=BN618_01591 PE=4 SV=1MKKISMFLRNQPPGRMIVGGFAGVILFGMILLLLPISVKDGAEVSAIDALFTSTSAVCVTGLIAIDTADHFTAFGQGIVAALIQIGGL GVTSLGVGLMLVARKRVGIKSRMLVKEALNIDSYKGIVKLVKAVLLMTLCFEAGGAILSFFVFSQDYDTVHAVGISIFHSIAAFNNSGFDI LGGLRNLTIYQDNVLLNLTTCILIIFGGLGFLVILDILKQKRFRKLTLHSKVVIVTSLVLLVAGTVILKLTENVTWLGAFFQSVSARTAGFST YPIGEFTNAGLFVLCILMFIGASPGSTGGGVKTSTFFIMFQKIRGTCTKGTVHAFHRNISEQNITKAFMITILSGTVVCIATFFMCVLEPE YSFMQLLFEVVSAFGTVGLSTGITPELSVAGKAVIIIVMFIGRVGIITLLSMWVNRVEPRARYSEEEVSIG
8.1E-56	199	11.9	2.2E-55	197.5	8.3	1.5	1	F4G9A 0_ALID K	Trk system potassium uptake protein	Alide2_ 4455	Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	488	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Alicycliphilus, Alicycliphilus denitrificans, Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	596154	>tr|F4G9A0|F4G9A0_ALIDK Trk system potassium uptake protein OS=Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601) GN=Alide2_4455 PE=3 SV=1MRDLFPVLRVLGMLMCMFSLGMVLPGLLSWWLQEAVWRVYPASVLATLGAGLVLWWLLRGHRQELQPRHGVILVTLVWVLL PLCASLPLWLAMAQLGQPITFTHAYFEAVSGLTTTGSTVLSGLDALPLSVNFWRTFLQWMGGMGILILAVAVLPLLGVGGSQLFKAEA AGPIKDTKLTPRMTETAKGLWGVYAALSVVCALCFWVGGMTPMDAVMHMFTTVSLGGLSSHDASFAFFESPVLEAMAVFFMLVASC NFTLYFVALRKGHWRGFWRDPEVRATMAVLIGGGLLVALLLWANGVYEPLQALRHGMFHVVSVATTTGYATQDYLAWPVFAPVFM LLLSGVATSAGSTGGGIKMVRMLILVQQARRELTRLVHPRAVQPVLLGGRVVDNRMIFSVLAFMLVYGATVIVLSMVLLLTDLDPLTAF SAVLASVHCTGPGLGTIGPSSNYAGLTDFQIWICTLGMLLGRLEILSFMALLSPAFWRR
8.5E-56	199	21.9	8.1E-28	106.6	6.2	2.1	2	R5Z87 3_9FIR M	Uncharacterized protein	BN700_ 01406	Firmicutes bacterium CAG:536	508	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:536	1263028	>tr|R5Z873|R5Z873_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:536 GN=BN700_01406 PE=4 SV=1MMFWLRRQGRKLNWHVIGNVIGNVLLVMAFLFVFPIIGGIIYHEEVLSFLFVMIACLVVGFPLSRIKVKHRMYFARDGLMAVGLC WVVLSIVGALPFWFSGTIPHFIDAFFETVSGFTTTGSSILKEVESLPKCMLFWRSFTHWIGGMGILVFVLAILPKSNDRSMHILRAESPG PVIGKLVPRLRKSAMILYAIYMGMTILEVVLLLLGKMPLFDALCNTFGTAGTGGFSITNQGIGQYHNAYYEWVIGIFMALFGVNFNFYFF CLIHEWKEAFHMEEVQTYFKVIGFSTLFIAINILPLIHGGFIDAVRLAFFQVSSIITTTGYSSCDFNLWPTFSKMILLLLMVLGACAGSTGG GIKVSRMIVVVKKIRADIQKTIHPLKVTLITFDGKALDNKVVDQIMSFFCCFILILALCMVLVSLDGFDFETTISACFACIGNIGPGFAMVGP FGNFSAFSDLSKIVLSFAMLIGRLEIFPILIFLAPFIGKGKKYRPTKADQVLLDEKNY
8.7E-56	199	16.2	2.5E-28	108.2	3.4	2.1	2	D4M1X 4_9FIR M	Trk-type K+ transport systems, membrane components	RTO_0 4760	Ruminococcus torques L2-14	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, [Ruminococcus] torques, Ruminococcus torques L2-14	657313	>tr|D4M1X4|D4M1X4_9FIRM Trk-type K+ transport systems, membrane components OS=Ruminococcus torques L2-14 GN=RTO_04760 PE=4 SV=1MNKKMIVYILGKMMGVEGLLLLIPALVSLIYHEKSVISFLIVAAILLAIYMVFGRKLPASKQIYGKEGFVIVGLAWILWSAFGALPFVI SGSIPHYIDALFETISGFTTTGSTILVDIEALPMGISFWRSFTHWIGGMGVLVFVMMITSLDDENAMPLMRAEVPGPEADKLVPKARHT ARLLYGMYFVLTAAEVVFLLFGGMNLYDALLHAFSTAGTGGFSNRAASVSFYDSAYIDGVITVFMILFGINFNLYFFILLKDWKSILKNEE LWAYLGIVGVSIAIITGNILKIYGTVAHAFRYASFQVGSIITTTGFATADYDQWPELSKSILLALMFVGACAGSTGGGIKVSRLLIIVKSIRR EVRKMLHPNAVTIIKVNGKKIGQDTLKNVNLYLTCYIIIMIVSILLVSIDNFDFATTFSGVLTTMSNVGPGISKVGPVMNFHPFSALSKLVF CFDMLIGRLEIFPYLLLLSPELWRRRF
8.7E-56	199	21.2	1.7E-55	197.8	14.7	1.4	1	Q315M 8_DES AG	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Dde_05 67	Desulfovibrio alaskensis (strain G20) (Desulfovibrio desulfuricans (strain G20))	443	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio alaskensis, Desulfovibrio alaskensis (strain G20) (Desulfovibrio desulfuricans (strain G20))	207559	>tr|Q315M8|Q315M8_DESAG H(+)-transporting two-sector ATPase OS=Desulfovibrio alaskensis (strain G20) GN=Dde_0567 PE=4 SV=1MRQKYLSPFWLPVYAFGIVIVAGACLLRLEDSLNGVSISFIDALFTATSAVCVTGLAVVDTPSTFSTTGRTVLMVLIQLGGLGIMT YSSLIFFLLRRRVSLTDKAAVGQVLLHDPSFDLGRFLTHMVIFTLCIELAGAAALMALIPQDMPWFHALFHAVSAFCNAGFALFSDSLM RWEGHAGVNLVFMLLIIAGGLGFSVMEESVLRIRGEIPALSRHTRIVLRTTLWLIFGGAACLFLAELHSGGSADMPTRVLQALFQSVTA RTAGFNTVDIGGMANVSLLVMLFLMFVGGSPGSCAGGIKTTTLRALSAFVAAQLSGRRQTVVMERALDDATMNKAITLFIFAVLTVTG ATLALSITESAGGALAQEKGMFLELLFESVSAFATVGLSTGVTPQLSDPGKLIVTALMFIGRIGPIWLLSALQRFQHEPKYRWPETQLPI G
8.8E-56	199	10.2	1.5E-55	198	7.1	1.3	1	A0A0F 6W2P1 _9DEL T	Potassium uptake protein, integral membrane component, KtrB	DB32_0 03099	Sandaracinus amylolyticus	659	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Sorangiineae, Sandaracinaceae, Sandaracinus, Sandaracinus amylolyticus	927083	>tr|A0A0F6W2P1|A0A0F6W2P1_9DELT Potassium uptake protein, integral membrane component, KtrB OS=Sandaracinus amylolyticus GN=DB32_003099 PE=4 SV=1MSNETAASLDIARERTSEFLDLSRAFHCHRGVSEPRPSTPPPRGSLPPEERASRASLLDVAHAPVAKGRAAAQSLGLTGVLVAA LVIVVVDFGLAIHLWASIPLTVLQTALAFPWMELVLRAETGERRPRGWLPKARMLLAHFVNIGLLAFALVEKWIALVGALHASDVTPFV SSYRSFSVVALVMATLGILGRGHRAQRFLADAADHPARLMVLSFGITAFLGGFLLTLPEAVVRVEDASFLDGLFTATSAVCVTGLAVND VGATYTFFGEAVIVVLAQIGGLGIMVLSASFVVLAGRKLRVKQSAVLVEMIDAGSLAALRRTLIAIVGYTLLFEAIGALLLYAFTGFHPEV MRGPDDPHPIAGAGDRAWWSVFTAVSAFCNAGFCLSHANLAGFAASWPICLTVAALITVGGIGFPVIDELRRHAWERVRRRRPDRL SLHARIVLGTSAMLTLGVAAILLVLEWSQSLAHLPWHARVLASLFQSVSMRTAGFNTIDLGAMRAVSIALACVVMVIGASPGSTGGIK TTSFAAICAEVWAELRGHASARLLDRRLEPGVVRRAMGVTFLSLAIVMLGTFAMLMTEDHEPLRILFEVCSAFSTAGLSTGITSSLSPA GKLVLIVMMFAGRTGPLTLALAMATETKRTPVQLASERVMIG

9.4E-56	199	21.7	1.2E-54	195.1	15.1	2	1	R6SJR6_9FIRM	Uncharacterized protein	BN586_02430	Dorea formicigenerans CAG:28	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea formicigenerans CAG:28	1263073	>tr|R6SJR6|R6SJR6_9FIRM Uncharacterized protein OS=Dorea formicigenerans CAG:28 GN=BN586_02430 PE=4 SV=1MNGKMVRYILGRMLGVEALLLLLPAFVGILYGEEKEALSFVIPAVILTCIFVIAGRKRPEGQVIYGKEGMVVVASAWITWSLFGAL PFTLSGSIPNFVDAFFETVSGFTTTGSSVLRDVEALPQCMLFWRSFTHWIGGMGVLVFVLMLTNLDKKNSMYLMRAEVPGPEKDKLV PKTKTTARILYGIYFGLTLILVIFLMFGGMNLFDSLIHAFGSAGTGGFSNYADSVGHFDSAYIDYVISIFMILFGINFNLYYFMLLGDFKAF WKNEELRVYLGIIATATILITLNTNQMYGSIMKAFRYALFQVSTIITTTGYATTDFNLWPTFSQCIVVLLMIIGACASSTGGGIKVSRLMIV FKGVKREIKQLVHPKSVNLIRINRKKISDETLRGVYVYLMAYALLAIVSVLIISLDNQDFTTTFTSVMATLNNIGPGLSAVGPTGNFADFSI LSKIVFCIDMLAGRLEIFPFLTFLTMFAWKRKF
9.7E-56	199	17.1	1.2E-53	191.8	11.9	2.1	1	D4LX27_9FIRM	Trk-type K+ transport systems, membrane components	CK5_06190	Blautia obeum A2-162	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, Blautia obeum, Blautia obeum A2-162	657314	>tr|D4LX27|D4LX27_9FIRM Trk-type K+ transport systems, membrane components OS=Blautia obeum A2-162 GN=CK5_06190 PE=4 SV=1MNFRIIAYIVGWVCNFQAIFMVLPCITALVYQEHEFFAFLISMILCLIAGIPLTARKPKNKVFYTKDGCVAVALSWLALCIFGSVPFV LSGSIPHPIDAFFETVSGFTTTGSSILTDVEVLPHCILMWRSFTHWIGGMGVLVFLLSLLPLAGGYHMNLMKAESPGPSVSKLVPKVQ QTAKILYSIYIGMTFLQIVLLLIGNIPLFDTLCIAFGTAGTGGFGIRNDSMGSYSTYCQIVTTIFMILFGVNFSAYYLILTKKIRQALKFEEVR YYFGIIAAAVLVIGLNTMHLFQNLGVSIQQAAFQVGSIITTTGFSSADFNQWPALSKTILVLLMFVGACAGSTGGGIKVSRILILCKAARK EFQLYLHPNAVKKIKMDQKTITHDILRSTNIYLTLYLLIFAVSILLVSLDNFDMTTNFTAVTATLNNIGPGLEIVGPMGNFSSFSYFSKCILIF DMLAGRLEIFPLLLLFFKGTWKKF
9.7E-56	199	29.2	1.3E-55	198.2	20.3	1.1	1	D3UG98_HELM1	Putative K+ uptake protein	ktrB HMU02570	Helicobacter mustelae (strain ATCC 43772 / LMG 18044 / NCTC 12198 / 12198) (Campylobacter mustelae)	447	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter, Helicobacter mustelae, Helicobacter mustelae (strain ATCC 43772 / LMG 18044 / NCTC 12198 / 12198) (Campylobacter mustelae)	679897	>tr|D3UG98|D3UG98_HELM1 Putative K+ uptake protein OS=Helicobacter mustelae (strain ATCC 43772 / LMG 18044 / NCTC 12198 / 12198) GN=ktrB PE=4 SV=1MNLKSIKFLLLSYFGIALIGSFLLSLPFSHKGHISFIDAFFTATSALTCTGLIIKDTALDFTSTGHVIILFLIQLGGFGYMTMLGLIYLLF RRRMGNAERNILKEALNHANYDDLTDFIKKILIYVFFVELIGAILLSIDFSLRFGLADGIWYGVFHAISAFNNGGFSVFPNSLIDFRTDVLV NTVICVLIFLGGIGYICLVELRFFLLNRVTKQRKHRFSLHFKIVFSVSILLIVLCAMMLLVLEWDNPETFGSFGFFERIIAAVFSSVNYRTA GFVSYDMSGLRDSSLFFSIIFMLIGGAPGGTATGIKVTTIAVLYAFARSVFTRSEVRLFNRAVSEESIQRALMVFIISGVYFLGLSLLLTLI EPKTNFFALVYEVNAAFSNVGISTGDGGILSLSASFHDAGKSLIILSMILGKAGVMIFTLALFGSAQESRIKYQKEKIIL
1E-55	199	30.1	4.8E-54	193.1	20.9	2	1	Q6LKF2_PHOPR	Putative potassium uptake protein, Trk family	KTRB PBPRB0325	Photobacterium profundum (Photobacterium sp. (strain SS9))	454	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium profundum (Photobacterium sp. (strain SS9))	74109	>tr|Q6LKF2|Q6LKF2_PHOPR Putative potassium uptake protein, Trk family OS=Photobacterium profundum GN=KTRB PE=4 SV=1MVLWHPSITPVERKPKAAKKIIGAPPFILCGSFILLVIIGACLLKLPIATEVPISWLQSLFTATSAVTVTGLVVVDTSTTFTPFGQVIIN VLIQFGGLGLMTFAIVTLIALGGKISFLQQTVAREAFNQTDTSTLVSTAKSVLVFSLAIELIGILILSVYWSGELGWKASLFHGFFYTISAF NNAGFALSADSLMPYVEDPVVNFTITGLFIIGGLGFSVLIDLLRNKCWSKLTPYSKMMITGTVLINAVALIAIYCIEYNNPNTLAPLSNMG KWLASWFQAVTTRTAGFNTLAIDQLEDATTMVILMLMFIGGGSLSTASGIKVVTFMVLILATYRYLRRDEGIHIFQREITKETVSKALALT MISIGITWIAIFALLLSEDAPILDIIFEAVSALGTVGLSRGLTTSLSETGEFIIIFMMFIGRLGPLTLAYFLASPRTKRLRYPETKVTIG
1E-55	199	33.6	1.1E-54	195.1	23.3	1.9	1	A0PZN5_CLONN	Potassium transport protein	NT01CX_1764	Clostridium novyi (strain NT)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium novyi, Clostridium novyi (strain NT)	386415	>tr|A0PZN5|A0PZN5_CLONN Potassium transport protein OS=Clostridium novyi (strain NT) GN=NT01CX_1764 PE=4 SV=1MKKGYKRRFTPVQTLALGFFILIMIGSMLLMLPIASKNGSSTPFIDAFFTSTSAVCITGLTTVNTAAHWNYFGTTVIIALIQIGGLGF MSFATLFALILGKRITLKERLIMQEAMNSFSLQGLVKLAKYILIFTFSVEGIGALFLSTKFIPKYGLLKGIYFSLFHSISAFCNAGFDLTGDS LVPYYNNTVVILTISFLIIISGLGFSVWAEIYNYKGVGNFSTHSKVAIAMTLFLVISGWALMYLFEMRNPETIQYMSFKGKILSSFFASVSP RTAGFYSVNLPNMTLAGKVLTIILMFIGGCPGGTAGGVKTTTIGILMMTIVCVIKNREDTEIFERTIGKNLVYKSFVIATLAMGVVIIDTVIL SFTETGASLEYILYEITSAFGTVGLTLGLTPQLSVIGKFIICATMYIGRIGPLTLIMALSSKKDKNLIKYPDGKILVG
1E-55	199	21.9	1.5E-54	194.7	15.2	2	1	Q465Z0_METBF	Sodium transport protein	Mbar_A3429	Methanosarcina barkeri (strain Fusaro / DSM 804)	483	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina barkeri, Methanosarcina barkeri (strain Fusaro / DSM 804)	269797	>tr|Q465Z0|Q465Z0_METBF Sodium transport protein OS=Methanosarcina barkeri (strain Fusaro / DSM 804) GN=Mbar_A3429 PE=4 SV=1MGGRWFLIDNSAVFNALGKILFLLAFTMLVPLLVAFYYREPLVPFIVSFFITLVSGLLLMRFKGREDWQQKEALAIVALSWLAAAIF GAIPFLFEGVSFIDAVFESMSGFTSTGSSILTNIESYSRGLLFWRSFTAWLGGMGIIVLFIAVLPKLGVAGRQLFRAEAPGPTEDKLKPR IRETARILWTLYILISALEVVALFLGGMSLYDALNHSFACMACGGFSTYNAGIEAFHSPIIEFILTFFMFIAGANFALYYRVIRVNKFALFRD EEFKAYSFFILGFTGLLTLVLFKDMGFSPFNSFRYAIFQITSVMTATGFASTDFNMWKDSAKILVLSVMFIGGCAGSTGGGMKVVRFLL MLKYARRELFKFVHPRLVRSIRLNNKAVPEDILQSILSFVVLYIGVFVVGTVLLTLLGVDMVSSVTASITTLGNIGPGFNIVGPMANFESIP LLGKIILISNMWVGRLEVYTVLVLFTREFWHS
1.1E-55	199	28.7	1.3E-55	198.2	19.9	1	1	F6FFH5_MYCHI	Potassium uptake protein KtrB	ktrB MHF_0055	Mycoplasma haemofelis (strain Ohio2)	493	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma haemofelis, Mycoplasma haemofelis (strain Ohio2)	859194	>tr|F6FFH5|F6FFH5_MYCHI Potassium uptake protein KtrB OS=Mycoplasma haemofelis (strain Ohio2) GN=ktrB PE=4 SV=1MVNRSTDLSIFKNFLKNPFGKTIYQKFLRIYLLTTLIGAFLLYLPISRKGSLDFFSAIFISLSAFSNTGLTTHVTSDTFNFFGQLVILCL IQFGGLGFLTVLIFLWSWIKSGGNINVEHRRFLHFERGSFKKVESLETVKGGITVLLIAELVGALILTVFFYFATPATQASESLPSAKGDF GKALWYAIFHSISATNNAGFDILGQNSIMPYRHGANNILSAVLLVESVLGGIGYPIFYDLYLWRKNQKLRRNYQVSLFTKTCVSTYFFIS LISVVLIVFFETILGLGYSNSTVLYSSDSELGSKFDRLWNVIYTSFSARSAGFSSIDISKVTEETKWLLSILMFVGTSPASTGGGIRNITIFL ILARMFFTIRGRRYLTIYNKTVSENIIADAYVVFSAASILVMLSIFAITMSLQSRQYKIGDAFFEATSAFGTVGLTSGVTKSCNFLGKLTLM LLMFVGQLGISNAILSLTNQQPKFKNARYCVETLRII
1.1E-55	199	36.8	1.6E-55	198	25.5	1.1	1	A0A0D1W8T3_ANEMI	Strain NCTC 7096 contig_138, whole genome shotgun sequence	TS65_17360	Aneurinibacillus migulanus (Bacillus migulanus)	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Aneurinibacillus group, Aneurinibacillus, Aneurinibacillus migulanus (Bacillus migulanus)	47500	>tr|A0A0D1W8T3|A0A0D1W8T3_ANEMI Strain NCTC 7096 contig_138, whole genome shotgun sequence OS=Aneurinibacillus migulanus GN=TS65_17360 PE=4 SV=1MLRKNIYKLSPIQIIVSAYFIAIVVVTGLLMLPISLKPGVSLSFVDALFTATSAVSVTGLTTVSTPETFSTFGSVVLISAFQLGGIGVM TLGTFIWILFGTPIGLSQRRLIMVDQNRYNLSGLVQLMKLVLGMALLFEAVGAVIFGLYFYFAGYYDSLATSFYYGIFHSISTYTNAGFDL FGNSLLDFADDYFVISLTAILIILGAIGFPVLVELREYFFGGHKRFRFSLYTKVTTFTFGILLVLGTIGVWVVEDSRYLAGMTWHEKFFYS MFLSVTARSAGLVTVDPSDLSVTSQFFTSILMFIGASPSSVGGGIRTTTLAVMILTIITFARGRNEVRIFGRSLRQDDINKSFVFFSTASIL VISGILILEMVDGHRFSLSAIIFNICSAFGTCGMSIGAISESTPVSKMVLVLLMYIGRIGMMPFLSIFISGKAKADIHYPEEKIIIG

1.2E-55	198	18.3	5.2E-55	196.2	12.7	1.8	1	A0A0D6JKM9_9RHIZ	Trk system potassium uptake protein	BN1229_v1_3957	Candidatus Filomicrobium marinum	481	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Filomicrobium, Candidatus Filomicrobium marinum	1608628	>tr|A0A0D6JKM9|A0A0D6JKM9_9RHIZ Trk system potassium uptake protein OS=Candidatus Filomicrobium marinum GN=BN1229_v1_3957 PE=3 SV=1MIQFRPILFALGLILCTIAAAMVLPAVVDVADGHEDWRVFFTSAVATFFIGGLLILVAYEDQPAPLGIKEGFLLTTLCWVTVAAFAA APFAGLGLGFADAYFEAMSGLTTTGSTVLTQLDQLPRGILLWRAILQGLGGIGIILTAIIMLPFLRVGGMQLFQMESSDKSEKVLPRAIE LTLAIAGVYVVGLIVACIAVYMALGMTPFDAICHGLSTVSTAGFSTHDESFGFFRSPALEWACVLFMILGALPFVVYVKAMRNHPEALWR DTQVRGFLMFLIGLWLIMTFWLITARGLEPTTALRMSAFNLTSIMTTTGYASSDYMQWGPFAVGLFFLVTFIGGCAGSSAGGIKIYRLQ VTALLTRSHFVHLMSPNRVVTLVYNGKRLPADVPFSVVAFLTIYMSTVGIFTVVLSAMGLDFVTAMSSSAQAIGNVGPGLGDIVGPAG NFSSLPAAAKWVLSFAMLLGRLELFTVLVLFRIEFWRG
1.2E-55	198	20.4	1.6E-55	198	14.2	1.1	1	D4K7Z0_9FIRM	Trk-type K+ transport systems, membrane components	FPR_05560	Faecalibacterium prausnitzii SL3/3	465	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii SL3/3	657322	>tr|D4K7Z0|D4K7Z0_9FIRM Trk-type K+ transport systems, membrane components OS=Faecalibacterium prausnitzii SL3/3 GN=FPR_05560 PE=4 SV=1MEKIKNIRKRLRHQRSVRRRKLGLSTPTQIICVSFIIVIALGTLLLTLPIASRHGRLDVLNAMFTATSATCVTGLVVRDTWTQFTWF GQAVVLLLIQVGGLGLVTLTSFFALAMRRRMGFRDLRLLGESVSADGYDQAKSVLKIVVGLAAMFEGIGILLLLFAFVPQFGLEGVWIS VFTAISAFCNAGFDLFGRFGAYSSLAPYVNNYYVQAVIMFMIISGGLGFMVWVELCQWYQKRRLSLHAKVVLSFSVILWLGGALGLGL MEWNNSATLGGLSVPGKVMASLFQSVSTRTAGMNTVDLASCGTLSKLLMSVLQFIGAAPGSTGGGVKVTTFAVIILTIRSVAQGRDD CVIADHHIESKTVYYRALTIIVLGAAAVIGSAIVVYYNTSDAVSVVDAIFESCSAFGTVGLSVGVTSQLNNGAKILYMLVMFMGRVGPVAF AMSLTAKPDDNKRKIMPVGHINVG
1.2E-55	198	15.5	3.9E-55	196.7	10.7	1.7	1	B8DLW2_DESVM	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	DvMF_1540	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	454	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	883	>tr|B8DLW2|B8DLW2_DESVM H(+)-transporting two-sector ATPase OS=Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637) GN=DvMF_1540 PE=4 SV=1MLHRRLLSPLILPVYSFAATILAGAVLLYLDISHAPSAGEAGISFVDALFTATSAVCVTGLSVVDTGTTFSRAGQWIILALIQLGGLG IMTYSSLLLFLLRRRVSLTDRLAVGQALMHDPSFHLGRFLYRLVRTILCIELAAACLLYIFAPQGMGAFGALFHAVSAFCNAGFGLRPDN MMPWQEHTGVNLVIMFLIVVGGIGFSVIDELLGAARTRLTGKPYRPLSRHTRLVLSTTAFLIVAGAALIWLAEYLSDYTGLSPAGLVLPA FFQSVTCRTAGFNTMDIGRLTDFTLMVMICLMFVGGSPGSCAGGIKTTSFRVLAGFVEMQLRGRRQNVLLGRAVDAPTQAKALTLFL FAIIVVTVGTMVLSLTEGGIAPHTHGQFEQLDLMFEVVSAFGTVGLTTGVTPHLSVPGKLLISFLMFIGRIGPVWLLATLQHLQSEPKFR WPEVDYPIG
1.3E-55	198	26	5.3E-55	196.2	18	1.7	1	I0GST2_SELRL	Putative potassium uptake protein TrkH	trkH SELR_21110	Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421)	456	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Selenomonas, Selenomonas ruminantium, Selenomonas ruminantium subsp. lactilytica, Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421)	927704	>tr|I0GST2|I0GST2_SELRL Putative potassium uptake protein TrkH OS=Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421) GN=trkH PE=4 SV=1MVDNLQEATAFKAQQKFRLKPTQTILLSFVLMISIGTVLLMLPVSTTNRVGLPFMDALFVSTSASCVTGLTVVDVQNDLSFFGKC VLLLLIQVGGLGIMTLATMVAHAMGYRFPLKQSIIVQESLSQSGRAGLFALIRRMIFYTFMVEGFFALLLTVHFYPEFGVDAIGYGIFHAV SAFCNAGFDLFGNYDSLCKRADDFVLLAGIGLPIILGGIGFTVIYDVLHCRSWRQYSLHTKIVLISNLFLLTVGTLLIWALEANNGGTLAD VPVAGQLAQSAFMSVSCRTAGFNTFDLAKATQITQLIMIILMFVGASPLSTGGGIKSTTMFVIVRSVWAVFRGESELVVFGRTITKDLR DQAFATFTVGTIWVVSMGMLLSVLDGEVHDLEEVIFETVSAFGTVGMGIGITLSWNDWGKGLLALTMLLGRVGIMSFMLSFIKQKQSA VIKYPKEEVMLG
1.3E-55	198	25.3	3.7E-54	193.4	17.5	2	1	R7R583_9FIRM	Uncharacterized protein	BN450_01491	Roseburia sp. CAG:100	465	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:100	1262940	>tr|R7R583|R7R583_9FIRM Uncharacterized protein OS=Roseburia sp. CAG:100 GN=BN450_01491 PE=4 SV=1MDCYNEPSTPYKGDNRELKKQNKNKIKRSTTRLVALGFALIIMIGTMLLSLPISVHSGQPNIMNALFTATSATCVTGLIVADTYQN WTTFGIIVIFTLIQIGGLGFMTIGVYISIILKKKIGLKQRENLQESVNSMEIAGVVRLARKIVQGTFLIEGIGALLLSTRFIPRFGLQRGIAFSI FHAVSAFCNAGFDLMGYEEAYASLVSFEGDVLVNMVVMFLILTGGIGFIVWDDLMRNKWHFKKYLLHTKIVLTFTIGLTVIATIVFLVLE NHGVLAGLTPVEKALGAAFCSVTPRTAGFNTTDVAGLSNAGKMLTILLMFIGGSPGSTAGGAKTTTIVVLLLYAVAMIRNHEDINLFGR RLTDDVVKKANAVVVTNFMLASLAAVIIMAMQPFDMADVLLEVFSAINTVGMSTGITRDLNTVSRLILIVLMYCGRLGSLSFALVFAQKN TSDTIRLPQEKIIVG
1.4E-55	198	23.6	1.9E-55	197.7	16.3	1.1	1	Q8DRK5_STRR6	Trk transporter membrane-spanning protein-K+ transport	trkH spr0070	Streptococcus pneumoniae (strain ATCC BAA-255 / R6)	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pneumoniae, Streptococcus pneumoniae (strain ATCC BAA-255 / R6)	171101	>tr|Q8DRK5|Q8DRK5_STRR6 Trk transporter membrane-spanning protein-K+ transport OS=Streptococcus pneumoniae (strain ATCC BAA-255 / R6) GN=trkH PE=4 SV=1MLFKLSKEKIELGLSRLSPARRIFLSFALVILLGSLLLSLPFVQVESSRATYFDHLFTAVSAVCVTGLSTLPVAHTYNIWGQIICLLLI QIGGLGLMTFIGVFYIQSKQKLSLRSRATIQDSFSYGETRSLRKFVYSIFLTTFLVESLGAILLSFRLIPQLGWGRGLFSSIFLAISAFCNA GFDNLGSTSLFAFQTDLLVNLVIAGLIITGGLGFMVWFDLAGHVGRKKKGRLHFHTKLVLLLTIGLLLFGTATTLFLEWNNAGTIGNLPV ADKVLVSFFQTVTMRTAGFSTIDYTQAHPVTLLIYILQMFLGGAPGGTAGGLKITTFFVLLVFARSELLGLPHANVARRTIAPRTVQKSF SVFIIFLMSFLIGLILLGITAKGNPPFIHLVFETISALSTVGVTANLTPDLGKLALSVIMPLMFMGRIGPLTLFVSLADYHPEKKDMIHYMKA DISIG
1.4E-55	198	28.8	1.4E-55	198.1	20	1.5	1	G8R8R7_OWEHD	Trk-type K+ transport system, membrane component	Oweho_1506	Owenweeksia hongkongensis (strain DSM 17368 / JCM 12287 / NRRL B-23963)	603	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Cryomorphaceae, Owenweeksia, Owenweeksia hongkongensis, Owenweeksia hongkongensis (strain DSM 17368 / JCM 12287 / NRRL B-23963)	926562	>tr|G8R8R7|G8R8R7_OWEHD Trk-type K+ transport system, membrane component OS=Owenweeksia hongkongensis (strain DSM 17368 / JCM 12287 / NRRL B-23963) GN=Oweho_1506 PE=4 SV=1MIFQEIREKVKLFIYDSRDIVLKLFRVSSVIVAFIAVLSILYFHGFNITSEENKVITIILRVAFGYFVIKYLVRLLFSLQPLKDFKNSLFEG VLILLVILNASFAFLFDWELIHHLGQFLNIENINWFFAVGIQLYFVLILVNEVGRAGSRLSSFNLSPPAMLIGSFFILILFGSGLLVLPEMTS SGESMPYFDALFTSISASCVTGLIVVDTATYFSLKGQMVIMLLIQLGGLNIISFASVFALIARRGIGLKHQSMLQESLNAESLSASSSLFR QIFLFSMLIEIAGAVLIFFSWKDIPEVSATSDKIFYSIFHSISAFNNAGFSVFSNGLFEEGVRNAYTLHLVIALLIILGGIGFTTMRDLFSFSR IKERYQKSWRSLRIDTKLSLYSAAILILSGFVVFYVFEVNNTLKDASIWGQVVGALFQSVTTRTAGFNTVDVGALAKPALIFSIFLMFIGA SPGSTGGGIKTNTFAIIILGAWSTARGKPRLELFKRTIPYDLLNKAFLIFFISICFIALGIFGLAISEPDKSLIALSYEEVSAFCTAGLSTGITA DLSTTGRVIIMLSMFLGRVGILSLAFALGRNTKVHDYKYPKASLLIG
1.4E-55	198	19.6	7.5E-55	195.7	13.6	1.9	1	F7XPL6_METZD	Cation transporter	Mzhil_1612	Methanosalsum zhilinae (strain DSM 4017 / NBRC 107636 / OCM 62 / WeN5) (Methanohalophilus zhilinae)	478	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosalsum, Methanosalsum zhilinae, Methanosalsum zhilinae (strain DSM 4017 / NBRC 107636 / OCM 62 / WeN5) (Methanohalophilus zhilinae)	679901	>tr|F7XPL6|F7XPL6_METZD Cation transporter OS=Methanosalsum zhilinae (strain DSM 4017 / NBRC 107636 / OCM 62 / WeN5) GN=Mzhil_1612 PE=4 SV=1MRHSTVLHVMGNLLFMLGVIMFVPLLIALYYGESLYPFAVAIVASILSGSLLSINFEEKERWYHREGFAIVAGGWLLAAAFGSIPFI LSGISPINAFFESMSGFTTTGSTVLMDIESYSRSLLFWRSMTQWLGGMGIILLFIAILPKLGVAGREMYYAEVPGPDKEGIKPRVRETA KLLWMVYLLLSVIMVLIFLILGLSLYDSVTHTFTTVACGGFSPYADSIAAFNSPLIEGTITLFMFLAGINFVLHYRTLYGPRKDILRDEEFRF YLAVVFLAIVALAFVLWRDMNFGIFDSLRYASFQSLTIITSTGFASADFDLWTDSSRMILLALMFTGGCASSTAGGIKMVRILLLLKYTYI RLKGPVLPLSVNVLRLNGREVPLIQLQSVIAFVVLYLAIFCVSSLILAELGLDIVSAITASIATLGNIGPGLGMVGPMENFAMIPVMGKIILIF NMWAGRLEIFTVLVLLTPEFWKNR

1.5E-55	198	27.3	5.7E-55	196.1	18.9	1.7	1	A0A089L1J7_9BACL	ATP synthase subunit J	R70331_26210	Paenibacillus sp. FSL R7-0331	437	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. FSL R7-0331	1536773	>tr|A0A089L1J7|A0A089L1J7_9BACL ATP synthase subunit J OS=Paenibacillus sp. FSL R7-0331 GN=R70331_26210 PE=4 SV=1MSPPQTLVLGFAAVILVGTLLLMLPFSSTSGHSLTFIDALFTATSATCVTGLVVVDTGSYFSLFGQTVILVLMQIGGLGFMTMATL FALLLRRRISLRDRLILQEAMNQSSMEGIVRLIRKVLVYSLVIEAAGAVLLTLRWAADMPFARALYYGVFHAVSMFNNAGFDLFRDYRG LTAYASDPVINLVVMLLIVSGGIGFIVMADLIDYRKTRRLLLHSKVVLTMTAALILTGAAVIFVFEFTNARTLGPLNIGGKIWAAFFQSVAP RTAGPNTVDIGGMRQASQFFIVMLMFIGASPGSTGGGIKTTTFTLMIGAVVSMLRGREDIVLFRYRLAQERVFKALTITLLAVLLIVTVS MILSTTEGWPFLMILFETTSAFATVGLTMGVTPELTDAGKILLCLTMFAGRLGLLTLAYALGPKQGKPLYKYPEGKMIIG
1.5E-55	198	23.2	2.1E-54	194.2	16.1	2	1	R6R5K9_9FIRM	Cation transport protein	BN606_01191	Butyrivibrio sp. CAG:318	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, environmental samples, Butyrivibrio sp. CAG:318	1262761	>tr|R6R5K9|R6R5K9_9FIRM Cation transport protein OS=Butyrivibrio sp. CAG:318 GN=BN606_01191 PE=4 SV=1MNYSIIRYILSSVVCFEGVFLALPSIIGAIYGEEEGFIYGIVSIICILAGFAGRYRKPKSNTFYSREGFVAVSLSWILLSIIGALPLCLTG EIPFYIDALFEIVSGFTTTGASIMPSVEILSHASAFWRLFTHWIGGMGVLVFIMAVLPLSGGSNMHLMRAESPGPSVSKLVPRVKHTAMI LYGIYCIITIMETAALLIAGMKFFDALTLSFATAGTGGFALLNSSIASYSAAVQNIITVFMLACSVNFNVYYLLLIRKGKEALLNEEVRYFLII VFASALLIALNIMGSFGSFFEAFHHSIFQVASVISTTGFATCDFNMWPEFSRAILVLLMFVGACAGSTGGGLKISRLIILAKAVKNEARSI VHPRSVNRVRINGKGIQDSAVKTVLVYLAAYVLIVIISFLIVSLDRYDMTTNFTAVAATFNNIGPGLGAVGATGNYGGFSVLSKLVLIFDM LIGRLEIFPMLVLLSPGTWRVRQSSSTK
1.5E-55	198	38.4	4.3E-53	189.9	26.7	2	1	D3PBS9_DEFDS	K+ transport (Trk) system, membrane component	DEFDS_0570	Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1)	426	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Deferribacter, Deferribacter desulfuricans, Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1)	639282	>tr|D3PBS9|D3PBS9_DEFDS K+ transport (Trk) system, membrane component OS=Deferribacter desulfuricans (strain DSM 14783 / JCM 11476 / NBRC 101012 / SSM1) GN=DEFDS_0570 PE=4 SV=1MKKIKLSPWTYLILTFLILIFVGSILLKLKGTYNGNLSYIDALFTSTSAVCVTGLIVTNTSNFTLFGQSIILLLIQLGALGIMTLSSSLYIF LRGELGLDQRIMVAKITDVFALHEVENILVYIIKYTFIIELIGAILLSVGFLLQGFHLSSAVYYGIFHSISAFCNAGFSTFDDSLINSNAIVKITT MCLIILGGIGYYVIYDLQKSFQKKVRLKLHTKVVLMTTFLLIIVGFLVFSIIEKEMGIVDGFFQSVTARTAGFNSVDLGQLHNISKFMLIILMI IGASPGSTGGGVKTTTFFIAFVSILRVIKGENKIIIFKRQIPYQTILRAFALIFLYLAVDVVSTLILLYFYNYDFLEMLFEVTSALSTVGLSLGI TTKLTMAGKIVIICCMFLGRVGPAALVMAMLGKEKRTFVQYPEEKVVLG
1.5E-55	198	14.4	1.8E-52	187.9	10	2.1	1	U1FB33_TRESO	Cation transport protein	HMPREF1325_2228	Treponema socranskii subsp. socranskii VPI DR56BR1116 = ATCC 35536	481	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema socranskii, Treponema socranskii subsp. socranskii, Treponema socranskii subsp. socranskii VPI DR56BR1116 = ATCC 35536	1125725	>tr|U1FB33|U1FB33_TRESO Cation transport protein OS=Treponema socranskii subsp. socranskii VPI DR56BR1116 = ATCC 35536 GN=HMPREF1325_2228 PE=4 SV=1MAVLTFLKIISIIVAFIGVSFLIPIGTALALGETSVIASFAVPMVASWIAAIVIFIAGRKTEIRLSTRGTFVIVALAWISGSVFGALPLWC SRAIPHFADAIFESVSGFSTTGATILSEVESLPRSINLWRCEMHWLGGMGIVALTVALLPLLGVGGFQLIKAETTGPEKGKVTPKITTTA KILWISYTALTVVQTVLLLFAGMDFIDALSHAFATLGTGGFSTKNSSVGTYGSVSIDVICTVFMFLSGINFSLYYYAVTGKFSEIRDNSEL KAYFAVFIVASLGIAFVITKQYGSFLQALRYGSFQVASILTTTGFGTADFTTWAPTAQLLIFILYFLGGCAGSTGGGIKVVRWVVLAKQL HNETEKMLHPHGIFNIRLNGKVAGKDLAPNVAAFVSLYLLLVFITTAIGCLFDLDLFSALTGALSMVGNVGPGFGKLGPVCNYGFLPDT VKWWYSFAMLAGRLELYTMILYFLPAFWKK
1.5E-55	198	17.9	1.8E-53	191.2	12.4	2.1	1	R6EUB3_9FIRM	Trk system potassium uptake protein TrkH	BN749_00338	Firmicutes bacterium CAG:65	481	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:65	1262994	>tr|R6EUB3|R6EUB3_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:65 GN=BN749_00338 PE=4 SV=1MNFAILSFIIGFILQFEALFLLLPWIVGMIYGEYHVALIYLATAVVCFILGKLLSFRHTGRFKELYVREGFTAVALGWFVMSVFGAIP FVLTGEIPFYIDALFETISGFTTTGSSILSDVEALSYASLFWRSFTHWIGGMGVFVFIMAILPMMGGSTMNLMRAESPGPSVSKLVPRV RDTAKILYGLYMAITVLGVIMLCLCGMPLFDSLCTTFGSVGTGGFGIKNSSIGGYSPLIQNAVTVLMILSGVNYTVYFCLLSRQFKEAFSI EEVRWYFLIIFASALTIAWNIRPLYATLGETLRHSFFQVGTIITTTGFATTDFNMWPQLSKTILLLLMMIGACAGSTGGGIKVSRVLILFKA IRKELSMMIHPRMVKKIKMDGHNLSHETLRSTNVYMTAYFIVLFVSLLIVCLDEYDLSTNFTAVLATLNNIGPGLELVGPTQNFALFSPLS KCVLMFDMLAGRLELFPMLVILLPSCWKKY
1.6E-55	198	28.5	2.3E-55	197.4	19.8	1.2	1	Q5M5Y3_STRT2	K+ transporter (Trk), membrane-spanning protein	trkH2 stu0314	Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311)	461	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus thermophilus, Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311)	264199	>tr|Q5M5Y3|Q5M5Y3_STRT2 K+ transporter (Trk), membrane-spanning protein OS=Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311) GN=trkH2 PE=4 SV=1MITRRFSVINHLSVTQKLVLSFAFVIIVGSILLSLPISHYANSPETSYLDHLFNAVSMVCVTGLSVVPVSKAYNGFGQIISILLIQTGG LGLVSLIAFSTYTLKNKLGLSDQDLLQSALSRDNQKDLKAYLFNVYKITFSIEALAALVIMTDFIPRFGLGHGIFNSLFLAVSAFCNAGFDN LGTNSLQDYATNPTINLSVAFLIMSGGLGFAVWIDLIQMIRCYIKDRPRNWKLASRPFSNQSRLVLISTSCLLLGGTLLAWFLEMDNSKT IGTLNVWQQLLVSFFQTVTMRTAGFATISYTNANFTSNLLFMIQMFIGGGPGGTAGGIKVTTASIMFLLFKSVLSGNSRVVFRNRIISNK TVMQAFTVILFYLTMLLVGYVILLQTNPTLSPLALLFESVSAIATVGVSMDLTSSLNTMGRLVIMALMFIGRVGPITVLLSLMTKKEKHVS YAPTHISVG
1.6E-55	198	22.2	9.5E-54	192.1	15.4	2.1	1	R6PIH4_9CLOT	Uncharacterized protein	BN618_01678	Clostridium nexile CAG:348	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	1263069	>tr|R6PIH4|R6PIH4_9CLOT Uncharacterized protein OS=Clostridium nexile CAG:348 GN=BN618_01678 PE=4 SV=1MNYRMTSFILGRMLGVEALVMVIPAIVSAIYGEETMRAFLITSAVLMVLFLIFGRKKPENAMIYAKEGFVIVALAWILWSVFGALPF YISGTIPKYIDALFETVSGFTTTGSTILTDIASLPMGMNFWRCLTHWIGGMGVLVFVLVLTSLDDKNTMHLMRAEVPGPEADKLVPKVR GTAKILYGMYLALTLIEVGFLLAGGMNLYDSVIHAFSTAGTGGFNNRNNSVAFYDSAYIDGVITVFMILFGINFNMYFLLLLKNVKSVFKN EEVRAYLGIIAATTIIITFNIMHIYETPLKSFRYAVFQVASIITTTGFATADYNLWPELSKCLLLMVMIVGACAGSTGGGMKVSRILILLKSIK QEVKKTLHPKSVSVVKVNGKRVSGETMHAVYVYFMAYIFIVIASVLVVSINNFDFATTFTGVLTTLNNVGPGIAAVGPVENFAKFSVLSK IVFCFDMLVGRLEIFPFLMLFSSNLWRRKF
1.6E-55	198	14.1	4.7E-27	104	4.9	2	2	L0ID41_HALRX	Trk-type K+ transport system, membrane component	Halru_2092	Halovivax ruber (strain DSM 18193 / JCM 13892 / XH-70)	509	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Halovivax, Halovivax ruber, Halovivax ruber (strain DSM 18193 / JCM 13892 / XH-70)	797302	>tr|L0ID41|L0ID41_HALRX Trk-type K+ transport system, membrane component OS=Halovivax ruber (strain DSM 18193 / JCM 13892 / XH-70) GN=Halru_2092 PE=4 SV=1MSIRVDWRSSASLTGTVLKWLAVPLLAPLALALYDGADVVPFAVSVAVTVVLGLALEQLSDVRELEHREGLLIVASTWLGVALIG AIPFILVGQGAPSQSAFAGPVDGPINALFESMSGLTTTGATIMSGWDFEHQSRAILLWRQLLQWLGGLGILIVAIGLLSNLMVGGAQLM ETETQTRSVNKLTPEIEQTARIIWGLYVGLTLVTIAVLYGLNVVGLADEMTLFNAVAHALTSVSTAGFSPEAESIAAFAPIVQWVLIPVML LGATNFILLWYLVHGDFDRPRQSEELRFYLGVVAFASSLVIGVLVVDPGHIESVEASVRHGLFNVVSMITTTGYASFDYTTWGPGAQH VLFLSMFVGGMAGSTTCSIKTLRWLVILKGLYRNLFLSIHPQAVRPIRLGDSVVDEETIGDIFSYVMLALLIFFGLTVFVVTDASLAGRAV SEFDALGAAASIALNIGPAFGEAGPMDNYAVFPTSTRFVMVVMMWIGRIEFVPVLVLLLPAFWKS

1.6E-55	198	22.2	1.5E-28	109	3.8	2.1	2	R5C6S4_9FIRM	Uncharacterized protein	BN499_00806	Blautia hydrogenotrophica CAG:147	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	1263061	>tr|R5C6S4|R5C6S4_9FIRM Uncharacterized protein OS=Blautia hydrogenotrophica CAG:147 GN=BN499_00806 PE=4 SV=1MNYSMIRYIIGWILILEAAFLSLPCIVAAIYQETDGWVYAAVLLVCLTCGLLLKRTKIQTKIFFAREGLVTVSLSWIVLSIFGSLPFIFTGAISNPVDALFETVSGFTTTGASILTDVEALSHCNLFWRSFTHWIGGMGVLVFMLALLPLTGGSHMNLLKAESPGPSVSKLAPKVQTTAKILYMIYIAMTLIQIVFLLIGKMPLFDALTTSFGSAGTGGFGIKNDSMASYSPYLQNVVTIFMILFGVNFNFYFLLLHKKFRQAFHFSEVRLYIGIILAATATIALSLGNTYDNFLEALHHSAFQVASIITTTGFATTDFNLWPEVSRTILVMLMFIGACAGSTGGGIKVSRFIILMKALVKELHQYIHPKGIKTIHIDGHTLGHEVLRSVNVFLFAYVLIFAASSLLLTFDGKDLITNFTAVAATLNNVGPGLELVGPSSNFSCFSMFSKLVLTFDMLAGRLEIFPLLLLFVRDTWKKF	
1.6E-55	198	30.9	1.8E-55	197.8	14.6	2.3	1	A0A0A0X5D9_9SPIO	Potassium transporter	JO41_07950	Treponema sp. OMZ 838	480	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema sp. OMZ 838	1539298	>tr|A0A0A0X5D9|A0A0A0X5D9_9SPIO Potassium transporter OS=Treponema sp. OMZ 838 GN=JO41_07950 PE=4 SV=1MKFLQCLTIIFMILSIVAGSFLIPVAVAVFLHEWNMLPAFFIPMAVLWVITILLFIRTKRQPIRLTVREGILLVSAAWLGAGLLGAVPFMLSGFVPHFSDAFFESVSGFTTTGASVLQNIESYPMALRVWRTQMHWLGGMGIVALTVALFPLLGVGGFQLIKSETSGPDKGKVTAKITHTAKALWFIYLGMTVLQIILLCIAGMPFLEAMCHSFSTLGTGGFSTQNTSVGYYNSAAIEIICTVFMFLAGVNFSLYFHLFTGKPEEFFRNSELRAYIRIALFTGIGIALVLVPVYGLSAAFRHSFFHVASIMTTTGFSTVNYCAWPAFAQALLFLLMFTGGCSGSTAGGIKVIRWVILRKQALNEMQRLLHPHGVFSIQLNRRPGRKDVVYSVAGFMFVYFVCLLVTFLTAALTGADLLTDITAALTLVGNIGAAFGRVGSGGDFSFFPHWAKVVFSFSMLAGRLELYTIVILCVPAFWRR	
1.7E-55	198	30.6	1.1E-53	191.9	21.2	2.2	1	G7V995_THELD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Tlie_0731	Thermovirga lienii (strain ATCC BAA-1197 / DSM 17291 / Cas60314)	441	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Thermovirga, Thermovirga lienii, Thermovirga lienii (strain ATCC BAA-1197 / DSM 17291 / Cas60314)	580340	>tr|G7V995|G7V995_THELD H(+)-transporting two-sector ATPase OS=Thermovirga lienii (strain ATCC BAA-1197 / DSM 17291 / Cas60314) GN=Tlie_0731 PE=4 SV=1MNPKKFYGKLEPEKVILWGFLMLIMSGTLLLWISNYSYKPLTFIDSLFTATSAVCVTGLVVVDTASDLTFYSKSIVAVLIQLGGLGVMTAFTFLFILRGARVSLQQRYYLSNSLGLESVSGVIRLLGHIVKMTLAIELFGTLLLFGKLIDYYEPLSALGHATFQSVSAFCNAGFSTFPGNMMPFSKDIYLTSVIMILIVLGGIGFVPLTEIVGVEKRGKRLSPYCKMVLIMTVMLIVLGCIFLFLSEHCRSNQQISVFQGFWDALFQSVSARTAGFNTVDIGKVSPLGSFILILLMIVGASPGSTGGGMKTTTLGVLLLSLYSEILQREDVVFFGRRVPYSVLRKAVSLAIVYVMTIFLSSFIMGFMEPYSFREILFEVTSALGTVGLSTGITPKLSTGSKLLLILLMFWGRVGLIIFFYGIARKEEKGRVTYADVNVPIG
1.7E-55	198	32.5	2.3E-55	197.4	22.6	1.1	1	A0A059XWB4_9MOLU	Potassium transporter KtrB	ktrB MCFN_01930	Mycoplasma californicum	512	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma californicum	2113	>tr|A0A059XWB4|A0A059XWB4_9MOLU Potassium transporter KtrB OS=Mycoplasma californicum GN=ktrB PE=4 SV=1MNKSDMSNRWRNSRFRAKISATLHWLRKVSNVRIIFFTYLLIVLASSLLWSPITHAEEGKNKISYMDAIFTTASAFSDTGLVSVDSYSTWNMFGQAIIATLILSGGIGIFALKIFFISILFPRAKNSVNSMRVIAHERGSDELGTTKQIILHSVATLLIITFISGMFLSLYFYLASPRSTGNIDFHGQFISPKGNVSLAFRYGFFHTISAINNAGFDIIGQNSLMSYYWNIELQLYFAFLFLIGGLGYPVIYDITGFIKHLLTNRKNRQRYIFKLITKISVTTYLITTLIGFSLLCAFEFAAKSNSFASNGDYGNWAQKTWQLFFLSLSTRSAGFSTIQINHLTNGSIIVLTILMFIGAGPVSTGGGVRTTTIAILVLAIFNKILGRPTVRVFKRRIPDETVKMSSIVFCISAFLTFAWVLIISSSLDTYGGKLNAIEYNFVHLAFEVCSALGTSGLTVGVTRDLNIVSKIFLIIMMFIGQFGITSSVLVWGKKANNSFKYEYIQEEVMIG
1.8E-55	198	27.8	2.5E-55	197.3	19.3	1.2	1	Q5WEL0_BACSK	Na+-transporting ATP synthase	ABC2665	Bacillus clausii (strain KSM-K16)	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus clausii, Bacillus clausii (strain KSM-K16)	66692	>tr|Q5WEL0|Q5WEL0_BACSK Na+-transporting ATP synthase OS=Bacillus clausii (strain KSM-K16) GN=ABC2665 PE=4 SV=1MDNKHARLSNSFQIIITAYLLTIFLFSLLLMIPWFHQDGVTLAYRDSLFTAVSAVSVTGLTTISVADTFNGTGIMVLSLAIQLGGIGIMTLGTFTWIVLGKRINLAQRMLIIADQNRVQNHMSGLVLLMRQLLLLALAIECVGGLVLGTYYLRYFDTWTEAYVQGFFAALSAFTNAGFDLTGQSLQPFAGDAVVQLVMILLIIAGSIGFPVLVECREFLLKRKAGFRFSLFTKLTVSTYFLVFAIGALGIWLFESFGAFAGLPWFEQFGHSLFQSATTRSAGLSTIDISQFEQSTLLFMSGLMIIGASPSSVGGGIRTTTLAVMVLTIRGYALGRNRVNAFGRQIHKDDQEKAFIVLSVAALLIAVSLISIAFFERDSGIRLLALIVEVASAFGTCGLTMGETGSLSYPSQIILMCLMFIGRVGIVAMLFSFKKKHTKSHYHYPTEPVIIG
1.9E-55	198	32	3.4E-55	196.9	22.2	1.3	1	A0A089MC30_9BACL	ATP synthase subunit J	PGRAT_26905	Paenibacillus graminis	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus graminis	189425	>tr|A0A089MC30|A0A089MC30_9BACL ATP synthase subunit J OS=Paenibacillus graminis GN=PGRAT_26905 PE=4 SV=1MNNFRFLKLSPPQILVLGFAAVILIGTLLLMLPVSSTSGESLQFIDALFTATSATCVTGLVVVDTGTYFTVFGQIVIMVLIQVGGLGFMTMATLFALVLKRRISLRDRLILQEAMNQGSMEGIVRLIRKVLIYSLVIEAGAAVILSMRWAFDMPLGRAVYFGIFHAVSMFNNAGFDIFGDFRSLTEYVSDPIVNIVVMFLIVSGGIGFIVMSDLVDYRRRTRRLSLHSKVVLSMTAALIVIGTVVIFVFEFTNSRTLGPLNFGGKIWAAFFQSVTPRTAGANTLDIAGLRQASQFFIVILMFIGASPGSTGGGIKTTTFTLMIGAVISMLRGREDIVLFRYRLAQERVFKALTVTLLALLLIVTVSMVLSTTEDRAFLMILFETTSAFATVGLSMGLTPELSQAGKILICLTMFAGRLGLLTLAYAIGPKQGKQLYKYPEGKMIIG
1.9E-55	198	30.2	3.4E-54	193.6	20.9	2	1	R7FU03_9FIRM	Potassium uptake protein TrkH family	BN797_00295	Eubacterium sp. CAG:841	442	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:841	1262894	>tr|R7FU03|R7FU03_9FIRM Potassium uptake protein TrkH family OS=Eubacterium sp. CAG:841 GN=BN797_00295 PE=4 SV=1MEILKRKLSSFQIILLGFAGVILLGALILTLPISSKSHEWTSFIDALFTSTSAVCVTGLIVFDTATHWTIFGQIIILLIQIGGMGVVTIAVSLAVASGKKIGLFSRETMKNAISAPNVSGIVRLTGFIIKGIFLIEIIGALIMLPVFCKDYGAEGIWMAVFHSVSAFCNAGFDIMGTKSGEFTSLTHYSAQPVINITIMLLIIVGGIGFLVWEDICKHKWRIREYRTQSKLVLIVTAVLIVLSAVYFFFFECGDLPVTERILASLFQSVTPRTAGFNTIDLTAISDTGLYLMIILMLIGGSPGSTAGGMKTTTIAVLFSSAFSVFRKKDNAEVMKRRIDDETVKTASAVFLMYITLFLVGGMAISTIENLPITSCLYETASAVGTVGLTLGITPTLGSASKMILIMSMFFGRVGGLTLIYAAFGANKKQVAKLPADTIAVG
1.9E-55	198	32.9	9.5E-54	192.1	22.8	2	1	R6XKE9_9FIRM	Potassium uptake protein TrkH family	BN605_00324	Dorea sp. CAG:317	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea sp. CAG:317	1262873	>tr|R6XKE9|R6XKE9_9FIRM Potassium uptake protein TrkH family OS=Dorea sp. CAG:317 GN=BN605_00324 PE=4 SV=1MDYIENRLHRHITSFQIIILGFFSVILLGSFFLMLPQATQDGMGASFSDALFTATSAVCVTGLVVHDTATYWSFFGQTIIILLIQIGGMGVVTVAVAIATVSGRKISLMQRSVMQEAISAHQVGGIVRMTKFILKTSILIELIGAVLLASVFVRDFGVEKGIWYGVFHSISAFCNAGFDLLGIKEQFSSLTLYARDPVVNLVIIGLIIIGGLGFLTWADVHKNKWHWKKYRMQSKVILVVSAVLIFVPSICFYFFEFSSLPAQERLWSSVFQAVTPRTAGFNTADLTLLSETGQMLMIILMLIGGSPGSTAGGMKTTTIGVLFSSAVSVFQKNESAQLCGRRISDDAVKNAATIFMLYVTLFLGGGMFISSIEGISLMSALFETSSAIGTVGLSLGITPSLGYISRGILIGLMFFGRVGGLTLIFAAFSERNNYHCRLPQEKITVG
1.9E-55	198	19.5	3.8E-54	193.4	13.5	2	1	R5HD95_9FIRM	Trk system potassium uptake protein TrkH	BN469_02206	Firmicutes bacterium CAG:114	465	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:114	1263001	>tr|R5HD95|R5HD95_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:114 GN=BN469_02206 PE=4 SV=1MQLEALCLLLPLVVCLIYREDPKPFLYTIGLVGLLGSLLVRLRARPDFFSREGFAVVGLIWVFLSLFGALPFWFSGEFASFADCFFEIVSGFTTTGASILTEVESLPRGILFWRSFSSWIGGMGVLIFTLAFLPKVGGRTQVLVQAEATGPVSNKLVPKTALSARILYLIYISLTLLEILALCLAGMPFYDAVVNTFATVCTGGFSVRNLSIASYGLPACEVIITVFMLLCSLNFAVFFLVLTGRLRQALGSDELRFFLLAVALSSAIVFFNVLPLYESAGHALRDTLFQVSSVVSTTGFSTADFALWPTVSQFVLVLLMFLGGCAGSTAGGLKASRVLLLLRCARRSLRRLSHPRAVKVVKLDGKAVDEETLNTVFVFFTCFFLVLGGTCLVVSLDGFSLTTSCSAALACISNTGPGLEAVGPLGNFAAFSSLSKVVLSMAMLVGRLEIFPILILFQPSTWGRN

1.9E-55	198	27.1	3.6E-55	196.8	18.8	1.3	1	U5NFV1_9MOLU	Uncharacterized protein	PRV_01450	Mycoplasma parvum str. Indiana	503	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma parvum, Mycoplasma parvum str. Indiana	1403316	>tr|U5NFV1|U5NFV1_9MOLU Uncharacterized protein OS=Mycoplasma parvum str. Indiana GN=PRV_01450 PE=4 SV=1MIKAQAKNKPNKLTIFWRCCVGKNIYQRISRIYFIVVLIGFGLLNIPGISLNGSCKVCSSNGSTNENDIFSKLFISVSAFTTTGLTMN PLHCSFNTWGKIIILVLIQVGGLGLVTSWMFIKHFFLKAKKHTIEERLNLYSERGGMSRGNSFEIVMSALKILLSCEVIIAILLTFFFYFVTP DLSCNNGSQKDFWNSLWNGIFHSVSSINNAGLDILSSKSIMPYSKNWGVILSIIFSISSIIGGIGYPVLYEFKEWCKKKRKHKSSKNIFSL FTKISILMHFLITVIAAGAVLGSEFSENGRTLDKIKHCCLSTGEKVWQLLYLIISARSSGFSGLDLTSLTERTQWILLILMFIGASPSSTAG GIRSITLFLIMGKVWSTMRGRKSLSVFSKTVSSQTIENSFLVFFLSSALVLIASLIIPNSSNGGNNLLRHEKLFEASSAFGTSGLSLGTTT KTNWVGQVVLMVLMYIGQMGVPNVLLYYSKSRPSKQKIIYPEEKLRIA	
2E-55	198	24.3	2.7E-55	197.2	16.8	1.1	1	Q7V5D6_PROMM	Possible sodium transporter, Trk family	PMT_1628	Prochlorococcus marinus (strain MIT 9313)	467	cellular organisms, Bacteria, Cyanobacteria, Prochlorales, Prochlorococcaceae, Prochlorococcus, Prochlorococcus marinus, Prochlorococcus marinus (strain MIT 9313)	74547	>tr|Q7V5D6|Q7V5D6_PROMM Possible sodium transporter, Trk family OS=Prochlorococcus marinus (strain MIT 9313) GN=PMT_1628 PE=4 SV=1MPFPKAVHRTQDLYRRLTVPQFTVVTGLLVIIAGTLILATPVCSNAKVGLWEALFTATSAVTVTGLCIIDIGQDLTNVGQGVLAAMI LAGGLGLMAITTFLQGFVVRGTELRCRLDRGKTLDEFGVGGVGTTFRGIALTATVLILIGAIVLYIFGFNDITNHGERLWAALFHSISAYN NAGFGLWSDSLEHYRSNAVVNIVIIVLIVLGGLGWRVTSDLWSNRKQLQRRNLSLHTRLVIRTSLILILIGTVGLVITESLSQDHFLSSIG WSERLMSSLFGSISARTAGFTTVNLSLESISDSGLLLLMALMFIGASPGGTGGGIKTTTLAALMAATRSTLRGQDDVVIRNRQISDKVV LKAVGITVASLLFVLVMALLLGMSSSLNGEQAFTFLEMLFTCISAFATVGFDVGVTQNLSHFGQLVLIVGMFVGRLGILLLLSAIWEAVN KDRLHRQNRIGYPREDLYV	
2E-55	198	16	1.5E-54	194.7	11.1	1.9	1	U7G8U0_9RHOB	Trk system potassium uptake protein	Q669_05025	Labrenzia sp. C1B10	474	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Labrenzia, Labrenzia sp. C1B10	1397530	>tr|U7G8U0|U7G8U0_9RHOB Trk system potassium uptake protein OS=Labrenzia sp. C1B10 GN=Q669_05025 PE=3 SV=1MNVLGFLYVGLATAMLIPAIVDVAQKNADWQAFVFSALLTGMIGMLLSLAVGGSLREGLDTRQTFVLTTLAWTTLPAFGALPFL WLGIGYADAVFEAVSGFTTTGSTVLTGIDSLPPGLLVWRSLMQWMGGVGIIVMAIVLLPFLRIGGMQLFQSENSDRSEKIVSRSVELIR LIGLAYLFLTFLCIVAYLVTGIELFDAFNHALTTIATGGFSTHDQSFGYFTNPASGWVAIVFMIIGALPFVLIVQALRGHPLQLWRDPQVR ALLGFLAVVALTLTVYLGLNMHFPFDEALLRATFNVVSIVTGTGYALGDYSQWGAPVVGIALLLMFVGGCTGSTTGGIKIFRFLVFFGT VRAHLRRMVRPHRIMSEEYGGTRLTPELSFSVLAFLVVYMGSVGIITVALSFFDLDLVTAISAAATSVGNVGPGLGPVIGPAGHFAPLP DGAKWLLSFAMLVGRLELFTILVLLDPDFWSK	
2E-55	198	27.5	1E-53	192	19	2	1	J1JX38_9RHIZ	Trk system potassium uptake protein	ME5_01721	Bartonella tamiae Th239	466	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bartonellaceae, Bartonella, Bartonella tamiae, Bartonella tamiae Th239	1094558	>tr|J1JX38|J1JX38_9RHIZ Trk system potassium uptake protein OS=Bartonella tamiae Th239 GN=ME5_01721 PE=3 SV=1MGATMILPALVDLRVGNSDWIVFLRASTLTLMLATLVFLATRGSSYRFSARLGFLLTVSLWVTGCLLGALPLYFSHIPLSFASAIFE SVSGITTTGATVLKQLDDLPPGILLWRSLLCWIGGIGFIALALLILPSLRIGGVRLFHMESSDKSEKIFPRINQIANGIIVAYVSLTILCLICYF AAGMSLFDAANHAMTTVATAGFSTHDASLGFFSQTPLVLIIATIFMVLSALPFALYVKLVLPGKTRKLLDPQIILFFLIIAFASISLSSWLYF QNTMTFRHAFLTSLFHFVSIITTGYTSENYLLWGPLAIGFFFIASFIGGCAGSTAGGIKINRLIIFWGVLKAAFTQLLSPNSIVKVRYGHF DVSQNIIIMTVLLFLCLYIFSLIVGATLLMITGLDIISAFTGALTALSNIGPGFGSKIGPVGNFSTIEDPALWVLSFLMLIGRLEIVTVFILFTPA FWQK	
2.1E-55	198	18.9	4.8E-54	193.1	13.1	2.1	1	C4L7Y0_TOLAT	Trk system potassium uptake protein	Tola_0149	Tolumonas auensis (strain DSM 9187 / TA4)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Tolumonas, Tolumonas auensis, Tolumonas auensis (strain DSM 9187 / TA4)	595494	>tr|C4L7Y0|C4L7Y0_TOLAT Trk system potassium uptake protein OS=Tolumonas auensis (strain DSM 9187 / TA4) GN=Tola_0149 PE=3 SV=1MINFKSITFVIGLTLSKLALFMWLPLLMAFFSGTAGTAEFLAAAVLTHIVSLLFIRLGYQQAFRLSVRDMFVMTSLIWLVSCAFATL PFIFLSKLSFTDAYFEAMSGLTTTGSTVMQGLDKMPPAILLWRSLLQWLGGIGFIVLAVAVLPYLNVGGMKLFQMESSDRSEKDSPRM SNVARNILIVYLMLSLICCLGYWFSGMSLFDAINHAMTTLSTGGFSTRDASMSAFSPQAQWIASGFMFLGGLPFILYVQSLRRREGLIF RDAQVRGFFWLVITASLIMSIWLWHSDVFSFEDALRITTFNVISVLTTTGYGLTDFGTWSYMTSVLFVFLMLFGACSGSTAGGLKLFRI QIAGALFQKQARQLMHPAGVFPQKYNGRPVNDAIVRSIVAFVLGYLTVIIVSAILLGMLNLPPLEAISGAITAVGNVGPGFGSTIGPLGNF TSLPDAAKWILSAGMMMGRLEILTVAVLLFPSFWKD	
2.2E-55	198	36.2	1.4E-54	194.9	25.1	1.8	1	B0S1P9_FINM2	Putative potassium uptake protein	FMG_0871	Finegoldia magna (strain ATCC 29328) (Peptostreptococcus magnus)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptoniphilaceae, Finegoldia, Finegoldia magna (Peptostreptococcus magnus), Finegoldia magna (strain ATCC 29328) (Peptostreptococcus magnus)	334413	>tr|B0S1P9|B0S1P9_FINM2 Putative potassium uptake protein OS=Finegoldia magna (strain ATCC 29328) GN=FMG_0871 PE=4 SV=1MKHLKKYLEDNPPLVLILSFLFLIIIGSLLLSLPISQNTTRVPYIDCFFTATSAVCVTGLVTVATYSAWSVLGKIIIIILIQMGGLGFMTF ATLIALVMGRRITLKDRLIIKEQTNSIDMQGMVKLIKYILISTFSIETIGAFLLMTKFVPVYGFKGVFYSFFHSISAFCNAGFDILGPNSLIDIN TNIFVLLIIGLLIVIGGIGFNVILDVLHNNFKFKKYSLHSKIVLTTTILMLSITSILIFAMEFSNPGTIGNLGFIDKITNSIFQAITLRTAGFASINQ SKLLDSSSVLSILNMFIGGSPAGTAGGIKTTTFALLIIVALSEIKGQEDVEVFNRRIRFSQVKKALAIITLSMAWVIFVTFAILVIDKAKYLDV VFEVVSAFGTVGLTRSLTPGINISKIILISTMYIGRVGSLTILYALSNTKNKKAYKEAHENIIIG	
2.3E-55	197	23.4	1E-53	192	16.2	2.1	1	A0A090I3G8_9FIRM	Trk system potassium uptake protein TrkH	ING2D1G_1231	Peptoniphilus sp. 1-1	487	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptoniphilaceae, Peptoniphilus, Peptoniphilus sp. 1-1	875453	>tr|A0A090I3G8|A0A090I3G8_9FIRM Trk system potassium uptake protein TrkH OS=Peptoniphilus sp. 1-1 GN=ING2D1G_1231 PE=4 SV=1MNYAIIFKILGIIFAVEALFMLPPLILSIAIKDGATSSFLITIIILVLLAVATKFFDTKSLRITPGDGLLTVSTAWIAASLFGALPLYFSNSL PTYIDCLFEIVSGFTTTGATVVVNPEILPDSIILWRSMTHWIGGMGILVFTLILLPKIGTGAYQIFKAESPGPVAGKIEPKMTDTAKKLYKIY IVITIVLFLLLLIGKMTPFDAIVHTFGIVGTGGFSSKAKSIGHYSSYGPYIPIVIGIFMIICGTNFTLHNYLYKGKIKNILKDEEFRAYYAIIFGA VTLIAVDLYINNYGGVGKSILDSFFTVTSVSSTSGFVTADYDLWPSFSKYILFLLMIIGSSAGSTAGGMKVIRVVVVFKLVKREVKRILHP HAVIPIRVNGRVLSEEIISGIYAFTAVYMIIALIAATIISLSGIDFLSSISSALTMLSNVGPAFGATGPTRNFLFFAPFYKLVFCVLMLLGRLEF FTLIALFSIFTKKKNPVAD	
2.3E-55	197	18.9	4.7E-55	196.4	13.1	1.5	1	F4KJQ4_PORAD	Cation transporter	Poras_0681	Porphyromonas asaccharolytica (strain ATCC 25260 / DSM 20707 / VPI 4198) (Bacteroides asaccharolyticus)	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, Porphyromonas asaccharolytica, Porphyromonas asaccharolytica (strain ATCC 25260 / DSM 20707 / VPI 4198) (Bacteroides asaccharolyticus)	879243	>tr|F4KJQ4|F4KJQ4_PORAD Cation transporter OS=Porphyromonas asaccharolytica (strain ATCC 25260 / DSM 20707 / VPI 4198) GN=Poras_0681 PE=4 SV=1MRRINLPFVGSIVGGICLIECIFLFLSIVVSLIMRDYTVVPLLVTLGIALLVGIVLLLCGRLKHSDKLGRREAMLAVSMTWLVVALIGM IPFLVGGYLPRFSNAFFESVSGFTTTGASTFTSVEHLPKGILFWRSIMQWQGGIGVVVFSLALSPVLGKDIGLLYQAEVTGVDHDRFM PRIKEVAIRLAAVYTLLTIVLILLLRLTPIPLFDATCMALTCLSTGGFSIYDQPFEVINSPYFETILMIFMVIGGLNMTLIFFAFKGQVKQLFK DEQTRWFLGIILVTAMLVTLHLVISQIQPHLGKAIRDAFFQIVSLISTTGYVYADYGSWGPFFMLCGLFVMLICGCAGSTAGGLKVIRFVI MSKTLPKEIAHRVSPNLVAPLRINGKSVPDEAVYKVMGFFFGYIALIFLGTFCLTFTGNDFISAGTASVSAIGNVGPAFGDYVFNFSSAS SFDLFVLSFLMLAGRLELFTVLSLFAPAFWRR	
2.4E-55	197	22.7	2.6E-54	194	15.7	1.9	1	A0A0F7JSB5_9DEIO	Potassium transporter KtrB	SY84_11640	'Deinococcus soli' Cha et al. 2014	471	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, 'Deinococcus soli' Cha et al. 2014	1309411	>tr|A0A0F7JSB5|A0A0F7JSB5_9DEIO Potassium transporter KtrB OS='Deinococcus soli' Cha et al. 2014 GN=SY84_11640 PE=4 SV=1MSASLPPHAPEPGRASRRKPLLARLNPPQLIALSFAVAILIGGLILTMPGLHGVNEDGTRRSVNFLQALFTSTSALCVTGLNVIDP SRDFNRAGQLVIMLLIQLGGLGIITFGTSFALLSRRRVNFTERMRVAQQVGALNAGGVLGLIRSIFLYTFVIELVGAALLAFRFVPLEGW GRGLFYALFHSVSAFNNAGFALYSDNLMGFVDDPLVSLVIALLIILGGTGFLVQLNVVAHLLSPRRNRLMVHSKLVLTMMAALLVVGTL VYLVFEWSNPRTLAPLGFGGKLLASFFQSVTLRTAGFNTLDYGAMQLPALFMSIILMFIGANPGGTGGGIKTSTFYVMMASAWSMVR GRRDTTLFRRRIDTDTILRAMTVGLLSIGLVNGMFLLLLVFNTRADVLFVNLFFEAVSAFGTVGLSMNTTPLLNPEQHVVLIALMFLGRIG PLTFAVAFNRPDSRALIRYPADKDILIG

2.4E-55	197	16.7	9.1E-54	192.2	11.6	2	1	Q885N0_PSESM	Trk system potassium uptake protein	trkH PSPTO_1801	Pseudomonas syringae pv. tomato (strain DC3000)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas syringae group, Pseudomonas syringae group genomosp. 3, Pseudomonas syringae pv. tomato, Pseudomonas syringae pv. tomato (strain DC3000)	223283	>tr|Q885N0|Q885N0_PSESM Trk system potassium uptake protein OS=Pseudomonas syringae pv. tomato (strain DC3000) GN=trkH PE=3 SV=1MSLPTFRIIGFIIGIFLITLAVAMIVPMATLVIYDRFEDLRSFLWASAITFIAGLALVVPGRPDNVQLRPRDMYMLTVSSWIVVCIFAALPFLLTQHISYTDSFFESMSGITATGSTVLSHLDSMSPGILIWRSMLHWLGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSEKVMPRSHMVAKFIVLAYVGFTALGSLAFWAAGMSLFDAINHAMSAISTGGFSTSDLSLARWPQPAVHWVAIVVMILGSLPFTLYVATLRGNRKALIKDEQVQGLIGLLLITWLVMTVWYANTTDLPWTEALRHVALNVTSVVTTTGFALGDYSLWGNFSLMLFFYLGFIGGCSGSTAGGVKIFRFQVAYILLKTNLNQLIHPRAVMKQKYNGHRLDDEIVRSILTFSFFFTITICLIALMLSLLGLDWMTALTGAASTVSGVGPGLGEVIGPAGNFSTLPDAAKWILSGGMLLGRLEIITVLVLCVPAFWRH															>tr|C4Z7N7|C4Z7N7_EUBE2 Trk system potassium uptake protein TrkH OS=Eubacterium eligens (strain ATCC 27750 / VPI C15-48) GN=EUBELI_20169 PE=4 SV=1MLNPFFNIILVDFNYVRKGEFFMFDNRIRKHLSSFRVITIGFGGLIILGALLLMLPVSSASGCVTPFGDALFTSTSAVCVTGLVVLDTGSYWSLFGQLVIITLIQIGGLGVITVAVAFSLLSGKKVSLMQRSFMQESVSAPVVGGVVRLTGFILKGTFIIELSGALLMMPVFCRDYGLKGIWFAIFHSISAFCNAGFDVLGTADNQFASMTTYACNPVINITLMLLIVIGGIGFVTWEDIKNNKYHFKRYKMQSKLIIVTTAVLITVPAIIFMINDMMTGNEKMPVFKALFQSVTLRTAGFNTVDLNAMKQASVMIMIALMLIGGSPGSTAGGMKTTTFAVLMGNMVATFKRNKNIHFFERRIDNDTVKNAATIAMMYITLFVTGAFIINVTDGISLGKCLFETASAVGTVGLTLGITPQLGILSRIVLIILMFMGRVGGLTLIYAAFSGNGNSYSKFPEEKINIG															>tr|S0L0G9|S0L0G9_ENTAV Uncharacterized protein OS=Enterococcus avium ATCC 14025 GN=OMO_02528 PE=4 SV=1MNKKMVLFTLGKLLKVEAVLLLLPLVVSFIYQEHIGLSYAIVAVFVFLVGLLMSRKLPKNRNIYAREGFFIVGVSWVLLSVFGALPFMLTGEIPSFTDAFFETVSGFTTTGSSILSNLDGLSHASLFWRSFTHWVGGMGILVFTVAFIPLASGRTMHILKAEMPGPVIGKLVSKVRVTARILYVIYAALTLVQIILLILGGMPVFDSILNSFATAGTGGFSMSNEGIAVYNSAYIDGVITVFMILFGINFNLIYFFLIGKIAPVLKSEELRGYLAIIAGSTLLITLNIASQYPSYLKAFRYAVFQVASIITTTGFTTTNYDKWPMFSQTILLLLMFIGACAGSTGGGIKVSRIIMLSKQAIQELKKMIHSRSVTTLNFEGEAIAPKTISNVYSYLVLYLLVFAASLLILSLENLDFQTTFSAVATCINNVGPGFKAVGPTGNFGFLSDFSKWTLSFAMLAGRLEIFPILLLFSKSLWKS															>tr|F4GSS4|F4GSS4_PUSST Trk system potassium uptake protein OS=Pusillimonas sp. (strain T7-7) GN=PT7_1126 PE=3 SV=1MLFLVGLVLLATAAMMLVPMAVDIYYGSEDWRAFALSLGLTVLIGGVLVHYSRRPLKVGLTIRQAFMLTPLSWLSVAVVSALPFFFSSFGSVSGHASNAFFEAVSGITTTGATVISGLDDAPPGMLLWRAILQWMGGIGIIATAIAILPALGIGGMQLFRTESSDRSEKAMPRVRQLATVIGLVYLGLTVLAAIVYWLAGMRLFDAAAHALTSIATGGYSTSDGSFGMWEENGIQWFATAFMLSGSIPFVVYVRFFAGESKALWDRQIKTMLAFISMVVLVLGLWLIFSERYGIEAAFRHAAFNVVSVVTTTGFATTDYSLWGNAVVGLFFGLTFVGGCTGSTSGGIKIFRFEVLAVMMKAHVMRLLYPNGVFSRTYGERVLDDEVIGSVAAFLTVFFLFYFVATISLMTFGLDFLTSASGAATALANVGPGLGDIIGPAGNFSTLPDGAKWILSISMLLGRLELFTVLILFVPRFWRG															>tr|R6CJY7|R6CJY7_9BACT Trk system potassium uptake protein TrkH OS=Prevotella copri CAG:164 GN=BN510_01053 PE=4 SV=1MINSKLIYKILGQLLFIEAFLLFVSLLVAFYYQQDDIFAFIVATLTTIGGGLVLKWRGHGADNSMSRRDAYLVVTLSWIVFSFFGTLPFMVSGYINNFTDAYFETMSGFTTTGATILDDVECFPHGLLFWRSLTQWIGGLGIVFFTIALLPSLVGGQTKVFAAEATGPIKTKLHPRLSTSAKWIWSIYLMLTIACIISYYVAGMNLFDSFNYAMSTTATGGFATHNSSTEFFHSPALEYICTFFCFLSGVNFTLLYAAVIKFKIKDLFKNSEFKFYAFLVAAFSAFIMVELMVMRNYDVEHAFRSAIFQVVSFITTTGLFNDDAAVWPHVTWVVLAACMFFGACSGSTSGGLKCIRGVMLVRMVKNEFRQILHPNAVLPLKIDGVNVPMQKRVTLLAFLTTYLIICLVISFTMIAMGIDNTNAITITLSCVGNVGPTLGTEIGPTMSWSELPDVAKWFCSLMMLIGRLEIFSVLVIFTPAFWREN															>tr|R7KUF0|R7KUF0_9FIRM Potassium uptake protein TrkH family OS=Ruminococcus sp. CAG:353 GN=BN622_01513 PE=4 SV=1MSRFRDLLDDITGGKYSPVKRMSSARIIAAGYLILILIGTCLLMLPFASKGEPPRFADAMFTATSASCVTGLIVYDTFSQWTIFGQIVLIILQIGGMGFMTIISLAALATGRKIGLKERSVLSESVNKPELGGIIRMVKKIATGTFICEGIGALLLSTRFIPKMGLLQGIGNSAFLAISAFCNAGFDLNGQYGAYSSLCEFRSDPVVNITACLLILSGGIGFMVWDDIVKYKLKFRSYRLHSKIALSMTAALTLIGTALFFIFEHNNTAAGLGFGEELLLALFNSVTPRTAGFNTVDTAALSPASTILTICYMFIGGSPGSTAGGVKTVTVAVLFLAAIASMRNDEDINLFGRRLEEDMPKKALSVAAFSLTLIVIGVTAICGIQPELDPTDVVFEAVSAINTVGMTTGITRDLNSISRIIIMLMMYCGRVGSVSFALIFTNTKRYSGVRNPEETISVG															>tr|G8M1Z5|G8M1Z5_CLOCD Trk-type K+ transport system, membrane component OS=Clostridium clariflavum (strain DSM 19732 / NBRC 101661 / EBR45) GN=Clocl_0340 PE=4 SV=1MNYKLIFKLIGNVLRIEALFMLFPLAVSFIYGGGDHPAFLWSILILAAAGTILAKLNPKNKNFRTRDAFVVAGFSWIMLSLFGALPFYFSGYFNSFIDCVFESISGFSTTGSSVLTNVEVLPKGILFWRSFSHWIGGMGILVFIIAVMPSINASSVNLLRAESTGPSPDKIVPKIRETARIMYTIYFAMTVILIILLKIAGLSIFDSFTNAFSVAGTGGFSNTNASIGGYNNIVAEIIMTVFMFLFGINFSLYFTLFGRKFTKFANDIELKIYLGIVITAILIITINISGLYNGIWEALRHSSFQVTSIISTTGFATTDFNLWPTLSKSVLIFLMFTGCCAGSTGGGIKLIRFIILFRAAKVELGKIFHPGSVKTVSINGKKVSNDIVSKTALFFFIYFAIFFVSLLLISIENKDIVSSATAVIASLSNVGPGLGIVGPTGNYATFSSFSKIVLSFCMIAGRLEFFPLLVLFTPHAWKR															>tr|V6F6H4|V6F6H4_9PROT Trk system potassium uptake protein OS=Magnetospirillum gryphiswaldense MSR-1 v2 GN=trkH PE=3 SV=1MSSPPWVAGMNLWTATRNRANSRADSRGEARLIDFRPVIFVNGILLIVLAAAMAVPAAVDWLYDDKDWQVFIVSGLFTLLAGLAMVLGARPEGRPELTTRQAFLLTTSVWVLMTAFGALPFTLSGLKISYTDAFFEAMSGLTTTGSTIIIGLDSMPHGILLWRALLNWMGGIGIIVMAVAILPLRIGGMQLFKMESSDKTDKVKPRTSQVAGGIVMVYVVLTLLCTLFLWLAGMTPFEAFCHAASALATGGFSTSDSSLGNWSNPWIHWILTIFMGLGGATFVLFISPWRRGRWAILTDSQIRWYLHFLVFFTLVLTLWQWAVNDWSPSDALRHSAFNVTSIVTTTGFVSTDYSLWGGLPQIIFFMLTFIGGCTGSTSGAVKIFRWEVLFAMAGVHLKRLLHPHGVFVIDFNRQRISDAVVDSVLGFVVMYFLTFAVFALLLTMTGMDFVTAITGSATALGNVGPGLGNIIGPAGTFQPLPDTAIWLLSFEMMLGRLELFTVLVLFSRSFWRG															>tr|R5LZR0|R5LZR0_9FIRM Potassium uptake protein KtrB OS=Butyrivibrio crossotus CAG:259 GN=BN569_01381 PE=4 SV=1MNPKLKPKNRLTQTRFICLGFIMIILLGTLLLMTPIASRSHTVTPFLDSMFTALSATCVTGLVVVDTFTHWTLFGQLVIITLIQIGGLGFITIGVAFSLLLRNRIGLKARGLMQESINSVKIGGIIKLAKKILVGTFIVEGTGALILGIRFSFDFGFVRGMYYGIFHAISAFCNGGFDLMGRLEPYSSLTYYAGDVVVNVVICSLIIIGGIGFVVWDDITTNGLHFKKYRLHTKIVLVTTAFLLLSGTLLFYITEYNNTMKGMNVGERILASFFSASTARTAGFNSVDTGSLTSASKLLTCVLMFIGGSPGSTAGGIKTTTIFILVVSLWSGITDRHKTAIFKRRFEDDAIKKASIVFTLNMFLAVSALFTILAITDLSLSDVMFEVFSAIGTVGMTTGITRDLSSAARIIIMVLMFCGRVGSLSFALTFLQGKKDPPVYYPEEEISVG														

3E-55	197	25.9	1.4E-54	194.8	17.9	1.9	1	A0A0A2E7N7_9PORP	Potassium transporter	HQ47_02835	Porphyromonas macacae	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, Porphyromonas macacae	28115	>tr|A0A0A2E7N7|A0A0A2E7N7_9PORP Potassium transporter OS=Porphyromonas macacae GN=HQ47_02835 PE=4 SV=1MSRINCKFISRIVGMMCIIEGVVLLFCLLVSLIYRENIFPILISSLVFATIGFVFFLPSKNYREKKIGSREGMLTVTLTWLILSLIGTLPF LLSQSTNNFIDAFFETISGFTTTGATIFTEVENLPKGILLWRSITQWQGGVGIVVFSIALIPLIGGGASSLFNAETTGITHDRFLPRITQVA KRIFTIYLFLTLLLFILLLIGPMELYDAICHSLTCISTGGFSTKNNSIGSYNSPYLEYIVSIFMFIGSLSLALLYFAILRKQPQKLLRDEESRWY AGILGVCVIITMSWLIYHNEYPSIESNFRHALFQVTSLFSSTGYLTADIGSWGAFFGILAVSMMAVNGCAGSTSGGLKMGRFLILLKNLN NEFHKRVSPNQVVPVKVNGHTLAVSTVHQVLAFTFLYFFLILTGAMLLMLMNDHSFIEGISVATSAISNSGPALGSFVNNFEHAGFFTKI IMCFLMLAGRLEVFTVITILTPTFWRK
3.1E-55	197	14.7	3.9E-45	163.7	4.3	2.5	2	D8QVJ7_SELML	Putative uncharacterized protein (Fragment)	SELMODRAFT_22409	Selaginella moellendorffii (Spikemoss)	439	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8QVJ7|D8QVJ7_SELML Putative uncharacterized protein (Fragment) OS=Selaginella moellendorffii GN=SELMODRAFT_22409 PE=4 SV=1YYHLHILYFVGLSLLGALLLRSFGTREGSTHSHLSFLDCFYTAVSAMCLSGLSSIQIEDIPAPGQVLVMVLMVLGGQVLSLVVPLL VKKHRYCKIARMALRPRSFKVVFLEHQAICHLADIVVWYLLAVHLLGFVVAWISIQCSSNAKSVLESKTINPGFFALFATISAFNNVGFVL TNENLVAFNTNSVLLLDLGLVILLGNTLFPVALRGILWLVHRYTTGTKKEVYTLLLEHPRKYYLHLFPKTATLWLLLAVTGSNALGGLIFC ALDWNNEALDGLRPGEKLVNGLFQAFSTRSGGMNSLNLVELSQAMLFFYCVMMYIKPYPVLLRGEQSREDDTTLLTQSRRNLANDN TFLFLLVVFISISLNSQMEKDPRNFNLFAILFEVASAYGCVGLTLGYSCNLRLQPGHCKDTTLSFSGTWNAPGKMFIIAVMFIGR
3.1E-55	197	24.8	1.4E-54	194.8	17.2	1.8	1	C5BKG9_TERTT	Trk system potassium uptake protein	TERTU_4685	Teredinibacter turnerae (strain ATCC 39867 / T7901)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadales genera incertae sedis, Teredinibacter, Teredinibacter turnerae, Teredinibacter turnerae (strain ATCC 39867 / T7901)	377629	>tr|C5BKG9|C5BKG9_TERTT Trk system potassium uptake protein OS=Teredinibacter turnerae (strain ATCC 39867 / T7901) GN=TERTU_4685 PE=3 SV=1MNNRALTLFLLALPLGLMGSVQLVFAGVSHFIFDDHEEVEFLLPALGLVACSLVLLLFKRRINMQSIGYRTALLYAVVTWVAMGV TGAIPIINATGVSFTDGVFESVSALTTTGATVLSGLDAMPKTFLMYRQFLQWLGGLGVVIFVVAVLPMLNVGGMRLLKAETPGPIKDDK LTPRIASTAHYLWLVYLAITLLCALAYWAGGMSLYDAIAHSFTTVSTGGFSTHDASMGYFQSHTLLMISNVFMLAGAINFALHFRVWES RDFIAYWQDEENRVFILTVLAMTAAITWVLVSSHYSELTLETLSDTLFHVISFITSTGYGASSFTEWPVLATFLLVIAGYMGGCAGSTAG GNKFVRNILAVKYVAREMKRLVHNWGMFSIHYQGRAIENSVLNATMSFLFLTAISSLVFSLVLVATGLDFWSSITAVAACVNVLGPAFG ELGSNFQPVSDVGTWVLSFAMILGRLEYFTVLAILSPMFWRR
3.1E-55	197	31.2	4.4E-55	196.5	21.6	1.2	1	C4L2A8_EXISA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	EAT1b_2238	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	460	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	360911	>tr|C4L2A8|C4L2A8_EXISA H(+)-transporting two-sector ATPase OS=Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b) GN=EAT1b_2238 PE=4 SV=1MQQKFMKRNLQLFFRNLTPVQTLVLIYSAAAILSVLLLALPIAHKPGVTITFTDLVFFAVSCVSVTGLTPIVVTDTFSTFGLFIILFIVQ VSGVGLISLHVIMWILLGKRIGFRERQLILRDQNQTSMSGIVKYITEIVITVIAIEAVGAVLLGVHYLNYFDTAGEAFLQGLFGSVSATTNA GFDITGSSLAPFREDPFVIFTQIALMTGGAIGFPVLVEIRTYLVSRITRKRHTFPSRFSLFTKLTVSTFFILIAVGTVGLFIFEYNNAFKDLP LWLALSDSLFQSVTTRNGGLSTVDVNLFSEASMLLLSILMFIGASPSSVGGGIRTTTFAVAVLGVVAFIRGDSSIKIFGREIVLEDIWKAF VIITVSLAVLLSGVMVMAYFEDASLTRILFEACSAFGTTGLSVGLSSEFSNVGKWVLTILMFIGRIGVIAFILILQRRQPKRMYNYPKESIIL G
3.2E-55	197	26.7	1.3E-54	195	18.5	1.7	1	A0A0G1I1H4_9BACT	K+ transport (Trk) system, membrane component	UW45_C0044G0003	Parcubacteria bacterium GW2011_GWC2_44_22	492	cellular organisms, Bacteria, unclassified Bacteria, Parcubacteria, unclassified Parcubacteria, Parcubacteria bacterium GW2011_GWC2_44_22	1618930	>tr|A0A0G1I1H4|A0A0G1I1H4_9BACT K+ transport (Trk) system, membrane component OS=Parcubacteria bacterium GW2011_GWC2_44_22 GN=UW45_C0044G0003 PE=4 SV=1MNLKGIFKIISPVIITVGLAMVGCALAAYLFKEDARPLLAGAFGALVFGVAVYFITRKAGISNLGIEEGCVVVTLSWIIACIFGALPFY VLDLIEHAHSVSITKAIFETVSGFTTTGATIYKNVESLPKSLLLWRSLTQWLGGMGIVVLAIAILPKLGFGGRQAFKMESPGPVKTEKLV PRISETGKILYTVYLGMTAIQIIFLLMAGVSFYDAVIHSFSTVATGGFSNYNNSVAGLGNIYAEYIIAVFMWLAGINFGLIYVMLWRRQLK KFFRNVEFKVYAVITVVAVVLISGSLFFSHYHNWALGRVIRYVVFQVPSVLTTTCFTTADYSRWPVFAVAVLLLLMFIGGSTGSTSGSIK VLRHIISYKLIKHEILKIIRPNLVTTVKVGSQAIEHKVVVSVLAFILIYVATVVVGGVVLTLFDLDLVTALTASIASLGNFGPGLGAVGPASNY VALHPVALWILMFEMIIGRLEIYTVFALFNVALWRRRI
3.2E-55	197	29.5	5.4E-55	196.2	20.4	1.3	1	A3DG02_CLOTH	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cthe_1658	Clostridium thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) (Ruminiclostridium thermocellum)	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminiclostridium, Clostridium thermocellum (Ruminiclostridium thermocellum), Clostridium thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) (Ruminiclostridium thermocellum)	203119	>tr|A3DG02|A3DG02_CLOTH Potassium uptake protein, TrkH family OS=Clostridium thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) GN=Cthe_1658 PE=4 SV=1MRKYIRKLKSLSYPQIIALGYFLIIIAGTFLLSLPIASRNNLFPGLINALFTATSATCVTGLVVFDTYTQWSLFGQVVILLLIQIGGLGF MTVVTMFSIFLKRKIGLKERGLLRESINAMYIGGIVRLTKRILLGTLLFEGIGAVLLSLRFIPKMGLLEGIYNGIFHSVSAFCNAGFDIMGKY GKYSSLTNFAGDAVVNLTIISLIIVGGIGFFVWDDIEKNKYHFRKYQLHTKIVLTMTAILIVSGTICFYIFERNNLLYGMTTGEKVLVSLFGA VTPRTAGFNTVDVASLTSASKLLTIVLMFIGGSPGSTAGGIKTTTLAVIMISLWSSLKNRKGDNIFGRRLEDNALKRSSAVVTVNILLILSA ALLISATNKALGLDAVLFEVTSAIGTVGLSTGITGGLNTFAKIIIILLMYSGRVGSLSFALLFTEHGVTSSIQNPVEKINIG
3.3E-55	197	35.1	1.2E-54	195.1	24.3	1.7	1	R3WJY8_9ENTE	V-type sodium ATP synthase subunit J	UC3_02566	Enterococcus phoeniculicola ATCC BAA-412	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus phoeniculicola, Enterococcus phoeniculicola ATCC BAA-412	1158610	>tr|R3WJY8|R3WJY8_9ENTE V-type sodium ATP synthase subunit J OS=Enterococcus phoeniculicola ATCC BAA-412 GN=UC3_02566 PE=4 SV=1MRKKKRQATKQMTAVQLLAVGFLVLILLGGGLLTLPFFSNSGTFTPFIDAVFTATSAVCVTGLTTLNTVEHWNEFGQFLILLLIEIG GLGFMMMPIIFFTLAKKKISLSTRIVLREALNLDEMSGVMNLMIYILKLAGAIQLIGSVALSFVFIPKFGWLKGIWYSVFHSISSFCNAGFD LLGDSLAGYQSNVYVIMVVSALIISGGLGFLVWRDLLNYKKNRRFSLHTQITLIVTVTLLIGGTLVFFFTEQNARLLAPDASYIERFVNTFF MSVTPRTAGYFSIDYAQMSHAGLIMTMFLMYIGGTSGSTAGGLKTTTFGVLVIQMYSMFKGRTRAEFRERTIRSTAVIRALTLFFLTLT LCVVTIMILSITETIPETSGIEYIAFEVFSAFGTVGLTMGLTPELSFVGKIIIISLMYIGRVGVLTVVFSLITKAQRQEAKYKYPEESVMIG
3.6E-55	197	30.5	5.4E-55	196.2	21.2	1.2	1	D5BH27_ZUNPS	V-type sodium ATP synthase subunit J	ZPR_0851	Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87)	587	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Zunongwangia, Zunongwangia profunda, Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87)	655815	>tr|D5BH27|D5BH27_ZUNPS V-type sodium ATP synthase subunit J OS=Zunongwangia profunda (strain DSM 18752 / CCTCC AB 206139 / SM-A87) GN=ZPR_0851 PE=4 SV=1MSKYKILEYLRRFSFWLSFFAVIAIIFDLGFSHEKFVEIEIRTFYFITLLVGIPSIALRYFIANDRFPNKVRFFDTIIFSLFGLLALAQVD AIRENLVFFEFFNKMGWIYLAIVIYFIRELSRFELKIDREIINPAQLFIISFLILIIIGTLCLMLPKATHNGISFLDALFTSTSAVCVTGLIVVDTG SYFTTFGQSIILVLIQLGGLGIMTFASYFSYFFRGSTSYENQLMMKNVTDSETLGEVFSALKKILFITFVFEFIGGLLIYMSLDPQLFETVG DRIFFSVFHTISGFCNAGFSTLEYSLYQPEYRFNFPLHIILSVLFILGGLGFPIVLNIYKYGKYFIKKNFLRFKRPDQPVHMPWILNLNSRIV LVTTAILLVGGTVFFMFFEYNNTLKDYNFLGKLAASFFGSSTPRTAGFNSVDMGALHFSTIMVIMFLMWIGASPGSTGGGIKTSTIAIAT LNFLSLAKGKDRVEVYNREIANNSLRRAFAIMTLSILFVGLSILMISYFDPDMHLLDVAFESISAYSTVGLSLGITANFSGASKIVIIMTMFA GRVSMLTIMAAFLADVKHLNYKYPTEEVLIN

3.7E-55	197	14.5	2.4E-53	190.8	10.1	2	1	R7B1I5_9BACE	Uncharacterized protein	BN656_00252	Bacteroides pectinophilus CAG:437	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides pectinophilus CAG:437	1263051	>tr|R7B1I5|R7B1I5_9BACE Uncharacterized protein OS=Bacteroides pectinophilus CAG:437 GN=BN656_00252 PE=4 SV=1MNYGIIRYIIGKVIEIEGAFFVIPVLTALVYHEWSGLGVYVLLACLYMFAGFIMSSKEPEKKEFYAREGYVLAALAWIIMSILGAIPFV ITGDIPSMADAVFEIASGFTTTGASILASPEPLLKCNLMWRSFSHWIGGMGVLVFLIAILPSGGGESIYIMRAESTGPSVGKIVPRIKQTS KILYEIYTALTFILFVLLVLGRMPVFDAICLTFGAAGTGGFGILADSVASYNTYCQVVITIFMLLFGVNFTFFYMLLIGKARDAFRMEEVRG YLAIYCAITLLITLNLWAQNGHFMHQLQQVSFQTSSVMTTTGYSTQDFNAWPQFSKILMGLLMAIGGCTGSTGGGIKVSRILVYVKGII KEISEQVHPRRVKVLRVDGKRVDDSILRAIYIYLALYTLIFVISLVIVGIDGYDWETTFSAVLATININGPGFGLVGPTGNFGMFSVMSKLV LTFDMIAGRLELIPLFVLLMPDTWKKNG
3.7E-55	197	18.8	5E-55	196.3	13	1.1	1	Q7U4A3_SYNPX	Possible sodium transporter, Trk family	SYNW2168	Synechococcus sp. (strain WH8102)	469	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain WH8102)	84588	>tr|Q7U4A3|Q7U4A3_SYNPX Possible sodium transporter, Trk family OS=Synechococcus sp. (strain WH8102) GN=SYNW2168 PE=4 SV=1MPLRQAIERSQGWHRRLTVPQFTVVTGLLVILLGTLLLATPLCSSSKVGLWEALFTATSAITVTGLSIIDVGADLTTAGQLVLAMMI LAGGLGLMAITTFLQGFVVKGTGLRRRLDRGQTLDEFGVGGVGSTFRGIAATAALVILVGALVLYGFGFSDIPDRGERLWASVFHSIS AYNNAGFGLWSDSLERYHDNVLVNAVVMVLIVMGGLGWRVTSDLASQGVRRGRRRLSLHTRLVLRTTLLLVVFGTLGLALTEWLNR GEVFIGMAWRERWMTALFESVTARTAGFTTVPFSLENITDSGTLLLMALMFIGASPGGTGGGIKTTTVAALMAATRSTMRGRDAVVIR NREIPDKVVLRALGITVASLLFVLAMALLLSIASNLNGAEPFTFLEMLFTCISAFATVGLDLGVTEQLGRFGQAVLMLGMFVGRLGILLLL SAIWEVMTREQIHIHRQNRIGYPREDLYV
3.8E-55	197	15.6	6E-55	196	10.8	1.2	1	W0J0F4_9BACT	ATPase	OPIT5_08600	Opitutaceae bacterium TAV5	610	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Opitutae, Opitutales, Opitutaceae, unclassified Opitutaceae, Opitutaceae bacterium TAV5	794903	>tr|W0J0F4|W0J0F4_9BACT ATPase OS=Opitutaceae bacterium TAV5 GN=OPIT5_08600 PE=4 SV=1MLPARNATSTKRTDARSRAVVFFLLNTLLVLCSVAALALFVLVAGWPLEPETHQLVRIATGLVLKLFVFQEACRMWLQRHRMT WLKTRRLEAGLCMLIVLEMILGPRLHGWLNHHFPDIGSGTLTLFILAASQLTLLALICLRALRRNRLLATRRLTPGMALILSFALLIVIGTL MLKTPRATTQGIGWIDALFTATSSVCVTGFGTVDITTQLTRYGQWIVLGLVQTGGLGIMTLTYFFAHFLTGGVSLRNRIALQNLLSEDN LGQIGTVLGMIVGFTLTVELAGAVAIWLLAGQGSVAATPIVAGDRAFFALFHAVSAFCNAGISTLPGNLTDPALAGIGMKGVLVVIMLLV VAGGIGFPVIRNLHEVVIARIRQRIGLRLATPPRITTNSRVVLVTTAVLLAGGAVLIYITEFATGNGDPGALGPWMAAIFHSVAVRSAGFN VIDTANLAPATVILTMFLMFVGGSPSSTAGGIKTSTLAVAVLALRRVLLGRPEIEAFGRRISDDIANRALAVLLLAGAFVTLVATTLCVLHP ELPALDLLFEAVAAVSTAGLARGVTSQLGDPAKLVMIVAMFVGRIGVLMFLLSFIRRRDHKGYRYPGATIVIT
3.8E-55	197	7.9	6.1E-55	196	5.5	1.2	1	D3PQU1_MEIRD	Cation transporter	K649_04945	Meiothermus ruber (strain ATCC 35948 / DSM 1279 / VKM B-1258 / 21) (Thermus ruber)	495	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Meiothermus, Meiothermus ruber, Meiothermus ruber (strain ATCC 35948 / DSM 1279 / VKM B-1258 / 21) (Thermus ruber)	504728	>tr|D3PQU1|D3PQU1_MEIRD Cation transporter OS=Meiothermus ruber (strain ATCC 35948 / DSM 1279 / VKM B-1258 / 21) GN=K649_04945 PE=4 SV=1MKRKTKPWLITNLRFAYYFLGVVYLALGAVMLGLEVLSLALGESPWGFLLGTAVGLSLGWWFRSLGDPRHEPGRAEALLSIALI WLLVPLLGAIPFWVAGGMNYLDAVFEAMSGFTTTGATVLANFEQFGYSLFFWRSLMQWFGGVGILVLVVALLAHLAVAGRQLFITES TGIQKEPFTPRLRTAALSILKVYTSLTLAAALCYWIAGVPAFEAICNALTTLPAAGFSPNPRSFETYSPLAQWFGTLFMFLGGAGFVLQ YRLFFTRDPRPLLRDVELRVYTLIVLVFSTALAAFLITHHAQDMNYTWSDAIRHAFFNVTSIITTTGYASADFALWAPAAQAILVAAMFV GGCAGSGAGGIKVIRWLVVGAIVRRELIRSLHPQAVMTLRLGNKSLGEDVMRSVAAFITLYAALVAAGAVLISLLENDFVVGFTASAQA VGNIGPGLGEVGPMGSYAGLEPLSKLILIVQMWAGRIELIPVFLLLTPELWRKLKG
3.8E-55	197	26	8.3E-54	192.3	18.1	2	1	R5TM93_9CLOT	Potassium uptake protein KtrB	BN544_02896	Clostridium hathewayi CAG:224	451	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	1263067	>tr|R5TM93|R5TM93_9CLOT Potassium uptake protein KtrB OS=Clostridium hathewayi CAG:224 GN=BN544_02896 PE=4 SV=1MNEKKLIHARRHVSQTQFIAYGFFCVIITGTLLLMLPFASRDGQSEPFLNCLFTATSASCVTGLVVADTWSQWSLFGQLVILTMI QIGGLGFITVGVFISIILRRKIGLKERGLMMESVNTLQIGGVVRLAKKIIIGTCIFEGTGAVLLAIRFIPQFGFLRGLFYGIFHSISAFCNAGF DLMGGQAPYSSFVAYYDDWLVNLVIMSLIVIGGIGFIVWDDLSRNKLHFRKYMLQTKIVLVTTAILVFGGGLLFYLMERNNLLVGMNTS GKILTSLFSSVTARTAGFNTTDTAALTDGSKLLTIILMFVGGSPGSTAGGIKTTTLVVLLLCVHSNIKQTYGINIFGRRLENDAVKRAGTIL TINLLLALTASLAIMAIQPLGFSDILFETFSAIGTVGMTTGITRALHPVSRLIIILLMYCGRIGSLSFALAFVQSKRKPHVQQPAEAINIG
3.9E-55	197	23.9	1.1E-53	191.9	16.5	2	1	R7QVA8_9FIRM	Cation transport protein	BN520_00792	Roseburia sp. CAG:182	492	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:182	1262942	>tr|R7QVA8|R7QVA8_9FIRM Cation transport protein OS=Roseburia sp. CAG:182 GN=BN520_00792 PE=4 SV=1MNYSMIRYILCSVLGFEGLFLLLPALVGAIYGEKEGLVYLAVAAASLLLGMLGRIKKPKSSVFYSREGFSAVSLSWIVLSLVGAVPL RLTGEFPSYVDALFETISGFTTTGASVLSSVEELTHATAFWRCFTHWIGGMGVLVFIMAILPLSGSSSLHLMRAESPGPSVGKLVPKIR STAMILYGIYLLITLSEMVALKIAGMSVFESVTLTFSTAGTGGFGLVNTSIASYTLAVQIIITVFMLLCSINFNVYYLFLIRRPKDALLNEEVR YFLIIVFTSAALITVSIHGQYKSVFYAFHEALFQVASVVSTTGFATADFNLWPEFAKMILVGLMFIGACAGSTGGGFKVSRLMIVFRAVK NEIQSVTHPRSVQKVRMDGRRVPDNVVKSALCYMAGYFLILLISILLLSLNGYDMTTNVTAVMATFNNVGPGLNMVGPTGNFGAFNIF SKFVLMFDMLIGRLELFPMLVLFAPGMWRLPARRADRKEPGLDI
3.9E-55	197	19.7	8.6E-54	192.2	13.7	2	1	R6VAW7_9FIRM	Trk system potassium uptake protein TrkH	BN546_01088	Firmicutes bacterium CAG:227	482	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:227	1263010	>tr|R6VAW7|R6VAW7_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:227 GN=BN546_01088 PE=4 SV=1MNYSIIAYIIGWILNFEALFMALPCITAIFYHEHSGWAFFLSAMFCLLIGIPLVQKKTKNKIFYTREGCVTVALSWIILSIMGALPFLIG GVISNPIDAVFETVSGFTTTGASILPDVESLPKCMLMWRSFTHWIGGMGVLVFILCLLPLTGGDGGYHINLMKAESPGPSVSKLVPQV QSTAKILYSIYLTLTVIEFVLLLFGKMSVFDALTTSFGTAGTGGFGIKNDSIAGYSPYIQYVVTIFMILFGINFSAYFLLLSKKLRQAIHMEE VRWYLIIIFASIVFISFNARAMFSTLEETIRHVSFQVASVITTTGFATTDFDLWPEFSRTILVILMFIGACAGSTGGGIKVSRFILLIKTMKKE LHTYLHPRSVRKIQMDGKVVEHNVLRSTNVYMIAYILIFVASVLLISLDNFDLTTNFTAVSATLNNIGPGLALVGPTQNFSLFSNGSKLILI FDMLAGRLELFPLLLLFVRDSWRRF
4E-55	197	16.3	9.9E-30	112.9	3.4	2.1	2	R7N4J8_9FIRM	Cation transport protein	BN816_02181	Firmicutes bacterium CAG:95	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:95	1262988	>tr|R7N4J8|R7N4J8_9FIRM Cation transport protein OS=Firmicutes bacterium CAG:95 GN=BN816_02181 PE=4 SV=1MNTGKIMNIIGRILFVEVLLMLPSLFVSLIYRDGDTKAFVYTMIPAAIVSVLLMLVRQQQKRMSSRDGYFIVAMAWIIISIVGAFPLYL AGGFASYWGALFEIVSGFTTTGASVLAEPGTLGHGVAFWRCFTHWVGGMGVLVFVLMVIPMENDNSMHLVRAEVPGPTAGKLVPR MRTTSMILYGIYAVMTLILVVILKCLGMKVFDAFCIGFGTAGTGGFALNSAGIAGYGSPAIEIVLGIFMILFGINFNTYFLLLLRKFKEALTS EETAVYFGVIGVSVVAISINILSCFSNTGEAVRSAFFQVASIITTTGFATVDFNLWPEFSKHLIVLLMIIGACAGSTGGGLKISRVIILFKSFI AEIKQILNPKEVVSIRLNGKNVDKKTLNSTRIYFGAYVILICIFTLIISLDGLDLTTNLTAVLSCFNNIGPGLNLVGPMENFGLYSDWVKVVL SLAMLTGRLEIFPMFLLFAKSAHDR
4.1E-55	197	18.1	4.9E-30	113.9	3.5	2	2	Q92YF2_RHIME	Trk system potassium uptake protein	SMa1691	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Rhizobium meliloti (Ensifer meliloti) (Sinorhizobium meliloti), Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	266834	>tr|Q92YF2|Q92YF2_RHIME Trk system potassium uptake protein OS=Rhizobium meliloti (strain 1021) GN=SMa1691 PE=3 SV=1MNASLFRHAMHIAAILGLYLSAAMLIPAMLDLYYGHYDWQVFAAAAFVTSGLSATTFMATRGGPPPFSKKFGFLLVNVLWSAFA LIGALPLWMSSLDLDFAQALFESVSAITTTGSTVIVGLDDAPPGILIWRSLICWLGGVGIVVLGLFIIPYLRVGGMSFFKMESSDTNEKPF ARLATFSRAFFTVYVGITLLCAIGYNLTGMNRFDAINHAMSTVATGGFSTHDASFAYFGSIPLLWTATFFMTLCSLPFSILIVFVARGRL DALRDPQIFVFLAYLTVFAFSVAIYHRLTNGVEFHIALAHAFFNFSSILSTAGYMSEDYQLWGPFVVMAAFIATFMGGCSGSTAGGIKA YRFIVLFNAIHSGLRKLIYPAAVYPVRYGRNSLDADTLRAILLFFVTYILLWIFGSLTMAALGYDFLTAVSAVITCLSNVGPGLGTLVGPAG NFSTLEDPELYLLSLMMMMGRLEVLTVLVILTPVFWKQ

4.2E-55	197	22.8	7E-53	189.2	15.8	2	1	M1NZ81_BARAA	Trk system potassium uptake protein	trkH BAnh1_08710	Bartonella australis (strain Aust/NH1)	464	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bartonellaceae, Bartonella, Bartonella australis, Bartonella australis (strain Aust/NH1)	1094489	>tr|M1NZ81|M1NZ81_BARAA Trk system potassium uptake protein OS=Bartonella australis (strain Aust/NH1) GN=trkH PE=3 SV=1MLLPIFVDLCDGNRSWVTFLHPCAVTVMLATLILLATRGSTCRFSARLGFTLTVCLWLTGSIVGALPLYLSPLPISLAGAIFESVSG ITTTGSTVIIGLDYLPRSILLWRSIMCWIGGIGFIGLALLLLPSLRVGGVQLFHMESSDKSEKILPRINQIANGIITAYIGLTLACMISYFAAG MTLFDSVNHAMSTIATAGFSTHDTSFGYFSNKPAILIVATIFMLFSALPFVLYVKLVLPGHSKRSIDPQVIVFLNIVFFFSLALAVWLRFHN HLAFHSAFLDAIFHITSIISTTGYSAKDYQLWGPFALGIFFIVSFAGGCAGSTSGGIKINRLIILWRIAQANMAKLLSPNAVVKVRYDHSNV SSDIAKAVLLFVCLYMSCLLTGTALLLTTGLDFTSAFTGVLTALSNIGPGFGDIIGPAGNFSTINDNALWILSFLMLVGRLEIVTIFVLFIPA FWRKQF
4.4E-55	197	27.7	4.3E-53	189.9	19.2	2	1	R5HPQ5_9FIRM	Uncharacterized protein	BN501_01989	Roseburia inulinivorans CAG:15	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia inulinivorans CAG:15	1263105	>tr|R5HPQ5|R5HPQ5_9FIRM Uncharacterized protein OS=Roseburia inulinivorans CAG:15 GN=BN501_01989 PE=4 SV=1MPELIRKKKKMSSFEMIAFGFAGVILFGAIILMLPISSSAGVVTPFDKTLFTATSAVCVTGLVVVDTGSYWSAFGQAVILLLIQTGG LGVITVVASFSMVSGRKISLMQRSTMQDAISAPKVGGIVRLTKFILQGTFLIELVGAILMLPVFCRDYGWKGIWMSVFHSVSAFCNAGF DILGTTEQTFPSLTGYIANPLINLVIMLLIVIGGIGFLTWDDFCTNKWNLKRYRLQSKIILVTTAVLILLPAVFFFLIDFTGFSVGKRILASLF QSVTLRTAGFNTADLGAMSDSSKAIMILMMLIGGSPGSTAGGMKTTTIAVLILNAFATFGREPETEVFGRRFDNTVVKNAATIAILYFFL FFAGGIAISQIEHVALSDCLFETASAVGTAGLTLGITTELGLVSHLILVVLMYLGRVGGLTLIYAAISVKIQSGAKRPLDKITVG
4.5E-55	197	34.7	1.4E-53	191.5	24	2	1	R5G2D4_9FIRM	Potassium uptake protein TrkH family	BN756_00396	Coprobacillus sp. CAG:698	444	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:698	1262856	>tr|R5G2D4|R5G2D4_9FIRM Potassium uptake protein TrkH family OS=Coprobacillus sp. CAG:698 GN=BN756_00396 PE=4 SV=1MEIMKPKKKLSSFQIILLGFAGVILLGTFLLMLPISSQSHQWTSFIDALFTSTSAVCVTGLVVFDTSTYWTIFGQIIILLMIQIGGMGV VTIAVFLAVISGKKIGLFSRETMKSAISAPNLSGIVRLTGFIIKGILLIELLGALIMLPVFCIDYGAEGIWYAIFHSISAFCNAGFDIMGSKSGE FTSITYYSAQPVINITIMLLIIIGGIGFLVWEDVCKYKLQLKNYKTQSKVVLIVTAIIIVLPAIYFFFFEFTDLPMGERILASLFQSVTPRTAGF NTINLTLISDTGLYLMIILMLIGGSPGSTAGGMKTTTIAVLFSSTISIFRKKDNAELMKRRISDETVKTALAIFIMYITLFLFGGMAISKIENLPI TSCLYESASAVATVGLTLGITPSLGIISKLILILSMFFGRVGGLTLIYATFGANKKQIAKLPTDTIAVG
4.5E-55	197	22.1	9.3E-55	195.4	15.3	1.4	1	A0A089N5Z0_9BACL	ATP synthase subunit J	PSTEL_14980	Paenibacillus stellifer	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus stellifer	169760	>tr|A0A089N5Z0|A0A089N5Z0_9BACL ATP synthase subunit J OS=Paenibacillus stellifer GN=PSTEL_14980 PE=4 SV=1MFNLLLKRLRLTPPKILSLGFIILIAIGTVLLALPISSQEGHMSWIDALFMATSATCVTGLAVVDTGTGLSTFGQLVLLVLFQLGGLG FVTMATLITLVLNRKISLKERLLLQESMNQNSMQGIVRLIRRVLIYSVVIQLSGALVLALRFLKDMSAGKAVYYGIFHSISIFNNAGFDLFG DVHGPFSGLTRYAEDPVVNITAMLLIFLGGIGFIVLSDLVDFTKRRRLTLHSKVVLTTSAFLIGAGALFFFWLEVYHSLKPLHTGGKIMAS FLQALTPRSGGVTTLDIQALRESSQFLIIVLMFIGAAPGSTGGGIKVTTFALLLAAVYSRIRGREDVVLFRNRLSKDNVYRAITMTLLSLLL VVAATMLLSITEQADFLAVLFEAVSAFGTSGLTMGLTPELTEAGKILIVILMFVGRTGPLTLAYAIRPKKDKQLYRHPEGQIMIG
4.6E-55	196	26	2.5E-28	108.2	7.3	2.1	2	F3ZNL1_9BACE	Cation transporter	Bcop_2394	Bacteroides coprosuis DSM 18011	482	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides coprosuis, Bacteroides coprosuis DSM 18011	679937	>tr|F3ZNL1|F3ZNL1_9BACE Cation transporter OS=Bacteroides coprosuis DSM 18011 GN=Bcop_2394 PE=4 SV=1MINTKLILRIIGVLLLIESAMLLCSTAVSFFYQEDDLNSFLLTTGLTAACGAILTLLSKGAEKYLGRRDGYFIVSISWIIVSLFGMIPFY HSGYIPTITDAFFETISGVSSTGSTILDNIEEFPHGLLFWRSMTQWIGGLGIIFFTIAVLPLFGVSSIQLFAAESSGPTHDKVHPRISVTAK WIWSIYAGMTIIETFLLCAGGMTFFDSICHAFGTTGTGGFSTKQTSIAFYNSPYIEYVISFFMILSGVNFTILLLFVTGKFQKVIKNSELKY YLGSVLVLTLVITVGLYYTSNYGLEEAFRKAIFQIGSIHTSTGFATDNYMNWNPFLWGILFIPMIIGACAGSTSGGFKCIRIVILSKITKNEF KRIIHPNVVLRVKVNNQILPNTVQSTVLAFSFIFIIIVLFSTLSLMAMGVEFLESFGVVISSISNMGPGFGKFGPDFSWSALPQTAKWISS FLMLCGRLELFTILLLFTPSFWRG
4.9E-55	196	11.6	6.6E-53	189.3	3.5	2.2	2	S7Z3R7_PENO1	Uncharacterized protein	PDE_00096	Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	624	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Penicillium, Penicillium oxalicum, Penicillium oxalicum (strain 114-2 / CGMCC 5302) (Penicillium decumbens)	933388	>tr|S7Z3R7|S7Z3R7_PENO1 Uncharacterized protein OS=Penicillium oxalicum (strain 114-2 / CGMCC 5302) GN=PDE_00096 PE=4 SV=1MASLLESKLLPLHLAYFFLFSMIGSGILYATSTQIVNLPYVDALFMSVSAMTGAGLSVVDPSVLGTLPQITIFILFILGHSIPINGVITL LRALSLRKRLIRGQEATEKGHIDCQESLPEKHMIPTEICSIVNPAKSLSPLKTNVTDREIPADGPSPVGSEDMRHSRGPLIFTFARSPSR VSAGPTATRERPKLAKLGSVLAMAGSKIDSLMAHKDHVGTLNTTSEDWTEYRALMIISVSTLSYAVICPLIGILSVGFWFQMCRPDVPR EDGVAPFWAGAFLVMSSFANNGMSLVNRNMEPFQREAAPLLICGILILAGNTLFPCLLRLVIWTSRRMIPLTPKWAIWRQTFDLVLTQ PQNLCGFLYPAGHTWFLVGTVVLLNVIMWGGFELAALRDLEIGTLPPKFRVLDGLFQAFAIRGGGFAVVAIDKLPQALLVIYAIMMYLS ALPTCAAFKDTFSPQISEAGNASCLEAGVAGFRNGTRHGAESMLCRSTFYYERLRSHLSRDMWWLSFAVIIICVAESRKFIDFPLAFS TFNIIFEVVSAYSFVGVSVGYPGKTYAFCGEWTSFSKLLLIMISVVGRHRDVPNMIMRKPRFVNIDQTVHRQTIAPGCDLELVPAHARL D
4.9E-55	196	37.1	6.6E-55	195.9	25.7	1.1	1	A0A0A8JKS9_BACSX	Trk-type k transport systems, membrane	OXB_1863	Bacillus sp. (strain OxB-1)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus sp. (strain OxB-1)	98228	>tr|A0A0A8JKS9|A0A0A8JKS9_BACSX Trk-type k transport systems, membrane OS=Bacillus sp. (strain OxB-1) GN=OXB_1863 PE=4 SV=1MKFSRENLRRFTPAQIIVFYYFLAIAFSYLLLNLPGVYLPGVEVSFLDSLFTAVSAVSVTGLTPISIAGTYSVFGLCMLMLVLQLGGI GIMSIGTFFWLLVKKRIGLRERQLIMVDHNQYSLAGVVHLIREIVKIIFLVEMIGGLLLTIYIRPFFETFSDALLHGMFLAVSATTNAGFDIT DASLLPYFNDYFIQTVIMVLIILGAIGFPVLIEVKSYFSNKVPNFRFSLFTKITTTTFGILLVFGALMIFLLESVHSFKGLAWHEKVFASLFH SVSSRSAGLTTYDITEFSEATDIFISSLMFIGASPSSVGGGIRTTTFAIALLFIINFARGNQVINIFHRQIKLIDVFRSYAVILLAGAMVMAAL LILLITEPGIPAVTLLFEITSAFGTCGMSLGITSELSPIGKMIIMILMFIGRVGLISFLYTLGGKTKTIHYHYPKERVIIG
4.9E-55	196	27.4	4.6E-28	107.4	11.5	2.1	2	F0T884_METLA	Potassium uptake protein, TrkH family	Metbo_0244	Methanobacterium lacus (strain AL-21)	479	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium lacus (strain AL-21)	877455	>tr|F0T884|F0T884_METLA Potassium uptake protein, TrkH family OS=Methanobacterium lacus (strain AL-21) GN=Metbo_0244 PE=4 SV=1MIAYLRRKDFYLIFKNLGTVMEGIGIVMLIPLIVALIYGENDFAGFLVAGILSMSIGYVLKIKFSDSINLKLKHGMIIAALAWLWAALM GSICLMYATDISFLNAYFESMSAWTGSGLTMYTNVQILPQSVLFLRSLEQWVGGLGVVIVVIGILIRPGTAASRLYKAEAREEKIKPSIA NTVRTIWWIYLFYTILGIVLYILAGMSLFDAINNCFTNLSTGGMSIKNDNIGFYNSVPITIVTILLMILGGTSFLVHYKALKGRIWDVFRDIQ FQAMVIIVAVFSIMLFTVSHFTSLNSIFYIVSALSCTGSNTVTAGTMFGWTDYTKVILIVCMIIGMAAGSTTGALKLIRVVTLIKGIYWEVV KVLSPEGSVFPRKISGKTVKDAEIKEAGSYTFLYLFFILITWFIFLSYGYGGIDSLFEIASAQGNVGLSVGITGPTMPKLPEILLIIGMWIGR IEIIPALVLLKGSFDLFKRFNR
5E-55	196	22.8	2.9E-54	193.8	15.8	1.8	1	G8PR70_PSEUV	Trk system potassium uptake protein	PSE_3993	Pseudovibrio sp. (strain FO-BEG1)	471	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Pseudovibrio, Pseudovibrio sp. (strain FO-BEG1)	911045	>tr|G8PR70|G8PR70_PSEUV Trk system potassium uptake protein OS=Pseudovibrio sp. (strain FO-BEG1) GN=PSE_3993 PE=3 SV=1MLGYFLVGLAILMLAPALLDIYFSNPDWIAFALSSLFVGLLGLLLAVSTANYKLEHLTIRQAFLLTTTSWFVMPVCGALPFLSLGIG FENAFFESVSGFTTTGSTVLIGLDGMPPGLLFWRSLTQWIGGIGIIVMAILLMPLLRIGGMQLFRTESSDRGEKIVARATDLTRLIGGVYI MLTLTCAILYVFSGMSLFDAVNHAMTTLSSGGFSTHDASFAYFESTAAEWVAVVFMLASGLPFVVLIKSLTKNPMALLQDPQARAFIFV IIILSSMTALYLGIENKFTFGRAVVEALFVVISIITTTGYGLGDYTAWGPPMMGFFLMLTFIGGCTGSTSGGIKIFRFIVFFGTVRAYMNK MIRPDQVVPVRYGDTKITPDLAFSVLAFLVVYMATVGLITVILGGLGLDLVTAMSAATTAVSNVGPGLGDVVGPVGNFADIPSSAKIVLS AAMLLGRLELFTVLVLFNPEFWR

5.1E-55	196	17.2	6.8E-55	195.9	11.9	1	1	A0A075U3A1_9CORY	ATPase	CATYP_08330	Corynebacterium atypicum	462	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium atypicum	191610	>tr|A0A075U3A1|A0A075U3A1_9CORY ATPase OS=Corynebacterium atypicum GN=CATYP_08330 PE=4 SV=1MLPVVAMQNSPGWLHPARLTAVGFLALILLGTGLLMLPTSAVGEHATPFLPAFFTATSAVSLTGLIVVDTATYWQPSGQAIILALI QLGGLGIMTLAALSGMVLTGRISLRARQRTAAEGRPVIHGSIKHTLVSTLAVTLLCEAVVAGVVGTRVWCTGQVSVARAAWVGVFHAI SAFNNAGFSTYSDNLAGFSHDAWVLIPLAFALIVGGLGYPVLAEVLRLARGIATRALHRTHPRVHRVSITAKMTFIATLVLLVGGTGFLL AVEWNGWFSGMPVGTRILNAFFQAASPRTAGFNTMDYDQAHPITLMGTDVLMFIGGGSAGTAGGVKVTTACVLIASMAAEFLGRED TTVGRRRLPLTVVRQALALAVAGIAVIAFGVAVLRIFDPQFTGDQVTLEVVSAFATVGLSTGITAKLTAASQVTLCFIMYLGRVGPTTLV AALAARSFPHRYRYPEERPFIG
5.2E-55	196	35.3	6.5E-55	195.9	24.4	1.1	1	S6A959_9SPIO	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	TPE_2532	Treponema pedis str. T A4	406	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema pedis, Treponema pedis str. T A4	1291379	>tr|S6A959|S6A959_9SPIO H(+)-transporting two-sector ATPase OS=Treponema pedis str. T A4 GN=TPE_2532 PE=4 SV=1MFTSVSAVCVTGLSTLSMDIYSRTGFIIIMLLIEFGGLGIITFVSFYIALPAKKVSIVNRKLIRDFFIDDIEYRPRRILKRILTYTLIIQLIG FILLMCGLYLAKDENFIFNALFISISAFCNAGFSTTSNSLSGFAENKYILSVIMILIILGGIGFAVITNLVQKIKSFFYTKKEYISVHTKIVILMT LFLIITGAVYNFIFEFNYAFNNLPLPQKILNSLFQSITLRTAGFETLPQNKFTPPSTLLHIVFMFIGGSSGSIAGGVKTTTVFIAFLYAFNGD EEVNAVIYKKRQISAQIVNKSITIISRSFIILFCSIFLLALAENVKLTNGTFSSIDIIFECTSAFATVGLSRGITGELNFAAKIIIILTMFIGRTGVF AMALKINKSKNSLNTVSYPKETVMVG
5.4E-55	196	15.2	1.9E-54	194.4	10.5	1.7	1	Q3SMR6_THIDA	Trk system potassium uptake protein	Tbd_0022	Thiobacillus denitrificans (strain ATCC 25259)	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Hydrogenophilales, Hydrogenophilaceae, Thiobacillus, Thiobacillus denitrificans, Thiobacillus denitrificans (strain ATCC 25259)	292415	>tr|Q3SMR6|Q3SMR6_THIDA Trk system potassium uptake protein OS=Thiobacillus denitrificans (strain ATCC 25259) GN=Tbd_0022 PE=3 SV=1MSAILPVIHILSKVLMLFALAFALPLGISVALEDGAERAYDEAIAIAFVSGLVLWMLSRRGRRELQTRDGFLLVVLIWAVLPLYSAV PLLVYMPELSFTDAYFEAVSGLTATGATVLSGIDDLPPSINIWRTQMHWIGGMGVIVLVVAVLPMLGVGGRQLFKAETPTPMKDSKLT PRMAETAKGLWQVYAAITLVCMGALWLGGMSWVDAIVHGFSVMGLGGLSSHDASMAFFDSVLLEVIVMVFALIAGISFSTHFLAFRT RSLLTYRVDSEIRWYFAVLALSVAGLTWFLWAKGFYLDLPEALRYAAFNTVSVATTLGFSNTDYNVWPYFAPLWMLFLSSFIASSGST GGGIKMLRAVLLYKQVYREMIKLVHPNAAIHTKLGRQPVPNKIIYAVLAFLFIYVASVVILSFILSASGLDVFTAFTAVVAMVNNTGPGLG QVGPASTYAVLNDFQTWVCAFAMLLGRLEFFTLLVVLTPVFWRK
5.5E-55	196	26	5.2E-54	193	18	1.9	1	A0A077C260_9RICK	Trk system potassium uptake protein	IM40_04220	Candidatus Caedibacter acanthamoebae	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Rickettsiales genera incertae sedis, Caedibacter, Candidatus Caedibacter acanthamoebae	244581	>tr|A0A077C260|A0A077C260_9RICK Trk system potassium uptake protein OS=Candidatus Caedibacter acanthamoebae GN=IM40_04220 PE=3 SV=1MIAFQPIFFTSGLFLISLALGMVGPGLVDFFHHDINWQAFALASGVTLFIGLLLVLANRSQKIQNLTVRDTFLLTAINWLTTSIFAAL PFIFTYSTPSLTDSFFEAISGLTTTGATAIVRLDYASHGIILWRSLLQWFGGIGIVLMALTILPLLRIGGMQLFRSEFSDRSEKILPKVSQIA SAIFGTYIFLTFACTLALWWAGMTFFHAFCHALSTVSTGGFSTFEASIEYFNDPYIEIVLIIFMIMGAITLTLFVRCIQGEAKTLFKDNQVR TLFKILIIASLATTFWLWQDGHELMYALRHSIFNVTSILTTTGFNSQDYSLWGNFPIMIMLALSVIGGCTGSTSGGIKIFRFHVMYATVKT QILQLRRPHGVFIPMYNGKPIPEGIFLSVFTFFALFVACLGALALALSLFELDLLTCLFAALSVLNNMGTGFGDILGDTGTYAAALPTGAK WLLMFGMLVGRLEYITILILFSPKFWRD
6E-55	196	19.6	3.6E-53	190.2	13.6	2	1	R6GWA6_9FIRM	Trk-type K+ transport systems membrane components	BN557_01626	Oscillibacter sp. CAG:241	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, environmental samples, Oscillibacter sp. CAG:241	1262911	>tr|R6GWA6|R6GWA6_9FIRM Trk-type K+ transport systems membrane components OS=Oscillibacter sp. CAG:241 GN=BN557_01626 PE=4 SV=1MTEEMPCRKRRLSSFQIIILGFAGVILLGALLLMLPLSTTAGCVTPFHEALFTATSAVCVTGLVVQDTGSYWSGFGQTVILTLIQIG GLGVVTVAASVALLSGRRISLMQRSTMQDAISAPKVGGIVHLTRFILRGTFLIELVGALVMLPVFCRDYGWHGIWMAVFHSVSAFCNA GFDILGTNNNLYPSLTGYVQNPVINITIMLLIITGGIGFLTWDDICENKLHFHRYRMQSKVILVTTLTLIVLPALFFFFADFDALPLGERIQA ALFQSVTPRTAGFNTVDLPAMSSASLSVMILLMLIGGSPGSTAGGMKTTTLAVLLANAAATFRQRDSAQLFGRRVDCGAVKTAATILT MYLALFFGGGVFISVYEDLPLSSCLYEAASAVGTVGLTLGITPQLHIPSQMVLIALMYLGRVGGLTLIYAAVSSKKTGSAKLPQESITIG
6.2E-55	196	29.4	8.4E-55	195.6	20.4	1.1	1	C6CR87_PAESJ	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Pjdr2_0619	Paenibacillus sp. (strain JDR-2)	454	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. (strain JDR-2)	324057	>tr|C6CR87|C6CR87_PAESJ H(+)-transporting two-sector ATPase OS=Paenibacillus sp. (strain JDR-2) GN=Pjdr2_0619 PE=4 SV=1MFKTSREWVSRRSPAQVITGYYILAVLISILLFSIPAVRRPGIEVSFFDTVFTAVSVVSDTGLSVFNVAETYSVFGYFVIMLVLQFG GIGIMAMSTFFWLLIGRKIGLRERRLIMVDNNQFALSGLVQLVKEILRITLLTELLGAVIFGLRFLRYFPTWQEAFLQGLFASVSATTNAG MDITGQSLIPFKDDYFVQLVTILLIIFGAIGFPVLIELKAFLSRNKLDLNHPFRFSLFTKLTTFTYFALLGIGTICILLFESQHYFKGLTWHES FFYAFFQAATTRSAGLTTMDITHLTLPTLLLLMCVYMFIGGSPNSVGGGIRTTTFALNMLFIFHFARGRRDYKVFKRELHIDDILKSLAISM MAIVMCSLSVVAISFSDKQHQLVAIILEVCSAFGTVGLSTGITPDLSIFAKCILMLLMFIGRIGLTSFLYIIGGQQTTSKYRYPVERVMTG
6.2E-55	196	30.5	8.5E-55	195.5	21.1	1.1	1	A9B9G9_PROM4	Possible sodium transporter, Trk family	trkG P9211_00931	Prochlorococcus marinus (strain MIT 9211)	467	cellular organisms, Bacteria, Cyanobacteria, Prochlorales, Prochlorococcaceae, Prochlorococcus, Prochlorococcus marinus, Prochlorococcus marinus (strain MIT 9211)	93059	>tr|A9B9G9|A9B9G9_PROM4 Possible sodium transporter, Trk family OS=Prochlorococcus marinus (strain MIT 9211) GN=trkG PE=4 SV=1MRFSKTINLKQAWYRRLSVPQFTIATGFLIVVVGTFILATPLCSKEDVGLWESFFTATSAITVTGLTIIDIGNDLTIFGQMILALLLLIG GLGLMAITTFLQGFVISGTELRTRLDKGKTLDEFGVGGVGKTFRGIVLTATVLICIGAFFLFYFGFNNISNLRERFWAALFHSISAYNNA GFGLWADSMQSYRNNWVVNVVVILLIILGGLGWRVTSDLWMNRKNFSFRKLSLHTRLVIRTSALLITLGTVGLLVTESIGQGYFFSEIS LLERLVTSLFESVSARTAGFTNMPISVQSITDSGLLLLMTLMFIGASPGGTGGGIKTTTIAALMAATRSTLRGQDDVIIRNRQISDKIVLKA VGITVGSLVFVLVMALLITMNNSFEGKELFSFLEILFTCISAFATVGFDLGVTEQLSHFGQFVLVVGMFVGRLGILLLLSAIWQMLNTGS MHIHNRVGYPREDLYV
6.2E-55	196	23.5	5.3E-53	189.6	16.3	2.1	1	G2T0Z3_ROSHA	Trk system potassium uptake protein TrkH	RHOM_04325	Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, Roseburia hominis, Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	585394	>tr|G2T0Z3|G2T0Z3_ROSHA Trk system potassium uptake protein TrkH OS=Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183) GN=RHOM_04325 PE=4 SV=1MLEIIHRKKRLSSFKLIALGFAGVIVLGALILMLPFSSNTGSVTPFHEALFTSTSAVCVTGLVVQDTGSYWSAFGQAVILLLIQIGGL GVVTVAATFAMLSGRKISLMQRSTMQDAISAPKVGGIVRLTRFIVRGTFLIELIGMVAMLPVFCRDHGFKGIWMAAFHSVSAFCNAGF DILGTTENKYPSLTGYVGEPTINIVIMILIIVGGIGFLTWDDICTNRWHFKKYRMQSKVILVTSVILIIVPAIFFFLFDFTGLPPGEKILASLFQ SVTPRTAGFNTADLTAMTESSKAIMILLMLVGGSPGSTAGGIKTTTLAVLILNAFSVCRKKNDTEVYGRRLECSAVKSASTIAVIYFLLFF IGGIIISTAEGMPLSACLYETASAVGTVGLTLGVTPQLSVFSQFILIVLMYLGRVGGLTLIYAAISNKNQSGAKLPLEKITVG

6.5E-55	196	21.9	1.5E-53	191.4	15.2	2	1	A0A0F5VGB1_9GAMM	Ktr system potassium transporter B	KY46_04810	Photobacterium halotolerans	454	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	265726	>tr|A0A0F5VGB1|A0A0F5VGB1_9GAMM Ktr system potassium transporter B OS=Photobacterium halotolerans GN=KY46_04810 PE=4 SV=1MVLWHPSVSPIERRPKAGKKLLGAPPFILSASFMLLILMGAGLLKLPFATHEPISWVQSLFTATSAVTVTGLVVVDTGTVFTPFG QTVIALLIQCGGLGLMTFAVVTLIALGGKIGFLERTVAREAFNQTDSSTLATTAKSVLGFALVVELIGIAVLTLYWREELGWQTSLFHGF FYTISAFNNAGFALSADSLMPYVDDPVVNITITGLFVIGGLGFSVWMDLRRNRCWSRLTVYSRMMISGTVIINLVALIAIYLIEYDNPNTL APLSESGKWLASWFQAVTPRTAGFNTLAIDQLEDATTAIMLVLMFIGGGSLSTASGIKVVTFIVLILATYAYLRRDEAVDVFQREITKETI SKALALTIISAGVTWLAIFALLLSEKAPMLDIVFEAVSALGTVGLSRGLTGNLSAAGEFIIILMMFMGRLGPLTLAYFLASPRKKKVRYAET RLAIG
6.6E-55	196	28.8	9.1E-55	195.5	19.9	1.1	1	M9WCK3_9MOLU	K , Na uptake protein bound cytoplasmic subunit	ktrB MPUT9231_10020	Mycoplasma putrefaciens Mput9231	546	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma putrefaciens, Mycoplasma putrefaciens Mput9231	1292033	>tr|M9WCK3|M9WCK3_9MOLU K , Na uptake protein bound cytoplasmic subunit OS=Mycoplasma putrefaciens Mput9231 GN=ktrB PE=4 SV=1MVPKDHDQKETNSNQNNTSKRFKKPFFKKWKIQEKDKFFIKFKNFWPLSKTSGKIFLIYLCIILLGALLLSIPNFALTPTANPRYSW DYLTGIFLASSAFSDTGLTVIDVSHSYTFTGQLILLLLIEAGGIGVLTFKVVLFLIINKKISISDTMVAQSERGSTITNSTIHLIKDGFIWLSIV QVTSAFILFFLFFFNKPGTVNSVGVQLNVVSPYHNFWKSLWFAIFHSTSAINNAGFDIISPNSLQPYNVDNHRVYAIQVIFMLEWIIGGL GYPTFHDIKRKIQARKQGQKVKFSLFTKLNFWVYLTLFILGPIGVLSTEYASYDNSLIFHSFVNGQKITKPFIISFVDILFNTTASRNAGFS TISIDNFNPGSKSVLAILMFIGSAPSSTAGGIRTTTFAILLLSTISIIKNRKYTSVFKKTIPDETVRRSYATFFISSFLIFIALFIIYIDSHQVFENI AKTGSTNNQSVTTQILVLITSAFGTVGLSPLGYDDMYKLKATTKILLVLIMFIGQLGVSNTLLIFIKPAREEALKFLDEDVTIG
6.7E-55	196	27.5	4.6E-53	189.8	19.1	2	1	G2SP92_LACRR	K+ transport system, membrane component	LRC_11430	Lactobacillus ruminis (strain ATCC 27782 / RF3)	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus ruminis, Lactobacillus ruminis (strain ATCC 27782 / RF3)	1069534	>tr|G2SP92|G2SP92_LACRR K+ transport system, membrane component OS=Lactobacillus ruminis (strain ATCC 27782 / RF3) GN=LRC_11430 PE=4 SV=1MNFNECWGGFLKKVRLTSFQIIILGFLCLILLGTLLLMLPISQANGNATSFKDALFTSTSATSVTGLVVRNTATYWSLFGKCVILCLI QIGGLGIVTVAMAFSLLGRKKIGLMQRTVMQESISAFYVGGIVKFTSFIIRTVVCCELLGALLMLPVFWHQFGGIHGIFYAVFHSISAFCN AGFDLFGRTHPYASLARYVDNLPINLVIMSLILIGGLGFRTWEDVRQNKQHFSRYCLQSKLVLATTAILIIIPFLYFFFAEFGHYPLKERIL AALFTTVSPRTAGFNTVDLNRLSDDGVVMNIMLMLIGGATGSTAGGMKLTTVAVLAISAHSVLHRKKDATAFGRRIGTGVIFDAAAIFSL YFVTCVISAMAISAIEGLPFLKCMFETASAVATVGLTLGITPHLSTLSQLILIVLMFMGRVGGMTLVFATIARRHVVDPLKPEEKVQVG
6.7E-55	196	31.2	1.2E-54	195	21.6	1.3	1	D9QUE7_ACEAZ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Acear_0393	Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Acetohalobium, Acetohalobium arabaticum, Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	574087	>tr|D9QUE7|D9QUE7_ACEAZ Potassium uptake protein, TrkH family OS=Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288) GN=Acear_0393 PE=4 SV=1MRIISFKLDSLSPAQFLALGYIIVITVGALLLMLPAATVDGQGLGLINSLFTATSATAVTGLIVVNTGAYFTLFGQAVILLLIQIGGLGF MTTSTLLALILGKRINLKKRIIIQEDLNYFNLSGLIRLVQYVTLLTLGVELIGAILLFAPLSVEYSAGKAAFFSIFHAVSAFCNAGFDLFGNSL ANFTNDVYINLVITALFIIGGIGFAVIADVYRKQRFIDYSLNTKLVLVITLILILGTCFVFLLEFSNPATLQGLSFKGKLLAAYFQGVTPRTA GFNTIPTGQMRNATLFFIIILMFIGASPGSTGGGLKTTTIGALLAVVYNLVKGNEDIELFERRLSQSIIYKALAVTIISLIWIGLVVTVLTITEE ANFLSILFETVSAYGTVGLSTGITGGLSEAGRIIIILTMFLGRVGPLTLAVAIGERDKEGQMRYPEEKILIG
6.8E-55	196	19.9	2.3E-54	194.1	13.8	1.7	1	A0A0A2EMY8_PORCN	Potassium transporter	HQ35_05855	Porphyromonas cangingivalis	475	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, Porphyromonas cangingivalis	36874	>tr|A0A0A2EMY8|A0A0A2EMY8_PORCN Potassium transporter OS=Porphyromonas cangingivalis GN=HQ35_05855 PE=4 SV=1MMGFLCTMQVPFLVIAILISLYYHDAGLRPLEITAGLMAVVGLILLFIGRNAKDYNAGRREGMLSVAVSWFVVSLIGMLPYLLGDF VPTFADAFFETISGFTTTGGTILTDIEALPRSILFWRSVTQWVGGIGIVVFVVALVPIMGGSASLLYNSETTGVTHERFLPRVGMMAKW VSLIYVGLSMLCVLLLWAGPMGLYDAVCHATTCISTGGFSPRNASIAAYDSFYIQVITVIFMLCGATNFSLLYFALRGRGAKLFTDVEFR AFLAIIGVLTLIASLFLFFKGVKPNLFEAVWGAFYHIVSIITSTGYVLDDYNNWYPFFSFVMLFAMFVGGCAGSTSGGLKVARFIILGKNL RNEFHKRTHPNAMLPVRIDGHPIPGKVVHQVLAFFFAYLCLMMIGAVIVSMDGFTVEESISAALTSISNTGPGIGTFGPVNNFASLSSH SKILLSVIMVMGRLEIFTVLTIILPSFWRS
7.1E-55	196	30.4	2.2E-54	194.2	21.1	1.6	1	B8DYW8_DICTD	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Dtur_0268	Dictyoglomus turgidum (strain Z-1310 / DSM 6724)	456	cellular organisms, Bacteria, Dictyoglomi, Dictyoglomia, Dictyoglomales, Dictyoglomaceae, Dictyoglomus, Dictyoglomus turgidum, Dictyoglomus turgidum (strain Z-1310 / DSM 6724)	515635	>tr|B8DYW8|B8DYW8_DICTD Potassium uptake protein, TrkH family OS=Dictyoglomus turgidum (strain Z-1310 / DSM 6724) GN=Dtur_0268 PE=4 SV=1MNLFMFEKELISKKRGFNPAVFFIISFAIVILTGAILLSLPISSAKGEFTNFLTALFTATSATCVTGLVVVDTGTYWSHFGHLVILLLIQ IGGLSYAVISTGMMLLLNRRLQLRERLILQYSLNTTSLRGIVSFLKNVLITVFIFESIGALSLFFVFIKRYPLLRSIKFAIFHSVSAFCNAGLD LIGGFRSFTDYVSDPHLVFTITTLIIVGGIGFIVIHDIIQRFMGKRIHLSLHSKMALFTTLFLILIGTIVIFILEYNNPNTLKPLNFWGKFLGAYF QSVTPRTAGFNTLDIGKMNPSTLLFIIVLMFIGASPGGTGGGIKTVTFLVLWLSVSTIILERKNVHFKDRTIPWENVKRAYIVFLLSLTLVII SWFLLLITEPFPPLNILFEVVSAFGTVGLSTGITPYLSPFARLVIILTMFLGRVGTVTAGMAILIPVSKRSQVEYPSEEVSIG
7.7E-55	196	43.4	1.3E-54	194.9	30.1	1.4	1	B2TS58_CLOBB	Potassium uptake protein, TrkH family (Putative potassium uptake protein)	CLL_A2476	Clostridium botulinum (strain Eklund 17B / Type B)	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum B, Clostridium botulinum (strain Eklund 17B / Type B)	935198	>tr|B2TS58|B2TS58_CLOBB Potassium uptake protein, TrkH family OS=Clostridium botulinum (strain Eklund 17B / Type B) GN=CLL_A2476 PE=4 SV=1MGKVLTKKSRLNAVQVLAIGFAIVALIGALILTLPISSASGESTNFIDAIFTSTSAVCVTGLITLDTGTYWSTFGQVIIIILIEIGGMGFM SFTTFIAILLGKKITLRDRLLMQEAMNTFNIEGLVRMVQYVFALTFSVQFFGALLLSTQFIPQFGFSKGLFYSIFHSISAFCNAGFDLFGN FTSLTGYSSNVVVILSISALIIIGGLGFTVWLEIYNYNKSSKRLSLNCKVVLLITIFLIIFGFICIFIFEYNNIQTIGGMSFKDKILNSFFASVSP RTAGFNSMSTDDMTMSGKLITIILMFIGGSSGSTAGGLKTATFGVLILTVISVLKGREDTEAFEKRFSKDLVYKAFTLFFIAMMLVIVVTM ILTIVEPNQSFINLLYEATSAFGTVGLTTGVTQQLSFAGKIVIMLTMYCGRVGPLTVILALLNRKKKKGYRYPEGKILIG

7.9E-55	196	26.2	1.6E-54	194.7	18.1	1.4	1	B2A3S6_NATTJ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Nther_0103	Natranaerobius thermophilus (strain ATCC BAA-1301 / DSM 18059 / JW/NM-WN-LF)	443	cellular organisms, Bacteria, Firmicutes, Clostridia, Natranaerobiales, Natranaerobiaceae, Natranaerobius, Natranaerobius thermophilus, Natranaerobius thermophilus (strain ATCC BAA-1301 / DSM 18059 / JW/NM-WN-LF)	457570	>tr|B2A3S6|B2A3S6_NATTJ Potassium uptake protein, TrkH family OS=Natranaerobius thermophilus (strain ATCC BAA-1301 / DSM 18059 / JW/NM-WN-LF) GN=Nther_0103 PE=4 SV=1MVRATRFNPARTLVLGFLSLIIIGAVLLSLPIATIEAGRLPLLDALFTATSAVCVTGLVVVDTGTTFTVFGQTVIMLLIQAGGLGFMT SATLIFLALGRKITLRERIVIQESLNQFDLQGVVRLVRSILILAFSIQGIATMILGIRFSQELGWAKGFFFGLFHSISAFCNAGFDLIGDFRS LMPYVNDPLISLLLPLLFIIGGLGFTVLVDLYFTRYITRLGFHTKVALIITGSFLLIGFLTVTLLEWNNPKTLGSVTGGAKIWSAFFTAATPR TAGFNVLPTDELNQATTLFIMVLMFIGASPASTGGGIKTTTFGTLLLAVISVVKGKNQVSFLRKRIPYNLISKALAIIIFISLGIVVLVAMVLLV TEDANFEEALFEAISAFGTVGLSKGITPDLSAVGRIVVIVTMFVGRVGPLTLAFALAKESDDTGIKYPEERLIG
8.2E-55	196	23.9	3.1E-53	190.4	16.6	2	1	Q87G87_VIBPA	Putative Na+-transporting ATP synthase	VPA1430	Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	454	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio harveyi group, Vibrio parahaemolyticus, Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	223926	>tr|Q87G87|Q87G87_VIBPA Putative Na+-transporting ATP synthase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1430 PE=4 SV=1MVLWHPSIIPIERKPKAGKKLLGAPPLILSLSFACLIMLGTVLLKLPIATTEPTTWIQSLFTATSAITVTGLVVVDTGTAFTPFGQVVI AFLIQCGGLGLMTFAIVTLLALGGKIGFLERAVAREAFNQTDSSTLIATAKSVLMFALLVELIGFTILSVYWSEELGWKTSLFHGFFYTIS AFNNAGFALSADSLMPYVDDPVVNFTITSLFIIGGLGFSVVIDLKRNRRWHRLTVYSRMMILGTMIINVVALIAIYLIEYDNPNTLAPLSEA GKWWASWFQAVTPRTAGFNTLAIDQLEDATTAIILVLMFIGGGSLSTASGIKVVTFMVLVLATYSYLRRDEATYAFQREIPKETISKALA LTLISVGVTWFAIFTLLLTEKASMLDIMFEAVSALGTVGLSRGLTGSLSEPGELVIIFMMFMGRLGPLTLAYFLASPRKKKARYASTKLAI G
8.3E-55	196	33	1.4E-54	194.8	22.9	1.3	1	A0A099W0X9_9LIST	ATP synthase	EP56_13165	Listeriaceae bacterium FSL A5-0209	471	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, unclassified Listeriaceae, Listeriaceae bacterium FSL A5-0209	1497679	>tr|A0A099W0X9|A0A099W0X9_9LIST ATP synthase OS=Listeriaceae bacterium FSL A5-0209 GN=EP56_13165 PE=4 SV=1MLEKKRNKRDNYMIGGKSRRGRARARMSRLTPIQVIITFYFLSITFATALLSMPFTQKPGVKIPFIDTLFTAASSVSVTGLASVNV GESYSRAGIWVLMGIFQVGGLGVMMLSTFFYLVLKRRVGLRQRQLIMTDTNQFSMSGMVRMLREILVLIFGIQIIGGLILGIYFIPFYNG DVGEAMFQGLFNSVSAVTNAGVDITGYSLTPFVNDYFVQFITILLIIAGGIGFPVLIEARRFLFEKNTLIPFRFSLFVKVTTVTYMALLVIG GLLIWAMESQHYFKGTSIDEGFFNSMFLSATSRSAGLSTIDTSALTDPTLLVVSALMFIGASPSSVGGGIRTTTFFAITILFLYSVMRGRN HIYIFGRELYQEDVRKALAVAVFATLLCVGAITILGYTEQAELMAIIVEVFSAFGTCGLSMGLTADLSHFGKIIIILLMFIGRVGIMYMMLSF RTKDGKKNAIRLPKEKIITG
8.7E-55	196	29.9	2.4E-53	190.8	20.7	2	1	S0K3C5_ENTAV	Trk system potassium uptake protein TrkH	OMU_04283	Enterococcus avium ATCC 14025	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus avium (Streptococcus avium), Enterococcus avium ATCC 14025	1140002	>tr|S0K3C5|S0K3C5_ENTAV Trk system potassium uptake protein TrkH OS=Enterococcus avium ATCC 14025 GN=OMU_04283 PE=4 SV=1MVKEKHWPFKIYPIQFIALGFAGIILFGSVLLTLPIVTKSGQGTPFIDALFTATSATCVTGLTTLTTSEHWNMGGQLIILSMIEIGGL GFMMMPFIFMAIMKRKVGLMTRIILQESLNLDSLSGVMRLMLYIFRFAMGFQLLGALLLAIDFIPAYGLGRGLWYSFFHSISAFCNAGFD LFGDSLVGFQDNAYVLFVISGLIVGGGLGFIVWQDLMNFRKTRKLSLHSKLALTVSLSLLIIGTLVFCISESGGRYLVGNSSPINRFANML FMSVTARTAGYFSVDYGSVSQAGILFTIVLMFIGGTPGSTAGGLKTTTFGVLLVQTISMLKGRMHAEAFRRTIRPSVVSRALTLFFITLT LCIAVTMLMSVTEVLPRFRGIEYLLFETFSAFGTVGLTMGLTPSLSLMGKILIIIGLMYIGRVGILTVGFSLTIRLTKKEQGNYKLPEESVMI G
8.8E-55	196	26.2	5.4E-53	189.6	18.2	2	1	I5AVL5_EUBCE	Trk-type K+ transport system, membrane component	EubceDRAFT1_2077	[Eubacterium] cellulosolvens 6	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium cellulosolvens, [Eubacterium] cellulosolvens 6	633697	>tr|I5AVL5|I5AVL5_EUBCE Trk-type K+ transport system, membrane component OS=[Eubacterium] cellulosolvens 6 GN=EubceDRAFT1_2077 PE=4 SV=1MEEINNRIRHLKPVQIIILGFALVIISGTLLLMLPVAKRGAGSAGFADALFTAVSSTCVTGLVVQDTATYWSAFGQAVILLMIQIGGL GVITVAISIAIVSGRKIGLLQRNIMQASISAPQISGIVKFTRFILLATFGCELAGAVVMLPVFAGMYGIRKGCWYAVFHSVSAFCNAGFDL MGGSGRFSSLTSLSVHPVINVTIMALIILGGIGFFTWMDVVVHGIHFSRYRMQSKVSITVSVILILIPALFFYFCEFGNLETGRRIWYSLF QAVTPRTAGFNTADLTKLGENGIFLMIILMLIGGSPASTAGGMKTTTVAVLFASAFSVFQRKKDAGLFGRRISTDSITNAGAILLLYAGLF AVCGMCISAIEKLPLLTCLFETASAIGTVGLTLGITPSLSLVSRTILVILMYVGRVGGLTLIFAAVSEKGLHKGRLPEESITVG
8.8E-55	196	16.6	1.8E-52	187.9	11.5	2.1	1	U7DDY0_PSEFL	Trk system potassium uptake protein	B723_07405	Pseudomonas fluorescens NCIMB 11764	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens NCIMB 11764	1221522	>tr|U7DDY0|U7DDY0_PSEFL Trk system potassium uptake protein OS=Pseudomonas fluorescens NCIMB 11764 GN=B723_07405 PE=3 SV=1MALPTLRLIGFIIGLFLITLAIAMVVPMATLVIFERTGDLPSFLWASMITFVAGLALVIPGRPEHVHLRPRDMYLLTVSSWLVVCIFA ALPFLLTQHISYTDSFFESMSGITATGSTVLNHLDDMSPGILMWRSLLHWIGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSEKVMPR SHMVARLIVAAYVGITIFGSLAFWWAGMSPFDAINHAMSAISTGGFSTSDQSLAKWTQPAVHWVAVVIMILGSLPFTLYVATLRGNRR ALIKDQQVQGLLGMLLVTWLVLGTWYWWTTQLHWLDALRHVALNVTSVVTTTGFALGDYSLWGNFSLMLFFYLGFVGGCSGSTAG GIKIFRFQVAYILLKANLNQLIHPRAVIKQKYNGHRLDEEIVRSILTFSFFFAITICVIALLLSLLGVDWMTALTGAASTVSGVGPGLGETIG PAGNFATLPDAAKWILSFGMLLGRLEIITVFVLCIPAFWRH
9E-55	196	20.1	2E-53	191	13.9	2	1	E7GTF8_CLOSY	Trk system potassium uptake protein TrkH	HMPREF9474_04203	[Clostridium] symbiosum WAL-14163	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	742740	>tr|E7GTF8|E7GTF8_CLOSY Trk system potassium uptake protein TrkH OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_04203 PE=4 SV=1MNYSIIFYIMGWILNFEAAFMVPPCIVALIYGEQAGWSFVITMALCLLIGVPLVIKKPKKQIFYTSEGFVTVSLCWVVMSIMGALPF LFSGSITSPVDALFETVSGFTTTGASILSDVEVLPKSILFWRSFTHWIGGMGVLVFILSLLPLTGGSHMNLMKAESPGPSVSRLVPKVR LTAKLLYSIYIFMTVVEILFLLAGKMPLFDAVTVTFGTAGTGGFAIKNNSIAGYSPYIQNVVTVFMILFGVNFNVYFLILMKRVGQAFRTEE LRWYLIIIAVSIGIITVNTAGLYRSLGDALHHASFQVASIITTTGFATQDFDLWPQASKTILVLLMFIGACAGSTGGGVKVSRLVVLVKTVR KELIQFLHPQVIRKIKMDGKVVEHEVVRSINVFMVAYTLLFSLSVFLLAFDGEDLITNFTAVAATFNNIGPGLELVGPSKNFGIFSEPAKL VLIFDMLAGRLEIFPVLILFSRETWKKF
9E-55	196	28.7	2.1E-54	194.3	17.2	2.3	1	Q08A32_SHEFN	Trk system potassium uptake protein	Sfri_00020	Shewanella frigidimarina (strain NCIMB 400)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella frigidimarina, Shewanella frigidimarina (strain NCIMB 400)	318167	>tr|Q08A32|Q08A32_SHEFN Trk system potassium uptake protein OS=Shewanella frigidimarina (strain NCIMB 400) GN=Sfri_0020 PE=3 SV=1MFNVKQIIFILGIFLSILTGFMLVPMAFALFYGEETIGDFMLSGLFTGFIAILCIQNGRNHHFSLNIRDMFMLTSITWFVVSLFAALPF TLYHGINYTDAFFETMSGITTTGSTVLSGLDSMDHSILVWRSLLQWLGGIGFIVMAVAILPFLNVGGMRLFRTESSDWSDKTIPRTQH MAKHLFLIYVALTLLCTLSYHLAGMHWFEAINHAMTTLSTGGYSTSDSSMAAFSHEAHWVGIVFMLAGGLPLLMFVQTIQQRSLRLW NDQQVKGFLRFVLLVSFSLAFWLWQHQQIDFMDALRLASFNVISVITTTGYGLTDYQSWGSVASVAFLFLMFIGSCSGSTSGGIKIFR FQIAFSIMRQQIKQQFHPNGVFKDKYNGHRIQDDIVRSIMAFFMLMIVVILLLSITLVLTGLDPMTSFTGAITAVANVGPGLGPIIGPAGNF APLPDVAKWALAIGMLLGRLEILTVAVLFHPKFWRF

9.1E-55	196	25	1.5E-54	194.8	17.3	1.2	1	K9S331_9CYAN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	GEI7407_0069	Geitlerinema sp. PCC 7407	444	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Geitlerinema, Geitlerinema sp. PCC 7407	1173025	>tr|K9S331|K9S331_9CYAN Potassium uptake protein, TrkH family OS=Geitlerinema sp. PCC 7407 GN=GEI7407_0069 PE=4 SV=1MTVSRTICLGFLAVITLGSLLLMMPFSVTSGTWGDPITALFTTTSAVCVTGLAVVDTGTYFSTLGQGILLLLIQVGGLGYMTATTF LLLLLGRRFGLRDRLALQQSLDMPGMKGVVQLVRSIIATTLIFELTGIFIMLPAFSADYGLDRGLWLAIFHSISAFNNAGFSLFPDNLVGY VSSPLVNIAVTGLVIWGGIGYQVIMELFLWLRDRLLRRPECVVFSLNFKIVTSTTLVLLIGGTVLVFCVEFDNPATLGALDWNGKLWAA WFHSVITRTAGFNSISVGQMETASLFASIAFMFVGAGPGSTGGGIKTTTLRILYVCTKAVLQGKEYVHCYQRQIPLSLILKAVGVVVGS MATVVGSTILISLFDPDLQFIEILFEAVSAFGTVGLSMGITADTSVLTKLVLIMTMYVGRVGVLLLMSALLGDPKPSVVRYPEEELLVG
9.5E-55	195	16.5	2E-53	191.1	11.4	2	1	R5HH33_9FIRM	Ktr system potassium uptake protein KtrB	BN469_02097	Firmicutes bacterium CAG:114	448	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:114	1263001	>tr|R5HH33|R5HH33_9FIRM Ktr system potassium uptake protein KtrB OS=Firmicutes bacterium CAG:114 GN=BN469_02097 PE=4 SV=1MPFLKHDRITPAQVVILGFLFQILIGACLLSLPVATRSGESVPFLDALFTATSATCVTGLVIHDTALFWSPFGQGVILLLIQVGGMG VVTMAVAIFMFSGRKIGLKQRWVMQESISAPQVGGIVRMTGFILKTAFLIEAVGALLLALRFCPQFGLGKGIWYGIFHAVSAFCNAGFD LMGETGAFSSLTGYVGDPLVNLVICLLIVVGGLGFLTWHDVAAHGRHVSQYRLQSKLILLTTLSLLVGGFLFFRFYEFSRPQWAALTG GERGLAALFQSVSPRTAGFNTVDLTQLSACSQLMTILLMLAGGSPGSTAGGFKTTTLAVLLLSVGAVIRRQGSARCFGRRLPDQVLR NACAIFLLYLLLFLAGGMLICCMDEIPLMQALFEAASAIGTVGLSLGATAEASEGGSRLILIFLMYFGRVGGLTMIYAMAAGSNGSSSQYP QEQVTVG
9.9E-55	195	29.2	8.7E-53	188.9	20.2	2	1	S0P3R3_9ENTE	Uncharacterized protein	I573_02199	Enterococcus sulfureus ATCC 49903	443	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sulfureus, Enterococcus sulfureus ATCC 49903	1140003	>tr|S0P3R3|S0P3R3_9ENTE Uncharacterized protein OS=Enterococcus sulfureus ATCC 49903 GN=I573_02199 PE=4 SV=1MHSLRKKRRPFHFSPAEIITGTFIGLILLGTGLLMLPISNQQDSPQWIDALFIATSAICVTGLSPLLIDQQFSLFGQSVILMLIEIGGL GFMSIPIFIYFVGKKRIHLSTRLVLRESMNMESRSGEVKLALAILKIAGSIQLVGIGLLAIRFIPKYGVATGIWYSVFHAISSFCNAGFDLFG TSMVAFKGDPIIILTISFLIISGGLGFLVWTDLLQIRHKKLSLHSRLALKMTGILLLVGWGLFYLIMPKTSLGKSLLDSFFLSVTPRTAGFFT LDYANMPQAGLMLTMMLMFIGGTSGSTAGGLKTTTLAVLIAKVRSLFKGRTRTEISGRTIREVAVAKAMTLFFLALAICTISLFILTITETT SNETLVVLGFEVVSAFGTVGLTMGATSSLSLVGKLVIISLMFIGRVGILTILYSLSRKIYQQEVKIKYPEESVLLG
9.9E-55	195	24.3	3.9E-52	186.8	16.8	2.1	1	R7L888_9BACT	Cation transporter	BN601_01642	Coraliomargarita sp. CAG:312	489	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Opitutae, Puniceicoccales, Puniceicoccaceae, Coraliomargarita, environmental samples, Coraliomargarita sp. CAG:312	1262865	>tr|R7L888|R7L888_9BACT Cation transporter OS=Coraliomargarita sp. CAG:312 GN=BN601_01642 PE=4 SV=1MNYSIIFKILSMVFAVMAGAFSVCAGVSVIYADTPLEGEAMPSWICVIALSLMLALAFFIPSRNAPTKLFKKEAMCIIGLAWTLASL VGALPYVLILDCPFATAFFESASGLTTTGASVFASFSEFPHSLMFWRCLSHWIGGLGVVVFFVAILSFLGFGGRILYAHESSANSGGG METERIQSGAIRILEVYTAISVVCLITFKLCGMGWFDGICHMFATVSTGGFSVYENSIAHYDSRLIDWAVIVFMFIGGVSFTAIILALEFRH KRLAQNTEFWTYLGIITASSFIIFALICTSQPSILDAFTHSVFQTVSIMTTTGLASAPYQNWLPSTHIVLFALMIIGGCAGSTSGGLKVSRV VASFKILLRDVEKSFRPRVVRNITLNGKTLDESDTNSILSFVVLYSFIALIAFIVFTIFEPDASITTCISSVLSMIGNVGPGFGDVGPDKTYG FMEDHTKIFLSMLMIMGRLEFYAILVLFMPSLWKKFE
1E-54	195	19.5	1.4E-54	194.8	13.5	1.1	1	A4XYA5_PSEMY	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Pmen_3573	Pseudomonas mendocina (strain ymp)	442	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas mendocina, Pseudomonas mendocina (strain ymp)	399739	>tr|A4XYA5|A4XYA5_PSEMY H(+)-transporting two-sector ATPase OS=Pseudomonas mendocina (strain ymp) GN=Pmen_3573 PE=4 SV=1MKASLHPSRTVALLFLAVIVVGTLLLMLPYASADGQSASLLTAAFTAVSAVCVTGLVVVDTGSYWSTFGQWVILLLFQFGGFGM MTLATLLGLMVNRSFRLRTKLVAQVESHSLGLGDITSVAKLVLVVTLGMEALITALLTLRLHVGYGLPWDQAAWSGLFHAVSAFNNAG FSIHADSLMGYAGDSLILTPVMAAIIIGGIGFPVLQDLRNRLRDPRHWSLHTKLTLSGTVLLLLGGFLVMLLAEWSNPRTLGAMTLDDKL LSAAFASVSARTAGFNSIDIGALTHESWAVHYFLMFIGGGSAGTAGGVKITTVAVLVLLVVAEIRGRSDTEAFGRRVSDSAQRQAITVL VLGSAMVVLGTLVILRNTEIPTDQVIFEVISAFGTVGLSTGITADLPPSSQWMLTLLMFAGRVGTITLATSLALGEHRMPYRYPEEHPIV G
1.1E-54	195	32.1	6.5E-53	189.3	22.3	2	1	R5VV37_9CLOT	Potassium uptake protein TrkH family	BN512_00485	Clostridium sp. CAG:167	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:167	1262777	>tr|R5VV37|R5VV37_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:167 GN=BN512_00485 PE=4 SV=1MADFIHKKNRFTSFQIIIGGFIAVILIGALLLMLPVSSKAGIITPFNEALFTSTSAVCVTGLVVQDTATYWSWFGQGIILVLIQIGGLG VITIAVSFALLSGRKISLMQRSVMQEAISAPKVGGIVRLTGFVLKGTFLVEFTASIIMMPVFVKDFGVKGIWMAIFHSISAFCNAGFDLMG TENAKYASLTSYISHPLINITIMLLIIIGGIGFLTWEDILKNKYRIKSYRMQTKVILTTSLLLILFPAFFFFRDFADMPMQERIFSSLFQAVTP RTAGFNTADLTMMTKDGLGIVIVLMLVGGSPGSTAGGMKTTTLAVLIANTLACFRRKEDAQMFGRRIETSTIKNAATIFMMYIVLFFGG AIVISTVEDLSFSTCLFETASAIGTVGLTLGITPELGVISQTILMILMFLGRVGGLTLIYAALSGSGKKISKLPQEKMTVG
1.1E-54	195	14.1	2.4E-53	190.8	9.8	2	1	Q9HZ30_PSEAE	Trk system potassium uptake protein	trkH PA3210	Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	208964	>tr|Q9HZ30|Q9HZ30_PSEAE Trk system potassium uptake protein OS=Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228) GN=trkH PE=3 SV=1MALPTLRILGFIIGIFLITLAASMLVPILTMLAFDRTEGIQAFIWSSVATFVTGLGLVLPGRPEHVHLRPRDMYMLTVSSWVLVCIFA ALPFVLQQHISYTDAFFESMSGITATGSTVLSGLDDMSPGILIWRSLLHWLGGIGFIAMAVAILPMLRIGGMRLFQTESSDRSEKVLPRS HMVAKYIVATYVGITLLGSLAFWGAGMSPFDAVNHAMSAISTGGFSTSDQSLAKWKQPAVHWTAVVVMILGSLPFALYVATLRGHRK ALIKDQQVRGLLGLLLVTWLLMGTWYAVTSKLPWMDAFRIVAVNVTSVVTTTGFALGDYSMWGHFSIMLFFYLGFIGGCSGSTAGGI KIFRFQVAYTLLKANLYQLIHPRAVLKQNYNGHRLDEEIVRSILTFSFFFAIVVCLLALGLSLIGLDWMTALTGAASTVAGVGPGMGPIIG PSGNFASLPDAAKWLLAAGMLLGRLEIITVLVLLTPAFWRH
1.2E-54	195	20.3	4.5E-54	193.2	14.1	1.8	1	A7ICI4_XANP2	Trk system potassium uptake protein	Xaut_0469	Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	498	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Xanthobacter, Xanthobacter autotrophicus, Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	78245	>tr|A7ICI4|A7ICI4_XANP2 Trk system potassium uptake protein OS=Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2) GN=Xaut_0469 PE=3 SV=1MHAARIPTVEAEAVSLSLRPVAATLGVLLAILGVAMLVPAIVDFATRSGGQGAFVGASAITIFVGVLLWMSGRSQKVSKLDLRQ AFLLTSSVWVVLSLFAALPLMWGHSRLSFTAAMFESMSGLTTTGASVMSGLDAMSPGILLWRALLHWFGGIGIVAIAIAVLPMLSIGG MQLFRTESSDKSEKFLPRAGAIAKRLLVAYVLLTAVCAGFYLMAGLKPFDAVTIAMSTLSSGGFANSDSSLTVFAKPAVDYVAVVFML MAALPFPLYVRALSGDPWRIFSNPEVRLFLAIVALFTGLSFVQLTVSGVASGETALRWALFTVASLISTTGFMAADYTNWGTTSDAIFF VLMFIGGCTGSTSGGLKALRLAITAKAIRQHLKRISFRAGVFPLRYGGAPVADDVVASVLSFVFLYLLAFFLFGVALNMLGLDLKTAFSA TIACLANVGPGLGPLVGPASNYSVLPDSALWLLTAAMLLGRLEILTVLVLFLPRFWVR
1.2E-54	195	12.7	3.1E-52	187.1	8.8	2.1	1	R6QC68_9FIRM	Cation transport protein	BN792_00056	Faecalibacterium sp. CAG:82	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, environmental samples, Faecalibacterium sp. CAG:82	1262898	>tr|R6QC68|R6QC68_9FIRM Cation transport protein OS=Faecalibacterium sp. CAG:82 GN=BN792_00056 PE=4 SV=1MNYAIVFRLLSYILFCEAALLLLPVTASLCYGEWSVLGVFVLTAALCLVLGLLLRRIKPSSKVFYMREGFATTALSWVVISIMGAIPF VLTGCIPNPVDAMFETVSGFTTTGASILPAVEGLPKGVLFWRSFTHWIGGMGVLVFLLSLLPLTGGSHVNLMKAESPGPQVDKLVPKV QSTAKILYGIYFALTVLEFLFLLVGRMPVFDAMLTAFGTAGTGGFGFKNDSFGSLSPYIQWVVTIFMILFGVNFNTYFLLLLRRFRRAAA SEEVRGFYLIILVAIGIITLNIHGMYDSLGVALRHAAFQVGSIITTTGFSSCDFDLWPTLSKEVLVMLMFVGACAGSTGGGIKVSRLLILGK TLGKELKQALHPQVVAPARMDGKLINHETIRATNVFLAAYIFIFAASLFFISLDGFDMVTNFTAIAATLNNIGPGLNQVGPMMNFGGFSN PAKLVMIFDMLAGRLEIFPMLVLFLPDTWRKF

1.3E-54	195	27.5	1.9E-54	194.4	19.1	1.2	1	C0MG46_STRS7	Cation transport protein	SZO_03020	Streptococcus equi subsp. zooepidemicus (strain H70)	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus dysgalactiae group, Streptococcus equi, Streptococcus equi subsp. zooepidemicus, Streptococcus equi subsp. zooepidemicus (strain H70)	553483	>tr|C0MG46|C0MG46_STRS7 Cation transport protein OS=Streptococcus equi subsp. zooepidemicus (strain H70) GN=SZO_03020 PE=4 SV=1MKRSFFKSLSVTQRLTFSFAIVILIGSLLLSMPFTHYSNGPNTIYLDHFFNVVSMVCVTGLSVVPVADVYNGIGQTIAMMLMQIGGLGLVTLIAVSTFALKRKMRLSDQTLLQSALNRGDSKDLKKYLFFAYKVTFSLEAFAALVIMTDFIPRFGWKNGIFNSIFLAVSAFCNAGFDNLGSSSLKDFVLNPTINAIITFLIISGGLGFAVWVDLGTAFKKYFFERPHCYGITFKKFSNQSRLVLQTTLVILVLGTFLSWFLEKDNLNTIARYNLPQQLMVSFFQTVTMRTAGFATISYNDTLAPTNILYMIQMVIGGAPGGTAGGIKITTAAITFLLFKAELSGQSEVTFRNRIIANKTIKQTMTVLIFFFAVLMIGYILLLSVEPDIAPIPLLFESISAIATVGVSMDVTPHLSSAGRLIIIVLMFVGRVGPITVLISLIQRKEKTIQYATTDILVG	
1.3E-54	195	16	3E-54	193.8	11.1	1.5	1	B6IP70_RHOCS	Trk system potassium uptake protein	trkRC1_2185	Rhodospirillum centenum (strain ATCC 51521 / SW)	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum centenum (Rhodocista centenaria), Rhodospirillum centenum (strain ATCC 51521 / SW)	414684	>tr|B6IP70|B6IP70_RHOCS Trk system potassium uptake protein OS=Rhodospirillum centenum (strain ATCC 51521 / SW) GN=trkRC1_2185 PE=3 SV=1MAVLDVRPILYVIGYLLIVLAGAMLVPMSADLAAGSPDWQVFAVSGALTLFFAVLLVLTNRTHGISLNLRQTFVLTSLAWIIVCLFSSLPFMLSSLRLGFADAFFEAMSGLTTTGSTVITGLGDLPPGILLWRALLLQWLGGIGIVGMGIVILPLFRVGGMQLFRSESSDKSDKVVPRASDLALAFCWIYLALTCICTAALMVSGMDAFDSICHAMAAALSTGGFSTEDASVGYWREPAIHWTLIVFMILGSLPFVRYVSLVRGDARPLLRDTQVRAFLGLLAVSSLGLALYLGIVQHMPAEEALRQATFNVVSVSVVTTTGFASADYTLWGSPAVALFFVLLFTGGCTGSTAGGVKIMRFEILWLTLWAQMTRLISPNRVIPLSYNGKPVDSDIILSVMSFISIYIGTMFVFTQLLAATGLDLVTSVTGVAQALGNIGPGLGTIIGPAGNFKPLEDEAKWILSLAMLMGRLELFTLLVMLSPSFWRT	
1.3E-54	195	28.3	9.2E-54	192.1	19.6	1.9	1	A0A0C5WIQ9_9GAMM	Trk system potassium uptake protein	H744_2c0279	Photobacterium gaetbulicola Gung47	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium gaetbulicola, Photobacterium gaetbulicola Gung47	658445	>tr|A0A0C5WIQ9|A0A0C5WIQ9_9GAMM Trk system potassium uptake protein OS=Photobacterium gaetbulicola Gung47 GN=H744_2c0279 PE=3 SV=1MVNFRPILFVIGLVLSKIALFMYVPTLVAFATGTEGFIDFATAVLITHVVAFLCLTFGRTSEFKLGVRDMFLITTLVWTIASAFAALPFVFINHISFTDAYFETMSGITTTGSTVLSGLDDMAPSILLWRSTLQWLGGIGFIVMGVAILPMLNVGGMRLFQTESSDWSDKSSPRTKSVAKNIVNVYLSLTGLCFLGYLLTGMNTFDAINHAFTTLSTGGYSTSDGSMNHFSNSAHWVAIVFMFAGGLPFLLFVQALRKREARTLLSDAQVRGFTLLVLAAGLAVALWLTWQLDYRFIDAFRVSLFNIISVVTTTGFGLDDFTAWGPFPTIVFAFIMLVGGCSGSTAGGIKIFRFQVAFALLRKQMMMQLIHPSGVFIQRYNGRPVTDGIVRSVVAFALTFVLTIVVVAAVLGMQGLDAVTSITGAVTAVANVGPGMGNVIGPTGNFATLPDLAKWTLSFGMLMGRLEILTVLVVFFPAFWRN	
1.4E-54	195	37.2	3.3E-54	193.6	25.8	1.5	1	A0A0F7KK77_9PROT	Ktr system potassium transporter B	AAW31_17905	Nitrosomonas communis	455	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas communis	44574	>tr|A0A0F7KK77|A0A0F7KK77_9PROT Ktr system potassium transporter B OS=Nitrosomonas communis GN=AAW31_17905 PE=4 SV=1MKPWDPHVLPYKHIIAAKKNLLNLSPPAVLFLGFALLIAIGTVLLKLPIASHSETSLLQSIFTATSAVTVTGLILLLDTGTHFTLFGQIVIALLIQAGGLGFMTFAIVAAVSLGAKLGIGQQVVVQEAFNQTNLEKVIYIAKYVLIYSLFIELTGFILLVLTWFNELGLSTAIHHAFFYTISAFNNAGFALSSNSLTPYFNNLSINLVITALVIIGGIGFLVLIDIKTQKSWHRLNVNTKTVLLSTFIINICAFTLIWVLEVKNPATLGQLSILDQALTAWFQAVSPRTAGFNTVPIEELTQATTTLMILLMYIGGGSLSTASGLKIGTFVVLIMATYAFLRRRDDVVILQRTVPPTQVMRALALAIVSIIMIFIGIFILTLTENAQFIDIVFEVVSALSTVGLSRGLTTQLSITGEIVIIFFMIIGRVGPLTFAYFFASPKKKYIKYANADIQVG	
1.4E-54	195	20.2	1.3E-29	112.5	5.7	2	2	R7B3P2_9CLOT	Trk-type K+ transport systems membrane components	BN653_02091	Clostridium sp. CAG:43	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:43	1262805	>tr|R7B3P2|R7B3P2_9CLOT Trk-type K+ transport systems membrane components OS=Clostridium sp. CAG:43 GN=BN653_02091 PE=4 SV=1MPEEITRRKRRLSSFQIITLGFAGVILLGALLLMLPISTTGENVTPFNETLFTATSAVCVTGLVVQDTGSYWSTFGQAVILALIQIGGLGVVTVAASFALLSGRKISLMQRSTMQDAISAPKVGGIVRLTRFILRGTFLIELLGALAVLPVFCRDYGWRGIWMAVFHSISAFCNAGFDILGTESNRYPSLTGYADSPVINITIMLLIVIGGIGFLTWDDIFENKWRFHRYRMQSKVILVTTGFLIFLPAMFFFFSDFSALPAGNRLLASFFQSVTPRTAGFNTVNLSTMSGASQGVIILLMLIGGSPGSTAGGMKTTTLAVLLANATATFRQRDSAQFFGRRVDCSAIKTAATILTMYLMLFFSGAVFISAYENLPLSACLYETASAVGTVGLTLGITPQLHIPSQMVVLITLMYLGRVGGLTLIYATFSSKKAGNAKLPQEKITIG	
1.5E-54	195	17.6	1.1E-53	191.9	12.2	1.9	1	R5HAJ0_9FIRM	Uncharacterized protein	BN555_01484	Firmicutes bacterium CAG:24	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:24	1263012	>tr|R5HAJ0|R5HAJ0_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:24 GN=BN555_01484 PE=4 SV=1MNYSIIFYIIGWILNLEAAFMLPSCLVALIYQESSGWSLVAAVLLCLLIGLPLVIRKPKNRVFYLREGFATTALCWIVLSCVGALPFVLSGYIPNPVDALFETVSGFTTTGASILTDVEALPHCLLFWRSFTHWIGGMGVLVFLLTLIPLTGGSHMNLMKAESPGPSVTRLVPKVKSTAKILYMIYIVLTIIEIFLLLFGGMPLFDSITLSLGTAGTGGFGIKNDSIAGYSTYCQVIITIFMILFGINFNAYFLILIRKFRQAWESEEVRAYLLIIAAATLAITFNVRGYFSSFAQAFQQTIFQVASIITTTGYATTNFDLWPEFSRTILVLLMFVGACAGSTGGGIKVSRILILLKTVKKELIQLLHPRSVRRIQIDGKAIEHEVVRSTNVYMGVYIFIFAFSMLLIALNNFDLITNFSAVAATLNNIGPGLSLVGPIGNFSMFSDFSKLVLIFDMLAGRLELFPLLLLFVPNTWKRF	
1.5E-54	195	27.7	1.1E-52	188.6	19.2	2	1	R6G042_9FIRM	Potassium uptake protein TrkH family	BN476_01230	Eubacterium hallii CAG:12	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium hallii CAG:12	1263078	>tr|R6G042|R6G042_9FIRM Potassium uptake protein TrkH family OS=Eubacterium hallii CAG:12 GN=BN476_01230 PE=4 SV=1MSKDIHKKKHLSSFQLIILGFASVILLGAIILMLPVSSAEGVITPFNQTLFTSTSAVCVTGLAVLDTGSYWSVFGQVVILLLIQIGGLGVVTVAVSVFMLSGRKISLMQRSTMQNAISAHKVGGIVRLTKFILKGTLFIEMAGALALLPVFYHDFGRKGIWMAVFHSISAFCNAGFDILGTPANPFPSITAYAENPIVNVVIMFLIIAGGIGFLTWEDICINKTHFRKYHMQSKIILVTTALLIVLPAVFFFFSDFTHLSVGKRLLASAFQAVTPRTAGFNTMDISKMTEVSKAMIIILMLVGGSPSSTAGGMKTTTFAVLILNAFATFRSQENVETFGRRIEWSVIKNASTIAMMYCMLFLCGGITISVYEGLPLSECLYEAASAVGTVGLTLGITPKLHIVSQFILIILMYLGRVGGLTLIYAVLSKKKKGNARLPLEKLTVG	
1.5E-54	195	27.8	1.9E-54	194.4	19.3	1.1	1	E4TYS4_SULKY	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Sulku_1403	Sulfuricurvum kujiense (strain ATCC BAA-921 / DSM 16994 / JCM 11577 / YK-1)	442	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Sulfuricurvum, Sulfuricurvum kujiense, Sulfuricurvum kujiense (strain ATCC BAA-921 / DSM 16994 / JCM 11577 / YK-1)	709032	>tr|E4TYS4|E4TYS4_SULKY Potassium uptake protein, TrkH family OS=Sulfuricurvum kujiense (strain ATCC BAA-921 / DSM 16994 / JCM 11577 / YK-1) GN=Sulku_1403 PE=4 SV=1MHTQEIKIILFSFIALIFGGALLLSLPFAHNGELRFVDAVFTATSAVCVTGLIVKDTPVDFTPFGHVVILSLIQIGGLGYMTAVTFMAVMRKQKIGHRDRLILKESLNHPGMDGLVRFLKIVFASIIIEAVGMLILTLRFWVDMPFGKAVWFGTFHSISAFNNAGFSLFSDNMMSFRGDFVINMAIPLLVILGGLGYIVLLEIYNFRRRDRLLRISTHTKIVLWMSGILILIGMILLLSLEWNNPKSFGGLDTYEKILAAWFASVNYRTAGFNSIDFSTLTDSNLFFSTFFMMTGGSPGGTAGGIKTTAVALALIGVWYTLRGDTNAHIFRRRSIAQYQINKAYAVIFVASFYVVMTTIILSEVEHLPFLRILFETTSAFGTVGVSTGDGGVLSYSALFSDWGKINIIVLMLMGRVGVFAFTIIIVGKAVESRIKYAEGKVII	

1.5E-54	195	23.1	2.2E-54	194.2	16	1.2	1	R6HB03_9FIRM	Potassium uptake protein TrkH family	BN490_02168	Firmicutes bacterium CAG:137	462	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:137	1263004	>tr|R6HB03|R6HB03_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:137 GN=BN490_02168 PE=4 SV=1MSYVRHLLRLRLSVSSNRLSTTRIIALAFAAIILTGALLLTLPVASRNGESCGFLTALFTATSATCVTGLILVDTFVQWSGFGQVVIL SLIQIGGLGFMSIASIFAFSLHKKLGLKQRMLLAQAMSLNDMEGVVRLQKHVLVGTFSLESLGALVLFFRFLPSYGPWNALKWGVFHS VSAFCNAGFDILGVLKPGSSLMLFQKDPVVCLTIMALIVVGGLGFFVWEDLLRAVRTRSLRRLSVYSRLVLTCSGLLILIGAGLICAMEW NNPATLGPMTVPQKLLAGAFQSVTTRTAGFAAIDQGAMRESTRAVSIVLMLIGGSSGSTAGGLKTVTVAVLLLASVASARGQSHVRVF KRSISDRQVRDAMSITVIMLILCFTGAVVLVADSGLSFLNSLYETASALATVGLTANVTPLLHLPSKLIIIAFMYFGRVGILTISLGFLMGDR AVERFRYAETKLLIG
1.5E-54	195	25	6.6E-53	189.3	17.4	2	1	D4LNL5_9FIRM	Trk-type K+ transport systems, membrane components	CK1_37170	Ruminococcus sp. SR1/5	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus sp. SR1/5	657323	>tr|D4LNL5|D4LNL5_9FIRM Trk-type K+ transport systems, membrane components OS=Ruminococcus sp. SR1/5 GN=CK1_37170 PE=4 SV=1MPEKSYKKKHMTSFQLIIMGFAGVILLGTVLLMLPFSSAEKVITPFHEALFTATSAVCVTGLVVKDTGSYWSLAGQTIILALIQTGG LGVVTVAASVSLLSGKKISLMQRSTMQNAISAPKVGGIVRLTRFILRGTFLIEAAGTVLLLPVFMGDYGKKGIWMSVFHSISAFCNAGFD ILGTDSSMFPSLTGYSGNILINLVIMLLIITGGIGFLTWDDIYTNKLNFKRYRMQSKIILMTTACLILFPAVFFYICDLTKLPMGKRLLAAAFQ SVTTRTAGFNTINISEMSEASKAVMILLMLIGGSPGSTAGGMKTTTFSVLILNAIATFRSQENAGAFGRRLEYHVIKNAATIAMLYFALFF GGGIAISVYEGLPLLNCLYEAASAVGTVGLTLGITPELHVFSQVVLIILMYLGRVGGLTLIYAVFSGRNKGNAKLPLEKITVG
1.5E-54	195	31.3	7.8E-54	192.4	21.6	1.8	1	S0JBY5_9ENTE	Trk system potassium uptake protein TrkH	OMQ_00547	Enterococcus saccharolyticus ATCC 43076	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus saccharolyticus, Enterococcus saccharolyticus ATCC 43076	1139996	>tr|S0JBY5|S0JBY5_9ENTE Trk system potassium uptake protein TrkH OS=Enterococcus saccharolyticus ATCC 43076 GN=OMQ_00547 PE=4 SV=1MRRKRQSPFHLTVSQLITLGFGILILMGALLLMTPLATKNGESTNFLDALFTATSATCVTGLTTLMTNEHWSLFGQSVILVLIELGG LGFMTIPVFFFVLMKKKITLSTRMFLREAFNSQRMSGEIHLLLYVLKIALLIQGVGSLLLAVRFVPQFGWGKGLWYSVFHAISSFCNAGF DLFGDSLVGFQKDPWVLSIISLLIISGGLGFFVWHDLLEIRKNKRLSLHSQIALLVTAGLLVFGVIGFFFTEQNSGLLAEGNRWQRFFNTI FMAVTPRTAGFFSIDYFSMSHAGLVLTMVLMFIGGTSGSTAGGFKTTTFGVLLIKIRSIFKGRSRAEFRGRTIKEDTISRALTLFFAFLTVI IISTMILSVTETIPNVDQLGLEYIVFEVISALGTVGLTMGLTPDLTSIGKVIILSLMFLGRVGVMTVFFSFIFRANKNEANFKYPEESVIIG
1.5E-54	195	22	1.3E-28	109.2	6	2.2	2	O27332_METTH	TRK system potassium uptake protein TrkH	MTH_1264	Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NBRC 100330 / Delta H) (Methanobacterium thermoautotrophicum)	479	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanothermobacter, Methanothermobacter thermautotrophicus (Methanobacterium thermoformicicum), Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NBRC 100330 / Delta H) (Methanobacterium thermoautotrophicum)	187420	>tr|O27332|O27332_METTH TRK system potassium uptake protein TrkH OS=Methanothermobacter thermautotrophicus (strain ATCC 29096 / DSM 1053 / JCM 10044 / NBRC 100330 / Delta H) GN=MTH_1264 PE=4 SV=1MVLMRYVGKRDLFTVGKYLGTIMQGVGFVVALPVFVAIIYGEGNLQSFIIPAFISLGAGTVLKRYLPEECSVRLKHGMMVACLAW LWAGLIGSLIMISALNIDFTNAFFENMSAWTGSGLTIFSSVESLPKSILFLRSLEQWIGGLGVVIVVIGILIRPGTAASRLYKSEARDERIK PSIANTVKTIWWIYITYTVLGIVLYGLTGMPLFDAINNTLTNLSTGGMSIKNMNIGYYHSAAVYLVTMLLMILGGTSFLVHYQLIKGRFFS VLHDIQLQATVVFISIFTILAVYVGGVAPLESIYHVISALSCTGSSISSTPQMVAWPAYFKVLLITCMLIGMAAGSTTGAVKIIRVITVLKGV YWEIMRILAPEGSVMPRKISGKSVSDTEIREAGSYISLYFVLLFFTWSVLVVYGYDPLNSLFEAASAQGNVGLSMGITSFNLPVVPKMA LILSMWLGRLEIIPVIVLIRGLVEAFKAG
1.5E-54	195	24.9	2.2E-54	194.2	17.3	1.2	1	S5MIS1_9MOLU	Potassium uptake protein KtrB	ktrB SDIMI_v3c01210	Spiroplasma diminutum CUAS-1	552	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma diminutum, Spiroplasma diminutum CUAS-1	1276221	>tr|S5MIS1|S5MIS1_9MOLU Potassium uptake protein KtrB OS=Spiroplasma diminutum CUAS-1 GN=ktrB PE=4 SV=1MKNSSKDEKDNIKKKSFKKKKDLKNNNEKFFYKLKNWWPFSRVSGKIIMAYLIAIITGGFLLSIPGIVKDPENHWDFITGMFTASS AISDTGITMIQTNTGYSFMGQLLIIIMCQIGGIGILTIKITLLVMIGRKVSLDDQNIAQTERGNNSLSNTVEMIKDAFIFLLSLELIGSIVLFFG FYFTPISLSGTVELDPNSVTSPYNDFGKSLWAAIFHSISATNNAGFDIISGNSLVPYNQGNSHAYLIQITFLLQWVIGGLGYPTYHDIKKK IKARREGKKVKFSLFTKLNFITYITLFILGPILVFLTEYLTVENSQILLNGYYLDKEVLSEKSGEIIKTKVWVSDGWKPTHVWMMDLIFNVS STRNAGFATVDVNSFTAGSKYLLSIWMFIGAAPSSTAGGIRTTTFAICVLAIFSIMRNKKSVEAFKRKIPDETVKRAFAVVFISFFIVITSIF VVYLDSNKMLYGTDTTEHTEATIIKLIMYVCSAFGTVGFQPFPNEQIIQLGVLSKIMLVITMFIGQLGISNTLLAFVKQKNKQNYGFLEEE VTIG
1.6E-54	195	25.6	2.1E-54	194.2	17.7	1.1	1	R7C807_9CLOT	H(+)-transporting two-sector ATPase	BN737_00550	Clostridium sp. CAG:62	456	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:62	1262828	>tr|R7C807|R7C807_9CLOT H(+)-transporting two-sector ATPase OS=Clostridium sp. CAG:62 GN=BN737_00550 PE=4 SV=1MKRFGRKKEFTTTRIIAVGFFVAIVIGTFLLMLPLSSKTGKVTGIVDALFTSTTSVCVTGLVTVPTYAHWSLFGQVVIALLAQVGGL GVITFTTMFMLILRRRIGMKERLLIQDAYNLDTIQGLVVLVKKILKGTLVIETVGALLYMTVFIPDYGLAGIWYSVFNAVSAFCNAGMDVI GPDSLSRYVGNPVVNITTMGLIILGGLGFPVWWNVLDVMKQGKRKRRTGRESLHYLSLNAKLVLFMTAFLIVVGAIFILILEYQNPATLG PLSFFDKIQAAFFQSVTTRTAGFCTISQSGLNKSTALVCCLLMFIGGSPSGTAGGIKTTTMAVLVLTVVSIIKGRRDTEMFGRRVSDMA VRRALSIFAVSFGVMLGATVILAAVQPGNFMDCLYEIVSAIATVGLSRDFTPHLTTVSRLIIIVTMYIGRIGPISLALFFNSKRFVNVKTYPK ERVSVG
1.6E-54	195	18.9	4E-53	190	13.1	2	1	R6PCQ4_9FIRM	Trk system potassium uptake protein TrkH	BN627_01282	Lachnospiraceae bacterium CAG:364	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	1262983	>tr|R6PCQ4|R6PCQ4_9FIRM Trk system potassium uptake protein TrkH OS=Lachnospiraceae bacterium CAG:364 GN=BN627_01282 PE=4 SV=1MNYLIVKSIIGRVLYFEAAFMLLPCFTALIYQEYSGWSFVFTALLCVLVGAVLTRKKTKNTVFYVKEGFVSVALSWIVLSFMGGLP FLFSGVISNPIDALFETVSGFTTTGASILKDVEVLPHCMLMWRSFTHWIGGMGVLVFLLTFMEMHGGSHMNLMKAESPGPSVSKLRP TVRSTAKILYIIYIVLTTVEILLLLAGGMPLFDSLTTSFGTAGTGGFGIKNDSIGGYSPYIQIVVTVFMILFGVNFNAYFLIWCRKFTQAFRM EEVRCYFGIIFASIAVITLNIAHLYSGVGEALRHAAFQVGSIITTTGYATTDFNLWPQASRTILVLLMFIGACAGSTGGGIKVSRFIILIKTIK KELHTLLHPRSVRKLKLDGHTLEHEVVRSTNVFLIAYVLVFALSILISFDGLDMVTNFTGVSAALNNIGPGLELVGPTQNFSIFSNGAKL VLTFDMLAGRLELFPMLLLFVRETWKKY
1.6E-54	195	28.3	3.1E-54	193.7	19.6	1.4	1	E7RQV9_9BACT	Potassium uptake protein, TrkH family (EC 3.6.3.14)	ktrB HMPREF0663_11560	Prevotella oralis ATCC 33269	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella oralis, Prevotella oralis ATCC 33269	873533	>tr|E7RQV9|E7RQV9_9BACT Potassium uptake protein, TrkH family OS=Prevotella oralis ATCC 33269 GN=ktrB PE=4 SV=1MIHFKIIYKILGSLLFIEASLMICCLVMALCYNEDDLFAFIVSVITTLFCAFVLRHVGRNADNFLSLRDAYLVVTLAWMVFSLFGTLPF IISGYVPSFTDAYFETMSGFTTTGATVIDNVDILPHGLLFWRSLTQWIGGLGIVFFTIALLPSMVGGSVKVFSAEATGPINSKLHPRLSM SAKWIWMVYLVLTAACFGCYLLGGMNWFDGLNFSMSTTATGGFATHNESISYFHSPTLEYVCTVFTFLSGVNFTLLYFSAAKFKFKQ LFSNAEFRFYLLLIVSFSLFIMLELIIRNHYDIEHAFRSGIFQVVSFITTTGLFNDDAGKWPHVTWVILAICMFFGACSGSTSGGMKCIRG VMLLKIIKNEFRQILHPNAVLPMKIDGVNVQQQKRVTLLAFLTVYLILCLIVSFTMIAVGVDNTNAITITLSSIGNVGPTLGIEIGPTMSWSM LPALVKWMCSLMMLIGRLEIFTVLVIFTPQFWKEN

1.6E-54	195	37.6	4.8E-54	193.1	26.1	1.6	1	C7NEH9_LEPBD	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Lebu_0427	Leptotrichia buccalis (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249 / C-1013-b)	445	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Leptotrichiaceae, Leptotrichia, Leptotrichia buccalis, Leptotrichia buccalis (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249 / C-1013-b)	523794	>tr|C7NEH9|C7NEH9_LEPBD Potassium uptake protein, TrkH family OS=Leptotrichia buccalis (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249 / C-1013-b) GN=Lebu_0427 PE=4 SV=1MLKKQKEISPYIIILASFIIIILIGGFLLSLPIATENGQKTNLLEGMFTATSAVCVTGLTVNDVSKVYNLFGKTVIMILIQLGGIGIITFSAI VVMMISKKMGYFTKKLIQEDINANTTFEIQKFVKKVLITVFTIEIIGAAILFLKFIQIFDYKKAIYYSIFHSISAFCNAGFALFTNNLSDFKNSVI INTIIPLLIFFGGIGFAAILNIYQYFLKKDRRLTTTTRIAIKMSIFLIIFGTILTFILEYSNNKTLGTLPFFEKIGAAFFQSVTTRTAGFNTISIAEL REPTVFLFVVLMFIGASPGSTGGGIKTTTVGLILFGIVTTIKNKEHLEYNKRRISWKIYNKAMVIVFISIMYVVVILFLLIWLEDIRVIELGFE LVSAFGTVGLSRDLTPQLSDISKLLIMITMFVGRVGPLTIALALSKVKNSKGRYVYPKEDILIG
1.7E-54	195	17.5	3.8E-54	193.4	12.1	1.5	1	B1I1A7_DESAP	Cation transporter	Daud_0265	Desulforudis audaxviator (strain MP104C)	466	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Candidatus Desulforudis, Candidatus Desulforudis audaxviator, Desulforudis audaxviator (strain MP104C)	477974	>tr|B1I1A7|B1I1A7_DESAP Cation transporter OS=Desulforudis audaxviator (strain MP104C) GN=Daud_0265 PE=4 SV=1MGEAAALLLCLGIAVYYQSTDAAALAVGCAVTALAGIILVRRKVDYQDVGYREGFVVAALGWFLTALFGSVPFVVSGAIPHPVDA FFETMSGFTTTGASILTDIEALPPGLLFWRSLTHWIGGIGTVVLLVALIPSLRIAGMQFYRAEVSGPTKAKALPRVAQTSRQLFKVYMVF TLLQIVALRAAGMTWFDSLIHTFGTVATGGFSNRNLSVGAYDSLAVELIIVFFMVICGMSFALHIKALQGNPAVIWKDSETRVYLLVMLA AVAVISHNLVSTAGYSVETSVRHSLFQVSSVMTSTGFATADFDQWPDLSRLVLLLLMFVGACAGSTGGGIKIIRIMILAKLALRQLQKLI HPQAVIPIRVGRSVIPAEVADGVQAFLVLYLGLFSGAVLVMGALGLDLVSAFASVVATMSNIGPGLGLVGPAANYAAVPVAGKLVLSFC MLVGRLELFTVLALLNPGFWRK
1.7E-54	195	12.2	2.5E-54	194	8.5	1.1	1	E6SIU9_THEM7	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Tmar_0829	Thermaerobacter marianensis (strain ATCC 700841 / DSM 12885 / JCM 10246 / 7p75a)	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiales incertae sedis, Clostridiales Family XVII. Incertae Sedis, Thermaerobacter, Thermaerobacter marianensis, Thermaerobacter marianensis (strain ATCC 700841 / DSM 12885 / JCM 10246 / 7p75a)	644966	>tr|E6SIU9|E6SIU9_THEM7 Potassium uptake protein, TrkH family OS=Thermaerobacter marianensis (strain ATCC 700841 / DSM 12885 / JCM 10246 / 7p75a) GN=Tmar_0829 PE=4 SV=1MDTSLGGGAPQRPATGAAGLDAGAPPERRRRTAPAEAREPNPARILALGFAGVILLGSVLLSLPVAWEPGQRVGYLDALFTAT SAVCVTGLVVVNTAETFSTFGEMVILALIQVGGLGVMTMSTLFALLVGKRITFRERLIIQEAWGQLSPAGMVRLVQYVTLVSVAFEAAG TLLLTLYWWQAYDMPFGLALYRGFFHAVSAFNNAGFDVFDSRRPSLERFAGDPVVTLVIGGLIIAGGLGFTVLADLGRRLRHRRHRLS LHTRLVLWTTAALLVAGTVLVAVAEWSNPATLGSLPVDRKLWAAFFHAITPRTAGFNMLPMAELTSLTVLTTILLMFVGGSPAGTAGGI KTTTLALLLATVRATIRGEDELVLMDRRVPTLTAAKALALAVLGAGLVLVVTMGMLLWDHHPLTATLFEAVSAFGTVGLSLGITPDLAPV SKVLILLTMYAGRVGPLTLAVALTRRGRRPPAVRYPEERVLVG
1.7E-54	195	10.4	3.8E-54	193.4	7.2	1.5	1	W0K5C5_9EURY	Potassium transporter TrkH	HALDL1_12860	Halobacterium sp. DL1	515	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halobacterium, Halobacterium sp. DL1	751944	>tr|W0K5C5|W0K5C5_9EURY Potassium transporter TrkH OS=Halobacterium sp. DL1 GN=HALDL1_12860 PE=4 SV=1MARTLSTYVDFRTSVAFVGSVLKYIGVTPLFPLVLAFYYGEDPLPFVATSVVMVGGGVLLEQLSDDTDLGNREAFLLVSLAWLV VPLAGTVPYLVAGVGSVANPVNAMFESMSGFTTTGATVLGEISVDRHGHAMLLWRQLTQWLGGMGILVLMVAILPELSVGGAQVMN EEAPGLSLEKLTPRIQKTARGLWGIYAGFTVLAALAYYGLHLVGAAPNMDLYNAVAHALTTLPTGGFSPEARSVEAFTPAVQWMVMP FMLVAGTNFALFWYVFRGEPSRLTENTEFRSYLLAIAGFGAVISAVLFAGVGLAETPVNVDVIPGNVEDSLRQGLFQVIAVVTTTGYAS MDVNTWDASAQTILLFAYFLGGSAGSAAGSIKIVRWVLVKKAVVRSLFTTVHPDAVKPIRVGDDAVDEGTIRDVFVFVLLFVGLFALST VLLYLDSFRTAGVSMSGLDAMSVAMATLGNVGPGFGVVGPMNSFLPFTDAAKLYMVFLMWIGRLEVLSVLVIFTPAFWKR
1.7E-54	195	24.1	2.3E-54	194.1	16.7	1.1	1	R5Z764_9FIRM	Potassium uptake protein TrkH family	BN504_01492	Eubacterium sp. CAG:156	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:156	1262880	>tr|R5Z764|R5Z764_9FIRM Potassium uptake protein TrkH family OS=Eubacterium sp. CAG:156 GN=BN504_01492 PE=4 SV=1MKVDKAIKATFNTNLIILNGFLVALLVGTILLMLPVSSASGNGTDFITALFTATTSLCVTGLVVVPTYAYWSIFGKVIILILIQLGGLGII SFTIGFLIIIGKKISLKERKMIQESYNLDSAQGVLKILRKIFGITVKIEGIGAILYSIQFIPEYGIVKGICYSVFHSVSAFCNAGIDIIGNDSFVKY HGNVLVNFTTVMLIICGGIGFIVWLDIGGIISEIRNKKLRPNKFIERMKLHTKLVLITTAILVGGGFLFILLFEYNNPDTLGNMTFGNKCLAA LFEAVTLRTAGFITVPQAGFRDGTFMIMCGMMIVGGSPLGTAGGIKTTTLALVFLLTWATIKGKDDIEVCRRRINKQNVRSAVAIGTIVL SILAVAIMALSFTEGAPLKVITFEAVSALGTVGLSMDFTASLTAIGKLIIIVLMFFGRVGPITIAMAMTGRARKDRKIKNYPEKRVMIG
1.8E-54	195	33.8	2.4E-54	194.1	23.4	1.1	1	B7K5T7_CYAP8	Potassium uptake protein, TrkH family (EC 3.6.3.14)	PCC8801_4053	Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	454	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	41431	>tr|B7K5T7|B7K5T7_CYAP8 Potassium uptake protein, TrkH family OS=Cyanothece sp. (strain PCC 8801) GN=PCC8801_4053 PE=4 SV=1MTIARTICLGFVAVITVGTLLLILPFSTVDGHWNNPIIALFTSTSAVCVTGLTVVDTGTYFSFWGQLIITLLIQVGGLGYMTTTTFLM LLIGRRFDLRQKLAIQDSFDRPFRQVSSRMMISSIISMTLLFEITGVIFLFIFFKDRYELPYSLWLSIFHSVSAWNNAGFGLFKDNLMSVQ GSLIINFTITILIIFGGLGYQAILEIYMWIIHKIKNKQERVVLSLNFKVVTSTTLFLLIFGTVIFLLVEYNNPETLASMSLKDKLLGAWFQSVTT RTAGFNTIDNGKMTIAGLLLTMGLMFIGASPSGTGGGIKTTTVRILSNCTRSVLRGNDQVILYQREVPVPLILKAVSVVFGSTILVISISFFI SFIEVSINPDVFEVSFNSLQVLFEVISAFGTVGLSTGITASLSPISQILLVLTMYTGRVGVLLLMAAIVGDARPRVVQYPEESLLVG
1.8E-54	195	23.4	1.1E-52	188.6	16.2	2	1	D4JAC1_9FIRM	Trk-type K+ transport systems, membrane components	CC1_26590	Coprococcus catus GD/7	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, Coprococcus catus, Coprococcus catus GD/7	717962	>tr|D4JAC1|D4JAC1_9FIRM Trk-type K+ transport systems, membrane components OS=Coprococcus catus GD/7 GN=CC1_26590 PE=4 SV=1MPGENIRRKRRLSSFQIIILGFAGVILLGALLLMLPISTTAGGVTPFNETLFTATSAVCVTGLVVQDTGSYWSAFGQAVILTLIQIGG LGVVTVAASLALLSGRKISLMQRSTMQDAISAPQVGGIVRLTRFILRGTFLIELLGALAMLPVFCRDYGWRGIWMALFHSISAFCNAGF DILGTEDNLYPSLTGYAGSPVINITIMLLIVIGGIGFLTWNDICENKWRFHRYRMQSKVILVTTGLLILLPAVFFFFSDFSALPAGNRLLAS FFQSVTPRTAGFNTVNLSAMSSASQGVMILLMLIGGSPGSTAGGMKTTTLAVLLANAVATFRQRDSAQFFGRRVDCSAVKTAATILM MYLVLFFGGAVFISAYENLSLSTCLYETASAVGTVGLTLGITPQLHITSQMVLITLMYLGRVGGLTLIYAAFSGKKATGAKMPKEKIMIG
1.9E-54	194	35	2.8E-54	193.8	24.3	1.2	1	Q9K8B2_BACHD	Na+-transporting ATP synthase	BH3094	Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus halodurans, Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)	272558	>tr|Q9K8B2|Q9K8B2_BACHD Na+-transporting ATP synthase OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) GN=BH3094 PE=4 SV=1MKSALNQFMTPFRMIMVSYIIAMFLFSVLLFLPISQQPGVNLTFSEALFTSVSAVSVTGLTVVNVSETYSYIGILFLALAIQLGGIGI MTLGTFVWMLFGKKIILSQRMLIMVDQNQNQFSGLVNLMRGILLVALSIEFIGALILGTYYIRYFDTVGEAYYQGAFAALSAFTNAGFDIT GESLIPFADDYYVQLVTILLIFAGAIGFPVFLEVRAYFSKENPNFTFSLFTKITTTTFFAVFIFGVIGIWALEKNHYFVVGLEWHQQLFTAVF NSATSRSGGLTIMDISDLSLATLLFISGLMIIGASPSSVGGGIRTTTLAVMFLTIRSFALGKQDVKVFGREIHPEDQQKSFIVISVFLVLLFA AVIMISAFERGSAIPLIAIIFETASAFGTCGLSMGITDELSLPSQFILMVLMFIGRVGLIAFLFSVRRKETKSYYKYPTERIIIG

1.9E-54	194	29.5	2.4E-52	187.5	20.4	2	1	A0A089MMX6_9BACL	ATP synthase subunit J	PODO_16140	Paenibacillus odorifer	438	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus odorifer	189426	>tr|A0A089MMX6|A0A089MMX6_9BACL ATP synthase subunit J OS=Paenibacillus odorifer GN=PODO_16140 PE=4 SV=1MTPPKVLSLGFLILITAGTFLLSLPVSSTSGQISFIDALFMATSATCVTGLAVIDTGTQLTTFGQVVLLILFQIGGLGFVTMATLITLV LNKRISLKERILLQESMNQNSMQGIVLLIRRVLIYSLVIQLSGAVLFAGRFMMDMPFGKAAYYGIFHSISIFNNAGFDLFGDIHGPFSGLT RFVNDPIVNFTSMSLIFLGGIGFIVLSDLMDFPKRRRLTLHSKVVLWTSLILIIIGAGLFFLLEYNSTLKPLSASGKFWATFLQAVTPRSGG VTTIEVPLLRQSTQFLMILLMFIGAAPGSTGGGIKITTFAVLVTAVAARLRGKEDIVMFRHRIAKENVYRALTITLMSLMLLVIATMLLSLTE SAEFLTVLFEAVSAFGTSGLSMGLTPELTTAGKVLVIILMFMGRTGPLTLAYALKPKGSKELYRYPEGKITIG
1.9E-54	194	20.9	1.2E-28	109.3	5.5	2.1	2	A3QJF8_SHELP	Trk system potassium uptake protein	Shew_3740	Shewanella loihica (strain ATCC BAA-1088 / PV-4)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella loihica, Shewanella loihica (strain ATCC BAA-1088 / PV-4)	323850	>tr|A3QJF8|A3QJF8_SHELP Trk system potassium uptake protein OS=Shewanella loihica (strain ATCC BAA-1088 / PV-4) GN=Shew_3740 PE=3 SV=1MLNFRPLLFILGVFLSTLTAFMFFPLLFALLYGEETVGAFMIASLITGTCASACMHQGQSENIRLNIRDMFLLTSLTWFIVSLFAAM PFTLYHGINYTDAFFETMSGITTTGSTVLSGLDTMDHSILIWRSLLQWLGGIGFIVMAVAILPFLNVGGMRLFRTESSDWSDKAVPRTQ DMAKHLFYVYIILTVCCGVAYHLAGMTWFQAINHAMTTLSTGGYSTSDSSMAAFSKPAHWVGTIFMAAGGLPLLMFVHSLSQRSLRI WNDAQVKGYLIFLAFVSCSLAFWLWHGHEMTAADALRLASFNVVSVVTTTGYGLTDYTSWGAVANVAFLFLMFAGSCSGSTSGGIKI FRFQIAIAIMREQLKQQFHPNGIFKERYNGRPITEDIVRSLVTFILLFMLVIVLLSVILVSTGLDPTTSFTGAVTAVTNVGPGLGPVIGPAG NFSSLPDIAKWSLAIGMLLGRLEILTVAVLFHPNFWKY
2E-54	194	26.5	1.5E-53	191.4	18.3	1.9	1	D6GSY4_FILAD	Trk system potassium uptake protein TrkH	HMPREF0389_01221	Filifactor alocis (strain ATCC 35896 / D40 B5) (Fusobacterium alocis)	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Filifactor, Filifactor alocis, Filifactor alocis (strain ATCC 35896 / D40 B5) (Fusobacterium alocis)	546269	>tr|D6GSY4|D6GSY4_FILAD Trk system potassium uptake protein TrkH OS=Filifactor alocis (strain ATCC 35896 / D40 B5) GN=HMPREF0389_01221 PE=4 SV=1MNYKMIRYLIGKMLRIEALLLLIPTLVSVYYREPIAKTIFQICVGLTVLGSILSYEEPDKSEFYAKEGLVIVATTWLVLSLCGALPFYL TGEIPSYIDSFFETVSGFTTTGSTILTDIEVMSKGLLFWRSFTHWIGGMGVLVFAFAIFSQSSVNSMYIMKAEVPGHKVGKLVSKISLTA RILYGIYILLTVIEVGFLYAGGMSFFDCWIHAFSTAGTGGFSSHNASIAYFDSVYIETVITVFMILFGINFQLYYFLLLKKFKDCFGSEELR YYLLIILGAIILISFNIRAVAGSWGEAVRGSSFQVAAIITTTGFVTRDYQQWPFLSQGILLTLMYIGAMSGSTGGGIKVSRIILMIKNTVMGI RKIQHPNRVFSIQIENSPVPTGVMQELQAYFNLYLCIMVISLLVLLSQGMDLLSTFGAVSCCLNNVGPGLGVVGPVDNFSSLTNISKLIL SFDMLAGRLELFPMVIIFLPTTWRKN
2E-54	194	25	7.2E-52	185.9	13.5	3.2	2	Y2412_DICDI	Putative potassium transport protein DDB_G0292412	DDB_G0292412	Dictyostelium discoideum (Slime mold)	648	cellular organisms, Eukaryota, Amoebozoa, Mycetozoa, Dictyostelida (dictyostelid cellular slime molds), Dictyostelium, Dictyostelium discoideum (Slime mold)	44689	>sp|Q54DR4|Y2412_DICDI Putative potassium transport protein DDB_G0292412 OS=Dictyostelium discoideum GN=DDB_G0292412 PE=2 SV=1MVGFIGSVLIKLIEFEVPFIDCLYIGYSALTTTGLVTVDISGWSSGTLFLLVILVQLGSTVLLTLPIVLLRRFFIRSVYSNSSIISAANAS PDLISTIIHSHLPHHDFKDDDDENDNNNNEENDDNDDESYQHNNNNNEEHDDNDIEIGGILKLDSPIDHNLPNGFQDDNAPHHYNIPIV GKIDKKSRKFSLDSPSSPIIQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQPSTTTTTTTTTNSTLNKSTNNSTNNNNNTNDSQSIQKE VNIDINRIDSLQELQEQQEHQQQQRQLSKPLNLNSYEDNMEYRSLGKLLVIIPCYIITIYILGFISIGAYIAGSESARSIMKANGVNGWWW SLFHTFSAFNNAGLALFSDSLIQINEKYFLLITLSILIFLGNTLFPVFLRIILLVVSKFTKDPEPYRNLLENPRSIFTHLFPYKETVQLFVIWCI FNVSQIALMALLDVNDKAFTNMNYGTILLNYYFSSISTRTCGFNSVDLNLLSESVLLLFVGLMFVSSYPFIISLRRSAVNNKYSNQSREV MKEVLIRDIFVPYICILFIAIFESQLLESGVITVFQILFEAISAFGNVGLSISITLSTYSKLVFIALMLAGKHRQLPESVDESVNPALLKKNAVI SKIITRYKRRKL
2.1E-54	194	42.6	4.8E-54	193.1	29.5	1.6	1	R5LQB9_9SPIR	Cation transport protein TrkH	BN758_00057	Brachyspira sp. CAG:700	580	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Brachyspirales, Brachyspiraceae, Brachyspira, environmental samples, Brachyspira sp. CAG:700	1262760	>tr|R5LQB9|R5LQB9_9SPIR Cation transport protein TrkH OS=Brachyspira sp. CAG:700 GN=BN758_00057 PE=4 SV=1MLNKKNRYANKNIIHTINELVSRFSNLLAIAGSIFAIFVLLMQIRSINAYNFYIANYGKIINIITICFIFILLEQIRIAPRKLYIIVPIIQIIGLILI NFLSKKYYNIYSYRIAWTIAGSILFFLIIVINWLRLSYSKFTLYQLIIASFVFVITLGSLLLYLPLSTVKGNMHFIDALFTATSAVCVTGLTVIDI SKELTLFGRIVLITLIQIGGLGIMSISAIVLLFSVSKGSVRDRIRTLEMFNTQNKDIIQSTIKVIFLATFLIEFAGAISLFTVIKNDAGGVGEKIF YSLFHSISAFCNAGFSLYANSLHRFSNNITVSVTIGLLIILGGIGYPVLLTVFFAIKNKIMGKRYIIDTQTTIVLFTTIILLLFGFLFIFFNEYDG VLKDLSLREKILISAFQSISPRTAGYETISYNSMNSVTIGIIVFLMFVGASPSGTGGGVKTTTLFVFVSSIITAISNRPFIVVRGRKIKESAV NKSVAIFTLAIAISAFAALLIFYIDGYKTMTPVLFESVSALSTTGLSLGITPSLSIWSKIIVMILMFIGRVGYLTLFMSVGSIDKGRYGLIDLPT SDVTIG
2.1E-54	194	36.4	4.1E-54	193.3	25.3	1.4	1	C2W5H9_BACCE	H(+)-transporting two-sector ATPase	bcere0022_10460	Bacillus cereus Rock3-44	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock3-44	526986	>tr|C2W5H9|C2W5H9_BACCE H(+)-transporting two-sector ATPase OS=Bacillus cereus Rock3-44 GN=bcere0022_10460 PE=4 SV=1MREIKKFLQKLRPVQLIVLFYFIAVIVSVILLSFPFFIKPGVKWTFIDALFTSVSAVSVTGLSVVSIPDTFNTAGIIVLALVLQLGGLGI MALGTFVWMLTGKKIGLQRRRLIMADHNQGNLSGLVELMRSILILVSIEAVGALLLGTRFLQYFPTWQEAYFHGFFAAVSATTNGGFD LTGQSLIPYKNDYIVQIIHMLLIILGAIGFPVLMEVKQYLSKKRHELFRFSLFTKLTTTTFFSLVIVGTIVIFLLERNQFLVGKSWHETIFYTL FQSVTTRSGGLATMDIRDLSQPTLLFMSVLMFIGASPSSVGGGIRTTTFAVNILSLYTFAKGGRTVRVFKRQLHEEDILKASVVMTMGI VLCASALFILSMTENVPLMSLIVEVCSAFGTTGLSTGITSELTTIGKLVLIVLMFIGRVGILTFILASGGREQPPRYKYPKERIIIG
2.1E-54	194	28.6	1E-52	188.7	19.8	2	1	R7FQV3_9CLOT	Trk-type K+ transport systems membrane components	BN588_01134	Clostridium sp. CAG:288	442	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:288	1262791	>tr|R7FQV3|R7FQV3_9CLOT Trk-type K+ transport systems membrane components OS=Clostridium sp. CAG:288 GN=BN588_01134 PE=4 SV=1MKILKRKLSSFQIILLGFAGVILLGALILTLPISSKSHEWTSFIDALFTSTSAVCVTGLIVFDTATHWTIFGQIIILLLIQIGGMGVVTIAV SLAVASGKKIGLFSREAMKNAISAPNVSGIVRLTGFIIKGTFLIEMIGALIMLPVFCKDYGAEGIWMAVFHSVSAFCNAGFDIMGTKNGE FTSLTHYSGQPVINITIMLLIIVGGIGFLVWEDIYKHKWRIREYRTQSKLVLIVTAVLIVLPAVYFFFFECDDLPVTERILASLFQSVTPRTA GFNTINLTAISDTGLYLMIILMLIGGSPGSTAGGMKTTTIAVLFSSAFSVFRKKDNAEVMKRRIDDETVKTASAVFLMYITLFLVGGMAIS AIENLPITSCLYETASAVGTVGLTLGITPTLGIASKMVLIMSMFFGRVGGLTLIYAAFGTHKKQVAKLPTDTIAVG
2.1E-54	194	36.1	1.5E-52	188.1	25	2.1	1	E4TK32_CALNY	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Calni_1400	Calditerrivibrio nitroreducens (strain DSM 19672 / NBRC 101217 / Yu37-1)	428	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Calditerrivibrio, Calditerrivibrio nitroreducens, Calditerrivibrio nitroreducens (strain DSM 19672 / NBRC 101217 / Yu37-1)	768670	>tr|E4TK32|E4TK32_CALNY H(+)-transporting two-sector ATPase OS=Calditerrivibrio nitroreducens (strain DSM 19672 / NBRC 101217 / Yu37-1) GN=Calni_1400 PE=4 SV=1MSKNNVWSVFTSTFLFLIVLGSVALMIPGMYKGSLHYIDALFTSTSAVCVTGLVVTNTSNFTLMGQFVIITLIQLGGLGIMVLTTSL LLFLRGELDLKRRIVITNLIDVYALSEAEYVLKYIVLYTFFIELIGAILLTFGFLMDGHSLLSSIFYGVFHSVSAFCNAGFSPFDDSIIGMNWL IKVTIMLLIIFGGLGFYVIYDLHNYFKKRENRLKRLKVHTKIVLITTAGLIIFGVVILSILEHDMSLLDGFFQSVSARTAGFNSVDLTKLTNISK FALIILMIIGASPGGTGGGIKTSTFAITLLSIKNILKGDNRITLFNREIHYINILKSFSITAMYIFVLIVATLLMLYFYNYDFMDMLFEVASALGT VGLSLGITMKIGLAGKIILMICMFVGRIGVSALFLSLVGYEHVSNIRYPEEKVILG

2.1E-54	194	36.6	2.7E-54	193.9	25.4	1.1	1	D3EQQ9_ATETH	Potassium uptake protein, TrkH family	UCYN_11400	Atelocyanobacterium thalassa (isolate ALOHA)	454	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Candidatus Atelocyanobacterium, Atelocyanobacterium thalassa (isolate ALOHA)	713887	>tr|D3EQQ9|D3EQQ9_ATETH Potassium uptake protein, TrkH family OS=Atelocyanobacterium thalassa (isolate ALOHA) GN=UCYN_11400 PE=4 SV=1MTIARTICLGFLAVILVGTLLLMLPFATSDGSWSNPLVALFTSTSAVCVTGLVVVDTGSYFSFWGQLIILLLIQVGGLGYMTTTTFLILVLGRKFDLRQKFAIKEPFDSSHLYGSSQNIIISIVATTLIFEILGILLMLNVFSDKYGTFQGLWIATFHSISAWNNAGFSLFSDSLISVGDSFIINFAISILIIFGGIGYQVIIEMYIAIRHKLKNKQERLGFSLNFKVATSTTIALLVAGTITFLITEYNNQATLGLLNFHNKLLTAWFQSVTTRTAGFNSIDIKNMTFAGLFLTMGLMFVGASSNGTGGGIKTTTLCILTNCTRSVLKGNHEVVMFRREVPVSLILKAVAVVFGSTNMVVLMTLLISLSEASLNPTFFDSGVSSLQVLFEVISAFATVGLSTGITANLSSLSQLLLILTMYVGRVGILVFIAAISKKSQPRLIQYPEETLLVG
2.1E-54	194	31.8	3.6E-54	193.5	22.1	1.3	1	A0A077LBW0_9MOLU	Potassium uptake protein KtrB	trkG MCAN360_0479	Mycoplasma canadense	518	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma canadense	29554	>tr|A0A077LBW0|A0A077LBW0_9MOLU Potassium uptake protein KtrB OS=Mycoplasma canadense GN=trkG PE=4 SV=1MKNKKLNPKKTNIVLRFLRKLGAVRYIFIIYILFTILISLLLFWNVSHKSDLKEPIKYIDALFVSSSAFSDTGLTPVVILNTFNSFGQFLIAISMVVGGIGIFTFKIYIFQSILGLKSNIFSNTVSQTERGAITVSETRKMIKIAISFLIISTIIASFIFTMILYLKPNNNFITEELAKKTNPLIFNNKVVMKANEIPYNNFFQSLKLGIFHAISSINNAGFDLFGNKSLQPFYNDYTFQLVTIITFLIGGIGFPVIYDIWKKIESLKKDKPRHRFQLFTKFTIITYLSTTVLGFALTAILEYSSKSKDTFWYQEAYGNVGDKLFAIYFQVSSTRSAGFSTVDYINFTHSTILLHSILMFIGFSPVSTAGGIRNTTVAVIFLSLVTMLTGRKKINAFKRQIGKETLIKAVNVFALAIVLVFAVTIISYSTLPKETKSIDNTHLPMIFVLFEACSAFGNTGLSTGLSSGINNLHIAGKLSLITIMITGQFGILQTIRIFGREKSKPEHYQYIYEDVSVG
2.2E-54	194	6.7	8E-53	189	4.7	2	1	E4U524_OCEP5	Cation transporter	Ocepr_1922	Oceanithermus profundus (strain DSM 14977 / NBRC 100410 / VKM B-2274 / 506)	482	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Oceanithermus, Oceanithermus profundus, Oceanithermus profundus (strain DSM 14977 / NBRC 100410 / VKM B-2274 / 506)	670487	>tr|E4U524|E4U524_OCEP5 Cation transporter OS=Oceanithermus profundus (strain DSM 14977 / NBRC 100410 / VKM B-2274 / 506) GN=Ocepr_1922 PE=4 SV=1MGGFVRYALGTALRAVGLVMLAFVLVAWAWSEDVRGFLLGAGVGLALGQLLRMTGTPKAEPRRAEGLFIVAVIWLLVPLLGALPFWVSGHVGLLDAYFEAMSGFTTTGATILPDFTLFNRSLFLWRGLTQWFGGVGIIVLFVAVLPHFAVAGRQLFFAESTGVQKEKLTPRLRHTAEMVLRVYVLLTGLAVLGYWLAGMPLYDAVANALTTMPAGGFSPNPLSFAGYPAAAQWVAVVFMFFAGANFLLIASALFGRASRTPWRDPEFRVYSGAFLAGSLLLAVYHVYLHDYGIEAALRHAFFQVASLLTSTGYASVDYTQWVVPAQAILIFLMFVSGSAGSAAGGVKSVRWLVMTNHVVLRELKRTLHPNAVLPLRLGTKAVGEDVLRSVSSFVILYLFVFVLGTMVIVFTEGDLVVAFTSSAAFIGNVGPGLGAVGPMGSFAELHPLAKLVGIFQMWAGRIELIPVLLLFHPDTWRALRRSR
2.2E-54	194	21.7	6.1E-28	107	4	2.2	2	R7R5V2_9FIRM	Cation transporter	BN450_02720	Roseburia sp. CAG:100	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:100	1262940	>tr|R7R5V2|R7R5V2_9FIRM Cation transporter OS=Roseburia sp. CAG:100 GN=BN450_02720 PE=4 SV=1MNFRLINSILSRVIMLQGILLLPSCLVGILYHEWHDVLVYLIVSICCTLFGLLLYQVKPKSSTFYAREGFVAVSLSWIIMSVIGAMPFYFSSDIPDFTDALFEIISGFTTTGSSILLDVEALSHANLFWRSFSHWIGGMGVLVFILAILPMSGGSTMNLMKAESPGPSVGKLVPRIQQTAFLLYAIYFAMTIIELILLLCGSMRPFDALCLTLGTAGTGGFGIRNDSLASYSTYSQIVVTVFMFLFGVNFTFYYFILINKVKDALHMEEVRGYFILFAAASVAIAVNLCLTDTPGFWHNLQQSAFQVASVMTTTGYATADFNLWPTFSKVVLVGLMFIGACAGSTGGGIKVSRILIYVKQVRKELMQQIHPRQISVTKLDGKGIEHTTIRSCNVFLMTYGVVFIVSILLISLDGFDFTTTFTSVAATLNNIGPGLDMVGPTGNFASFSVFSKYILMFDMLAGRLEILPMLILFHPATWKK
2.3E-54	194	27.2	2.2E-53	190.9	18.8	2	1	R7NS92_9FIRM	Cation transport protein	BN720_00377	Eubacterium sp. CAG:581	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:581	1262890	>tr|R7NS92|R7NS92_9FIRM Cation transport protein OS=Eubacterium sp. CAG:581 GN=BN720_00377 PE=4 SV=1MNYRAVVNVLGKIMFMEGALMILPLIVAIIYGEYDTLIAFLIPIVILVSIGLAFGVKTPKNKMLLAKEGFMICGLAWIFMSAFGCLPFVISGMIPNYLDAFFETVSGFTTTGSSILTKVEGNPYGLLFWRSFTNWIGGMGVITFLMAIVPQGDGQAMHLMRAEVPGPKAGKIVSKLTDTARILYILYFILTALEIVMLMFSGIGFYHSVVTAFATAGTGGFSVKGASIAGYHSPYVEYVVATFMLLFGVNFNLYFFMILRKFKAVFQDTELKVYLGMVTASVVLICVNLLSTGKMAFETAFRDSYFTVASIVSTSGFVTADFEQWSVFSKVILISLMFVGGMAGSTAGGIKVTRIVLYFKQMIRDIKQMVRPRQVMSVRINKKSVDNSILKGINTYLVIYVFILLASTLLVSIEGESLVTTFTAVVTCFNNVGPGMDGVSATSNFAHLSALSKIVLSFDMLAGRLEIFPMMILLIPSTWKRRV
2.3E-54	194	28.9	2.6E-53	190.7	20	2	1	C7LSQ9_DESBD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Dbac_1352	Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) (Desulfovibrio baculatus)	448	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfomicrobiaceae, Desulfomicrobium, Desulfomicrobium baculatum (Desulfovibrio baculatus), Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) (Desulfovibrio baculatus)	525897	>tr|C7LSQ9|C7LSQ9_DESBD H(+)-transporting two-sector ATPase OS=Desulfomicrobium baculatum (strain DSM 4028 / VKM B-1378) GN=Dbac_1352 PE=4 SV=1MKHAHKFLSPAVLPVYFFAATILLGGVLLHLPVALNGTHLTWLDAMFTSVSATCVTGLVVVDTGTVFSTFGQTVIAVLIQIGGLGVMTYTSLVFYMWRRRVSLTDRIAVGQSLQGDPSFKLGRFLVQLFLVCFGIEALGAVAMYAFSLGELDWFSAFFHSVSAFCNAGFSLYPDSLMRFSGNLPINLLFMTLIFLGGIGFYVLVELPGFFGAALRGRPLRGALSWQGSLVIRTSLWLILIGWVVFFLIEQRQDGMATALLQSLFQSVTARTAGFNTMDIGIMTDTSLFIMILLMIIGGSPGSCAGGIKTTALRVLLGFAVSQIKGRDQVVVEGYGVDASTVNKAMTLVIFAFVLIMGSVFILTVTEGANQPHQLVRGKFMELFFEASSAFGTVGLSTGLTPHLSTPGKFIIMLLMFVGRLGPIVFLTMLQAWQTRERFKRAEKSMLIG
2.3E-54	194	17	2.6E-30	114.8	3.8	2	2	F6A938_PSEF1	Trk system potassium uptake protein	Psefu_1994	Pseudomonas fulva (strain 12-X)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas fulva, Pseudomonas fulva (strain 12-X)	743720	>tr|F6A938|F6A938_PSEF1 Trk system potassium uptake protein OS=Pseudomonas fulva (strain 12-X) GN=Psefu_1994 PE=3 SV=1MAWPTLRLIAFINGIFLITLAIGMIGPMFTLFVFDRAAEVSPFAWSSLITFIAGLSMIARGKPQDVHLRPRDMYMLTVSSWLMVCIFAALPFMFTQHMSYTDAFFESMSGITATGATVLIGLDNMSPGILIWRSMLHWLGGIGFIAMAVAILPMLRIGGMRLFQTESSDRSDKVMPRSHMVAKYMAVAYFGISLLGCLAFWLAGMSFFDAINHSMSAISTGGFSTSDLSLAKWTQPAVHWVAVVLMILGSLPFVLYVSTLRGNFGAVLADQQVRGFLGILLGVWLTMGTWYYFTTDLHWLDALRHVAVNATSVMTTTGFALGDYSLWGGFAGMLFFYLGFIGGCSGSTAGGLKIFRFQVAYILLKANLMQLVHPRAVIKQQYNRHRLDEDIVRSILTFSFFFTIIIAVLALALTLCGLDWITALSGAASTVAGVGPGMGPIIGPAGTYASLPDMAKWLLTLGMLMGRLEILTVLVLFMPAFWRH
2.4E-54	194	28.7	1.4E-53	191.5	19.9	1.8	1	Q7MMB0_VIBVY	Trk-type K+ transport system, membrane component	VV1162	Vibrio vulnificus (strain YJ016)	456	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio vulnificus, Vibrio vulnificus (strain YJ016)	196600	>tr|Q7MMB0|Q7MMB0_VIBVY Trk-type K+ transport system, membrane component OS=Vibrio vulnificus (strain YJ016) GN=VV1162 PE=4 SV=1MKPFSHNNGLFYLADKTSKQSKGNEPRIILLSFLAVLLPSAILLTLPVFSVSGLSITDALFTATSAISVTGLGVVDTGEHFTLAGKILLMLLMQIGGLGQMTLSAVLLYMFGVKLSLRQQALAKEALGQDRQVNLRRLVKKIVIFACVAELIGFVLLAFRWVPEMGWQSGLFYALFHSISAFNNAGFALFSDSMMSFVDDPLVIFTLAALFIFGGLGFTVVGDVWMNWRRGFHFLHLHTKIMLVATPALLIIGTLLFFVLEQHNANTMGELSTSGQWLAAFFQSASARTAGFNSVDLAQFTQPALLIMIILMLIGAGSTSTGGIKVSTFAVAFMATWAFLRQKKHVVMFQRTVNWPTVTKSLAIIVVSGAILTTAMFLLMITEQAQFDKVMFETISAFATVGLTAGLTAELSEPGKYIMIVVMIIGRIGPLTLAYMLARPEPTLIKYPEDTVLTG
2.5E-54	194	36	1.7E-53	191.3	24.9	1.9	1	R6XF90_9FIRM	Potassium uptake protein TrkH family	BN602_01249	Firmicutes bacterium CAG:313	444	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:313	1263017	>tr|R6XF90|R6XF90_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:313 GN=BN602_01249 PE=4 SV=1MKKHHLSIVGILFLGYFITILIGTILLLLPISKNITEKIEWYDAMFAATSATCVTGLIPFPTTNWSTFGQIVLLVLIQIGGLGFMTIISLILMMFKKNIGIYHRTVLMQSAGSYSISGVTNLIKRIILVTLFCEIVGAIILSLRFSSDMEIGKAIYFGIFHSVSAFCNAGFDLFGVSLINYQSDWIVLSTIMLLIIFGGLGFVVWSDFFDHGLKFKKYELHSKIVLVFNGIIILVPAIFYFIFEFTNFGNAGKFTYLPFNEKILNALFLSVSPRTAGFNSLDLNNLTSSGKLLTMVLMFIGGSTGSTAGGVKVTTIVVVIANLVSLARGKDKIVLFKRRVVNNNIVKQSSALVLAYLIITISTLVICAIEPNVMFESVLFEVISGIGTVGLSLGLSSYACVATKLILTFLMYVGRLGAFSLFDLLLKKSENIYLEKPEGKVLVG

2.5E-54	194	20	7.5E-53	189.1	13.9	2	1	F2KTY0_PREDF	Potassium uptake protein, TrkH family	HMPREF9137_0231	Prevotella denticola (strain F0289)	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella denticola, Prevotella denticola (strain F0289)	767031	>tr|F2KTY0|F2KTY0_PREDF Potassium uptake protein, TrkH family OS=Prevotella denticola (strain F0289) GN=HMPREF9137_0231 PE=4 SV=1MLNLKLISKILGSLLWIEGLLLLNCLAVSLWYQSVDVMPFVWSILITVGTGFLFRLLGRNADNLLGRRDAYFVVTVAWILFTLFGTLPFMISGYIHSFTDAFFEAMSGFTTTGATIIDYPERLPKGLLYWRSLTQWIGGLGIVFFTIAILPSIVGGSVKVFAAEATGPIKSKLHPRLSTSAKSIWVVYLMLTVACILSYKLCGMGWFDAFNYSMTSTATGGFATESGSIMTFHSPAEEYVCSLFCFLSGVNFTLMYASAVGMDIRKLLKNSEFRLYALMVLSFALFIAFELVYRNHYDIEHAFRSAIFQVVSFITTTGLFSDDAGKWPHVTWVVLAACMFFGGCSGSTSGGIKSIRGVMLLKVIRNEFRQILHPNAVLPMKIDGVNIPQSKRVTLLGFIGLYLVLTLFCAFTMIAFGIDNTNAITITLSSLGNVGPTLGMEIGPTMSWAQLPDIAKWICSFLMLVGRLELFTVLVLFTPAFWKEN	
2.5E-54	194	20.4	2.8E-52	187.3	13.1	2.4	1	A0A0F2NJ71_9DELT	Trk system potassium uptake protein	VR65_06960	Desulfobulbaceae bacterium BRH_c16a	485	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, unclassified Desulfobulbaceae, Desulfobulbaceae bacterium BRH_c16a	1629713	>tr|A0A0F2NJ71|A0A0F2NJ71_9DELT Trk system potassium uptake protein OS=Desulfobulbaceae bacterium BRH_c16a GN=VR65_06960 PE=3 SV=1MKREHIYSSLGIILVAFGIILLSPIVVALIDKNYFCILPFSVASVSSIAVGLLLQKAGGFLRNFDNLNRNEGFLIVALAWIVTAAMGAIPYLFYGLNPLDAYFESVSGITTTGATIFIDFSLYPKSLFFWRSLSQWLGGMGIVVLFVAILPQFKVAGRQMFFAESPGPTEEKVTPRITHTAKALWLVYFILTLLEIICLIWVGMPVFDAVCNSFSTMAAGGFSPHPQSIMGYNSPAITWIIIGFMFLAGSNFAWQYQTVARRRLAALVKREEFRGYSIIIVISALLAVVLFINESENWSTSIRESLFQVVSILTTTGFSSSDFALWSVAAQTLLFSVMLVGGCAGSAGGGVKVIRVLLGAKYMLREIVQLVHPRVVTPIKIDGKTVPDAIQFQVLGFLLFYIFLMTLSAYAVTIIEGSPTIGLIGTAATIGNIGPGFGEIGPMGTFGNLAWPTKVIFIINMIVGRLELIPFLAMLHPDFWRMRK	
2.7E-54	194	25.4	8.6E-53	188.9	17.6	2	1	D2YRB0_VIBMI	Potassium uptake protein	trkH VMD_22660	Vibrio mimicus VM573	454	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio mimicus, Vibrio mimicus VM573	671076	>tr|D2YRB0|D2YRB0_VIBMI Potassium uptake protein OS=Vibrio mimicus VM573 GN=trkH PE=4 SV=1MVLWHPSVRHIERKPKSGRKLVGAPPLILCGSFLLLILLGTVLLKLPIATHEPITWIQSLFTVTSAITVTGLVVVDTGTQFTVFGQVVIALLIQCGGLGLMTFTIVTLIALGGKIGFLERTVAREAFNQTDSSTLVATAKSVLLFALVVESFGMAILTWHWSGELGWQTSLFHGFFYTISAFNNAGFALSADSLMPYVDDPVINFTITGLFIVGGLGFSVWMDLKRHRCWSKLTVYSRMMITGTVLINAVALIAIYLIEHDNPNTLAPLSESGKWLASWFQAVTPRTAGFNTLAIDQLENATTSIILVLMFIGGGSLSTASGIKVVTFMVLILSTYAYLRRDEQVYVFKREIAKETVSKALALTMISVVVTWLAIFALLLSEDAPMIDIVFEAVSALGTVGLSRGLTGNLTEAGELIITFMMFMGRLGPLTLAYFLASPRQKKLRYAETKLAIG	
2.8E-54	194	9.8	1.9E-26	102	0.9	2	2	Q8TWM3_METKA	Membrane subunit of a Trk-type K+ transport system	trkG MK1010	Methanopyrus kandleri (strain AV19 / DSM 6324 / JCM 9639 / NBRC 100938)	490	cellular organisms, Archaea, Euryarchaeota, Methanopyri, Methanopyrales, Methanopyraceae, Methanopyrus, Methanopyrus kandleri, Methanopyrus kandleri (strain AV19 / DSM 6324 / JCM 9639 / NBRC 100938)	190192	>tr|Q8TWM3|Q8TWM3_METKA Membrane subunit of a Trk-type K+ transport system OS=Methanopyrus kandleri (strain AV19 / DSM 6324 / JCM 9639 / NBRC 100938) GN=trkG PE=4 SV=1MDVKLVSSILGTVVKVAAVLPLLPLPISLLYGELDCIAPLLLTSLIMLVCGVALERIARVERHVRPRHAIVAVPIIWLVIPLFTSLPYRFCEHMSWLDAYFESMSGWTTTGLTVLPDIDHAHRTILFWRSLEQWVGGLGIVVSIISILRFETPSLLYVAEAREERIRPNVVNTAKEMWKIYITITAVGFLALWAAGMNPFDALNHSMTAVATGGFSTRSESVTAWHSPTVELITVVLMVLGATSFVTHYRVAKTFRTSPAELPKRIIKALRQYLQDRQFLTMIGLTAAVTAYAGAVSGDRAWDVVRYYGYQAVSAITCCGFSNADVLSFPEYAKLAITILMIVGGSTASTAGAIKVLRFLIMAEAVKAAIARRTQPIRGVVVPRIGSRVLSEDEISDAFAIASAYMFFLLIGTLLLTAYGYPLVDALFEVASAQGGVGLSSGITAPNAPAFVKILLIFHMWIGRLEVLPCLAALYWLTLILKRLAVKGRD	
2.8E-54	194	25.2	5.5E-54	192.9	17.4	1.4	1	R5GYZ7_9FIRM	Uncharacterized protein	BN782_01554	Eubacterium sp. CAG:786	477	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:786	1262893	>tr|R5GYZ7|R5GYZ7_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:786 GN=BN782_01554 PE=4 SV=1MNYKMISFILGWILIFEGMFLAVPGITALFFGESALWSYLLSISICLLIGSLLILKKPQKRQLYAREGCVIVSLSWIVLSAFGALPFFLSGEIPNYVDALFESVSGFTTTGASILNDVEAISYASRMWRSFSHWVGGMGVLVFIMAFIPLSGGQNMHILKAESPGPSVSKLVPRVKTTAMLLYSIYLVLTLIEFILLLCGGMTPYEAINTAFATGGTGGFGFYNSSMGSFSPYIQIVVTVFMLLFSVNFNCYFLLMTRKIKDAFNLELRTFLIMYISVTALITLNVAGSFKSAGEALRNSAFTVASIMSTTGFSVVDFNQWPELSRTLLVILMFIGSCAGSTCGGIKISRVIILFKGMAKELHTMIQPHQVKKIKMDSHTIDHETVRSVNVFMVAYLMIFIISLVIISFDNHDMITSFTAVATTINNVGPGLEMVGPSSNFSFFSDPAKIVLIFDMLAGRLELFPMLLLFTPATWKK	
3E-54	194	12.5	8.2E-53	189	8.7	2	1	A0A023X2V4_9ACTN	Trk-type K+ transport systems membrane component	RradSPS_1248	Rubrobacter radiotolerans	482	cellular organisms, Bacteria, Actinobacteria, Rubrobacteria, Rubrobacterales, Rubrobacterineae, Rubrobacteraceae, Rubrobacter, Rubrobacter radiotolerans	42256	>tr|A0A023X2V4|A0A023X2V4_9ACTN Trk-type K+ transport systems membrane component OS=Rubrobacter radiotolerans GN=RradSPS_1248 PE=4 SV=1MHPRVIANALGVVLAAVGATMIVPTAYALLYGDGNFLPFLLPMLAGVTGGAALFYSTRSSEQSYVSIRDVFLIVVSGWFLVGTLGAVPFVVSGALGPVNAFFDSMAGFTTTGASTISTPEGLDPSLLLWRSMSQWAGGIGIIVLFVAIAPIVGFGATQLYAAEMPNPTQERLTPRIQDTAKVLTYIYLSLTAGIALALLLAGMGAFDAVNHALTTVSTGGYSTRSDSVAAFDSAAIEYVIVFGMIFSGTNFGFYFLAIQGRLRRALRSPELLAYLGIISVATLLLTLSLFRDGAAGSLSESFRAALFQSASLSTGTAFTTESWDAWDPFAQSILMLLMAIGGCAGSTSGGIKVVRAVVLTKNALQDALRLLHPRAVTPLKLGERIIPERLRQGVLGFVFIYLATLALGTVIIAAHGVAVGDAFGSVFACINITGTSLGSAGDPAFYASLPPSAKLVLTFCMLMGRLELLTVLVVLTPAFWRR	
3.1E-54	194	31.3	1.4E-53	191.5	21.7	1.7	1	A0A0A1GUR4_9LACO	Trk system potassium uptake protein TrkH	trkH LOOC260_101910	Lactobacillus hokkaidonensis	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus hokkaidonensis	1193095	>tr|A0A0A1GUR4|A0A0A1GUR4_9LACO Trk system potassium uptake protein TrkH OS=Lactobacillus hokkaidonensis GN=trkH PE=4 SV=1MSKIQQHRLSLPKILTLGFLVIIIGSLLLKLPVATQAGLTTKYSDAFFTATSATCVTGLTTLNTAAHWTIFGQLVIMILVEIGGLGFMTFTVLLFSMLRRQPNLTTRVLVKESLNLESLADVKTVMKYVISLSLAIQALGVGILMFDFIPRYGWLKGSYFSVFHSVMAFCNAGFDLFGNSLESFSNDPYLIFVLSLLIIAGGLGFLVWRDVLLWHKKHQISLHTKIALSTTATLLVGATVIFWVTESQLQQLKGAANGWARFVDTFFLAVAPRTAGLDVMPYSKMTMAGIVLTMVLMFIGGTSGSTAGGIKTTTIGILWLQSWAVDRGDEDVEFAHRRFTQNNVFRAAMLIFVAAIIVVIAVMILAATEAVPKQFGLEYIVFEVLSAFGTAGMTMGLTPNLTLIGKIIIMVLMFIGRVGIFTVMFTVLNSDHPQKRYRYVEEGVMIG	
3.1E-54	194	10.8	7E-54	192.5	7.5	1.5	1	I0HXE6_RUBGI	Trk system potassium uptake protein	trkH RGE_43470	Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	484	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Rubrivivax, Rubrivivax gelatinosus (Rhodocyclus gelatinosus) (Rhodopseudomonas gelatinosa), Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	983917	>tr|I0HXE6|I0HXE6_RUBGI Trk system potassium uptake protein OS=Rubrivivax gelatinosus (strain NBRC 100245 / IL144) GN=trkH PE=3 SV=1MDALAVVAMIGRMVAMFSLLMLVPLAWAVYAAEPVVDALVKAAATSFAIGVAASLLTRRFRRELQPRDGFLLVGLTWTVLPAFGALPLLLMLPGSSVTDAYFEAVSALTASGATVFSGLDTMPGAVHVWRCLMTWVGGLGIIVLAVAILPMLGIGGSQLFRAEVTGPMKDSKLTPRIADTARAIWGVYVLLSLACALAYRAAGMSWFDAFVHMGSTVSLGGFSSYDASFGHWNSPAIEAVSVVFMMLSGVNLTMYYVWRERSPAPLWRNAEARAFYLVVLGSALLIALYLWASGAYASLTLALRHSLFHVVSVATTAGYATYDYAQWPLFASLWMILLGCFATCAGSTGGGIKMVRLILLLKQARHEFVRIVHPNVVVPVLNGRAIGDRTMQNVIGYMMTYGAVLVGLTMALLATGLEPVTAFTAVIACVNNIGPGLGEVGPAVNYGGSLSDVQTWICAFAMLVGRLELLTVLVLFMPAFWRD	

3.1E-54	194	21.5	4.3E-52	186.6	14.9	2	1	R7JW89_9CLOT	Trk-type K+ transport systems membrane components	BN584_02248	Clostridium sp. CAG:277	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:277	1262790	>tr|R7JW89|R7JW89_9CLOT Trk-type K+ transport systems membrane components OS=Clostridium sp. CAG:277 GN=BN584_02248 PE=4 SV=1MPEKTYKKKHLTSFQLIILGFAGVILLGTVLLMLPFSTLDKVSTPFHEALFTATSAVCVTGLVVKDTGSYWSMAGQTIILVLIQIGGLGVVTVAASVSILSGKKISLMQRSTMQDAISAPKVGGIVRLTRFILKGTFLLEAAGALLLLPAFLPDYGGKGIWMSAFHSISAFCNAGFDILGTADNPFPSLTRYSGNAFVNVEIMLLIIVGGIGFLTWDDIYTNKLNFKCYRMQSKIILMTTAGLILFPTVFFFVCDLKNLSAGKRLLAAVFQSVTTRTAGFNTINISKMSEASKAVMIMLMLIGGSPGSTAGGMKTTTFTVLILNAIATFRSKENVGAFGRRLEYPVIKNAATIAMLYFNLFFLGGIAISVYEGLPLLDCLYEAASAVGTVGLTLGITPGLHVFSQTVLIILMYLGRVGGLTLIYAVFSGRDKGNAKLPLEKITVG
3.2E-54	194	20.5	6.6E-54	192.6	14.1	1.4	1	Q2GBC8_NOVAD	Cation transporter	Saro_0397	Novosphingobium aromaticivorans (strain DSM 12444 / F199)	443	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Novosphingobium, Novosphingobium aromaticivorans (Sphingomonas aromaticivorans), Novosphingobium aromaticivorans (strain DSM 12444 / F199)	279238	>tr|Q2GBC8|Q2GBC8_NOVAD Cation transporter OS=Novosphingobium aromaticivorans (strain DSM 12444 / F199) GN=Saro_0397 PE=4 SV=1MPLRLTHPARLVPLVFSAAIVLGTVILMLPIARAGAGSAPFLTALFTSTSAICVTGLIVQDTPVYWSSFGQWVILLLFQVGGFGIMSAATLLGLLVGRGFRLSDRLRTRVERSHFDLHDARSVLRLILLVTIVVEGTLALLLTLRLHFGHGYDWADAAWHGIFHAVSAFNNAGFSTFSDSLMGFQNDWLFLVPVMLAIVLSSLGFPVLHEIRNRRDGPGPWTLHSKITVLGTGMLLIVGFLAVLMAEWSNPATLGAMPLGDKILNGAFQSVTTRTTGFNALDIGALQEETLLVTYILMFIGGGSAGTAGGIKVTTFFLLGIVVWSEARGERDAAIFGRRIGPAIERQALTVVLLSTALIGVGTLIILSATHLPLQAVLFETISAFATVGLSTGITAQLGPIGQVVLIILMFIGRVGTITISTALAMGMGRTAFRYPEERPIVG
3.2E-54	194	34.3	3.2E-54	193.6	23.8	1.5	1	I3ZZK9_ORNRL	Trk-type K+ transport system, membrane component	Ornrh_0950	Ornithobacterium rhinotracheale (strain ATCC 51463 / DSM 15997 / CCUG 23171 / LMG 9086)	581	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Ornithobacterium, Ornithobacterium rhinotracheale, Ornithobacterium rhinotracheale (strain ATCC 51463 / DSM 15997 / CCUG 23171 / LMG 9086)	867902	>tr|I3ZZK9|I3ZZK9_ORNRL Trk-type K+ transport system, membrane component OS=Ornithobacterium rhinotracheale (strain ATCC 51463 / DSM 15997 / CCUG 23171 / LMG 9086) GN=Ornrh_0950 PE=4 SV=1MKFIKIINEFFNKSKKYIYKLTFYLSVLSVLIFIYDLGFKHSHEYYHWADYIYKLAVFFGAFSIILKHTYTDKKYFLTVKIFDLLSVIFFFYVLYRSMVIHKSMWAFAIFFVFVREVSAMHINYGKNVINPARLFLFSLLIIILFGSFLLMLPQASNVELSYLDALFMSTSAVCVTGLSVMDISSGLTHFGQGIILVLIQIGGLGIMTFASYFSYFFRGSSSYSNHLTLSEFTNSDNLSDVFSTLRRIVLITLIIEFIGAILIYFATSFNDLDENAIFFSMFHSISAFCNAGFSTLPDGLYASSVQHDYDLHLIIALLITFGGLGFPIVYNVYKYFVYKISNLYRKILRRDRIQYKPWLISINARITLTTTFALFFLGFISFFIFEYDYTLSNYDLKGKIVESIFGSVTPRTAGFNTVDMANLSFPTLMVYFLLMWVGASPGSTGGGIKTSTFAVSILNFMSLAKGKDRVEAFRREISQTSIKRAFATIVLSLFVIGVAIAIIESVEHDKGLLSIAFECFSAYSTVGLSLGITDSLSSVSKVVIICVMFIGRVSMLSILIALLKKKEKYKGYKYPTEDILIN
3.3E-54	194	22.9	2.5E-52	187.4	15.9	2	1	R5AGI7_9FIRM	Potassium uptake protein TrkH family	BN453_01895	Firmicutes bacterium CAG:102	442	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:102	1262998	>tr|R5AGI7|R5AGI7_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:102 GN=BN453_01895 PE=4 SV=1MGKLERKLSSSQMIILGFAAVILLGALLLMLPVSSKSGEITPFLDCLLTSTSAVCVTGLVVYDTAAHWTVFGQAIIIVLIQIGGMGVITVAAAITMAAGKKISLMQRSTMQDAISAPQVGGIVRFTGFILKGIVIIELLGAAIMAPVFIGDYGFGEGLWMAVFHSISAFCNAGFDIVNDGILFNSLMGYAANPIINLAIMLLIIIGGLGFLTWSDICTNGIDIKRYHMQSKVILTVTSGLILVPTVYFFFFELVHLPFAERFWGALFQAVTPRTAGFNTVDLNAMSETGQMITSLLMIIGGAPGSTAGGMKVTTFAVMISVAAAVFQKRQNGCFFGRRIDDDTVKNAATVFFMYISLFLLGGIAISKLENLPLVTCLYESASAVGTVGLTLGITPELGAISKLILIAQMYIGRVGGLTLIFAILPATKNTLSKLPVEKISVG
3.4E-54	194	24.4	6.4E-54	192.7	16.9	1.4	1	R6BR11_9BACT	Trk system potassium uptake protein TrkH	BN731_01635	Prevotella sp. CAG:604	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:604	1262932	>tr|R6BR11|R6BR11_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:604 GN=BN731_01635 PE=4 SV=1MINSKLIYKILGQLLFIEAFLLFISLLVALYYQQDDIFAFIVATLTTIGGGLILKWRGHGADNTMSRRDAYLVVSLSWIVFSLFGTLPFIISGYIHSFTDAYFETMSGFTTTGATILDDVECFPHGLLFWRSLTQWIGGLGIVFFTIALLPSLVGGQTKVFAAEATGPIKSKLHPRLSTSAKWIWSIYLVLTIACILSYYIAGMNLFDSFNYAMTTTATGGFSTHNSSTEFFHSPALEYICAFFCFLSGVNFTLLYAAVIKFKIKDLFKNSEFKFYTLFVMAFTAFIMIELVTLRNYDLEHAFRSAVFQVVSFITTTGLFNDDAALWPHVTWVILATCMFFGACSGSTSGGLKCIRGVMLVRMVKNEFRQILHPNAVLPLKIDGVNVPMQKRVTLLAFLTTYLIICLVISFTMIAMGIDNTNAITITLSCVGNVGPTLGTEIGPTMSWSELPDLAKWFCSLMMLIGRLEIFSVLVIFTPAFWKEN
3.5E-54	194	15.6	2.7E-26	101.5	2	2.1	2	R6WBG9_9FIRM	Trk system potassium uptake protein TrkH	BN636_00117	Ruminococcus sp. CAG:382	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:382	1262957	>tr|R6WBG9|R6WBG9_9FIRM Trk system potassium uptake protein TrkH OS=Ruminococcus sp. CAG:382 GN=BN636_00117 PE=4 SV=1MNYKMIRYFFGIMLMLEAAFMLIPTATALIYSEDITPFIITIGILLFFGIPSVAFKPNNTRIYAKEGFICVAAAWILLSLFGALPFVISGAIPNYIDAFFETVSGFTTTGATILCEIESLPRGILLWRSFTHWFGGMGVLVFMLALFPSGDGQTIHLMRAEVPGPVKGKLVPKIKRTAMILYGIYFALTVVQTVALLCTGMPFYDSLVNSFATAGTGGFSVKNQSIMSYENPAAEWVIAVFMFIFGVNFNLFYLMLVKHIREVLKNEELRSYLIICLVATGAIALSTYKTFDGFEHCLRTSFFQVTSIISTTGFSTTDFNLWHIFPKTVLTVLMFIGACAGSTAGGLKVSRVIILFKSIRREIKHMLKPRSVNIIRVDGEVIPEENVKAALNYFALYIVLIILSTVLISVVDGLSMETNITAAVTCVNNVGPGFDTVGPMGNFSTYSAFSKIVLSLDMLLGRLEIMPMFILFSPMAWKKR
3.8E-54	193	25.1	4.8E-54	193.1	17.4	1.1	1	R5I787_9FIRM	H(+)-transporting two-sector ATPase	BN729_01847	Ruminococcus sp. CAG:60	463	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:60	1262964	>tr|R5I787|R5I787_9FIRM H(+)-transporting two-sector ATPase OS=Ruminococcus sp. CAG:60 GN=BN729_01847 PE=4 SV=1MFIQNLQYKLHKLNTAQIITLSFAGVIFVGGLILWLPLCTAPGQTTSFSDAMFTATTCVCVTGLVTVVTATHWSLIGKLVILLLIQIGGIGLIALASVIFIYLNKKISMKNRRMIQESYNLEQMSGLVKVVRKVVLCVFAAEGIGAISYGIYFIPRVGLVKGAGQAVFTAVSAFCNAGIDLLGDNSLADYVTNPLLNFTTISLIIASGLGFTVWWDLGKRFKLIFQKKLSFGRFYRTLHLQSKIVLVTTGILLVGGTFLIFLFEYDNPASIGKLTLGQKLMASLFQAVTTRTAGFFTVDQAAFTNGTAMLCLFLMLIGGSPMGTAGGIKTTTLAVLVLSIITNLRGKKDVEVCGRKIRSSYVRSALVVAGMAVSVLFVSLLAFFAVMPDAPFIDVLYELTSAVGTVGLSRGLTSVLNTPAKWIVIFTMYIGRIGPLTLGAAVVSRAQKKSEKVHLAEENIMIG
3.9E-54	193	38.3	6.2E-54	192.7	26.5	1.2	1	C8W5Y3_DESAS	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Dtox_0518	Desulfotomaculum acetoxidans (strain ATCC 49208 / DSM 771 / VKM B-1644)	457	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum acetoxidans, Desulfotomaculum acetoxidans (strain ATCC 49208 / DSM 771 / VKM B-1644)	485916	>tr|C8W5Y3|C8W5Y3_DESAS H(+)-transporting two-sector ATPase OS=Desulfotomaculum acetoxidans (strain ATCC 49208 / DSM 771 / VKM B-1644) GN=Dtox_0518 PE=4 SV=1MAYLKSTRLNFNKRFSLTPVQLMVLGYFLFTIIGAMLLISPFSLNTGKQLNLIDAFFTATSAVSVTGLTVVSTPDTFSLTGRIILSFLLQFGGIGIMVLGTLVYILSGTKIHLRTYAMIRIEQNQTSIHGMVSLMLFILKVAVIFEILGAIILTSRFFINYHMPFSDALGMGIFYSISGFTNAGFDLFGHGLQNFQQDYLIQSVISILLLSGAIGFPVLLEAHSYYLSLRKKTRFTFSLYTKVTTMTFLILLFLGFIFVLLSELHGPLANMSWQEKVSVAFFHSLNTRSGGFSTIDINVFSTPTLLFLSLLMFIGASPSSCGGGIRTTTFAINLISVFSYMRGRNSVKIMNRELYPEDILRSFMVSFFAAMLVILSVIFLMETENFASREILFEVCSAFGTTGLSTGIATNLSVTGKLIIIFLMFVGRVGILSLLMLLHNHRLRDKYHIIKERIIVG

4.2E-54	193	12.6	7.5E-34	126.4	0.3	2.1	2	W0PBG6_9BURK	Trk system potassium uptake protein	trkH MIM_c07260	Advenella mimigardefordensis DPN7	489	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella mimigardefordensis, Advenella mimigardefordensis DPN7	1247726	>tr|W0PBG6|W0PBG6_9BURK Trk system potassium uptake protein OS=Advenella mimigardefordensis DPN7 GN=trkH PE=3 SV=1 MRNILNVLHALSLTMLGFSTILLFPLAVSLYFDDGAHNAFLLSLGIAIGVSAALWKFTRRSRDEINPRNGLLLVSLVWLVFPLIASLP FVFDAYIEGQSLTFTHAYYEAMSGLTTTGASVLNNISSLPPSVNIWRVTLIWVGGMGILVMAVAIMPLLGVGGHQIMRGEIPGPMKEEK LTPRIAGTAKALYAIYISASTLCVLCYRLAGLSWYDAWCHAASTMALGGFSIYDDGFQHYDSPMVDTVACVFMMFAGINFATHYNVFR FRSLRYYVTCPETKIFVAILLLGGLGVSAWLYFDGVYPTLTQSLRFGMFNTISLATTTGFANTDYLHWPVLLPVVMLLLGSFCSSAGST GGGIKLIRVVLIAKQIRAELRKLLHPHAICPVKLGRRIVPPPIISSIMAFVILFVIMNVALTGLMVMSGLDFATASSAVFASLTNIGPGLGEV GPMSNYSGLSNFQMWICTFAMLVGRLEFFTVLVLFTPGFWKK
4.2E-54	193	27.8	4.2E-54	193.3	19.3	1.6	1	R2Q1J7_9ENTE	Cation transporter	UAS_00152	Enterococcus asini ATCC 700915	478	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus asini, Enterococcus asini ATCC 700915	1158606	>tr|R2Q1J7|R2Q1J7_9ENTE Cation transporter OS=Enterococcus asini ATCC 700915 GN=UAS_00152 PE=4 SV=1 MDSLQRFYEVFSRRARYFVTNKISSIQIIVSYYILMTIFSLILFHLPFFREVDSYGQVTFMDLLFMAISTVSVTGLTTFDINSVFNDR GVVLLEILFQIGGLGVMMISTFFFIISRRRITLKQRQLIMTDMNQPRLSGIVRLIRTTFTIILAFQGIFGVFFSLYFKFQGYYDSWRDAIFYG FYQAVSAVTNSGFDVTGDSIMPLSHDYFFLFWIIFLIFIGGIGFPVLMDFREWLKYRKQRHLRKKAKQKAGLPFRFSLFTKIAVLAFVILF VGGTVIIWLLEKDHLFRNLSDFGTWMNSAFYSMTTRNAGLQIHNLNDFQVTTLILFSLLMFIGCSPSSVGGGIRTTTLAIIGLYLYSFLKG EAKINIFGRRISDDDVRKSVVVFMLSLGMCFFCVIFLTATEEEPLIAIIVEVCSAFGTTGLSLGITADLSGIGQAVIAALMFIGRIGMLYTLLL FVPKETQDLGYEYPTEQIIIG
4.3E-54	193	16.1	1.2E-51	185.2	11.1	2.1	1	Q88EF8_PSEPK	Trk system potassium uptake protein	PP_4507	Pseudomonas putida (strain KT2440)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas putida (Arthrobacter siderocapsulatus), Pseudomonas putida (strain KT2440)	160488	>tr|Q88EF8|Q88EF8_PSEPK Trk system potassium uptake protein OS=Pseudomonas putida (strain KT2440) GN=PP_4507 PE=3 SV=1 MALPTLRIIGFIIGIFLITLAVSMAVPMATLVIFERTGDMPSFLWSSLITFIAGLALVVQGRPEHVHLRPRDMYLLTVSSWLVVCVFA ALPFLLTQHISYTDAFFESMSGITATGATVLSGLDNMSPGILMWRSMLHWLGGIGFIAMAVAILPLLRIGGMRLFQTESSDRSEKVMPR SHMVAKSIVGVYVGFSILGALAFWWAGMSPFDAINHAMSAISTGGFSTSDQSLAKWDIPAVHWVAVVVMIMGSLPFTLYVATLRGNR KALIRDQQVQGLLGMLVVTWLVLGTWYWYSTNLHWLDALRHVALNVTSVVTTTGFSLGDYSLWGNFSLMLFFYLGFVGGCSGSTA GGIKIFRFQVAYILLKASLNQLIHPRAVIKQKYNGHRLDEDIVRSILTFSFFFAITICVMALLLSLLGVDWMTALTGAAGTVSGVGPGLGE VIGPSGNYATLPDAAKWILAAGMLLGRLEIITVLVLCMPAFWRH
4.3E-54	193	18.2	4.2E-53	190	12.6	2	1	R7BK71_9FIRM	Trk system potassium uptake protein TrkH	BN803_00370	Firmicutes bacterium CAG:882	493	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:882	1262991	>tr|R7BK71|R7BK71_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:882 GN=BN803_00370 PE=4 SV=1 MNKSIIRYILGHVLLLTSALMLLPALVGLIYLEHEGFTYLFVAACCFVVGFFFMTRSKPNNTTLYLKEGCISTSLAWILLSLVGCIPFCI TGEITSFTDALFETISGFTTTGASILSDVEALSHCSLLWRSFTHWIGGMGVLVFLLAIVPLSGGSNINLMRAESPGPSVGKLVPKMKYTA RILYIIYFGLTLIQFILLLVGRMPVFDAVCTAFGTAGTGGFGIRNDSIAGYSPYLQWVITIFMLLFGVNFNAYYFILFGNARKAFKMEEVRC YFIIVAVSVAVITIELFRSAVPFANALRDSSFQVASIITTTGFSTADFNLWSGTSRTILVMLMFVGACAGSTGGGMKVSRFVILFKTVFKE LDSYIHPKRIQKLSLDGKPIEHDVVRSINVYFITFTVIFAASLLLVSLEGKDLVTNFTAVAATINNIGPGLELAGPTQNFVHFSILTKYVLMF DMLAGRLELFPLLILFHPAVWRDIHTTHRRWKRKRMEE
4.3E-54	193	35.5	9.6E-54	192.1	24.6	1.5	1	J9W8D1_LACBU	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	trkH LBUCD034_2134	Lactobacillus buchneri CD034	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus buchneri, Lactobacillus buchneri CD034	1071400	>tr|J9W8D1|J9W8D1_LACBU H(+)-transporting two-sector ATPase OS=Lactobacillus buchneri CD034 GN=trkH PE=4 SV=1 MNLKTRLALPQILTLGFLIIILVGTFLLSLPIASKSGHMTGYINAFFTATSATCVTGMTVVNTALHWSVFGKIVILMLVEIGGLGFMT FAVLLFVFMRRKVDLTTRLLTQQSLNLQSFANTSSVVFLVVRISLAIQVLGTALIFIDFYPRYGFAKGLGYSIFHSISAFCNAGFDLYDNS LEQFQTDPYLLFVLTILIISGSLGFLVWKDILFYKEDHHLSLHTKLALTTYLGLIGLSFVVYMLTEGNFGQESHLTMFQRIMNTWFLAVTP RTAGFYTLPVTHITMGGMFFTMILMLIGGTPGSTAGGIKTTTVGILLIRVWSTLRGKRDATFWGRRFSNDNVTRSLSLVFLVAVVLSIAT MILTFTETIPKNQGLEYITFDVISAFGTTGFSLGLVAHLSVVGKLIFAALMFMGRVGIFTVMYSLLNSKRPEDAFRYPEENVMIG
4.4E-54	193	42.6	1.3E-53	191.6	29.6	1.6	1	B7GJK2_ANOFW	Trk-type K+ transport system, membrane component	Aflv_1302	Anoxybacillus flavithermus (strain DSM 21510 / WK1)	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Anoxybacillus, Anoxybacillus flavithermus, Anoxybacillus flavithermus (strain DSM 21510 / WK1)	491915	>tr|B7GJK2|B7GJK2_ANOFW Trk-type K+ transport system, membrane component OS=Anoxybacillus flavithermus (strain DSM 21510 / WK1) GN=Aflv_1302 PE=4 SV=1 MKVRRLSRLSTVQLIVLFYFVAVCISTFLLWLPFFHQPGVKLSFVDALFTAVSAISVTGLTVVSTADTFNVPGIFILAFILQFGGIGI MALGTFIWLMFGKKIGFRERQLIMTDQNRSTFAGLVKLMKEILTLIITIEIIGAIVLGIYFLRYFPSWKEAFFQGFFASVSATTNAGFDITG QSLIPFANDYFVQTVHMILLVLGAIGFPVLIEVKEFLFHRQKQQYRFSLFTKLTTVTFFLLVLFGTWAILLIEWNRFFANKTWHEALFYAL FQSISSSRNGGLATMNVAEFSEPTLLVLSALMFIGASPSSVGGGIRTTTFAIMVLTIFFYAKGKNSIKVFQREIHDEDILKSFIVFGTAFILC FLAIVLLSFSESFTMIEIVFEVCSAFGTTGLSMGITSELSTFGKLVITALMFIGRIGILSFLFLIRGNNQKETYHYPKERIIIG
4.4E-54	193	24.8	1.4E-28	109.1	6.4	2.2	2	A0A0E9LQK6_9BACT	Potassium uptake protein TrkH	JCM15548_14411	Geofilum rubicundum JCM 15548	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Marinilabiliaceae, Geofilum, Geofilum rubicundum, Geofilum rubicundum JCM 15548	1236989	>tr|A0A0E9LQK6|A0A0E9LQK6_9BACT Potassium uptake protein TrkH OS=Geofilum rubicundum JCM 15548 GN=JCM15548_14411 PE=4 SV=1 MNFRFILNIFGRVLILLGLFMLTSIIWALVYNEEVVEELLVSSLITLVSGAGMYLLTFRNLKKELGLKDSYFTVTFTWVIISLFGTLPY LLTGAIPSVVDAVFETVSGFTTTGSSILVDLESLPKSVLFWRSLTHWIGGMGIIVLVVAILPLLRIGGYNLFKNEASGISYEKLTPKTASTA KRLWGIYVSLTFILMGLLLLGDMSFFDAMNHAFSTMSTGGFSPRNTSLGGYSSYVQYVVILFMFLAGMNFYLHYFHVKGRFRRVFSN LELRTYFGIVMAVTIGVAVIIYREGGIGIEKAIRDALFQVVSIITTTGFATYDYLSWPQEAWTLIFMLMFVGACVGSTGGGVKVIRHVVSF RNVTLHFSRMLHPNSVKRLKINGEIIDDEKVGSLVSFLVLYLLTFTIGSIIMVLLGEDTLTAVGSVAANMGGVGPGIGSVGPASSYAHIHE TGKIVLSFLMLIGRLELTTVLILFTSLFWER
4.6E-54	193	25.4	1.2E-35	132.3	4.9	2.2	2	F2NWG7_TRES6	Cation transporter	Tresu_2292	Treponema succinifaciens (strain ATCC 33096 / DSM 2489 / 6091)	480	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema succinifaciens, Treponema succinifaciens (strain ATCC 33096 / DSM 2489 / 6091)	869209	>tr|F2NWG7|F2NWG7_TRES6 Cation transporter OS=Treponema succinifaciens (strain ATCC 33096 / DSM 2489 / 6091) GN=Tresu_2292 PE=4 SV=1 MAFTLCIIIFFIISIIGLSFSIPIATAIFCHEYFVIPSFLIPMIASLILGAMTLFFFRNKKSRLTIRSSFAAVALAWISASLFGAIPLYFSGAI PNFTDAFFESVSGFTTTGATTLSEIEKLPRSINLWRCLSHWLGGMGIVALTVALMPVLGVGGFQLIKAETTGPEKGKFTPKITTTAKIL WFIYLGMTLIQTALLKIAGMDFIDALCHAFSTLGTGGFSTRNASIGAYNSAAIEWICFVFMFLAGINFSLYYYFFTRNFSEIKCNSELKAYI WINIISIAAIAVAQASSYGGFFKSLRFSAFQTATILTTTGFSTADYTKWKSASQIVILMLLFIGGMSGSTAGGVKVIRWVVLYKQFKNEIL KMIHPHGVFSIRLNQQTGRKDVVFSVSAFFFLYFSFVILTAFFTSFFGLDMQTSFTGALTMIGNCGPAFGALGPSNNCGWLAAPVKW WYSFAMIAGRLELFTLFIFLTPAYWKK

4.6E-54	193	15.8	1.3E-51	185.1	10.9	2.1	1	G8PZM2_PSEFL	Trk system potassium uptake protein	trkH PSF113_1525	Pseudomonas fluorescens F113	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens F113	1114970	>tr|G8PZM2|G8PZM2_PSEFL Trk system potassium uptake protein OS=Pseudomonas fluorescens F113 GN=trkH PE=4 SV=1MALPTLRIIGFIIGIFLITLAIFMVVPMATLLIYERTSDLPSFLWSSMITFVAGLALILPGRPEHIHLRPRDMYLLTVSSWLVVCVFAALPFLLTQKISYTDSFFESMSGITATGATVLSGLDNMSPGILMWRSLLHWLGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSEKVMPRSHMVARLIVASYVGITILGTLALWWAGMSLFDAINHAMSAISTGGFSTSDLSLAKWTQPAVHWVTIVIMILGLSLPFALYVSTLRGNRRALIKDQQVQGLIGVLLVTWLVLGTWYWATTDLHWLDALRHVALNVTSIVTTTGFALGDYSLWGNFSLMLFFYLGFVGGCSGSTAGGIKIFRFQVAYILLRANLNQLIHPRAVIKQKYNGHRLDEEIVRSILTFSFFFAITICVIALLLSLLGVEWMTALTGAASTVSGVGPGLGETIGPAGNFAPLPDAAKWILSGGMLLGRLEIITVFVLCIPAFWRH
4.6E-54	193	27.1	3E-53	190.4	18.8	1.8	1	R5WPF9_9BACT	Uncharacterized protein	BN505_00838	Alistipes sp. CAG:157	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes sp. CAG:157	1262692	>tr|R5WPF9|R5WPF9_9BACT Uncharacterized protein OS=Alistipes sp. CAG:157 GN=BN505_00838 PE=4 SV=1MRTGLVLKYIGAVLLLDSAFMLLSAGISWINGMDSGFTPLFLSFLLTAILGMFPTLFVRRREQINAKEGYCIVTGAWLLSCFVGTFPYLLYGGEFNFVNAWFESVSGFTTTGSTILTDVESLPNGLLFWRSATHWIGGIGVVMFALAILPSLGKTKMTLYSVELSTLAKDNYRFQTRKIVYILLFVYVGMTAMATVMLRIAGMDWFDAVNHAFSAISTGGFSTKNASIAYFDNLWIELVIVFFTFVSGLHFGLMYSTLTGSRNNLFRSEVTRYYFLCAVTGVFLITLSLWLSGTYGSFATALRYGLFQGVTVLTTTGFATADTNLWTPLAMTVLFFFTLQCACAGSTAGGIKCDRILLSFKVLRNRIRQQQHPNAVLRIKLNGVTQEESTINFAMLYIAVYFLFIILGTLINTACGVDFITSLTASATCMGNVGPGFGEVGSMESFAAMPGVMKFSSTALMLFGRLEIFGLIQLFMIKWWV
4.7E-54	193	30	8.2E-52	185.7	20.8	2	1	R7DDV4_9FIRM	Potassium uptake protein TrkH family	BN639_00223	Ruminococcus obeum CAG:39	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus obeum CAG:39	1263107	>tr|R7DDV4|R7DDV4_9FIRM Potassium uptake protein TrkH family OS=Ruminococcus obeum CAG:39 GN=BN639_00223 PE=4 SV=1MPEHLHKRKHLTSFQLIILGFAGVILIGALILTLPVSSASGVVTPFDQALFTSTSAVCVTGLVVQDTGSYWSVFGQAVILALIQIGGLGVVTIAVSVFMLSGRKISLMQRSTMQDAISAPKVGGIVRLTKFILRGTFLIEALGAVLLLPVFCRDFGIKGIWMSVFHSISAFCNAGFDILGTTDHTFVSLTGYSRNIWLNIVIMLLIITGGIGFLTWEDFYINKFKFKRYRMQSKIILMTTAILIFLPAIFFFTNDFKMFSGEERTLLSFFQSITTRTAGFNTADMALMTESGKAVMIFLMLIGGSPSSTAGGMKTTTFAVLILNAFATFRSREDAGAFGRRFDRQIIKNAATIAMLYFMLFFFGGITISVYEGLPVLTCFYEAASAVGTVGLTLGVTPGLHIISRLILIALMYLGRVGGMTLIYAVFSGKNNNGARMPLEKITVG
4.7E-54	193	25.5	1E-53	192	17.7	1.4	1	R6Q8Y8_9BACT	Trk system potassium uptake protein TrkH	BN637_00025	Prevotella sp. CAG:386	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:386	1262925	>tr|R6Q8Y8|R6Q8Y8_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:386 GN=BN637_00025 PE=4 SV=1MINWKLIYKVLGQLLFIEASLLLLSLLVAVYYQQEDIFAFIVATLTTIGGGLILKWRGHGADNSMSRRDAYLVVSLSWIIFSLFGTLPFMVSGYINHFTDAYFETMSGFTTTGATILDDVECFPHGLLFWRSLTQWIGGLGIVFFTIALLPSLVGGQTKVFAAEATGPIKTKLHPRLSTSAKWIWSTYLVLTIACILSYYVAGMGLFDSFNYAMTTTATGGFSTHNTSTEFFHSPSLEYICTFFCFLSGVNFTLLYAAVIKFKIKELFRNSEFRFYIFLVTVFSVFIMVELMVMRNYDIEHAFRSAIFQVVSFITTTGLFNDDAALWPHVTWVVLSMCMFIGACSGSTSGGLKCIRGVILLRMVKNEFRQILHPNAVLPLKIDGVNVPMQKRVTLLAFLTIYLIICVIISFTMIAMGIDNTNAITITLSCVGNVGPTLGTEIGPTMSWSELPDLAKWFCSLMMLIGRLEIFTVLVIFTPAFWKEN
4.7E-54	193	17.4	1.1E-52	188.6	12.1	2	1	R7XUB6_9ACTN	H(+)-transporting two-sector ATPase	CF8_3257	Nocardioides sp. CF8	459	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Nocardioides, Nocardioides sp. CF8	110319	>tr|R7XUB6|R7XUB6_9ACTN H(+)-transporting two-sector ATPase OS=Nocardioides sp. CF8 GN=CF8_3257 PE=4 SV=1MENRTPTRRYGDPVGRLRQSVLHPARVVPVAFFAAIVVGTVLLALPWSTPGPERTPILTAAFTAVSAVCVTGLATVDTATYWSPFGQGVIMALIQVGGFGIMTLATLLGLLVGGKLRLKSSLIAQAETHTLNIGDVRHVIGRIAITILAFEIAFATMLTFRFRAAYDDTWGQALWHGAFHSVSAFNNAGFALYSDSLIGFVDDAWIIFPICVAVIAGGIGFPVLFELRRRWRSPDRWTVHTRLTVYGTGILLVVGTAAFLALEWTNAGTLGPLDTWGKLVGGVTGGVVPRTAGFNSVDYGQITPETMAVNYVLMFIGGGSAGTAGGIKVTTFFLLAYVIWSEVRGERDTNVAHRRISSETMRQALTVALLAIAAISTGTMVILLSTDYALDVVLFESISAFATVGLSTGITPDLPPVAEVTLMLLMFVGRVGTITVATALALKTRHRHFHLPEERPIVG
4.8E-54	193	23	1.3E-52	188.3	15.9	2	1	R5IGI0_9CLOT	Potassium uptake protein TrkH family	BN757_01587	Clostridium sp. CAG:7	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:7	1262832	>tr|R5IGI0|R5IGI0_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:7 GN=BN757_01587 PE=4 SV=1MELFQKKKSLSSFQIIIFGFLAVILVGTLLLMLPFASREPGSAPFLDALFTATSATCVTGLIVHDTATYWSCFGQVVILLLIQIGGMGVVTITIAVAMVSGKKIGLMQRSLMQESISAPQVGGIVRFTGFFLKGIALIELLGAILLAPVFIKDFGVGKGIWYGVFHSISAFCNAGFDLMGVRQQYSSLTYYAGNGLVNAVIVLILIGGLGFLTVEDIKTNKLQFKKYRMQSKVILVTDILLVIVPTVIFYFGEFHGSQWGNGLERFWLSLFQAVTPRTAGFNTADFGQMSEGGLFLMVMLMLIGGAPGSTAGGMKMTTIAVLLLSTAAVFRRKEDAQCFGRRIPTETVRYAAVVMLMYMVLCTVGGLFLCYAEGLPVLTSLFEAGSAIATVGLTLGVTPTLGAAARLVLIVLMYCGRVGGLTLVFAALSGMRPSMTKFPQEKITVG
5E-54	193	27.4	8.7E-54	192.2	19	1.3	1	A0A0B4XUL9_9PROT	K+ transporter Trk	TH3_00385	Thalassospira xiamenensis M-5 = DSM 17429	447	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Thalassospira, Thalassospira xiamenensis, Thalassospira xiamenensis M-5 = DSM 17429	1123366	>tr|A0A0B4XUL9|A0A0B4XUL9_9PROT K+ transporter Trk OS=Thalassospira xiamenensis M-5 = DSM 17429 GN=TH3_00385 PE=4 SV=1MPFYFPNRTGKPIRIPPPLLLAILYLALILIGAVVLVLPVAVTHPISFSDALFTATSAVTVTGLAVVDTGSSFTLFGQAMILILIQLGGLGLMTFAALVLSALGLPIGLRHHNFLREDLNQTSLHQLVGLVKTILAVVLFCELIGGILLLTVFVPDFGWARGTWFAVFHSVSAFNNAGFALMPDSLSRWATNPVINLTIPALLLIGGIGFSVISDLWIHRGWRHLSLHSKLMLTGSAILIVWSVTMFAILEWHNPDTLGAFASPIDKLQISWFQGLTTRTAGFNTVDIGSIHDTTALMFILLMVIGAGSTSTAGGIKVTTFIVLVLATIAFFKRHNQLHAFGRSIGLEEVMKVLALTMISMFVVMSGIFLITMSHDGDFLDLVFEVTSAFGTVGLSRGTTGELDTLGRIVIELIMFIGRVGPLTLGFFLARRVPPRISYPSSQVYLG
5.1E-54	193	37.2	2.8E-53	190.5	25.8	1.8	1	F9VCT3_LACGL	Potassium transporter protein	LCGL_0674	Lactococcus garvieae (strain Lg2) (Enterococcus seriolicida)	440	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Lactococcus (lactic streptococci), Lactococcus garvieae, Lactococcus garvieae (strain Lg2) (Enterococcus seriolicida)	420890	>tr|F9VCT3|F9VCT3_LACGL Potassium transporter protein OS=Lactococcus garvieae (strain Lg2) GN=LCGL_0674 PE=4 SV=1MQKNLKKLTALQIIFIAFLTLVIVGGTLLSLPISSKTGQFTHPIDALFTAVSATCVTGLTVIDTSAHWSLFGQVIILLLIEIGGLGFMTLVVSIFLLLNQKMSLKSRLIIQESYSLSDMSSGVRVVMNVLIISFLIQFCGSVLLSFAFVPKFGLVKGLWYSVFHAISAYCNAGFDLFGNSLMLYEHSPYVLVMVIASMIVCGSLGFIFVGMMDLLNYKKQRKLSLHTRLALTTTTFLIFGGMILFLISDFESVSNNPAILTMQSLFLSISQRTAGFSIQEYTLFSQASIFLTIMLMIIGGTSGSTAGGLKTTTIGVLALNVRSIIKRDKHTSFKNRTIPQSVVKQAYESVFLYFFMMVIATFALLLTNPKFRVDQLLFEVISALSTVGLSMGVTPGLNVPGKIIVGLLMFIGRVGVFTIIYSLNAKDSHESLYKYPEEKVMVG
5.1E-54	193	31.7	8.4E-54	192.3	22	1.3	1	A0A0D8MYB9_PHOLE	Ktr system potassium transporter B	UB34_03520	Photobacterium leiognathi	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium leiognathi	553611	>tr|A0A0D8MYB9|A0A0D8MYB9_PHOLE Ktr system potassium transporter B OS=Photobacterium leiognathi GN=UB34_03520 PE=4 SV=1MSFIPNRGMYVPIKTENRDKRWSEPKIIIFSFLAILIPAAILLTLPVFSVSGLSFTDALFTATSAISVTGLGVVDTGSHFSISGKILLMLLMQIGGLGQMTLSAVLLYMFGLRLSLRQQALTKEQLGQEKFTNIRRLVKHIIIFVLICELIGVFFLSIRWVPEMGWEQGLFFAVFHSISAFNNAGFSLFSDGLTRYVDDPLVIITIASLFIFGGLGFTVISDLKRNAHRGFHFLSLHSKIMIIATPVLLFVGTVMIWLLEHHNSYTLGSLNESGQWLAAFFQSATARTAGFNSVDIGQFTQPGLLIMMLLMLIGAGSTSTGGGIKVSTFVVAILATWSFLKQRDRVVLFKRTISNQTVTKSLAIIVVSGIVLTIAMFALMITEKAPFYEVMFETISAFATVGVTAGLTATLSEPGKYIMIIVMIIGRLGPLTLAYMLARPKPTLLKYPEDNVAAG

5.1E-54	193	31	1.9E-53	191.1	21.5	1.7	1	C4ZDM1_EUBR3	Uncharacterized protein	EUBREC_3270	Eubacterium rectale (strain ATCC 33656 / VPI 0990)	453	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium rectale, Eubacterium rectale (strain ATCC 33656 / VPI 0990)	515619	>tr|C4ZDM1|C4ZDM1_EUBR3 Uncharacterized protein OS=Eubacterium rectale (strain ATCC 33656 / VPI 0990) GN=EUBREC_3270 PE=4 SV=1MNDIKHDIKKRHKNLTEFRYIAVGFFLTILSGAIMLSLPFSSRDGQWTNFLDSLFTATSATCVTGLVVFDTFRHWSIIGQLVILVLIQIGGMGFISIGVAFSMLLHKKIGLRQRDLMQESVNALEIGGIVRLFSVIIRGTFLIEGIGAVLLAIRFIPDFGILRGIYFSVFHSISAFCNAGFDLMGINEEYSSFTKYVADPLVNITIMLLIIIGGIGFTIWNEVRTKKLKFSRYSLHAKIVISTTLILVFGGGLFMYIFEKSNTIAGMDTPGAIFASLFGSVTARTAGFNTVDTAALTQESKLLTIVLMFIGGSPGSTAGGIKTTTMAVMIIYIVSYMRGSNGCNVFGRKISSEVIKKAGMVLIINLVLGLTAVIAILATSNMKMDDVLFEVYSAISTVGMTTGITRDLNTVGRIIIIIMMYCGRIGSMTFVLSFVHRPDKANIELPEEKVIIG
5.3E-54	193	29.2	7E-54	192.5	20.2	1	1	E0UE58_CYAP2	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Cyan7822_2204	Cyanothece sp. (strain PCC 7822)	453	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7822)	497965	>tr|E0UE58|E0UE58_CYAP2 Potassium uptake protein, TrkH family OS=Cyanothece sp. (strain PCC 7822) GN=Cyan7822_2204 PE=4 SV=1MTIARTICLGFIAVIAAGTLLLILPFSTSAGSWGNPIVALFTSTSAVCVTGLVVVDTGTYFSFWGELFITLLIQIGGLGYMLTTTFLMLLIGKRFELRQKFAIRESFDRPFLQGSQNIVRSVIATTLAFEIAGALLLFIKFTSDFGPIRGLWFAIFHSVSAWNNAGFGLLKDNMISYRSSSYIINFTIPILIIFGGIGYQVIIEMYSWFIDRFKRERFDFSLNYKVAVHTTIFLLIFGTLGYLFLEFTNPQTFGGFNLKDKLLAAWFQSVVTRTAGFNSIDFGQLTISGLFLTMGLMFIGASPSGTGGGIKTTTLRILTSSTRAVLRGQEQVVLYEREVSVSLVLKAVAVVFGSAMTVLGITFAIAIIEYSFLKNPIFINGTYNSIHIAFEVISAFCTVGLSTGITAPLSPYSQLLLVLAMYTGRVGVLLFMAAIIGDPRPSALHYPEENLLVG
5.5E-54	193	18.3	1.8E-53	191.2	12.7	1.7	1	A1S1J5_SHEAM	Trk system potassium uptake protein	Sama_0039	Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella amazonensis, Shewanella amazonensis (strain ATCC BAA-1098 / SB2B)	326297	>tr|A1S1J5|A1S1J5_SHEAM Trk system potassium uptake protein OS=Shewanella amazonensis (strain ATCC BAA-1098 / SB2B) GN=Sama_0039 PE=3 SV=1MLNLRPLLFILGTFLSMLAGFMLIPLLFALLHGDETSGAFMISSLATGAAASFCISSGQQKNIKLNIRDMFLLTSITWLVVSLFAAMPFTLYHGINYTDAFFETMSGITTTGSTVLSGLDSMDRSILIWRSLLQWLGGIGFIVMAVAVLPFLNVGGMRLFRTESSDWSDKSTPRTQDMAKNLFLVYILLTILCGLGYHLAGMDWFEAINHAMTTLSTGGYSTSDESMAHFSPAAHWVGTSFMLAGGLPLLIFVQMLRGRSLTVWNDAQVKGFLLFVALVSVALSFWLADVKDLAFMDALRLTSFNVVSVVTTTGYGLTDYGSWGPLANVAFLFLMFVGACSGSTSGGIKIFRFQIAGAIMREQLKQQIHPAGIFRERYNNRPISEDIIRSLVTFILLFMGVTVALAVFLVAVGVDPMSSLTGAITAVTNVGPGLGPVIGPAGNFASLPDSAKWALSLGMLLGRLEILTVAVLFHPKFWHY
5.5E-54	193	15.1	3E-52	187.1	10.4	2.1	1	D8K3A2_DEHLB	Cation transporter	Dehly_0090	Dehalogenimonas lykanthroporepellens (strain ATCC BAA-1523 / JCM 15061 / BL-DC-9)	484	cellular organisms, Bacteria, Chloroflexi, Dehalococcoidia, Dehalogenimonas, Dehalogenimonas lykanthroporepellens, Dehalogenimonas lykanthroporepellens (strain ATCC BAA-1523 / JCM 15061 / BL-DC-9)	552811	>tr|D8K3A2|D8K3A2_DEHLB Cation transporter OS=Dehalogenimonas lykanthroporepellens (strain ATCC BAA-1523 / JCM 15061 / BL-DC-9) GN=Dehly_0090 PE=4 SV=1MNLLTIVHFLGLLVSLLGGIMAVPATLSLIQGENASGAMWTATVITVVTGALMFLLTRSQRQKLNQREVFLLVVASWVAATAFGALPYYFSGALPNYLDSFFEAMSGFTTTGATVMTSIGDQAHGVLLWRSLTQWLGGMGIIMLFVALFPLLGIGAAQMADAEMSGESGERMTSRIRETAKALWLIYVVLTLICFGALVISGLPVFDSLNISLTTMPTGGFAPVDFSIEEYGHVPAQLVVNVFMYIGGINFALLYFMFVKRRPGKLFRNPEFQLYSGILALSALFVTFNLMSNNIYDNLSEALREGAFSVTTIMTSTGYTGANYDEWPAFSRALLLLMLMVVGGSAGSTAGGLKVIRLLVLIKYSYRRVILAFNPHAVIPLKVGGTVLPEKTVSRIMSLTVLYLAVLWSGFLIMSALGLDIDTALSSVVSAVSNIGPGLGGVGPYENFAWIPDLGKGVLIVMMLAGRLEFFTLLVLFVPAFWRRY
5.6E-54	193	24.5	1.1E-52	188.6	17	2	1	A0KEW6_AERHH	Trk system potassium uptake protein	AHA_0254	Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Aeromonas, Aeromonas hydrophila, Aeromonas hydrophila subsp. hydrophila, Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	380703	>tr|A0KEW6|A0KEW6_AERHH Trk system potassium uptake protein OS=Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240) GN=AHA_0254 PE=3 SV=1MIKLRPIIFTLGLVLSKLALFMWLPTLLALLTGSEGFVEFLKSVLITHGAALLCLHYGRKAVFHLGVREMFLLTTSVWVVACIFGALPFFFINHIDFTDAYFETMSGVTTTGSTVLSGLDGMAHSILLWRSILQWLGGVGFIVMAVAVLPYLNVGGMKLFQTESSDWSDKSAPRAKTVANNIVLVYLVLSMLCFLAYWVSGMTLFEAVNHSMTTLSTGGYSTSDQSMSHFSNSAHWIGTVFMFLGGLPFLLYVQSLSRRDNSLLKDAQVQGFFWLVVWVTVVVTFYLWLRDIYGFMDALRISCFNIVSVLTTTGFGLGDFGTWGPLTSIIFIILLALGACSGSTAGGLKIFRVQVAFALFKKQMRQLMHPSGVFPQKYNGRPVNDAIIRSMISFVLAYFAVILLIAALLAAIGLDPLTAISGSITAVANVGPGMGPIIGPSTNFATLPDSAKWILSFGMLLGRLEILTVALVLLFPSFWKQ
5.9E-54	193	14.5	9.8E-53	188.7	10	2	1	A6V2L2_PSEA7	Trk system potassium uptake protein	trkH1 PSPA7_1916	Pseudomonas aeruginosa (strain PA7)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	381754	>tr|A6V2L2|A6V2L2_PSEA7 Trk system potassium uptake protein OS=Pseudomonas aeruginosa (strain PA7) GN=trkH1 PE=3 SV=1MALPTLRTLGFIIGIFLITLAASMLVPILTMLAFDRTEGIQAFIWSSVATFVSGLGLVLPGRPEHVHLRPRDMYMLTVSSWVLVCIFAALPFVLQQHISYTDAFFESMSGITATGSTVLSGLDDMSPGILIWRSLLHWLGGIGFIAMAVAILPMLRIGGMRLFQTESSDRSEKVMPRSHMVAKYIVATYVGITLLGSLAFWGAGMSPFDAVNHAMSAISTGGFSTSDQSLAKWKQPAVHWTAVAVMILGSLPFALYVATLRGHRRALIKDQQVRGLLGLLLVTWLLMGTWYALTSRLPWMDAFRIVAVNVTSVVTTTGFALGDYSMWGHFSIMLFFYLGFIGGCSGSTAGGIKIFRFQVAYTLLKANLYQLIHPRAVLKQNYNGHRLDEEIVRSILTFSFFFAIVVCLLALGLSLIGLDWMTALTGAASTVAGVGPGMGPIIGPSGNFASLPDAAKWLLAAGMLLGRLEIITVLVLLTPAFWRH
6E-54	193	5.3	7E-53	189.2	3.6	1.9	1	Q5SJ41_THET8	Trk system potassium uptake protein (TrkG)	TTHA1173	Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579)	490	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Thermus, Thermus thermophilus, Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579)	300852	>tr|Q5SJ41|Q5SJ41_THET8 Trk system potassium uptake protein (TrkG) OS=Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579) GN=TTHA1173 PE=4 SV=1MRSWLPSSRSKGALEALLYLLGLTFRGFAFVHLGFAALALVLGEEAWGFLGAAALGFALGYLGTFRGRPKAQPQRAEVFAGVALLWLLVPVLGAVPYWISGGLAFLDALFESMSGYTATGATVLQDFSLSRSLFLYRGFTQWMGGIGIVVLFLAVFPQLHVAGRQAFFAESTGVEKERLTPRIRQTAQAVLLLYLALTGAAALGYALAGVPLFEAVANALATVPAGGFSPNPQSFAGYPPLAQWLGVAFMFLAGVNFLLQYRLFFRGEVGPLLRDAEFRAYVLVVLAAGLALSGYLYTHHTYDLEASLRHAFFQVISILTGTGFASVDFAQWVVPAQAILVLLMFVGGSAGSAAGGIKLVRWLVLFGFLRREITRTLHPQAVLPLRLGGRVLSEEVLRQVSVFILLYTLLFVLGAVALAFLEKDFVVAFTASAQAIGNIGPGLGEVGPMGSYAGLHPLSKLLLVGLMWAGRIEVVPVVLLLTPELWRRLR
6.1E-54	193	35.4	8.6E-54	192.2	24.5	1.1	1	A0A0B5AQG4_9BACL	ATP synthase	JMA_14660	Jeotgalibacillus sp. D5	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Planococcaceae, Jeotgalibacillus, Jeotgalibacillus sp. D5	1508404	>tr|A0A0B5AQG4|A0A0B5AQG4_9BACL ATP synthase OS=Jeotgalibacillus sp. D5 GN=JMA_14660 PE=4 SV=1MWQMLKDRIRKLKPAQLIVTYYFLAISLSFGLLRLPWVHQPGQEVSLIDSLFTAVSAVSVTGLTVIQITDTYTVFGIVMVMLILQLGGIGIMSLGTFVWLLIGKRIGLRERQLIMLDHNQYNLSGVVKLIIEIIKILLLIEAIGALLLSLYFTQFYETWAEAVLHGVFASVSATTNGGFDITGQSMIPYANDYFVQIITILLIILGAIGFPVLIELKQFLSHKSGPFRFSLFTKLTTITFGILLVVGTILIYLIEYNQRFADVSWHQGLFYALFQSVSTRSGGLVTLEVSTFTEPTQLILSLLMFIGASPSSVGGGIRTTTLAIAVLFLINFSRGRHHIQVFGREIHLIDIFRSYVVIILAVLMSMISVITIMIIEDLDVIAVIFEVTSAFGTSGMSMGITPTLSTPSKMILMVLMFIGRVGLISFLFMIGGNNKKEKYHYPKERVIIG

6.2E-54	193	18.3	1.8E-53	191.2	12.6	1.6	1	F0ST30_RUBBR	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Plabr_0558	Rubinisphaera brasiliensis (strain ATCC 49424 / DSM 5305 / JCM 21570 / NBRC 103401 / IFAM 1448) (Planctomyces brasiliensis)	447	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Rubinisphaera, Rubinisphaera brasiliensis, Rubinisphaera brasiliensis (strain ATCC 49424 / DSM 5305 / JCM 21570 / NBRC 103401 / IFAM 1448) (Planctomyces brasiliensis)	756272	>tr|F0ST30|F0ST30_RUBBR H(+)-transporting two-sector ATPase OS=Rubinisphaera brasiliensis (strain ATCC 49424 / DSM 5305 / JCM 21570 / NBRC 103401 / IFAM 1448) GN=Plabr_0558 PE=4 SV=1MAELTATEVFVLSFLALIVVGVFLLKFLPGLHTGEELGWVDAVFMSTSAVCVTGLTVVDTETYFTPLGQAVLLLLIQLGGLGMLVLTSLIITMLGGRPSLRTETLAAGGRHLIPEISSRRLIRDIVMFTFALELTGAVGLYLTWGPRLGWTEAIWPSIFHSVSAFCNAGFSTNSQSLMEYQNSPLTLGLISWLICAGGIGFIALEELWLFVIRFRKKRQRLSVHTKLVLSTSAVLLLGAWPVFAVLEWRGVLADMTLTERLANSFFMSVTPRTAGFNSIDYAAASDSSNFLTIILMMIGGSPGSTAGGMKTTTFALLGLLAWSRLRSYQTVTFASRSIPPETIQRATGLFVIATGVVVVNVMIFTSLGDLYQFDQPFLAQLFESVSAFNTVGLSMGLTGTLSPAEKWLLVLLMFVGRTGPLAIATALIVRISRGARYRLAYEDVVVG
6.5E-54	193	21.1	3.3E-53	190.3	14.6	1.9	1	A7HTK0_PARL1	Trk system potassium uptake protein	Plav_1614	Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966)	490	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhodobiaceae, Parvibaculum, Parvibaculum lavamentivorans, Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966)	402881	>tr|A7HTK0|A7HTK0_PARL1 Trk system potassium uptake protein OS=Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966) GN=Plav_1614 PE=3 SV=1MDGARVSFADSTKVVGLVIGALLIALSVVMLVPVLAEIVAESGDWEAFLSSAVVTGFVGGALMLSNQTEDRDLGHRATFLVTTLGWLSLSAFSALPFAFSKVDMSYTDAFFEAMSGFTTTGSTVMVGLDATPPGLLLWRSLLQWMGGIGIIVTAVAILPFLRVGGMQLFRTESSDRTEKVLPRPGQIAVAIGEVYLLLTLLCALAYIIGGMSAFDALNHAMTTISTGGYSTHDASFGYFDSSFIHWAAIIFMVSGALPLILYVQTLRGTGETLWGDPQVRAFITMLAVTSVLMALWLAARGDYHFFEALQLTAFNVVSVVTTTGFASTDYTLWGPFAIMAFFLMFIGGCTGSTSGGLKMFRLQILALLFKSQVRQTLYPHVAQTLRYADRTVSREIVFSVALFVFVYMGSILAVSLALAAFGLDLVTALSSAVTAIANVGPGLGPVVGPAGNFSSLPDGPKIILAFAMLLGRLELLTVLVMFSKDYWER
6.6E-54	193	12.8	1.4E-51	184.9	8.9	2.1	1	D4K4V3_9FIRM	Trk-type K+ transport systems, membrane components	FP2_09910	Faecalibacterium prausnitzii L2-6	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii L2-6	718252	>tr|D4K4V3|D4K4V3_9FIRM Trk-type K+ transport systems, membrane components OS=Faecalibacterium prausnitzii L2-6 GN=FP2_09910 PE=4 SV=1MNYAIVFRLLGYILMIEGALLLLPAVTSLIYAEWAVMGVFLLTAAISGALGFALQAIKPRSKVFYMREGFAATALSWITISIMGAVPFVLTGCIPNPVDAMFETVSGFTTTGASILPGVEGLPNGILFWRSFTHWIGGMGVLVFLLSLLPLTGGSHVNLMKAESPGPQVDKLVPKVQSTAKILYGIYFALTVVELCFLLAGGMNVFDSLLTAFGTAGTGGFGFKNDSFASFSPYIQWVVTVFMILFGVNFNAYFLLLLRRFRRAASSEEVRAYFAIILAAVAVITVNIRSLYGTFGEALRHAAFQVGSIITTTGFSSCDFDLWPTLAKEVLVLLMFVGACAGSTGGGIKVSRFLLLGKTLGKELKQALHPQVVAPVRMDGKLVNHETIRTTNVFLAAYIFIFAASFMLVSLDGFDMVTNFTSVAATLNNIGPGLNQVGPMMNFGAYSNFAKLVLIFDMLAGRLEIFPMLVLFLPDAWRRF
6.7E-54	193	22.4	3.6E-52	186.9	15.5	2	1	R6PNU9_9FIRM	Uncharacterized protein	BN668_02114	Firmicutes bacterium CAG:466	481	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:466	1263025	>tr|R6PNU9|R6PNU9_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:466 GN=BN668_02114 PE=4 SV=1MNYKMMAYILGNIMQAEGLLMSISALLALYKGEINELRAFLITIILLLVIGTAMKHFAPKNKRIYGREGFVIVALSWIVMSIFGAMPFYLSGAIDGAVNCFFETVSGFTTTGATVLSEIEGLPMSILFWRSFTHWIGGMGILVFVLAIVPLGDDRSMHLMKAEAPGPVVSKLVPKIKSTAKILYGIYIVMTILEMIFLFAGGMPLFDSINHALSTAGTGGFSIKNSSIAAYNSPYFEYVITVFMLLFSINFNMFYLLLVRDFRAVFKNEELRYYLVIVGISTAVITANIVHLYPTLESAFRHAVFQVATITSTTGFITANYEEWPELSKTILVVLTMLGACGGSTGGGIKVSRFIILLKLTLREIRHIVHPRSVNIIKLEGQRVSDETIQGTTGYFITYIMLLFGSFILVSIDNYDFTTSITAVITTLGNVGPGLSLVGPVENFSLFSDFSKIVLSLDMLFGRLEIFPMIMLFSPSIWRKA
7E-54	193	36.1	1.2E-53	191.8	25	1.3	1	R3W4F5_9ENTE	Cation transporter	UC3_02829	Enterococcus phoeniculicola ATCC BAA-412	466	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus phoeniculicola, Enterococcus phoeniculicola ATCC BAA-412	1158610	>tr|R3W4F5|R3W4F5_9ENTE Cation transporter OS=Enterococcus phoeniculicola ATCC BAA-412 GN=UC3_02829 PE=4 SV=1MNLGRFVRLSKKRGNRFISSHFSSIQIIVSYYILMTVVSTGLFYLPFFREPDVHVSFIDMLFMAVSTISVTGLSTFDINSVFNERGVILLELLFQVGGLGIMMISTFFFIISKRKISLKQRQLIMTDMNQPRLSGIVRMIRITFGIIIWFQVIFGLLFSIYFYVNDYFDNWGDALFNGFYQAISAVTNSGFDVTGDSIIPFAGDYPFLLSIMFLIFIGGIGFPVLMEIREWLGYRRQKHKLPFRFSLFTKIALLAFVLLFVVGTLLIFFLEKDHLFLGMNPVSQWMNSMFYSITTRNAGLQIHNLQDFQVTTLIVFSLLMFIGCSPSSVGGGVRTTTIAIIGLYLFSFLKSEEKINIFGRQIDDDDVRKSIVVFMLSLGMCFFSVLFLTAIEDHSLISIIVEVASAFGTTGLSFGITGDLTVVGKLTIAALMFIGRIGMLYTLLLFVPKETRDLGYEYPSEKIIIG
7.1E-54	193	32.7	1.1E-53	191.9	22.7	1.1	1	M1WP46_DESPC	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	BN4_10797	Desulfovibrio piezophilus (strain DSM 21447 / JCM 15486 / C1TLV30)	454	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio piezophilus, Desulfovibrio piezophilus (strain DSM 21447 / JCM 15486 / C1TLV30)	1322246	>tr|M1WP46|M1WP46_DESPC H(+)-transporting two-sector ATPase OS=Desulfovibrio piezophilus (strain DSM 21447 / JCM 15486 / C1TLV30) GN=BN4_10797 PE=4 SV=1MRIKFLSPYWLPVWFFAGAILIGTIILHLDVSHPGGPLSFVDALFTATSAMCVTGLIVVVDTGSFFSVLGQDVILILIQFGGLGIMTFTTLFIYLFGKHVSLGDRMAVGQSLLHDPSFSLVKFLGRIVIATFVLEGLGAFALWWMDPIGFSPYSAIFHSVSAFCNAGFSLYSDSLSQWSNHAGINMVFIVLITAGGLGFYVLYECSSLLKKMILNKRAIRRGVPLLSWHSSIVLKTSFFLVIAGAIVIFSAESAANNAPASMSERVLTALFQSVTCRTAGFNTVDIGSMSNVSLVFMMGLMLIGGSPGSCAGGIKTTSFRALCSFVVAQFKGHSQVKVSRFALSSEALNKVLTLFMVSVLLVILGTMVLTTLESAGASYLMGRGKFMVNMFEVISAFGTVGISTGLTANLNTAEKVMIIVLMFVGRLGPMWLLSALQSWQTERRYKLPTGDLPLG
7.1E-54	193	15.6	2.1E-53	191	10.8	1.6	1	W0SB32_9RHOO	Trk system potassium uptake protein	SUTH_00130	Sulfuritalea hydrogenivorans sk43H	484	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Sulfuritalea, Sulfuritalea hydrogenivorans, Sulfuritalea hydrogenivorans sk43H	1223802	>tr|W0SB32|W0SB32_9RHOO Trk system potassium uptake protein OS=Sulfuritalea hydrogenivorans sk43H GN=SUTH_00130 PE=3 SV=1MERYYPVVRVFGVLLMGFALAMLVPLVVSWSLHDGAESAYDEAFLLTFGTGATLWWAARREKRELKVRDGFLMVVMVWSLLPVFAGLPLILHLGVSFTDAYFEAMSGLTTTGSTVLSNLDTLPLSINLWRGMMVWLGGMGLIVLAVAVLPLLGIGGRQMFKAETPGPMKDSQLTPRMTQTAKGLWAVYAGVTVLCIFSLRWAGMSWFDAVMHAFTTMGLGGFSSHDASFGYWNSPLIEAVTIVFMLAAGMNFATMFLALHGRSFQPYLRDPEARWFLGVTFASVLGIAIYLWAMGTYPEFMTALRHSAFNVVSIATTTGYASVDYNLWPFFAPLWMLFLCSFVTSAGSTGGGIKMIRAIILYKQVYRELLRAMHPNIAWPVRIGDNPVPHNILFAVLAFGFMYMASIVSLTLLMSLSGLDIVTAFSAVVASINNTGPGLNQVGPATTYEILTDFQTWVCSFAMLLGRLEIFTLLVVLTPAFWRR
7.2E-54	193	32.3	1.1E-53	191.8	21.9	1.6	1	Q03PZ2_LACBA	Trk-type K+ transport system, membrane component	LVIS_1655	Lactobacillus brevis (strain ATCC 367 / JCM 1170)	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus brevis, Lactobacillus brevis (strain ATCC 367 / JCM 1170)	387344	>tr|Q03PZ2|Q03PZ2_LACBA Trk-type K+ transport system, membrane component OS=Lactobacillus brevis (strain ATCC 367 / JCM 1170) GN=LVIS_1655 PE=4 SV=1MEKIKQSQLFDTLSKKMVWGFVFLITIGTVLLSLPVATNGMRGTSFIDTVFTATSATCITGLTVVNTAEHWSIFGQVIILGLAEIGALGYMTFAVLLFNLMRRNLDLSTQLMVKESLNLENLSDTKSVMTYVVGLSALFQIGGSLLLAVDFVPRYGWVRGLYISVYHAVMSFCNAGFDVFGDSLMRFRNDSYLLLVTIILIIGGGLGFLVWRDLLLFHERKRLTLNSKLTLTTTGALFVIGFLLLLVTERNLSILPAHTSWFNRTINTLFLSVTPRTAGLITVPTNSLQSGSIFLIMILMFVGGTPGSTAGGIKTTTFGVLMLQSIAQLRGKKDVEFSRRRFSASNINRALLLIFLASIVMVVATLILTQTEKIPKGFGLEYILFEVLSAFGTVGLSLGLTPHLTVIGKLVIMLLMFIGRVGIFTSLYSLSKRQTTVNKIRYPEENVLIG

7.8E-54	192	16.5	4.8E-52	186.5	11.5	2.1	1	R6KTV0_9FIRM	Cation transport protein	BN552_01754	Blautia sp. CAG:237	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:237	1262755	>tr|R6KTV0|R6KTV0_9FIRM Cation transport protein OS=Blautia sp. CAG:237 GN=BN552_01754 PE=4 SV=1MNFRIIAYIVGWVCNFQAAFMMLPLLTAGIYREKDFSAFLLVMLVCLVVGVPLTRKKPKNKVFYIKDGCVAVALSWLALCIFGSIP FVVSGCIPHPIDALFETVSGFTTTGSSILSDVEVLPHCILIWRSFTHWIGGMGVLVFLLSLLPLAGGYHMNLMKAESPGPSVSKLVPKV QSTAKILYTIYFGMTLIQLALLLIGRVPLFDSLCITFGTAGTGGFGIVNDSLGSYSTYCQVVTTIFMILFGVNFSAYYLILTKKFRQAFKYEE VRYYFGIIAVAIVIIALNTAHLFRNLLTAFQQAAFQVGSIITTTGFSSTDFNQWPALSKTVLVLLMFVGACAGSTGGGIKVSRILILCKAAK KEFQLYLHPNAVKKIKMDDKVITHDILRSTNIYISLYLMIFAASVLLIAIDNFDLITNFMAVTATLNNIGPGFEIVGPMGNFSSFSYLSKCVLI FDMLAGRLEIFPLLLLFFKGTWKKF
7.9E-54	192	31.9	3.8E-53	190.1	22.1	1.8	1	R6PC11_9FIRM	Potassium uptake protein KtrB	BN627_00062	Lachnospiraceae bacterium CAG:364	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	1262983	>tr|R6PC11|R6PC11_9FIRM Potassium uptake protein KtrB OS=Lachnospiraceae bacterium CAG:364 GN=BN627_00062 PE=4 SV=1MKFKFKKKNFSSFQIISLGFFIVILTGGFLLMLPISTKGPGGAPFLDAMFTSTSAVCVTGLVLHDTATYWSYFGQFVIILLIQIGGM GVVTVAVSIAMFAGRKIGLMQRNTMREAIAAHHVGGMVRMTGFILKTTLCIELIGAALMAPVFCKDFGFFKGLWYAIFHSVSAFCNAG FDLLGVRGEFSSITTYASQPIINLTIMALIVTGGIGFLTWEDIKTNKFHVKKYRMQSKVILTVTSFLILLPAAYFFFVEFSQEQWSNLSLYE KILASFFQSVTPRTAGFNSVDLTLFTEAGIMIMIVLMLTGGSPGSTAGGMKTTTVAVLFASTSSVFRRRENAQVFHRRISESTVNDAATI LLMYVVLFLSGGIISCIEDIPILTLCLFETASAIGTVGLTLGITTEVGIVSHLILMLLMFWGRVGGLTLVFAAVSGKHIEVGRFPEEKITVG
8.3E-54	192	9.4	4.3E-52	186.6	0.8	2.1	2	G4TLU2_PIRID	Related to potassium transporter TRK-1	PIIN_06219	Piriformospora indica (strain DSM 11827)	794	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Sebacinales, Sebacinales group B, Piriformospora, Piriformospora indica, Piriformospora indica (strain DSM 11827)	1109443	>tr|G4TLU2|G4TLU2_PIRID Related to potassium transporter TRK-1 OS=Piriformospora indica (strain DSM 11827) GN=PIIN_06219 PE=4 SV=1MNRSKTLPAATGLAPHAPMHPNLHKAKSENDKPAQIDAELANGVLPMEDIVVEAPERQSKHPWIRWLRKHLNFFRIHLLVFTFL PFFDAILLWAVNGSFKISFIDSLFLAYSAFTNTGLSPIDLSHTTRLQQVILFITMFFGSTIVVSWVVVLVRRNILASQCAHWVAQRRSLAS RARSALAGVRRKTMHDPPTKSFATGDMQEKGTPPTVVPAPSTTPTSAGEDAPRRTPSRAATGMIVPFRKYSIRRVDTELKLVDPSGR ISRGQTLQAVPQEGTDARTPNPQSFFHTIPPSPDREVGDQEPVAPTEVFDSPRSNAIDIDDSKLHLDKDGNMRADEGLPTTGNTPVS PALSSPAPPVFVTSPLSMQTFPSAISASEMGKSTPRQVGFELPAGNGTPRTVSVVGTDHEGLRQRRTAHMPQRQFTYTEIDVRPRG KTMSQNPSYQMPKVDERFVSKDSIGLGGFPGPIELTRRLFRALSARWDTTRFGRLFRPYPSVLVPIGSSAGAQFPRSETKEVPYFSF AAIVGKNSTFHGLTEEELDELGGVEYRGLRLLSKLVPAYYVGVQAIAWAINAPSFSKSKYTSLFAGQWAWIPPSWAGVFMGTSSMTN TGMSLVDTALIPFQNEFGVLIITSFTSLAGNTAFPILLRLIVWIGTKVTRKTGETWATLHFLLDHPRRCFLYLFPSHQTWFLLIVIFLLNMI DWAGFMLFDLGNPAFEAIPVNQRVINGFLQATSVRCAGVASVSLAAVAPATQVFIAPFPIALAIRSSNTYLDRSLGIYEQDSDSDDEEIG GPF
8.6E-54	192	17.8	4.3E-51	183.3	12.3	2	1	R5BC33_9CLOT	TrkH family potassium uptake protein	BN545_01805	Clostridium sp. CAG:226	486	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:226	1262781	>tr|R5BC33|R5BC33_9CLOT TrkH family potassium uptake protein OS=Clostridium sp. CAG:226 GN=BN545_01805 PE=4 SV=1MNIKAVGFYIGHVLRLLAAMMLPPLLIAFFANEEGTVAAFALSMGITMAAGCILLLLKRPGSGGVRPAEGFITVSLSWILISLFGCL PFYFSRYIPRFVDCVFETVSGFTTTGATILTDVELLPNSLLYWRSFTHWIGGMGVLVFMMAVVPLAKGNGESMHLLRAESPGPVVGK LTAKMKDTTRVLYLIYIAMTVLLFVLLLAGGMPLFDSVVNAFATAGTGGFGIKNASIAAYQSRYLQTVIAVFMMLFGVNFNVYYFILIGKG AQALKGEEFRAYIGMVIAGTLMIALNILPLYGNSFAQALHQSFFQVSSIISTTGFATADFDKWPEFSRMILMALLISGASAGSTAGGIKVA RIVMLFKGLKAEVMRAVKPRRVVTICMDGKRIDASVMRGTYGYVAAFVAICAASMLLVSLDDFDFTTTVTGVLTCIGNVGPGLSMVGP SGNFSAFSDASKLVLSLDMLFGRLEIFPLILMFSPRIWGRRG
8.6E-54	192	13.9	2.3E-53	190.8	9.6	1.6	1	A0A0B6TTU6_9CORY	Sodium transport protein	B840_07050	Corynebacterium marinum DSM 44953	447	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium marinum, Corynebacterium marinum DSM 44953	1224162	>tr|A0A0B6TTU6|A0A0B6TTU6_9CORY Sodium transport protein OS=Corynebacterium marinum DSM 44953 GN=B840_07050 PE=4 SV=1MALGFLLVIAVGTAVLASSWAGVDGRPTPLLDALFTATSAVSLTGLITVDTATHWSTAGQVTILLLIQVGGLGFMTLASLLGLLLA GRLGLRRRLGATAEGRGLHLGDVAWVIRATVAFSFIVEAVVALALALRFRAAYGHSWGRAAWEGIFHAVSGFNNAGFALYTDNVMA FALDAWILLPLAVALIFGGIGFPVLLEAVRRTRSAASGRPRPRWSLTARFTFTGTVVLGLAGTALVGLGEWNGALAQAGEAAGAGSA PGTGVRLLNAFFAGVSPRTAGFNALDYADFHPSTLLGTDLLMFIGGGSGGTAGGVKITTAAVLVAAVVAETRGDSSVAAHGRTVGGG VVRQALVIVSASVTLVAGSTMAILFIAPAFTTDQVAFEVVSAFATVGLSTGITADLPAAAQLLLVVLMFAGRVGPLALATALAAARTRGRL FDYPEERPFIG
8.7E-54	192	32.5	8.7E-54	192.2	22.5	1.4	1	L0FYW0_ECHVK	TrkA-type K+ transport system, membrane component	Echvi_1565	Echinicola vietnamensis (strain DSM 17526 / LMG 23754 / KMM 6221)	593	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cyclobacteriaceae, Echinicola, Echinicola vietnamensis, Echinicola vietnamensis (strain DSM 17526 / LMG 23754 / KMM 6221)	926556	>tr|L0FYW0|L0FYW0_ECHVK TrkA-type K+ transport system, membrane component OS=Echinicola vietnamensis (strain DSM 17526 / LMG 23754 / KMM 6221) GN=Echvi_1565 PE=4 SV=1MNVNKKLLKQIIEKVILVLSFTAFALVIYEEGFKKPFLTVTDSHLLLKVMLSSIWAGYLALYFLVKSKTGGFTKKRISELIAILLISGILL FIFTDYSVPGLDVITQATTDRFLVDLLVAGVFLIELSKVSLGVNELQLNPPLIFILSFLVLILIGTVLLMLPNATHQPIHLVDALFTATSAVCV TGLIVLDTAKDFTLFGQLIIMLLFQLGGLGMMTFSFFGFFFRGSFSIQNQLFLKDFINEDDFGQIFSTLMKIILFTFLVEGVAAVLIFVSLD NDLFGGVGEMIFFSIFHSISGFCNAGFSVLSNGLYEEGFRDNYTMQLVIAFSIIFGGIGFPVVLNYYGYLRHFVRGMYRKIAYGESYRHL PRVVNIGTRLIVLTTGILILVGFVSYWMLEYDHTLAGLDTYGKVVTSFFGAVTPRTAGFNTVDMTALSVPTVLIYLLLMWIGASPGSTGG GLKTSTFAVAILSAFSIAKGKDRVEVFRREISSSTLRKAFTVTFLSFMIIGLAVFALTLFDRDLPLISVVFEAFSAFSTVGLSLGITGSLSFG SKMVLIMTMFIGRVGILTLLIALSKGVKNQSYRYPEESVFIT
8.7E-54	192	25.6	2E-53	191	17.7	1.4	1	B1I237_DESAP	Potassium uptake protein, TrkH family	Daud_0545	Desulforudis audaxviator (strain MP104C)	458	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Candidatus Desulforudis, Candidatus Desulforudis audaxviator, Desulforudis audaxviator (strain MP104C)	477974	>tr|B1I237|B1I237_DESAP Potassium uptake protein, TrkH family OS=Desulforudis audaxviator (strain MP104C) GN=Daud_0545 PE=4 SV=1MANKDRFQTGPTGFGAGRGTPELFTPQRILLLGFGLLIAAGTFLLSLPAAVAPGGDNSFLVALFTATSATCVVGLVVVDTGTNW SPFGQAVILGLIQVGGLGFIVVASLILVLTGRRIGLRQRLLIRESLSQNRVGGVVRLVIQIIVITLAIQAFFAAVLAARFIADFGWPRGLWM GVFHGVSAFNNAGFDLFGGFRSLTAYTEDVIVNLAVAIPVILGGLGFIVIVDLYQQRSFKKLTLHSKIVIVTTVVLLVFSTLVVLLEHNRA FADLTGPGKVLAAFFQAVTSRSAGFSTVATEALHPATQFFTIGLMFIGGGPNSVTGGIKVTTFAILLLSVWTLSRGSESIDVRDRRIPLA QFYKAVALTIILFGLIFLAALILSVTEQADFLTTLFEATSAVGIVGLSMGLTPELSPAGKLVVTICMFIGRLGPLTIIWALTKPIKKSKLKYPE EQVIIG
9E-54	192	18.3	1.5E-51	184.9	12.7	2	1	R6NRP1_9CLOT	Trk system potassium uptake protein TrkH	BN649_01198	Clostridium sp. CAG:413	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:413	1262803	>tr|R6NRP1|R6NRP1_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:413 GN=BN649_01198 PE=4 SV=1MNYRAISFNIGRILAVEAALLIFPAIGSIIYRDGTLLSFAITIAVLTVCSLAALSAKPKSRTLHARDGYVIVALSWILMSLFGALPFVLS GHMPNLFDAFFETVSGFTTTGSTCLRNVEALPKSLLFWRSFTHWIGGMGILVFVIAIMPKTDSSSMHVMRAEVPGPTVGKLVSKLSVS ARILYGIYCVMTLIEIVMLALGGMPLFDSIVNSFATAGTGGFAVLNKSIEGYNSLYAEMVIAVFMVLFGVNFNLYYFILIKQGKQAVKNEE LRWYLGIIGGATLIIAGDLILTKHSVGESFRYAFFQVSSIITTTGFSTTNFDMWPVLSKAVIVLLMFCGACAGSTGGGLKVSRIIILTKGSV REVRKAANPRRVESVKIDHHSVDESVVKSVFVYFAAEMFLIAVSTLLLCFEGRDLVTSFTAVLSCVSNVGPGLEAVGPAGNFADFSGL GKLLLSFDMLAGRLELVPMFMLFSPLAWSKKYA

9E-54	192	28.1	7.8E-53	189.1	19.5	1.8	1	K4LJ80_THEPS	Ktr system potassium uptake protein B	ktrB Tph_c28960	Thermacetogenium phaeum (strain ATCC BAA-254 / DSM 12270 / PB)	463	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Thermacetogenium, Thermacetogenium phaeum, Thermacetogenium phaeum (strain ATCC BAA-254 / DSM 12270 / PB)	1089553	>tr|K4LJ80|K4LJ80_THEPS Ktr system potassium uptake protein B OS=Thermacetogenium phaeum (strain ATCC BAA-254 / DSM 12270 / PB) GN=ktrB PE=4 SV=1MQRIIFIENSKRRRTVYLRKIFGRFTPAQILVFGFAALIMMGTFLLMLPVAAREGQATPLITAFFTATSAVCVTGLVVVDTATHYSLFGQLVILGLIQAGGLGIMTMTTLFAMLIGKKINLRERLLIQEGLNAIRLEGVVSLVKSIIKMTILIEGTGGLILSLRFIQDFGWAKGIYYGFFHAISAFCNAGFDLFGTVSGPFSSLTAFKEDPVVSLTIPALIILLGGLGFVVIRDVAAHRRFSRLSLHSKLVITITLVLVVAATAVIWLLERDNTLRGLTPLGTFLASFFQAVTPRTAGYNTLSISSSLRGATQFFIVMLMFIGASPGSTGGGIKTTTFGTLLIATWSVVRGEIDVGAFERSITQDIIFKALAITMLAVSLIATVTMILTITEKATFLDILFETTSAFGTVGLTTGITPDLSEIGRILISLTMYAGRVGPLTLALAIWQHRDQLGFHYPEEKIIVG
9.3E-54	192	15.6	1.5E-40	148.5	2	3.3	3	A0A0D2UL57_CAPO3	Uncharacterized protein	CAOG_006235	Capsaspora owczarzaki (strain ATCC 30864)	975	cellular organisms, Eukaryota, Opisthokonta, Opisthokonta incertae sedis, Ichthyosporea, Capsaspora, Capsaspora owczarzaki, Capsaspora owczarzaki (strain ATCC 30864)	595528	>tr|A0A0D2UL57|A0A0D2UL57_CAPO3 Uncharacterized protein OS=Capsaspora owczarzaki (strain ATCC 30864) GN=CAOG_006235 PE=4 SV=1MASSEPTSSPPTLVGGGSERRVNFNHVAISVGAPQKETNPPATAAENAKNPETAAPQGRSDWINDGDDENGQEKTLETAAVRDPRPQRVLTGRRWLTTIPQDDRHNIFLQVPPTGWAGVAQGETSATTADCRCRTASTSIPVPVSSESLPADFYTSTAQYQHAKPVPMTAASRRRATIDTLRVFVPNVIPTSEKNAAKLAAEKHAGSSKWRRFLPDITYYKVHLLYIIVMALICATIVWGIEDISYTNAAYLGFASVSQAGLISVDLSTLHTGSQVTLILTVLFTWTIPLTLMPVTIRRYYFAKRLRAAGVSPEDAQHCITEYAALRTITHIVIGFIVVWLVLGFLGLFFYMQFSSTAQQTLDANNDQSAPYFSFFQCISALSNTGFSSFSSNMVALNTQAYPLMWIAVMGLVGDTFYPILLRFIVYCLYRWSKSRVLERFRQWQDRRRKKAHPAAVPERKDSGVDADSMEVPFSEANSNKRQTAGGVPQIIVTSTDGDANEIRPIVTPAASSSAEHAAEGTQRDREDGSSVTAVPPTAATLSQLNRAALTTASMDWWHRTTLIGAPPCPCVCHRADNFNDAAHVLRSCCLAAREYFAPRSSSASTSTSAPSTSLSTSTADGIIQRKRQSRYVTQNEQTIPHHDNFLHRHLHNHHHYRKQYRTFMERFTAHHHVVQTSDIYLFLLRQPRRCYTHLFRWPETRWLIFVFVTLNVLQIALFLGLDWNSDALASLDTGEKIYNGIFQSFVARRAGFNSVDFSQLAQSMLVCYIAFMYISSTPVVAVVRQTDRSAASQLPSTELDMSGLPVRTNRGSLKVQTRRLFTQDLALVYLGLVVICIIERDQLEEQHTTDFTVFKTVFEIVSAYGGIGLSLGYPGTTASFSSIWRPGSKWVLMLIFLLGKQRGLPYSIDHAVQLTFNFGSRRPWSPSASSAPTSSTAGSGRSSPTNATLSRDVSREQPASVPASPFEQNGKSGQVT
9.3E-54	192	21.2	1.8E-52	187.9	14.7	2	1	D7CNH2_SYNLT	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Slip_1494	Syntrophothermus lipocalidus (strain DSM 12680 / TGB-C1)	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Syntrophomonadaceae, Syntrophothermus, Syntrophothermus lipocalidus, Syntrophothermus lipocalidus (strain DSM 12680 / TGB-C1)	643648	>tr|D7CNH2|D7CNH2_SYNLT Potassium uptake protein, TrkH family OS=Syntrophothermus lipocalidus (strain DSM 12680 / TGB-C1) GN=Slip_1494 PE=4 SV=1MLVKNNGVWKLSPAKLVVLGFAAVIFVGSVLLTLPAAVAGARDNSYVDALFTATSAVCVTGLVVVDTGTFYSRFGQVIILLIQVGGLGIVTVASIYAFLLRKRIGLRERLVMKEALNVESLGGIVRLVRAILLMTFLIEGVGALLLTLTLWNYFGFGKALYYGVFHAVSAFCNAGFDLFGREFYQYCSLIPFRHDWRVLGIIGSMILLGGLGFPVLVDLRRQRRFKTLSLHSKVVLITTGLLIILGCFLFWGIERDGVLQGTGVFKSMVNSLFMSITPRTAGYTSVDVAKLEPSTLLVLTVLMFIGASPVSTGGGIKTATMAVLVMAVYSRLRGRFDTEAFGRRIDSEIVYRALTVAVLSALLVGIGIIVLSLVCQVDIMKLIFEAVSAFGTVGLSTGITPQLNTGSKVILIVLMFAGRLGPLTLAFSLLQQERKETARYPRGNVIIG
9.6E-54	192	23.3	1.5E-30	115.5	6.4	2.1	2	F2JIW0_CELLD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Clole_0281	Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Cellulosilyticum, Cellulosilyticum lentocellum, Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	642492	>tr|F2JIW0|F2JIW0_CELLD H(+)-transporting two-sector ATPase OS=Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) GN=Clole_0281 PE=4 SV=1MSFYVNIIETFYMKRRMAMNRNDLKKIAPAKIIALGFIMVILIGAILLSLPIFANEGVEVSFLDALFTSTSAVCVTGLIAIDTADTFNVFGRTIVALLIQIGGLGVTSIGVGIILIAGKRVGLKQRTLVREALNLNSFQGIVRLVKAVLLMTLGFELAGAVLSFIVFRADYNTWDAIGISVFHSIAAFNNSGFDILGNLQNLSPYKDNVLLNLTTCGLIIFGGLGFLVIIDVAKNRSFKKLTFHSKVVLTMTGSLLLIGTLLLLKWTEDIPWLAAFFNSTSARTAGFSTYPLGDFTNAGLLVLIVLMFIGASPGSTGGGIKTTTLFVLIQSLKSTATNQHCQAFKRSIPCEAIMKAFMITLLSLGIVVAGTFALCVFEPENTFVQNIFEVTSAFGTVGLSTGITPGLTGPSKMVLIIIMYIGRIGPLTVASLWFTKEKASVKYSEGLITIG
9.8E-54	192	38.9	1.3E-53	191.6	27	1.1	1	K0IVR8_AMPXN	Putative Ktr system potassium uptake protein	AXY_03880	Amphibacillus xylanus (strain ATCC 51415 / DSM 6626 / JCM 7361 / LMG 17667 / NBRC 15112 / Ep01)	453	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Amphibacillus, Amphibacillus xylanus, Amphibacillus xylanus (strain ATCC 51415 / DSM 6626 / JCM 7361 / LMG 17667 / NBRC 15112 / Ep01)	698758	>tr|K0IVR8|K0IVR8_AMPXN Putative Ktr system potassium uptake protein OS=Amphibacillus xylanus (strain ATCC 51415 / DSM 6626 / JCM 7361 / LMG 17667 / NBRC 15112 / Ep01) GN=AXY_03880 PE=4 SV=1MSLIYRVHNKHAISPVKLIVLFYFLAIIISTALLNMPIFWREGQSVTVFDGLFTSISAISVTGLSVVAIDEVFNTAGYFVLSFIFQLGGIGIMTLGTAIYMLIGKKIGIRERQLISVDHNQATLSGLVRLTKKILKTILTIELVGMIVLSIYYLNYFDTWQEALLQGYFASVSATTNAGFHITGTSLALFADDYFVQFVHIILMILGAIGFPVLIELQQWLKNRKSGNSHFRFTTFMKLTVSTYFILLIFGTIVIFLLENNHMFANQPWYQALFSSLFQSVSTRSGGQVTIDIANYSTATLIIMAFLMFIGASPSSAGGGIRTTTFFAVMLLAVYNYAKGRQSIKIFRREISHQDTIRSFVVVLTTAIALTFISIFILAITESHSILEITFEVFSAFGTTGLSLGITSELSVIGRIVIMMMMFIGRIGIFSFLFLISSPPTKDRYSYPKARMLIG
9.9E-54	192	30.8	1.4E-53	191.6	21.4	1.2	1	E3C740_9LACO	Putative ATP synthase F0, A subunit	HMPREF9265_0990	Lactobacillus oris PB013-T2-3	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus oris, Lactobacillus oris PB013-T2-3	908339	>tr|E3C740|E3C740_9LACO Putative ATP synthase F0, A subunit OS=Lactobacillus oris PB013-T2-3 GN=HMPREF9265_0990 PE=4 SV=1MIEINKRKYSFPKILTLGFLLVIASGTLLLLLPCATVSGEQTSFMTAFFTSTSATCVTGLTLVNTATHWTGFGQAVIALLMEVGGLGFMTFAVMMSLMIRRRVRMSTRLLTQEALNLDHLSQLSVVYLIIKLSLLIQLVGSVFLFFDFYPRYGLGRGLWLSIFHAISAFCNAGFDLFGNSMENYLNDPYMICVLAVLIVAGSMGFLVWKDLLNYHKYHHLSLHTQLALRTGAVIFLISFLVYLLTERNLAQLSGQISGPQRLLNTVFMAITPRTAGLITFPYTKLSAAGISVTIILMFIGGTPGSTAGGVKTTTIGLLATQSIATLRGQRDTNFAHRRFTQENINRALTLFFVALFIVLLAILLLVLTQQLPAHDSLAYVTFEVLAAFGTTGISLGITQSLNLFGQLVVMVLMFIGRVGIYTVMFSIFNSQPKVKSYHYPEESVLIG
1E-53	192	21.5	8.7E-28	106.5	6.6	2.1	2	R5DUQ2_9FIRM	Trk system potassium uptake protein TrkH	BN798_00268	Eubacterium sp. CAG:86	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:86	1262895	>tr|R5DUQ2|R5DUQ2_9FIRM Trk system potassium uptake protein TrkH OS=Eubacterium sp. CAG:86 GN=BN798_00268 PE=4 SV=1MNRRRVLKILGKILMTEAMLMVPSLIVSLIYGDGDAMYFIGTIAFAAIAGFILSCVKAPERKMGSRDGYCIVALAWIIICIIGAVPLFLTGQFRSYWSALFEIVSGFTTTGASVLSNPEYLPHGVLFWRSFTHWVGGMGVLVFVLMIMPMENENSMHLIRAEVPGPVAGKLVPRMKKTSIILYGIYTAMTAILIVLLLFGGMNVFDAFATAFGTAGTGGFATSSVGIAGYDSAYIEIVLGIFMLLFGVNFNAYYLILIKRFTDALKIEEIQWYFGIVGVSVIAIAINICHSLSAVSVSLRQAFFQVSSIITTTGFATVDFDKWPEFSRHLLVLLMIIGACSGSTGGGIKVSRVIVMVKSFFTEIRHIINPSSVTAVRTNGKPMDKETLIAVRVYVASYFILICLFTLVISLNGLDFTTNLTAVLSCFNNIGPGLNLVGPMSNFSCYADWAQVILSVAMLTGRLEIFPMFMLFSKSVHRR

1.1E-53	192	18.2	2.3E-52	187.5	12.6	2	1	M4WZM3_PSEDE	Trk system potassium uptake protein	H681_17005	Pseudomonas denitrificans ATCC 13867	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas pertucinogena group, Pseudomonas denitrificans, Pseudomonas denitrificans ATCC 13867	1294143	>tr|M4WZM3|M4WZM3_PSEDE Trk system potassium uptake protein OS=Pseudomonas denitrificans ATCC 13867 GN=H681_17005 PE=3 SV=1 MALPTLRTLGFIIGIFVITLAVAMLVPMATLLYYGRGTELHPYIWSAIITFTCGLGMVIPGRPEQVHLRPRDMYMLTVSSWVIVCFFSALPFVFARHISFTDAIFESMSGITATGSTVLSGLDKMSPGLLIWRSLLHWLGGIGFIGMAVAILPMLRIGGMRLFQTESSDRSDKVMPRSHMVAKYIVGVYVGITILGALALWWAGMGLFDAVNHAMSAISTGGFSTSDQSLAKWHQPAVHWVAVVIMILGSIPFVLYVATLRGHRKALIRDHQVHGFLGLLLFTWVVMGTWYSVNSDLSWFDAFRIVAVNVTSVVTTTGFALGDYSLWGHFSIMLFFYLGFIGGCSGSTAGGIKIFRFQVAFTLLRASLYQLIHPRAVIKQSYNGHRLDEEIVRSILTFSFFFGGTVGVLALGLSFLGLDWMTALTGAASTVAGVGPGMGPIIGPSGNFAPLPDAAKWLLSAGMLFGRLEIITVLVLFTPAFWRH	
1.1E-53	192	23.8	2.7E-52	187.3	16.5	2	1	H1Z486_9EURY	Cation transporter	Metlim_2592	Methanoplanus limicola DSM 2279	489	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanomicrobiaceae, Methanoplanus, Methanoplanus limicola, Methanoplanus limicola DSM 2279	937775	>tr|H1Z486|H1Z486_9EURY Cation transporter OS=Methanoplanus limicola DSM 2279 GN=Metlim_2592 PE=4 SV=1 MVFRMNRLEQFSIIADDLGTVFRFLSVGTVFPLFIALYYREWDMLIPMGLVPVALFTLGTMLLNFPENKREAKVSQALFSVAFIWLVCAFIGAIPFTIGIDMPYLDAVFESMSGWTDTGITMIRDVDSTPHTLLFWRSLMQWMGGLGIVAFTVVMLSRTGLNPSRFYRSEGRSEAFMPSVVQQGLQMWKIYLILTGISIIVILISGVPLWDALNIAMVAIATGGFSVHTAGISYYDNALLEALIPVMIAGALPFKIYYTLYYRKKTEFFKDEQIKLLFMLILIGCTIITADLIMYRGLEGFDALRKGVFMAVAGATSTGFQTGSVNLWAPVTVLILIFLMFIGGSSGSTAGGIKLSRAAMAYRGILWWFRRSYISCKVIVPFRFGGKIIPKAQAETEVSRNILIIILYMLTIFVAMILIMHFETPDHDTSMVLFDVVSATCNNGISTGFAGPDLSPFSKIVFIFIMWIGRLEIFAVIMFFMGLFKGFE	
1.1E-53	192	44.3	2E-28	108.6	14.7	3.1	2	I1A5N4_9MOLU	Potassium uptake protein B	MCAN UFG4_01926	Mycoplasma canis UFG4	602	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma canis, Mycoplasma canis UFG4	1131455	>tr|I1A5N4|I1A5N4_9MOLU Potassium uptake protein B OS=Mycoplasma canis UFG4 GN=MCANUFG4_01926 PE=4 SV=1 MKKIKSFFKKTFFGKTIDKAFIYLKKVSKLKYLLVVYFLIVLFSSLLLWSPITQKNPTSDWTSAKNYVDALFTTASAFSDTGLVVYNTYSHWNVLGQATIAILILSGGIGIFALKFFVINFIFRKNITSLNTLKMIQHERGHEDVNKISHVLKSSVTFILSVSLISGLGMTFYFYFATPTHTYGISQFIGEFVSPQHNWELSFRFGFFHTISAINNAGFDIISGHSLMPYYQNYVLQIWFITLLIISGLGYPVIYDVHRFIKHKLRRKQNKYRFSLFTKVSSITYLLVFIVGFLILFGYEYSSNSASSLWNKIYVPNNMQDDYVKWVTVVGNYKQDNTIQGQVIYNELINLHKIANKDELTTTIAKEFFDLINKETFNGSLKNYIEKGYMYGNDFDKTFAILFSSLSTRSAGFATVNMRDFTRSSVIVMIIMMVIGAAPSSTGGGIRTTTLAVVVLSVISVILSRNRVRIFKRAIEPRTVFMSGQVLVIALIILIISSLICFTSFDIHGGKIHTDELSIINGQNIHDSFYETEHIWFEVASAFGTTGLSAGLTKDFNIISKITLIFVMFIGQFGISSSLLVWRRKKSTQRNYEYIITTDIVIG	
1.1E-53	192	24.4	9.9E-53	188.7	16.9	2	1	R7CRY8_9FIRM	TrkH family potassium uptake protein	BN625_01579	Dialister sp. CAG:357	482	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Dialister, environmental samples, Dialister sp. CAG:357	1262869	>tr|R7CRY8|R7CRY8_9FIRM TrkH family potassium uptake protein OS=Dialister sp. CAG:357 GN=BN625_01579 PE=4 SV=1 MNLKVIYTMLSRIMLVSGAMVALPLAISLIMGGPILAFIFSMAVAGLASVVLKKRGVAQENSLTPREGTAITALSWLFVSLLFALPYIFSGTLGPLDSLVESISGLTGTGATVIDDLGAVPQSILFFRAMTHWLGGLGIIVIFVAIFPQIGRGSAKMVNAESTGPTSSKALPRIKETASALFTVYLIFTIAAAAAYMLCGLTFLDAIDTSFSTIATGGFSTKDASIAYYNNPVLELVIAFFMIISSANFGIYVEARKRGLSAITGDMEFRTYIGIVLAATVLMTISLVLQGNYGFVEALRETTFFQSASLSSTTGFVSADFDQWPSFAKFIILLIIIVGGCGGSTAGGLKVIRLILLVKSFTSILKLHIHPRAVLHVTVSHERYSQDTIFRVLCFFFIYMALSTLWAACMMMDGVAFMDAIGVSFSTMSNAGPAFGQFGATCTYSALPDFSKFVVCLSMLFGRLESVTLLAIFIPSFWKKSGW	
1.1E-53	192	24.2	3E-53	190.5	16.8	1.6	1	R5WLE4_9FIRM	Cation transport protein	BN751_00146	Coprococcus eutactus CAG:665	499	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus eutactus CAG:665	1263071	>tr|R5WLE4|R5WLE4_9FIRM Cation transport protein OS=Coprococcus eutactus CAG:665 GN=BN751_00146 PE=4 SV=1 MNNSMIIYILGQVVRLEGILMIIPCITSLIYQEHEGFAFLVVILACVIVGTLMTIRKPSNQTIYLKEGCIATAFSWVLLSIFGCMPFVISGEIPSFTNALFETVSGLTTTGASILSDVEAMSHGMMFWRCFTHWIGGMGVLVFLLAIIPMNSASGSNMNLMKAESPGPSVGKLVPRLKHTARILYAIYFAMTLLEVVLLLFGRMSLFDAFCTAFGTAGTGGFGIKNDSFTSFSPYIQWVVTIFMMLFGVNFNFYYYILYRNVRKALSMEEVRTYFLIILGAIGIIFVNLMQTMSNAWDALRHASFQVASIITTTGYASADFDQWTQTCKTVLVILMFIGACAGSTGGGMKVSRLIIMFKTVVKELSSYFHPKNIKKIKMDGKPVEHEVVRAVNVYFITLMGIFTISVFLVSFEGRDLVTNFTAVAACLNNIGPGLSQVGPTQNFGMLTGFSKYVLMFDMLAGRLELFPLLLIFNPGVYRDMIMGAVRYVKRKIAARRVS	
1.2E-53	192	25.7	7.8E-33	123.1	3.7	2	2	A1UTF8_BARBK	Trk system potassium uptake protein	BARBAKC583_0982	Bartonella bacilliformis (strain ATCC 35685 / KC583)	466	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bartonellaceae, Bartonella, Bartonella bacilliformis, Bartonella bacilliformis (strain ATCC 35685 / KC583)	360095	>tr|A1UTF8|A1UTF8_BARBK Trk system potassium uptake protein OS=Bartonella bacilliformis (strain ATCC 35685 / KC583) GN=BARBAKC583_0982 PE=3 SV=1 MGVTMILPALIDLRDGSQNWTAFLYPCTITTMLATLILLATRGANCRFSARLGFTLTACLWLTGSIVGALPLYLSPLSLSLAEAVFESVSGITTTGSTVITGLDNLSRSILLWRSLMCWIGGIGFIGLALLLLPSLRVGGVQLFHMESSDKSEKILPRINQIANGIIIAYVGLTLACTFSYFAAGMTLFDAINHAMTTIATAGFSTHDASFGYFSNKPAILVISTIFMLLSALPFVLYIKLLFPSYSKRPIDPQIIVFLNIVFLFSFSLAVWLRFNDHLSFHQIFLDVIFHLTSIITTTGYSAQNYQLWGPFALGIFFILSFTGGCAGSTSGGIKINRLIILLWRIAQTSMAKLLSPNAVVKVRYDNSNISNDLAQSVLLFVCLYMFCLLIGTALLLFTGLDFISAFTGVLTALSNIGPGFGDIIGPIGNFSTINDNALWILSFLMLAGRLEIITIFILLTPAFWHE	
1.3E-53	192	35.5	1.3E-53	191.7	24.6	2.7	1	D4H7Q6_DENA2	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Dacet_1283	Denitrovibrio acetiphilus (strain DSM 12809 / N2460)	668	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Denitrovibrio, Denitrovibrio acetiphilus, Denitrovibrio acetiphilus (strain DSM 12809 / N2460)	522772	>tr|D4H7Q6|D4H7Q6_DENA2 H(+)-transporting two-sector ATPase OS=Denitrovibrio acetiphilus (strain DSM 12809 / N2460) GN=Dacet_1283 PE=4 SV=1 MNQYTFRNFFASDHEVSWGILTLTPLPLLSLIITPVLPFSYQIRCGISVLSVILNLIFAFYNGTKTGKFSGLLSMVLIYFSFLPMLLENPVYMLAGNVLFIILFFFAVYLSSSMQYFEGYLVKKYFRNVSVALHVFTVIIILIVVFTEKDVTSLLLAIPLTSFVFSQFAFVRWSVSSENWFNVFTSIMYITIGVAVTVLGVEFWDFVLLFFSVAATAQLYICRKQHGSAENWWDVFMSHPGRVLFSSFFILCLVGTVLLLIPAATSKGDISFIDAVFTSVSAVCVTGLIVLDTPKDFSMFGQIIIILILQLGGLGIMSLTTVAIQTFGKRLSLKHETVLTSMTETDHKTLLSSLAMILKYTFTLEFIGGAVLIVLFYRTGDSIDEAVWRGVFTSVSAFCNAGFALQSDSLISYNNNSYILNTVALLIFFGGIAPVIALSIPALVMGKKIPLGATLALWTSIILIFAGALLLLIFEWNGIFKGMNLVNKLFNSLFQSVTLRTAGFNSVELGHITNPSLIIMLIFMFIGGSPGGTAGGIKTTAVSILALTFWANITNRKSIVLQNKKIAQSTVNKAVTIVISGFIFWFLSVIMIEVTQQIPTRELIFEVTSAIGTVGLSTGATGMLDGVGKIIIIVTMFAGRLGPMTLFTIMSGTGNTSGTEYIEENITIT	
1.3E-53	192	30.5	4.2E-53	190	20.2	2.1	1	B3PGK6_CELJU	Trk system potassium uptake protein	trkH-2 CJA_1857	Cellvibrio japonicus (strain Ueda107) (Pseudomonas fluorescens subsp. cellulosa)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Cellvibrio, Cellvibrio japonicus (Pseudomonas fluorescens subsp. cellulosa), Cellvibrio japonicus (strain Ueda107) (Pseudomonas fluorescens subsp. cellulosa)	498211	>tr|B3PGK6|B3PGK6_CELJU Trk system potassium uptake protein OS=Cellvibrio japonicus (strain Ueda107) GN=trkH-2 PE=3 SV=1 MKLLGPTLFILGAILNLLALFMLVPLAFSVIDDSDNQLAFFASATITSLVGIVFLLIGRKANFDYMQPRQVFLITSGSWLGVCLLSSLPFLLIDNPLSLADSIFEAVSGVTSTGSSVISGLEKLPRDILLWRSLLNWIGGIGIIGMAIVVLPFLRVGGMRLFKTESSEWSDKAMPRARSLIAMIIYCYISLSVLCFLLYWLAGMDWFNAINHAMATVSTGGFSTADSSFAQFNNLLIHWICILFMFAGAMPFVLFVRLVVSHNWRVFTDTQVKGLLLAIVSTSLVVSIHLIISEQMPPLQAITMATFNLVSVITTTGFASADYQTWGSLAVMIFFFAMFIGGCSGSTSGGVKIFRLQIFGGLMREQIITAIHPRAIISRRYNNRLISSEIIASSISYMFLMMGCFIVIAIILALTGLDLVTAITGSATAVMNVGPGLGNIIGPAGNFAPLSDTAKYALSAGMLLGRLEFLTILVLFSRVFWRS	
1.3E-53	192	43.2	3.7E-53	190.2	29.9	1.5	1	G4L4D2_TETHN	Putative Ktr system potassium uptake protein	TEH_01550	Tetragenococcus halophilus (strain DSM 20338 / JCM 20259 / NCIMB 9735 / NBRC 12172) (Pediococcus halophilus)	468	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Tetragenococcus, Tetragenococcus halophilus (Pediococcus halophilus), Tetragenococcus halophilus (strain DSM 20338 / JCM 20259 / NCIMB 9735 / NBRC 12172) (Pediococcus halophilus)	945021	>tr|G4L4D2|G4L4D2_TETHN Putative Ktr system potassium uptake protein OS=Tetragenococcus halophilus (strain DSM 20338 / JCM 20259 / NCIMB 9735 / NBRC 12172) GN=TEH_01550 PE=4 SV=1 MSIKLFIRDTLQKSRFFLKHKLSSVQVIVSYYLLVTLIAIVLFYLPIFRQPGSHVSFIDMLFMAVSTISVTGLSTFSVTDVFNEQGVILLEILFQVGGLGIMMISTFFFILSKRKVTLKQRQLIMTDMNQPRLSGIVRLIRTTFVIILGVQIISGIGFSIYLKLNEYYTSWTDAFYYGFYQAVSSVTNSGFDVTGDSVSPYANDFLFLLTIMFLIFIGGIGFPVLVDVKEWIAYKFHRRPRLSQFRFSLFTKIALLSSVILFIGGSIVIFLLEKNHLFANMSTLGQGIHSMFYAVTTRNGGLQIHDLDSFQTTSLIVFAMLMFIGCSPSSVGGGIRTTTIMIIGLYIYSFLKGKAHVHIFGRNINKEDIRKSIAVFMLSLIMCFSCVVFLTAIEDVSLISIIVEVTSAFGTTGLSLGITSDLSTIGKLVIAGLMFIGRVSMLYTLMLFIPQNPHDSGYRYPTEKIIIG	

1.3E-53	192	37.3	2.7E-53	190.6	25.8	1.4	1	A0A075U7X9_9LACT	Ktr system potassium uptake protein B	ktrB_1WS74_1335	Weissella ceti	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Leuconostocaceae, Weissella, Weissella ceti	759620	>tr|A0A075U7X9|A0A075U7X9_9LACT Ktr system potassium uptake protein B OS=Weissella ceti GN=ktrB_1 PE=4 SV=1MHKLFDRLTPPQILTAGFLAIIFVGAGLLSLPIAQNPGVSVSFIDALFTAVSATAITGLTVVNTSETWSFFGQVVLLIMIEVGALGFMTFAVLVLTLTRQRLDLKARLLMREALNLRNLGDVKSMLTFVFSLSFIIQIIGAILLMFAFIPRFGIGQGIYFSIAHAISAFGNAGFTFFKEPITIFQNSPYVLFVWMFLITAGSLGFLVWRDLLSLKRGGRLSLHTRMALTTSSWLIVGGFTVFLFTEKLMHNLSGLSLWERVSDTLFLAVVPRTAGLEVIPLSSLSVGGLFIIMVLMFIGGTPGSTSGGIKTTTLGILWLQSVAALRGQEQVNFGNRRISQKTIVKALMLAVISTAFVMFVSLLLCMTETIPKGFGLEYITFEVISAFSTTGFSLGLTPNLSVIGKIIIMFVMFIGRVGLYTVMFSVLNIREKPSHYQYPTEEIIIG	
1.5E-53	192	14.6	5.1E-33	123.7	0.5	2	2	A0A0F7KHL4_9PROT	Trk system potassium uptake protein	AAW31_11985	Nitrosomonas communis	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas communis	44574	>tr|A0A0F7KHL4|A0A0F7KHL4_9PROT Trk system potassium uptake protein OS=Nitrosomonas communis GN=AAW31_11985 PE=3 SV=1MNQFLSVTNVLSKIILVFGFTMLVPYGVAYWSEDGSSVVFGEAILMTMSCGAIIGLMTRRYKRELQIRDGFLLVVLVWLLLPLFGMLPLLRFFPDISFAKAYYEATSGLTASGGTVLTGLDILPHSINLWRGEMVWLGGMGLIVLAVAILPMLGVGGRQIFKAEIPGPMKESKLTPRIAETAKGLWLVYVLLTLICMIAYKLAGMNWFDAVMHAFTTLGLGGFSSHDGSYGYWNSPIIELVAIIFMMISGINFATHFMVWRAKSFSSYYHDPEIKPYFVIVLASCIGLAGYLWLTGVYTDPLTALRYASFNVVSVATTTGYSNTDYSLWPIFAPLWMLFLSGFCTSSGSTGGGIKMIRVRILYQQFFRELITIMHPQAISPVKLGKNVVANRIIFAVFVFLFVYLASMILLTLVLTLSGLDEITAFSAAVANINNLGPGLNQIGPATTYASLTDFQISLCSFAMLLGRLEFYTFLIVFTAAFWKK	
1.5E-53	192	31	2.8E-52	187.2	21.5	2	1	A0A0B5AUX7_9BACL	Potassium uptake protein KtrB	JMA_32300	Jeotgalibacillus sp. D5	387	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Planococcaceae, Jeotgalibacillus, Jeotgalibacillus sp. D5	1508404	>tr|A0A0B5AUX7|A0A0B5AUX7_9BACL Potassium uptake protein KtrB OS=Jeotgalibacillus sp. D5 GN=JMA_32300 PE=4 SV=1MTGLVTVDTGTVFTLFGEAVIMILIQVGGLGFMTFAVLVILFLRKKITLKERLLIQEALSQTSIGGVVRLVLSLFIFSLVIELAGMILLATVWVPEYGWREGLHVSLFHSISAFNNAGFSLWSDNLMGYVGDPVINLVITGLFILGGLGFTVLVDVYKKPQFKKLTLHSKLMIIGTLVINTVALLFIFFSEYGNPATIGGMPLIDQLWASYFQGVTTRTAGFNSLDIGSMEDSSILFMMALMFIGAGSGSTGSGIKLTTAIIILLTFITFLQNKSEVAVFGRTIKNNIVIRAFAITFAGFMTVFVCLLGLTLTDPQLPFLEVAFEVFSAFGTVGLSMGITAELSVPGKLIIIVMMFLGRVGPITLAFSLAVIKPDKVRYAKEDVYTG	
1.5E-53	191	25.8	4.2E-53	190	17.9	1.6	1	S2VYN9_9ACTN	TrkH family potassium uptake protein	HMPREF9306_01546	Propionimicrobium lymphophilum ACS-093-V-SCH5	414	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Propionimicrobium, Propionimicrobium lymphophilum, Propionimicrobium lymphophilum ACS-093-V-SCH5	883161	>tr|S2VYN9|S2VYN9_9ACTN TrkH family potassium uptake protein OS=Propionimicrobium lymphophilum ACS-093-V-SCH5 GN=HMPREF9306_01546 PE=4 SV=1MMPMSTVHPGGLPLLPALFTATSALCVTGLTIVDTSSYWTVFGKVVIASLIQVGGFGVMSFATILGQAVVRRANLNANLVTAAERRSSMGGMGVLLRRVVLVSFAVEGVVAAVLTGRFLTLGYSFSRAICHGVFHAISAFNNAGFALYPDNLTRFAGDWWICVPLMCAIIIGGLGFPVIFQLRHNLFKPHRWNLNTRMVLAGTTALLLGSSLLVTAFEWSNPRTLGSLDNSSAILAGIFQAVQTRTTGFNSIDISAMSDSTLFAMDMFMFIGGGPAGTAGGIKITTLFVLLATVFSVIRGRNDASVFGKAISPNVIRQAITVVMLSFGLVATATLAILLLTDFNLSETLFEVLSAFGTVGLSTGITPLLNSPSQIILISLMIVGRLGPITVATALAFAPASSAISLPIERPIIG	
1.5E-53	191	27.9	2.1E-53	191	19.4	1.1	1	A0A099V604_9HELI	TrkH family potassium uptake protein	LS79_06365	Helicobacter bilis	458	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter, Helicobacter bilis	37372	>tr|A0A099V604|A0A099V604_9HELI TrkH family potassium uptake protein OS=Helicobacter bilis GN=LS79_06365 PE=4 SV=1MQIQSIKVLLAGYLGVILLGTLILSMPPMYHTNVSFLEALFTSVSAMTCTGLAIKNTGLDFTTYGQIVICVLIQLGGFGHMSMAGILFLLIGKRLSAAEKDLINVVDNLNNNSVQGIDKAILKAIVFVLIVELIGASLLCPYFVWQLGDTKEGMWVGIFHAISAFNNSGFTILKDGLLPYQADIVVNLVIPMLIIIGGFGYLSSLEFSHFCYAKVRYNRLFTHKAPRMRLSLNTRIVFVMSVLLLICGMINVLIFEWSNPRTLENVPFWDKIMNAFFVSTNYRTSGFHIFDISGFEERTMFFSIFFMMIGGGPGGTAAGIKVTTFAVLVALSIAIVKNRKNTTIFGRTIPQDIVSKVFCVFIIALVYLSVATFFLAIFEPNIPFLPLLFEVVSAFSTVGMSMGDGDSLSLCADFNTIGLLIIMILMISGKIGILAFTLIFMGGARTKHVQYVQEKVLI	
1.5E-53	191	13	3E-52	187.2	9	2	1	F8GID2_NITSI	Trk system potassium uptake protein	Nit79A3_0469	Nitrosomonas sp. (strain Is79A3)	485	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas sp. (strain Is79A3)	261292	>tr|F8GID2|F8GID2_NITSI Trk system potassium uptake protein OS=Nitrosomonas sp. (strain Is79A3) GN=Nit79A3_0469 PE=3 SV=1MNRLFVVVNVLGKMVLIFGLTMLIPLGLALWNNDGARFAFEESILITMSCGLLMWLVTRRYKRELQTRDGFLLVVLVWAALPAFAMLPLLIYLPDLNLSMAYFEATSGLTATGGTVLSGLDALPPSINLWRGEMVWLGGMGLIVLAVAILPLLGVGGRQLLNAEIPGPMKENKLTPRIAETAKGLWTIYASLTLACVVAYRWAGMDWFDAVMHAFTTLGLGGFSSHDASYGYWDSPLIESVAILFMLVAGINFATHFLAWRAKSLSIYRYDSEVGWYVMIVLFSCIGLASYLWFVDVYTDPLVALRYAVFNIVSVATTTGYSNTDYSLWPMFVPLWMLFLSGFCTSSGSTGGGIKMIRARILYQQVYREMITIMHPNAVIPAKLGRSVVANRVILAVLGFLFVYSASIVSMTLALTFTGLDVITSFSAAVACINNLGPGLGEIGPATTYASLTDSQIWICSFAMLLGRLEFFTILVIFTPAFWRK	
1.6E-53	191	16	1E-51	185.4	11.1	2.1	1	A0A077L974_9PSED	Trk system potassium uptake protein	PSCI_0193	Pseudomonas sp. StFLB209	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. StFLB209	1028989	>tr|A0A077L974|A0A077L974_9PSED Trk system potassium uptake protein OS=Pseudomonas sp. StFLB209 GN=PSCI_0193 PE=3 SV=1MALPTLRIIGFIIGIFLITLAISMIVPMLTLVIYDRFEDLRSFLWASAITFIAGLALVMPGRPEHVHLRPRDMYMLTVSSWIVVCIFAALPFLLTTHISYTDSFFESMSGITATGSTVLNHLDSMSPGILIWRSMLHWLGGIGFIGMAVAILPLLRIGGMRLFQTESSDRSEKVMPRSHMVAKYIILAYVGFTVFGSLAFWWAGMGIFDAINHAMSAISTGGFSTSDLSLAKWPQPAVHWVAVVVVMILGSLPFTLYVATLRGNRKALFRDEQVQGLLGLLLVTWALMTLWYGLTTDLPWLDALRHVALNVTSVITTTGFALGDYSLWGNFSLMLFFYLGFIGGCSGSTAGGVKVRFFQVAYILLKANLNQLIHPRAVIKQKYNGHRLDDEIVRSILTFSFFFTITICVIALLLSSLLGLDWMTALTGAASTVSGVGPGLGEVIGPAGNFASLPDAAKWILSAGMLLGRLEIITILVLCVPAFWRH	
1.6E-53	191	22.5	3.6E-53	190.2	15.5	1.4	1	Q2S0A8_SALRD	TrkH potassium uptake protein	trkH1SRU_2269	Salinibacter ruber (strain DSM 13855 / M31)	474	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidetes Order II. Incertae sedis, Rhodothermaceae, Salinibacter, Salinibacter ruber, Salinibacter ruber (strain DSM 13855 / M31)	309807	>tr|Q2S0A8|Q2S0A8_SALRD TrkH potassium uptake protein OS=Salinibacter ruber (strain DSM 13855 / M31) GN=trkH1 PE=4 SV=1MSTSSQQPPPGRRGVLWRLWSWWRSLSPPQLFVGAFLTLILAGTVGFMTLPGLYAGPPLNWVDALFTATSAVCVTGLIVVDTATYFTTWGQAYVLLLIQLGGLGIISFTSVILAALGQRLSLRHEQLAGSGTSLVDDIDYRALTWAILRFTFVAELIGGVLLYAAWVPRFGWGGAAWHAVFHTVSAFCNAGFSTFTTSLEGFQANLPLLMVVMGLIVVGGLGFLTLEELNVWRRKRRAEGRFRLSVHSQIVLGTTAFLIVAGWVAFTAFEWHNTLAGMSVGERLVNGLFASITPRTAGFNTIDYAQVETETNFLTIVFMMIGGSPGSTAGGIKTTTFALLGLLAWSRLQGRPTTSISSSRTIPESTLQKAMSLFIGAFGIVTVAIFVFSVTEFGDGVAAGAAPFLSYMFEAFSAFNTVGLSMSATGTLTTPGRLCTVVLMFIGRVGTLTFVAAMAREPKRIKGGFRYAYEDVSIG	
1.7E-53	191	24.2	3.2E-53	190.4	16.8	1.3	1	X4ZJ73_9BACL	TrkH family potassium uptake protein	PSAB_12140	Paenibacillus sabinae T27	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	1268072	>tr|X4ZJ73|X4ZJ73_9BACL TrkH family potassium uptake protein OS=Paenibacillus sabinae T27 GN=PSAB_12140 PE=4 SV=1MANLSYGGLRLTPPKILSLGFILLIAVGTVLLSLPVSSAGGDISWIDALFMATSATCVTGLAVIDTGTGLTTFGQIVLLVLFQFGGLGFVTMATLITLVLNKRISLKDRLLLQETMNQNSMQGIVRLIRRVLIYSLVIQFAGAVALTLRFLEEMPAGKAVYYGIFHSISIFNNAGFDLFGDVHGPFSGLTRYVEDPVVNITAMLLIFLGGIGFIVLSDVVDFRKRKRLTLHSKVVLSTSLILIGAGAALFFWLELFHTLKPLHFGGKVMASFLQALTPRSGGITTLDIYQLRESTQFLIILLMFIGAAPGSTGGGIKVTTFALLIAAVYSRVRGREDVVLFRHRLSKENVYRAITMTLLSLLLVIISTMLLSITEEADFLAVMFEAVSAFGTSGLSMGLTAELSAAGKILIILLMFMGRIGPLTLAYALRPNRGKELYRHPEGHIMIG	

1.7E-53	191	17.3	3.8E-26	101	4.9	2.1	2	R5XKI1_9FIRM	Uncharacterized protein	BN537_00694	Firmicutes bacterium CAG:212	481	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:212	1263009	>tr|R5XKI1|R5XKI1_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:212 GN=BN537_00694 PE=4 SV=1MNKKMIIYILAKMVGVEGLVLLLPAIVSLIYREKSGFCFLIVSAVLILIYFLLGRKVPKNKRIYAKDGLVIVGAAWILWSLFGAVPFYISGSIPNYLDAFFETVSGFTTTGSTILTDIEVLPMGMSFWRSLTHWIGGMGVLVFVMVLTSLDDDDSMHLMRAEVPGPEADKLVPKARYTARILYAMYFVLTAAEVIFLMFGGMNFFDALLHAFSTAGTGGFSNKNSSVAHYDSAYIDGVITVFMILFGVNFNLYFLLRLRNWKEALKNEELHAYLGIIAGSIAIISLNIVGMYGNILHAFRYASFQVASIITTTGFCTANYNLWPELSKTILLCLMIIGACAGSTGGGIKVSRLLIMLKSIKKQVKNMLHPKAITIVKVNGKRINESTMKGVYIYFICYIMITMVSVLLVSINNFDFATTFSSVLTTLNNVGPGISQIGPVENFYKFSALSKIVFCMDMLLGRLEIFPYLLLLSPELWRRRF	
1.7E-53	191	13	2.2E-52	187.6	9	2	1	D0LJG6_HALO1	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Hoch_4041	Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2)	709	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Nannocystineae, Kofleriaceae, Haliangium, Haliangium ochraceum, Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2)	502025	>tr|D0LJG6|D0LJG6_HALO1 H(+)-transporting two-sector ATPase OS=Haliangium ochraceum (strain DSM 14365 / JCM 11303 / SMP-2) GN=Hoch_4041 PE=4 SV=1MASSPDSGHSDALPAPPRAERPRAAATTLHVAALSGALAAAAPAPVAVASWLRVEISWPAVPTLAILSLVATLCLGLSSVVVRRRARPGRWLGALGIVLGTAGAADLLLASPVLALIMLVGATAAVNRLWAPEPMMRRLIHLAHPSVATARARGAAMAAVAVWLVVALRGLSPQPVGQAVLAVSLLAALGIIAGWLRREYRYRWRAWIFIATAGCAAAAVAAAALAGSARVDALMLVPGAACLLLPMVTRPGLGRMDWWEPILGHPARFLVVSFAGLCVLGTVLLALPVALEADVPGVLPGAGLPLVDAAFTAVSAVCVTGLGVVDTPHTFGRLGELILLVLIQLGGLGIMAFSTAALGLLGRRMSLRYEGMVASLMSAQDRNRLHGATRQLIGFTLLTEAVGALVLALLFWQQGDDVASALWRGLFTSVSAFCNAGFSLQSDSLIPYQAAPAILHVIALLIIAGALSPAAALAVPTLVRRRKARVSAQIKLALVTTAALLFGGALLMLTMEWDASLAGMSALDRVHNAWFHSVTLRTAGFNSTDLATTRPETFTVMLVWMFIGGNPGGTAGGAKTVTAALMILAVVAAIRGRAQAHAFGRRISHASVYRAAAIVTVGVLSVLGAVIALELTQAAELTPRMAIFEVVSALATVGLSIGGTALLDEVGKVVIIACMFMGRVGPLTMFMFLQSRSAEDHWQRPEEEINVG	
1.7E-53	191	28.6	2.4E-53	190.8	19.8	1.1	1	E8JXT9_9STRE	Potassium uptake protein, TrkH family (EC 3.6.3.-)	HMPREF9423_0052	Streptococcus infantis ATCC 700779	470	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus infantis, Streptococcus infantis ATCC 700779	889204	>tr|E8JXT9|E8JXT9_9STRE Potassium uptake protein, TrkH family OS=Streptococcus infantis ATCC 700779 GN=HMPREF9423_0052 PE=4 SV=1MTALTVLWYNVTMLFKSFSEKINTTLGRLSPARRIFLSFALVILAGSLLLSLPFVQATSSQATYFDHLFTAVSMVCVTGLFTQPVATTYNIWGQLICMFLIQIGGLGLMTFIGIFYIQSKQKLSLRSRETILESFSYGETQSLMVFIRSIFLTTFIVEGLGAFLLSFRFVPEFGWGRGIFTSIFVAISAFCNAGFDNFGSTSLVAFQTDPLINLVLAALIITGGLGFMVWFDLATQLSKKKRRLRFHTKLVLFLTAGILFTGTVSTLLIEWNNPGTIGNLSIPDKLLVSFFQTVSMRTAGFASIDFTQARPVTLLIYILQMFLGGAPGGTAGGLKITTFFVLLVFARSELLGLPHANVARRTILPRTVQKSFSVFIIFLLLTFLLGLILLGVTAEGNPRFIYIMFETISALATVGVTANLTPELGRLALSIIMLLMFIGRIGPLTLLVSLAEYQPDKKDMIHYMKDAITIG	
1.8E-53	191	24.3	1.8E-51	184.6	16.8	2	1	D4LYW4_9FIRM	Trk-type K+ transport systems, membrane components	CK5_13770	Blautia obeum A2-162	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, Blautia obeum, Blautia obeum A2-162	657314	>tr|D4LYW4|D4LYW4_9FIRM Trk-type K+ transport systems, membrane components OS=Blautia obeum A2-162 GN=CK5_13770 PE=4 SV=1MQENFHRKKHLTSFQMIILGFAGVILLGTLLLMLPVSSADGIVTPFDEALFTSTSAVCVTGLVVQDTGSYWSGFGQTVILILIQTGGLGVVTVAVAAFMLSGRKISLMQRSTMQSAISAPQVGGIVRLTKFILRGTFLVEAIGAILLLPVFCHDFGRRGIWMSIFHSVSAFCNAGFDILGTEGHRFVSLSGYGDNIWLNMVIMLLIIIGGIGFLTWEDVYENKLNFRRYRMQSKVILITTVLLIILPAILFFANDFGEFLFKKRLLYSIFQSVTTRTAGFNTADLPLMTEAGKSVMILLMLIGGSPSSTAGGMKTTTFAVLILNAFATFRSREDAGVFGRRFDVQVIKNAATIAMLYLMLFFGGGIIISAYEGLPVLTCFYEAASAIGTVGLTLGVTPDLHIISRLILIVLMYLGRVGGLTLIYAVFSGKNNSNARMPMEKITVG	
1.8E-53	191	23.2	6.3E-30	113.5	7.3	2.1	2	Q8EKR2_SHEON	Trk system potassium uptake protein	trkI SO_0028	Shewanella oneidensis (strain MR-1)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella oneidensis, Shewanella oneidensis (strain MR-1)	211586	>tr|Q8EKR2|Q8EKR2_SHEON Trk system potassium uptake protein OS=Shewanella oneidensis (strain MR-1) GN=trkI PE=3 SV=1MLNFRALLFILGLFLSMLTAFMPAMLVAVVNGEETVGSFMLSALATGICASLCLHNGQSKGINLNIRDMFLLTSLTWLIVSLFAAMPFTLYHGIGYTDAFFETMSGITTTGSTVLVGLDTMDHSILIWRSLLQWLGGIGFIVMAVAILPFLNVGGMRLFRTESSDWSDKAVPRTQSMAKHLFFIYILLTIICSVAYHLAGMTWFQAINHAMTTLSTGGYSTSDSSMAAFSNSAHWVGVVFMAAGGLPLLMFVQMIQQRDVKVWNDAQVKGFLFFLTFVSCSIGFWLWQTRDIALIDALRLSSFNVVSVVTTTGYGLTDYGAWGAFANIAFLFLMFVGSCSGSTSGGIKIFRFQIAGAIMREQLKQQCHPNGIFRERYNNRLITEDIVRSLITFVLLYMFVIVGLSVILVLTGLDPVTSFTGAITAVSNVGPGLGPIIGPVGNFSTLPDLAKWALSLGMLLGRLEILTVAVLFHPSFWKY	
1.8E-53	191	19	5.8E-52	186.2	13.2	2	1	R5NRM2_9CLOT	Trk system potassium uptake protein TrkH	BN482_00504	Clostridium sp. CAG:127	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:127	1262774	>tr|R5NRM2|R5NRM2_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:127 GN=BN482_00504 PE=4 SV=1MNYSVVIYILGWIMEIEAAFLALPGIVSAIYGEKGGFAFLWVALGSAVAGSAIILRKPKNMRFYLREGFVTVALSWILMSVIGCLPFVINGDIPHFADALFEMISGFTTTGATVVSDVEGLTKGSLFWRSFSHWIGGMGVLVFLLAIVPMAGGSHMNLMKAESPGPSVGKLVPKVRQTAKYLYIIYFALTMIEVIFLLFGGMNLFEALTTSFGTAGTGGFAIWNDGFVSVSPYNQWVVTIFMLLFGVNFGFYFLILTGKLRDALKFEEVRIYFIIVIAAAVFIFINLRHFALYAPAEGIRQAFFQVASIITTTGFASADFNLWPETSRTILVLLMFIGACAGSTGGGIKVSRFIIACKSFIKEIISYLHPRSVKKIKIEGKPLEHETLRATNVYFMTYMVIFAVSVLLVSIENKDLVTNFAAVAATFNNIGPGLSLVGPMANFGHFTDFTKYILMFDMLAGRLEIFPMMLLFCPAVWKRRRA	
1.8E-53	191	29.6	1.2E-51	185.2	20.5	2.1	1	A3DKA0_CLOTH	Cation transporter	Cthe_3184	Clostridium thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) (Ruminiclostridium thermocellum)	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminiclostridium, Clostridium thermocellum (Ruminiclostridium thermocellum), Clostridium thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) (Ruminiclostridium thermocellum)	203119	>tr|A3DKA0|A3DKA0_CLOTH Cation transporter OS=Clostridium thermocellum (strain ATCC 27405 / DSM 1237 / NBRC 103400 / NCIMB 10682 / NRRL B-4536 / VPI 7372) GN=Cthe_3184 PE=4 SV=1MNYRLIFKLIGNVLRIEALFMLFPLLVSFIYGGGDHPAFLWSILISAAVGTILAKLNPKDKNFRVKDAFVVAGFSWIFLSLFGALPFYFSGYFNSFVDCVFESISGFTTTGSSILTNVEVLPKGILFWRSFSHWIGGMGILMFMIAVMPSINASSVNLLRAESTGPAPDKIVPRIQETAKIMYIMYFAMTVILVVFLKIAGLPIFDSMLNAFSVAGTGGFSNMNASIGGYNNIAAEIIMTVFMFLFGISFSLYFALLGRKFEKFIKDTELKIYFGVVIVSILIITINISGLYNGIWEALRHSSFQVSSIISTTTGFATTDFNLWPTLSKSILVFLMFTGCCAGSTGGGMKLIRFIILFKAAKVELDKIFHPGSVKAVSINGKKISNDIVFKTSLFFFIYFAIFFVSLLLISIDNKDIVSSATAVIASLSNVGPGLGTVGPTGNYAAFSSFSKIVFSFCMIAGRLEFFPVLVLFTPHVWKRRVIK	
1.9E-53	191	35.9	2.8E-53	190.5	24.9	1.2	1	A0M4E3_GRAFK	V-type sodium ATP synthase subunit J (EC 3.6.3.14)	ntpJ GFO_2532	Gramella forsetii (strain KT0803)	596	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Gramella, Gramella forsetii, Gramella forsetii (strain KT0803)	411154	>tr|A0M4E3|A0M4E3_GRAFK V-type sodium ATP synthase subunit J OS=Gramella forsetii (strain KT0803) GN=ntpJ PE=4 SV=1MKFSGFRSWLQNERFLRYLNRLSFLLSLITVLIAIYDLGYRHAEYEEEQLSHFYFGALIIGVLAILLRYFLFKVHFRLKVRIFDSVLGTLFALLIFIKIDGVLENLPFMEFMNQMVYVYIAALIYFVREFSTVEFSLNSQYLNPAQLFISSFLLIILAGTALLMLPKATYEGISLLDALFTSTSAVCVTGLIVVDTGSYFTLFGQTIILMLMQIGGLGIMTFASYFSYFFRGQTSYQSQLMLKDATNSDKIGEVFSVLKKILFITFIVELLGTIFIYFSLNNSEITHIGHRLFFSIFHAVSGFCNAGFSTLENSLYEPDFRFNYPLHLIIASLFILGGIGFPIVLNIYKYTKYTMKNLYSKIRNKEKLPYSPWVINLNTRIVIVTTFILLSLGTIGFYVSEYNNTLAEHNWFGKIVTAFFGAATPRTAGFNSVDTSALNFSTIMLMFILMWIGASPASTGGGIKTSTIAVATLNFFSLAKGKDRIEVYRREISQASIRRAFAIISLSLMIIGISIFLIASFDQDKTLLSIVFESFSAYSTVGLSTGITSDLSANSKVVIIFTMFIGRVVSMLTLLIAILRRVKHLNYRYPSDEILIN

1.9E-53	191	17.4	2.9E-52	187.2	12.1	1.9	1	Q1QXG7_CHRSD	K+ transporter Trk	Csal_1488	Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)	453	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Chromohalobacter, Chromohalobacter salexigens, Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)	290398	>tr|Q1QXG7|Q1QXG7_CHRSD K+ transporter Trk OS=Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768) GN=Csal_1488 PE=4 SV=1 MSFWQRLSRPWRHTPHGRVLRLSPPETLLLGFTLLCLIGGGLLRLPMAATVTLDWQEALFTATSAVTVTGLAVVDTSAFTPFG QVVLLALIQIGGLGFMTFGALTLLLLGARLPLQQQNLVREALGETSLGELSQLVRLVVAFAVLVEAVGAGLLALHWVPELGWSRGLWA SLFHAVSAFNNAGFSLWPDSLTRDVGTPLVTLVVSSLFIVGGLGFVVISDIREKRRWGRFSMQTKIVLCATLAINLVAMAAMAALEWH NPATLGGLESLGDKLQAAWFQAVTPRTAGFNSVDTAAMSDASSLLTMLLMFIGGGASSTASGIKLTTFIVLLLVARAFLRGTQPTAYG RAIGEQTVMKAVAVALAGVALVFVTLLVLCITDGRLAFLDLAFESVSAFGTVGLSRGITNELSLPGQWMLMLTMLLGRVGPLSLGYFLA TRRTRGMRYAEGHIQIG
1.9E-53	191	28.7	3.2E-33	124.4	12.3	2.1	2	R5TM99_9FIRM	Potassium uptake protein TrkH family	BN481_02116	Ruminococcus gnavus CAG:126	434	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	1263106	>tr|R5TM99|R5TM99_9FIRM Potassium uptake protein TrkH family OS=Ruminococcus gnavus CAG:126 GN=BN481_02116 PE=4 SV=1 MKKINMFLRNQPPGRMIVAGFAAVILLGMLVLLLPISVKDGAEVTLIDALFTSTSAVCVTGLIAIDTADHFTAFGQGVVAALIQVGG LGVTSLGVGLMLVARKRVGIKSRMMVKEALNIESYKGIVKLVKSVLLMTLCFEAGGALLSFLVFSRDYSTVHAIGISIFHSIAAFNNSGFD ILGGLRNLMPYHDDVLLNLTTCTLIIFGGLGFLVILDIGKQKCFKKLTLHSKVVIVTSLVLLVVGTLTLKLTENVTWLGAFFQSVSARTAGF STYPIGQFTDAGLFVLCILMFIGASPGSTGGGIKTSTFFIMFQKIRGTCTKGTVHAFHRNISEQNISKAFMITILSGTVVCVATFFMCVLE PEYSFMQLLFEVVSAFGTVGLSTGITPALSVAGKAVIILVMFTGRVGAFTLISMWVNRTEPRARYSEEEVSIG
1.9E-53	191	36	2.5E-53	190.7	25	1.1	1	A5IYG5_MYCAP	Potassium uptake protein KtrB	ktrB MAG3760	Mycoplasma agalactiae (strain PG2)	536	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma agalactiae, Mycoplasma agalactiae (strain PG2)	347257	>tr|A5IYG5|A5IYG5_MYCAP Potassium uptake protein KtrB OS=Mycoplasma agalactiae (strain PG2) GN=ktrB PE=4 SV=1 MYNLILLYLHTIWRLNKMRSKKFAYWWRNSKIRSFFKKIRLWTKNGTKVKFILLMYALVVLIITLFLHSKITHNLDYVAENKITFWD AFFTTCSAFSNTGLVSHSTYKAWNMFGQSLIAIAALLGGFGLFALKIFLINVIFMKGHVSLSDVELVSYERGHSDFFKNKRMIIDSMIFLM VTLLLASIGLSFYFYVVSPKTELAHLREVVGNNSANFDNPYHNWSHSFRFGVFHAISAINNAGFDIIGDNSLMPYYKNIGLQVIIMALFLI GGIGYPVIHDVLNYIRIKSINKNAYYNWSLFTKISIVTYLIVLTLFGFIFVISFELSSTDSIFKSNLQYYGNNAYKTWSLLFMVISTRSAGFST LNLHLLSEPTLWVLGTLMFIGAAPASTGGGIRTTTFAILFLLVISKVFGRPNVRAFKRQVDSDTVKMSTIVLTISVVLVGFVSLVVMSSFD NFSGLIPRAKYSATHVFFEVFSAFGTSGLTTGITSSLNVGSKIVLSILMFIGQFGVSSSVLIWTSKKNYAYKYNYISESVTIG
2E-53	191	28.1	6.7E-27	103.5	7.5	2.1	2	F6D434_METPW	Potassium uptake protein, TrkH family	MSWAN_2203	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	477	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	868131	>tr|F6D434|F6D434_METPW Potassium uptake protein, TrkH family OS=Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1) GN=MSWAN_2203 PE=4 SV=1 MIGYLRKKDFFLIFKNLGTVMEGIGAIVLIPLIVSLIYNEHTYLSFLLPSLFSLIIGYTFKKIFPGTGNLRLKHGMIIAALAWLWAAFIGS LCLIYSTDMSFLHAYFESMSAWTGSGFTMYTNVEILPKSILFLRSLEQWVGGLGVVILVIGILIRPGTAAARLYKAEAREEKIKPSIVNTV KTIWWIYLFYTVLGIVLYVAAGMSIFDAINNCFTNLSTGGMSIKNGNIGAYNSNIITMITIVLMTIGGTSFLVHYKAIKGRAIDVFKDIQFQA MIVLVSIFSILLFVNAHFTSLNSVFYVVSAMSCTGSNTLSVSAMAAWGDYAKVVLTICMVIGMAAGSTSGAVKLIRIVTLFKGIYWEIVKI VSPEGSVIPRKIAGKSVTDAEIKEAGTYTFLYLLFIFITWLVFMQYGYGGIDSFFEIASAQGNVGLSVGITGPTMPSIPEIFLIFGMWIGRI EIIPALVLFKVGIDLFKRF
2.1E-53	191	15.3	1.5E-52	188.2	10.6	1.9	1	F2J504_POLGS	Trk system potassium uptake protein	trk SL003B_1618	Polymorphum gilvum (strain LMG 25793 / CGMCC 1.9160 / SL003B-26A1)	472	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, unclassified Alphaproteobacteria, Polymorphum, Polymorphum gilvum, Polymorphum gilvum (strain LMG 25793 / CGMCC 1.9160 / SL003B-26A1)	991905	>tr|F2J504|F2J504_POLGS Trk system potassium uptake protein OS=Polymorphum gilvum (strain LMG 25793 / CGMCC 1.9160 / SL003B-26A1) GN=trk PE=3 SV=1 MLGFLYVGLATAMLIPAIVDVAAKNPDWQAFVFSALLTGLVGMLLSIAVGGSLHEGLDMRQTFILTTMAWVTLPAFGALPFLWL GVSYVDAVFEAVSGFTTTGSTILSGLDSLPPGLLVWRSLMQWVGGIGIVVMAIVLLPFLRIGGMQLFQTESSDRSEKIVGRSVELIRLL GLVYLFLTALCVVGFLLSGMDLFDAVNHGLTTIATGGYSTHDVSFGFFTNSAAGWVAVVFMTIGALPFVLLIQALRGKPLLLWRDPQV RTLLAFLALVSLGLTIYLGVKLDFPLDEALLKATFNVVSVVTTTGFAMGDYSEWGAPVVGLALLLTFVGGCTGSTSGGIKVFRFLVFFG TVRAHLRRMVRPNRVMSEKYGGARLTPELSFSVLAFLVVYLGSVGIITLLLSLFDLDLVTAVSAAATAVGNVGPGLGPIIGPAGNFASLP DGAKWILSAAMLLGRLELFTVLVLLDPDFWSK
2.1E-53	191	24.6	5.5E-52	186.3	17	2	1	R5D9W0_9FIRM	Potassium uptake protein TrkH family	BN457_00554	Dorea sp. CAG:105	443	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea sp. CAG:105	1262872	>tr|R5D9W0|R5D9W0_9FIRM Potassium uptake protein TrkH family OS=Dorea sp. CAG:105 GN=BN457_00554 PE=4 SV=1 MMKNIGRHFTPFQLITMGFAAVILFGAFLLTLPISSVEGVFTPFHKALFTSTSAVCVTGLAVLDTGSYWSFFGQLVILILIQIGGLGV VTVTVSITLLSGKKISLMQRTTMQDAIAAPRIGGIVRLTKFILKGTFLVELIGAVLLLPVFGKDFGVKGIWMSIFHSISAFCNAGFDILGTTK NTFPSLLQYAGNALVNVVIMLLIIIGGIGFLTWEDVCTNTYHFRRYRLQSKIVLVTTAVLILLPSLFFFWNFKNLAMEERLLASFFQAVTP RTAGFNTVDIGKMAEPAQTLIIILMLIGGSPSSTAGGMKTTTIAVLLLNAFATFRSKDTVSAFHRRIDNHVIRDAATLLMLYVMLFFGGGI AISMYEGLPLAECLYETASAVGTVGLTLGITPHLHMASQLILIVLMYLGRVGGLTLIYAVFSSRNKSTAKFPVEQITVG
2.2E-53	191	27.4	3.1E-53	190.4	19	1.1	1	V5RIN1_SPIAP	Potassium uptake protein KtrB	ktrB SAPIS_v1c01140	Spiroplasma apis B31	541	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma apis, Spiroplasma apis B31	1276258	>tr|V5RIN1|V5RIN1_SPIAP Potassium uptake protein KtrB OS=Spiroplasma apis B31 GN=ktrB PE=4 SV=1 MDNSNNNSLTTGEPKSGKKKRSKRKYSTEKSEKTFFAKPKNWWPFSRVSGRIISVYLLTIVIGGFLLSIPGVVKEESNFWNFITG MFTASSAFSDTGITMIQTNTGYSFFGQFLILLLIQMGGIGILTVKIVFLVFLNKKISLDDQSVANTERGSNSLANTVEMIKDAFFFLLSVEII GAFILFFGFYFTPMSKSYLQENPNTTTNPYHNFGTSLWASIFHSVSAVNNAGFDILSGNSLQPYNQDDSRGYILQFTFLAQWIIGGLGY PTYHDIKRKFRARKLGKTVKFSLFTKLNFIVYVTLFILGPVLVFLSEYLTIENSAILLNKDSNGEHSEKIWKPAYVWIIDILFNVSSCRNAG FASVDINNFTAGSKFILSIWMFIGAAPSSTAGGIRTTTLAICFIAIFSIMRNKSSTEAFKKRIPDETVKRSFAVVLLSFMIVLVSIYVVYLDSN EMLFNTDDSKNTESTIIKLIVYVCSAFGTVGFQPFTNGQIIQMGVISKIMLVITMFIGQLGISNTLLAFVKPKNKQNYGYLEEDVTIG
2.2E-53	191	40.6	5.5E-53	189.6	28.1	1.5	1	R2SH50_9ENTE	Cation transporter	UAW_03190	Enterococcus haemoperoxidus ATCC BAA-382	466	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus haemoperoxidus, Enterococcus haemoperoxidus ATCC BAA-382	1158608	>tr|R2SH50|R2SH50_9ENTE Cation transporter OS=Enterococcus haemoperoxidus ATCC BAA-382 GN=UAW_03190 PE=4 SV=1 MNRFRLLWLAQRNGRRYISNNFSSIQIIVSYYVIMTVVSYLLFCLPFFREPGSHVSFIDMLFMAISTVSVTGLSTFDINSVFNDRGV ILLEVLFQVGGLGIMMISTAFIILSKRRISLKQRQLIMTDMNQPKLSGIVRLRITFTIILWFQVIFGTFFSIYFYFSGYYKTWPRAIFFGFYQ SISAVTNSGFDVTGDSIIPFANDYLFLIVIMFLIFVGGIGFPVLMEVREWLFFKKKKRGLPFRFSLFSKIAVLAFVILFIGGTILIYLLEKDHLF VGMGEIQRWITSMFYSMTTRNAGLQINDLGDFQVTTLMVFSLLMFIGCSPSSVGGGVRTTTVAIIGLYLYAFLKSEDKINVFGRRIDDD DVKKSIVVFMLSLIMCFFAVLFLTATEDHPLIAIIVEVASAFGTTGLSLGITSDLTTVGKLMIALLMFIGRIGMLYTLMLFVPKETRDIGYEY PSEKIIIG
2.3E-53	191	19.7	7.9E-53	189.1	13.7	1.7	1	A1U0J4_MARHV	Trk system potassium uptake protein	Maqu_1427	Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)	472	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Marinobacter, Marinobacter hydrocarbonoclasticus (Pseudomonas nautica), Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)	351348	>tr|A1U0J4|A1U0J4_MARHV Trk system potassium uptake protein OS=Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8) GN=Maqu_1427 PE=3 SV=1 MFILLSVFMTLPVLLLAATPSGAPNAIAFAESAAIVCVLGVLGLLLTYREPRELKPRYMFVLTVSSWFVIALLSALPFYLSDNDISAA DAFFEGTSGITTTGATVFTGLDTMDKDLLLWRSILQWLGGIGIIGMFVAVLPFLRVGGMRLFATESSEWTEKALPRMKTLSRGLLLVYL VFSVVAVVTYWLSGMSLFDAFNHGLTSIATGGFSTSDLSMGKFSDLILLEATFFMIIGSLPFFLFVREMHGQHGVLFRDQQVRLFLGIL FAVPAMLTLYRWWVSPVPFDPIHNYAATLFNVTSVVTTTGYASEDYSAWGPLAFVVFFFLMFVGGCSGSTAGGMKIFRFQLSLIIRE QLMRLLHPRAVFTRNYNGRAVSDEIISSMIAYTFIFLLCLLVITVLLASLQLDFVTALSGALTSLTNVGPGLGDIIGPAGNFSPLPDAAKWI LSVGMLMGRLEILSVVIVLSPGFWRG

2.3E-53	191	28.6	1.2E-51	185.2	19.9	2.1	1	A0A0C3R885_9PORP	Potassium transporter	BA92_01525	Sanguibacteroides justesenii	482	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Sanguibacteroides, Sanguibacteroides justesenii	1547597	>tr|A0A0C3R885|A0A0C3R885_9PORP Potassium transporter OS=Sanguibacteroides justesenii GN=BA92_01525 PE=4 SV=1MINFRFIVNIIGKLLLVESAFLVLCIVVALIYGENDLLAFIYSAVITLTAGSLMAFTVKVKDRVLAKKDGYFIVTSTWVIFTVFGCLPYLFGNTIPSIVDAVFETMSGFTTTGSSIINNVEALPHATLFWRSLTQWMGGIGIIVLLLAILPGFGIEGRDMFVAEVTGPTHDKFTATFTSTAQRMWTLYLSLTLLQTVFLLLGGMDLFDSICHSFTTMATGGYSTKQNSIAYWDSAYIQYVFIIFMFLAGTNFGLMYSVILKKIRNPFRDEEFKLYFLIVVVSSTIIALGLYFNGYSDLEKSIRDALFQVVTIQTTTGYATTDYLLWPPLLGIIIFVLMFVGASAGSTSGGLKCVRISLLFKNSFIEMKRIIHPNGIINVKYNNKSVHPNIMSGVMGFAILYIFIFGISSVIMSFFTKDIATACSAVITSLSNVGPGFGEIGPMGNFSILPGIAKIFLAILMLVGRLEVFTVLVLFSRTFWKK
2.3E-53	191	20	4E-51	183.4	13.9	2	1	R7N126_9FIRM	Trk-type K+ transport systems membrane components	BN816_01862	Firmicutes bacterium CAG:95	446	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:95	1262988	>tr|R7N126|R7N126_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:95 GN=BN816_01862 PE=4 SV=1MPEEIIHQKHRLSSFQIIISGFVGVILLGALLLMLPVSTTEGCITPFNETLFTATSAVCVTGLVVQDTGSYWSGFGQAVILALIQIGGLGVVTVAASFALLSGRKISLMQRSTMQDAISAPKVGGVVRLTQFILRGTFLIELLGAAAMLPVFCRDYGWRGIWMAVFHSISAFCNAGFDILGTENNLYPSLTGYTGSPIINITIMLLIVIGGIGFLTWDDICEHKWHFHRYRVQSKVILAITGFLIVVPAAFFFEDFSALPTGTQLLVSFFQSVTTRTAGFNTVALSAMSSASKGIMILLMLIGGAPGSTAGGMKTTTLGVLLANAVATFRQRDNAQFFKRRIDCNTVKTASTILTMYLTLFFGGGIFISVYEHLPLSDCLYETSSAVGTVGLTLGITPQLHIPSQIVLIILMYLGRVGGLTLIYATLSGKKAGNAKLPQEKITVG
2.4E-53	191	28	4.2E-52	186.6	19.4	2	1	A0A0D8P2D9_9GAMM	Trk system potassium uptake protein	UB37_09715	Photobacterium iliopiscarium	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium iliopiscarium	56192	>tr|A0A0D8P2D9|A0A0D8P2D9_9GAMM Trk system potassium uptake protein OS=Photobacterium iliopiscarium GN=UB37_09715 PE=3 SV=1MVNLRPILFVLGLVLSKIALFMYVPTLVAFFTGTEGFMDFATAVIITHSVAFLLLSYGKTDEFKLSVRDMFLITTLVWTVASAFAALPFVFINHISFTDAYFETMSGITTTGSTVLSGLDQMAPSILLWRSTLQWLGGVGFIVMGVAILPMLNVGGMRLFQTESSDWSDKSSPRTKSVAKNIINVYLILTVLCIIAFMFAGMNTFDAINHAFTTLSTGGYSTSDGSMNHFSHSAQWVATFFMFAGGLPFLLFVQALRKRHPRTLFGDAQVKGYTLFVVVASLIVAACLIFNKGYSVLDAMRLSFFNIISVVTTTGFGLGDFTAWGPLPTIIFAFTLLVGACSGSTSGGIKIFRFQIAFALLRKHIMQSIHPSALFIQRYNGRPVTDDIVRSVVALVFTFIMTIIVIAAVLALQGLDPITSITGAVTAVANVGPGMGTVIGPTGNFASLPDLSKWTLSLGMLMGRLEILTVLVVFAPAFWRD
2.4E-53	191	31.5	2.7E-52	187.3	21.8	2	1	N9GRE9_ACIHA	Uncharacterized protein	F927_01091	Acinetobacter haemolyticus CIP 64.3	445	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter haemolyticus, Acinetobacter haemolyticus CIP 64.3	1217659	>tr|N9GRE9|N9GRE9_ACIHA Uncharacterized protein OS=Acinetobacter haemolyticus CIP 64.3 GN=F927_01091 PE=4 SV=1MTTKTQTQKIFNLSPPSLLAIGFLSFIVIGTLLLKLPISHTGQISWMDAIFTATSAVTITGLSVVNIGESYTHFGQFIILLMIQSGGLGFMTFAILAALSLSPKVGLKQQMMAQESLGQTSLSKVTFIAKGVVAYTIFFELIGAIILSTSFIPLYGIPKGLYYSVFYSISAFNNAGFSLFDNGLSNFYGNYFICLTISLLYILGGIGFLVLMDIKQNKKWRKLSPNTKLVVSTIVIINIFAFIMIWLLESRNPMTLGSMSFGEQAVNSWFQATVPRSSGFNTIDTGSMNNSTTLLTMLLMFIGGGSLSTAGGIKVGTFVILVLCVVAFLRRNDEIRIFNHAISQETTYKALAVAAITGMLIFLGGFIILILEPELDVLDLMFEVLSAACTVGLSRGATGELHDGSLLVLCLLMFTGRLGPLTLAYLIATPKKSRLKHPTANIQIG
2.4E-53	191	25.4	6.8E-52	186	17.6	2	1	E6UKE2_RUMA7	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Rumal_3700	Ruminococcus albus (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7)	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus albus, Ruminococcus albus (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7)	697329	>tr|E6UKE2|E6UKE2_RUMA7 H(+)-transporting two-sector ATPase OS=Ruminococcus albus (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7) GN=Rumal_3700 PE=4 SV=1MDKVKGKLQDDISKKKRKGRTSFQIIISSFAALILLGTLLLMLPISSKGRVVTPFSDCMFTALSATCVTGLIVKDTATYWSLFGKGVIITLIQIGGMGVITIGLAIMTVSGKKIGLAQRSTMQESINAPQVGGIVKLTGFILRTSAIIELTGAALLSPVFIKDFGVLKGIGYSLFHSISAFCNAGFDLMGVREPFSSLTTYSSNAYVNAVIMLLIILGGIGFLVWGDVGAHKFKLSKYSLQSKVVLTTSLILIFVPAVYFFFCEYEDMGVKDRILSSLFQSVTARTAGFNSQDLAQMDESGTLIMIILMIIGGSPGSTAGGLKTATFAVLFLTALTVFSRRTDVQAFKRRIPDEAVRNAGAILFMYLTLFITGGIVISRAEGLPLLTCLFETGSAVGTVGLTLGITPSLHMLSRVILMFLMFFGRVGGLTLIYAAVSSAETSKVKMPMEKISVG
2.5E-53	191	39	4.2E-53	190	27.1	1.3	1	F4L4X9_HALH1	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Halhy_6221	Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	580	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Saprospiraceae, Haliscomenobacter, Haliscomenobacter hydrossis, Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	760192	>tr|F4L4X9|F4L4X9_HALH1 H(+)-transporting two-sector ATPase OS=Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O) GN=Halhy_6221 PE=4 SV=1MWTRRVIQLFTLSALGLVIYDFGFTQDPIKEIFLLNAYFFLTLAFTVLESYRLYKKQIPFTFFYFVRLILPFTAFTVIAIDWIVQQESFRAAVMRNEGWFFANILLLVLYGMSNIASRLYRRSFSPAVIFVSSFMIVIFFGTLFLMLPNATNNGIRFIDAIFTITSAVSVTGLAVVDTRAAFTTMGQTIILVCIQLGGLGMLTLTAFFAYFFKGKSSYVEGLFIRDFLSSDQFEGLLGLAMKIVFLTFGIELTGAFLIYINLPQQEFRSFFDMVFFCVFHSVSAFCNAGFSTLTNGLYEAPFRFNYNIHLTIAFLIIIGGLGFSIMFNLFILMKHTLTSWYKHFIVHLVFYRQAVRVATLNTRVVIFTTVVLLIVGTIAFAFFEWNGVMQEHKTLWGKFVTAFFGSVTPRTAGFNTVNMTELSRPTILVTILFMWIGASPASTGGGIKTSTFAIAILKSVISIMRGKERVEIFRRQISNETLQKAFAVIALSFLFIGLGIFLVMLFNPELALIDVAFEVFSAFSTVGLSLGITSQLGAASKVVIMICMFMGRVGTLTILIAIVRKAGQQRYKYPEESVFIT
2.5E-53	191	28.9	3.9E-53	190.1	20	1.2	1	A0A0D3VAG6_9BACL	ATP synthase subunit J	UB51_11880	Paenibacillus sp. IHBB 10380	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. IHBB 10380	1566358	>tr|A0A0D3VAG6|A0A0D3VAG6_9BACL ATP synthase subunit J OS=Paenibacillus sp. IHBB 10380 GN=UB51_11880 PE=4 SV=1MKRKKILRFLLTPPKILVLGFMLIILTGAILLSSPLATSEAEPLSFVNALFMATSATCVTGLAVIDPGIHLSTFGELVLLFLVQIGGIGFTTMATLIALLFNKRISLKERLILQQAMNHGSMEGIVRLIRKVILYSLLIELIGTILLAIRFSLDMPFWKAAYFGMFHSISTFNNAGFNIFGNIHEFSDGFNSYVNDPYINLILMVLIFLGGIGFIVISDLLSYRETRKLSLHSKIVLSTSVCLIVLGTIVIYLSEYSNQDTLKALSEPGKLMASLLQSVTTRSGGITTLDTASLRQSTQFFMIILMFIGAAPGSTGGGIKVTTFAILIGAVISMARGKEDVVFFRNRISKEVVYKAITLTLLSFLLVIAFTMLLSITEDQQFLSILFEATSAFGTCGISIGLTQQLSPIGKIAITFLMFLGRLGPLTLAYALTPKKQKTPFRYPEGKITIG
2.5E-53	191	34.6	2.5E-53	190.7	24	1.7	1	A3HUF6_9BACT	Potassium uptake protein KtrB	ALPR1_01015	Algoriphagus machipongonensis	604	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cyclobacteriaceae, Algoriphagus, Algoriphagus machipongonensis	388413	>tr|A3HUF6|A3HUF6_9BACT Potassium uptake protein KtrB OS=Algoriphagus machipongonensis GN=ALPR1_01015 PE=4 SV=1MKPKFKFFSNPDRNLYFLRKLETVLEKVVRYSSFITFGLLLYHLGYDPNPTIYAISSFFFTICLFLIGFGYILKILLKEPSIFVGRVLAEIFLSLVLIGFSLLRWNAFGLEFSEGILNYSRHYFLVNILVVILFFIEISKYSLHINRLKASPTLVFISSFLLLIFVGAILLSLPHATTNGISFIDALFTSTSAVCVTGLIVMDTAKDFTFFGQTTIMILFQIGGLGMMTFTSFFGFFKGNYSIENQLFIRDYINENNVGEIYSTLLKIIFFTVITEVAAAFLIYHFTDDALFANKGDQLFFAAFTAISAFCNAGFSNLSNGLYESGFREAYNMHLVLAMAIILGGIGFPVFINYYNYLKHVVVGGTKKILGIESYKHVPRITNISTKLSLYTTGILLVFGFFTYAIFESNHTLEGLSPYGKFVTTIFGAVTPRTAGFNTVDMTMLSVPTILIYYLILIMWIGASPGSTGGGLKTSTFAVAILNTLSIATGKKRVEIFRRQISNETLQKAFAVIALSFLFIGLGIFLVMLFNPELALIDVAFEVFSAFSTVGLSLGITSQLGAASKVVIMICMFMGRVGTLTILIAIVRKAGQQRYKYPEESVFIT

2.5E-53	191	18.7	3.5E-53	190.2	13	1.1	1	Q5P4U7_AROAE	Cation transporter (Trk-type K+ transport system, membrane component)	trkG ebA2741 ebA5555	Aromatoleum aromaticum (strain EbN1) (Azoarcus sp. (strain EbN1))	444	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Aromatoleum, Aromatoleum aromaticum, Aromatoleum aromaticum (strain EbN1) (Azoarcus sp. (strain EbN1))	76114	>tr|Q5P4U7|Q5P4U7_AROAE Cation transporter OS=Aromatoleum aromaticum (strain EbN1) GN=trkG PE=4 SV=1MRIREIQHPARVVPLAFLITILIGTGLLMLPISRPDAVSAPWIVALFTSVSAVCVTGLITVDTGTYWSPFGQWVIMALFQVGGFGM MTAATLLGLMVNRSFRLRTRLTAQAETHTLGIGEVSSVARLVLFVTLIVEGIAALALIVRLRTGYELPWAEAAWSGLFHAVSAFNNAGF SIHADSLMRYASDGFLLTPIMLAILIGGLGFPVLHDLRRKLRSPHHWSVHTKLTLVGTGVLLAGGTIILLAFEWSNPRTLGPMAVADKVL SAIFASVSARTAGFNSVDIGALTHESLGLHYLLMFIGGGSAGTAGGVKVGTAMILVMLVIAEIRGRMDTEAFGRRISHSAQRQAITVLVL GSAVVVLGTVFILHTTRIATDRVIFEVVSAFGTVGLSTGITAELPASAQLILALLMYIGRVGTITLAASLALGEHRMPFRYPEEHPVVG
2.6E-53	191	35.4	1.4E-52	188.3	24.5	1.8	1	J9YX56_9PROT	Trk system potassium uptake protein	HIMB59_00000950	alpha proteobacterium HIMB59	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Pelagibacterales, Pelagibacteraceae, unclassified Pelagibacteraceae, alpha proteobacterium HIMB59	744985	>tr|J9YX56|J9YX56_9PROT Trk system potassium uptake protein OS=alpha proteobacterium HIMB59 GN=HIMB59_00000950 PE=3 SV=1MLNLKPIALVGGTVVCAVGFLLFIPLITEIFYQSESWQSYAVPILIYLIVGGSLVITNRNVELKISIKEAFIITVLSWILLAFLSAVPFIYT KVNLSVVDAIFESMSGITTTGSTVINNLDYLPKGILIWRAMLQWLGGIGIVVIALFILPFLRVGGMQLFHLEGDDPYDKFLPKISSVIKKIVI LYLFLTLILTLYFSYGMNFFDSLAHSFTTISTGGFSTHDQSFAYFQNDSILLIAIIFMIIGSLPFLVIAQTSLNNIFATIQDHQVRIFLLILFVSI FIIYFFAETYIDGNVFQKIITISFNSISIISIGSTGYVSENFESWGNYASVLFLILMFIGGCAGSTTGGLKVFRFQILFKYIGLHFKKMLQPHVVI AGYFNNKSIPESTYESVMSFFFLYIFTFASSALLLSFSGLDFLTCISAAASAISNVGPGLGDIIGPEGNYSTLSDYSKTILTATMFLGRLEM LTILILFLPSFWKN
2.6E-53	191	16.8	9.4E-53	188.8	11.6	1.7	1	Q12H12_POLSJ	Cation transporter	Bpro_0215	Polaromonas sp. (strain JS666 / ATCC BAA-500)	443	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Polaromonas, Polaromonas sp. (strain JS666 / ATCC BAA-500)	296591	>tr|Q12H12|Q12H12_POLSJ Cation transporter OS=Polaromonas sp. (strain JS666 / ATCC BAA-500) GN=Bpro_0215 PE=4 SV=1MNRHFFQPASVLVLSFLAVISIGTLLLMLPLAHAEGAGASALTALFTATSAVCVTGLVVVDTGTYWSGFGQGVILALFQLGGFGM MTSATLLGLLVNRQLRLRSRLLLQAETHSLGLGDVKSIARLVLIVTVVVELGTALLLTLRFALGHAMPWGEAAWHGLFHAVSAYNNAG FSTWSDSVMGFAGDAWVLGPLMMGIVIGGLGFPVLHELMLERGRRRHRSMHTVLTLWGSAALVLAGSLVIYLAEMNNPRTLGPLG WTDQALRALFSAVSARTAGFNAVDVGQLSPESLMLHYALMFIGGGSAGTAGGVKITTFFVLLLVVWNEVRGHQDVEFRGRRIATAVQ RQALTILVLSVAVIVLAMLVLLPMTNLPLDKVLFEVISAFATVGLSTGITAELPPAGQLVLVVLMFTGRVGVVTLAASMAMNHARRDFRY PEEKPIVG
2.6E-53	191	25.2	4.4E-53	189.9	17.5	1.2	1	I3TQY1_TISMK	Trk system potassium uptake protein	trkH TMO_3331	Tistrella mobilis (strain KA081020-065)	483	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Tistrella, Tistrella mobilis, Tistrella mobilis (strain KA081020-065)	1110502	>tr|I3TQY1|I3TQY1_TISMK Trk system potassium uptake protein OS=Tistrella mobilis (strain KA081020-065) GN=trkH PE=3 SV=1MIDVKPVLFIIGVLLALLGATMLVPAAFDAVAASPDWSVFVVSSLVTIFAGVSLVLTTRTAHPTSLSLRHAFLTTTLSWLSVAAFAA LPLLFASPHITYAGAFFESMSGLTTTGSTVLSGLDTAPPGVLIWRGMLHWLGGIGIIVTSVAIMPMLRIGGMQLFRTESSDNSEKIVPRA AQLAAAFGRVYVVVMTLACMALLWAAGMTGFEALVHAMATVSTGGFSTSDASIGHFDSPLIEMIIVVFMIGGALPFVLYIRVLGQDRDAL WRDTQVRAFFLAILVWTVTLSLWLVLHEHVAPLQALRVSLFNVVSVITTTGFATADYNLWGTFPFAVFFWLILVGGCTGSTSGGIKVF RFVILVTAARRHLRQLVHPNAVIVPTYNRRPVPEAILLSVLSFTTVFFAVFVVLSIVVALLGVDFITAATAVSQALANVGPGLGPIIGPAGN YATMTDPVLTVLAFAMLLGRLELFTVLVLFTRAYWRG
2.7E-53	191	40.5	3.7E-53	190.1	28.1	1.2	1	C5J7D4_MYCCR	NtpJ protein	ntpJ MCJ_007120	Mycoplasma conjunctivae (strain ATCC 25834 / HRC/581 / NCTC 10147)	495	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma conjunctivae, Mycoplasma conjunctivae (strain ATCC 25834 / HRC/581 / NCTC 10147)	572263	>tr|C5J7D4|C5J7D4_MYCCR Ntpj protein OS=Mycoplasma conjunctivae (strain ATCC 25834 / HRC/581 / NCTC 10147) GN=ntpJ PE=4 SV=1MKKQMLKILKLLYSKIKTIQIIFFTYLTIILIGAGILSTPWARLPNAENIGFFKALFTSVSAFSDTGLSLVDTGTTFSVFGQIIIACLIFIG GVGFFAIKFFIFNYIFGFKLGIVSREILKIERSSNKISELKSVIKTTIYFFLIIIFVFSFILSIHFYSYEAPAHKFPINQNPYKNIGLSIRFGIFHTIS ALNNAGFDLVGGNSFEPYYSDYFLQTLFILLTVLGGIGYPVIYDFYIYFKNKVFTKKKKAFSFSLFTKISLISYFTILVISYTLFIIFEVTTKTK TFWNLNSSGNTFNKLFALLFHNFSTRSVGFSIFDVNTLTSPSVFLSSILMFIGSAPSSTGGGIRVTTFWILILAIIAKFRHLKEIYTFKRKIS NERVSASAIVFVVSIILNLTLIFISSVSLDEINNLNQNNPAFRFEIHHIIFEVSSAFGTTGLSTGLIRFLPPVTQFCFMLIMVIGQLGVSSSVL VWRGTTIERSSHKYIEEDVIIG
2.7E-53	191	18.9	3.1E-52	187.1	13.1	1.9	1	G0VQR6_MEGEL	Potassium uptake protein	MELS_1546	Megasphaera elsdenii DSM 20460	484	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megasphaera, Megasphaera elsdenii, Megasphaera elsdenii DSM 20460	1064535	>tr|G0VQR6|G0VQR6_MEGEL Potassium uptake protein OS=Megasphaera elsdenii DSM 20460 GN=MELS_1546 PE=4 SV=1MNIRIILFVLGKLAQACGLALMIPFVVALFYGESSLMAFLVAIVISLFLGRLFMGQGHRPTDSLTVREGVAITALGWIMITLLGMIPY AAGGYLSVLDSIFECISGLSGTGATVIDDIEGLPASLVLWRALTHWFGGLGIIVIFIAVFPQPGKGIVHMFNAESTGPRSDRTLPRIKEMA KALFTVYVAFTIVSTLVFMLCGMPFLIAADHAFATIATGGFSPYNDSVAHFHSPVIELCLSFFMLISSANFGMYVAAWQKGFKVILDDTE FRVYLAIVAVATAAMSLDLVLAQQWDGVESLRQAFFQSVSISSSTGFVSNDFDQWPVFSKFILLVLMFVGGCAGSTTGGLKVTRIMLL VKTLAAIIRQKMHPNLVLHIRSNGEEFSMDLIYGVARFFFVYTMLGVLWTFILVFDGVAIFDAIGLSVSTMGSCGPGFGQFGATATCSA LPPLSKVALCFSMLMGRLEAFPVLAILMPSFWRHRNSW
2.7E-53	191	33.2	7.4E-53	189.2	23	1.6	1	A8EUC2_ARCB4	TRK system potassium uptake protein TrkB, putative (EC 3.6.3.14)	ktrB Abu_1289	Arcobacter butzleri (strain RM4018)	442	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Arcobacter, Arcobacter butzleri, Arcobacter butzleri (strain RM4018)	367737	>tr|A8EUC2|A8EUC2_ARCB4 TRK system potassium uptake protein TrkB, putative OS=Arcobacter butzleri (strain RM4018) GN=ktrB PE=4 SV=1MMDHRYVKSIFLGYVLIIFLGALILSLPICHIGELKFIDAIFTSASATSVTGLIVKSTSEDFTFWGELVILILIQSGGIGYMTLVIIFFLSL KQNINFDAKRAIKQSLDLPNLDAKEFVKKIILVVFLIELIGATILSFQFLEKYELKDAIWYGIFHSISAFNNAGFSLFTDCLISYQGDFITLFTL SMLIIFGGLGYFVLIEIYENRKFSKRFSIHTRIMLYGTLILIIGGMFLFLSIEWNNAKTFGELDFFEKILNSFFLSVNFRTSGFNSIDLSSLKD SSLFFSTIFMMIGAGQGGTAGGMKITTVAILIISVIYILKDSNQQPSIFKRTIEQKHINKALAIIISSSFFVLFATLLLVETQNLPFIKILFEVVS AFGTVGVSTGNGGILSLSEQFDSFGKSLIIVLMIGGRLGVFAFGIILLGKAKTKHFKYPVGKIVI
2.7E-53	191	42.6	3.8E-53	190.1	29.6	1.1	1	Q4A9D6_MYCHJ	Potassium uptake protein	ktrB MHJ_0549	Mycoplasma hyopneumoniae (strain J / ATCC 25934 / NCTC 10110)	494	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma hyopneumoniae, Mycoplasma hyopneumoniae (strain J / ATCC 25934 / NCTC 10110)	262719	>tr|Q4A9D6|Q4A9D6_MYCHJ Potassium uptake protein OS=Mycoplasma hyopneumoniae (strain J / ATCC 25934 / NCTC 10110) GN=ktrB PE=4 SV=1MNLKINFKSFLKSLFRLKKIHIIFAVYTIVIFLGAGFLVTPFAHTNAVDKISFLSALFTSVSAFSDTGLSLVDTGTSFNVFGQTIIAILIS LGGIGIFAVKFYIFNLIFGKKISILSREILKIERGSSRLNDLKGVIKISINLFILVLISSLALMLHFYYYEISPKKFSFQQSPYKNLVLSLRFAIF HSISAINNAGFDIIGAYSFEPYYYSYFLQIIIIILTIIGGIGYPVIFDFYSYFRIKLSKQKVKNFRFSLFSKISLLSYFVISFFGFILFIAFEASSKS NLTFWNQVENGNWFDKSFALLFHNFMSRSTGFLTFDLKQLSQASTFLTSLLMFIGSAPASTGGGIRVTTFWIFILVIISRIRGSQDVNAF RRKITTDKVVSASIVFFISLVLVIFLVFVASFSLDDSINRGKTIPYQIHHLIFEVTSAFGTSGLSTGLIRDLSTVSQVGFMIIMLIGQLGITSFI YVWQGDNIGKQNKTYITEDILIG

															>tr|R5F4S0_9CLOT Uncharacterized protein OS=Clostridium bolteae CAG:59 GN=BN723_03390 PE=4 SV=1
2.7E-53	191	23.5	3.5E-51	183.6	16.3	2	1	R5F4S0_9CLOT	Uncharacterized protein	BN723_03390	Clostridium bolteae CAG:59	457	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	1263064	MNEKLFGKKPKHYRLKKHISQTQFIAYGFFLIIMTGSLLLMLPIASRDGQSEPFLNCLFTATSASCVTGLVVADTWTQWSLFGQMVLLVLIQLGGLGFISIGIFLSIVLRRKIGLKERGLMQESVNTLQIGGMVKLAKKIIIGTAVFEGAGAVILACRFIPEYGLVHGTWYGIFHSVSAFCNAGFDLMGHTSQYSSLCNYEGDWVVIGTISFLIITGGIGFIVWDDLSRKKLDFRHYMLHTKIVLVTTAVLLVTSTILFYLMERNNILVGMNGSESFLACFFSAVTPRTAGFNNVDTAALTDGSKFLSAILMFIGGSPGSTAGGIKTSTLAVLLLYVHSNIRQTYGVEIFGRRLEDESIRQSACILTINLGLMLAATIAIMVSQNLPMSDVFFETCSAIGTSGMSTGVTRSLNSFSRIVIILLMYCGRIGSLSFALAFTRSNRKPHVQLPAERITIG
															>tr|A0A0E2EPE3|A0A0E2EPE3_VIBFU Potassium uptake protein, TrkH family OS=Vibrio furnissii (strain DSM 14383 / NCTC 11218) GN=vfu_B00805 PE=4 SV=1
2.8E-53	191	25.1	6.2E-53	189.4	17.4	1.5	1	F0LYL9_VIBFN	Potassium uptake protein, TrkH family	vfu_B00805	Vibrio furnissii (strain DSM 14383 / NCTC 11218)	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio furnissii, Vibrio furnissii (strain DSM 14383 / NCTC 11218)	903510	MNPLERSGIFYALDKDKNSNNGSEPKIILVSFLSVLLPAAVLLTLPVFSKSGLSFTDALFTATSAISVTGLGVVDTGTHFTIHGQILLLLLMQIGGLGQMTLSAVLLYMFGVRLSLKQQAIAKDALGQDRAVNLQKLVKRIIIFALIAEGIGWAILSFRWVPELGWSQGLFSALFHAVSAFNNAGFSLFSDSMISYADDPTILLTLAGLFIFGGLGFTVVGDVWAHWRSGWRYFSLHTKLMLVATPVLLLIGTLFFWCLEHNNPHTMQPLPLWQQWLSAFFQSATARTAGFNSVDIAQMSQPALLIMIILMLIGAGSTSTGGGIKVSTFTVAFLATWTFLRQKKHVVMFKRTINWPTVTKALAIIVVSGALLTIAMFLLMLTEQASFEAVLFETISAFATVGLTAGLSAQLSEPGKYIMIVVMIIGRIGPLTLAYMLARPQATLLKYPEDNVLTG
															>tr|L0EGJ6|L0EGJ6_THECK Potassium uptake protein, TrkH family OS=Thermobacillus composti (strain DSM 18247 / JCM 13945 / KWC4) GN=Theco_2726 PE=4 SV=1
2.8E-53	191	20.3	4.8E-53	189.8	14	1.3	1	L0EGJ6_THECK	Potassium uptake protein, TrkH family	Theco_2726	Thermobacillus composti (strain DSM 18247 / JCM 13945 / KWC4)	444	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Thermobacillus, Thermobacillus composti, Thermobacillus composti (strain DSM 18247 / JCM 13945 / KWC4)	717605	MKFKFTAALWSPPRVLAIGFALIILLGASLLSLPAVSADGQPMRFIDALFTATSAVCVTGLVVADTGTFFNAGGQLIILALIQVGGLGFMTMATLFALVFKRRITLRERLILQEAMNQTSMEGIVRLIRRVIIYSLTIEAAGTAVLTARFAAEMPLGRAAFMGLFHAVSLFNSAGFDLFGNYRSYTPYVSDPVVNITAILLVTLGGLGFIVISDLLEYRKRRRLSLHSKVVLATSGALLSIGAVVIFVFEFTNALAPLGWDGKIWASLFQSAAPRSIGVNTLDIGSLRQATQFFLILLMFIGAAPGSTGGGIKVTTFTTLVGAVIAMMRGKDEVVLFRYRLARERIFKALTITMISLAVVVAVTMVLCTTEDRAFLRILFETVSAFGTCGLSTGITPQLTDFGKLLLSLTMFAGRLGPLTFAYALRPKDEKELYRYPEGRIIIG
															>tr|M9R9Z7|M9R9Z7_9RHOB Trk system potassium uptake protein OS=Octadecabacter antarcticus 307 GN=OAN307_c15380 PE=3 SV=1
2.8E-53	191	22.7	4.6E-53	189.8	15.7	1.3	1	M9R9Z7_9RHOB	Trk system potassium uptake protein	OAN307_c15380	Octadecabacter antarcticus 307	483	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Octadecabacter, Octadecabacter antarcticus, Octadecabacter antarcticus 307	391626	MFDVRPVGYVIGLLVAALGATMFAPLLADLVAGNGHWPVFFESAVITILVGGLVALACQNGVSSGLTIRQTFLLTTLVWLALPLFGSLPFMLGGSDLDFTDAFFEAMSGLTTTGATVITGIEGLPEGLKLWRAIMQWLGGIGIIVVAMVFLPELRVGGMQIFRSEAFDTMGKILPRAAEISSRISVIYVAITLACAICYSIVGLNSFDAITHAMTTVATGGFSNYDNSFGAFGAGPHYVASVFMILAALPFVRYVQLISGNGARPLFRDSQIRTFFAVVFVLVGVMTLWLWRTFHGVGEIGFREALFNVTSIITGTGFASADYMQWGPFAVTMFFFIGLIGGCAGSTACSVKIFRYQLLFTSIKAQIRRIHSPHGIFTPRYQGRAVSDDVLNSVMAFFVAFMVAIGVVGVALAFTGLDFITSISGAASALANVGPGLGTEIGPAGNFAGLNDTAKWILAIAMLVGRLEIMAVFTILSWHFWRE
															>tr|R6DMI4|R6DMI4_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:230 GN=BN547_01176 PE=4 SV=1
2.9E-53	191	32.3	3.8E-53	190.1	22.4	1	1	R6DMI4_9CLOT	Potassium uptake protein TrkH family	BN547_01176	Clostridium sp. CAG:230	455	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:230	1262782	MKSIKKSLSTTQIIALGFFVAISIGTALLMLPVSSADGRVTPLIDSLFTATTSICVTGLVVVPTYLHWSAFGKVVILLLIQLGGLGIISFTTGIMMVIGRRITLHDRILLEDALNLNTLSGLVAFLRKIFCGTFIIEGIGALGYTFLFIPKYGFLRGIWYSIFHSVSAFCNAGIDLLGDNSLCNYLTNTWMNVVTMFLIISGGIGFIVWWDLLDAFKNLTKKKKAFSYIVKKLHIHTKLVLITTFILLFGGMLLILLFEYDNTATIGNLDFYHKILASLFQSVTTRTAGFLTISQSSLRPHTALICMFLMFIGGSSIGTAGGIKTTTFALLVLNTIMIVKGQNHVTVFHKTIPHKTHQKAIAVTLVSFLVLGVAIITMSCFETGSLMDIAYEVTSAIATVGLTRDFTPHLHLIGKTIIIICMYLGRIGPLSLAILFNNNTKRSLIAYPHEDVTVG
															>tr|A0A095ZGM9|A0A095ZGM9_9BACT Potassium transporter OS=Prevotella buccalis DNF00853 GN=HMPREF2137_10405 PE=4 SV=1
3E-53	191	25.2	4.1E-51	183.4	17.5	2.1	1	A0A095ZGM9_9BACT	Potassium transporter	HMPREF2137_10405	Prevotella buccalis DNF00853	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella buccalis, Prevotella buccalis DNF00853	1401074	MINLRTIYKVIGSLLFIEAFILFACFGMALFYGEDDAMAFLLSVFISLFTAFILRYLGRNSNNTLSRRDAYLVVTLSWIVFSFFGTFPFTLSGYIHSFTDAYFETMSGFTTTGTTIIDDVEVLPHALLFWRSLTQWIGGLGIVFFTVALLPSMVGGSVQVFAAEATGPIKSKLHPRLSTSAKWILTVYLVLTIACIGCFILYGMNWFDAVNYSMTTTATGGFSTHNSSTEFFHSPALEYICTIFCFLSGVNFTLLYTAVVKRRFKALFKSSEFKFYLSVVILFSLFIMLELMINRGYDLEPAFRSGIFQVVSFITTTGLFNDDAGQWPHVTWVILATCMFIGACSGSTSGGFKCIRVVMLLKTIRNEFKQILHPNAVLPLKVNDTNIPYQKRGTLLAFLTMYLILCLLASFVLMMAHIDSTNSITIILSCIGNVGPTLGLEIGPTMSWSMLPGFVKWVCALLMLIGRLEIFSVLVILSPAFWKDN
															>tr|A0A0D5AEL9|A0A0D5AEL9_9NOCA Potassium uptake protein, integral membrane component, KtrB OS=Rhodococcus sp. B7740 GN=NY08_3281 PE=4 SV=1
3.1E-53	190	14.1	4.8E-53	189.8	9.8	1.2	1	A0A0D5AEL9_9NOCA	Potassium uptake protein, integral membrane component, KtrB	NY08_3281	Rhodococcus sp. B7740	437	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. B7740	1564114	MATGFALAIALGAGVLMLPAATVPGSETGFLQALFTSTSAVSLTGLIVVDTPVYWSGFGQGVILGLIQIGGFGIMTIASLVGLVLADRIGLRGRLNAAAEVRTSGLGDVRSVVVGVFRTSLIIESVVAIALAARFFIGYDEPLGRALWLGTFHAVSAFNNAGFALFSDNMIGFATDPWICIPLLIAVVLGGIGFPVLFEIARHLRARAGGVRARKRWSLHTRMTLTVTGILLILGPAVVLLFEWSRTLGEFGLWDKMLVATFQGVMPRTAGFNSVDYADVDNATLLVTDVLMFIGGGSGGTAGGIKVTTFALLLFVILAEIRGDREVTVFDRRIDARVQRQALTVALIGVALVMLPVVALLAGTNFDLDVLLFEVVSAFATVGLSTGITAQLPGWGQVILALMYLGRIGSITLVSALAARDRGRRYTLPTERPFIG
															>tr|R6DPD3|R6DPD3_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:238 GN=BN553_01412 PE=4 SV=1
3.1E-53	190	23.3	4.2E-52	186.7	16.1	2	1	R6DPD3_9FIRM	Uncharacterized protein	BN553_01412	Firmicutes bacterium CAG:238	488	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:238	1263011	MNAVFKNFIRIQGAIFLLMAASLLIPLFLAFYYDEDSCKFAFLLVSGSCALAGIIIRLGVKPADAKFKVRDGFLIVSTAWLVCSVIGALPFLISGAISSAADAFFESCSGFSTTGASILTDVEVLPKSIMFWRSFTHWLGGMGIIVFVMALMPVLGINGQIAANAETPGPTKDKLTARFSDTAKNLYKLYLVFTLVQVVLLCLGGMSVYDSFLHTFGSLGTGGFSNYNDSVGHFNTYIQIVILIFMILAGMNFNLFFVLQRKGLRKFLHDDELRFYLAVIGIASTAIFICNQVNSNFKDTARSLLDSFFQVVSILTTTGYVTDDYDLWPTFSRMILFCLFFFGGCSSSTSGGIKCVRVLVCLKLVRRSVSLRLHPNRIAPITLNESEVPSEVIINITNFVFTYIAVIFAGMFLISVDNLDFMSTFSAVATCVGNIGPGFNLVGPTCNFSVLSDFSTVICSLLMLVGRLELITVLALFSKYYWNSNKTK
															>tr|W3TWJ8|W3TWJ8_BARQI Trk system potassium uptake protein OS=Bartonella quintana JK 73 GN=Q649_00647 PE=3 SV=1
3.1E-53	190	24.6	5.8E-51	182.9	17.1	2	1	W3TWJ8_BARQI	Trk system potassium uptake protein	Q649_00647	Bartonella quintana JK 73	464	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bartonellaceae, Bartonella, Bartonella quintana (Rochalimaea quintana), Bartonella quintana JK 73	1402976	MLLPILADLHDSNRNWITFLCSCAMTTMLATLILLATKGATCRFSARLGFMLTVCLWLTGSVVGALPLYLSHLPISLAGAIFESVSGITTTGSTVITGLDNLSRSILLWRSIICWIGGIGFIGLALLLLPSLRVGGVRLFHMESSDKSEKILPRINQIANGIIIAYVGLTLACMLSYFASGMSLFDAINHAMSTIATAGFSTHDASFGYFSDKPAILIISTIFMLLSALPFVLYVKLVLPGHSKRFIDPQVIVFLNIVFLFSFALAAWLRFHDHRAFHWIFLDVIFHLSSIISTTGYSAEDYQLWGPFALGIFFIVSFTGGCAGSTSGGMKINRLIILWRITQTNIAQLLSPNVVVKAHYDHSNISSDVAKAILFFVCLYMFCLIIGTALLLITGLDFTSAFTGVLTALSNIGPGFGDIIGPTGNFSTINDNALWILSFLMLAGRLEIITIFVLFIPAFWREQF

3.1E-53	190	11.1	6.4E-50	179.5	4	2.5	2	D8RMU3_SELML	Putative uncharacterized protein	SELMODRAFT_97685	Selaginella moellendorffii (Spikemoss)	485	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8RMU3|D8RMU3_SELML Putative uncharacterized protein OS=Selaginella moellendorffii GN=SELMODRAFT_97685 PE=4 SV=1MTFFRVHLTCFVIVAFIGSLILWGIGNERGGHFPFVDCFYGITSALCLSGLTTVPVEDIPPGGQVVLMIMMLLGSQVVTSTVPLLV KKHRYCRVARIAIDPSDHEPHQATIVLIRIIVIYGVLVHLMGFFIAWLSILCGRPYPRNLIRHKKKTNLGFFSLFAVVSAFCNVGYIASSEN LMPFNSSLVLLLDMILLIMLGNGIYPPCLRGIIRLLHHFSKGNTKQACEFLLDHPRKCYTHLFPPNTTRWLLISFFGLNGFEICVIYILDWN STAFDGLDTGEKIVNGIFQCVNTRSGGMNSVAITGLSPTTLFIFAVMMYVSAYPVFLSRQATRQKSVDDEGAISHLSARKQRDILDTTL ATQFRRLLAQDTAYLFLATFFICVSVNHGLKHDPLNYNIFSVVFEIISAYGGVGLSYGYSCSLRTEPGYCVDEPVSFSGKWGVTPKIIMI VVMLLGRHRGLPDNIDSAILLPEQKFSNIMRRQTSE
3.3E-53	190	14.8	1.1E-50	181.9	10.2	2.1	1	R6E6G7_9BACT	Trk system potassium uptake protein TrkH	BN487_01445	Prevotella sp. CAG:1320	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:1320	1262922	>tr|R6E6G7|R6E6G7_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:1320 GN=BN487_01445 PE=4 SV=1MINVKLICKILGQLLLFEAFWMLISLGISLYYQEDDSFAFLVSIITTVGVGLLLKGKGRGAENSLSRRDAYLVVTLTWVVYSLLGTLP FLVGGYLNSLADAYLEAMSGFTSTGATVFDDVERLPHGILFWRSLMQWVGGLGIVFFTVALLPSLVGGSVKVFSAESSAPLRAKLHP RLSTTAKWIWSIYVTLTVACTAAYWLGGMSFFDSLNHAMCTTPTGGFSTRNDSFGYYDSPYLEYMCSLFTFLSGANFALLYAVVLKR RVGELAKNSEFKFYLGAVLVFTLFVAIQLFNECGYQFEEAFRKALFQVVTLMTSTGFCSDDTALWPAVTWGVLLVCMFMGGCSSST GGGVKQVRLVMLFQIVKNELRQILHPKAVLPVRVNGVNVPIQERVTLLAFLGVYLGLLLAQTFAMVAVGIDLGNALTISFSSLGNAGPSL GTLSGMDLSWSALPDVAKWITSLSMLLGRLEIFTVLVIFTPGFWKDN
3.3E-53	190	22.7	4.4E-53	189.9	15.7	1	1	R7JLC5_9FIRM	Potassium uptake protein TrkH family	BN630_00707	Blautia sp. CAG:37	461	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:37	1262757	>tr|R7JLC5|R7JLC5_9FIRM Potassium uptake protein TrkH family OS=Blautia sp. CAG:37 GN=BN630_00707 PE=4 SV=1MAEKQSKNKWHTPAERIMMLGFAAVILLGTILLCLPVSAADGKSVYWLDALFTATTSVCVTGLVTVPTATTWSTFGKIVILGLIQF GGLGIMACLTMVFLILRRKISLQSRKLIQDTYNLPVLKGSVGIVRRLLIGTATVEIAGAVLYSFWFVPEYGFWKGIGYSIFHAVSAFCNAG IDLVGEASFAPFVTNPLINFTTMGLILLSGLGFPVWWEVMERVQELVKGKRPRKNFVRGFTLHTKLVLTTTMILVFGGALLIALDWNH APSLGSLKPAQKVMAAFFQSVTTRTAGFETIPQADFSDSSAMVSMVLMFIGGSPMGTAGGVKTTTVAILVVLVASYIRGDSDTVAWG RKVMEENIRTAVVIFFFVLTTVFTATVLLISVTRSPLLDCTYEIISAVATVGLTRSLTPTLPFMGKVIVILVMFMGRIGPVTLAVALRRRTG RKDVDIQRPEQRILIG
3.4E-53	190	26.6	1.3E-51	185	18.5	2	1	A0A0D8MTE7_PHOLE	Trk system potassium uptake protein	UB34_12160	Photobacterium leiognathi	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium leiognathi	553611	>tr|A0A0D8MTE7|A0A0D8MTE7_PHOLE Trk system potassium uptake protein OS=Photobacterium leiognathi GN=UB34_12160 PE=3 SV=1MVNYRPILFVLGLVLSKLALFMYVPTLVAFFTGTEGFIDFATAVLITHSVAFLFLTLGKTPEFKLSVRDMFLITTLVWTVASAFAALP FVFINHISFTDAYFETMSGITTTGSTVLSGLDDMAPSILLWRSTLQWLGGVGFIVMAVAILPMLNVGGMRLFQTESSDWSDKSSPRTK SVAKNIVNVYLTLTLLCIISFMFAGMNTFDAINHAFTTISTGGYSTSDGSMNHFSHSAQWVATVFMFAGGLPFLLFVQALKKRHPKTLF GDAQVKGYALFVTVASLIVAACLIFNKDYSVMDALRLSFFNIISVVTTTGFGLGDFTAWGPLPSIIFAFTLLVGACSGSTSGGIKIFRFQIA FALLRKQIMQSIHPSALFIQRYNGRPVTEEIVRSVVALVLTFIMTIIFIAAVLGLQGLDPITSITGAVTAVANVGPGMGDIIGPTGNFASLPD LSKWTLSLGMLMGRLEILTVLVVFSPAFWRD
3.4E-53	190	34	9.8E-26	99.7	6.2	2.3	2	D1B054_SULD5	Trk system potassium uptake protein	Sdel_0635	Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175)	479	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Sulfurospirillum, Sulfurospirillum deleyianum, Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175)	525898	>tr|D1B054|D1B054_SULD5 Trk system potassium uptake protein OS=Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175) GN=Sdel_0635 PE=3 SV=1MSVKSILKFISAVGLVVFFILLLPPLVGFFYDEDVFIYTLVMFALFIVNLSTFLILKSSEMHLGIKESIISVNLIWILLGIGGAIPLVLYSKI DPAGAFFEAISGFTTTGASVYRDVEILPKSILFHRSLTHWIGGIGIVLGVGLLPLINPSGSLSLFKAESTGISIDKITPKIKDTANRIWAVYI LFTLVNFILLMLFGMNWFDAINHAFATISTGGFSTKNSSLGGFSDGVIWTTTFFMTISGINFLAHIRFFNGDKYAFNTEENRWYLGLIIAL SFIMAWQHVTISKDSFYYSLMHSFFTVSTLATTTGFASLDYEKWGQFTMMIALLAMIMSANAGSTAGGIKMIRFVLFFKNIALEIKRTIQ PDVITSLFIDGKQIRSSIINSVFGFFALFIITVFLVMMYLYARGFDFLTAFATAISMVGNIGPGLNLTGPSQNYAFFSWYDKIILSFAMIIGR LECYTVFIMLSRSFWKKF
3.5E-53	190	10.2	2.9E-52	187.2	7	1.9	1	A1TVU2_ACIAC	Trk system potassium uptake protein	Aave_4543	Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	498	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax citrulli (Acidovorax avenae subsp. citrulli), Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	397945	>tr|A1TVU2|A1TVU2_ACIAC Trk system potassium uptake protein OS=Acidovorax citrulli (strain AAC00-1) GN=Aave_4543 PE=3 SV=1MSVPSALSEALPDLLPVLRVFGALLAMFSWALAVPLGASLWAGEGLWPVYAASLGFALACGVALWLGLRRHARELQPRHGVM LVSLVWLLLPLFASLPLMGALHAIDRPIGFTHAYFEAVSGLTTTGATVLSGLDSLPLSVNIWRTFMQWIGGMGILILAVAVLPLLGVGGS QLFKAEAAGPVKDTKLTPRMTQTAKGLWGVYVVFSLVCALAFWAGGMVVPDALMHMFATVSLGGLSPYDASFGHFHSPLLEAIAIVF MVLASCNFALYFVALRKGHWRTCWRDPELRATVCTLLGSGLFVALLLWFKGIYGPLDALRHGMFHTVSVATTTGFATTDYLGWPVF APVFLLMLSGVATSAGSTGGGIKMVRVLILLQQARREMTRLVHPRAVQPVRLGATVVENRMIFAVLAYMLVYGATITVLSMVLLLTDLD VVTAFSAVIASVHCTGPGLGLIGPAANYAVLTDFQLWVCTLAMLLGRLEILSFMALLTPAFWRR
3.6E-53	190	25.6	1.6E-52	188	17.8	1.8	1	E6K6K5_9BACT	Potassium uptake protein, TrkH family (EC 3.6.3.15)	ktrB2 HMPREF6485_1254	Prevotella buccae ATCC 33574	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella buccae, Prevotella buccae ATCC 33574	873513	>tr|E6K6K5|E6K6K5_9BACT Potassium uptake protein, TrkH family OS=Prevotella buccae ATCC 33574 GN=ktrB2 PE=4 SV=1MINKELLYKIIGQLLFLEAMLMGCCFVIAFFFHEDDTLAFLESTIISIFAGVVLKLFGRHADNSMSRRDAYLVVTLCWVIFSLFGTLP FLISGYITHFTDAYFETMSGFTTTGATIIDDVEALPHGLLFWRSLTQWIGGLGIVFFTIALLPSMVGGSVKVFAAEATGPIKTKLHPRLST NAKWIWVIYLVITMACTASYWLGGMGVFDSINYAMTTTATGGFSTHNTSTEFFHSPTLEYVCTFFTFLSGVNFTLLYLTVIKGKVSLLC KNTEFKFYLFLVGIFTLIITIELMARNGYDVEHAFRCGIFQVVSFITTTGLFNDDAGTWPHVTWVVLAVCMFFGACSGSTSGGFKCIRG VMVLHVIKNEFRQILHPNAVLPIKIDGSNVPNQKRVTLLAFLTVYLILCLITSFTMIAMGIDNTNAITITLSSIGNVGPSLGLNIGPTMSWSS LPDVCKWMCAVMMLVGRLEIFSVLVIFTPEFWKER
3.6E-53	190	26.6	1.3E-30	115.8	9.3	2	2	R6GAV9_9FIRM	Potassium uptake protein TrkH family	BN476_01903	Eubacterium hallii CAG:12	434	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium hallii CAG:12	1263078	>tr|R6GAV9|R6GAV9_9FIRM Potassium uptake protein TrkH family OS=Eubacterium hallii CAG:12 GN=BN476_01903 PE=4 SV=1MKQIFDSLKKQSPSRIIALGFSAVILVGAVLLMMPFSLKKGVHLSFLNALFTSTSAVCVTGLVVVDTADSFTAIGQAIVAALIQIGGL GIASVGVGFIIAAGKRVSIKSRLMVKEALNVDTYHGMVRLVRIVLAITLGFEAAGAIISFFVFRKDYSPLHAVGISIFHSIAAFNNAGFDNL GGMHNLIPYKDNILLNITTDVLVIVGGIGFLVLVDIVKQKSFKKLCLHSKVAISMTAVLLIGGTLILKATENITWMGAFFQSMTTRTAGFST YNIGNFSKAGLFAMCILMFIGASPGSTGGGVKTTTIFVMIQALKCMGRKKSAHAFKRSISEENISKAFMITVLSAGILCVATFLMCVFEPE YDFIQIIFEVASALSTAGLSTGITPELGVAARILIILLMFTGRVGAFTLLSVWGKVSTPNARYSEEMISIG
3.7E-53	190	28.6	7.7E-31	116.5	5	2.1	2	A6Q6U9_SULNB	Trk system potassium uptake protein	SUN_0248	Sulfurovum sp. (strain NBC37-1)	484	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, unclassified Epsilonproteobacteria, Sulfurovum, Sulfurovum sp. (strain NBC37-1)	387093	>tr|A6Q6U9|A6Q6U9_SULNB Trk system potassium uptake protein OS=Sulfurovum sp. (strain NBC37-1) GN=SUN_0248 PE=3 SV=1MDIHALKNIFKFVSVIGMALSLFLFTAIIVGWIYHEDMSRFLYFDLTLFSINAIIVLLLREHRMKLSIKGGILSVNLIWVLLGVAGAVPF LLYTGITPADAFFEAVSGFTTTGATVFSDIESLPKSILCLRSLMHWLGGMGIIVLGVGLFSLINPSGSMTLFKAESTGIKMEKITPKVKDT AIRLWGIYVLFTVADAIALKLAGMNIFDAVNHAFSTISTGGFSTKNASLGYYDSNVIIWITTFFMIISGINFLAHLKLFSTGKADGYKREEV LWYLAIFIALSLLLSSVDIFVDYDSYFHALTHASFTVASVLTTTGFATLDYEQWGHMAISVIFVAMLIGGNAGSTAGGVKVIRYIVLFKNIS VQFKRTLHPNAVLGVFIDHQKVSSQIISSTTGFIFLFVMTNMFLTLYLFARGFDAMTSVSTALACVGNIGPGFALTGPAHNYGFFSDIDK IVLSMGMIIGRLEFYTVFLLFSRSFWKKF

3.7E-53	190	29	5.1E-53	189.7	20.1	1.2	1	A0A0D8PR03_9GAMM	Ktr system potassium transporter B	UB37_14455	Photobacterium iliopiscarium	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium iliopiscarium	56192	>tr|A0A0D8PR03|A0A0D8PR03_9GAMM Ktr system potassium transporter B OS=Photobacterium iliopiscarium GN=UB37_14455 PE=4 SV=1MSFIPNRTMYVPIKTNKRDKRWSEPKIIIFSFLAILIPGAILLTLPVFSVSGLSFVDALFTATSAISVTGLGVVDTGTHFSTSGKVLLM ILMQIGGLGQMTLSAVLLYMFGLRVSLRQQSLTKEQLGQEKFINIRLLVKHIIIFVITCELIGTFFLSLRWVPMMGWDKGLFTAVFHSISA FNNAGFSLFSDNLTQYVDDPLVIITVAMLFIFGGLGFTVISDLHRNLHRGFHFLSLHSKIMIIATPILLLSGTVMIWLLEHDNMQTLGSLNT SGQWLAAFFQSATVRTAGFNSVNIGAFTEPGLLVLMLLMLIGAGPTSTGGGIKVSTFVVAILATWSFLKQRDRVVLFKRTISNQTVTKS LAIIVVSGIVLLIAMFALMLTEKAPFYEVMFETISAFATVGVTAGLTATLSESGKYIIIVVMIIGRLGPLTLAYMLARPKPTLLRYPEDNVLTG
4.1E-53	190	22	1.9E-25	98.7	4.1	2.1	2	R6DGR6_9CLOT	Cation transporter	BN547_01528	Clostridium sp. CAG:230	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:230	1262782	>tr|R6DGR6|R6DGR6_9CLOT Cation transporter OS=Clostridium sp. CAG:230 GN=BN547_01528 PE=4 SV=1MNYSIISYILGWVLTIESIFMFIPCIVAAIYREKEGFAFLIVALLCLAIGLLRIRKKTKSQVFYAKEGFVTVALSWIIMSIFGALPFVINR DIPSFTDALFETISGFTTTGASILSDVEALSHCSLFWRSFTHWIGGMGVFVFLLAILPLTGGYNMHLMRAESPGPSVGKFVPKVRETAK ILYAIYIVMTLVEIILLLSAGMPLFDSLTVSFGTAGTGGFGIKNTSIADYNMVIQAIISIFMILFGVNFGAYFLLLGNNKKDAFKLEEVHWYLT IIAGAVAIITINTKDMFHNLFTAFHHALFQVASVITTTGYSTTDFDLWPQLSRAVLVIVMFIGACAGSTGGGIKVSRIIILVKSVKQELGYFI HPRSVKVIKMDNKPLSANSIRGVNAFFVTYTLIFVASLLIITFDNFDLVTNFTAVTATLNNIGPGLKLVGPTGNFGIFSPVAKYILMFDMLA GRLELYPILLLFTPSVWKKH
4.2E-53	190	36.4	6E-52	186.1	25.3	2	1	A0A060RBE6_9BACT	Potassium uptake protein KtrB	BN938_00614	Mucinivorans hirudinis	460	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Mucinivorans, Mucinivorans hirudinis	1433126	>tr|A0A060RBE6|A0A060RBE6_9BACT Potassium uptake protein KtrB OS=Mucinivorans hirudinis GN=BN938_00614 PE=4 SV=1MKRKFSLTHFIVSMLRFDFERILTFGYISKHPHRQLIFGYLSYIVVGTLLLCLPFMTSTNVGFLDHIFSATSAVSTTGLSTVDVSSAY TFSGKLVILLLIQLGGLGYMTMSCFVMFSLTKHFTIIKKGIIAAEFTMPGGITAKNLVKSVVGFTFFFEVIGALLLYFLFADKGVENPVGTA IFHSVSAFCTAGFSTFSDSLMQFRDDWGVNLVVIVLSYAGAMGFIVMHDLWQKITTRGYKITFTSKVIVLVTLALSALATTQMFFFEPSL LQYPASERFLMSLFQSMSALTTVGFNTINIGGLIPITLLSLTMIMYFGASPSGTGGGLKTTTLTATMAFVKSKLGQNRDVTLFGRTLPTY RIDTALATFVLYTAVICLSSLILTATEDFDYLVILFESASALGTVGLSTGITPELSSEGKLVLIVVMFIGRVGVLTFGFSMLHRMKQRTTQIT KQDDLAV
4.4E-53	190	0	4.9E-49	176.5	0	2.5	2	G0S8P6_CHATD	Putative uncharacterized protein	CTHT_0039880	Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719)	868	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Sordariales, Chaetomiaceae, Chaetomium, Chaetomium thermophilum, Chaetomium thermophilum var. thermophilum, Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719)	759272	>tr|G0S8P6|G0S8P6_CHATD Putative uncharacterized protein OS=Chaetomium thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719) GN=CTHT_0039880 PE=4 SV=1MKLSPKTSDRFRTRFSSIASRLADHLSPLRPYLPPINFITLHYAYFIFLSLFLSLIFYAAHSPTPSKSSNEDIARRRISYLDALFHTVS SLTGTGLNTVPLCDMSVGQQVVLFLAMLAGHPVLVSLGAVWFRKDVFEKKFREIVQRERERKEKMEGGRLGKALVRRVTFNLALTLT RERSRDGDGDRGGLAGLGTRIKERREGERMSPTPTPNSSSNQTRERDRDRERDLEPGLPPIHEQQDPNPNTSSLLSPQPQFLFPSP PSHSPASRSIQFIEPPRPDRPSPSLSPSPDPNNNNNNNESGNDTPDFIARLRHSHTRNASFANLTLSERQYLGGVEYRALEVLIVTVTA YFILWPLFGAIALGAWLSRHGGQVSEQETGEKSPSPNPWWEGIFLSVSAFGNGGMVLGPEMGSFLDRGVGGVFVLLVVSLLTLAGS QASPVFLRVIFLGLWGILKRVVADEGGYAVWRETFEFILRYPRRVYINMFAARDTWRLAGWLAAFLAVDWVLFWLLNIGNGEVEGMP RGKRVLGGLAQSISNLSGGFAIIPVSAVSFSLQVFWLIKIYASAYPTSITVRGSNVYEERSLGIYMGDEPPDSDDSGSDNEKRPAKAKP LPESEPEPEGTTTGLMIPSLPRPPLTPVSTTSQVSRLSTASRRGLTKLVGITRQGTAFMGRQIQRRMTTGFQGVGVSASAALPIPQKS TLPTFNTPATSTSSKTTTAPTPAPKPDLTTHHARSQLSHDIPLLALSFLLLVLIETPHISSSPLIYSLWNILFELVSAYANNGITVGFPGRD YSFCGGWRKLSKLLLVGVMLRGRHRDLPVALDRAVKLPREGDWDGEEEEDGEIRKIISRSPAVGRSPMLGRLNGL
4.4E-53	190	25.9	6.6E-53	189.3	18	1.1	1	W5WPB9_9CORY	ATPase	CFAL_05180	Corynebacterium falsenii DSM 44353	453	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium falsenii, Corynebacterium falsenii DSM 44353	1451189	>tr|W5WPB9|W5WPB9_9CORY ATPase OS=Corynebacterium falsenii DSM 44353 GN=CFAL_05180 PE=4 SV=1MGNEGSLKKLGPARVVAAGFLVLIFSGALLLTLPVMTASGTSTSFKDALFTATSAVSLTGLITVDTGSHWNLLGQAVVVILIQLGG LGIMSMTSVAGWLLTGRVGLKSRMNAAAEGRSQSAGGVRRILGWTLALTFTTEAFVAVIITGRMMINYDMSFKHAIWEGIFHSVSAFN NAGFGLRSDSLVPYVGDAWIIPIALSFMIGGLGFPVLSELVSRTLRKLRGIQVPSHLSVTCQMTLFGTTILVLAGWFMVLALEWSGVLS GMGFGEKLLASFFQGVTPRTAGFNSLDYGQMHPITLMGTDILMIIGGGSAGTAGGIKITTIVVLAAGMAAEFKGEKSAIVAKRRISSGVI RQAMTVAAAGVTFVVIAIGALRWMDPQFNGDQVTFEVVSAFATVGLSTGITAQLSTGSQLVLCAMMYLGRIGPITLVSSLAMRNIKRR FEYPVERPFIG
4.6E-53	190	19.8	3E-52	187.1	13.7	1.9	1	R6AMV5_9FIRM	TrkH family potassium uptake protein	BN678_01741	Dialister sp. CAG:486	482	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Dialister, environmental samples, Dialister sp. CAG:486	1262870	>tr|R6AMV5|R6AMV5_9FIRM TrkH family potassium uptake protein OS=Dialister sp. CAG:486 GN=BN678_01741 PE=4 SV=1MNIQIIYSMLSRVLAASGAALLLPLLLSLYERGPILPFLVPMLLSAVLSLFLKRKGAAIESSLTPREGTAITALSWIAVSLLYALPYWV SGSLSPLDSLVESISGLTGTGATVFPDLTCVPESLLFFRSLTHWLGGLGIIVFFVALFPQAGRGTVRMMQTESTGPTSSKALPRIRETA RALFAVYAVFTSVCFLSYLLCGLSPLDALNHAFSTIATGGFSTRNESIAYYHDARLEMVIAFFMIISSANFGIYVEAWKRGVSVIWKDTE FRTYLSIVAIATVLMTLSLVLQGGASLLPALRETFFHAASISSTTGFVAADFDRWPDFCRFLLLLLILVGGCGGSTAGGMKVIRFILLGKS IFSLLKLHLHPRAVQAVSAGENRYSSDVLYRVLCFFFLYIMLAFLWAAIMMFDGLAFLDALGVSFSTMGSVGPAFGQFGATQTYAALP TLSKMVVCLSMLFGRLESITLMCIFIPSFWKRSGW
4.9E-53	190	35	2.3E-52	187.5	24.3	1.8	1	R6MVS8_9FIRM	Potassium uptake protein TrkH family	BN531_00019	Eubacterium sp. CAG:202	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:202	1262884	>tr|R6MVS8|R6MVS8_9FIRM Potassium uptake protein TrkH family OS=Eubacterium sp. CAG:202 GN=BN531_00019 PE=4 SV=1MISKLISKLGYTRFIALSFIPVILLGTFLLCLPISSKTGEWTNFIDSLFTSVSATCVTGLIVFDTFTHWTVFGQIVILIMIQIGGLGLMTII TMISIFLRKKINMRERKMMMQSSGNTQIDGTLKLVKKIVGGTFIFEGIGAVLLAFRFCPQMGMLKGIYYSCFHAISAFCNAGFDLMGFR QPYSSLTYYTNDYYVNIIIMSLIVIGGIGFIVWNDILKNKFHFSKYLLHTKIVLVTTAILLVAGGLGFFVFEYNGELADKTVPQKIVNAMFMS VTTRTAGFNTIDLSNLSDSGTLLSLILMLIGGSPGSTAGGLKTTTIAVVVIAVFAMAKGGDDINTFKRRIVSDVVKQSAVIILIYLFAVMLSS MIICSVEGLGMSQVLFETASAAGTVGVSKGITNQISAISKIILMIMMYGGRIGGLSLVLVFGQRKPEAPVKRPTEQILIG
4.9E-53	190	19	1.5E-29	112.3	2.9	2.1	2	R2Q247_9ENTE	Uncharacterized protein	UAS_00356	Enterococcus asini ATCC 700915	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus asini, Enterococcus asini ATCC 700915	1158606	>tr|R2Q247|R2Q247_9ENTE Uncharacterized protein OS=Enterococcus asini ATCC 700915 GN=UAS_00356 PE=4 SV=1MNKKMIFYIIGKILQVEGILLLLPVIVSLIYQEQVTRIYGVIALLLLVLGSLISRSAPRDKDFFIKEGLFIVGISWFLMAVFGALPLVFSG EIPHFVDAFFEIVSGFTTTGATVLSDIDQLSHASLFWRSFTHWVGGMGILVFTVAFIPLTSGRTMHILKAEMPGPIVGKLVSKAQVTAQI LYILYGALTLIEVLLLLVGGMPLFDSLLTTFSTAGTGGFTMSNAGIIGYHSPYIEGVLTVFMIIFGINFNLIYLAALGRGWLVLKNEELRWY LGIIATSTVLLTVNIRRLYGSMGEAFRYAVFQVASIITTTGFATTDYDQWPMFAQNVLLLLMFVGASAGSTGGGIKVSRIVMVAKSGLKE IKRMLHPHGVVTVDFEGATVTARTLNNIHSYLLLYALVFCGALLVVSLENLDFHTTFSAVATTINNVGPGFNGVGPMKNFGDLTALSKY TLAFTMLAGRLEIFPVLLLFSKYFWQE
4.9E-53	190	22.3	2.3E-51	184.2	15.4	2.2	1	R6YP16_9FIRM	Uncharacterized protein	BN600_01814	Roseburia sp. CAG:309	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:309	1262945	>tr|R6YP16|R6YP16_9FIRM Uncharacterized protein OS=Roseburia sp. CAG:309 GN=BN600_01814 PE=4 SV=1MKKRIVVYILGWLLVFEGFFLMLPCFVGLMYQEVEAVWFAVVALVCLCLGFIITRLIPKDKTMYAREGFVITALSWVLLSLFGALP FVLCDVVPSYIDAVFETASGFTTTGATIFQEVETLPYCINFWRTFFTHWIGGMGVLVFMMAVVSLADGRNMYLMKAESPGPSVSKLVP HVKSTAKILYGLYIGLSALEFSLLIFGDMTVFQAVTTTFGTAGTGGFGIMNDSMGSFSNYTQIVVVTVFMIAFGINFSFYYLLLKKAWKD ALKLSEVRVYISIIIVASLVVMFNIRGQMGSYPNAMKHAFFQVASIITTTGYSTVDFNQWPEFSKTIMIGLMFIGACAGSTGGGMKISRFII WAKTFFKELKVMIHPRNIYKISMDGRKVEHETVRSVNVYLVAYVLLFSVSLLIVSINGHDFETNFTSVATTINNVGPGFHLAGPVSNFSF FSPLSKVVLIVDMIAGRLELFPLLLLFSASTWKK

4.9E-53	190	16.2	2.3E-29	111.7	4.8	2.1	2	R6JUR5_9CLOT	Uncharacterized protein	BN486_00397	Clostridium clostridioforme CAG:132	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium clostridioforme CAG:132	1263065	>tr|R6JUR5|R6JUR5_9CLOT Uncharacterized protein OS=Clostridium clostridioforme CAG:132 GN=BN486_00397 PE=4 SV=1MNRSIIIYMLGWIMNMEAIFMTLPVITAVVYRESIGFIYLGVAVVCGLLGFLCTRKKPCTKMFFAREGFVTVSLGWIVLSFFGCIPFVISGEIPHIIDAMFEIVSGFTTTGSSIIPKVEDMSHATLMWRSFSHWIGGMGILVFILAILPMAGDYNMHIMRAESPGPSVGKLVPKIRITAKLLYSIYFCMTIVMMILLLLGKMPLFDSICMSFGAAGTGGFACRNSGQADYTVYQQAVITIFMLLFGVNFNVYYLLLIRRPKDAGRCEELRGYLAVVAIAILLITINIRNLFPSLFMAFHQAAFQVSSIITTTGYSTIDYNSWPEFSKTILLLIMFIGACAGSTGGGMKVSRVMIAFKEIKKEMASVIHPRSVKVLKFEGKPLEHNILRSLNAYIIVYFIIFGISILIVSLDNYDFMTSFSAVAANLNNIGPGMSVVGPSSNYSMMSYLSKTVLIFDMLAGRLELFPMLVLLSPGTWKRS
5E-53	190	22.3	2.6E-52	187.3	15.5	1.8	1	A0A0D6TAW7_9RHOB	Ktr system potassium transporter B	SY26_14350	Paracoccus sp. 361	428	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 361	1603292	>tr|A0A0D6TAW7|A0A0D6TAW7_9RHOB Ktr system potassium transporter B OS=Paracoccus sp. 361 GN=SY26_14350 PE=4 SV=1MLAVGYLTLIAVGGLLLMLPPMTHTPITLSDALFTSTSAVTVTGLNVVDTELVYAFWGQLVIAVLIQLGGLGLMTFAVLIWSALGRPLGITQGTYLREDLNQTSYGKLTRLVWTILRIVVMAEVAGAMLLCLSFMPHHGLGPGLWHAIFHSVSAFNNAGFSTFSPGLTGYALDPVVNVVIPVLFIAGGIGYVVIADLYQRAFWRGWSLHTRMMMVGTAILIVGGVAMTAILEWDNPNTLAQYHSITARLTVAWFQGVTTRTAGFNSTDIAGLEDSTSFMYMILMIIGAGPTSTGGGLKVTTVFVMLLATWAFLRRRTEVTGFGRSIPLGDVLKAMALMAMASAVIVTAIFLLLISEGGDFVDIAFEVSSAFGTVGLSRAYTPELSEFGRAVIMVVMFLGRVGPLTLGFFLATRMVPRVRYPAGQVHLG
5.1E-53	190	28.6	1.9E-52	187.8	19.8	1.7	1	Q5FKC5_LACAC	Na+-transporting ATP synthase	LBA0999	Lactobacillus acidophilus (strain ATCC 700396 / NCK56 / N2 / NCFM)	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus acidophilus, Lactobacillus acidophilus (strain ATCC 700396 / NCK56 / N2 / NCFM)	272621	>tr|Q5FKC5|Q5FKC5_LACAC Na(+)-transporting ATP synthase OS=Lactobacillus acidophilus (strain ATCC 700396 / NCK56 / N2 / NCFM) GN=LBA0999 PE=4 SV=1MIHLFHRRITFSLALTIGFLILIFIGSILLSLPFADKVGRATDYSDALFTATSAVCVTGLSTVTTATHWSFFGQLIIMILVEIGGLGFMTFAVMLSNFAHQRMSLGARMLTEEALNLHHLSQLRVVQLIIRLSLIIQLVGAALLFIALEPSLGVKKGIWYSLFHSAAAYCNAGFDLFGPSVEQLNNNPYILTVFMLLIGAGSFGFLVWRDLLTYHIRHKITLHTRFALTVGLIILVLSIIGFLFSEQNLKQFSSSLNGVDRFFNTLFLAVTPRTAGFFSVPYTKLSTAGIVITIILMFIGGTPGSTAGGVKTSTIGILFLQSIGTFTGKEPAFSHRRFTRDNINRALTLFFSAILLIILATLLLTMTQPSLGHNGVTKAVFEAVSAFGTVGLTLGLTPHLNLFGKIIIMALMFIGRVGIYTFMYSIFKSHPSKQSYRYPEEEIIIG
5.1E-53	190	31	4.7E-32	120.5	12.4	2	2	R7AWV6_9FIRM	H(+)-transporting two-sector ATPase	BN599_01126	Firmicutes bacterium CAG:308	438	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:308	1263016	>tr|R7AWV6|R7AWV6_9FIRM H(+)-transporting two-sector ATPase OS=Firmicutes bacterium CAG:308 GN=BN599_01126 PE=4 SV=1MENSQKKIRRALYYFSAPQLLMVGFASVILTGAVILMLPISVREGATVSFIDALFTSTSAVCVTGLIAIDTADHFTVFGRAVVAALIQIGGLGVTCVGVSLILAAGRKIDFHTRKLIKESWNIDSYQGLVKLVKQVLKLTFAFEVVGAVLSFLVFSQDYSFWDAWGISIFHSIAAFNNSGFDILGNLQNLIPYSDSILLNLVTAGLIICGGIGFLVILDIKKKKRFKKLTLHSKVVITMSIVLILVGTILLKSTENITWLQAFFHSVSARTAGFSTTPLGEFTNAGLFVLVILMFIGASPGSTGGGIKTSTFFVLITVFRGIVKNQPFGAFKRRISNKVIMQAFNVVFLSLMVVVIGTLLLCVTAPECTFIQILFEVTSAFGTVGLSTGITPYLNSISKFILILIMFIGRLGAMTVATMIANKKPRTAVYSVEDISIG
5.4E-53	190	11.9	1.9E-30	115.2	0.4	2.2	2	H0UMH5_9BACT	Trk-type K+ transport system, membrane component	JonanDRAFT_1314	Jonquetella anthropi DSM 22815	485	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Jonquetella, Jonquetella anthropi, Jonquetella anthropi DSM 22815	885272	>tr|H0UMH5|H0UMH5_9BACT Trk-type K+ transport system, membrane component OS=Jonquetella anthropi DSM 22815 GN=JonanDRAFT_1314 PE=4 SV=1MKNPLVLKILGWFGLVVSGTLVLPLAWALWDASADWLPILCSLAAGGVLSGLMIFVGTGLSAQKEQNINAGDAAVIVTGAWVLASALGALPYWLGGYCSYTDAFFEAMSGFTTTGASVFPLVEALPRGILFWRALTHWLGGMGIIVLGLTVLKLSGVGGMELYKAEAPTPLPEKLTPRLCQTALWLWLIYMGLTAAETAALVVCGMTPFHALCHAFSTMATGGFSTFNGSVGQLNSPAVEWVIIVFMVLAGVNFTLHFLALRGEVSCYWKDDECRLYGGILLAGGAFAAVLAMRAGFFTQWGEAFRRGLFTVVSTMTTTGFVVCNYDLWPAAAKFLLMLLICIGASAGSTGGGMKCARIIVLFRQCRRELRHSLAPYRVDVLHYGGGQLKDRDVSSIGTFFVAYVSCLGLLSLLAALLGCDATTALTSVITCLGNTGPGLGSVGPVGNYAALAGSVKWVLSFAMLLGRLEIITVALAFFSSFRRL
5.4E-53	190	42.3	1.7E-52	188	29.2	1.8	1	K7XA93_MYCHR	Potassium uptake protein, integral membrane component, KtrB	MOS_752	Mycoplasma hyorhinis SK76	531	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma hyorhinis, Mycoplasma hyorhinis SK76	1118964	>tr|K7XA93|K7XA93_MYCHR Potassium uptake protein, integral membrane component, KtrB OS=Mycoplasma hyorhinis SK76 GN=MOS_752 PE=4 SV=1MKFSDIKIKNIWEILKNRFNNFLKFNKVKWIFLTYILIIFFGALLLTSKISLQQGQEITFFEALFTSVSAFSDTGLVVKTTASTFNQFGQAIVAILILIGGAGFFAWKIYIINYIFRFKLSLFQKTLLKTERGANKFGDIKGVIISSLTVFIILIILSSFVLSFYFYNVQGNFDPLKSTAQSPEFNNPYKNASISIRYSIFHTITALNNAGFDIVGKYSFAPYYSDYFILIWLIILFVIGGIGYPVIYDVYLYIKSKIFKNQRYAMKFSLFSKISVLTYVIVTIVGASLILIFETQSQNPDSFWNKASSSQGFWGDESAFSYGTKSNKVFALIFYTFSTRSAGFSIFDTYDLSQPSLIISSLLMFIGSSPSSTGGGIRTTTLAIIILSIWSKILGKKSIHSFKKTISFENSDRASVVFFISLFLVTITLLVGSSSFANLSTKTVENPLFLKQINKARTFNLFHLLFEINSAFGTTGLSTGILNHLNIYTKILLIVIMFIGQLGISSSILIWSSEKSKFNKYEYLSEDVLTG
5.5E-53	190	28.1	7.4E-53	189.2	19.5	1.1	1	B9DTP2_STRU0	Cation transport protein	SUB0372	Streptococcus uberis (strain ATCC BAA-854 / 0140J)	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus uberis, Streptococcus uberis (strain ATCC BAA-854 / 0140J)	218495	>tr|B9DTP2|B9DTP2_STRU0 Cation transport protein OS=Streptococcus uberis (strain ATCC BAA-854 / 0140J) GN=SUB0372 PE=4 SV=1MFFSWIRTWSITRRLTFSFALVILIGSILLSLPFFQYQNASESVYLDHLFNVVSMVCVTGLSVIPISEVYNGFGQMVAIILMQIGGLGLVTLIAFSTFALQKKMDLSGHSLLQSALNRNDSTNLKHYLFFAYKVTFAIESIAFLVILTDFIPRFGLKNGIFNSLFLAVSAFCNAGFDNFGSNSLTDFVVNPTINFVVALLIIFGGIGFAVWYDLSNNLKRYFYDKPKCHGLFYQKLSNQTRLILQTTLIILITGTLITWFLEKDNPNTIANYNLWQQLMVSFFQTVTMRTAGFATLSYTDTLAPTNFLYMIQMIIGGAPGGTAGGVKVTTVAIVFLLLKSELKAQSQVTFHHRMIASKTVKQTMSVLIFFFTILTIGYILLLAVEPYIDPVALLFEAISAIDTVGVTMNVTPKLSTPGRIIIMLLMFIGRVGPITFLLSLIARKEKTIRYATTDILVG
5.6E-53	190	26	2.8E-28	108.1	4.6	2.5	2	F4GL50_SPHCD	Cation transporter	Spico_1177	Sphaerochaeta coccoides (strain ATCC BAA-1237 / DSM 17374 / SPN1) (Spirochaeta coccoides)	484	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Sphaerochaeta, Sphaerochaeta coccoides, Sphaerochaeta coccoides (strain ATCC BAA-1237 / DSM 17374 / SPN1) (Spirochaeta coccoides)	760011	>tr|F4GL50|F4GL50_SPHCD Cation transporter OS=Sphaerochaeta coccoides (strain ATCC BAA-1237 / DSM 17374 / SPN1) GN=Spico_1177 PE=4 SV=1MLNWKQDARLLSSILMVFTLVMSIPTAIAWSSREHDAFRGFLWAMFTALVLAALLYHISLSASSRKLGTRDGYILVTTTWLLVTAIGAIPLRASGAFPTYTAAYFEIMSGFSTTGASVIPVHDAIPSSIHFWRSATNWLGGMGIIVLFVALVPVMGSGGAKLVGAEFVGPTKDKLTPKIRNTALSLWLIYVGLSVLQAILLLAGGIPLYDAATITFSTMSAAGFSPYAGGVVSFFSSRYVLVIVIIFMFLSGVNFALFFKALMGQGKLAIRDKELRTYGIITLVVATAGGISLAFSGMYDIGESFFQSLFQTVSFISTTGFVTADYQTWPAFNQMLLFILIFIGGCAGSAAGGIKVMRIMTMARLAKVHMRQRLHPNGVFPVHVGTKILSPEVTRGVSAYFGIYFTTALAGILVISLTGVDFETAVSSVLTCLSNVGIGFGQVGPKGSFAMFPPWAHWVFSFLILAGRLEFFTVFTVFTRDFWKR

5.6E-53	190	13.1	1.8E-27	105.5	1	2.5	2	G7ZI23_AZOL4	Trk system potassium uptake protein	trkH AZOLI_p50076	Azospirillum lipoferum (strain 4B)	486	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum lipoferum (strain 4B)	862719	>tr|G7ZI23|G7ZI23_AZOL4 Trk system potassium uptake protein OS=Azospirillum lipoferum (strain 4B) GN=trkH PE=3 SV=1MPNFRPILFIVSIVLLALAGTMLIPAAVDFAYGNPDAGVFLYSAAFTGACGGALALGTRCHLHGGLSLRQAFLLTPLTWTSTAAFA ALPFQFGHFPELSLNYANAFFETMSGLTTTGSTVLVGLDRTTEGILLWRALLQWMGGIGIIGVAIAVLPALRVGGMQLFRTESSDRSQ KVLPRAQQIAKAIAGVYAGLTAICGVCYWLAGMTPFEAVVHALTSLSSGGFSTSDSSIGHFESPVLHWLVTLFMLLGSLPFVLYVRTLT GQRDALWKDSQVRTYLAFLAAVILPLSIWLAATHGHGFHDALRLVAFNVVSVVTTTGYAYTDYSQWGNLAVGVFFGLTFIGGCTGST AGGIKIFRFEVMVTVLRTHFLHLIYPRGVFPRQYGNRRLDDDVLGSVIVFFALFFTAYSVITIALMALGLDFITSASAAVTALANVGPGLG DIIGPAGTFSSLPDSAKWLLSLAMLLGRLELFTVLVLFMPQFWRG
5.7E-53	190	31.6	7.5E-53	189.1	21.9	1.1	1	B1YJ13_EXIS2	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Exig_0461	Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sibiricum, Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	262543	>tr|B1YJ13|B1YJ13_EXIS2 H(+)-transporting two-sector ATPase OS=Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15) GN=Exig_0461 PE=4 SV=1MDLAYQQKLQHFIRKLTPIQSLVIIYFVAVIIGVILLGLPWSTKGNYDWDFTDLVFMAVSCVSVTGLTTVSVSDTFTTFGYFMIMIL VQVSGIGLMSLHIAMWVILGKRIGFRERQLVVRDQNQTTMQGVVKYIREVIIIILSIEIIGALILGLYYTKYFPTLGEAMLQGLFGSVSATT NAGFDITGESLLPFRGDLFVVFMQILLLTLGAIGFPVLVEVRRYISYRATRQATRQPYHFSLFTKLTASTFFILVLFGTVSLLLFEWNQSF KGLPVNEKMVDALFQSVTTRNGGLTTVDITSFSQASIFVLSILMFIGASPSSVGGGIRTTTFAVAVLSVIAFIRGEYGIKIFGREIGQSDIW KAFVVIVVSTGVTMIGLIVLLIFEDAPFLVLFFEACSAFGTTGLSLGITNELSDVGKWTLSVLMFIGRIGVISFVLLLKANQPKRNYNYPKE SVIIG
5.7E-53	190	44.4	1.6E-52	188.1	30.8	1.6	1	U5S803_9LACT	Uncharacterized protein	Q783_03440	Carnobacterium sp. WN1359	457	cellular organisms, Bacteria, Firmicutes, Bacili, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium sp. WN1359	1266845	>tr|U5S803|U5S803_9LACT Uncharacterized protein OS=Carnobacterium sp. WN1359 GN=Q783_03440 PE=4 SV=1MNYYKFMGRFSNQFSTIQLIVLYYFIVVVVACLLLALPIFRNPDVSISFIDLIFTAVSTVSVTGLATINLGETYNFAGIILLQILFMLGSL GVMMISTSFMLLRKKKVSLKQRQLIMTDMNQPRLSGTVRLIRNTILIILGFEFVGGVILSSYFFLFSNWSLKEVLFQGFFTSFSAVANVG VDLTGQALIPFHDDYFVQIIIMLLIVVGGIGFPVLLEIKDFLQYKKEKKALPFRFSLFTKITVFSFLILLIGGAICIWLLEFKQFFKGMPFTDS VFYSFFYSVTTRNAGLMTTSLSNFSEGSLLLFSILMFIGASPSSVGGGIRTTTLAIVVVYLISFIRGHDQVALFKRRIDRDDVQKSITVFIL SMVLCIFSVMVLSVSESHDLITLIVEVTSAFGTTGLSLGVTPTLTVVGKLIIIVLMFIGRIGMLYMLMLLVPKHKEDKNYHYPTEKIIIG
5.8E-53	190	10.8	5.7E-51	182.9	7.5	2	1	C9LUT7_SELS3	Cation transporter (Potassium uptake protein, TrkH family)	Selsp_2217 SELSPUOL_01227	Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	483	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Selenomonas, Selenomonas sputigena, Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	546271	>tr|C9LUT7|C9LUT7_SELS3 Cation transporter OS=Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28) GN=Selsp_2217 PE=4 SV=1MDIKVVAYFLGRIAQAEGLIFLVPLAVSLWYVESSRLPLFATALLSAAAGTALRRAGKEPGERLTLREGIAITGGGWLLATFLGML PYLLGGYLGYLDGVFESISGFTGTGATVVEDIEALPQGVLLWRSLTHWLGGLGIIVIFIALLPATGQGAITMYNAESSAQGSERVLPRLK DLTSVLFRIYVVLTGAAFLAFFACGMSALDAVNHAMSTIGTGGFSTYNASAAHFGSPAIELWMSLFMFISGGSFGLYYRVYKKGPQVL WRNSEFKAYLGIVGGAVLLIAANLFYRGLYNVPDALRFALFQATSLSTTGFVSADYELWPGFSKGILLLLMLTGGCVGSTAAGLKIARIL VLFRMVRTIVLEKLHPRVTTPVRINGASVDEATLHRTAVFFFLYVLSIAFFAVLMTADNIKTFDAIGISVTTVGCIGPAFGIAGATENYAGL SDFTKGILCFAMLLGRLEFFTLLVMLYPSFWRSKKNW
5.9E-53	190	21.8	1.6E-52	188	15.1	1.5	1	Q31PA9_SYNE7	K+ transporter Trk	Synpcc7942_1080	Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	447	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus elongatus, Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	1140	>tr|Q31PA9|Q31PA9_SYNE7 K+ transporter Trk OS=Synechococcus elongatus (strain PCC 7942) GN=Synpcc7942_1080 PE=4 SV=1MQRSWRLTVPRTISLGFLAVILAGTFLLMLPWSQSSGQWGGWLPALFTSTSAVCVTGLSVVDVGTYFSPFGQLVLILLIQVGGL GYMTATTFLLMLLGLRFGLRDKVAIQQSLDRSGMAQIRQVLRAIAIATLACETVGAIALFTPLMSRHETLMGAAWSAIFHSVSAFNNAG FSIYPDNLVGFVGSLRVNWIIAILIVLGGIGYPVILEGWQLLKGKRRLSPLSLHFRLAILTTLGLLIGGWLLFLGAEHLNPKTLGPLPINDQ MLAAWFQTVTPRTAGFNTIDQTQMSLFAQMVTIALMFIGASPGGTGGGVKTTALAILIGCTISVLRGRESVLMFQRQIPQRIVQKATAV VVGSSSFTIILGTLIMAVFDRDLEFIQLLFEAVSAFATVGLDLGVTATANAGVQLVLIALMYIGRVGILLLMQALLGDPHRSRLRYPEEELLV G
6.2E-53	189	30.6	1.1E-52	188.6	21.2	1.3	1	A0A0F5VBD4_9GAMM	Ktr system potassium transporter B	KY46_13625	Photobacterium halotolerans	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	265726	>tr|A0A0F5VBD4|A0A0F5VBD4_9GAMM Ktr system potassium transporter B OS=Photobacterium halotolerans GN=KY46_13625 PE=4 SV=1MKGFIGKGGIFHLKTPHKQSQWSEPKIIIVSFLSILLPASVLLTLPLFSLTGLSFIDALFTATSAISVTGLGVVDTGTHFTHSGKVLL MILMQIGGLGQMTLSAVLLYMFGARLSLKQQAVTKGALGQENSINIRRLVILIILFTFISETIGTMILAIRWVPEFGLTEGLFTAVFHAISAF NNAGFSLFSDSLTRYQDDPLLLMTISLLFICGGLGFTVVADLFKWSKTRHHRLRLHSKLMLVATPTLLLSGTLLFWLLERNNAATLGQL PTGLQWINAFFQSATARTAGFNSVDISQFSQPALLVMMALMLIGAGSTSTGGGIKVSTFVVAVLATITFLRQQNNVVLFKRTIAWSTVL KCLAIIVVSGLILMLAMFLLMLTEKASFDRVMFETLSAFSTAGLSAGLSASLSEPGKVIMVVVMITGRIGPLTLAYLLARPTTTQLKYPED NVYAG
6.8E-53	189	21.2	4.2E-52	186.7	14.7	1.8	1	D5WS22_KYRT2	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Btus_2305	Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Kyrpidia, Kyrpidia tusciae, Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	562970	>tr|D5WS22|D5WS22_KYRT2 Potassium uptake protein, TrkH family OS=Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) GN=Btus_2305 PE=4 SV=1MSSRPSVWTPARVLVLGFAAVIFVGGVLLSLPVSSQSGRGLDFLDALFTATSAVCVTGLVVVDTGTYFSHFGQVVILLLIQIGGL GFMTVATFLLIMSRHRIGLKERLVIQESLNVATLSGLVKFSRNVVLMTLTVEGIGALILAVRWSFDMLWWRALYFGLFHGVSAFCNAGF DLFGDFRSLSGYAEDPVVNLTIMALITLGGLGFTVIVDLMKRRRSRRLSLHTKLVVITSLGLLLVGAAAFLALEWDRPQTFGPLDWRGKI LSALFLSVTSRTAGYTTVDISQLSTPSLFLDIVLMFIGASPGSTGGGIKTVTFAAIVLFTWSVITDKENVVLYGRTISTKTIYKSLSIAIMSIM LIATWTFILTLMEPVNFIRLLYETTSAFGTVGLSTNLTPELSPPGRFMILLMMYIGRVGPLTLGLALAQRGRKKAILRYPEENLFVG
6.8E-53	189	37.2	9E-52	185.6	25.8	1.9	1	R6T9C2_9STAP	Potassium uptake protein TrkH family	BN609_00852	Staphylococcus sp. CAG:324	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, environmental samples, Staphylococcus sp. CAG:324	1262969	>tr|R6T9C2|R6T9C2_9STAP Potassium uptake protein TrkH family OS=Staphylococcus sp. CAG:324 GN=BN609_00852 PE=4 SV=1MRKLIKSITPTQLIALGFMLVILIGSFLLSLPISAKNLKWTNYLNALFTATSATCVTGLVTYDTNTHFSIFGQIVILVLIQIGGIGFMTIL STIGIYLKKKINLYERKIIMQASGSISTQGVIALVKRIGKTTLIIEGIGAILLASRFIPVFGMGKGIYFSIFHSISAFCNAGFDLMGSLGNEFCS LTNFVGDWVVNLTIMGLIISGGLGFFVWSNIIDTKCCFRKMKLHTKIVLSATAFLIVPSFLFFIFEKDNPMTIKNLPIDEKILASLFQSVTTR TAGFNTIDLSKINDSSALLTIFLMAIGGSPGSTAGGIKTTTFVVSILSIVFSTKQQSTIVIGKRQLENNIIKQASAIISLFLFSIILSSLMIIAIDNI TLLDALFETTSAIATVGLSNGVDVSSSLSSISKLVLIFLMYIGRIGVISIAFLFNKKGDNELLKRPVEKILIG
7E-53	189	17.5	6.3E-52	186.1	12.1	1.9	1	R6FVG9_9FIRM	Uncharacterized protein	BN525_00922	Eubacterium sp. CAG:192	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:192	1262883	>tr|R6FVG9|R6FVG9_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:192 GN=BN525_00922 PE=4 SV=1MNYKVVGKFISQILAVEAAFMLPALIISAACQNLNAVIGFIVSIVIILGIASLLYVLCRKANKRFFAKEGLVSVGIGWIVLSILGCLPFFI SREIPSFVDALFETVSGFTTTGASILTDVEAMSKGMLYWRSFSHWLGGMGVLVFLLAIAPADGKSNRFTMHLLRAESPGPTVGKLAP RMRDTALILYLMYIGLTLGNFIFLIIGKMPVFDAVCTAFGTAGTGGFGIKGDSMAGYSPYIQNVCTIFMLLFGVNFSCYYLVLLRRFKSIIK DSELRTYVVIILSSVALITINISGMFSSVGQALHHAAFTVSSIITTTGFATEDFNLWPNFSKTIILMLMFVGACGGSTGGGLKCGRLLIILKS VKRNIRKTLNPRKVEVIRMGGNVVKEEVVSAVNSYFVAYIVIVFLSFIFISVDGHSILTNFSSVASCFNNIGPGLDMVGPASNYSMFSDW SKLVLIGDMLAGRLEIFPILILLSKTTWSRKR

7E-53	189	23.6	2.7E-52	187.3	16.4	1.7	1	A0A089NJ41_9BACL	ATP synthase subunit J	PGRAT_16730	Paenibacillus graminis	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus graminis	189425	>tr|A0A089NJ41|A0A089NJ41_9BACL ATP synthase subunit J OS=Paenibacillus graminis GN=PGRAT_16730 PE=4 SV=1MVPFAHPKLTPPKILSLGFMVLIAAGTILLCLPAASTGERIIFIDALFMATSATCVTGLAVIDTGTQLTVFGQIVLLVLFQFGGLGFVT MATLITLVLNKRISLKERLLLQESMNQNSMQGIVRLIQRVLIYSLVIQLGGAVLLAARFTLDIPFGKAVYYGLFHSISIFNNAGFDLFGDIH GPFSGLTRYAEDPVVNITSMLLIFLGGIGFIVLSDLIDYPKRRRLTLHSKVVLSTSAVLILGGAAVFFWLELASTLKPLHAGGKVMASFLQ AITPRSGGVTTIEIPLLRESTQFLMILLMFIGAAPGSTGGGIKITTFAILAVTAYTKIRGKEDIVMFRHRISKENVYRAITMTLLSLMLVVAAT MLLSVTESADFLTVLFEAVSAFGTSGITMGLTPNLTTIGKVLVILLMFVGRTGPLTLAYALKPKNSKELYRYPEGNITIG
7.1E-53	189	25	2E-51	184.4	17.4	2.1	1	C4Z2J5_EUBE2	Trk system potassium uptake protein TrkH	EUBELI_01578	Eubacterium eligens (strain ATCC 27750 / VPI C15-48)	495	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, [Eubacterium] eligens, Eubacterium eligens (strain ATCC 27750 / VPI C15-48)	515620	>tr|C4Z2J5|C4Z2J5_EUBE2 Trk system potassium uptake protein TrkH OS=Eubacterium eligens (strain ATCC 27750 / VPI C15-48) GN=EUBELI_01578 PE=4 SV=1MNSSIVRYILGHVLKIEAALMVIPVIVGVIYREKAISAFLITIALCAVCGILMTIKKPANTVFYLKEGCITTALSWILMSIFGCLPFFISRE IPSFTDALFETISGFTTTGASILSEVEGLSQSIMFWRCFTHWIGGMGVLVFLLAVIPLTGGSNINLMKAESPGPSVGKLVPKIRYTARILYI IYFGMTVLQTILLLFGGMTFLDALNTAMGTAGTGGFGIRNDSFTSFSPYIQWVVTIFMILFGVNFNAYYLIVLRQFKKAVKVEEVRCVFG IILAATAIIFVNIYRSVVGTVELTLRQSMFQVASIITTTGFSSVDFDMWPSLSKSVLVVLMFVGACAGSTGGGIKVSRFIIVIKTIFREIQSYIH PKSVKVIKTEGKPVDSETCRSVSIYFITFMMIFTASLLLISIEGKDIVTNFTAVAATINNIGPGLSAVGPTQNFGSYSDFSKYVLMFDMLA GRLELFPLIILFTPSVWKDLVTKKVSERKMRRIRRG
7.1E-53	189	29.7	1.2E-52	188.5	20.6	1.2	1	R7LD19_9BACT	Potassium uptake protein KtrB	BN805_01267	Prevotella sp. CAG:891	465	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:891	1262937	>tr|R7LD19|R7LD19_9BACT Potassium uptake protein KtrB OS=Prevotella sp. CAG:891 GN=BN805_01267 PE=4 SV=1MTKKLVNIYRNALKTVRRKLMKTSLEQFICFGVKSDMPQKQIMAVYAGYSLIGTLLLLLPVSSKCDIPFIDHLFTVVSAISTTGLATV DVASAYTFFGQFVILLLIQMGGLGYMTLSSYVMLKLTGRFGSDKAKLFQIQFAVPDTFDSEVMLKSIVKYTFSFELLGFVLLCPYFLLQG TAQPVWSAMFHSVSAFCTAGFSIYSDNLMQFQSDVYVNVVIMVLCIAGAMGFIMMTDISKWITQKHYKISFTTKVIMSITGLLALWGTV HLYFCEDSFQHLPVGERWMASLFQSISAMTTVGYNTVDVSQMVPISLLILTITMYIGASPSGTGGGLKSTTISALYAYTKCALEFRNKV SLCGNVIPRYRITSALTTVLFYTFILFVGIYLIGLFEPDDADFLKISFEAVSALATAGLTSGILSDITIGSKVVLVLLMYIGRVGVITFGNVML AGKEESIKGKHDIAV
7.2E-53	189	29.3	1.9E-52	187.8	20.3	1.6	1	R6TQY1_9FIRM	KtrB	BN580_01979	Firmicutes bacterium CAG:272	440	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:272	1263015	>tr|R6TQY1|R6TQY1_9FIRM KtrB OS=Firmicutes bacterium CAG:272 GN=BN580_01979 PE=4 SV=1MKIPLKKPTQMQVVALGYLAVMIVGTLLLALPCSSREGTWTGFTDAFMTSTSAACVTGLIPVSTYHHWSAFGQAVLLVLMQVG GLGIMTLMASFTRLLGRNMTLGERKLFMLSTGNDSVGGVTKLIRSVLLYTFSFEAAGAIILAARFIPQHGAYGIWEAVFHSVSAFCNAG FDLMGKYGQSSLTGYAGDVTVNLVIMALILCGGVGFIVWQDIFACRFDPKKFTLHTKVVLVMTGILLFSGAVLFLLFESGKTMPFGERIL TAFFNSVTARTAGFNTVELAALSPASAALMIILMIIGGAPGSTAGGIKVTTFVTLLAGTLASARQVSATNIFKRRIEGDLVRQASAIATIYF SVVSLGIVSVAAIERIDLSWVTFEVVSALSNVGVTMGITGSLSVASKLILCLLMYFGRVGMMSLVIALAAKRENIPISRPAENLLL
7.2E-53	189	29.6	1.9E-51	184.5	20.5	2	1	V5XPX7_ENTMU	V-type ATPase, subunit J	EMQU_2028	Enterococcus mundtii QU 25	448	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus mundtii, Enterococcus mundtii QU 25	1300150	>tr|V5XPX7|V5XPX7_ENTMU V-type ATPase, subunit J OS=Enterococcus mundtii QU 25 GN=EMQU_2028 PE=4 SV=1MKQRITKQLSPVQLIAVGFFLLILVGGSLLTLPFFSKSGEPTNYIDALFTATSAVCVTGLTTLNTAAHWNEAGQFLIMVLIEIGGLG FMMIPIIFFAVAKKKVSFSMRILLKEALNLEIMSGVMSLMLYILKFAMVIQGLGALALSFTFVPTYGWTKGIWYSIFHAVSSFCNAGFDLL GDSLANDQPNIYLLMVVSALIIAGGLGFIVWRDLLSYHKVKKITLHSKIALIVTGGLLVGGFIVFFFTEQNAIHLVEGTYLERLANTFFMSV TPRTAGYYSIDYLQMSHAGLMLTMILMYIGGTSGSTAGGLKTTTLGILLIQMHATFNGKTRAEAFGRTIRPAAVLRALTLFFVTLSLCML AIMVLSVTETIPETSGIEYIAFEVFSAFGTVGLTMGLTPDLTEVGKLIIMSLMYIGRVGILTVFFSILVKGNQVGTKYKYPEESVLIG
7.8E-53	189	30.2	1.4E-50	181.7	20.9	2	1	F4GTH7_PUSST	K+ uptake system component	PT7_1220	Pusillimonas sp. (strain T7-7)	455	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Pusillimonas, Pusillimonas sp. (strain T7-7)	1007105	>tr|F4GTH7|F4GTH7_PUSST K+ uptake system component OS=Pusillimonas sp. (strain T7-7) GN=PT7_1220 PE=4 SV=1MRNWLPLYGYHSYQHIKRTGLFRASPPVVLAAGFLALILIGTLLLSLPMASQHDISPFTAFFMATSAVTVTGLTNIEPSITLTHFGQ IVLITLVQLGGLGFVTFAVVAAITLGKKMSLSHQALALEALNQTSVSKIQKTAFSVFKLSIVIELIAAVTLALWWWRDYPLATATYRAIFHA IGAFNNAGFSLFPNSLAQFIGDPVTVFVFTGSIILGGIGFSVLGDIGQKKRWSTLLTYTKVVVMGTIALNLAGFAVIWALEFNNPDTLANL PWHGQALAAWMQSVTSRTAGYVTLDITQLHDSSTLIIMLLMFIGGGSLSTASGIKVGTFIILLAAVYSYIRHRKEVVLFKRSISPDTIQKS LALLLANSALVFLGVLILTTLEKAPFISILFEVVSAVSTTGMSRNLTPQLSTASQAVLTLLMFAGRLGPLTLIYSLATQQRSRVRYPETEF QVG
7.9E-53	189	14.5	1.1E-52	188.6	10	1.1	1	D3PW58_STANL	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Snas_1511	Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	452	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Glycomycetales, Glycomycetaceae, Stackebrandtia, Stackebrandtia nassauensis, Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	446470	>tr|D3PW58|D3PW58_STANL H(+)-transporting two-sector ATPase OS=Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21) GN=Snas_1511 PE=4 SV=1MRRRAQSTFVRPSLRHPARLVPLAFLGVAAVGTGLLSLPISREGSDAAEPITALFTAVSAVCVTGLVTVDTGTYWSGFGEVVIAA LMQVGGFGIMTMASLLGLIVSGRMRLSDKLVTATETKMLGLGDVRKVVVRVALVAICVETVVAVILGLQFRFSYDYAPAKAAWYGIFH AVAAFNSGGFALYSDSLESFVTDPVVILPVTIASLVGGIGFPVVVELIRRTFKPSKWSIHTKITVLGTGVLLAAGFVFYLAIEWNNAKTLG PLDIQHKIQAAFFSAAMPRSAGFNAVPTGDLRPETWAVTDILMFIGGGSAGTAGGIKVATFFLLAFVIWAEVRGEPDVSVFGRRIPHST QRQALTVALMGVAAVACGTIALLFASDAPFDQLLFEVTSAFGTAGLSTGLTGDLNNAGQIVIIVLMFAGRVGTVAVATALALRVRHRRF RFPEERPIVG
7.9E-53	189	7.4	1.5E-52	188.1	5.1	1.4	1	A9GMD3_SORC5	Potassium uptake protein, TrkH family	trkH sce3261	Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	649	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Sorangiineae, Polyangiaceae, Sorangium, Sorangium cellulosum (Polyangium cellulosum), Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	448385	>tr|A9GMD3|A9GMD3_SORC5 Potassium uptake protein, TrkH family OS=Sorangium cellulosum (strain So ce56) GN=trkH PE=4 SV=1MDPSPPPSSWSGAPRSAQPGGRGNRAEPALTVASPGAPSVPPPSAAAGAAAAAAAAVAPRPRAVWMRPASLLAGSAVLLGLD LAFAISPRVSMALTALETLLVPAWVVAVVSLERAHRTLTGAQAEASRPRLALFLLALGLLLACIGEKWHLVWQPTGDTGHRGVVLYRS YTVLAFFLALGGLLGRRPLERLMATAAEHPARLMAVSFGVATLIGSFLLTLPQSLRNIEDASFVDGLFMSASAVCVTGLAVHGIAETYT PFGQAVLILLVQIGGLGIMVLSTFFAILAGRRLRLRDAAVMAELIDAESFARLRRNVAAIVLFTLGVELVGAIALLFSFLPYHAIASGPVPG EPLSGAGDHLWAAVFHAVSAYCNAGFSLFGGLVPLVGSPAVSAVLGGLVIFGSLGFPVHDELVRRLRLRLRGERPPRLSLHSRVVL LTTAVLLVVGAAGFLLLEWRRSMAGLSWPVKVMASFFQSAMTRSAGLTTVDFGLMGPAALMLTSMMMFIGGAPGSTSGGVKVTTV AALFAALRAELRGDEAPHLLGRTLPAATVRRALGVAFLSMVLVSVFVLILLALEPHDPMGLAMEAVSAFATAGLSANVTPSLSAPGKVV VTLAMFIGRIGPLTMALALANQARARSYRLPEERVGIG
8E-53	189	25.5	2E-51	184.4	17.7	2.1	1	E1RJX2_METP4	Cation transporter	Mpet_2108	Methanolacinia petrolearia (strain DSM 11571 / OCM 486 / SEBR 4847) (Methanoplanus petrolearius)	486	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanomicrobiaceae, Methanolacinia, Methanolacinia petrolearia, Methanolacinia petrolearia (strain DSM 11571 / OCM 486 / SEBR 4847) (Methanoplanus petrolearius)	679926	>tr|E1RJX2|E1RJX2_METP4 Cation transporter OS=Methanolacinia petrolearia (strain DSM 11571 / OCM 486 / SEBR 4847) GN=Mpet_2108 PE=4 SV=1MNRLAQFSIIADDLGNVFRFISIGTCIPIIVALIYGEWNMIIPMAMVPLILFLLGTLMLQFPENKREAKLSQALFSVALIWMVCALVGA VPFTLGLGMPYLDAVFEAMSGWTDTGLTMIADVDAVPHTLLFWRSLMQWLGGLGIVAFTIVMLSRTGMNPSRFYRSEGRSEAFMPS IVEQGLNMWKIYLILTFVSVLLILISGVSIWDAVNIAMVAIATGGFSVHTAGIPYYNNPLLEMLIIPVMIAGALPFKIYYLSYYKRKLSFYHD EQPWILFFLVILGFIVITSDLILFNGLESIDAVRQGIFMAVAGVTSTGFQVSSPDTWAPVSVLFLVFLLFIGGSSGSTAGGIKLSRVALAYR GIVWWFKRIFVSGKAVVPFRYSGRIVPKAEAEAEVSRNMLIILLYFIVVFFSAIIIMHFESPMVDTSNVIFEIVSATCNNGISTGFVNSDLT PFSKVVFIFVMWIGRLEVLPVIVFFMGLIRGFEK

8E-53	189	19.6	2.2E-36	134.8	3.6	3.1	3	Q5KL75_CRYNJ	Potassium ion transporter, putative	CNC00490	Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) (Filobasidiella neoformans)	854	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Tremellomycetes, Tremellales (jelly fungi), Tremellaceae, Filobasidiella, Filobasidiella/Cryptococcus neoformans species complex, Cryptococcus neoformans (Filobasidiella neoformans), Cryptococcus neoformans var. neoformans, Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) (Filobasidiella neoformans)	214684	>tr|Q5KL75|Q5KL75_CRYNJ Potassium ion transporter, putative OS=Cryptococcus neoformans var. neoformans serotype D (strain JEC21 / ATCC MYA-565) GN=CNC00490 PE=4 SV=1MKRPRFRVRKAFRKPKMPTVAEARDTWQKLKCHFNFFRIHLLVFTFIPIIAACIFYAANGSASGNANSGLTGRQKVTFIDSLFLCF SAMTTTGLCTVNLSALHPFQQVILFFLFIVGDYSFVSLIMVLVRKHYFRTHCEQLLINDLFRRIPTISYDTGAQGGLNYSSKSFKSTIKKL RGKNIAISGPIDGHKMDNFAEDGLVTAGDQEQHMMTDSPVDMTFEERGRRERAEASEIPADNQTPGPRVPSTLGKSTAALLNPANA APPPATSSAQAEDHRSPFVDPLFQARQRLRTQTRAKSISAAQHGRSTSDHRPTPPHVTSDVPNHMGGGAIPPKRKNNVHIKDYSHH DQSQHPHLHTAAQIVTHHTIDPTRGLPIPFGHKNTGYGGFPSLLHIFHHFLPERAKQRLYRPVRRVGIVMHPTYAHEFENGHAGHEES WSEAIRGSVAKWMPEGLQGLVIGRNSRFWTEELDDEELEQIGGVEYRALKLLSSIVSSYIFLYQMIPFAILSIYFAKVDYWNSALLETA GEQAGTVNKTWFSLFLSASAYTGCGMVLTDEGLVPFQTCYLMIYVLIVALLVGNHALPIMLRFIIWIGTKITRKGVKHESLHFLLDHPRR CFLYLFPSHQTWYLLFILLAFTVVELFSFLVLNIGLPVVDSLGGWERFSDGLLQSLSVRASGFGIITISDMAPSVLFLYILLPCLSDLQMC TKSGRSDCTNMMIPIRQVKMNRNLKVTVEKSSGGFDLPVCLCKGNVSDIGLTHSWFTIFRIIFECTSGYGTIGLTLGTPNNNYAFSGEF GTASKLVMIVIMLRGRHRQFCFLESIPASSNPPKAYNQRYLTPIHLPVHRMKMIDRDR
8E-53	189	37.5	9.4E-52	185.5	26	1.9	1	R5ZK40_9FIRM	Potassium uptake protein TrkH family	BN700_00950	Firmicutes bacterium CAG:536	441	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:536	1263028	>tr|R5ZK40|R5ZK40_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:536 GN=BN700_00950 PE=4 SV=1MKLKKKRLTSARIIIGGFMGVILIGAFLLMLPISSKSGAVTPFINALFTSTSAVCVTGLVVYDTATYWTWFGQFVILLLIQIGGMGVV TIALSLTMLSGRKIGLLQRATMQDSISAPRMGGIIKMLRFILKGVFLLEALGALAMTFVFIPMFGWIQGIWFSIFHSISAFCNAGFDLMGV YEPFSSVTYFAGNPIINITIMCLIVLGGIGFFVWHDIVKYKNHFRKYSLQSKVVLCMTFCLIVLPSIYFYFFDFASIHSVSERIFMSLFQSVT ARTAGFNTANFGKMSQTGLMVMIFLMLIGGSPGSTAGGMKTTTFAVMLANLVGIFQKGKAHLFRRRIEETTVRSASAIFMLYITLFISA AMIISRVEGLSILDCMFETSSAVATVGCTMGITPHLMSISKAILIALMYFGRVGALTLPFALARSDRYVNSLPEESIVVG
9.1E-53	189	26.6	1.5E-52	188.2	18.4	1.3	1	S5MAQ1_9MOLU	Potassium uptake protein KtrB	ktrB STAIW_v1c01540	Spiroplasma taiwanense CT-1	554	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma taiwanense, Spiroplasma taiwanense CT-1	1276220	>tr|S5MAQ1|S5MAQ1_9MOLU Potassium uptake protein KtrB OS=Spiroplasma taiwanense CT-1 GN=ktrB PE=4 SV=1MDNSSKKPNKLIKEKQTKKKERKSLDKENNFFSKLKNWWPFSRISGRIISIYLISILIGGFLLSIPGVVLTEQNYWQFITGMFTASS AISDTGITILQTNTNYSFIGELLIIIMCQIGGIGILTVKIVLMVMLGRKISLDDQSVAQTERGNSALSNTVEMIRDAFIFLLWLEIIGVFFLFFG FYFTPMDLGTVYNEKFQPLENLINENSVTNPYHDFSKSLWAAIFHSISATNNAGFDIVSGNSLLPYNQGNSHAYLLQVTFLFQWVIGGL GYPTYHDIKRKIKAKREGKTVRFSLFTKLNFIMYSILFILGPLLVFMTEHFTVEEESKILLDGKYIKDTEGNINWVTTGEWKKTHIWIMDLLF NVSSTRNAGFATVDVNEFTAGSKFVMSVWMFIGAAPSSTAGGIRTTTFAICILAIYSIMRNKKSVEAFKKKIPDDTVKRAFAVVFLSFFIV VTSIFVVYLDSNKMLYATDTTKHTESTIIKLIMYVCSAFGTVGFQPFSNEQIIQLGVISKLMLVITMFVGQLGISNTLLAFVKPRNKQNFGY LEEEVVIG
9.2E-53	189	33.7	1.5E-52	188.2	23.2	1.3	1	D1J7H3_MYCHP	Potassium uptake protein KtrB	ktrB MHO_0330	Mycoplasma hominis (strain ATCC 23114 / NBRC 14850 / NCTC 10111 / PG21)	515	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma hominis, Mycoplasma hominis (strain ATCC 23114 / NBRC 14850 / NCTC 10111 / PG21)	347256	>tr|D1J7H3|D1J7H3_MYCHP Potassium uptake protein KtrB OS=Mycoplasma hominis (strain ATCC 23114 / NBRC 14850 / NCTC 10111 / PG21) GN=ktrB PE=4 SV=1MIKKGNPKKSNVLFVFLKKLGTIRFIFLIYILFTILMSLMLYWEVSHNPSKHISYLDALLLAASSFTTTGLSGVAVSEVFNMFGQILIA VCFILGGIGIFTFKLYIFQSLLGLRTNLFSGQIHQTERGGSNIYETKKMIKISISFLIIISILFSLIFSLIFVYDNTALFSDEKMSQLNALSKNNP WTFNPYEESIRNPYHNFGMSLRFGIFHTLSAINNAGLDIIGTKSLQPYYHNYYFLFLTSILFLIGGMGFPVFYDVWQKIKSIKKDNPRHC FTLFTKFTIITYIFTSLIGLLLTFIFETTAKGANYFWNSSEYGSIGDKVFAIYFQTMSTRSAGFSTVNYYNFTQPTIMVHGILMFIGFSPVST AGGIRNITVAIIFMSIITLIKNRKNINAFHRQIGKESLIKAVNIFAIAIFITLIMTIVIYHTLPSDLKNVYNESYPMVYVMFEVFSAFGNSGLNIG LTPNLGITGKILLIITMIVGQLGISQFLKIFTFSKSKPQRYQYIYEDISIG
9.3E-53	189	30.6	9.3E-53	188.8	21.2	1.4	1	W8GNQ3_9MOLU	Ktr system potassium uptake protein B	ktrB X271_00580	Candidatus Hepatoplasma crinochetorum Av	536	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Candidatus Hepatoplasma, Candidatus Hepatoplasma crinochetorum, Candidatus Hepatoplasma crinochetorum Av	1427984	>tr|W8GNQ3|W8GNQ3_9MOLU Ktr system potassium uptake protein B OS=Candidatus Hepatoplasma crinochetorum Av GN=ktrB PE=4 SV=1MKSFFGKKDKANHNEILIPKQNIVRNKKWEEGGFFKRFLHKNHAILTVLGWYLFFSILGGILLYIPIFQKDDIEHVSFINSLFISSSAF SDTGLSTVSVSDTYNFFGQLIILILILIGGVGWFTIKVILVEYIFEKKITIKDQNEIMNEIGGETNRHALEVAKVAFISTVSFTIIFGLIFAGLFY SVDPKYPANWTEDSNTPASINLGLQGDFLQSFWTGIFHAGSSINNAGFDIFTGDYSLAVYYQNYFIQFLTIFLFVFGGVGFAVIYDCYN YLKNKAKGQKFRFSIFTKIAALSYFSVAFIGLFLVFIAEGFDVLISDQNSFYRSDFYGDPSAKSFALIFNTFSTRNAGFSTINIYDLSEATK VIFILMMFIGSGPGSTAGGIRTTTLFVLIVALIAKIKRKKEVTCFNRRIANENVRDAFRIFIFSALIVFVSSFLIYIPENVIDNEDVTYIDSLFIS ASAYGTTGLATNNLQLIDIFASIVLIIVMFIGQFGIYNILNLFKSNRSDYIFSKKHHYYRVYNSKYLETKIRLG
9.6E-53	189	16	6.9E-52	185.9	11.1	1.9	1	R5NJL1_9FIRM	Cation transport protein	BN730_00114	Eubacterium sp. CAG:603	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:603	1262891	>tr|R5NJL1|R5NJL1_9FIRM Cation transport protein OS=Eubacterium sp. CAG:603 GN=BN730_00114 PE=4 SV=1MNYKKINRFLSGILILEAVFMIPAMLICIYDKETKVALSFLATIGISIVLAGILYLFSRNPSNGFHPREGLVCASACWILISLVGCLPFFI SRQIPSFIDALFEIVSGFTTTGASILSDVESLSRGLLYWRSFSHWLGGMGVLVLLMVFVPKSDHNSGSTMHLLRAESPGPNVGKLVPR MKKTALVLYGIYMAMTILNFLFLFIGGMPLFDSVCTTFGTAGTGGFGIKSDSMASYSPYLQNVTTIFMLLFGINFSCYYLILTKHLLSVW RDEELRAYLSVFVVSTALITLNIYHIYSSVTTGLRHAAFQVSTVMTTTGFATTDFDKWPVFSKQLLLCLMFVGASAGSTAGGLKFQRLL LLLKNLRRHIHRTLYPNKVQVVRMNGQKVSEKILDGTDLYLIAYSLILIFSFMLISIDNFSITTNFSAVVACFNNVGPGLDAVGPTCNFGG FSIFSKLVLIFDMLAGRLEILPLLCTLNISTWKRR
9.6E-53	189	17.7	1.2E-50	181.9	12	2.2	1	M1P2A9_DESSD	Trk system potassium uptake protein	UWK_01046	Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	485	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfocapsa, Desulfocapsa sulfexigens, Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	1167006	>tr|M1P2A9|M1P2A9_DESSD Trk system potassium uptake protein OS=Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1) GN=UWK_01046 PE=3 SV=1MKLSNVLNALGIILVAFGTILLTPIVVALVEHEYSSVLPFITAASTSIGLGLLFQKYGGFSRNFDDLKRNEGLLIVSLAWIVTAAMGAI PYLFYGLSPLDAYFESVSGITTTGATILTDFSLYPKDFFFWRSLSQWLGGMGIIVLFVAILPQFAVAGRQIFFAEAPGPTEEKVTPRITHT AKALWLVYLLLTLLEIFCLAAAGMPLFDATCNALSTMAAGGFSPNPLSIMGYESSTVTWIITCFMFLAGSNFALQYRFLIQGKKPLPLLKN EEFHFYTSIVLFVSVCLCIALLLDGTATFLDAVRDSLFQIVSIITTAGFSSADFALWSVTAQTILFTVMLVGGCAGSAGGGIKVIRVLFGLK YLKREITQIIHPKAVLPIKIDHKSVAEDIQRQILGFLLFYLVLMTFSALLVTIIEGDAAVGIVGTAATIGNIGPGYGEIGPMGSFGGLSILTKII FILNMIVGRLELIPFLAMLHPDFWNFRR
9.8E-53	189	28.2	2.2E-52	187.6	19.6	1.5	1	R5KL06_9BACT	Trk system potassium uptake protein TrkH	BN467_02396	Prevotella sp. CAG:1124	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:1124	1262920	>tr|R5KL06|R5KL06_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:1124 GN=BN467_02396 PE=4 SV=1MINAKLVYKVIGSLLFIEAIMMLSCLLVSVYYKEDDIPAFLITITITVLAAIGLKYKGYGAENSMGRREAYLLVTLIWIIFSGLGALPFVI SGYLTSYTDAFFETMSGFTTTGATIIDDVEALPHGLLFWRSLTHWIGGLGIVFFTIAILPSLVGGSVKVFSAESTGPIKSKLHPRLSTSAK TIWAVYIVLSISCAAFFYIFGMGLFDSVNYAMSIIATGGFATHNESTAYFNSAAIDYTSIVFMLLSGANFSLLYLVVIKGRIKEFFKDAEFR FYMLVVLLSTATIMYFLITHNDYSISKALRNSLFQVAAFITTTGIFNDDAAKWPHITWIILSLCMVFGACAGSTSGGIKCIRCAILFRIIRNE FKRLLHPRAVLPVKINGNIVPNQSVPTLLVFFTLYIAAVFFSYFTFTLLGVDSTNSMTIAISSASNVGPTLGLEIGPTMSWSSLPDIGKWI CSMLMLMGRLEFFSVIVLFTKAFWKEN

9.9E-53	189	12	1.8E-50	181.3	8.3	2	1	L0ADE5_NATGS	Trk-type K+ transport system, membrane component (Trk-type transport system (Substrate potassium) 1, subunit 2.1)	Natgr_0191 C490_12105	Natronobacterium gregoryi (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2)	505	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natronobacterium, Natronobacterium gregoryi, Natronobacterium gregoryi (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2)	797304	>tr|L0ADE5|L0ADE5_NATGS Trk-type K+ transport system, membrane component OS=Natronobacterium gregoryi (strain ATCC 43098 / CCM 3738 / NCIMB 2189 / SP2) GN=Natgr_0191 PE=4 SV=1MRIRVAWRHSLTLTGTVLKWLAVPLCFPLVLAVYYGEPVAPFLATIVVTLALGLSFEQLESDGRLGPREAFLMVALTWLLVALVG AIPFVVAGHGTISHPVNAAFEAMSGLTTTGATVLRSFDEHAQSIMMWRQLIQWLGGLGILVLVTAVFSQLSVAGAQLMETETQYDNV NRLTPHIEDTARLILKLYTGLTAAAIGVLYSLYLLGLAPNMTLYNAVAHAFTSVATAGFSPEPLSIEAFEPIVHWALMPFMILGSTSFVLM YFVLQGNFDRLRNSEEFWFYVGSIVFFAGLVMTILTLEGNPTGDGFGDTVRQSAFNVVSIITTTGYANADFNAWSPFAKHLLFMCMFL GGMAGSTTCSIKSLRWLVVFKAFRRDLFTSFRPEAIRPVRLSGQPVDEETIRDVYSYTLVAVLGVFLVTLLIVVDGARTGLYDVGDGSF GEFEALGAAASTFLNIGPAFGPAGPVGTYDVFSTTTKAAMVVVMWVGRIEIIPVLVLLTPSFWRS
1E-52	189	24.6	1.3E-51	185.1	17	2.1	1	R5JXF3_9CLOT	Uncharacterized protein	BN743_00324	Clostridium sp. CAG:632	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:632	1262830	>tr|R5JXF3|R5JXF3_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:632 GN=BN743_00324 PE=4 SV=1MNYQILIYVLGWVLNFQAVFLLLPSLVALIYQEKSGWCFLLAAVVTGMIGIALTVKKPKNTQLHAREGFVLVALSWIIISLISAAPLCI SGEVPNYIDAVFEMVSGYTTTGASILTAVEDLPNCMNFWRCFSNWIGGMGVIVFMVTILPMVGANANMYLMKAESPGPSFGKLVPKL KKTASLLYIMYIGMTLMQIILLLIGKLDFFHAVCVSLATAGTGGFGIKNDGFSGYTSYVQIIVTIFMFLFGVNFKFYFLLLIRKFKDAIAIEEV RWYTILYAVATIVIAIDIFIHLIGTVGGSLKHAAFQVATVMTTTGFATADFNQWPILSQTILVLLMFVGACAGSTGGGMKVSRFIIYIKSAQ KEIACLLHPSSVKKIKMDGKVVDHETIRSANVYLIIYILLLAVSILLVSINGFDLVTTTTSVIACFNNIGPGLGVVGPMGNFSSLSWLSKLVL ILDMLAGRLEVFPIVVLLFRDTWKR
1E-52	189	14.7	5.6E-52	186.3	10.2	1.8	1	V4KCY1_9ACTN	TrkH family potassium uptake protein	B590_16884	Streptomyces sp. PVA 94-07	447	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. PVA 94-07	1223307	>tr|V4KCY1|V4KCY1_9ACTN TrkH family potassium uptake protein OS=Streptomyces sp. PVA 94-07 GN=B590_16884 PE=4 SV=1MVTRPWPHLRHPAQVVVAGFATAVAAGTGLLMLPVARAGPGGAGVMEALFTSTSAVCVTGLAVVDTPGYWSGFGQAVILALI QVGGFGIMTFASLLVLLVSHRIGLKARMTAAAETKTLGLGDVRSVVTGVVKVSLLLEAVTALALTLRFATAYDEPWPRAAWLGVFHAV SAFNNAGFALYSDSLTGFVTDPWICLPIALAVIAGGLGFPVLFELRRRFRKPRGWSLHTKIVLWASGVFLVGGSAFITALEWSNPATLG PLDAQGKLLAGFFQGVMPRTAGFNSIDTSQMSPASWLGTDVLMFIGGASAGTAGGIKVTTFAVLFFVIYAEIRGEGAVDIFHRRLHGD LQRQALTVVLLSVAAVAITTVVFMVFSDHTLDQSLFEVTSAFATVGLSTGITADLAPGLQLLLVALMFIGRLGPITVASALALRSRHRLYD LPEERPIIG
1E-52	189	18.7	1.6E-52	188.1	13	1.2	1	C3PJ84_CORA7	Potassium uptake protein, TrkH family	trkH cauri_0143	Corynebacterium aurimucosum (strain ATCC 700975 / DSM 44827 / CN-1) (Corynebacterium nigricans)	454	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium aurimucosum, Corynebacterium aurimucosum (strain ATCC 700975 / DSM 44827 / CN-1) (Corynebacterium nigricans)	548476	>tr|C3PJ84|C3PJ84_CORA7 Potassium uptake protein, TrkH family OS=Corynebacterium aurimucosum (strain ATCC 700975 / DSM 44827 / CN-1) GN=trkH PE=4 SV=1MKRGHFLGPARLTAVGFVLLILVGTVLLMLPISANVPQWTPFLPALFTATSAVSLTGLVVEDTGTYWTPFGQVVIITLIQLGGLGI MSLASLSGMLLTGRISFKARRTIAAEGRAVAFGGIRRALVLTLVMTLICEAIVAVFIGVRLATEHGVAPGRAAWEGAFHAISAFNNAGFS TYSDSVISFAADGWILLPLAFALIIGGLGYPMLAEFVRRARARLTRWRGGTPRIHRMSMTARMTLGATAFLLLGGTVVFFLSEGSGVLH GMPLGQKLINAFFMSASPRTAGFNAIDYGEAHPLTLMVTDILMFIGGGSAGTAGGIKVTTACVLGAAMISEFLGREDTSIGHRRRLPLST FRQALALTAAGMIVVAVGVATLRIWDPEFTADQVTFEVMSAFATVGLSTGITASLSAPSQLMLCLIMYVGRVGPTTFVAALAARTVSLR YRYPEERPFIG
1E-52	189	18.6	1.4E-52	188.2	12.9	1.1	1	C4ZIV0_THASP	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Tmz1t_0458	Thauera sp. (strain MZ1T)	444	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Thauera, Thauera sp. (strain MZ1T)	85643	>tr|C4ZIV0|C4ZIV0_THASP H(+)-transporting two-sector ATPase OS=Thauera sp. (strain MZ1T) GN=Tmz1t_0458 PE=4 SV=1MKVREVQHPAHIVPLAFLITILIGTALLMLPVSRADAVGAPWIAALFTAVSAVCVTGLVTVDTGTYWSSFGQWVIMALFQIGGFG MMTAATLLGLLVNRSFRLRTRLTAQAETHTLGIGDVSSVAKLVLFVTVIVEVMTALALALRLHLGYDLPLAEAAWSGLFHSVSAFNNAG FSIHADGLIRYASDSYFLAPVMLAIVIGGLGFPVLQDLRNKLRDPQHWSVHTKLTLVGTAVLLAGGAILLAFEWANPRTLGSMPAGDK LLSAIFASVSARTAGFNSIDIGGLTHESLGLHYFLMFIGGGSAGTAGGVKVGTAMILVMLVIAEIRGRMDTEAFGRRISHSAQRQAITVL VLSSAVVVLGTVFILHTTEIATDRVIFEVISAFATVGLSTGITADLPDSAQLMLILLMYIGRVGTITLAASLALGEHRMPFRYPEEHPVVG
1E-52	189	26.2	1.5E-52	188.2	18.1	1.1	1	A8AXU1_STRGC	Sodium transport family protein (EC 3.6.3.14)	ntpJ SGO_1320	Streptococcus gordonii (strain Challis / ATCC 35105 / CH1 / DL1 / V288)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus gordonii, Streptococcus gordonii (strain Challis / ATCC 35105 / CH1 / DL1 / V288)	29390	>tr|A8AXU1|A8AXU1_STRGC Sodium transport family protein OS=Streptococcus gordonii (strain Challis / ATCC 35105 / CH1 / DL1 / V288) GN=ntpJ PE=4 SV=1MKHLFSRLSPAQKIILSFLLVIFCGSLLLSLPWVQTASSQAGYLDHLFTAVSMVCVTGLFTRSVVDTYNVWGQLLCMLLIQIGGLG ILTFIGFFTMESRKKLSLKDRRILRDSFSYGHNRTLGQFVRSIFITTFTIEGLGALLLMIRFIPKFGLRKGIFNSIFLAVSAFCNAGFDNFGN DSLLGLQTDVLVNITLALLIITGGLGFMVWFDLATKLGGKQKGLHFHTKVVLLLTAGLLVFGTVTSLWTEYNNPGTIGNLSFGNKLLVSF FQTVSMRTAGFASIDYTAARPVTLFIYLLQMFLGGAPGGTAGGLKITTFLVLLLFARKEILGLPHTNMGRRTLSPQLVQKAFGVTVIFQL TFLLGLLALGLVTDSSHRFIYLIFETVSALATVGVTANITTSLNTAGMIVIMLLMFIGRVGPLTLMVSLNHYQPKNAATLHYSKADIMIG
1.1E-52	189	12.1	2E-26	102	1.2	2.2	2	A9D5V8_HOEPD	Trk system potassium uptake protein	HPDFL43_09062	Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43)	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Hoeflea, Hoeflea phototrophica, Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43)	411684	>tr|A9D5V8|A9D5V8_HOEPD Trk system potassium uptake protein OS=Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43) GN=HPDFL43_09062 PE=3 SV=2MYGQTIRSAISIAATAGLYLSFAMLLPAALDFYFGNPDWQVFAASSFVVGSICLGTAMATRGAPAPFSRRLGFLVVNLLWITLSV TGAVPLYMSSLGLDMADALFESVSAVTTTGATVIMGLDEAPPGLLLWRSLLQWMGGIGIVALGLLVLPFLKVGGFTVFKMESSDTSER PFARFSMFIRAFFAIYIGLTASCALLYGVFGMGELDAINHAMTTIATGGFSTRDASFGAFQSPGLLWTATIFMALAGLPFSVMILFAVRG RLDALRDPQIAAYAGLILVLVTVLIALSVRLGNGEDFAHALTHAAFNVVSIVTTTGFVSADYALWGPLPVALLFLATFLGGCSGSTSGGIK AYRLVIIASSVRSGLMKLIYPHAIQPVRYGAVTVEPDMQRTVFLFVCAYMGIWALGAVALSATGLDIETALSGSITALANVGPGIGPVIGP SGNFSSIGDAGKMIMVFLMLLGRLEILAVLVLLAPAFWRD

1.1E-52	189	37.2	1.7E-51	184.6	25.8	2	1	A0A0G0LVG5_9BACT	YubG	US76_C0014G0003	Parcubacteria (OD1-vii) bacterium GW2011_GWA2_38_13b	416	cellular organisms, Bacteria, unclassified Bacteria, Parcubacteria, unclassified Parcubacteria, Parcubacteria (OD1-vii) bacterium GW2011_GWA2_38_13b	1618780	>tr|A0A0G0LVG5|A0A0G0LVG5_9BACT YubG OS=Parcubacteria (OD1-vii) bacterium GW2011_GWA2_38_13b GN=US76_C0014G0003 PE=4 SV=1MLPQATVSGEISFIDAVFMATSAVCVTGLVVLDTAVDFTRFGQTILLILMQIGAFGIITATAIFFMMIKKKIGIAYGATLRRSLDMEFTNEAVSLVKFIFIFVFSFELIGSLLLFFYWDIQGISGLTKVFYSIFHSVSAFANAGLSLFSDSFYGFRYNAFLNIIISILIITGGLGFMVFDDLKDYFFSWVKRGFKTRKLYVHTKLMLIGTIIFIFIGIAGLLIFERNNSDFSGNPILVSYFQSVTTRTAGFSTVDIGNLSHPTYLLFMALMFVGGGSGSTAGGIKVVTIVILFLMFWAFILNKKRVSVFGRTLLWENLKHAMAVFIFAFFILLLFSGLLLYTEKGDFRDIIFEAFSAFGTVGLSAGITPNLTYIGKILIILLMFLGRIGPLAIAMIISGEDRSLRLRYPKERVVVG
1.1E-52	189	28.2	2.3E-51	184.2	19.5	2.1	1	R7G1S8_9PROT	Potassium uptake protein TrkH family	BN767_01254	Acidiphilium sp. CAG:727	451	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acidiphilium, environmental samples, Acidiphilium sp. CAG:727	1262689	>tr|R7G1S8|R7G1S8_9PROT Potassium uptake protein TrkH family OS=Acidiphilium sp. CAG:727 GN=BN767_01254 PE=4 SV=1MPFYTAFYMRNFFKKISVAQGMILAFMSVILLGSFLLSLPVSSVSGEWTGYGDALFTSVSATCVTGLVVVDTAAHWSIFGQMVILLLMQIGGLGVITIAIGVTTWTKHKIGLHERTAVRDSLAATQIGGVVRLMRFIVTVTFVIEFIGALLLSIAFIPKFGFFKGLWYGIFHSVSSFCNAGFDVLGGKGNEYASLTAYAANPLVNITVMFLIVSGGIGFLTWDDVRKHKWRLREYRLQSKIILSATAILILPALWFFFFDFSGESAGKRVLLSLFQAITPRTAGSNTADLTKMKSSSQFLMMLLMLIGGASGSTAGGIKINTVTVLFIAMLSIFRRNKDVTVFRRRISDGIIRRAAAVAALYITLWVIGGVTISAIENLPVFDCLFETASAIGTVGLTLGLTPTLGAASRTILAIFMFVGRMGGITFAFATIIRKNDPSARLPEEKINVG
1.1E-52	189	20.7	4.2E-52	186.7	14.3	1.7	1	S0GLT4_9PORP	TrkH family potassium uptake protein	C803_04245	Parabacteroides goldsteinii dnLKV18	471	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides goldsteinii, Parabacteroides goldsteinii dnLKV18	1235789	>tr|S0GLT4|S0GLT4_9PORP TrkH family potassium uptake protein OS=Parabacteroides goldsteinii dnLKV18 GN=C803_04245 PE=4 SV=1MCILETLFMLMATVVAFLYKGGDFYPLLISSGILFGVGISLYAIGFRANEYTAGRREGMLTVTLTWLLLSLLGMLPFYLGGYIDNITDAFFETMSGFTTTGSTILTDIEALPKGVLFWRSLTQWQGGIGMIVFTVALMPILGGGATQMFNAETPGITHERFRPRVTQVAKRLWGVYVFLTVLLIGLLWIGPMNLYDAVNHALTAISTGGYSTKNASIAYWHSAYIEYVITIFMFIGATNITLIYFCLNGNIKKLFFDEEFRWFFWFVLIMTGITTGWIMYHGFFTDFPTAFRQAAFQVVTLVSTCGFATENYIPWGPFFWMIALILMFICGCAGSTCGGLKMGRFVILSKNLFNEFKKQTHPHAIIPVRMDSHIVSGEVVHRVLAFAFAYMSLIVLSCAVLMLDGLGFEESIGAAVSAISNVGPGLGKLGPVDNFSEVPVVSKWFLSLLLMMTGRLEIFTVLTLLVPGFWKQ
1.1E-52	189	30	1.5E-51	184.8	20.8	1.9	1	E3EEU1_PAEPS	ATP synthase subunit J	ktrB1 PPSC2_00375	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus polymyxa (Bacillus polymyxa), Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	886882	>tr|E3EEU1|E3EEU1_PAEPS ATP synthase subunit J OS=Paenibacillus polymyxa (strain SC2) GN=ktrB1 PE=4 SV=1MKRSVKLSRFASPPFILVIGYVLIIALGTLLLMLPIANHGGHAPHWIDSLFTSVSAACVTGLVVVDVDSTYTVFGETVILVLMQLGGLGFMTLATLFALLLGRRLSLKDRLLLKEAINADSMEGIVRIIRKVLIFSFTIEAIAAVVLALRWMREMPVGQAIYYGIFHSVSLFNNGGFDLFGTSFQQYAGDFVFNMIASVLVISGGLGFLVLSDLFDFRRARRLTLHSKMVLSVSGALIVIGALVIFIFEFTNARTLGELNWEGKVYAAVFQSVSTRSSGTSTVDISGLRQASQFFIMLLMIIGASPGSTGGGIKTTTFLLMVGALIAVMRGQKEIVFFRHRVPQDIMMRALTIIVMALFIFSIVVILLLMTEDAPFLSLAFEAASAIGTVGLSVGVTPGLSDAGKLIICVTMFIGRIGPLTIAYAIRPRSTKTLYRRPEGHIVIG
1.2E-52	189	24.3	4.6E-52	186.5	16.8	1.7	1	R5CL09_9BACT	TrkH system potassium uptake protein TrkH	BN567_02424	Prevotella sp. CAG:255	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:255	1262923	>tr|R5CL09|R5CL09_9BACT TrkH system potassium uptake protein TrkH OS=Prevotella sp. CAG:255 GN=BN567_02424 PE=4 SV=1MINFKIIYKVIGSLLFIEAIMMLYSLCVSLYYKEDDIMAFVISIAITVTTAIGLKYKGYHAENSMGRRDAYLLVTLTWVIFSILGALPFVISGYIPSFTDAFFETMSGFTTTGATIIDDVESLPHGLVFWRSMTHWIGGLGIVFFTIAILPSLVGGSMKVFSAEATGPIKTKMHPRLSTNAKAIWAVYLLLTVGCAASFYVAGMSLFDCLNYSMSITATGGFAPHNSSTGHFHSAVIDYISIIFMFLSGTNFTLLYLSLFKGKIKSVVKDAELKFYFCVVALATAGIMFFLIKDLNYNLADSLRYALFQVVAFITTTGIFNADAGKWPHITWVILSICMFVGACAGSTSGGFKCIRSVILLKIIKNEFRHIIHPKAVLPVKISNNTVPYQAQATLLVFLSLYLAVCLFAYFSLTCMGIDSTNSVTIALSCASNVGPTLGLEIGPTMSWSGIPDAGKWICSILMLMGRLEFFSVLVLFTPAFWKEN
1.2E-52	188	29	5.4E-51	183	20.1	2.1	1	A0A0B4S2F0_9FIRM	Potassium transporter KefA	NW74_05325	Parvimonas micra	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptoniphilaceae, Parvimonas, Parvimonas micra	33033	>tr|A0A0B4S2F0|A0A0B4S2F0_9FIRM Potassium transporter KefA OS=Parvimonas micra GN=NW74_05325 PE=4 SV=1MNKKIIRYILSKILYIEAGFLLLPIIVSLIYKEDISNILSFLATIILLLLSGYAIGYKADGSGAFYEKEGFVIVALSWILLSAFGSLPFIFSGSIPSFIDAFFETSSGFTTTGASILTDVEALSHSILFWRSFTHLIGGMGILVFALAILPRSNRHSHIMKAEVPGPVFGKLVAKMSYTARILYKIYFAMTGILIIVLILAGHPVFDSFIHAFGAAGTGGFGIKASSIAYYYNSPAVEIILAIAMITFGINFNLFYIILIGKVRDGFKSEELKWYLFIVFGSVILIFFNIRNNYTSYLKAMRDIFFTVSSIISTTGYATVDFGKWTAFSHSILLFLMFTGACAGSTAGGLKISRLIILVKSSILQFRKAINPKRVLSVKVDNKPVPKEVLEEVKTYFVIYIFLVIIFTILISFSVSDFLTAFSAVMATFNNIGPGMGIVGPTGSYASLTDFNKIVLSFAMLAGRLEIFPILILFSSTTWKKK
1.2E-52	188	19.5	3.1E-51	183.8	13.5	2	1	R5FFP0_9FIRM	Trk-type K+ transport systems membrane components	BN468_00204	Faecalibacterium sp. CAG:1138	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, environmental samples, Faecalibacterium sp. CAG:1138	1262896	>tr|R5FFP0|R5FFP0_9FIRM Trk-type K+ transport systems membrane components OS=Faecalibacterium sp. CAG:1138 GN=BN468_00204 PE=4 SV=1MNFKMIFNTTGRVLKTEAAMLALPLLVSVIYKETCAWGFLAAIAVALALGFALTLAFRPDDRRIYTKEGLVTVALIWMSVSAIGALPFVISGDIPNYVDALFETISGFTTTGASIVTDVESLGKGILFWRSFTHWIGGMGVLVFVMAVTSKTTDRSIHLLRAEMPGQEVDKIVPRAKDTALILYVIYTVMTAVLVVMLLCGGMSLYDSVVHAFGAAGTGGFSIKADGIAGYNAYIQWVLAIFMLLFSVNFNLYYVVLIGKFKNFFKSTELWVFVGVVFVGVTTVTLNILSSCQNFAEALRLGTFQVSSIVSTTGYATADFNAWPTLSKTVLLLLMLMGGCAGSTAGGFKVSRLVIIKKIFGNLKKAVHPRTTNVIKMDGKRVPDETIEGVTSYSLVYMLLLFLIVLLLSFDTRLPSSSALETNITAAVSCFNNVGPGLSLVGPAENYAFYSHFSKIVLSFAMLLGRLEIYPILLTLSPMFWIKK
1.2E-52	188	25.1	1.9E-52	187.8	17.4	1.2	1	F0QR93_MYCSL	Potassium uptake protein KTRB	ktrB MSU_0477	Mycoplasma suis (strain Illinois)	491	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma suis, Mycoplasma suis (strain Illinois)	768700	>tr|F0QR93|F0QR93_MYCSL Potassium uptake protein KTRB OS=Mycoplasma suis (strain Illinois) GN=ktrB PE=4 SV=1MKPKKANLELFWKTLIGKNIYQRISRVYFLVVLLGFGALNLPFAKGNGGGSNGNWFSNLFIAVSAFTTTGLTTNSLNCSYSWFGQLVVLLLIQVGGLGLVTSWMFIKHCFFKSKKRTIEERLNLHSERGGMSQAHSYDIVMSALKILLSCEVIVAILLTFFFYFVAPSVGCADSFKGDFVKSLWGGIFHSISAINNAGLDIISQNSIMPYSSGWGIILSIIFAISSIIGGIGYPVLYEFKEWCKNKRRRKSSKNIFSLFTKISILMHFLITIIAAGAVILAETTSGNLSCIKSCCLSTSEKVWQLLYLIISARSSGFAGLDITSLHEKTQWILLILMFIGASPASTAGGIRSITLFLIIGKVWVTMRGRKSLSIFSRTVSSQTIDNSFIVFFLSSALVIVASLVIPDKNNGGNGIAQEIGRHAKLFESSSAFGTSGLSIGVTGKTNWVGHIVLMALMYVGQMGVPNVLSYYTKSRPSKQKISYPEEKLRIA
1.2E-52	188	21.4	1.9E-52	187.8	14.8	1.2	1	E6VUS9_DESAO	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Daes_1306	Desulfovibrio aespoeensis (strain ATCC 700646 / DSM 10631 / Aspo-2)	454	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio aespoeensis, Desulfovibrio aespoeensis (strain ATCC 700646 / DSM 10631 / Aspo-2)	643562	>tr|E6VUS9|E6VUS9_DESAO H(+)-transporting two-sector ATPase OS=Desulfovibrio aespoeensis (strain ATCC 700646 / DSM 10631 / Aspo-2) GN=Daes_1306 PE=4 SV=1MRIKLLSPYWMPVWFFAGTITMGALLLHLDTGHPGGPISLIDAVFTATSAMCVTGLSVVDTGSFFSLSGQNVILALFQLGGLGIMTFTTLIIHLMGQQVSLGDRIAVGQSLLHDPSFSLPRFLTRVVVGTLALEAVGAVCLWLMDPVGFSPYSAMFHSVSAFCNAGFSLYPDSLTRWQGHVGINVVFMVLITAGGLGFYVLNECATLGKSLLLGRRPQRRGAHLLSWHSTTVLRTSLFLVVAGTVVVIFFAEGLADTGPADPGQRLLTSLFQSVTCRTAGFNTVDIGMMSNVSLLFMMALMFIGGSPGSCAGGIKTTSFRALWGFVAAQLRGRDQVRIGRYALSQGALNTVFSLFIIAAMLVAVGTMVLTSLETVGESYLISRDRFMINMFEVISAFATVGLSTGLTPTLNGAEKGMIVVLMFVGRLGPVWLLSALHSWQTECHYRVPTETLPLG

1.2E-52	188	36.7	7.3E-50	179.3	25.4	2.2	1	R6RDH3_9FIRM	Uncharacterized protein	BN563_00628	Eubacterium sp. CAG:251	434	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:251	1262886	>tr|R6RDH3|R6RDH3_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:251 GN=BN563_00628 PE=4 SV=1MRIKKFVMSQSPARIIAFGFAATIILGSLILMLPISLNDGVNLKYIDSLYTATSAVCVTGLITVDPANTFTPFGRFILAVLIQIGGLGITSLGTGIIIAMGKRVNFKSRSLVKEALNLNSGKGIVKFIKEIFFTTISFELIGTILSFIAFSKDFSFSKALGISAFHSIAAFNNSGFDILGNFQSLAAYKNNVYLNVVTCMLIILGGIGFFVIKDIKTNKFKWKSLSMHSKVVIWVTIILIIFGAVMIKLTNNITWLGALFNSVSARTAGFSTFNLSNFSNAGIIVMIVLMFIGASPGSTGGGIKTTTVFVLFKGIVSAATNKGEKAFKYAIPKNAFRKAAVVTVLGINVVLIGTFLISIFEPQLELRDILFEVVSAYGTVGLTTGITTSLSAASKILSMIIMFIGRLGPMTIVTLWYFSRGERISYPEGNISIG
1.2E-52	188	38.9	4.2E-52	186.7	27	1.6	1	Q8Y8B5_LISMO	Lmo0993 protein	lmo0993	Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	444	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, Listeria, Listeria monocytogenes, Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	169963	>tr|Q8Y8B5|Q8Y8B5_LISMO Lmo0993 protein OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) GN=lmo0993 PE=4 SV=1MARMTPVQVIIAYYFLAVTISTIVLSLPFTLQKGVKVSFIDTLFTAASSVSVTGLTTVDVSQTYSTAGIWVLMAIFQIGGLGVMMISTFFYLILKRRIGLKQRQLIMTDTNQFTMSGMVRMLREILVLIFGIELIGALILGIYFIPLYPNFWDAMFQGLYNSVSLVTNAGVDITGKSLMPFANDYFVQFISILLIIAGAIGFPVLLETRRFLFEKNTLIPFRFSLFVKVTTLTYFVLLIVGGLLIWLFEYHHFFSGKSWDFGFFNSMFLSATSRSAGLQTIDSGALSISTLLLVSFLMFIGASPSSVGGGIRTTTFAITILFIYSVIRGRKHVYIFGRELHQEDVRKSLAVTLVAGFLSISAIVVLMQTETASLIAVIFEVFSAFGTTGLSVGLTPDLSTPGKIIIIALMFIGRVGIMYSMLSLRNKNQPKNAIRLPKEKIITG
1.3E-52	188	12.3	3.2E-26	101.3	3.2	2	2	Q5V337_HALMA	Potassium uptake protein TrkH family	trkH1 rrnAC1107	Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) (Halobacterium marismortui)	391	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Haloarcula, Haloarcula marismortui, Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) (Halobacterium marismortui)	272569	>tr|Q5V337|Q5V337_HALMA Potassium uptake protein TrkH family OS=Haloarcula marismortui (strain ATCC 43049 / DSM 3752 / JCM 8966 / VKM B-1809) GN=trkH1 PE=4 SV=1MSGITTTGATVIRDFDAHSQALLMWRQVLQWLGGLGVLLLATAVLSRLSVAGAQLMETETRTENVTKLTPGIEDTARILGLLYLGLTAAAAAILFALGVSGLAPKMTLFDAIAHAFTAIATAGFSPRAESIGAFSPPVQWAVTLFMIVGATNFVLLYALVRGDTDRLRQSEEFHFYVGILGVGTLLIGGLLVLDQGFTGGVGATVRHAVFQTAAIVTTTGYASTDFSTWSAGAKNVLFVMMFIGGMAGSTTCSIKTLRWLIVTKSFWRDLNVSAHRWSVRPVRLGREIVDEDTVRDVYAYTLVALVFFILGTVLLVADGERAGAPITEFEALSAAASMFFNIGPAFGQAGPYGTYEGFAQSSKVLMILLMWVGRIEIVPVLVMLTPTFWTR
1.3E-52	188	19.2	1.9E-50	181.2	13.3	2	1	D4KUJ9_9FIRM	Trk-type K+ transport systems, membrane components	RO1_02350	Roseburia intestinalis XB6B4	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, Roseburia intestinalis, Roseburia intestinalis XB6B4	718255	>tr|D4KUJ9|D4KUJ9_9FIRM Trk-type K+ transport systems, membrane components OS=Roseburia intestinalis XB6B4 GN=RO1_02350 PE=4 SV=1MNYSIVLYILGCVLKFESAFLVLPALVGLIYREHASVSYLAVAVLCLILGVLLTHKKPRSTNLYTREGFVAVALSWIIMSIFGAIPFVLTGDIPFYVDALFETISGFTTTGSSILTDVESISKASLFWRSFSHWIGGMGVFVFIMAILPMMGGSTMNLMKAESPGPSVSKLVPHVKDTAKILYGIYIAITICEATILRALGMPLFDSLTTTFGTVGTGGFGIRNDSIAGYSPAIQITITVFMILSGINYTAYFYILTGKIKELFKIEEVRWYLAIIFGSVAVITWNVRSLYPTFSETLRHAFFQVGSIITTTGYATTDFDLWPALSKTLLVTLMFIGACAGSTSGGIKVSRILILLKTIRKELSLIIHPRQVKKIRMDGHPVDHETLRSANVFLVVYFVLLLTSMLLISVDEFDFSTNFTSVVTVLNNIGPGLNLVGPTQNFSIFSPFSKFVLMFDMLAGRLELFPMMILLMPSTWKRK
1.5E-52	188	21.5	2E-52	187.7	14.9	1	1	D4LM33_9FIRM	Trk-type K+ transport systems, membrane components	CK1_30380	Ruminococcus sp. SR1/5	429	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus sp. SR1/5	657323	>tr|D4LM33|D4LM33_9FIRM Trk-type K+ transport systems, membrane components OS=Ruminococcus sp. SR1/5 GN=CK1_30380 PE=4 SV=1MPFCSAPGQAVTFPDAVFTAATSVCVTGLSTVVMAVQWSPIGKAVILCLIQIGGIGLIALANMIFISLRRKISLKNRRIIKESYNLDEMGGVVAVVRSVVKCVFLAEGIGAVLYAFCFVPEFGIKKGLVHAIFLAVSAFCNAGIDLFGETSLSVYYVSNPLVNITTIGLIIVSGLGFIVWWDLWDKFRKVLRKELSPSRVFRVLRLQSKLVLTMTGILVFSGAFLVFIFESGNPSTLKGAPLGTKLMASFFQSVTTRTAGFYTMDQSLLSTPTVIISLLWMFIGGSPMGTAGGVKTTTIAVLILSIAAYLQGKKDVEVYGRRIRESYLRSAMVVAGTSVLILFTMTVLLSAVMPGVDLADVLYEITSAGATVGLSRGLTPQLNVAGKWIVILTMYLGRIGPLTLGTAVVMRVRNRPGSTTHLGEEDIMIG
1.5E-52	188	19	2.1E-52	187.7	13.2	1.1	1	A1KA53_AZOSB	Putative potassium uptake protein, membrane component	trkH1 azo3092	Azoarcus sp. (strain BH72)	442	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azoarcus, Azoarcus sp. (strain BH72)	62928	>tr|A1KA53|A1KA53_AZOSB Putative potassium uptake protein, membrane component OS=Azoarcus sp. (strain BH72) GN=trkH1 PE=4 SV=1MKTLLHPARAVALAFLVTILAGTLLLKLPLAHAEGSAAPWITAFFTAVSAVCVTGLVVVDTGSYWSWFGQGVILVLFQVGGFGMMTGATLLGLMVNRSLRLRTRLITQVETHSLGLGDISSVARLVFVVTIASELLIAALLTLRFHLAYALDWHEAAWSGLFHAVSAFNNAGFSIHADSLVRYASDAFVLLPVMTAIVVGGIGFPVLHDLRTRLRDPRHWSLHTKLTLCGTGILLAGGFVIVLAFEWDNPKTLGAMPVATRLLSAAFASVSARTAGFNSIDIGALTHESWALHYFLMFVGGGSAGTAGGVKVGTVAILLMLVVAEIRGHNDTEGFGRRVSSSAQRQAITVLVLGSGMVVLGTLFILRGTDFPTDQVIFEVISAFGTVGLSTGITADLPASGQLVLTALMYAGRVGTITLAASLALGERRMPYRYPEEHPIVG
1.5E-52	188	39.1	3.4E-52	187	27.1	1.4	1	R6GD99_9CLOT	Potassium uptake protein TrkH family	BN706_00909	Clostridium sp. CAG:557	463	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:557	1262819	>tr|R6GD99|R6GD99_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:557 GN=BN706_00909 PE=4 SV=1MGESEKKVPKTLKDMSPVRLIVSSFFAIIILGTSLLYLPIASKNMHPVNFIDAMFTATSATCVTGLTPFDTYSQWSTFGQVIIMLLIQFGGLGIITFTTGFTLFFRKKLGLRDMQIAKEYTSGSVLNLTRLIKTIIIWSLGCEIIGALLFAIRFIPQFGISKGIWISVFTAISAYCNAGFDIMGFIKPGSSFIEYATDPLVSLTASFLVILGGIGFVVVSDIYSCITRKIENPKTHPKLNLHSFIVITMSFTLLFIGTVLFMFFEYDRTLSGFNFFEKLNISFFQSTVARTAGFFTVPIGQEKTLTKLLTIILMFIGASSASTGGGIKTTTFVVILATLRSVVKGYDDTVILRHKVEKSTVYKAFSLTMLAFFLVSIVTAIIAVAEASKNITVLDITFETVSAFATVGLTTGITSALSTLSKIFIMLMMFIGRVGPISFIFSVSLMKDKNSAKVLPSSKIIVG
1.6E-52	188	18	3.6E-52	186.9	12.5	1.4	1	R6Q503_9FIRM	Trk-type K+ transport systems membrane components	BN792_00085	Faecalibacterium sp. CAG:82	461	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, environmental samples, Faecalibacterium sp. CAG:82	1262898	>tr|R6Q503|R6Q503_9FIRM Trk-type K+ transport systems membrane components OS=Faecalibacterium sp. CAG:82 GN=BN792_00085 PE=4 SV=1MLKRKKEKFNLRKQKGWLAGSSATQTICVSFLLVIAAGTLLLSLPIASKQGRLGLVDALFTATSATCVTGLVVVRDTWTQFTFFGQAVLLLLIQVGGLGLVTLTSFFALAARRRMGFRDLRLLGESVSAEGLSKATEVLKIVIRLAATFEAMGAVLLMFALVPQFGPEGIWVSIFTAISAFCNAGFDLFGRFGAYSSVVPYGNNYYVQAVIMFMIMAGGLGFMVWVELGEYRKRRRLSLQARVVLEFSLILWVLGALLIGLMEWNNPATMGGLSVPGKIMASLFQSVSTRTAGMNTIDLEACGPVTKLWMSILQFIGAAPGSTGGGVKVTTIAVVILTIRSVAQGRDDCVIHDHHIESKTIYRALTIIMLGAVAALGSAVVVYYNSAEAVTVIDAIFESCSAFGTVGLSVGVTGQLNTGAKLLYMLVMFMGRVGPVSLAISLTAKPDDNKRKVMPVGHINVG

1.6E-52	188	38.8	4.8E-52	186.5	26.9	1.7	1	A0A0E3ZBS3_9FUSO	Potassium transporter KtrB	VC03_05665	Sneathia sp. Sn35	444	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Leptotrichiaceae, Sneathia, Sneathia sp. Sn35	187101	>tr|A0A0E3ZBS3|A0A0E3ZBS3_9FUSO Potassium transporter KtrB OS=Sneathia sp. Sn35 GN=VC03_05665 PE=4 SV=1MKKIKLSPYVLILLSFIIMMFLGAFLLMLPISLNNGHIGNFLESLFTATSALCVTGLVVNDVHSTYTIFGKIVIMILIQLGGLGVLTFSSMVILSISSKMGYYTKKIVSEDINYNILTEIPRYLKQVSIMVFSIEFLGALILFIEFIRKMPIKDAIGYSIFHAISAFCNAGFALFSNNLEGYQSSLLINLCVTTLIILGLGFAAIIDIYNVFKGVRRKISNSTHIAINMTIILIILGTVLTFVLEYSNSLTLGSLSLKNKILASYFQSITLRTAGFQTINLSGITLPTIIIYIFLMFIGASPGSTGGGLKTTTLGVLLLGITNSITGREDIQYRRRRISWTTFNKACAILILSLSYILFMIFLMSIFDSKMGFLPLLFELVSAFGTVGLSMGLTAKLSVITKIILIITMYIGRVGPLTILYAVSRKRKQEGKYKYSEETILIG
1.6E-52	188	18.4	1.1E-26	102.8	5.6	2.1	2	R6ZQZ0_9FIRM	Trk system potassium uptake protein TrkH	BN699_01375	Firmicutes bacterium CAG:534	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:534	1263027	>tr|R6ZQZ0|R6ZQZ0_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:534 GN=BN699_01375 PE=4 SV=1MNKRKIISFMGKIILIEVFLMIPSLIVALSYGDGDAMAFIETMVPALILGVLLCRVRQSEQRISSRDGYFIVAAAAWIVISLIGALPLYLSGGFESYFGALFEIVSGFTTTGASVLAKPELLGHGVLFWRSFTHWIGGMGVLVFVLMVPMPMNNDNSMHLVRAEVPGPTAGKLVPRMRTTSMILYGIYAAMTLILILLLLAFGMQPFDTFCIAFGTAGTGGFAVSSAGIAGYNSLAIEIILGIFMLLFGINFNVYHLLLLRKFREAFSMEEIKVYLGIAAFAVVSITVNIAGMVGNVGTALRQAFFQVSSILTTTGFSTVDYEAWPEYAKHLIVFLSLVGACAGSTGGGFKVSRAIILVKSFFQEIHQIINPKEVITVRLDGKAVGGRTLESTRIYAATYMVLICIFTLILSLDGLDFTTNVTAVITCFNNIGPGLNLVGPMSNFSVYSDWAKVLLSFVMLTGRLEIFPMFLLFARSAHDR
1.6E-52	188	37.5	3.7E-52	186.8	26	1.5	1	A0A0D5ZJ79_9MOLU	Uncharacterized protein	VO56_00615	Mycoplasma meleagridis	547	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma meleagridis	29561	>tr|A0A0D5ZJ79|A0A0D5ZJ79_9MOLU Uncharacterized protein OS=Mycoplasma meleagridis GN=VO56_00615 PE=4 SV=1MKLRERWRLWKNRTKIGSFFNKCNFLWIKHVKNKKNLKFLFLVYIAIVVISSLLLWSPWTQNLSPSSGNTAISYIDAIFTTSSAFSDTGLVVKDTYKHWNIFGQAIIAILIFAGGVGIFALKIFIFNWIFRRKNISILEMKLLQSERGGTDSAKVGKLVISAVKFLVLTIILFGFILSVYFYFTDINTTSGIKEYLAKNGEIDANGVWLNSPKGDLAKAFRFGFFHTISAINNAGFDIMSGFSLMPYYTDYFVQICFITLFIIGGLGYPVLFDLKGYFSHKIKRKKSRYHFTLFTKLSLSVYFLVFLFGLATSLGFELTSTNIESMWNKLDSSGQNYFYGNVFNRLFGIFFTSFSTRSAGFFTVHLKDFSLGSTITFMIMMFIGASPASTGGGVRTTTIGVFLMSIFNMVVDKPRVRIFKRAIKKDTVDMSSKVLGIAFIIVIVACFICFSSFSDYGGKIITSASQADGTKVPIYGAEHILFEVASAFGTTGLSSGITASLNTASKITILIVMFIGQFGISSTLLVWKRKRNNHRSYEYAEDDVAIG
1.7E-52	188	6.9	7.8E-52	185.8	4.8	1.8	1	D0IW70_COMT2	Trk system potassium uptake protein	CtCNB1_4560	Comamonas testosteroni (strain CNB-2)	454	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Comamonas, Comamonas testosteroni (Pseudomonas testosteroni), Comamonas testosteroni CNB-1, Comamonas testosteroni (strain CNB-2)	688245	>tr|D0IW70|D0IW70_COMT2 Trk system potassium uptake protein OS=Comamonas testosteroni (strain CNB-2) GN=CtCNB1_4560 PE=3 SV=1MKDLLPVLRVLGMLMIMFAGAMLLPFGISWFTQDGIWRIYPWSIGLTVGVGLLLWGGLHRHKQDLQPRHGVILVTLVWVVLPLCAMVPLMMGLNRVGISISLTHAYFEAVSGLTTTGATVLSGLDKLPVSINVWRTFMQWMGGMGILILAVAVLPLLGVGGAQLFRAEAAGPVKDTKLTPRITETAKGLWGVYALFSIGCFLTFWACGMQPLDALMHMFATVSLGGLSSHDASFAYFNSPLLEAAALLFMLLASCNFALYFVAMRKGRIDSFMRDPEMRATIGVLLGSGLLVALLLWVKGVYGPLDALRNGMFHTVSVATTTGFSTTDYLSWPVFIPVLLLLLSGVATSAGSTGGGIKMVRMLILVKQARREMTRLVHPRAVQPVRLGDAVVDNPMIFSVLAYMLVYGATVIVLSMVLLLTDLDPLTAFSAVLASVHCMGPGLGPLGPHPTTRC
1.9E-52	188	29.6	2.3E-50	180.9	20.5	2	1	R6KXX7_9FIRM	Potassium uptake protein TrkH family	BN552_00613	Blautia sp. CAG:237	443	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:237	1262755	>tr|R6KXX7|R6KXX7_9FIRM Potassium uptake protein TrkH family OS=Blautia sp. CAG:237 GN=BN552_00613 PE=4 SV=1MPEKHKRKHLTSFQMIILGFAGVILLGSLLLMLPVSSAERVVTPFDQALFTSTSAVCVTGLVVQDTGSYWSGFGQAVILLLIQTGGLGVVTVAVSVFMLSGRKISLMQRSTMQDAISAPKVGGIVRLTKFILRGTFLIEGIGAVLLLPIFCRDFGIKGIWMSIFHSISAFCNAGFDILGTADNTFVSLSGYAGNFWLNIVIMLLIIIGGIGFLTWDDVYTNKLRFKRYRMQSKIILLTTAILIFVPAIFFFVCDFGQVSIGKRTLLSLFQSVTTRTAGFNTADLSSMTEVGQAIMILLMLMGGSPSSTAGGMKTTTVAVLLLNAFATFRSREDAGAFGRRFDSQVIKNAATIAMLYFVLFFFGGITISVYEGLSLQLCLYEAASAVGTVGLTLGITPGLHILSRLILILVLMYLGRVGGLTLIYAVVSRRNTNAKMPLEKITVG
1.9E-52	188	30.3	3.3E-52	187	21	1.4	1	B3PMQ3_MYCA5	Potassium uptake protein B	ktrB MARTH_orf452	Mycoplasma arthritidis (strain 158L3-1)	523	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma arthritidis, Mycoplasma arthritidis (strain 158L3-1)	243272	>tr|B3PMQ3|B3PMQ3_MYCA5 Potassium uptake protein B OS=Mycoplasma arthritidis (strain 158L3-1) GN=ktrB PE=4 SV=1MKSKSQNAKGSNFLFRFFKKIAVVQYIFMIYLIFVVLSSLLLYWPATHTANLKTIKPDFNYSDALFLAASASSDTGLTSLPIGYAFNEFGQAIIAICILVSGFGIFSLKVYIIQGLFGFRLSIFNSKITQVERGADTVGETKKIIKVSITILLITLFISSILFTIFFYTSPHGKFDNALANSTTDENVFNPYELAERNPYHNLTLSKYGIFHAISSLNNAGFDIIGKKKSLNPYYQDYLLQFFTMILFFIGGVGYPVIYDIWCKLKSLKKNARRHRFSLFTKLTLITYACVTLIGFFMTLIFEETAKNSRSFWNQGAYYGTFPKLFAIFFQTTSTRSAGFATVDYYHFTQQTLMLHGLLMFIGFSPASTAGGIRNITIAVIFLSIISTISGRKRIVAFKRQIGKEILIKAITIFAIGTFLIFMGTLLTFSLSDHVTLKNGTNEIDWTKKQFTAVHAFFEISSAFGSSGLSTGLTSHLNIWAKLIFILYMFIGQLGIQQTVLVWGNRNRKAEYYSYIYEDVTLG
1.9E-52	188	17.8	6.5E-52	186	12.3	1.7	1	D3R168_MAGIU	Potassium uptake protein, TrkH family	HMPREF0868_0601	Mageeibacillus indolicus (strain UPII9-5) (Clostridiales genomosp. BVAB3 (strain UPII9-5))	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Mageeibacillus, Mageeibacillus indolicus (strain UPII9-5) (Clostridiales genomosp. BVAB3 (strain UPII9-5))	699246	>tr|D3R168|D3R168_MAGIU Potassium uptake protein, TrkH family OS=Mageeibacillus indolicus (strain UPII9-5) GN=HMPREF0868_0601 PE=4 SV=1MNLGIIRLMLGRLLWIIAGLMVFPLFVALFYQESWHNLLALSGSIVLALLGGLVLRIKMPTNKQMFAREGFILCALSWLALSIFGALPFYFSGAVPSYVDALFETASGFTTTGASVLTNVEALPKSMAFWRSFTHLIGGMGVLVFILAILPANERHSSSIYLMKAEVPGPTFDKLLSKIKDTSRILYQIYLAMTMVLILLLMAGGMSLFDACIHAFGTAGTGGFSNYAAGVGSFHSPYIEYVLGVGMLLFGINFNLYYLLLLKQFKSVFKDEELRWFLSIVGIAVLLISGSLWSSYTDHWRMFRDVFFTVSSVISTTGFATVNFGAWPLFAQVILLGLMFFGSCAGSTAGGLKISRVALIFKSFSAEIKSTLNPNRIVRLKFNAKPVPAETVHGIHSYFVLYIIIFAAAVLLVSPYCNSLLTAVSSVAATLNNIGPGLDAVGPSANFAFFPTWPKLLLTLTMIIGRLEILPVILLFSPRAWKKGC
1.9E-52	188	24.1	2.2E-51	184.3	16.7	2.1	1	C0QQU8_PERMH	Trk system, membrane component	PERMA_1271	Persephonella marina (strain DSM 14350 / EX-H1)	482	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Hydrogenothermaceae, Persephonella, Persephonella marina, Persephonella marina (strain DSM 14350 / EX-H1)	123214	>tr|C0QQU8|C0QQU8_PERMH Trk system, membrane component OS=Persephonella marina (strain DSM 14350 / EX-H1) GN=PERMA_1271 PE=4 SV=1MSNLRFSIIYKFETFILFILSLVTFIPPLVYSLYLEDEEILTFLIPVLLALFLYSLSVPIKSHKLSEKEALFIAVSIWFIFPVFTALGYILSGYIHDPIDAYFESVSGFTTTGASILEDIEKLPESVLLLRSITNWIGGLGFAVFAVSFLSTRLPIGRAIVKFESSKIVEEKIEPRVKEVTKIVFLVYITLTVIEIILLKISGLSWYNSITYTFSTVATGGFAPENESVGAFNSFAVEIIISLFMIMGAINLQLYYVAYKKRSVIRFFSDQEVIVFLAIICGSVMFATAVLYLSGFYPDMYESFRYALFQIVSTATTTGFSSTDYSDWHPSVLSLMMILSLIGAVGGSTGGGIKIFRAILVYKTVKAELKKIAHPKAVYRITIKGKPLDVSTISMFWAFLSLYVATTVFFGFLLTLSGHDLVTSFSASIACITSLGPGLGDVGPASNFSAFNDFEKLALSFEMIFGRLEIIPVISMLFIKNI
1.9E-52	188	21.9	2.6E-52	187.3	15.2	1.1	1	R5N3E7_9FIRM	Trk-type K+ transport systems membrane components	BN514_00189	Ruminococcus sp. CAG:17	464	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:17	1262951	>tr|R5N3E7|R5N3E7_9FIRM Trk-type K+ transport systems membrane components OS=Ruminococcus sp. CAG:17 GN=BN514_00189 PE=4 SV=1MNLKKVSDGLHKLNTSQIIALGFAGVIFVGGFILWLPFCSAPGQAVTFPDAVFTAATSVCVTGLSTVVMAVQWSPIGKAVILCLIQIGGIGLIALANMIFISLRRKISLKNRRIIKESYNLDEMGGVVAVVRSVVKCVFLAEGIGAVLYAFCFVPEFGIKKGLVHAIFLAVSAFCNAGIDLFGETSLSVYVSNPLVNITTIGLIIVSGLGFIVWWDLWDKFRKVLRKELSPSRVFRVLRQSKLVLTMTGILVFSGAFLVFIFESGNPSTLKGAPLGTKLMASFFQSVTTRTAGFYTMDQSLLSTPTVIISLLWMFIGGSPMGTAGGVKTTTIAVLILSIAAYLQGKKDVEVYGRRIRESYLRSAMVVAGTSVLILFTMTVLLSAVMPGVDLADVLYEITSAGATVGLSRGLTPQLNVAGKWIVILTMYLGRIGPLTLGTAVVVRVRNRPGSTTHLGEEDIMIG

2E-52	188	34.9	2.5E-52	187.4	24.2	1	1	A0A0D6DYB7_9LACT	Ktr system potassium uptake protein B	ktrB2 LACPI_1779	Lactococcus piscium MKFS47	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Lactococcus (lactic streptococci), Lactococcus piscium, Lactococcus piscium MKFS47	297352	>tr|A0A0D6DYB7|A0A0D6DYB7_9LACT Ktr system potassium uptake protein B KtrB OS=Lactococcus piscium MKFS47 GN=ktrB2 PE=4 SV=1MKFFLIKSWSITRQITFSFALVILIGSVLLSLPISQYQNNYHTTYLDNLFNVISMVCVTGLSIAPISEIYNGIGQTISIILMQIGGLGLITL IAFGIFALQKKMNFAGHTLLQSALNRKDSKNLKEYLFFAYKTTIIIESLFGIIIMTDFIPRFGIKHGIFNSIFLTVSAFCNAGFDNFGSSSLNA FVLNPTINFSVSALIIFGGIGFAVWDDVIANLKRLFFSKPVGHGVFYKKLSNQTRLILQTTVIILFLGTLLTWYLEKDNPKTISNYTFPQQI MVSFFQTVTMRTAGFSTISFKDTFAPTNFIYMFQMIIGGGPGGTAGGIKVTTFAIAFLLIKSELVGQSLVTFSHRVIASKTVKQTISVLLFF FTILVIGYTLLLSFEPNLDPFSLLFETISAMNTVGVTMDLTSKLSTQGRIIIMLLMFIGRVGPITFLFSLIQKKEKNINYAETDILVG
2E-52	188	24.2	7.7E-52	185.8	16.8	1.8	1	R6QNV1_9FIRM	Cation transporter	BN563_00622	Eubacterium sp. CAG:251	492	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:251	1262886	>tr|R6QNV1|R6QNV1_9FIRM Cation transporter OS=Eubacterium sp. CAG:251 GN=BN563_00622 PE=4 SV=1MNYRSVFYVLGKIMNILALLMLLPLFVSFYYNMQGFKEAKYISFIIPIALLFLLGMILKCFKPSSVKIYAREGLVICGVGWILVSLFGS LPFIISGIIPNFVNAFFETTSGFTTTGATILNKIESIPKSILFWRSFTHWIGGMGILCFLIAVVPKSNSNSMYVMKAEVPGPTAGKVTPKISE SARSLYIIYSVMTVIEIIVLFFGSRITGDNLRLFDSVVTSFATAGTGGFSVLNSSILGYNSKFVEWVCIIFMFLFGVNFNLYYFLLTKRYKE AFMDEEFRTYVIINVTFVALITLNIMGTYPHISDAIRDSFFAVNTCMSTTGFGTADFDLWPTFSKIILLLAMCIGCSAGSTGGGIKVSRVVL YTKQIFRDLRLSTRPNTIIKVRMNKRVVDDKVIRGVNVYLVIYVSITVISTLLLSIEGYSITTCFSGVVACFNNIGPGLELLGPTKNFDFLSM GSKIVLIIDMLAGRLELFPIIVLFSPNTWRKAK
2E-52	188	8.7	2.6E-52	187.3	6	1.1	1	F4H0T7_CELFA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Celf_2056	Cellulomonas fimi (strain ATCC 484 / DSM 20113 / JCM 1341 / NBRC 15513 / NCIMB 8980 / NCTC 7547)	462	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Cellulomonadaceae, Cellulomonas, Cellulomonas fimi, Cellulomonas fimi (strain ATCC 484 / DSM 20113 / JCM 1341 / NBRC 15513 / NCIMB 8980 / NCTC 7547)	590998	>tr|F4H0T7|F4H0T7_CELFA H(+)-transporting two-sector ATPase OS=Cellulomonas fimi (strain ATCC 484 / DSM 20113 / JCM 1341 / NBRC 15513 / NCIMB 8980 / NCTC 7547) GN=Celf_2056 PE=4 SV=1MSAGFGEALTADSGAGPHRPWRGLHHPVRMVVVGFGLGVLVGTAVLALPLSRTGPGGADLLTALFTATSALCVTGLVVVDTA TYWSPFGQATILALIQVGGFGIMTLASLLGLLISRRLGLSTRMAAATETKSVGLGDVRRVLLGVARITLTVEAATALVLTVRFATTYRHP LAESVWLGVFHSVSAFNNAGFALFADNLVGFAGDPWVCLPVVGAVIVGGLGFPVVLEVLREHRHARRWSVHTRLTLLMTAVLLVGG TLFMLAAEWTNPHTLGALDPPARVLAGFFQAVMPRTAGFNSVDPGAMNAGTLLASDVLMFIGGGSAGTAGGIKVGTFAVLLLAILAEL RGAPDVELFDRRLSPATIRQALAVSLLGVAAVVSATLLIATTSRYSLDQVLYEVVSAFATVGLSTGITDDLAPGHQLVLVVLMFAGRLGP VTFASALVLRESGRLFRRPEGRPLIG
2E-52	188	30.4	6E-51	182.9	21	2	1	F5WRP9_ERYRF	Potassium uptake protein, TrkH family	trkH ERH_0373	Erysipelothrix rhusiopathiae (strain Fujisawa)	446	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Erysipelothrix, Erysipelothrix rhusiopathiae, Erysipelothrix rhusiopathiae (strain Fujisawa)	650150	>tr|F5WRP9|F5WRP9_ERYRF Potassium uptake protein, TrkH family OS=Erysipelothrix rhusiopathiae (strain Fujisawa) GN=trkH PE=4 SV=1MKRKFKKLTIPQYIALGFALTIFVGATLLSLPISSQSGHATNFLDALFTATSAVCVTGQVTLNTAEHWNYFGKTVIITLIEIGGLGFM SIIVMFFVFIGKRLNLRQRLIVREAINTDSLSDAQFLIRYIIRFSLTIQAIGAALLAIDFIPRFGLFKGIYFSVFHSISAFCNAGFDLFGDSLEG FTRNPLVILTIGGLIVVGGLGFIVWRDVLSYRRNRKLLMHTKITLITTLSILGVSFLLFWLSESRNGTFADLPFHMQLINYLFMAITPRTAG YANVNYATVSSMGIFVTILLMFIGASAGSTGGGVKVTTVATIVLFVRAKLRDEQTHFKNRSISHEKVEKALLIVFAGIIMVLLASLILLITETI PERYGIEYVLVEVFSCFGTVGLTMGLTPNLTVIGKIVLIVLMFAGRIGLLTFFLSFGGRAEKKEPLIRYPEGNVLIG
2.1E-52	188	33.8	4.7E-52	186.5	23.4	1.5	1	R6QTA4_9CLOT	Uncharacterized protein	BN621_00782	Clostridium sp. CAG:352	464	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:352	1262798	>tr|R6QTA4|R6QTA4_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:352 GN=BN621_00782 PE=4 SV=1MINEKIEGGFLKKIKSFTPIRLVVLSFVLLMLLGGLLLKLPFSSADGVSKPFIDCLFTATSATCVTGLSICDTFTGWSYFGQAVILVLI QCGGLGLLTFASAFTLIARKKLGLRDLQIVKEYTSGSITDIPKLIKIIMLMTFSCEIVGAILLSFAFIPKFGLLGIWISIFTAISSFCNAGFDLF GFIEPGKGMILFANDIYVSVIVMLLIVVGGIGFLVVFDLQKQIKEKITRKRKRIEVSYHSKIVLITTGILIVFGAIAFFVSECSNTLSGRGIAEQ INVSFFQSVTSRTAGFAAVDLSQVHDVTKFITVILMFIGASPVSTGGGVKTTTIVVIFATVISVLKGKDGTVFGKHKINQKVVNSAIAISVI SLTYILVITGFIAAIESEQNISMFNILLETTSAYSTTGLSASVTANLSIVSKLILVLTMLIGRVGPLALFLSVSGRKANPNGKILPEGKVIVG
2.1E-52	188	20.4	9.8E-51	182.2	14.2	2	1	R6AYG7_9CLOT	Trk-type K+ transport systems membrane components	BN491_00801	Clostridium sp. CAG:138	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:138	1262775	>tr|R6AYG7|R6AYG7_9CLOT Trk-type K+ transport systems membrane components OS=Clostridium sp. CAG:138 GN=BN491_00801 PE=4 SV=1MPEENIRRKRRLSSFQIIILGFAGVILLGALLLMLPISTTAGCVTPFNETLFTATSAVCVTGLVVQDTGSYWSAFGQAVILTLIQIGG LGVVTVAASFAMLSGRKISLMQRSTMKDAISAPKVGGIVRLTRFILRGTFLIELLGALAMLPAFCRDYGWRGVWMAVFHSISAFCNAG FDILGTENNLYPSLTGYAGSPGINITIMLLIVIGGIGFLTWDDVCENKWRFHRYRMQSKVILVTTFALIVLPALLFFFVDFDALPLGERIQA ALFQSITPRTAGFNTVTLSAMSGASQGVMILLMLIGGSPGSTAGGMKTTTLAVLVANAAATFRRRESAQFFGRRVDCGAVKTAATILM MYLALFFGGAAFISVYENLPLSACLYETASAVGTVGLTLGITPQLRIPSQIVLITLMYLGRVGGLTLIYAALSGKKATGAKLPQEQITIG
2.1E-52	188	25	4.9E-52	186.4	17.3	1.5	1	I1YVE9_PREI7	Cation transport protein	PIN17_A0427	Prevotella intermedia (strain 17)	464	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella intermedia, Prevotella intermedia (strain 17)	246198	>tr|I1YVE9|I1YVE9_PREI7 Cation transport protein OS=Prevotella intermedia (strain 17) GN=PIN17_A0427 PE=4 SV=1MSLCLFVSLWYKDNDIAAFLWAILITVVVGAVFRLMGRHANNTIGRRDAYFVVAVTWVIFSLFGTLPFLISGYIPNFTNAFFETMS GFTTTGATIVDYPEHLPKGLLFWRSLTQWIGALGIVFFTIAILPSLVGGSLKVFAAESTGPIKSKLHPRLSTGAKWIWIVYFVLTVACILS YKVCGMNWFDAFNYAMTSTATGGFGTESGSIATFHSPAEEYVCTIFCFLSGVNFTLLYTSVAGFKFKQLFRNSEFKFYTTMIAAFTVFI MLELIFQCNYEVEHAFRSSVFQVVSFITTTGLYSDDAAKWPHVTWVVLAACMFFGGSSGSTSGGIKSIRGVMLLKVVKNEFRQILHPN AVLPMKIDGYNVQMSKRVTLLGFIGLYLFLAVICAFTMIAAGIDSTNSMTITLSCLGNVGPTLGLEIGPTMSWNELPDFAKWISSFLMLV GRLELFSVLVLFTPSFWKEN
2.1E-52	188	10	3.1E-52	187.1	7	1.1	1	A6WFX0_KINRD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Krad_4246	Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	450	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Kineosporiales, Kineosporiaceae, Kineococcus, Kineococcus radiotolerans, Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	266940	>tr|A6WFX0|A6WFX0_KINRD H(+)-transporting two-sector ATPase OS=Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216) GN=Krad_4246 PE=4 SV=1MDVSSPRRPRIMRHPAQVVALAFAAVVVVGTSLLWLPVARRGPGAATFVEALFTAVSALCVTGHVVVDTREHWSNFGLVVILA LAQVGGFGIMTSASLLGVFASRRLGLRSRMLTATESRGLDLGDVRTVLLGVVRVSVVVELVTAVALSSRLLAGYDRPLTSALWEGTFL AVSSFNNAGFVLRGNSMTDFVSDPWMCLPVVAASLLGGLGFPVLLELRRQFRVPRRWSLHTRLTLATTIPLLLVGWVFLTLNEWSNP ATLARLDWWARPLAGLFQAAATRSSGFNSIDITQMNGGSWLVMDVLMFIGGGSASTAGGIKVTTFALLAVALYAEFRGEPTVSVFGR RVPDRVVRQALTVALVSVAAVVVATIVLVEMTRAPLDMVVFEVISAFATVGLSSGLLVQLPESGQVILAFLMFLGRLGPITLGAALALRE RTRMYEYPEGRPIIG

2.2E-52	188	17	1.7E-51	184.7	11.8	1.9	1	R5MZI2_9FIRM	Uncharacterized protein	BN514_01542	Ruminococcus sp. CAG:17	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:17	1262951	>tr|R5MZI2|R5MZI2_9FIRM Uncharacterized protein OS=Ruminococcus sp. CAG:17 GN=BN514_01542 PE=4 SV=1MNYSIIIYILGWIMNVEAVCMLVPGITALIYREKSGIAFLITILACLAIGVPLVSRKPSKKAFYSREGLVTTALSWIVLSIVGAVPFVLS GAIPNPIDAFFEIVSGFTTTGSSILSDPSQMPYSINIWRCFSHWIGGMGVLVFILTLLPLAGGYHMNLMKAESPGPSVGKLLPKVQSTA KVLYKIYIALTIALIIFLLLGGMPLYDSLCAAFGTAGTGGFGIKSDSMGSYSLYIQIVITIFMILFGVNFNVYFLLLTRKFSQALKSEEVRCYF FVIIASALMITFNVRHLFDNVWEALQQAFFQVGSIITTTGYATTDFNQWPAVSRTILVLLTFCGACAGSTGGGIKISRLLLLAKSVRKELH LYLHPNAVKKIKMDGKAVSHEVMRATNIYMIVYLMLMAVSIFLISFDEFDLVTNFTAVATTLNNVGPGLSLIGPTGNFGIFSPLSKLVLSF DMLAGRLELFPILILFLRETWKKF
2.2E-52	188	15.1	4E-50	180.1	10.5	2	1	D4JZB2_9FIRM	Trk-type K+ transport systems, membrane components	FP2_19520	Faecalibacterium prausnitzii L2-6	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii L2-6	718252	>tr|D4JZB2|D4JZB2_9FIRM Trk-type K+ transport systems, membrane components OS=Faecalibacterium prausnitzii L2-6 GN=FP2_19520 PE=4 SV=1MIQYPRYRRHRFSSFQVIIAGFAAVDLVGALLLMLPIAAQQRCVTPFHEALFTSTSALCVTGLVVQDTGSYWSAFGQSVILLLIQI GGLGVITVGAAFALLSGRKISLKQRSTMQEATAAPQMGGIVRLTGFILRITALFELAGAALLLPTFCADYGLRGIWYALFHSISAFCNAG FDLLGTEGAKFVSLTRYAGDPLLTTVIAALIIFGGLGFLTWEDICTYRLDFRRYRMQSKVILVTTAFLLVLPTLYFYCFEFTAGSARQRILL SMFQSVTPRTAGFNTADLAAMDSTSQALMVVLMLLGGSPSSTAGGMKTTTFAVLLANMWATFRRRDDAEFFGRRIDGSAVKNAATI AGMYLTLFFLGAFVIAAAEQLPMSVCLYETASAVATVGLTLGITPQLGVLSQGVLIALMFLGRVGGLTLIYAAFGSSPAHSRLPQEKIAI G
2.2E-52	188	37.4	3E-52	187.2	25.9	1.1	1	W5USG1_9MOLU	Potassium uptake protein KtrB	ktrB MYB_00085	Mycoplasma bovoculi M165/69	496	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma bovoculi, Mycoplasma bovoculi M165/69	743966	>tr|W5USG1|W5USG1_9MOLU Potassium uptake protein KtrB OS=Mycoplasma bovoculi M165/69 GN=ktrB PE=4 SV=1MKKAIYFWKKTGFLFSKIKTIQIIFLVYISIILIGAGILSTPIAQENKNNPVDFFTSLFTSVSAFSDTGLSLVNVSQSFNIFGQALIAILIL VGGTGFFAIKFYFFNLLFRKKLGLKSREILKIERSSNNIGELKNVIKTTVTFFLITILIFSLILTLHFYFYNPGENKLEPGNNPYKNVNLAFRY GFFHTISALNNAGFDIVGSSSFSPYYGDIFLQTTFIFLIIFGGIGFPVIYDFSQYFKQKLFFKNKTKMQLSLFSKICIIANFSITAFSFVLFLLF EETRNTIYWNTTSGNWFTKSYTLLFHSFSTRSTGFAFFDVNHLSQPSLFLTSILMFIGSSPSSTGGGVRVTTIWILFLNIIAKFRNHNQIF CFKRKIGSEKITTATFVIFVSFILCVALILFSSVYLNTINLANKNNPDYVDFQLGHVIFEVTSAFGTSGLSTGLIQHLNRGVQVGFMLIMLIG QLGISSSILMWKGDGVDRTSHSYISEDFVIN
2.3E-52	188	35.6	3.8E-52	186.8	24.7	1.3	1	E6U0F5_BACCJ	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Bcell_3158	Bacillus cellulosilyticus (strain ATCC 21833 / DSM 2522 / FERM P-1141 / JCM 9156 / N-4)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cellulosilyticus, Bacillus cellulosilyticus (strain ATCC 21833 / DSM 2522 / FERM P-1141 / JCM 9156 / N-4)	649639	>tr|E6U0F5|E6U0F5_BACCJ H(+)-transporting two-sector ATPase OS=Bacillus cellulosilyticus (strain ATCC 21833 / DSM 2522 / FERM P-1141 / JCM 9156 / N-4) GN=Bcell_3158 PE=4 SV=1MNLGMSKFLSPFRIIVFSYIIAMFVFSIFLYLPISAQPGVNVTYSEALFTSVSAVSVTGLTVVNVSETYSGFGVFILALAIQLGGIGV MTLGTFIWLVFGRKINLSQRMLIMVDHNQIAFSGLVNLMRGILFVALGIEIIGALILGTYFLNYFDTVGEAYYQGAFAALSAFTNAGFDVT GASLIPFVDDYFVQLVSILLIFAGAIGFPVLMELKEYFTSKDRSFRFSLFTKIAASTYFIVFGIGVVGLWIIEKNAFYDGLSWHQQLFFSLF NSATARSGGLATMDVSQLTLASLLFLSALMIIGASPSSVGGGIRTTTLAVMFLTIRSFALGRKDVKAFGREIHEEDRQKAFIVLSVFVVG LFTAIILVSAFEHSSELELMAIIFEVSSAFGTCGLSMGITPTLTLPSQITLMVLMLIGRVGLVAFLFSIRGREKTSHYKYPTERIIIG
2.4E-52	188	15.2	2.3E-50	180.9	10.6	2.1	1	F7V3N9_CLOSS	Putative uncharacterized protein	CXIVA_14020	Clostridium sp. (strain SY8519)	507	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. (strain SY8519)	1042156	>tr|F7V3N9|F7V3N9_CLOSS Putative uncharacterized protein OS=Clostridium sp. (strain SY8519) GN=CXIVA_14020 PE=4 SV=1MNKRIVFYTIGFILLIEAVLMMLPLVVSVIYREAAGRNAFLISALISAAAGGLMIMKKPKKTRIFAREGFAIVALAWIMLSVFGCLPFV ISGEIPNFIDAFFETVSGFTTTGSSILTDVEAMSHSLVFWRSFTHWVGGMGVLVFVMIIVPLGGESNMHLLRAETPGPTAGKLVPRMR DTAKILYGIYLVMTVVEVVLLCCGGMSLFDSLINSFGSAGTGGFSNWGDSIGHYNSEFFEVVIGVFMLLFGVNFSLYYLLLLKRVKAVF KSEELRWYLGIIAFATITIAVNIEHIYGSFHQALRYSFFQVSSIITTTGYSSADFNQWPQYAKTILVLMLMICGACAGSTGGGLKVSRVLILF RTARRGLKRLIHSHSVEAVRFERKGLEEGTISNCGVYLIVYCMIAIGSLVVISIDNFSYETNVTAMLSCLNNIGPGLGTVGPMGNFAGYS WLSKLVLSFDMLAGRLELYPILLLFAPSIWRQGPYSRRGRKRTARRRIKKAGRVMHEEA
2.4E-52	188	22.1	4.1E-51	183.4	15.3	2	1	E8UFM8_TAYEM	Trk system potassium uptake protein	TEQUI_0704	Taylorella equigenitalis (strain MCE9)	490	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Taylorella, Taylorella equigenitalis, Taylorella equigenitalis (strain MCE9)	937774	>tr|E8UFM8|E8UFM8_TAYEM Trk system potassium uptake protein OS=Taylorella equigenitalis (strain MCE9) GN=TEQUI_0704 PE=3 SV=1MKRFLYISHSLGVTIVCWSLTFLIPYVASIYFEDGWDRNFLYAFFIAFSIGSFLFALGYYFKRDLQLRDGLMLVVLVWFLFPALGTL PFLMPFHTESEFSLSFSKAYFEIVSAITTTGGTAISDVGSLPKSINLWRHTIMWFGGMGILLLAVAILPLLGVSGHQVSRTEASGPMKEE KLTPRIAGTAKVLYSIYISASLICFLAYRLCGMSWFDAWCHAGSTMSTGGFSTYTGGFTEMNNPAAEIVACVFMLFAGVNFATHYSAL RTRNFKAYFNCPEALPFLVLTLFSGLIISIFLYLAGYYLDFGTTLRKGLFNTISLATTTGYASADYSLWPIGLSLWMLVLGTFATSAGSTG GGMKIIRMVILIKQIKNEIRKILHPHGVFPISIKGNKISNKIVLSILLFFIIYGAILVLGSSLLVISGVDFHTAFTSIIANMSNIGPGLGETGPMG DYSGFSNFSLWVCSIAMLIGRLDIFTVLVFMSPHFWKK
2.4E-52	187	19.5	2.8E-25	98.2	4.7	2.1	2	R5E3U3_9FIRM	Trk-type K+ transport systems membrane components	BN462_00716	Ruminococcus sp. CAG:108	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:108	1262950	>tr|R5E3U3|R5E3U3_9FIRM Trk-type K+ transport systems membrane components OS=Ruminococcus sp. CAG:108 GN=BN462_00716 PE=4 SV=1MNKRLIVYILGWVLIVEGAAMQIATVTSFIYGEHEGFYFLGVGALSALLGLLAVKVKKPKNPVLYQKAGFAATALSWILMSFVGCF PFWLSGEIPSFIDAFYETVSGFTTTGSTILTDVEALSHGMLMWRSFLHWLGGMGVIVFLLAIIPRLGGQQNIFLMKAESPGPIVGKAVP KMRNYAMLLYGIYFGLTALEFIFLIVGKMPVFDALNISFATAGTGGFGVTNAGIASYSNYLQTVIAVFMMLFGINFSVYILILAKKFKQAFR IQELWVYFGIIVLSTALIAFNIRSLYPSAYDAVHQSFFYVSSIITTTGFGLTDVNNWPEFSKTVIMIITFIGAMAGSTGGGFKVSRVILLFKE TRKEFSLLIHPRNVKTVKMDGKAIDHNVMRSTSIFLVLYIGIFALSWLVLSLDKTDFVTSFTAVAANINNTGPGLGMVGPVGNYSEFSIL SKIILIFDMLAGRLELFPLMLLFAPSAWKKS
2.5E-52	187	33.3	4.6E-52	186.5	23.1	1.3	1	A0A0D3V4W3_9BACL	ATP synthase subunit J	UB51_01765	Paenibacillus sp. IHBB 10380	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. IHBB 10380	1566358	>tr|A0A0D3V4W3|A0A0D3V4W3_9BACL ATP synthase subunit J OS=Paenibacillus sp. IHBB 10380 GN=UB51_01765 PE=4 SV=1MKFHLKWLRFSPPQILVMGFAGIILIGTCLLMLPISNTTGKPLGFIDAFFTATSATCVTGLVVKDTGIFFSTFGQVVIMSLIQVGGL GIMTVATLFSLMLKRRISLRDRLLLQEAMNQSSMEGIVRLIRKVLLFSFIIEGTAAILTIRWAFDMPFGKALYYGVFHAVSMFNNAGFDL FGHFHSLTGYVYDPVVNFVVMFLIVSGGIGFIVLADIVDFRKNRKFSLHSKVVLSMTAALIIFGALVIFVFEFTNPRTLGSLNWGGKILGS LFQSVTPRTAGANTIDIAGMRQASQFFMIILMFIGASPGSTGGGIKTTTFTIIIVAVIAMMRGRDDIVLFRYRLAQERIFKALTVMLLALLLV IGVSMLLSTTEDTNFLMILFETTSAFGTVGLSMGITPELSVFGKVLISLTMFAGRLGPLTLAYALGPKKGKELYRHPEGKIIIG

2.6E-52	187	21.8	3.6E-52	186.9	15.1	1.2	1	W6AF K4_9M OLU	Potassium uptake protein KtrB	ktrB SCULI_ v1c013 30	Spiroplasma culicicola AES-1	549	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Spiroplasmataceae, Spiroplasma, Spiroplasma culicicola, Spiroplasma culicicola AES-1	1276246	>tr|W6AFK4|W6AFK4_9MOLU Potassium uptake protein KtrB OS=Spiroplasma culicicola AES-1 GN=ktrB PE=4 SV=1MDNLKNEPNNEVQDKKRIKKRKRKLVKVKRSKSLDNTEKTFFAKLKSWWPLSKISGKIIIGYLSAIIIGGFLLSIPGIMINKEHEWNF ITGIFTASSAISDTGINMVYTYSDYSILGQFLILAMIKIGGIGLLTFKIVLLVMFNKKVSLDDQSVAKTERGSGTLANTVEMIRDAFIFLTVVE ILGSFALFFGFYFTPPGETIEAGTFVSPYQSFSKSLWYGIFHSISAVNNAGFDIIGQQSLMPYNQEGVQAYHLQWIFMIQWIIGGLGYP TYHDIKRKIKAKKEGKQVRFSLFTKLNFVVYLTLFLIGPLLVFCSEYFTQEHSRIMEYVDENNNSTERHWKPWYVWSMDIIFNVTSCRN AGFSTVDVNDFTAGSKFIMSIWMFIGSAPSSTAGGIRTTTFAICIIGIVSIMKNKHSVEAFKKKIPDETVKRSFAVVFLSMLIIMTSIFIVYLD SNVMLTQTTDGNEGLPQDSENTIIRLILYVCSAFGTVGFQPFKPDQIIQMGVLSKIALILTMFIGQLGISNTLLAFVKPKNKQNFGYLEEE VTIG
2.6E-52	187	27.7	5.4E-50	179.7	19.2	2.1	1	R6MRT 0_9FIR M	Trk system potassium uptake protein TrkH	BN647_ 02029	Firmicutes bacterium CAG:41	480	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:41	1263021	>tr|R6MRT0|R6MRT0_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:41 GN=BN647_02029 PE=4 SV=1MNYRMIAYSVGRILVAVAATMLAPLGLSLFYGESIALAYVIPIVISILIGLCVSAKAPKNKSLYGRDGMFIVAIGWIVISIIGCLPFYISG QIPSFVDSFFETVSGFTTTGSSILTNVEALDKSLLFWRSFTHWLGGMGVLAFAMAIFSSKDTRTTHMMRAEMPGPVVGKLASRWQF SLRILYGIYIALTVIEFVLLLFGGMPVFDSLLHTFGTAGTGGFGIKNSSVAYYNSAYIDYVIGIFMMLFGLNFNVYFLIIARKFSQIKSNDEV KWYIGMMIGAAVIIALNIMPMYHGFGRAFRYSFFQVSSIMTTTGYSTADFVRWPMLSQIILVLLMVVGACAGSTSGGMKVTRFIILMKT ATHSIKKAVSPRSVFSVKVDGKTVEKNIVNGVLGYFVVYMLFAAVSILLISFDNKDFTTTVTAVIATMNNIGPGLGLVGPTGSFADFSAL SKIVMSIGMLVGRLEFYPILILFSPYAWKRT
3E-52	187	22.6	3.8E-50	180.2	15.6	2	1	R6JPL 2_9CL OT	Uncharacterized protein	BN486_ 03185	Clostridium clostridioforme CAG:132	457	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium clostridioforme CAG:132	1263065	>tr|R6JPL2|R6JPL2_9CLOT Uncharacterized protein OS=Clostridium clostridioforme CAG:132 GN=BN486_03185 PE=4 SV=1MNEKLFGKKPKHYRLKKHISQTQFIAYGFFLIIMTGSLLLMLPIASRDGQSEPFLNCLFTAASASCVTGLVVADTWTQWSLFGQM VLLVLIQLGGLGFISIGIFLSIVLRRKIGLKERGLMQESVNTLQIGGMVKLAKKIIIGTAIFEGAGAVILSCRFIPEYGLVRGTWYGIFHSVSA FCNAGFDLMGHTSQYISLCNYEGDWVVIGTISFLIITGGIGFIVWDDLSRKKLDFRHYMLHTKIVLVTTAVLLITSTILFYLMERGNILVGL NGSETFLACFFSAVTPRTAGFNNVDTAALTDGSKFLSAILMFIGGSPGSTAGGIKTSTLAVLLLYVHSNIRQTYGVEIFGRRLEDESIRQ SACILTINLGLMLAATIAIMVSQNLPMSDVFFETCSAIGTSGMSTGVTRSLNSFSRIVIILLMYCGRIGSLSFALAFTRSNRKPHVQLPAER ITIG
3E-52	187	8.7	2.6E-50	180.8	6	2.1	1	Q1AW J3_RU BXD	Cation transporter	Rxyl_1 271	Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)	478	cellular organisms, Bacteria, Actinobacteria, Rubrobacteria, Rubrobacterales, Rubrobacterineae, Rubrobacteraceae, Rubrobacter, Rubrobacter xylanophilus, Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)	266117	>tr|Q1AWJ3|Q1AWJ3_RUBXD Cation transporter OS=Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129) GN=Rxyl_1271 PE=4 SV=1MHPRIIANVLGAVVAATGAAMLIPAALSRLVSDGYAGAFFLPAAAALLAGTLTFALSRGRGAYLSIRDVFLMVVLGWVAVAIVGS GPFVLSGLMSPVEAFFNSMAGFTTTGVSTVKSAPPSLLLWRSMSQWVGGIGIVLLFVAVAPLVGFGAAQLYSAEAATPLTERLTPRIR DTAKVLVYIYAALTAGLAAALLVAGMGLFDAVNHALTTVATGGYSTRPGSIAAFDSPAVELVLAAGMILSGTNFALYFQAVRGRLREAL TNAEYLTYLALILSATAVMAASLYAFDYQDSPLRALRLALFQSASLTTGTGFSTADWDSWDPLSQGLLMVLMAIGGCAGSTSGGIKVV RALLLAKNALQDAFRMVHPRAVTALKLGRKVVPERLRASLLGFFFVYVATLVAGTLLMALHQVPLGAAFGSAFACLNITGVAPGPAGD PAFYAGLPATAQLVLCLLMLLGRLELFTVLVILTPAFWRG
3.3E-52	187	29.8	6.7E-52	186	20.6	1.3	1	F9UQB 0_LAC PL	Potassium uptake protein	ktrB lp_2177	Lactobacillus plantarum (strain ATCC BAA-793 / NCIMB 8826 / WCFS1)	452	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus plantarum, Lactobacillus plantarum (strain ATCC BAA-793 / NCIMB 8826 / WCFS1)	220668	>tr|F9UQB0|F9UQB0_LACPL Potassium uptake protein OS=Lactobacillus plantarum (strain ATCC BAA-793 / NCIMB 8826 / WCFS1) GN=ktrB PE=4 SV=1MIMRQLAHFKFFDTLSKKMVAGFIILILIGTVLLSLPWATPANVHTSLIDVLFTSASATCITGLTVVNTAAHWTTFGQLVILVLSEVG ALGYMTFAVLLFNIMRRQIGLSTQLMVKASLNLERLSDTKSVMKYVVGLSLLFQLGGLGLLAIDFVPRFGWRHGLYVSLYHAVMSFCN AGFDVFGDSLQGFRNDPYVLTVTMILIIAGGLGFLVWRDVLLYHTRKRLTLNSKLTLLTTFSLFVIGFVLLLITERDLELLPTGMSWVNRT INTLFLSVTPRTAGLITMPTQGLQAGSLLVIMILMFVGGTPGSTAGGIKTTTFGVLMFQSIAQLRGRRDVEFSHRRFSQENINRALMLIF LASIVLTVATLILTQTEKIPKGFGLEYVLFEVLSAFGTVGLSLGLTPNLTLIGKIVIMMLMFIGRVGIFTSLYALSRRQARVNLIRYPAENILI G
3.3E-52	187	26.1	5.8E-52	186.2	18.1	1.3	1	R5GHT 7_9PO RP	Uncharacterized protein	BN460_ 00228	Porphyromonas sp. CAG:1061	498	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, environmental samples, Porphyromonas sp. CAG:1061	1262916	>tr|R5GHT7|R5GHT7_9PORP Uncharacterized protein OS=Porphyromonas sp. CAG:1061 GN=BN460_00228 PE=4 SV=1MPFIDHNEYETKRGFNYKFVALVLGLLSLFQAIFLLICLGVSLHYHDDGFKALLTTIGLNFVVGLPLALYGKGQNSYDTGRREGMV TVTLSWVLTSLLGMMPYLLGGFIPNVSEAFFESMSGFSTTGASILTDIEALPRSILLWRSITQWIGGIGIIVFIVALVPFAGESASVVYDH ETTGITHDRFVPRIGVMAKWIMFIYIILSILCVLLLWAGPFTLYEAVCHAATCISTGGFSIYNQSIAEVNSDYIIIVLTIFMLFGATSFTLIYFA TVRKEPKKLFRDSEFRWFISIIVVISIASALWLYFGEYYTSFPQALEHATFQVVSLFSTTGYVIQDYNFWGAPFWIIALFLMFVAGCSGS TSGGLKTIRFSILTRNLLNEFTRRTHPQAIVPLRYNGTVVKDKVITQVYNFFYAYLTLSIIATFSISLEGYSFTDAVSASIACISSSGPGLSA FGPFSNYASLGDFNTFLLSFLMLVGRLEIFTVITLLHRSFWRN
3.3E-52	187	32	3.1E-50	180.5	22.2	2	1	D4MY6 1_ANA HA	Trk-type K+ transport systems, membrane components	CL2_04 880	Anaerostipes hadrus	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, Anaerostipes hadrus	649756	>tr|D4MY61|D4MY61_ANAHA Trk-type K+ transport systems, membrane components OS=Anaerostipes hadrus GN=CL2_04880 PE=4 SV=1MPWKIHKKRHLTSFQVIILGFAGVILFGALILMLPISSVQGIITPFHKALFTSTSAVCVTGLAVLDTGSYWSVFGQTVIMFLIQIGGL GVITTATAVFILSGRKISIMQRSTMQNAISAPKVGGIVRLMSFILKGTLLIELIGALFMMPVFCHDFGLRGIWMSIFHSVSAFCNAGFDLL GTKWHPFVSLTSYAVNPVINIVIMLLIIIGGIGFFTWEDIYLHKFHFKHYHMQSKVILTTTLCLILLPAVFFFFQDYGNLSGIHRLLASLFQA VTPRTAGFNTTDLSMLTGASKAMMILLMLIGGSPSSTAGGMKTTTFALLLLNVLATFQSCDDVTAFGRRIDASVIKNATTIAMMYFILFF AGGMTISVYEGLPLSSCLFEAASAVGTVGLTLGITPKLHILSQIILIILMYLGRVGGLTLIYAVFSDKNKRKAKLPLDKIIVG
3.3E-52	187	26	1.6E-51	184.7	18	1.8	1	A0A07 7AXE4 _9RICK	Trk system potassium uptake protein	ID47_1 1775	Candidatus Paracaedibacter acanthamoebae	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Rickettsiales genera incertae sedis, Candidatus Paracaedibacter, Candidatus Paracaedibacter acanthamoebae	91604	>tr|A0A077AXE4|A0A077AXE4_9RICK Trk system potassium uptake protein OS=Candidatus Paracaedibacter acanthamoebae GN=ID47_11775 PE=3 SV=1MIAFRSVLYLVGMLLNAMAAAMVIPMVAELFVYKTLGWEEFLFGFFLTGALGSLLAMANRSPGRIELKVREAFLMTALCWIITPLF AALPIYWSDLNLTYLDSWFEAVSAITTTGSTIIPDLGKTSKGVLLWRSILQWLGGTGIILMALIILPTLRIGGMQLFRSEFSDKSEKILPRV SQISSAITTIYVFFTVACFFALFVAGMQPFDALCHAMTTVSTGGLSTKNASLAFYDSLSIEIITIFFMVMGSLTFVLFIRLWHGNASALLKD SQVRAYLGILFWFIVIVFFWTWSFLGMSASKALRESIFSVVSMSTSAGFTTIDYTLWGSFPCVLLLLVSIVGGCTGSTAGGVKVFRLQV LVKVTQSHLRQLRRPHGVYIPIYQGQKIPESVASSVLTFTTLYLFTAFCLTSLLTLFDLGMMDAFSASIAALSNTGPGVTKLVGPTGSLS VLDNGAKLLLMFGMTLGRLELLTIFVLLMPSFWRS

3.4E-52	187	15.9	3.2E-50	180.5	11	2.1	1	A0A068SP87_RHIGA	Trk system potassium uptake protein	RG540_CH14120	Rhizobium galegae	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Neorhizobium, Rhizobium galegae	399	>tr|A0A068SP87|A0A068SP87_RHIGA Trk system potassium uptake protein OS=Rhizobium galegae GN=RG540_CH14120 PE=3 SV=1MNANLLRSVIYMTALCALYLSLAMFLPAMVDLYYGHRDWQVFAMSGFMVGGLGAAAALATHGPPPVFNKRLGFLLVNVLWAM FSVVGAIPLFLAEHELSFAQALFESISGITTTGSTVIVGLDTMPPGILLWRSLLSWLGGIGIVGLGLFVLPFLKVGGASIFKLESSETNDKP FARLASFTRAFLIVYVLLTLACTVAYDLAGMDHFDALNHAMSTIATAGFSTHDMSFAYFDNNALLVVGTVFLAICSLPFSVLILLAVRGRL DTLRDPQILVFLGYLCVISIAVAVYHHLRNGIELDDALIHSFFNITSILSTGGFASDDYTLWGPFAVLVAFFATFMGGCSGSTAGGIKAYR FVVMVNVIRAGLNKLIYPNAIYPVRYGSLTVDAETQRAVFLFVSLYIFLWVVGSIGMALFGYDVLTATSSVITALSNVGPGIGPIVGPVGN FSTISDPALYLLSLMMLLGRLEILTVLVLLTPVFWRH
3.4E-52	187	24.5	5.6E-52	186.2	17	1.2	1	F5LJ82_9BACL	Potassium uptake protein, TrkH family	HMPREF9413_1572	Paenibacillus sp. HGF7	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. HGF7	944559	>tr|F5LJ82|F5LJ82_9BACL Potassium uptake protein, TrkH family OS=Paenibacillus sp. HGF7 GN=HMPREF9413_1572 PE=4 SV=1MGKKRRILIRFTPPQILALGILAIILIGSVLLSLPAASSTGEPISYLDAFFMSTSAACVTGLSVLNAGVHFSLFGQIVILMLVQVGGLG FMTMATLIALVLRKRITLKERLLLQEAMNQGSVEGIVRLIRKVLTYALAIELAGAVLLTVRWAFDMPLGQAVYFGVFHSISIFNNAGFDLF SSLPGAQGSLMAYVNDPYVNIVVIGLMVLGGIGFIVIADLLDFKRTRKLTLHSKVVLTATGLLILLGSVVVFIFEYTNPLTMQPLSLPGKIF AAFFQSATTRSTGVNTLDIESFRQATQFFVIILMFIGAAPGSAGGGIKITTFAILIGAVITMVRGKEDIVFFRKRLPEERIYKATTLTLMSLIL VVTGTMILSVLQDGPFIKILFEVTSAFGTAGISLGLTPELTSPSKVLMAILMFVGRLGPLTLAYALTPKGTKELYRYPEGKITIG
3.4E-52	187	24	3.9E-50	180.2	16.7	2	1	A8GYG9_SHEPA	Trk system potassium uptake protein	Spea_0027	Shewanella pealeana (strain ATCC 700345 / ANG-SQ1)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella pealeana, Shewanella pealeana (strain ATCC 700345 / ANG-SQ1)	398579	>tr|A8GYG9|A8GYG9_SHEPA Trk system potassium uptake protein OS=Shewanella pealeana (strain ATCC 700345 / ANG-SQ1) GN=Spea_0027 PE=3 SV=1MLNYRPLLFILGIFLSTLTAFMLIPGAFALYYGEETVGAFMISSLAAGSAASFCMHQGQSRKLHLNIRDMFLLTCLTWLIVSLFAAM PFTLYHGINYTDAFFETMSGITTTGSTVLSGLDTMDHSILIWRSLLQWLGGIGFIVMAVAVLPFLNVGGMRLFRTESSDWSDKTTPRT QHMAKNLFIVYCLLTFLCFLAYHGSGMNWFQAINHAMTTLSTGGYSTSDQSMAAFSNEAHWVGTTFMLAGGLPLLMFVYMVQQRS VKVWNDAQVKGFLKFVAFVSCALALWLWSSRGIAPLDALRLASFNVVSVVTTTGYGLTDYTAWGALANIVFLFLMFVGSCSGSTSGG IKIFRFQIAGVIMREQLKQQFHPNGVFKERYNNHIVRGDIVRSLVTFILLFVLVIVLLSIILVLTGLDPVTSFTGAITAVTNVGPGLGSTIGPA GNFSSLPDVAKWALAIGMLLGRLEILTVAVLFHPSFWKY
3.5E-52	187	13.6	8.6E-52	185.6	9.2	1.8	1	B2UQA4_AKKM8	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Amuc_0806	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	582	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales, Akkermansiaceae, Akkermansia, Akkermansia muciniphila, Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	349741	>tr|B2UQA4|B2UQA4_AKKMA H(+)-transporting two-sector ATPase OS=Akkermansia muciniphila (strain ATCC BAA-835 / Muc) GN=Amuc_0806 PE=4 SV=1MTTTRSGFTKLAAVCIAILLGAVVWELGWPLTRAEHEWSRLIAAVATLGHLTGILGSYFRKEINRPSLRLLIFQIISCLMIFLLIARE QQEAGYMRFTELSRLVITAGLIAIPTLMSLTRIFEWLVGKQKKGRPLMAPAMQFVASLGVVILAGTGLLLLPNSTYPGITLSFTDALFTS TSAVCVTGLNAVDFAHTFTPLGEMFTLALIQIGGFGIMTFAYFVAMMAGQGFSLRDRVLLTDLLDEDNLGAVVSFITTIVVSTLFIELCG AVLLYFSWEGKDINLMGEPLWWHSLFHSVSAFCNAGFSTFPMNLMEPGIRLCYSGQAVIMALIVCGGLGFGIYKEINSRLANRFFSKH RRLHMQWTPYFKLVMISTGILLAGGALAIFAVSSPHAAEPLGEHLWICLFDSVTARTAGFNISDYGRYLPAASLIMCGLMMVGGSPGG TAGGMRTTTCAIAGAEILRILRGRDHVEFFRRRIDQRTVARCVITVVVSCAWIGCFTVLICALEPSMSSLDIFFENCSAFATVGVSRGIT PDLSGPSKYLLIVNMLAGRVGLFAFLIALAGTPTPRHYRYPSVKIPLT
3.7E-52	187	17.7	1.2E-51	185.1	12.2	1.7	1	U7L7X8_9CORY	Uncharacterized protein	HMPREF1281_01127	Corynebacterium sp. KPL1855	473	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium sp. KPL1855	1203562	>tr|U7L7X8|U7L7X8_9CORY Uncharacterized protein OS=Corynebacterium sp. KPL1855 GN=HMPREF1281_01127 PE=4 SV=1MIFLRGVPPRSSAWGWTGLYFRFVKRLLFLRQWGPARLTATGFLLLILIGTALLLLPFAEAGDSRASFLSALFTATSAVSLTGLVV VDTGSFWSPAGQVVILALIQLGGLGIMSLASLSGWLLTGRISFKARKTGAYESRPILAGGIRRTLIFTFAFTALVESIIAAAVTARLMVGY GHSFPRALWEGIFHAISAFNNAGFSTNSDNLVPFVGDAWILLPLAGAVIGGGLGFPVWAELMRHMRRGSEAMRRISITARMTLAATG VLIVAGTIFFALTEWSGVLAPMTWGDKLLNAFFASVSPRTAGFNTFDYGEAHPVTLMGTDILMFIGGGSAGTAGGIKVTTACVLLAAM AAEFLGKEKTSIYHRSLPHSVTRQALALSFAGVLVVVTLGVAALRFFDPQFSGDQVSFEVMSAFATVGLSTGITASLSAPSQIVLCFIMYL GRVGPTTLVAALAAKNLSRRYSYPEERPFIG
4.3E-52	187	13	1.4E-51	185	9	1.6	1	D2Q2L6_KRIFD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Kfla_1093	Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Kribbella, Kribbella flavida, Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	479435	>tr|D2Q2L6|D2Q2L6_KRIFD H(+)-transporting two-sector ATPase OS=Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399) GN=Kfla_1093 PE=4 SV=1MKWRHPGQLVVAGFAAVTAVGTMLLMLPVASTTGESTGVVPALFTAVSAVCVTGLIVVDTPTYWSGFGEGVVLGLIQIGGLGV MTLASVLALLVARRLGMRLQLSAQAETKALGLGDVRQVVGGVIRLSLAVEVVIAILLALRFGLGYGESFGRAVYLGVFHAVSAYNNAGF ALYSDSLIGFATDPFICFPIMAAIVLGGLGFPVVLELLRRRRREWRGRPWSLHTRITLATYGGLLVVGTVAVTVVEWRNPATLGALELH HRLLVGLFHGVMPRTAGFNSLDVAQLEPTTLLVNDVLMFIGGGSAGTAGGIKVTTFALLAFVMLAEIRGEPTVHVLNRRLPGQVQRQA LTVALLGVGTVMAGTLALLAMTSFKLDDVLFETVSAFGTVGMSTGITAKLPVAGQFVLMALMFIGRLGPVTLASALAIRDRPRRYELPE ERPVVG
4.5E-52	187	20.9	8.1E-52	185.7	14.5	1.3	1	I5AWC4_EUBCE	Trk-type K+ transport system, membrane component	EubceDRAFT1_2363	[Eubacterium] cellulosolvens 6	458	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium cellulosolvens, [Eubacterium] cellulosolvens 6	633697	>tr|I5AWC4|I5AWC4_EUBCE Trk-type K+ transport system, membrane component OS=[Eubacterium] cellulosolvens 6 GN=EubceDRAFT1_2363 PE=4 SV=1MSLNQKGIKLAPVQIIPASFFLAILAGTILLMLPVSSASGRGTDVLTALFTATTSICVTGLVVVDTFAHWSFFGQLVILALIQIGGMG MIAMASTIMLLTRKKFSLKDRMLLRDAFNLNSDNRVLRFLVRVIKGTLLVEAAGAVLYCFVLIPEFGVKKGIWCSIFNSVSAFCNAGMDV MGGNSLGNYRSNPLFMTVTIALIVFGGLGFAVWFDVLGRMRDGFRRNFSPVTVIKRFSEHTKLVLSFTIFLLLAGTLIIFFLEYDNPGTI GGFGLGGKLANSFFESVTLRTAGFTTFPQENMRDASCMVAYILMFIGGSPIGTAGGIKTTTFFLLIMNVRSYLRNQDENVVFHHRVSE ESMRKASAIVFVSAGAVMLFTALLCIVNPVPMEDALYEVVSACGTVGLSRGLTPSLNALGRLTIIVAMYLGRIGPISLVALFAGNGADAN KIRYSEGKFYVG
4.9E-52	186	22.4	2.1E-50	181	15.5	2	1	K1LN25_9LACT	Uncharacterized protein	HMPREF9706_00134	Facklamia hominis CCUG 36813	482	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Aerococcaceae, Facklamia, Facklamia hominis, Facklamia hominis CCUG 36813	883111	>tr|K1LN25|K1LN25_9LACT Uncharacterized protein OS=Facklamia hominis CCUG 36813 GN=HMPREF9706_00134 PE=4 SV=1MNKKLVFSFIGKLCFIEALLLILPMVVAVIYRENWLNLQAFLITIIILIVVSFLSYQLKPKKNGYTLKEGLAITSLSWFALSFFGAPFV FSGQIPSLVDACFEMASGFTTTGSSILENVEELSQSMLFWRSFSHLIGGMGILVFAFAFAPQQGEGSVNIMKAEVPGPQFGKLVAKNK NTARINYRIYLGMTLIFIILLWLSGLNLFDAMIHAFGAAGTGGFSNKALSIAHFNNPAVEYILSIAMLLFGINFNLYYFLLNKQFKTIFKNEE FRLYLGLVLISLILIMINISTNYHHVEPLFRDSLFTVTTIVSTTGYATVDFDQWPLINKLIIMLLMFTGSMAGSTAGGIKISRLLVYLKTIKREI KLAIQPRRVFPLTIDRNPISEAFIKQTFIYLGTYVLIFITGLLLISFDRGDFLTDFSAVSATLNNIGPGFSGVGPRMNFSEFNDFSKIVMTVL MIIGRLEIFPVLILINTSIWKKR

5E-52	186	11.3	3.8E-49	176.9	7.8	2	1	R6HW78_9FIRM	Uncharacterized protein	BN490_01228	Firmicutes bacterium CAG:137	479	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:137	1263004	>tr|R6HW78|R6HW78_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:137 GN=BN490_01228 PE=4 SV=1MNKQMIRYVLGLVLLIEGALLLLPLAVALLYQETTWKHFGLTIAVCLILGGCMIIRKPRRRTLFPKDGFVIAALTWIVISLVGALPFSLSGQIPRYIDALFEVISGFTTTGSSILPRVEALDKGMLFWRSFSHWIGGMGILVFMLALLPAMGGATIHILRAESPGPNVAKVVPKIRESAKITYLIYLALTLLLVILYLAGGMPLFDSLCIAFGTAGTGGFAVRTSSCAEYTPYIQTVTTIFMALFGVNFTVYFLLLQRKFRQALHSSSELWTYVGIILTATLAISVNIYRSMPSFGQAVHHAAFTVSSIITTTGYGTLDFNLWPEFGRVILCFLMIVGACAGSTGGGFKVSRIVILCKYAKNELERLIHPRTVKVVKVDGKQVSKETVHGVLVYTLFYILIAMASMLLVSLDNFDASTTISSVLATLNNIGPGLGAVGPAASFAGLSDLSKAVLCLDMLAGRLEIFPLLVLLLPSTWAKK
5E-52	186	15.6	3.2E-50	180.4	10.8	2.1	1	R5L6Z7_9FIRM	Cation transport protein	BN508_01657	Eubacterium sp. CAG:161	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:161	1262881	>tr|R5L6Z7|R5L6Z7_9FIRM Cation transport protein OS=Eubacterium sp. CAG:161 GN=BN508_01657 PE=4 SV=1MNYKVMGRFISKILAVEAVFMTPAMLISVFDKEYKAFISFVLSILIIMAVSALLFVLGRKAKQRFFVKEGLACVGLSWIAISLLGCLPFYISGEIPHFIDALFEMVSGFTTTGSSILPEVETMSRGMLYWRSFSHWLGGMGVLVFLLAVTPANGRSNRFTLHLLRAESPGPNVEKLAPRMRDTAMILYMLYMALTVINVIFLLLGGMSLFDSVCTAFGTAGTGGFGIKNDSMAGYSPYIQNVCTIFMLLFGVNFSCYYLLLLRRFKTVLKDGELRLYLGLVVASITAITINIYHMFGSIGEALHHAAFTVASIITTTGFATVDFDKWPEFSKSIIVVLMMIGACAGSTGGGFKCGRLLLLKSIRRGIRKTLNPNKVEVIRNNGNAVNEKVISGINIYVATYFIIIFGSFLLIAVDGFSIITNFTAVLSCFNNIGPGLDQVGPTCNFGLFSDFSKIILIDMLAGRLEIYPILILFSRDVWSFKR
5E-52	186	25.3	5.9E-51	182.9	16.6	2.2	1	R7KSS8_9FIRM	Trk system potassium uptake protein TrkH	BN622_01249	Ruminococcus sp. CAG:353	488	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:353	1262955	>tr|R7KSS8|R7KSS8_9FIRM Trk system potassium uptake protein TrkH OS=Ruminococcus sp. CAG:353 GN=BN622_01249 PE=4 SV=1MAFALAKAATHMNFKMILNILGWILIFEALFFLVPIITAVVYGEAVLADFLISAGLCLICGGLLIMKKPENKALYSREGYVIVSLSWIVLSLFGALPFYISGVIPNFVDALFETVSGFTTTGATVLGEVETLPKAILIWRSFTHWVGGMGVLVFIMAFVPLSGGQNMHIMKAESPGPSVSKLVPRVKTTAMILYSIYFVLTFAEFIVLLIGGMRAFDALNTSFSTAGTGGFGFRNDSFASFSPALQIIVTVFMLIFSINFSSYYLLITGKLKEAFNSELKVFALIVISAITVITLNIRHLFPSVGDALRNASFTVASIVSTTGFSTADFDMWPELSRTIIVLIMFIGACAGSTGGGIKVSRIIILFKSMAKELSVMIHPKQVRKITVDSHAIDHETVRSVNVYMVCYIMVFVISMGVMSFDNYDLITNFTAVAATLNNVGPGLEMVGPIQNFGFMSSPTKLILIFDMLAGRLELFPMLLLFAPATWKK
5.5E-52	186	24.2	7.4E-52	185.8	16.7	1.1	1	D4M080_9FIRM	TrK-type K+ transport systems, membrane components	RTO_30360	Ruminococcus torques L2-14	468	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, [Ruminococcus] torques, Ruminococcus torques L2-14	657313	>tr|D4M080|D4M080_9FIRM Trk-type K+ transport systems, membrane components OS=Ruminococcus torques L2-14 GN=RTO_30360 PE=4 SV=1MYGFYIDEDRRKARRAKWNTVRIISIGFFGVILLGSLLLWLPFSNHQPIRYIDALFTAVTCVCVTGLVTVVPAAQFTVAGKVILLILIQIGGLGIIACTTAFLILVGKRINMKERVVIQEAYGLSTLQGMIRFIERVLWGTFLVEGIGAIGYSFQFIPEYGVAKGIFYSVFHSISAFCNAGVDILGDSSFTRYVNTPVITITTTMLVILSGLGYPVWIDLAKNIKMTIQSKGKRPVGRTITRLSLQSKIVLTMTLFLLTLGTVGFYLLEHHNPATMGTLNAAGKFQAAFFQSVTTRTAGFASISQSGLTNGSKLLASMLMIIGGSPAGTAGGIKTTTVAVLLLTAISVLRGNKDTECYGRKITFEIIRVGITITLVTFVFWLFGVTVMTVIEPQQKVLDLMFEATSAMATVGLTADLTPVLSDISHVVLMLMMYIGRIGPMTMALIFSGHVDKKNQFRTLPEAKIMVG
5.6E-52	186	1.4	7.2E-52	185.9	1	1	1	S3D711_GLAL2	Uncharacterized protein	GLAREA_06603	Glarea lozoyensis (strain ATCC 20868 / MF5171)	271	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Helotiaceae, Glarea, Glarea lozoyensis, Glarea lozoyensis (strain ATCC 20868 / MF5171)	1116229	>tr|S3D711|S3D711_GLAL2 Uncharacterized protein OS=Glarea lozoyensis (strain ATCC 20868 / MF5171) GN=GLAREA_06603 PE=4 SV=1MARNHGLHPKIPSQSIHPSLFPSTPTWYLLLVLLILNGIDFISFEALNHSNPTFNALSPAHRNLDGLVQTIFIRSAGFTVISISSLRIGLQALYVPMMFISAFPVAITMRSSNVYEERSLGIYASQLRAQAPNTTESASLLSRSSRTRLYFLRQQLAHQLSHDFWFVVICAIAVIWIETASYERDPLTFSVFNILFEVISAYACVGLSIGLPDQNYALSGAFHTSSKVILCFLMFRGRHRDLPVAIDRAVQLPDSILGTRGEEEGAEVGRV
5.7E-52	186	24.9	1.7E-51	184.7	17.2	1.6	1	H6N9C3_9BACL	K+ uptake transporter protein	PM3016_990	Paenibacillus mucilaginosus 3016	441	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus mucilaginosus, Paenibacillus mucilaginosus 3016	1116391	>tr|H6N9C3|H6N9C3_9BACL K+ uptake transporter protein OS=Paenibacillus mucilaginosus 3016 GN=PM3016_990 PE=4 SV=1MVGNKSFITPPRILAAGFALIIAVGTFLLALPAASQSGQRIPLMDALFTAVSATCVTGLVVMDTGRTFSLFGEIVILVMIQLGGIGFMTTATWIALALRRRISLRDRLVLKESLNQDSVEGIVRLIIKVFIYAFTVEAGASLVFAAQWAEEVPWKQALYYGVFHAVSLFNNAGFEIIGGFVPYVHDVGINFVSMFLIVAGGLGFIVMSDLVDYPRTRRLSLHSKVVLSVSGLLTLTSAVIFLVFEFANERTLGPMALEDKLLVSVFHAISLRSGGINTVDIAGLHAATQFMMVIMMFIGAAPGSTGGGLKITTFALLVGAVRAVLTGKEDVVLFRYRMPKRLIQKAVTMALIAVGVIVSATMILLTLQDRDFMTVLFEATSAFGTVGLSMGLTPELTPAGQGVIILLMFVGRVGLVTLAFALQSRPPKELYRYPEGRIIIG
5.9E-52	186	24.4	6.6E-51	182.7	16.9	1.9	1	R5SSG3_9FIRM	Trk system potassium uptake protein TrkH	BN540_00237	Dialister invisus CAG:218	482	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Dialister, environmental samples, Dialister invisus CAG:218	1263072	>tr|R5SSG3|R5SSG3_9FIRM Trk system potassium uptake protein TrkH OS=Dialister invisus CAG:218 GN=BN540_00237 PE=4 SV=1MNTAVVSALIAKLTAGCGLVLLLPLLTALFWEEPVLPFIYSMALCFLLAAFLRYKGKKKVINLNPRDGLAVTALSWICISILYLFPYFLSGLLSPLDALVESISGLTGTGATIFADLTVLPKSILFFRSLTHWLGGLGIIVIFVALFPQAGKGSARMIDAESTGPYSSRAVPRIKEMAKALFAVYLLFTVSAALIYTLLGMNFFDAVNHAFSTIATGGFSTKNESIAFYGSTPLKLSVIFFMVISSANFGIYVAAWKRGIRVLWENTEFKVYLSIVAAATILISLNLMLESGLYAPSALLEALFTSASLSSTTGFISYDFETWPHFSQVILLLMFIGGCGGSTSGGLKVTRIILLFKSMTAVLRQKLHPRAVIQTRAGGENFSESMLLEVFCFFFIYTMSIFLWTALIAASGADIPSALGLSIATMSNSGPALGQFGATCNWSAMPAMTKMVVALSMLMGRLESFTLLILFLPSFWRKNGW
5.9E-52	186	11.7	5.9E-50	179.6	8.1	2.1	1	D7CXF1_TRURR	Cation transporter	Trad_0133	Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24)	483	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Trueperaceae, Truepera, Truepera radiovictrix, Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24)	649638	>tr|D7CXF1|D7CXF1_TRURR Cation transporter OS=Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24) GN=Trad_0133 PE=4 SV=1MRGRFTIYVQGVGLLGLAGLGLVFATYAWLSAEPTDGFLAMALLSGALGGALLGLGRSDADPGRRESLIGVLLLWLLLPLLGGVPFAVTLELSVLDAVFESMSGFTTTGATMLVSFAEVPASLFMWRALTQWLGGVGIIVIFIAVFPPFGVAGRQLFFAEVPGPTEERLTPRLRNTAAAVLLVYLLLTLLCGLSYAVAGMSRYDALLHALTTIASGGFSSHPLSFEGFSPAQNWVAVLFMVFAGANFALQYQLVVGRPLALLRDREFQTYLAIVGVGGLLLTLTLWELYTPIEALRHGMFQSLTMVTTTGYASADFVRWPLPAQATLVLLMFVGGSAGSAAGGIKVIRWLILVKATAVELRRTLHPRVVKPVMVGRRVVREEVIRAVAAFITLYLLLFAATTWTVTVLGEDFTTALTAAVACIGNIGPGLGAVGPMANFAELHPVSKGLLTFGMYAGRLEVVTVFVLLNRDFWYLPRKKGARY
6E-52	186	17.7	6.9E-51	182.7	12.3	2	1	R5QVM5_9FIRM	TrkH family potassium uptake protein	BN521_01318	Coprobacillus sp. CAG:183	479	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:183	1262853	>tr|R5QVM5|R5QVM5_9FIRM TrkH family potassium uptake protein OS=Coprobacillus sp. CAG:183 GN=BN521_01318 PE=4 SV=1MNKKMIVFTIGKLLTITGLLMFMPVIVSLIYQETEGVYYAILGIIMLALGILISRKAPRKKNIYAREGFAIVALSWLLISLLGAIPFCLTGEIPSYVDAVFETVSGFTTTGSSILSNVEALSHTSLFWRSFTHWVGGMGILVFVIAFIPIASGRSLHILRAEVPGPVVGKLVSKVRLTARILYVIYAIMTVIEIILLLFGGMPLFDCILNAFGTAGTGGFGIKNASIAAYDSAYIDGVITVFMILFGINFNLIYFFILGRIKEVLKSEELRWYLIIIVAAIALITINILPLYDSILSAFRYSSFQVGSIITTTGFVTADYGQWPVFSQVILLSLMFVGACSGSTGGGIKVSRIVIYFKNARNELHKLLLHPHSVRAVEFENQPVEDNVIRTIHAYLVVYITIFALSLLILTFLNLDFKSAFSAIASCLNNIGPGLDVVGPVSNFGSLPDVSKIVLTFDMLAGRLELFPMLLLFSPSLWRK

6.3E-52	186	22.4	8.4E-52	185.7	15.5	1.1	1	Q1WVM8_LACS1	Potassium uptake protein ktrB	ktrB LSL_0068	Lactobacillus salivarius (strain UCC118)	462	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus salivarius, Lactobacillus salivarius (strain UCC118)	362948	>tr|Q1WVM8|Q1WVM8_LACS1 Potassium uptake protein ktrB OS=Lactobacillus salivarius (strain UCC118) GN=ktrB PE=4 SV=1MYGRRKMRTRQGLSRIQIITLSFLLAIMIGSLILMLPIMSANGESTDFVDALFTATTSVCITGLVTVTTATHWSSLGHIVILLLIQLGG LGTITLMSLAFFATGKRISLQNRLLMADAFNLDNNKGIVNFVIRVIKESLMIEGLGAIAYSIYFIPHFGFLTGSWYSIFHSVSAFCNAGIDLL ADNSLIAYAGNWWLNIVTMLLIVCGGLGFTVWNELIKGFVNQYRYYKNGRGKRLKNTLSQHTKMVLTTTFALIFGGAILYYLFERSNPN TLGSVKNSQAMLEALFQSVTTRTAGFVTIPQANLTIPSVMLTVFLMFIGGSPTGTAGGIKTTTLAVILAEVRATIKGEPEAICFKRQVPR QTTRKAIAITLISVAASVLAVLLMYFIQPGDMTDNVFEVYSALGTVGISRDLTPHLTTVAKYLIIVCMYLGRVGPISILLALMRRKHHANLK YAPGNIRVG
6.3E-52	186	28.4	8E-52	185.7	19.7	1.1	1	Q8DY63_STRA5	Sodium transport family protein	SAG1630	Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R)	459	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus agalactiae, Streptococcus agalactiae serogroup V, Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R)	208435	>tr|Q8DY63|Q8DY63_STRA5 Sodium transport family protein OS=Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R) GN=SAG1630 PE=4 SV=1MKHFFDYKTMSVARKLSISFIAVILLGSILLSLPIFQYANAPKTHYIDHLFTTVSMVCVTGLSVFPISKVYNGWGQIVAILLMQTGGL GLVTLMSLSYYTLRRKMSLNDQTLLQSAITYNSSTDLKKYLYMIFKVTLTLEVLAASILAIDFIPRFGLGHGIFNSIFLAVSAFCNAGFDNL EATSLAQFKLNPLVNIIVCFLIISGGLGFAVWKDLIEATIQTSHKGPKLIKTFPKRLSNHSKLVLKTTTIILLTGTLLSWLLEFGNFRTIANLS LPKQLMVSFFQTVTMRTAGFSTIDYTQTDFATNLVYIIQMLIGGAPGGTAGGFKVTVIAILLLLFKAELSGQSQVTFHYRTIPSSIIKQTLS ILTFFFIILISGYLLLLELNPHIDPFSLFFEASSALATVGVTMNTTNQLTLGGRIVIMFLMFIGRVGPITVLLSILQKKEKEIHYAETEIILG
6.4E-52	186	41.5	2E-50	181.1	28.8	2	1	U5S7D4_9LACT	Uncharacterized protein	Q783_01840	Carnobacterium sp. WN1359	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium sp. WN1359	1266845	>tr|U5S7D4|U5S7D4_9LACT Uncharacterized protein OS=Carnobacterium sp. WN1359 GN=Q783_01840 PE=4 SV=1MNKIILKGYLKQSTSRLNPSMTVVTSFFILILMGTVLLKLPIATTQTISWIDTLFTATSAVTVTGLIVVDTGTAFTLFGQTVIMFLMQL GGLGLMTSAVFIFFIFKRKIGMQQRNLIKTSLNQDSSGGIIRLVRYLLFFSFSIELVGFILLAIKWIPEFGLKKGSFYSLFHTVAAFNNAGF SLWSDNLSNYVGDPVVNLTITSMFILGGIGFTVLLDVWNKKKFKSLTLHSKVMIVGTLVINIIAILSIFILEYSNPQTLGNLSFGDKVWGAY FQGLTPRTAGFNSIDITALTVPAMLLTVLLMFIGAGSASTGSGIKLSTFIILLLTTITTLKGGEEVSLFGRRIKSNAVLRAFTLTMVSFLLVFI AILILTITENGSFIAIIFEVVSAFGTVGLSAGLTSELSTIGKFVIMIVMFIGRLGPVTIASTLIARKENSLLRYPQEDVFIG
6.5E-52	186	17.2	9.1E-52	185.6	12	1.1	1	C7MR33_SACVD	Trk-type K+ transport system, membrane component	Svir_36680	Saccharomonospora viridis (strain ATCC 15386 / DSM 43017 / JCM 3036 / NBRC 12207 / P101)	432	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharomonospora, Saccharomonospora viridis, Saccharomonospora viridis (strain ATCC 15386 / DSM 43017 / JCM 3036 / NBRC 12207 / P101)	471857	>tr|C7MR33|C7MR33_SACVD Trk-type K+ transport system, membrane component OS=Saccharomonospora viridis (strain ATCC 15386 / DSM 43017 / JCM 3036 / NBRC 12207 / P101) GN=Svir_36680 PE=4 SV=1MTAFGYVVAAGTALLMLPVATESGESSDFVTALFTATTSVCVTGLVVTDTAGHWSTFGELVILALVQIGGLGIMTLASLLGLLITR RIGLRMRLTAQAESKALGTGDMRRVLTGVALVSLTFETVTATVLTIRFATGYGYDIDSAAYHGVFHAITAFNNAGLALYPDSLTRFATD PWICVTVCLAVLAGGLGFPVWIELWRHSRGMLHRWSLHAKITLSTTALLLVLGTVAITTLEWNNPDTLGRFGVGGRLLTGFFHAVMP RSAGYNVLDVGEFRPGTLLVNDILMFIGGGSASTAGGIKVTTFALLAFVILTEIRGEPTVHVMGRKVPATAQRQALAVALLSVGTVMVA TLFLLTTTPFGLDVVLFEVISAFGTVGLSTGITPHLSGPATVVLTLLMFLGRIGPITLASALALREHTRRYELPEERPIVG
6.5E-52	186	22.3	5.2E-51	183.1	15.4	1.8	1	Q8EKN5_SHEON	Sodium-dependent potassium uptake protein integral membrane component KtrB	ktrB SO_0057	Shewanella oneidensis (strain MR-1)	453	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella oneidensis, Shewanella oneidensis (strain MR-1)	211586	>tr|Q8EKN5|Q8EKN5_SHEON Sodium-dependent potassium uptake protein integral membrane component KtrB OS=Shewanella oneidensis (strain MR-1) GN=ktrB PE=4 SV=1MVQWHPSLPLEQTQKAGKKLFGAPPFILSASFALLILVGTCLLKLPIATETPISWLQSLFTVTSAVTVTGLVVVDTGTVFTPFGQVI VALLIQCGGLGLMTFAIVTLIALGGKIGFLQQTVAKEAFNQTDTSTLVSTAKAVLVFSLLVEAVGMLILSVHWSDELGWQTSLFHGFFYT ISAFNNAGFALSADSLMPYVADPVVNLTITGLFIVGGLGFSVWIDLRRHKRWSKLTVYSRMMITGTILINAVALIAIYLIEYNNPNTLAPLS ELGKWLASWFQAVTPRTAGFNTLPIDKLEDGSALLILVLMFIGGGSLSTASGIKVVTFMVLILATYSYLRRDEAAYAFKREIPKETISKAL ALTMISIGVTWLAIFALVLTEKAPILDIAFEAVSAFGTVGLSRGLTSNLSGAGQGIIIFMMYMGRLGPLMLAYFLANPRVKKLRYAETKLAI G
6.8E-52	186	29.6	9.2E-52	185.5	20.5	1	1	R7C467_9FIRM	Trk-type K+ transport systems membrane components	BN579_00434	Firmicutes bacterium CAG:270	450	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:270	1263014	>tr|R7C467|R7C467_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:270 GN=BN579_00434 PE=4 SV=1MNELRPIQIILLGFFITIFAGSILLTLPIAAKSGQATSYIDALFTATTSVCVTGLVVETTMTHWSLFGQVVILLLVQIGGLGVVTITTGM FYVLGRRITLGNRMLIQESLGLNTLTGLVPLVKKIILGTAIVEGAGAVLYATQFIPEFGVGYGIWAAVFNSISAFCNAGMDIVKEDSFRSY VTNPVINFTTMALIVLGGLGFIVWKDLWQSMKKLIKEKIPVKRIVQQLKFQTKIVLSISTFLILFGTVLIFLFEYHNPATMGNLSLPGKVMA SLFQAVTTRTAGFETVAQGALTDASSLVSMFLMIIGGSPAGTAGGVKTVTFAILIFCVISAAKQEESISLFKRRVPGNLLSKALAIIVINLM VLMTSVLLLLVFDHGNFMESCYECVSALGTVGLTKGLTPNLTIAGKVIIIITMYLGRVGPISMAIGFSQKNRKKQVMYPEQDLIL
6.9E-52	186	22.3	1.2E-51	185.1	15.4	1.3	1	R5EXK2_9FIRM	Potassium uptake protein TrkH family	BN466_01976	Firmicutes bacterium CAG:110	459	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:110	1263000	>tr|R5EXK2|R5EXK2_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:110 GN=BN466_01976 PE=4 SV=1MSLRGKLVVFWMKHRPRHIATTQMVALMFAAIILLGALLLTLPAASRNGVSCGLRPALFTATSATCVTGLVLYDTWSQWSGFG QIVILCLIQIGGLGFMSVATLLIFLLRRKIGLQQRLMIAQSLSVNDIKGVVRLQKLVLTGSFSVEAVGAIILTLRFWPEYGFTRALRWGIFH SVSAFCNAGFDIFGAIAPGQSLIEFNADPVVLLTLSALIIIGGLGFLVWENIARKRSLRKFSVYTKLVLLITAALLAVGWAGTCLLEWNNP ETLGGMTVGEKLLNGFFQSATLRTAGFAAIDQAKLTESGKAFSSVLMFIGGSSGSTAGGIKTVTFLVLVLTIWARARGKSTVCAFKRTI PDEQTQNAMIIAFIVLALAVFGGIFISATSPMDFTDAVYEAVSALATVGLSAGGTASLSIPAQILIIIYMYFGRVGVLTISLGFLAGNRAEER FRYAETNLLIG
7.1E-52	186	28.1	1.2E-51	185.2	19.4	1.3	1	D3E9V0_GEOS4	Potassium uptake protein, TrkH family (EC 3.6.3.14)	GYMC10_2480	Geobacillus sp. (strain Y412MC10)	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Geobacillus sp. (strain Y412MC10)	481743	>tr|D3E9V0|D3E9V0_GEOS4 Potassium uptake protein, TrkH family OS=Geobacillus sp. (strain Y412MC10) GN=GYMC10_2480 PE=4 SV=1MKKKDLRNQMTPPKFLAIGFASITLIGTFLLKLPIATADGTSTPLVDALFTAVSAISVTGLTVVDTGTHWSIFGQIVMLMLVQLGGL GFMTSATWIALMFNRRISLRERMILQEAMGQYQIQGIVDLIRRVLVYTLIIEGAGALLLTLRFSATMPLSDAAYFGIFQSISIFNNAGFDLF GQIHGPFSGFATYVSDPFVNIIVMFLIFLGGIGFIVIFDLIEYPKCKKLSLHSKVVLTVTSLLIVIGAVMIFILEHSNPKTLGPLSYPVKIMASI FQSITPRSGGVSTLDIASLEQSSQFFMILLMFIGAAPGSTGGGIKVTTFAVLIGAVVTMIQGKRDVVLYRNRISQALVYRSITLTILSLLLL VGASMFLSVTESGEFLRILFEAVSAFGTAGLSMGLTTELSGVGKITIAMLMFLGRLGPLTLAYALSRKNNKELYRHPEGRITIG

7.3E-52	186	32.1	7.4E-52	185.9	20.3	2.1	1	A0A0F6A531_9GAMM	Trk system potassium uptake protein	RN22_01245	Grimontia sp. AD028	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Grimontia, Grimontia sp. AD028	1581149	>tr|A0A0F6A531|A0A0F6A531_9GAMM Trk system potassium uptake protein OS=Grimontia sp. AD028 GN=RN22_01245 PE=3 SV=1MVNFKPVLFVIGLVLSKIALFMYVPTLTAFFTGTAGFLDFGLSVIITHVAAFACLTLGKTEDFRLNARDMFVITTMVWLIASAFAALPFVFINHISFTDAYFETMSGITTTGSTVLSGLDDMAPSILLWRSILQWLGGVGFIVMGVAILPFLNVGGMRLFQTESSDWSAKSSPRTKNVAISIMKVYVSLSALCFVAYWLTGMTAFEAVNHAMTTLSTGGYSTSDSSMNHFSHAAHWVATCFMFAGGLPFLLMINALRRREPSMLVNDAQVRGFTYLVLATALMVAIWLVLTKDYGVMDAVRVSLFNIVSVVTTTGFGLDDFTAWGPFASVIFAFMLIAGGCSGSTSGGAKIFRFQIALALLKKQIQQLVHPSGVFIQRYNGRPVNEDIVRSVVAFAITYIMTILVVAMVLAATGLDGITSLTGAMTAVANVGPGMGTMIGPTGNFAGLSDTAKWVLSIGMLMGRLEILTVLVLLFPVFWRD
7.6E-52	186	26	5E-49	176.5	18	2.1	1	A5I1F4_CLOBH	Putative potassium uptake protein	CBO1319	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum A, Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	441771	>tr|A5I1F4|A5I1F4_CLOBH Putative potassium uptake protein OS=Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A) GN=CBO1319 PE=4 SV=1MNYPIVFKVLGDVIKYEALVMIFPLIASLYYGGKDANSFIITIAIMLCTAVIMSNIRPKNRTFYAKEGFLSVSVCWIVISLFGALPFYISGAIPSFVDCIFETVSGFTTTGATILTEVESLSKGILFWRSFTHWIGGMGILIFTLALMPSIGGTTIHLLKAESPGPTPGKIVPRIKETAKIMYLIYFAMTILQISLLLIAGMEPYDALIHAFGTAGTGGFSNMNSSVGAYNNVYIEVIITVFMLLFGVNFNVYFQLIAGNIKQAFKNEEVKYYIGMVLIAMTIIAFNIKGMYGGSLKEGFRQSSFQVASIVTTTGYATTNFDLWPTLSKSILALLMLTGCCAGSTGGGIKTVRIVLLFKAMKREISKIIHPRMVNSVKLDGKVVEDETISQVGLFVFAYVSIIVIAVLLVSIDGMDMETTLSSVLATIGNIGPGFKVVGPIGNFSSYSSFSKIVFSFCMLAGRLEIYPMLVMLSPSSMRKI
7.9E-52	186	21.4	5.2E-50	179.8	14.8	2.2	1	E0RYV5_BUTPB	Potassium uptake protein TrkH family	bpr_I2294	Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) (Clostridium proteoclasticum)	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, Butyrivibrio proteoclasticus, Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) (Clostridium proteoclasticum)	515622	>tr|E0RYV5|E0RYV5_BUTPB Potassium uptake protein TrkH family OS=Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) GN=bpr_I2294 PE=4 SV=1MNYSMIRFILFRLLRIMGTLFTLPLIVALVYKEYDSAISFLILAAVCFVVGTIFTIKKPANRVIYAKEGFAITAVAWIAVSMMGAVPFVITGTIPNYIDALFETVSGFTTTGGSILTTVDNIEKSVQFWRTFTHWIGGMGVLVFLLAVVPMADGYSMHLMRAESPGPVVGKIVPKVKDTAKILYIIYFGITVTEIVCLIISGMPIYDAITISFSTVGTGGFAVRDTGMMGYSLVSQAIIILFMALCGINFTVYYFLLNRKPKEAFAIDEVKFYLGTMLISAGIIAFNVYRSGCVTDPRLAFHHSLFSVASIMTTTGFCTLDFDTWPMLSKLMLVVLSLIGACAGSTGGGFKFSRALIVIRNARNELNFIVHPKAVKRVYMDGHSVEGTTVKSVTAYLGIYVITFIASTLIVALDNFDFQTTVTSVVATLNNIGPGLGMVGPTGNYSQFSYLSKLVLMFDMLAGRLELLPIFVILKPKTWRR
8.4E-52	186	20.3	4.9E-49	176.5	14	2.1	1	D4J3T8_9FIRM	TrK-type K+ transport systems, membrane components	CC1_00300	Coprococcus catus GD/7	495	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, Coprococcus catus, Coprococcus catus GD/7	717962	>tr|D4J3T8|D4J3T8_9FIRM Trk-type K+ transport systems, membrane components OS=Coprococcus catus GD/7 GN=CC1_00300 PE=4 SV=1MNGGMIRFILGSVLKVESVLLLFPCIVAVFYRESAGYWFLLTAVLSFVIGYLMVRKKPANTVFYLKEGCVTTALSWIMISLVGCLPFYLSGEIPAFTDALFETISGFTTTGASILSDVECLSQSILFWRSFSHWIGGMGVLVFLLAIIPLSGGSHMNLMRAESPGPSVGKLVPKVRATARILYLIYFGMTIVELIFLLIGKMPFLEAMMITFGTAGTGGFGVRNTSIGGYSAYIQWVVAIFMILFGVNFNAYYFLLMKRFKQAFDMEEVKGYFLVIAAASALIFINIYDKTMTAADTIRHVVFQVGSLMTSTGYSTVDFDLWPSASKVVLIIIMFIGACAGSTGGGIKVSRVIMMLKSVKRELNAYLHPKSVRMIKMEGKALDQGAISSVAVYFITFTLIFAVSFLLVALEGRDLTTNFTAVLTTMNNMGPGLADVGPSKNFGGLSILSKYVLMFDMLAGRLELFPMLVLFHPVLWKETWEGGKRRRRLKRKKVS
8.4E-52	186	29.8	6.4E-51	182.8	20.6	2	1	S1NH35_9ENTE	Trk system potassium uptake protein TrkH	OMK_00854	Enterococcus dispar ATCC 51266	450	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus dispar, Enterococcus dispar ATCC 51266	1139219	>tr|S1NH35|S1NH35_9ENTE Trk system potassium uptake protein TrkH OS=Enterococcus dispar ATCC 51266 GN=OMK_00854 PE=4 SV=1MKQLKKGHLATPQLISLGFATVILCGALLLMLPISSRSGGVTPFIDALFTATSATCVTGLTTVNTAQHWTPFGQFVILVMIETGGLGFMSLPVFFFMIARKKINLRTRMILKDSLNLEQMNGSVNLMRYILLTSVIIQGLGSIALSFSFVPQYGWLKGIWFSIFHSVSSFCNAGFDLLGDSLANNQQDIWMLSVIMILIIAGGLGFLVWFDLIQYRKQKRLSIHSKIALLMTGSLLILGAIGFYLTEHNGQLLVTGNWLQRFFNTMFMAVTPRTAGYYSVNYFEMSHAGLILTIVLMYIGGTSGSTAGGLKTTTFGVLLIQMKSILKGRNRAEFSGRTIPAGAIFRALTLFFITLSLCILATMILSVTEKIPDVDGLGLEYIVFEVVSAFGTVGLTMGLTPELSIVGKVIIISLMFIGRVGIMTVLLSLIAKARQQEQHFKYPEESVLIG
8.8E-52	186	29.3	4.5E-51	183.3	20.3	1.8	1	R6BIA0_9CLOT	Potassium uptake protein TrkH family	BN513_00555	Clostridium sp. CAG:169	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:169	1262778	>tr|R6BIA0|R6BIA0_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:169 GN=BN513_00555 PE=4 SV=1MKAVRKRSSSNPARIISESFVAVIAIGTLLLWLPISSRDGQFTPLLDSLFTATSATCVTGLVLYDTWTHWNPLGQGVLLMLIQIGGLGLVTLTSFFNLVVGKKLGLRGMKLASESINSTSFGDVPHLLRMIFTFTLTVESIGAVLLGLYFVPAYGLHGVFIAIFLAVSAFCNAGFDILGFLGEYTSLMTFNGRYLVIFTIMALIIVGGLGFIVWNDLLAYRKTKTLLLHTKVVLLTTAFLIFIGTVCFMLFEWNNPATLQPMGMKEKIGASLMQSVTMRTAGFNSVDLYAMRDSTKVFSIVLMFIGAAPGSTGGGIKVTTIAVIIMTAVSIIRGKEEPYLLKRRIAANVVYRSLAILFLGVVTVGVTAITLMATSPLEANGLTGIDATFEAVSAFATVGVSSGSTAIGSPFSKVMLILSMFIGRVGPVSFGLSLAAQQNVSRKLIVPEGRIVVG
8.9E-52	186	27.5	2.8E-50	180.7	19.1	2	1	A6W3U7_MARMS	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Mmwyl1_4481	Marinomonas sp. (strain MWYL1)	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Marinomonas, Marinomonas sp. (strain MWYL1)	400668	>tr|A6W3U7|A6W3U7_MARMS Potassium uptake protein, TrkH family OS=Marinomonas sp. (strain MWYL1) GN=Mmwyl1_4481 PE=4 SV=1MVNWDPAITVIERHPKAAKKIMAAPPLILCGGFLLLIIIGTLLLKLPIATTQSISWLHSVFTATSAVTVTGLVVEDTGTAFTTFGQVVIAILIQCGGLGLMTFAIVTLVALGGRIGFLQRTVAIEAFNQTDASTIVSTAKSVLLFSLIVEVIGMLILALHWSETLGWKTGLFHGFFYTISAFNNAGFALSSASLMPYVADPIVNFTISGLFIIGGLGFSVWIDLMKNRRWARLSPYSKMMITGTIVINFVALLAIYFIEYSNPNTLGPLSETGKWLASWFQAVTPRTAGFNTLAIEDLRDATTSLMLVLMFIGGGSLSTASGIKVVTFMLLLVLATYAYLRRDEEVNVFKREIPKEVISKALALSMISIGVTWLAIFVLLVSEKHAQMIDVVFEAVSALGTVGLSRGLTGSLSNTGEGIIIFLMFIGRVLGPVSFGLSLAAQQNVSRKLIVPEGRIVVG
8.9E-52	186	28.5	1.7E-51	184.7	19.7	1.3	1	A0A0F3RPR2_9LACO	ATP synthase subunit J	VC81_11715	Lactobacillus spicheri	453	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus spicheri	216463	>tr|A0A0F3RPR2|A0A0F3RPR2_9LACO ATP synthase subunit J OS=Lactobacillus spicheri GN=VC81_11715 PE=4 SV=1MKKLAKLSIFNTLSKKMVWGFILIIFLGSLLLSLPIATSHQQGTALIDILFTAASATCITGLTVVNTATHWSLFGQVVILGMAEIGALGYMTFAVLLFNIIRRHRSMGLSTQLMVKESLNLENLSDTKSVMKYVIGLSAVFQLGGVGLLAVDFIPRFGWKRGLYVSVYHSVMSFCNAGFDVFGDSLMRFRNDSYVLLVTIVLIVGGGLGFLVWRDLLLYHERKRLSLNSKLTLTTTGTLFVLGFVILLVTEGNLSGLLGDHMSWVNRTINTLFLSVTPRTAGIVTLPTNSLHSGSIFLIMILMFVGGTPGSTAGGIKTTTFGVLMLQSIAQLRGREDVEFSHRRFSQANISRALLLVFLASIVITLATLVLTQTEKIPQGYGLEYIVFEVLSAFGTVGLSLGLTPHLTVIGKVIIMILMFVGRVGIFTSLYALSKRQPKVSRLRYPEENILIG

9.1E-52	186	14.3	2E-30	115.1	1.7	2.1	2	A0A089WQY9_9PSED	Trk system potassium uptake protein	LK03_21520	Pseudomonas cremoricolorata	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas cremoricolorata	157783	>tr|A0A089WQY9|A0A089WQY9_9PSED Trk system potassium uptake protein OS=Pseudomonas cremoricolorata GN=LK03_21520 PE=3 SV=1 MALPTLRILGFIIGIFLITLAVSMTVPMATLVLFERTEDLPSFLWSSLITFGAGLALVLPGRPEHVHLRPRDMYLLTVSSWVVVCIFA ALPFLLTQHISYTNAFFESMSGITATGATVLSGLDHLSPGILMWRSMLHWLGGIGFIAMAVAILPLLRIGGMRLFQTESSDRSEKVMPR SHMVAKSIVLVYVGITVLGSLAFWWAGMSLFDGINHAMSAISTGGFSTSDLSLAKWDIPAVHWVAVVVMICGSLPFTLYVATLRGNRG ALLRDQQVQGLLGLLVATWIVLGTWYWATTDLHWLDALRHVALNVTSVVTTTGFALGDYSLWGNFSLMLFFYLGFIGGCSGSTAGGI KIFRFQVAYILLKANLNQLIHPRAVIKQKYNGHRLDEEIVRSILTFSFFFAITICVIALLLSLLGVDWMTALTGAAGTVSGVGPGLGEVIGP AGNYASLPDAAKWILAGGMLLGRLEIITVLVLCMPAFWRH
9.3E-52	186	37.8	3E-51	183.8	26.2	1.6	1	I3ZZL0_ORNRL	Trk-type K+ transport system, membrane component	Ornrh_0951	Ornithobacterium rhinotracheale (strain ATCC 51463 / DSM 15997 / CCUG 23171 / LMG 9086)	459	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Ornithobacterium, Ornithobacterium rhinotracheale, Ornithobacterium rhinotracheale (strain ATCC 51463 / DSM 15997 / CCUG 23171 / LMG 9086)	867902	>tr|I3ZZL0|I3ZZL0_ORNRL Trk-type K+ transport system, membrane component OS=Ornithobacterium rhinotracheale (strain ATCC 51463 / DSM 15997 / CCUG 23171 / LMG 9086) GN=Ornrh_0951 PE=4 SV=1 MRNELEPNVAKKSKFGSLYFKYRKFILKLSPQRHLIFGFALYTFIGWMLLSIPYLHRQPTSMLDNLFTTTSAISTTGLVTVSLSDTY NAIGLTVIALLVQIGGIGYMTMGSFLVMSRKNKMSNHQVRILTTEFSLPEGLEIKDFIRSIIVFTLVAETLGAIALYFIFVDANVPPSFAIWS SIFHSISAFCTAGVGLYNDSLESFASNIPLNIVISVLSLLGSLGFIVVTDIWSRFSGKTNKISFTTKVIVLILSILLIAGTLMFYFKEPATRFNN ENRFITSFFQSMSALTTAGFNTIPISNLSLPLLLFTIFLMYIGASPSGTAGGLKTTTLTAIIAIMWSRLRGDKRVTFMGKLIPIDRLYAATTA FIFYTAMIFFVTFLLSFTEKFSFSAILFEAASALGTVGLSTGITGDLSSWGKLLIIITMFIGRLGVITFGISILARKKQLTIYNETEDLAV
9.3E-52	186	24	3.5E-51	183.6	16.6	1.7	1	F7V7F2_CLOSS	Trk-type K+ transport system	TrkG CXIVA_26110	Clostridium sp. (strain SY8519)	415	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. (strain SY8519)	1042156	>tr|F7V7F2|F7V7F2_CLOSS Trk-type K+ transport system OS=Clostridium sp. (strain SY8519) GN=trkG PE=4 SV=1 MCLPFATVSGKSAGFFSALFTSTSASCVTGLIVHDTASYWSFWGQLIILLLIQIGGLGVVTMAVAIHMISGKKIGLGQRSQMQQSI SAPQIQGIVKLARFIILSALAIEGIGAAALAPRLIPDYGIIKGIWFAIFHSVSAFCNAGFDLFGTVESPYVSLVGYRYDPVVNTVIMALIFIGG IGFLTWHDIRTHGFHIRRWRLQSKVSLLAAAVLLAGGFLYFFFAEFHTLPLGKRIWMALFQSVTPRTAGFNTADQDALSDAGTLVTTIL MMIGGSTASTAGGIKTTTVVVMVCAAFAVFGMKKDVTVMNRRITENSIRSAGAIVFLYLTLQLLTAIIISLLEGLPILTCMYETASAIGTVG LTLGITPGLSPVSRLLLILLMYVGRVGGLTLIFAMRSPNSSGSGRFLTEDIAVG
9.4E-52	186	23.3	2.1E-51	184.3	16.2	1.5	1	M1FCX2_9ALTE	Trk system potassium uptake protein	trkG MRBBS_1998	Marinobacter sp. BSs20148	470	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Marinobacter, Marinobacter sp. BSs20148	490759	>tr|M1FCX2|M1FCX2_9ALTE Trk system potassium uptake protein OS=Marinobacter sp. BSs20148 GN=trkG PE=3 SV=1 MFILLSIFMMLPPLILMGSDAPNSAAFMESAGIVCILGLFGILATYRQSRDLKPRFMFMLTVSSWFFIAMFSSLPFYLSDNNISAAN AFFEGTSGITTTGATVFSDLDTMDRDLLLWRSILQWIGGIGIIGMFVAVLPFLRVGGMRLFATESSEWTDKALPRMKTLSRGLLGVYLL FSVVAVLTYWVSGMTLFDAFNHGLTSISTGGFSTSDLSMGKFNDLILLESTFFMILGSVPFFLFVRELHGQRGVLFRDQQVRLFLTILLI VPLLLTLYRWAVSAVPFNPVSNYISTLFNVTSVVTTTGYASEDYSAWGPLAFVVFFFLMFVGGCSGSTSGGMKIFRFQLSVIVLRENL MRLLHPRAVLTRNYNGRAVSDEIITSMIAYTFIFLLCLLILTVSLAAMQLDFTTSLSGALTALTNVGPGLGDIIGPAGNFGPLPDAAKWLL GVGMLMGRLEILSVVVVLSPAFWRS
9.8E-52	186	35.4	1.5E-51	184.8	24.5	1.3	1	Q0P8X4_CAMJE	Putative K+ uptake protein	ktrB Cj1283	Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	447	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Campylobacter, Campylobacter jejuni, Campylobacter jejuni subsp. jejuni, Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	192222	>tr|Q0P8X4|Q0P8X4_CAMJE Putative K+ uptake protein OS=Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168) GN=ktrB PE=4 SV=1 MKQFGLDRRTFKILLAGYIIIALFGALLLHSSWAHTTPIDFLDAFFTSTSAVSMTGLVVKNTAVDFTLAGQIIILALVQIGGLGYMGI GLFVYILIRKKVGFSARNLLKESLFYPSMDGLFKFFKKVLLFIFTIELIGAILLTMRFALEMNFKKALWFGIFHSISAFNNSGFTIFEHGFIA YKHDIAINLIITSLIIIGGLGYFVLVELYFFQRKKLQNLSLHTKMVVVASIFLIFSSTLIIFAFEYSNPQTIGHFSFFDKILSSYFIAINYRTAGFN TLDMGHLHDASLFFGSLFMVIGGAPGGTAGGMKVTTVMVLLLYAYWSIRDGRVRIFGHEIPRETISKAFIIAVGSAVYIVIAVILLSLLESK FDFIALLFETSSAFATVGISVGNGGTLSLCALFSDPSKVIIIIMMLSGRIGVFAFLLSVFKQDKAIHLKFPEGKVNL
9.9E-52	185	31.6	5.1E-49	176.5	21.6	2.2	1	R5H6S1_9SPIR	H(+)-transporting two-sector ATPase	BN676_01755	Brachyspira sp. CAG:484	436	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Brachyspirales, Brachyspiraceae, Brachyspira, environmental samples, Brachyspira sp. CAG:484	1262759	>tr|R5H6S1|R5H6S1_9SPIR H(+)-transporting two-sector ATPase OS=Brachyspira sp. CAG:484 GN=BN676_01755 PE=4 SV=1 MSSKIIKKLSDRFEQLAPYQVIVLGFLFYVVLGVFFISLPFAQKMDNGIVNNLFNVVSAMSTTGLTTGIINDMYTKFGLIVLLVLIQL GAVGYMTLTSFFIISGSNRLSTYRAKILSAEFPLPDCFHIKDFIKNIVLYTFFIELIGILLLWWQFEKLGSPTPLWSAIFHAISAFSTAGFSIY SNGLEGFRDNIAVNLVITFLCYAGATGFIVPMDVYRRVTGKSSEITFTTKVILFLTAVVAVFGTIFYLIGEHSSVLAAFFQVMSASTTAGF NTVPIGRLAPAALSVLILAMVIGASPSGTGGGIKTTGVSALIGVVASVMRGHPEHITLLKRHIPLNRVFTAVAAAFTYLSFLGISVYFLCLT EHFSFMELCFEASSALGTVGLSMGITSGLTWIGKLIITATMFFGRVGPLTLGIAFFKSSSNVVPKKSDLAT
9.9E-52	185	16.3	1.4E-48	175	11.3	2.1	1	R5FFR5_9CLOT	Uncharacterized protein	BN723_04302	Clostridium bolteae CAG:59	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	1263064	>tr|R5FFR5|R5FFR5_9CLOT Uncharacterized protein OS=Clostridium bolteae CAG:59 GN=BN723_04302 PE=4 SV=1 MNRSIIIYMLGWIMNMEAIFMTLPVVTAVVYRESIGFIYLGVAAVCGLLGFMCTRKKPCTKMFFAREGFVTVSLGWIVLSFFGCM PFVISGEIPHIIDAMFEIVSGFTTTGSSIIPKVEDMSHATLMWRSFSHWIGGMGILVFILAILPMAGDYNMHIMRAESPGPSVGKLVPKIRI TAKLLYSIYFCMTIVMMILLLLGKMPLFDSICMSFGAAGTGGFACRNSGQADYTVYQQAVITIFMLLFGVNFNVYYLLLIRRPKDAGRCE ELRGYLAVVAIAILLITINIRSLFPSLFMAFHQAAFQVSSIITTTGYSTIDYNSWPEFSKTILLLIMFIGACAGSTGGGMKVSRVMIAFKEIKK EMASVIHPRSVKVLKFEGKPLEHNTLRSLNAYIIVYFMIFGISTLIVSLDNYDFMTSFSAVAANLNNIGPGMSVVGPASNYSMMSYLSKT VLIFDMLAGRLELFPMLVLLSPGTWKRS
1E-51	185	17.2	2.2E-51	184.3	12	1.4	1	U5VU01_9ACTN	Putative cation transporter	AFR_04035	Actinoplanes friuliensis DSM 7358	446	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	1246995	>tr|U5VU01|U5VU01_9ACTN Putative cation transporter OS=Actinoplanes friuliensis DSM 7358 GN=AFR_04035 PE=4 SV=1 MRSRSPWRYPARIVPVAFLGAILIGTLLMMLPAARAEPGNAPFVTALFTATSAVCVTGLAVVDTPTYWSGFGQVLLTVLSQIGG FGIMTLATLLSLLVSRQLGLRSRLMAQAESSGLLGGNVGGVLIRVAIVMFASETAISIVLTLRFWLHYDYPFGRAVWEAVFHAVQAFNN AGFALYPDSLVRFVGDWWICVPLSLGVLAGSIGFPVLFELAREWRKPGYWSTHTRLTVWGTLLLSLTGFLVFLTFEWTNPNTLGPLG TPAKVLAAFTQDVMTRSGGFNSINLGGMNTETIAVTNGMMFIGGGSASTAGGIKVTTFLLLAFVIWAELRGEPDVVIRKRRIAEETQRQ AMTVALLGVALVASGTLALIGLTDHVPFDRALFEVTSAFATVGLSTGITPTLPQSAQVVLVILMYVGRVGTIAVGTAIALNTRRRLYRYP EERPLVG
1.1E-51	185	28	1E-49	178.8	19.4	2	1	R7HEN1_9FIRM	Potassium uptake protein TrkH family	BN634_01126	Eubacterium sp. CAG:38	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:38	1262889	>tr|R7HEN1|R7HEN1_9FIRM Potassium uptake protein TrkH family OS=Eubacterium sp. CAG:38 GN=BN634_01126 PE=4 SV=1 MLETLHRKKHLTSFQFIILGFAGIIFVGALLLMLPISSATGTITPFNEALFTSTSAVCVTGLVVQDTGSYWSFVGQLIILILIQTGGLG VVTVAAFVFMLSGRKISLMQRSTMQNAISAPTIGGIVRLTKFILKGTFIIEFLGALLMMPVFIHDFGINGLWMSVFHSISAFCNAGFDILGS KDCLYPSLTGYSNNYIINMIIMFLIIAGGIGFFTWDDIYTHKFHIKRYRMQSKIILTTTALLIILPAVLFFLCNFKELPFGKRLILSLFQSVTPR TAGFNTADISSMTDSSSQAVMILLMFIGGSPSSTAGGIKTTTFAVLLLNAFATFRSQEDVCAFGRRFDCQAIKNAATITMMYFILFFTGGI AISIYEGLPLSSCLYEAVSAVCTVGLTLGITPKLHILSRFILILLMYLGRVGGLTLIYAILSNKNRNNAKMPLEKITIG

1.1E-51	185	29.4	1.8E-51	184.6	20.4	1.4	1	F9Z5C0_ODOSD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Odosp_2837	Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) (Bacteroides splanchnicus)	602	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, Odoribacter splanchnicus, Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) (Bacteroides splanchnicus)	709991	>tr|F9Z5C0|F9Z5C0_ODOSD H(+)-transporting two-sector ATPase OS=Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) GN=Odosp_2837 PE=4 SV=1MFSTEFRYKLNNLRRILKKATVQLIRILFILASVATIVLMAYEYGYAISEAGKRYVTEGFNIIIRIFFFGSIATIFLDPKEIWQEKGYWIEIIVLALLLFVILTQTPAHFPTDNWLQKTDHILTHILLLFISIIHLSKVVVTGLQRHIRPEMTFVYSFLAIILTGAFLLMLPKAHHGSLSFIDALFTSTSAVCITGLTVVDTATTFTTTGQVVLLLIQIGGIGVMTFTSFIALSFFTQTSFNDQMALKNILSEESMNNIFRTLFYTLFTTIIVEAIGAWILWWEIRDLSPSLIPNKIFFAIFHAVSAFCNAGFSTLTGNLYHPGIRDLYGLQCWIATLIILLGGIGFPILFNYGKLVNHKVRNLFYRLTGSSKRMPSHVRIVNTTTRIVITATLLLLVGGTLLFWLSENNNCLRGLPLRGKLAVSFFSAVTPRTAGFNTVDLTSLLPSTWFLTLLLMWIGASPLSTGGGIKTTTITIALKNIINTLRGKEKIEIFKRQLPSENVRRAHAIILLSILWIGTATCLVAFWVPEGSVTQILFEVTSAISTVGLSLDFTSQLNTAGKIIISLTMFVGRVGLITLLSGLIPRQSSQSYTYAEENVIV
1.1E-51	185	37.9	1.1E-51	185.3	26.3	1.8	1	S0SA61_ENTAV	Cation transporter	OMU_02600	Enterococcus avium ATCC 14025	465	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus avium (Streptococcus avium), Enterococcus avium ATCC 14025	1140002	>tr|S0SA61|S0SA61_ENTAV Cation transporter OS=Enterococcus avium ATCC 14025 GN=OMU_02600 PE=4 SV=1MNFDRRVSFLKKSWQKLNNRFSSIQIIVFYYLAMTILSLILFHLPIFREPGSHVPFLDMIFMAISTISVTGLTTFDINSVFNDAGVLMLEVLFHIGGLGIMMITTFFFIVSKRRITLKQRQLIMTDMNQPRLSGIVNLIRITFTMLLAIEVLFGTIFSIYFYLAGYYHKISEAVFFGFYQAISAVTNSGFDVTGESIIPFSHDVFFIVTIMVLIFIGGIGFPVLMDFHGWIYHKKSKSRLPFRFSLFSKIALLAFFVLFIGGTVAIWLLEKDHNFAHMNLFDQWLNSSFYSMTTRNAGLQIHDLNLFQNTTLIIFSLLMFIGCSPSSVGGGIRTTTIAIIGLYLYSFLKNENDINIFGRKIAQEDVRKSVVVFMLSAGMCLFSILFLTATEDHSLISIIVEVTSAFGTTGLSLGITDDLSNTGKIMIAVLMFIGRVGMLYTLMLFVPKETQDLGYEFPEEKIIIG
1.1E-51	185	24.3	6.8E-51	182.7	16.9	1.9	1	D4ZDA8_SHEVD	Trk system potassium uptake protein	trkH-2 SVI_0059	Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella violacea, Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12)	637905	>tr|D4ZDA8|D4ZDA8_SHEVD Trk system potassium uptake protein OS=Shewanella violacea (strain JCM 10179 / CIP 106290 / LMG 19151 / DSS12) GN=trkH-2 PE=3 SV=1MLNFRPLLFILGIFLSTLTVFMFIPLIFALIYGEETVGAFMISSLVTATVATACMHQGKSKQLNLNIRDMFLLTSLTWLIVSVFAAMPFTLYHGINYTDAFFETMSGITTTGSTVLSGLDSMDHSILIWRSLLQWLGGIGFIVMAVAVLPFLNVGGMRLFRTESSDWSDKAIPRTQDMAKNLFYIYILLTVLCGFAYHMAGMDWFQAINHAMTTLSTGGYSTSDSSMAAFSNNAHWVGIFFMAAGGLPMLMFVNCIQQRSLLVWNDAQVKGFLLFIFTVSSCLAFWLWSSREIEPIDAMRLASFNVVVSVVTTTGYGLTDYTAWGALANVTFLFLMFAGSCSGSTSGGIKIFRFQIAIAIMREQLKQQFHPNGVFRQRYNNRPIGDDIVRSLVTFILLFMFVIIALSVILVMTGLDPTTSFTGAITAVTNVGPGLGDIIGPAGNFSSLPDVAKWALAIGMLLGRLEILTVAVLFHPGFWKY
1.2E-51	185	30.3	5.4E-50	179.7	21	2	1	Q8E9J5_SHEON	Sodium-dependent potassium uptake system permease component KtrB	ktrB SO_4282	Shewanella oneidensis (strain MR-1)	454	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella oneidensis, Shewanella oneidensis (strain MR-1)	211586	>tr|Q8E9J5|Q8E9J5_SHEON Sodium-dependent potassium uptake system permease component KtrB OS=Shewanella oneidensis (strain MR-1) GN=ktrB PE=4 SV=1MVSWHPSVYLAQRTSKAAKNILAAPPLILSISFIFLILIGTLILKLPISTTVPVTWSQSLFNATSAVTVTGLVVFDVGTVYTTFGQVVIALLIQLGGLGIMTFAIVTLLALGAKIGFLQNTIAKEAYNSTNTATLVTTAKSVLIFSLCVELIGMIILAVSWSDELGWRTSLFHGFFYTISAFNNAGIGLSPDSLMPYVEDPIINLTITALFIIGGLGFTVWIDLWRKKRWDKLTTYSKMMIIGTISINAIAVLAIYCIEYNNPKTLVPLSETGKWLASWFQAVTPRTAGFNTLAMNELEDATTAIMLMLMFIGGGSLSTASGIKVVTFMVLILATYGYLRRYDFVVYYHRGISKDTISKALALAMISVGTIWASIFFLLLSENASMIDIIFEAVSAFGTVGLSRGLTSNLTVTGQFIIIFLMFMGRLGPLTLAYFLASPKSKRIRYPETKLTIG
1.2E-51	185	22.8	3.3E-50	180.4	15.8	2.1	1	W0EWK5_9PORP	Potassium transporter	BARVI_12815	Barnesiella viscericola DSM 18177	487	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Barnesiella, Barnesiella viscericola, Barnesiella viscericola DSM 18177	880074	>tr|W0EWK5|W0EWK5_9PORP Potassium transporter OS=Barnesiella viscericola DSM 18177 GN=BARVI_12815 PE=4 SV=1MAKINVRVILKFIGMLLCMEAVFMLVPYFVALFYGDGDAPAFLLSTLIFATGGLLFYLFRNARNEVGKRESYLIVTSIWFFFTVFGMLPFCLMSNPLSITDAFFESVSGLTTTGASILVNVEAMPHGILFWRSFIQLIGGMGIILLTIAILPMLNHQGGLFLFNSEVTGISHEKLKPKIGETSKKLWYVYVSLTAILCLLLCLGPMEPFDAVCHAFSTMATGGFSTKQASLNYWNSAYIDYVITIFTFFAGINFALVYRAVTGDFKRLFSNEETRWYTFIVIGATLVVTAGLYATGQNDSFEETLRVSLAQVVTVITSTGYTVGDYVAWGPFFTTVFLLLMFFGACAGSTCGGAKIDRLVVLAKNTRNEFFRAIHPNAILPVRVNGKAISHEVVSKILAFILVYVMVLIAGSIILTALGLSIEESFGSTLSCLSNIGPGAGATGPVGSYAFIPDVGKWTLSFIMLIGRLELFTVLILFTSYFWKNS
1.2E-51	185	24.1	6.4E-49	176.2	16.7	2.1	1	D4N155_ANAHA	Trk type K+ transport systems, membrane components	CL2_16780	Anaerostipes hadrus	494	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, Anaerostipes hadrus	649756	>tr|D4N155|D4N155_ANAHA Trk-type K+ transport systems, membrane components OS=Anaerostipes hadrus GN=CL2_16780 PE=4 SV=1MNFSMIRYVIGLVMLFESAFLSLPCLIALIYHEKKGFSFWIMLFVCLIIGILFVMKKPKKTVYYAKEGFLTVAISWIVMSFFGALPFVINGDIPSVVDAMFETVSGFTTTGSSILTDVEALARCSLFWRSFTHWVGGMGVFVFVLAVMPLVGGQNIHLMRAESPGPSVGKLVPKIRKTSMILYKIYIFMTIVMVVLLLGKLPLFDSLLLAFGTAGTGGFSILNSGCASYSPYIQYLIAIFMILFGVNFNVYYFILIKKFKDAIHYEELKYYLLFIGASVAMITYNIHSLFPTIEQAFRHALFQVGTVITTTGYASTDFNKWPEFSKFILVMLMFSGACAGSTGGGMKVSRLVIMLKTVKKELLSYLHPRTVRKVKFNGRIVEHEVIRGINVYMIAYAFVLMFSVLIISIDNFDFTSNFTAVVATLNNIGPGLNIVGPTGNFSMYSNLSKIVMIFDMLAGRLELFPMLLLINPYTWKEIKIRKNKKNKKEGHSI
1.2E-51	185	17.9	1.7E-50	181.4	12.4	2	1	W8RBN2_PSEST	Trk system potassium uptake protein	CH92_12510	Pseudomonas stutzeri (Pseudomonas perfectomarina)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas stutzeri group, Pseudomonas stutzeri subgroup, Pseudomonas stutzeri (Pseudomonas perfectomarina)	316	>tr|W8RBN2|W8RBN2_PSEST Trk system potassium uptake protein OS=Pseudomonas stutzeri GN=CH92_12510 PE=3 SV=1MALPTLRIIGFILGIFLITLSVSMVIPMITLFAFERTDDLQAFIWASLITFSCGFALVAPGRPANTQLRPRDMYFLTTISWVIVCCFAALPLMLIQHISYTDAFFETMSGVTTTGATVLSGLDSASPGLLMWRSLLHWLGGIGFIGMAVAILPLLRVGGMRLFQTESSDWSEKVMPRSHMAGKYLIVIYLTFTLAAFVAFWLAGMSGFDAINHAMSTVSTGGYSTSDASLGKFSPASHWVAIFFMVLGSLPFTLYVATARGNRGALLRDQQVRGFLVMLTLTSLLFSGWYWLNHDDNLLDSLRIVTFSVVSVITTTGFAVTDYTQWGGFAVMAFFYLTFLGGCSGSTSGGLKMFRFQVAYALLRSNLKQLVHPRAVIRQQYNGHNLDEEIVRSILTFSFFITMTIGVLALCLALLGLDPITALTGAASAVCNVGPGLGPIIGPAGNFSTLPDAAKWLLSVGMLLGRLEIITVLVMLTPSFWRH
1.3E-51	185	35.5	1.3E-49	178.5	24.6	2	1	C2W5R1_BACCE	Potassium/sodium uptake protein	bcere0022_11240	Bacillus cereus Rock3-44	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock3-44	526986	>tr|C2W5R1|C2W5R1_BACCE Potassium/sodium uptake protein OS=Bacillus cereus Rock3-44 GN=bcere0022_11240 PE=4 SV=1MEATIKKGLYNRLIRFSPPQILAMGFFCLIIAGGMLLKLPFATKESISWVDAFFTATSAATVTGLGVVDTASTFTMFGQIVIMLLIQTGGLGLMTIAILVWVLGKKIGLRHRLLIGEAFNQTNIGGLVKLVKRVFIFSICIEFIGVVFLSIRFIPEFGFGKGLYYSIFHVIAAYNNAGFALWPDNLTRYVGDPIINIGICSLIIIGGLGFTVLIDIWYSRSFQKLSLHSKIMIVGTVALNVIAIIVIFLLEYNNVKTLGPLSLNEKLWASFFQGITPRTAGFNTVDYGGMEESSILFTMILMFIGAGSVSTGGGIKLTTFVILITSVVAFFRKKEDFILFRRTIKMSTVTRALAIAVASQILIFVAVFLLMLTEDFSFIQLLFETISAFGTVGLSMGITAKLSAIGKCIIMFVMFCGLIGPLTLVFSLARPAKQKIRYPSEDVFTG

1.3E-51	185	19	8.6E-50	179	13.2	2	1	Q2VZR3_MAGSA	Trk system potassium uptake protein	amb4108	Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum magneticum, Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	342108	>tr|Q2VZR3|Q2VZR3_MAGSA Trk system potassium uptake protein OS=Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) GN=amb4108 PE=3 SV=1MIDFRPVLFVNGFLLLVLALAMGIPAMVDLSAGDEDWKVFAVSAMVTAFAALSLIFGTRAKGRPTLSARQAFMLTTLAWISTAAFAALPFAFGNLHLSPTDAVFEAMSGLTTTGATVIIGLDHAPRGILIWRALLNWLGGEGIIIMAIAILPLLRIGGMQVFRMETSDKTETIKPRITQVATSITLVYVVFTVLAALAFWAAGMGRFDAVCHAMAAISTGGFSTSDTKLAHWNTAVQWVAVFAMMVGGSSFVLWTGPWRRGRPRIVDDAQAHWYLMFIGTAAGVVALWQWAVNDMSLGVAVRHATFNVVSTVTSTGFVSTDYGTWGGFAHVVFFILVFIGGCTGSTAGGVKIFRWELLFALAGIHLKRLLHPHGIFVIHYNQRPIAPSVLDSVQGFVVMYFFTFALFALGLSVVGVDFMTALSGSAAALANAGPGIGEVIGPFGSYRPLPDAAKWILAVEMMLGRLELFTVAVLFSRSYWRE
1.3E-51	185	30	1.7E-51	184.6	20.8	1.1	1	R5NZ17_9CLOT	Potassium uptake protein TrkH family	BN482_01626	Clostridium sp. CAG:127	462	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:127	1262774	>tr|R5NZ17|R5NZ17_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:127 GN=BN482_01626 PE=4 SV=1MDVAEKNEKKLRRQMRTTSKILLGFLLAILTGAVLLTLPVATVSGKSDFLTALFTATTSVCVTGLVVVPTFSYWTLFGKIVILALIQLGGLGIVALTSFVMLLMNRKFSLRNRMMIQDAFGLSTMQGMVVFIKRVIKGTVIVEMLGAVLYMFAFIPQFGVAHGIWYSVFNAISAFCNAGIDIIGPDSLMTYADSPLVLLTSSFLIICGGLGFVVWWDVVDVLSNVRAKKIPARDIWRRFNTHTKIILMMTFALILSGMVVTFLFECNNPLTLGNMSLGKKMLNAFFQSVTLRTAGFASISQKGLTEPTVLVSCVIMFVGGSPVGTAGGIKTMTAATLVFAVLAVVQGRKETVAFKKTIPTSIVRRSLAVTVIGFGTLILFSVLLLATNPLSLSDGVFEVTSAIATVGLSRDVTPGLNVIGKVIIILCMYLGRVGPITMFMFFGQRATNHNSVKYADAEIIVG
1.4E-51	185	20.6	4.8E-51	183.2	14.3	1.7	1	D5BMT6_PUNMI	Trk system potassium uptake protein	SAR116_1886	Puniceispirillum marinum (strain IMCC1322)	481	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, unclassified Alphaproteobacteria, SAR116 cluster, Candidatus Puniceispirillum, Candidatus Puniceispirillum marinum, Puniceispirillum marinum (strain IMCC1322)	488538	>tr|D5BMT6|D5BMT6_PUNMI Trk system potassium uptake protein OS=Puniceispirillum marinum (strain IMCC1322) GN=SAR116_1886 PE=3 SV=1MQFSPVLNILGLLTTILAATMLIPMCVDLYFGSGDWQVFAVSSLFTAFFGVTTWLATSQREPLDLGLRQAFLLTNGSWMLIGVFGSLPFMFSELQLSPTDALFESVSGITTTGSTVLQYIEMAPPGILMWRALLQWLGGVGIIVMAMAVLPMLSVGGMQLFRTESYERADKVVPRAAQLAGGIGLVYAGLTAAWTIMLAAAGMGIFDALTHAMTTLATGGYSTRTASIGAFDSVTIEWIVIAGMIVGSLPFAHYLAIVRGGWRNLVNDPQVRWFFILLIGLVALLAWHLSAGGYKIAHAIRESSFNTISILTGTGFGSANFSAWGGFASTMLLIAMFIGGCGGSTTCGIKVFRLQVLATTARVQISRLLRPHGVVLAYYNRKPVSSEVMDSVMAFFYVYILCFVILAILLGMMGLDFITALSGAATSISNVGPGLGNLIGAEGNFALLPDPAKWVMSFGMLLGRLELFTVLVMLNPGFWRR
1.4E-51	185	38.8	3.3E-51	183.7	26.9	1.5	1	D4W540_9FIRM	Cation transport protein	CUW_0337	Turicibacter sanguinis PC909	454	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Turicibacter, Turicibacter sanguinis, Turicibacter sanguinis PC909	702450	>tr|D4W540|D4W540_9FIRM Cation transport protein OS=Turicibacter sanguinis PC909 GN=CUW_0337 PE=4 SV=1MFIVKKLRNFIHSTPTRLIVGYYFMFTIGFAFLLWLPFSLNEGVSLSFLDALFISTSGLSNTGLSPVSPVDTFSIPGILILALNLQIGGLGLMMISTAIWLLAGHKISTRERALIMTDQNQINLSGVVKLVKSVLISFLAIELVFMLILGNYYYFAGYYPIYWQAMLQGFFTTVSAITNSGFDITGSSLMPFQKDYFVQTLHMFLMFFGAMGFPVILDIKKYFQCRRTKQRFKFSIYTKLTMVTTIILWVVGIVGFYLFEWNHFLADKGLIEGFFYATFNSLTTRNAGFATVDMNAFSTATLTMFCGLMFVGSSPNSSGGGIRTTTFALMVLAILSFARGKQYVNIYGREIETQTVYKSFMIYIVATFIVSLSTLLICMSDQFPLMEIFFEVCSAFGTTGLSMGITGSLTSFAKLVLIATMFIGRIGIIAFLMIFRANVHPAKVRYPKVDIIIG
1.4E-51	185	15.5	2.1E-49	177.8	10.8	2.3	1	F5YFU4_TREAZ	Trk system potassium uptake protein TrkH	TREAZ_2423	Treponema azotonutricium (strain ATCC BAA-888 / DSM 13862 / ZAS-9)	486	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema azotonutricium, Treponema azotonutricium (strain ATCC BAA-888 / DSM 13862 / ZAS-9)	545695	>tr|F5YFU4|F5YFU4_TREAZ Trk system potassium uptake protein TrkH OS=Treponema azotonutricium (strain ATCC BAA-888 / DSM 13862 / ZAS-9) GN=TREAZ_2423 PE=4 SV=1MKISRFAKQFILLRFLIILLGIIAIIMAPSLVIAIANGETAMIRAFAFPMGIVSVLAGLSLLLSLRKKNLHLNARDGFLLVFLTWVLASLLGAIPYFLGDAISLTDAIFESACSFATTGATTISDVEALPQSLLFWRSIGHWFGGIGIVLITVALMPVLGVGGFQLIKAETPGPEKEKITPKITVTAKLIFLAYGILTAALMLLYRLGGMNWFDAICHGFTVMASGGVSTRNAGIAYFNSGFIDGVSTVFMLLAGLNFSLYYRLLRGRFRDVDLDNTEARAYLIIFLVSAALITVNLIPVYGSPGAALRHASYQTASILSTTGSAIADYETWPSFARTVLFFLMFIGGCSGSTAGGIKVIRHVVLFKQMGNELRRIIYPRGVFSIQLNKKVGRKDVIYGVAGFFFLYLIVVAVTTLVTAASGTDLFSSFSAALSITGNVGTGFGAIGPRHNYSAFPDHIKWLFSFVMIAGRLELWTVLVIFTPAFWRK
1.4E-51	185	22	5.2E-27	103.9	5.3	2.1	2	R5U677_9FIRM	Trk system potassium uptake protein TrkH	BN683_01619	Roseburia sp. CAG:50	497	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:50	1262949	>tr|R5U677|R5U677_9FIRM Trk system potassium uptake protein TrkH OS=Roseburia sp. CAG:50 GN=BN683_01619 PE=4 SV=1MNKSMIAYILGWIMKLEGLFMLIPVLVALIYREHNGVWFAIVAVCALVFGAVVTHKKPESNVFYMREGCIATAMSWFIMSVIGCLPFFLSGEIPSFTDALFETVSGFTTTGSTILSDVESLSYCMLFWRSFTHWIGGMGVLVFLLAVIQMTGGSNMNLLRAESPGPAVGKLVPRMMHTARILYVIYLGMTVILFVLLVCGKMSVFESLTTAFSTAGTGGFGIRNDSLASCSPYIQWIVTIFMILFGVNFNAFYFLLLRKWKQLFHMEEVWAYFGVIVAAILIIMTNTYGWVGNVMENLRNTSFQVGSIITTTGFMTVDFDQWPSLSRYVMLFLMMIGACAGSTGGGMKVSRFLLSVKSALRELNSYLFPKSIKKIKMDGKTVDEEAIRGINVYFTAYMLLVILSTFLVCIDGTDLVSGFSSVLGTFNNIGPGLAKYGPACNFGAASTFSKCVYIFDMLAGRLEIFPVLILLYPPSWRGLLKRRIKRKKNSRTNISVS
1.5E-51	185	19.5	2.1E-51	184.4	13.5	1.1	1	A4VKV9_PSEU5	Putative cation transporter	PST_1936	Pseudomonas stutzeri (strain A1501)	442	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas stutzeri group, Pseudomonas stutzeri subgroup, Pseudomonas stutzeri (Pseudomonas perfectomarina), Pseudomonas stutzeri (strain A1501)	379731	>tr|A4VKV9|A4VKV9_PSEU5 Putative cation transporter OS=Pseudomonas stutzeri (strain A1501) GN=PST_1936 PE=4 SV=1MKSLLHPGRTVALVFLFAILCGTALLSLPIAHASGETGPLLTAFFTAVSAVCVTGLVVVDTGTYWSTFGQVVIMALFQLGGFGMMTLATLLGLLVNRSFRLRAKLIAQAESHVLGLGDISSVAKLVLVVTLVMELAVMLLLTLRLHLSYGLGWGEAAWSGLFHSVSAFNNAGFSIHVDGLVRYATDGFILLPVMSAIIIGGIGFPVLNDLRRRWSDPRHWSLHTKLTLSGTAVLLVGGFMAVLLFEWSNPGTLGPMAWADKLLSAAFVSVSARTAGFNALDIGALTHESWALHYFLMFIGGGSAGTAGGVKVGTVAILALVIAEIRGRADTEAFGRRVGSSAQRQAITVLVLGSAMVVLGTLVILRDTDIPTDQVIFEVISAFGTVGLSTGITADLPETSQLMLTLLMYVGRVGTITLAASLALGEHRMPYRYPEEHPIVG
1.5E-51	185	19.6	8.7E-51	182.3	13.6	2	1	C1DRN2_AZOVD	Trk system potassium uptake protein	trkH Avin_15550	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Azotobacter group, Azotobacter, Azotobacter vinelandii, Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	322710	>tr|C1DRN2|C1DRN2_AZOVD Trk system potassium uptake protein OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) GN=trkH PE=3 SV=1MALPTLRIIGFILGLFLITLATGMVLPMLTLVIYEHTHEIESFVWASMITLGAGVALILPGRPEQVHLRPRDMYLLTTASWLVVCVFAALPNLLQNISYTDAFFETMSGITTTGSTVLSGLDSASPGVLMWRSMLHWLGGIGFIAMAVAILPLLRVGGMRLFQTESSDWSEKVMPRSHMVAKYIVGIYVGFTLIGILAFHLAGMNWFDAINHAMSTISTGGFSTSDASMGKFSPAAHWIAIVFMLLGSLPFTLYVSTLRGNHQALFRDHQVRGFLLMLILTSLLFGLWYWRHSDHSLIDALRVVTLNVVSVVSTTGFALGDYTQWGGFATMLFFYLTFVGGCSGSTTGGLKIFRFQVAYVLLKSNMRQLIHPRAVLKQQYNGHNLDEEIVRSILTFSFFFTITIGAIALGLSFIGLDLITALTGAATAVCNVGPGLGPTIGPAGNFASLPDSAKWLLSIGMLLGRLEIITVLVLVTPSFWKH
1.5E-51	185	27.7	2.8E-51	184	19.2	1.4	1	B7VR07_VIBTL	KtrB	VS_II0392	Vibrio tasmaniensis (strain LGP32) (Vibrio splendidus (strain Mel32))	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio tasmaniensis, Vibrio tasmaniensis (strain LGP32) (Vibrio splendidus (strain Mel32))	575788	>tr|B7VR07|B7VR07_VIBTL KtrB OS=Vibrio tasmaniensis (strain LGP32) GN=VS_II0392 PE=4 SV=1MNSVKRKGTFYTLKSDKKPRKGSEPKIILTSFLGVLIPSAILLTLPVFSVTGLSFTDALFTATSAISVTGLGVVDTGQHFTLAGKILLMFLMQVGGLGQMTLSAVLLYMFGVRLSLKQQALAKEALGQDRKINLRKLVKKIIIFALVAEFVGFVLLCFRWVPEMGWATGSFYALFHAISAFNNAGFALFSDSMMSFVDDPLVIFTLAGLFIFGGLGFTVVGDLSSNWRKGFQHLHLHTKIMLTATPTLLLVGTVMFWLLERNNSATMEGLSVQGQWLAAFFQSASARTAGFNSVDLSQYTQPALLVMIVLMLIGAGSTSTGGGIKVSTFAVAFVATWTFLRQKKHVVMFKRTVTWQAVTKSLAIIVVSGALLTTAMFLLMLTEKAAFDRVMFEVISAFATVGLTAGLTANLTEPGKYIMIVVMVIGRIGPLTLAYMLARPEPSLLKYPEDTVLTG

1.5E-51	185	26.5	2.4E-28	108.3	6.3	2.1	2	D7BKZ5_ARCHD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Arch_1638	Arcanobacterium haemolyticum (strain ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018)	456	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Arcanobacterium, Arcanobacterium haemolyticum (Corynebacterium haemolyticum), Arcanobacterium haemolyticum (strain ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018)	644284	>tr|D7BKZ5|D7BKZ5_ARCHD H(+)-transporting two-sector ATPase OS=Arcanobacterium haemolyticum (strain ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018) GN=Arch_1638 PE=4 SV=1MRPTYILIVAFLVTLLAGTFLLMLPISVTGQPPWPYPLSTPPHEYGPRFAGGAPFSVAFFTATSATAVTGLAVVDTATYYTTFGQSIIAVLIQLGGMGTMTIVTLVAMVLARRLNMRTREVASASVSGMSMGNVRRVVFGVVALTALVETSIAGALLGRFLYLGHSFSTALGEAWFHSISAFNNAGFSLYTDSLIEFATDPWILPISAGIIIGGLGYPALLAFYGFGLHWWRWPMTTRLVAVGTSSLLVFGWVVFFALAEWNNPNTLGPEGPGGKILMAFFASVTPRTAGFNSLDVASLTDISRVLTDILMFIGGGPGGTAGGVKITTVFVIGFVVWSEMRGGRAVNVLGLRLPRSAQRQALTVMSLSSIAVMVGTMLIMVQTTVNLDQALFEVVSAFATVGLSTGITPSLPASSQLVLITLMIIGRLGPLTIATALALRTSPLTYELPKDRPLIG
1.5E-51	185	33.4	8.6E-51	182.3	23.2	1.8	1	A0A0F2Q260_9CLOT	Uncharacterized protein	VR72_14185	Clostridiaceae bacterium BRH_c20a	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, unclassified Clostridiaceae, Clostridiaceae bacterium BRH_c20a	1629719	>tr|A0A0F2Q260|A0A0F2Q260_9CLOT Uncharacterized protein OS=Clostridiaceae bacterium BRH_c20a GN=VR72_14185 PE=4 SV=1MQLLIMLPYMGIVLMILGVSMALPIFWGIYFNESEWVMFLLSSIITFSVGLIMNKATTRFKEDLRQRQALILVTLTWIVASVFSTIPYLLTKTFDTFTDAFFESMAGFTTTGASVIPDLEVLSYTVLFWRSLTHWLGGMGIIILFIAIMSTLKMGGTQLFRAEIPGSVVQKLKPRISQTALILWSTYVILTFVLTAILWALGMSIFDAINHAFGTMATAGCSTKNASLGYYNDPGIYWAVTIFMFLAGSNFALYFVALKEKSLLHFWKNAEFRLYTKIVVLFTFMMTTNLLFIENKSIADALTLSSFKVISSITTTGFTIYDYQGWTAFPQTIIIVLLFVGGCNGSTSGGSIKVGRYLIMFKQCIVELQQAVHPRAIINLKLDGKQINDQLIINVLTYFFLYIFLISMGTLFLTFLGLDLLSAFTAVLGSISNGGIGLTQLASGQFFTVFPTLGKHILALLMLLGRLEIYTVLILFSPSFWRK
1.6E-51	185	19.5	4.8E-49	176.6	13.5	2.1	1	R6MU04_9FIRM	Trk-type K+ transport systems membrane components	BN531_01412	Eubacterium sp. CAG:202	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:202	1262884	>tr|R6MU04|R6MU04_9FIRM Trk-type K+ transport systems membrane components OS=Eubacterium sp. CAG:202 GN=BN531_01412 PE=4 SV=1MNKRSIIYILGWVLIVDAVAMQIGTITSLIYGEKEAWYFVLTGVVSAILGVLAIKVKKPKNMVLYQKAGFASTALSWILLSLVGCMPFWLSGEIPSFIDAFYETVSGITTTGATILNDVEALSKGMLMWRSFLHWLGGMGVIVFLLAIIPKLGGQQNIFLMKAESPGPIIGKAVPRMRSYATMLYGIYIILTALEFILLLFGGLNVFEAINTSFSTAGTGGFGIYNSNAAAFDSYYVQTVIAVFMLLFGINFSVYLCLIARKFKQSLKFEELWIYLGIVAVSTAIIAFNISSIYKPYDAFHQSFFYVSSIISTTGFGLTDVNKWPELSKTVIIILTFIGASAGSTGGGFKISRIILLFKEVRKEFSLLVHPRNVKLVKMDGKAVNHDIMRTTSMYLVLYIGVFAISFLLVSIDNMDFTTSFTAVAANLNNTGPGLGAVGPVGNYADFSILSKIVFIFDMLAGRLEIYPLLLLFAPSAWKKS
1.6E-51	185	17.7	6.6E-28	106.9	5.5	2.1	2	A0A0F0CHZ0_9CLOT	Trk system potassium uptake protein TrkG	trkG CLFS41_19040	Clostridium sp. FS41	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. FS41	1609975	>tr|A0A0F0CHZ0|A0A0F0CHZ0_9CLOT Trk system potassium uptake protein TrkG OS=Clostridium sp. FS41 GN=trkG PE=4 SV=1MNRSIIIYMLGWIMNIEALFMLLPVLTAAVYKENIGYIYLGVAVVCGLLGFAWTRKKPKTKMFFAREGFVTVSLGWIILSFFGCMPFVISGEIPHIIDAMFEIVSGFTTTGSSIIPKVEELSKASLMWRSFSHWIGGMGILVFILAILPMAGDYNMHIMRAESPGPSVGKLVPKIRITAKLLYTIYFCMTVVMVILLLVGKMPVFDSICMSFGAAGTGGFACRNSGQADYTVYQQGVITVFMLLFGVNFNVYYLMLIRKPKDAFHCEELRGYLAIVAIAVLFITMNIRHLFPTLFMAFHQAAFQVSSIITTTGYSTIDYNSWPEFSKAILLLIMFIGACAGSTGGGMKVSRIMIAFKEIKKEMASVIHPRSVKVLKFEGKPLEHNTLRSLNAYIIVYFMIFAISTLIVSLDNYDFMTSFSAVAANLNNIGPGMSVVGPASNYSMMSYLSKTVLIFDMLAGRLELFPMLVLLSPGTWKRN
1.7E-51	185	28.6	2.3E-30	114.9	8.8	2	2	R5SDA2_9GAMM	Related to V-type sodium ATP synthase subunit J	BN527_00049	Acinetobacter sp. CAG:196	443	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, environmental samples, Acinetobacter sp. CAG:196	1262690	>tr|R5SDA2|R5SDA2_9GAMM Related to V-type sodium ATP synthase subunit J OS=Acinetobacter sp. CAG:196 GN=BN527_00049 PE=4 SV=1MAKRKNRFEFITKTPERILPATFFLLCLTGGIILYLPFCSPHGVSFLDAMFTAVSAVCVTGLSVVSVSDKFTGVGQLVLLLLIQAGGLGIMSISSIIFILLGKRMSLTHEKNARNIFEAESKEEIKKSLIRIFKYTFIVELTGAIILSACFTFSEHSLLTGLKFGFFTSISAFCNAGFFLKNDNLIGYNSFPLLTYTVSFLIILGGMSPAICLMLQNIFKGKKLPPVAVLVFYTTLALLIGGTLFFFLSEYNGVLSGMSIADKIHNAWFQSATSRTAGFNSVDLSSINPGTFLLMVALMIAGGSPGGTAGGLKTTTISVLFLTCYNAIRIKDNVVRNRVIKLDTIKKAVTLTVVYLSILVTIVLMLLTTQTANAEQLIFEAASALGTVGLSMGATSQLDGVGKVIIIAAMFLGRVAPATLICYLNTKNIDSRISYPDAKISLT
1.8E-51	185	19.9	3.2E-26	101.3	4.1	2	2	R5ZGR1_9FIRM	Cation transporter	BN504_00089	Eubacterium sp. CAG:156	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:156	1262880	>tr|R5ZGR1|R5ZGR1_9FIRM Cation transporter OS=Eubacterium sp. CAG:156 GN=BN504_00089 PE=4 SV=1MNYSIIRYILGIVLKLEGILMCLPLIVGIIYSEKSAYSYVITIAMCLIIGTILSHKKPKDTEFYATEGYITVSLSWVILSIFGCLPFVISGEIPSMVDALFETISGFTTTGASILSDVESLSYCNNMWRCFTHWIGGMGVLVFILAILPMRGGQRMYLMKAESPGPSVEKLVPKVRNTAMILYGIYTVMTFIEVLLLLISGMPLFDALTTSFGTAGTGGFGIKNDSITGYNSSIQIIVTVFMILFGLNFNIYYLILCKKFKQALHSEELKAYLLVIFATIGIITFNIRSFFPTIGEALKHAAFQVGSIITTTGFSTTNFDLWPQVSKTILIMLMFMGACAGSTGGGIKVSRLLILIKTLKKELFTIVHPRGVKKITMDKRPIEHETVRLTNIFMVAYIFILAFSILLIGIDNLDFTTNFTAVAATLNNIGPGLELVGPTRNFGIFSDFSKFILMFDMLAGRLEIFPMLMLFAPISWKRQ
1.8E-51	185	39.8	4.1E-51	183.4	27.6	1.6	1	Q4A5P4_MYCS5	Putative potassium uptake protein KtrB	ktrB MS53_0519	Mycoplasma synoviae (strain 53)	547	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma synoviae, Mycoplasma synoviae (strain 53)	262723	>tr|Q4A5P4|Q4A5P4_MYCS5 Putative potassium uptake protein KtrB OS=Mycoplasma synoviae (strain 53) GN=ktrB PE=4 SV=1MRLKRFRNFIKNKLYKVNNSVNRYKLSFNKTIYLFLAYFVIILIFSLILYSPITQNETFAGQKITPLNYLDVVFTTSSAFSDTGLVIADSYNQWNIFGQALIATLIFSGGIGVFALKIFIINWIFRKTKITLTDMNLMQSERGGSGFRNPTQVVITSVKFLIAVTIIFGFSLSFYFYFTDVKMTPGIKDYLGSNYISPKGSWSLAFRFGFFHTISALNNAGFDIMSSNSIMPYYGAVELQICMIILLIIGGIGYPVIFDIKLAIEHKIKGKKGRHRFSLFSKVTFVIYFLVFAIGTLLTFLLETTSKDPHTYWNKIYVPDELMAEYNQYLSDSSLVPSSQLQYYLNNGQMYGSVFQKSFGIVFINFSSRSAGFTSVVISDFSFPTVLLIGLEMIIGASPASTGGGIRTTTFALFIMAIISMFRSRKDITLFKRQISKENTEMTFKVIALSTILIIIGTFILSTSHSLYGGKLNNINLTGIFFNVASAFGTSGLSAGGISKLNVASKIMLIIIMFVGQFGISSTLLVWKRKKNKESQFKYLEEELAIG
1.8E-51	185	21	1.3E-36	135.6	8.3	3	3	D8SBD8_SELML	Putative uncharacterized protein (Fragment)	SELMODRAFT_54024	Selaginella moellendorffii (Spikemoss)	432	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8SBD8|D8SBD8_SELML Putative uncharacterized protein (Fragment) OS=Selaginella moellendorffii GN=SELMODRAFT_54024 PE=4 SV=1TFYRLHLAYFVTIAWVASICLWLFPKSDRAGADKLDFIDCVYNAVSSVCTTGLISVRMTSFSLPDNILIMILFTLGSPIFTSVLPLYIRLFQFRRKNINIHAANAVTKLRDALATMRLEHDALVSLNWVVSIYFVVWTILGFLVLEILLQCSAKDMAVLEQRSVNHLFFSLFASISTFTNSGILPLDDSIAAFRENNGILLWLSILILVGNTLFAPCLRTTIWCLKSLSATPARRAIYDYLLKNPRRCFTHLFPRNQTIWLVVTVMGFNAFESAFFYILSWRSQALDGLTTPQKLVNGIFQSITTRSAGENVVSISALSPSMLVLYIAMIQSKRLIATDTAYLFISIFVLCIIENRKINDDPLNFSIFNIIFEVISAYGNVGLSLGYSCSLLRKLTSFSSDTSCEDVPYSFSGTWSVPGKLLMIVIMFLGRHR

1.9E-51	185	23.7	3.6E-51	183.6	16.4	1.4	1	I7C6C6_MYCHA	Cation transport protein	MHLP_02360	Mycoplasma haemolamae (strain Purdue)	495	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Candidatus Mycoplasma haemolamae, Mycoplasma haemolamae (strain Purdue)	1212765	>tr|I7C6C6|I7C6C6_MYCHA Cation transport protein OS=Mycoplasma haemolamae (strain Purdue) GN=MHLP_02360 PE=4 SV=1MGKQAKGQGKFWKFCSQAKGHILGNTIYQKLSRIYLAIILLGFGALNIPGVSVNQGSADWFSKLFISMSAFTTTGLAVSSPKCSL NVWGQVVLLILIQVGGIGVVTIWMFIKNAVFKWKKSDFEERMRLHSERGSTGEESAFEVTKTALKILLSFEIVFASILVFFFYFVEPKAG CTDKFKGNFLKSLWAGVFHAISALNNAGLDIISDTRSIAPYSKGWGVILTVIFSFASIIGGIGYPALCDLQAKFSGRGRNRTSKPVFSLFT KISLLMYTVITITAGTGVLLAEGLSRGFNGNGKDCCLNTAEKIWQLVYLVISSRSSGFAGLDISSLHEKTQWILLVLMFIGAAPASTGGGI RGVTLFVIVGKVWFTLRGRKALTVFSKTISETTVDSAFLVFIMSSMLIVAGSLFITGGGQQSGQTLDKHAALFEASSAFGTTGLSLGMT EKTRWFGKVTLMILMYLGQLGIPNVLMHYVRPKVLKKDMIYPEEQLRIA
2E-51	184	34.6	1.8E-50	181.3	24	1.9	1	Q6FCI8_ACIAD	Putative potassium uptake protein (TrkH)	ACIAD1355	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	445	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	62977	>tr|Q6FCI8|Q6FCI8_ACIAD Putative potassium uptake protein (TrkH) OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) GN=ACIAD1355 PE=4 SV=1MKKQKINQKTFNLSPPSMLALGFLSFIVAGTLLLKLPISNNGHLSWMDAFFTATSAVTITGLSVINIGQSLTHVGQIILLFLIQCGGL GFMTFAILAALSLAPQLGLKQQLMAQDSMGQTSLSKVTFIAQAVFIYTLIFELMGTCILTFAWMNQFGFFHALYYAFFYSISAFNNAGFS LFPNNLMNFQTHYIACLTISFLYILGGLGFLVIMDIKERKRWKKLSPNSKIVIISIAILNTSAFLIIWLLEVNNPLTLYSMSFSEQALNAWFQ ATVPRSSGFNTIDIASMNNSSTLLTMFLMFIGGGSLSTAGGIKVGTFVILVFSVIAFLKRHDEVRIFNHSISYENTFKALAVVVITLILIFIGF FSILILEPHKNFLDLFFEIVSAACTVGLSRGITPQLNNSSLFVLSLLMYAGRLGPLTLAYLIATPKKSRLKHPSADIQIG
2E-51	184	24	1.8E-50	181.3	16.6	1.9	1	G4KWP9_OSCVS	Ktr system potassium uptake protein KtrB	ktrB OBV_36710	Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter valericigenes, Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	693746	>tr|G4KWP9|G4KWP9_OSCVS Ktr system potassium uptake protein KtrB OS=Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20) GN=ktrB PE=4 SV=1MNFLKIKSWSSTRLLSVGFALIILFGTVLLSLPISSRSGNGLGLLDAAFTAASATCVTGLALFDTYTQFTVFGQVVILLLIQVGGLGF MTVAIFFSLAVHRRIGLRERSLLADGVGSLHLAGVVRMVRRILFGTVVFEGLGTVLLAIRFVPRFGFLRGLWTACFHAVSAFCNAGFDL MGRLQPSSSLTFFYDDPLVVLTIAALIVIGGIGFVVWNDFADCAFHLRKLNYHSKVVITSTLALIAVGAALFFWMEKDASMAGMDMGG RLLSSLFQSVTPRTAGFNTVDTASLSDGGKALTMLLMFIGAAPGGTGGGIKITTFVVIAATAYASLKNKNNTNVGHYCIRVETIGRAFCS VTVYIGITLAGILVLCTQGVALTDAAFECISAIGTVGLSTGVTASLTEVSKLAVILLMYIGRLGSLTVFLAVSGRDAKAGFRYPIGKLLVG
2E-51	184	30.9	1.1E-49	178.7	21.4	2	1	R5FFA7_9FIRM	Potassium uptake protein TrkH family	BN468_00206	Faecalibacterium sp. CAG:1138	451	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, environmental samples, Faecalibacterium sp. CAG:1138	1262896	>tr|R5FFA7|R5FFA7_9FIRM Potassium uptake protein TrkH family OS=Faecalibacterium sp. CAG:1138 GN=BN468_00206 PE=4 SV=1MNRKRYKIKLSVWQNLTIGYFLVIVAGSLLLMLPFASTEKTTYINALFTSTSATCVTGLVPYDSGTHWTTFGQIVIILLIQIGGLGFM TFVTMVYRIINRNMAMHGKIAMMQSAGIGKLSDLKGISKRILLGTAIFESGGAILLATRFVPMFGWGKGIYFAVWHSVSAFCNAGFDLM GTQGAKFVSFTGQATDPVITLTLAFLIIIGGLGFVVWSDIKDNGLKFSKYGVYTKVMLVSTVWLLIVSTALFMIFERNNPTYDGYTFGQK LLVAFFNATTPRTAGFNTTDLLSLSDSGYLLTVVLMFIGGGSGSTAGGVKVGTMAVILMGMVAAFKGKRDVTIGSRRIDSSAINQALAV FSSCLLIVVFSTITLCAIEPDEILSFKQLLFEVVSALGTVGLSMSATPLLSSVSKLIVILLMFTGRVGILTFALAFGKTATSDDVKKPVGNILI G
2.1E-51	184	15.5	4.3E-51	183.3	10.8	1.4	1	A0A0F2R8F1_9PROT	Trk system potassium uptake protein	VR70_18090	Rhodospirillaceae bacterium BRH_c57	490	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), unclassified Rhodospirillaceae, Rhodospirillaceae bacterium BRH_c57	1629718	>tr|A0A0F2R8F1|A0A0F2R8F1_9PROT Trk system potassium uptake protein OS=Rhodospirillaceae bacterium BRH_c57 GN=VR70_18090 PE=3 SV=1MGTGGTPAVIDLRPVLLVIGFLLTIMSVGMLIPALVDLGVGHTDWQAFAWSGGLGVFLGLMLVFSNTMGRVSMNVRQAFLLTVA TWVVLPAFAAVPFTLADPGLSYTDAFFEAMSGVTTTGSTVMVGLDTQPPGILLWRGILQWLGGLGIIVMALTVLPMLKVGGMQMFKV EAFEAQEKIYSRATQIAAALTIVYGGLTLVWAFALWAAGMPFLEAVVHAMTTIATGGYSTRDASVGYFDSAAIDAIITFGMVAGGIPFLL FLQALRGRPWQLWRDTQVRWYLGVLVAFTVLMAWWLWQMRGFDAFQALRYASFNVVSVMTGTGFATADYNGWGGFPVAALFLL TFVGGCAGSTSCGIKVFRFQILYETAKVQLGRLLQPHAVFIPYFNGRPIQSGVPEAVMGFFFLYLLTVGLLTLALGLLGMDLITALSSAA TAVSNVGPGLGPIVGPAGNFSTLPDSAKWLLSLGMLLGRLEIYTVLVLLVPRFWKG
2.1E-51	184	32.4	2.6E-51	184.1	22.5	1.1	1	R5KKJ0_9CLOT	Potassium uptake protein TrkH family	BN572_00778	Clostridium sp. CAG:264	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:264	1262786	>tr|R5KKJ0|R5KKJ0_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:264 GN=BN572_00778 PE=4 SV=1MNKKKYVNRNYLTTTRIIALGFLITVIVGTILLSLPIASANGTWTDLLTAAFTSTTSVCVTGLVVVDTFSYWSLFGKGVILILIQIGGL GIVSIITLFMLLLRMKITLKSTMLLQDAFNLNSKQGLLKFTIKVIKGTFLIEGIGALIYSFYYCREYGFLKGIWFSVFHAVSAFCNAGIDIMG ADSLISYHSNLLMMLNTSFLIIMGGIGFIVWWDTVEAFRRIRTKRCSIRSAWNGVHLQTKIAIFMTLLLLIGGTIVIYFLERSNPDTLGNLS EKDRILNAFFQSVTFRTAGFAAVSQVALRPVTAFFGVLLMMIGGSPVGTAGGMKTVTIAVIFYTFAAMIRNHEDTEVFKRSIPVSVVKK AVAIVFLSMSTIFIMTILLLATNDVNLLDALYEVASAVCTVGLSRNLTPVLNTAGKIIIIICMYIGRVGPISMVVAFNTQNGKHRLLHYPEED VIVG
2.1E-51	184	31.2	3.1E-51	183.8	21.6	1.1	1	R6D3L9_9CLOT	Potassium uptake protein TrkH family	BN558_00709	Clostridium sp. CAG:242	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:242	1262783	>tr|R6D3L9|R6D3L9_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:242 GN=BN558_00709 PE=4 SV=1MNSAKKRASINPARMISESFAAVIVIGAILLWLPISSKSGEFTPLLSCVFTAASATCVTGLILFDTYTHWNAFGQGILMMLIQIGGL GLVTFTSFFNLVVGRKLGLRGMRLASESINSTSFGDVPHLLRMIITFTLTVESIGAVLLSLYFVPRYGLQGLWISAFLAVSAFCNAGFDIL GFLGEYTSLTTLNDSYLVLFTIMALIIIGGLGFIVWNDLIAYRKTKTLLLHTKIVLMVTIFLIISGAICFLLFEWDNPATMQPMNLKEKIGAAF MQSVTMRTAGFNSIDLYSMRDVTKVFSIVLMFIGAAPGSTGGGIKVTTMAAIIVMTAVSIIRGKEEPYVLKRRIAANVVYRSIAILFLGIVVV SVTSIILMTTSPLEQNSFSGIDAVFEAMSAFATVGVSAGVTGITSEISQVALILAMFIGRVGPVSFGLSLAAQQSVSRKLIMPEGKVIVG
2.1E-51	184	28.4	7.5E-51	182.5	19.7	1.7	1	Q87R92_VIBPA	KtrB	VP0905	Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio harveyi group, Vibrio parahaemolyticus, Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	223926	>tr|Q87R92|Q87R92_VIBPA KtrB OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP0905 PE=4 SV=1MTQFHQRGVFYVPDGKRDKAKGGEPRIILLSFLGVLLPSAVLLTLPVFSVSGLSITDALFTATSAISVTGLGVVDTGQHFTLAGKIL LMCLMQIGGLGQMTLSAVLLYMFGVRLSLRQQALAKEALGQERQVNLRRLVKKIVTFALVAEAIGFVFLSYRWVPEMGWQTGMFYAL FHSISAFNNAGFALFSDSMMSFVNDPLVSFTLAGLFIFGGLGFTVIGDVWRHWRKGFHFLHIHTKIMLIATPLLLLVGTVLFWLLERHNP NTMGALTTGGQWLAAFFQSASARTAGFNSVDLTQFTQPALLIMIVLMLIGAGSTSTGGGIKVSTFAVAFMATWTFLRQKKHVVMFKR TVNWPTVTKSLAIIVVSGAILTTAMFLLMLTEKASFDKVMFETISAFATVGLTAGLTAELSEPGKYIMIVVMIIGRIGPLTLAYMLARPEPT LIKYPEDTVLTG
2.2E-51	184	4.9	3E-50	180.5	3.4	2	1	E3CXV7_9BACT	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Apau_1141	Aminomonas paucivorans DSM 12260	439	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Aminomonas, Aminomonas paucivorans, Aminomonas paucivorans DSM 12260	584708	>tr|E3CXV7|E3CXV7_9BACT H(+)-transporting two-sector ATPase OS=Aminomonas paucivorans DSM 12260 GN=Apau_1141 PE=4 SV=1MRIYSSLRVERMLVLGFLSLITAGTLVLWAVDRLSGHPLSLLDALFTATSAVCVTGLAVVDTGRDLSLPAQGVLLLLIQLGGLGVM TATTALPLVFGMKIHLRQRLLFAGGLGMDTPQGAVRLLSTVLRYTLAVEALMAAPLFWGFLQREAPGRAAYLAVFHSISAFCNAGFSP YGDSLETFAGTFWVPGAVMVLVVLGGLGFPVAAELRACARRRHPLSAYTRMVLVVTAGLILLGTVLLAFSEWDRAFRDLPPLLKGWN ALFHSITPRTAGFDTVALRNFSGLGLGITLTLMFVGASPASTGGGIKTTTFGVLLACSWKEVQGEEETVVWGRRIDPRTQRKALALTV LYLATLFLAVLGLCLYEPFSFRDLLFEAFSAMGTVGLSVGITPRLTPEGKMILVFLMFWGRVGIVTFLYGILARTRPGKVQYPSAQMPIG

2.2E-51	184	17.8	3E-51	183.8	12.3	1.1	1	D7B4M3_NOCDD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Ndas_1634	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	479	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	446468	>tr|D7B4M3|D7B4M3_NOCDD H(+)-transporting two-sector ATPase OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_1634 PE=4 SV=1MRTGTGQYPPGPRAPRVPRIPARAGARADRRRLRDLSGWIKPPQLTAAAFAALILVGAGLLSLPAATEAGERAPFDTALFTATSA ASVTGLAVVDTASYWSGLGEAVILALIQVGGFGIMALATVLTLVVGRQLGLRMAVRTGSEAKVVTLGEVRQLVTGVLVVTVVFETALA VALALRWWLGYGLSLPEAVYTGVFHAVSAFNNAGFALYADSLMGFAEDPWITLPLALGVLAGGLGFPVWVELWRFTRRRAEHRHW TLHAKITLVVTGLLLVVGFVAFLALEWSNPATMGGLDLRGKLLTAFFQSVMPRTAGFNSLDFGQMNTQTLLVTDILMFVGGGSAGTAG GIKVTTFAVLAFVVYANVRGEPTVHVSGRRLAEGTTSQATTVALLALGLVLAGTLTLMTITPFTLDQILFETTSAFATVGLSTGITADLPL LGQAVLMFLMFVGRIGPITLASALALRRRPRLYELPEERPIVG
2.3E-51	184	7.9	1.3E-25	99.3	1.8	2.2	2	V4J951_9DELT	Trk system potassium uptake protein	N839_10960	uncultured Desulfofustis sp. PB-SRB1	486	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfofustis, environmental samples, uncultured Desulfofustis sp. PB-SRB1	1385624	>tr|V4J951|V4J951_9DELT Trk system potassium uptake protein OS=uncultured Desulfofustis sp. PB-SRB1 GN=N839_10960 PE=3 SV=1MKGGQVIAALGFILIAFGTIILSPITVALIEHEPEAIAPFVWASAIAISLGFLCRKMGGGRTNFDRLKRNEGMLIVCLAWLSAAAVTAI PYLFFGLSPLDAYFEAMSGITTTGATILLDFSGYPRCFFFWRSLSQWLGGMGIIVLFVAILPQFKVAGRQLFFAEAPGPTEERVTPRIT QTAKALWFVYVSLTLLEIGALVWAGMGPFDAVCNSLSTMAAGGFSPNPASIMGYGSDRICWIITVFMFLAGANFASQYWAFVRRRPR VLFGSEEFRGYLAIIVAAGGGVSAALLATTDASGVVALRDGYFQIVSLLTTTGFATADFARWAVPCQVILFSVMLVGGCAGSAGGGIK VVRILFCAKYIRREIVKIIHPRLVMPIKIDRKTVPEAIQQQILGFLLFYLLVLIASTLVVTAIEHDLVVGIVGTAATLGNIGPGYGEIGPMASF GTLVWPTKLIFIFNMVVGRLEIIPFLAMLHPDFWYLSKH
2.3E-51	184	30.1	3.1E-51	183.8	20.9	1.1	1	A0A0F5H1H0_9MOLU	Potassium uptake protein TrkH	MMELEA_03130	Mycoplasma meleagridis ATCC 25294	492	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma meleagridis, Mycoplasma meleagridis ATCC 25294	1264554	>tr|A0A0F5H1H0|A0A0F5H1H0_9MOLU Potassium uptake protein TrkH OS=Mycoplasma meleagridis ATCC 25294 GN=MMELEA_03130 PE=4 SV=1MSPITHQKINSSWGNVNFIDALFTASSAFSDTGLTSLNTYKTWNIFGQSLISILILIGGLGVFALKIYIINILFFGKLKISLNALNIVDSE RSSNDIGKGTREVIIDSISTLLIIMLIGAVGLSFYFYLAEPRNLFISQTKIIDPETNLSLSKSLYYNFVGDFINPKGNWSLSFRFGFFHAISAL NNAGFDIIGNSSLMPYYHNIELQFFFLILFFIGGIGYPVIHDIINFFRFKIKHPSRKYHWKLLTKLSLISYLLASLIGAILVVTFEILAKNGFW WTNSNEINKITEERFFGNNAEKTWALIFSVFSTRSAGFATIPINHLSDSSLVVLSILMFIGAGPSSTGGGIRTTTFAIITISIFSRILGRPSV RAFHRKIDNNTVKNSYTVFLTGIVLLIITSLVISSSSANYFGNVPANTHFSNYLFEASSAFGTTGITAGISANSNILSKIFLIIIMFIGQLGISS TILIWGKRRNYSYKYEYVPENVPIG
2.4E-51	184	21	1.8E-24	95.5	5.5	2	2	G9WM46_9FIRM	Uncharacterized protein	HMPREF9625_00429	Oribacterium parvum ACB1	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Oribacterium, Oribacterium parvum, Oribacterium parvum ACB1	796943	>tr|G9WM46|G9WM46_9FIRM Uncharacterized protein OS=Oribacterium parvum ACB1 GN=HMPREF9625_00429 PE=4 SV=1MNFSMIVYILAWVLKIEGASMILPLLCSLIYKENDIALCFFIIGTASVLLGYILTAKKPKKIAFYAREGFVIVAACWVVLSLVGALPFFI SGRIPHYIDALFEIVSGFTTTGSSVLSDVEALGKGLLFWRSFSHWIGGMGVLVLVLTVLPLGGGYNMMIMKAESPGPEVTKMVPRVAD TAKALYKIYFILTIIMILVFLLSGMPLFDALCIGFGTAGTGGFAIRNSGMADYSMLSQFLITIFMILFGVNFNVYYLIQRKKFSDAFHSEEAR GYFIIIAASTLFITFNIFQSIGKGFLFALHHAFFTVGSIITTTGFSTLDFNEWAVPSQMVILFLMICGACAGSTGGGLKVSRLIILLKSLAKEL HLIIHPEAIKKVRLEGKCLDHSVVRSVSTYLVAYCFIYMISIFLISFDGYDFLTNFSAISATFNNIGPGLGKVGPLSNFSVYSYFSKLVMIFD MLAGRLEIFPMLILFSIKTWKKTN
2.6E-51	184	28	2E-50	181.1	19.4	1.9	1	E3DNA8_HALPG	Cation transporter	Hprae_1399	Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL)	493	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium praevalens, Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL)	572479	>tr|E3DNA8|E3DNA8_HALPG Cation transporter OS=Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL) GN=Hprae_1399 PE=4 SV=1MKYKNLIISRYFLISKYIGVIIMFAGAAIASPLLFLTAYPEESFLAPQFLLAAGLSVLVGLALYSYGNKHQEEDVELSLNEGSIIVIFS WLGAIFFSAIPFVTILDMSWSHSIFEVVSGWTTTGLSLVDVTKAPKLILIWRSIMQFFGGAGLAVIALSSLLPVHGMGLYMAEARSDKLL PHVKRSTMMIMKIYTFYTVAGIFLYYFSGMPMFDSINHSMAAISTGGFSTQPDSIGHYNSLSIEVVTIILMFLGTINFATHYTLIKGKINTF FKNAEIRLMITLFTLLTPILMFFSLNSLYPKLGENFRITFFQIITALSTTGFSTIAFAGWPIFANFIIILIMLVGGGTGSTAGGIKQYRIYLIFKS IFWEIKEQFLPRRSVSSNYLWRGENKFYVKDQHIKDVANYIILYLFTFFVGVAIHTAYGYSLLDSMFEFGSALGTVGLSIGLISPTAPTGII WTQTIGMFLGRLEFFIILYAGIKLAKDGIYIVKK
2.6E-51	184	19.6	1.6E-50	181.5	13.6	1.8	1	G8AUF9_AZOBR	Trk system potassium uptake protein	trk AZOBR_p220031	Azospirillum brasilense Sp245	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum brasilense, Azospirillum brasilense Sp245	1064539	>tr|G8AUF9|G8AUF9_AZOBR Trk system potassium uptake protein OS=Azospirillum brasilense Sp245 GN=trk PE=3 SV=1MTGFDTRPVFFIIGALLSVLAVAMLLPMSVDLAAGNPDWMVFAIAFALTLFFGVQFMLANRMDRIALNLRQAFLLTALSWVVICAF AAVPFMVSQIDLSAADAYFEAMSSLTATGATVISGLDGLAPGLLLWRSLLQWLGGIGIIGMAIAILPFLQVGGMQLFRSESSDRSDKVT PRASDLAIAVGWIYLCLTAVCTAMLAYAGMSWFDAVNHAMTAVSTGGFSTRDASIASWNSPAIEWVLVIFMVLGGMPFVRFISLAQG RAASFWADTQIRWYLGFLAAVSFGMSVWLTLTRGVPWDDAIRVTTFSVVSVVTTTGYASIDYERWGPLASVVFFILTFVGGCTGSTS GGLKIFRFEILFIVLRALQRRLYSPNLVIPLNYNGKPVSADVMISVMSFGFVYLMSVFVLAFVLAFLGVDVVSALSGAATAVSNVGPGLG PTIGPVGNYATMPDGAKWALAAGMLLGRLEFFTILVVLSPSFWRR
2.6E-51	184	19.3	1.9E-49	177.9	13.4	2.1	1	A9DFA3_HOEPD	Trk system potassium uptake protein	HPDFL43_21539	Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43)	485	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Hoeflea, Hoeflea phototrophica, Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43)	411684	>tr|A9DFA3|A9DFA3_HOEPD Trk system potassium uptake protein OS=Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43) GN=HPDFL43_21539 PE=3 SV=2MNVLAEFRPVMLVTGALVSTLGVAMLLPALVDLAADNDDWMIFASSAMVTMLFGFGLFIANRGAPKGLSTRQAMLMTVVSWLA LVAFGALPFQWSGIVPSYTDAFFESMSGLTTTGATVITGLDTAPPGLLFWRGLLQWLGGLGIIVMAIAVLPMLQIGGMQLFKAEAFDT AEKILPRATQISTSITLVFIGITGVCAIAYMAVGMAADDAVIHAMTTVATGGFSTKDASIGHFANPGVEWVAVLFMILGSIPFILYVQMLQ GRFRPIFVDQQVKAFFAFLGVAVLAGWMMAHFSQYHLGLDGLRHAAFNVISIVTGTGYSSTDYGLWGPHAVAFFIIMFVGGCAGST SCGIKIFRFQVFFEAVGQHIAQVMYPHGVFRAQFNGKPIEGRVISSVMSFFFLFIASFVVLAILLRLSGLDAITSLSGAGTALANVGPGLG EIIGPAGNFQSLNDVQKWLLSAGMLLGRLELFTVLVLLLPRFWRS
2.7E-51	184	31.8	9.6E-51	182.2	22.1	1.7	1	D5V3L0_ARCNC	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Arnit_0051	Arcobacter nitrofigilis (strain ATCC 33309 / DSM 7299 / LMG 7604 / NCTC 12251 / CI) (Campylobacter nitrofigilis)	442	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Arcobacter, Arcobacter nitrofigilis, Arcobacter nitrofigilis (strain ATCC 33309 / DSM 7299 / LMG 7604 / NCTC 12251 / CI) (Campylobacter nitrofigilis)	572480	>tr|D5V3L0|D5V3L0_ARCNC Potassium uptake protein, TrkH family OS=Arcobacter nitrofigilis (strain ATCC 33309 / DSM 7299 / LMG 7604 / NCTC 12251 / CI) GN=Arnit_0051 PE=4 SV=1MEHKYVRSIFVGYVLVIFFGALVLALPICHKGHLAFIDAIFTATSATCVTGLIVTSTSENFTLLGEVIILLLIQIGGIGYMSLVIIFFLSFR QRLDIDEKRAMRQSLDLPSLHVRKFLRKIFAVVLVIEILGAIILTTQFLKKYDLLHSLWYGIFHSVSAFNNAGFSLFTNSLEGYQSDTISLV TICILVVLGGMGYFVLIEIYENRRFAKRFTIHTRIMIYGTVILIVAGMILFLSIEWNNPKTFGGLSVYDKLLNAFFLSINFRTSGFNSIDLGGL KESSLFFSTLFMMTGAGQGSTGGGMKITTVAILIITVIYILKESNQQPSIFKRTIEQKIINKALAIILSSSFFVLLATLILVETQDLPFLRILFEV VSAFGTVGVSTGNGGGVLSFSQEFDILGKSIIIVMMLAGRLGVFAFGLILVGKAKTKHFKYPTGRIII

2.7E-51	184	21	2.8E-51	184	13.8	1.5	1	R7CQ30_9FIRM	H(+)-transporting two-sector ATPase	BN806_00474	Ruminococcus sp. CAG:9	464	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:9	1262967	>tr|R7CQ30|R7CQ30_9FIRM H(+)-transporting two-sector ATPase OS=Ruminococcus sp. CAG:9 GN=BN806_00474 PE=4 SV=1MNKKMQLYNRLHKLNTAQIITLGFAGVIILGGLLLWLPFCTAPGYHTSFTDAMFTATTSICVTGLVTVVTATHWTLAGKIIILVLIQI GGVGLISLGSIIFISLRKKISLRNRRVIQESYNMDRMGGMVRLVKKVLICVFGAEGIGAVCYAVRFIPQFGLAKGLGYSVFTAVSAFCNA GIDLLGEDSLAQYVADPIVNFTSVGLIIMSGLGFVVWWDIWDKIKRVIRGKLPVGRIFKNLRLHSKIVLMMTLILVVGGTVLIFLFDHGNP ESIGTYSPGTKWMASLFQSVTTRTAGFFTVSQERFSNATYMLCLILMLIGGSPMGTAGGIKTTTVAVLLLSLKSNLQGKRDVEVHHRRI RDSYIRSAIVVTGMVLTVLILMSMLLCAAMPEAPIEDVVYEITSAVATVGLSRGLTPCLNTAGKWIVILTMYLGRIGPLTLGTAVTVRVQK MPADSHLAEEDIMIG
2.8E-51	184	32.4	6.7E-51	182.7	22.5	1.5	1	R7MIC9_9FIRM	Potassium uptake protein TrkH family	BN739_00829	Ruminococcus sp. CAG:624	442	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:624	1262965	>tr|R7MIC9|R7MIC9_9FIRM Potassium uptake protein TrkH family OS=Ruminococcus sp. CAG:624 GN=BN739_00829 PE=4 SV=1MKSIFSYTRMIAFGFLAVILMGTLLLSLPIAARSGDRTALIDCFFTATSATCVTGLTVLDTYMHWSSFGHVIILGLIQIGGLGFMTIIT MFSIFTRKHISLYERRLLMQSAGTIRLSGIITMIKRVVIGTFCVEGMGAVFLSLRFCPKLGFAKGLWYAVFHSVSAFCNAGFDLMGRFN EVSLTGYYNDPLVCITLMVLIVIGGLGFLVWSDVIKCRFVFKKMELHSKLVLTVTALLVFGGAAVLFMTEKNGAFKGMTTGEQVLSAFF QSITLRTAGFFTFDQSKLSNSGYILSTLLMFIGGSPGSTAGGVKTTTMAVAFLNLISVARNNDDVVIFKRKIINNKVVIQSVAIIGIHILMASI AIFIICYLEPIGLREVIYESVSAISTVGISMGITSDFNVASKLFIAGLMYSGRIGGMTIVLAIAENSHKVKLERPEEKILIG
2.8E-51	184	17.5	6.3E-49	176.2	12.1	2	1	A0A076NIC3_9CORY	ATPase	CIMIT_03810	Corynebacterium imitans	433	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium imitans	156978	>tr|A0A076NIC3|A0A076NIC3_9CORY ATPase OS=Corynebacterium imitans GN=CIMIT_03810 PE=4 SV=1MKQLLSSPARLTAFGFFFLIMVGTALLMMPFAGGASLLSALFTATSAVSLTGLVVEDTATFYSPAGQVIILVLIQLGGLGIMSLASL SGYVLTGRISFKARKTGAYEGRPITSGGIRRTLIFTFAFTAVVEATIAVLVGARLMLGYGYSFPRAAWEGIFHAISAFNNAGFSTHSDNL VSFAADAWILLPLAAALIGGGLGFPVWAELVRRKISITGRMTLWATGLLLLFGMVFFACAEWRGVLGPMPLGQKLLNAFFASASPRTA GFNAVDYGQAHPITLMGTDMLMFLGGGSAGTAGGIKVTTFCVLLAAMAAEFRGRKNTTIGHRSVPHTVTRQALALSVAGVAVVVVGV ATLRIFDPQFTADQVTFEVISAFATSGLSTGITADLSTTSKLVLCMIMYLGRVGPTTLVAALAARTVDRRFSYPEERPFIG
2.9E-51	184	24.1	6.8E-50	179.4	16.7	2	1	A0A0F0CAU4_9CLOT	Potassium/sodium uptake protein NtpJ	ntpJ CLFS41_24570	Clostridium sp. FS41	457	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. FS41	1609975	>tr|A0A0F0CAU4|A0A0F0CAU4_9CLOT Potassium/sodium uptake protein NtpJ OS=Clostridium sp. FS41 GN=ntpJ PE=4 SV=1MKEKLFESKPKHYRLKKHISQTQFIAYGFFLIIMTGTFLLMLPISSRDGQSEPFLNCLFTATSASCVTGLVVADTWTQWSMFGQV LLLIMIQLGGLGFISIGIFLSIVLRRKIGLKERGLMEESVNTLQIGGMVKLARRIIMGTAIFEGAGAVILSRFIPQYGLFRGIWYGIFHSISA FCNAGFDLMGHAEQYSSLCGYTGDWVVIGTISALIIIGGIGFIVWDDLYRKKWDFRHYMLHTKIVLVTTATLLAVSTVLFYLMERDNILV GMSGSEKFWACFFSAVTPRTAGFNNVDTAALTDGSKFMTAILMFIGGSPGSTAGGIKTSTLAVLLLYVHSNIRQTYGVEIFGRRLQDE SIRQSACILTINLSLMLTATILIMVFQNLPMSDVFFETCSAIGTSGMSTGVTRSLNTFSRIVIILLMYCGRIGSLSFALAFTRSSRKPHVQLP AERITIG
2.9E-51	184	17.8	1.7E-50	181.4	12.4	1.8	1	K0CBM8_ALCDB	Na(+)-transporting ATP synthase (Divided with OB1663 and OB1664)	yubG B5T_00798	Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	456	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Alcanivorax, Alcanivorax dieselolei, Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	930169	>tr|K0CBM8|K0CBM8_ALCDB Na(+)-transporting ATP synthase (Divided with OB1663 and OB1664) OS=Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5) GN=yubG PE=4 SV=1MRTWFPGLRARTEAVLSLRHPWRYSPPAILAGSFLLLIGIGTVLLWLPVSGTPPLTFFQALFTACSAVTVTGLVVVDTGSHLSPF GQSVVLGLMQLGGLGLMTFAALTLVALGGRLGLRGQRLVREATDQTSPADMLVLVRHTALLALIMEAIGAGLLSVVWIPELGVARGL WFSVFHSVSAFNNAGFALLPDSLSQWAANPMVNLVITALFIIGGLGFTVLLDLWRKRQWRTLSLHSKLTLAGTLVLCLGAWFLVIGFE WNNARTLGELPESGRLWAAWFTAVTPRTAGFNTVDMGGLMAPTVMLIMFLMFIGGGSNSTASGIKVSTFMVMLLATRAFLRGRQRP TVFRRAIAVESVFRAQAVVMLSLLAVALSGFLMVVLEPGRAVMDVLFEAFSAFSTVGLSRGITGELSWPSQCVLMILMFMGRIGPLAL AFSLARPQIPKLRYVEDHVQIG
2.9E-51	184	21.4	1.3E-50	181.7	14.9	1.8	1	A3CWW1_METMJ	Cation transporter	Memar_1935	Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1)	485	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanomicrobiaceae, Methanoculleus, Methanoculleus marisnigri, Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1)	368407	>tr|A3CWW1|A3CWW1_METMJ Cation transporter OS=Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1) GN=Memar_1935 PE=4 SV=1MDRIEQFSIIAADIGSIFKYMSIATALPLVVAVIYGEWDMILPMVSVPVVLFILGMFLLQVPREDREAPLSAALMAVALIWLIIALVSA LPFCLGLGVPYLDAVFEAMSGWTDTGLTMMRSVEEMPRTLLFWRSLMQWLGGIGIVAFTVAMASRTGLTQFRLYRSEGRSEALMPS VVATGFEMWKIYLALTAASIGLILLSGVPVWDAVNIALVAIATGGFSVHSAGIPFYNNPLLEVLIVPVMIAGALPFKLYYLLYRQKDTRFF GDQQARLLLMLIALGILVIAWDLVTLTATDLPTAVRQALFMATAAATSTGFQVASPNEWASVTVLFLAMLMVIGGASGSTAGGIKLSRV VLGFQSLVWWFRRMFVSGKVLVPFKYDGKVIPKNVADLEVSRNMLTIMLYFLIFVATILVMHLQPTSFDSSNVIFEVVTAMCNNGIST GFVSPDMEAPAKGLFILIMWIGRLEVIPVIMLVMGLFKRSD
2.9E-51	184	20.1	2.6E-26	101.6	5.8	2.1	2	R6RMF3_9FIRM	Cation transporter	BN583_01015	Anaerostipes sp. CAG:276	495	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, environmental samples, Anaerostipes sp. CAG:276	1262699	>tr|R6RMF3|R6RMF3_9FIRM Cation transporter OS=Anaerostipes sp. CAG:276 GN=BN583_01015 PE=4 SV=1MNYAVIRYILGLVILFEGAFLSLPCMVALIYREARGIPFFAVMLLCFFVGFLLSHKKPQNMQYYAKEGFVAVALSWILLSFFGCLPF VFNGDIPSFTDAMFEMISGFTTTGASILSDVEVLAKCSLFWRSFSHWIGGMGVLVFILAILPMGGGQNLHLMKAESPGPSVGKLVPKV RQTAKILYGIYCFMTLIEIILLMFGGLPLFDSMLLSFGSAGTGGFSILNSGFADYSPYIQYTVTVFMILFGINFNVYYFILIRKFKDAWKFEE LKYYLFVIAAAVLCITYNIRDLFPTLESAFRHASFQVGSIITTTGYSSVDFNVWPEFSKVILVLMLMFIGACAGSTGGGIKVSRVILMLKTVK KEMYFYIHPRSIRKIKFNQHVVEHEVIRSINIFLITYMMILAFSTLLIALDGFDLITDFTAVAATLNNIGPGLELVGPTSNFGMFSDFSKVVL MFDMLAGRLELFPMLVLISPITWRDTKVFKKIPKYRKNSPGV
3E-51	184	18.3	2.9E-49	177.3	12.6	2	1	D4LA55_RUMC1	Trk-type K+ transport systems, membrane components	RUM_02550	Ruminococcus champanellensis (strain DSM 18848 / JCM 17042 / 18P13)	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus champanellensis, Ruminococcus champanellensis (strain DSM 18848 / JCM 17042 / 18P13)	213810	>tr|D4LA55|D4LA55_RUMC1 Trk-type K+ transport systems, membrane components OS=Ruminococcus champanellensis (strain DSM 18848 / JCM 17042 / 18P13) GN=RUM_02550 PE=4 SV=1MFDLLHKKIQLSSFQLIILGFAGVILLGACVLMLPISSQLRQFTPFSEALFTATSAVCVTGLIVQGTGCYWSAFGQGVILSLIQIGGL GVVTIAVSFSLLSGRRISLMQRSTMQEAIAAPKVGGIVRLTGFILRGTFLIELLGALALLPVFCRDHGARGIWMAVFHSVSAFCNAGFDI LGTDQNPFPSLTEYAANPAVNIIIMLLILIGGIGFLTWEDIVVNKWRLRRYRMQSKVILLMTVLLMAIPAVFFYTDLTELPTGQRILAACFQ AVTPRTAGFNTVNLLSLGGASNAVTMVLMLIGGAPGSTAGGMKITTVAVLFANAFATFRKREDAQMFGRRIEPGAIRSAATILMLYMSL FFGGAVIISLCEQLPLSLCLYETASAVGTVGLTLGITPELGLVSKIVLILLMYMGRVGSLTLIYAAVSGKHLSPAKLPQEKIAVG

3E-51	184	32.5	8.6E-51	182.3	22.5	1.6	1	B1YFJ9_EXIS2	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Exig_2878	Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	463	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sibiricum, Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	262543	>tr|B1YFJ9|B1YFJ9_EXIS2 Potassium uptake protein, TrkH family OS=Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15) GN=Exig_2878 PE=4 SV=1MFSHKRRSRLAKFGRFGELIYHQLFDKPARFIATGFTLTILLGGFLLWLPIAQQDGQDIPFIDCLFVATSAGTVTGLSTVNIAESFN LLGQIIMMLLIQVGGLGFMTIALVLLSVTGRKIGIRQRIIIQEMFNLDSPGGTIRLARNIILTTVVVELIGMLLIALDLFIQYKYTFGKSLYYGL FHAVSAFNNAGFALWGDNLVGFQQDTTFILTISALLMIGGLGFTVIADISAKRNFKKISLHSKLMLLSLVVINGLGVLAMMIYEWVSHLG SLHDKSFFAALHIVFFQVVTTRTAGFQTIDLTTMVPLSIGLMMVLMYIGAGSASTGSGIKVTTAAVILKNVWTYLRGQRETVLMRRTVR PQAIQKAYAIAVFSLLFIALVTTLLALSQPNLSFVGLFFETVSAFGTVGLSLNVTAELNDFGKALIMFMMLLGRVGSLTILFTFAAQHDRLI RYPKENMLIG
3.1E-51	184	25.9	5.7E-51	182.9	17.9	1.3	1	D4LF45_RUMC1	Trk-type K+ transport systems, membrane components	RUM_22350	Ruminococcus champanellensis (strain DSM 18848 / JCM 17042 / 18P13)	440	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus champanellensis, Ruminococcus champanellensis (strain DSM 18848 / JCM 17042 / 18P13)	213810	>tr|D4LF45|D4LF45_RUMC1 Trk-type K+ transport systems, membrane components OS=Ruminococcus champanellensis (strain DSM 18848 / JCM 17042 / 18P13) GN=RUM_22350 PE=4 SV=1MTATKMIVLGYSTLILLGGCLLMLPHATRDGQGASLKDAMFTSASVTCVTGMTLHDTYHYWSLFGQLIQLVLIELGGLGFMSVMI FLLSFTKRKIGVKQRFVMQEAYSAPQVGGIVRMTQYIFFSSLAIELVGAAMLCLYFCPRLGALRGIFFSVFHSVSAFCNAGIDLMGYFS PGSSLMDVASDPFLNGVFMVLIIVGGLGFFVWFDVIEHRHHFAKYRLHTKLVLVTSGVLILLGAVQIFLLEHGGEAMAGCSTGEEWLR SLFQSVTCRTAGFFTMDLSAMTEATQFVCICLMLVGGSSGSTAGGLKTTTLALLFLSITVVFRKRKTVECFHRRIEEEAIHNACCVLML YLLLIVSSVSICAIESIGLLDSLFECAAALGTAGLTLGLTARLSALSQVILMFLMFVGRVGGLSVLLALGTTSGNVASQYPLEKVTVG
3.1E-51	184	21.7	1.9E-50	181.2	15	1.9	1	R7H9P4_9FIRM	Uncharacterized protein	BN634_00595	Eubacterium sp. CAG:38	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:38	1262889	>tr|R7H9P4|R7H9P4_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:38 GN=BN634_00595 PE=4 SV=1MNYSIIRTILGHVIRFEGAFLLIPVIIALIYGESSGIYFAVCGAACLVVGTHMTHRKSGNRSFFAKEGFVSVSLSWIVLSIIGALPFVL SGVIPNPVDAMFEIVSGFTTTGASILPEVESLPKCMLFWRSFSHWIGGMGVLVFILAILPLGGSSEVYLMSAESPGPKFGKLLPKLQKS AMTLYGIYLTMTVIEMLLLLAGGMSLFDSICTAFGTAGTGGFGVYNDSMGSFSPYLQNVVTIFMVLFGINFNFYFFLLVKEVREAFAME EVRWYLIIFAAATLMIAANLTIVQGGSPFYYLHHSAFQVASVMTTTGFATVDFNLWPNFSRSILVVLMFIGACAGSTGGGMKVSRYIIYF KTLRKELSTLIHPRSVKVIQCDGKAVDHDTIRSANIYLIAYIFIYMLSVLLISFDKFDLTTNFTAVAATFNNIGPGLNVVGPTGNFAGFSMF SKIVLIFDMLAGRLEIFPMLILLAPGTWKK
3.2E-51	184	17	1.2E-49	178.6	11.8	2	1	G0VQD0_MEGEL	Cation transport protein	MELS_1437	Megasphaera elsdenii DSM 20460	483	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megasphaera, Megasphaera elsdenii, Megasphaera elsdenii DSM 20460	1064535	>tr|G0VQD0|G0VQD0_MEGEL Cation transport protein OS=Megasphaera elsdenii DSM 20460 GN=MELS_1437 PE=4 SV=1MDLHVICQFLGRIAWAQSGVMTLPLVMALVFAEDSWLAFLGTMGTCALAGWGFLRYGHVRTKKLTMREGIAITGLGWLLATFL GMLPYCLGGYLNYFDGLFESISGFTGTGATVIPDLEILPQSLLFWRSLTHWLGGLGIVVIFIALLPEAGQSTVYMYNAESTGPTRERVL PRLHDMTQVLFRMYMAFTATAFVIFFLCGMDFLGALNHALSTVSAGGFSTYNASAAHFESPAVEAWMTFFMILTGGNYGLYYQAWQ KGAHVLWRNTEFKAYLLIAVAAALIGINLMDGFDVSAATALRYSSFQSASIATTGFVSADYDRWPSFSKGILLLLMISGGCAGSTAAGL KVSRVVIMVRYIWQAAKAKLHPRQVVALNMNGHRIGDDTVVRVAQFCFLYLMFIALWALLLTFDGIGAFDAIGISVSTMGCIGPAFGIT GATCTYAELSVFSKSILCLSMLLGRLEIFTLLVMLRKSFWKSKSSW
3.2E-51	184	23.3	3.2E-51	183.7	16.2	1.5	1	R6UDL4_9STAP	Trk system potassium uptake protein TrkH	BN609_00479	Staphylococcus sp. CAG:324	515	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, environmental samples, Staphylococcus sp. CAG:324	1262969	>tr|R6UDL4|R6UDL4_9STAP Trk system potassium uptake protein TrkH OS=Staphylococcus sp. CAG:324 GN=BN609_00479 PE=4 SV=1MNVKVIGKIVGKIMILEGILMFFPFVVSIIYKENYIYILSFLIPSCCLIIIGKLLQLLKPSRKGLYQKEGFAVCALTWIVMTIFGALPFVIN QDIPNYIDALFETMSGFTTTGASIVPDITQLAHSSLFWRSFTHWIGGMGILVFILIFIPESEDGSSLHLLKAESPGPQVGKLASKMKMTT RILYLIYLGLTIIEVILLLFSPKQVASDGTVYQMDLFNSLLTAFGSAGTGGFGFVTNSMEYFSAYSQYVIATFLILFGVNFSLYYLILIGKCK EAFKSEELRTYLMIIVISVFIICFNVISNQIDNLQSLGVVDLEEIFRHSYFQVASIITTTGYSTTNYEYWPELSKCMILILMLLGAMAGSTGG GIKISRLVISFKGIFTRIRKLINPRYVSKTKFEGKILEETTTNDVFAFITLYFFLTFIIILSCDPINGTVVNVAGKEVTHGFVSNFSATISCLS NIGPGLEAVGPYGSFNLYNHFSKIVLTFAMLIGRLEILPVLILFTPKTWKK
3.3E-51	184	20.7	2.7E-24	94.9	5.6	2.1	2	R6WTD8_9FIRM	Uncharacterized protein	BN605_00727	Dorea sp. CAG:317	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea sp. CAG:317	1262873	>tr|R6WTD8|R6WTD8_9FIRM Uncharacterized protein OS=Dorea sp. CAG:317 GN=BN605_00727 PE=4 SV=1MNRKMIAHILAKMLGVEALLILPAIVGVIYQEKSAVYFLPPIILLTLIYLIGGRKKPKNSTIYAKEGMVVVALAWILWSLFGALPFFLS GYIPSYLDAFFETVSGFTTTGSSIMPDVEILPQCMHFWRSFTHWIGGMGVLVFVMVLTSLDKKSSMYLMRAEVPGPEKDKLVPKMMS TARILYGMYFALTALEVILLMFGGLSLFDSLIHSFGSAGTGGFSNYADSVGHFDSAYVDGVITVFMILFGVNFSLYFLLLIKEYKAVWKN EELRVYFGIIAAATAVITINILPQYGSVLKSFRYAVFPQVGTIITTTGYATADFNVWPMLSKCVLIALMIIGACASSTGGGIKVSRFMIAVKSI KREIKQMAHPKSVNLICVNGKKMGNDVIRSVFVYFMAYAGIAGLSVLIVSADNFDFATTFSSVIATLNNIGPGIEDVGATGNFSAFSPLS KLVFCFDMLAGRLEIFPFLMLFTTKVWRRKFW
3.4E-51	184	9.7	2E-28	108.6	1.1	2.1	2	R4VPH8_9GAMM	Trk-type K+ transport system, membrane component	SPISAL_06570	Spiribacter salinus M19-40	489	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Spiribacter, Spiribacter salinus, Spiribacter salinus M19-40	1260251	>tr|R4VPH8|R4VPH8_9GAMM Trk-type K+ transport system, membrane component OS=Spiribacter salinus M19-40 GN=SPISAL_06570 PE=4 SV=1MREVLRGTGFLLHVPGIMALLSMPVAWWADERWGLVGLGWTAGLALFGGQGLVWMGRHAGAFQRYQSMQIAAISWLLIALL GALPFIASARLAPDGSAMALALAVFQFPVYAIFESVSGFTSTGLTVVATASELPAHIQWWRSFSEWVGIGVILLLIAVLPADRGALNLY FSEAREEKILPTVKSTVRAIWVIYLGYTIAGIGLLWLAGEPLWRAINHGMTAIATGGFSITDDSLMQASGAVQLAYIPVMLAGAVSFLVH YRLIVERRPLPSVWRTDELRLLVWLTVGGLVLLWLERWLAMGDWGGVSTAFLWVSALTTAGFTSVDLASWGDAALLLVLVAVITGG MAGSTSGGIKLLRVNVLLRDLLGQLRELRASPHEVVILPHDGERVTPGQFARLGRIAARLVGIFMLLWLLGVFLVLHTLPEEARLAHVF FDTASALFNSGLSTGIAGPDMPWATAGLMSLLMLLGRLEIFPLLVLAAWALAR
3.4E-51	184	19.6	5.7E-51	182.9	13.6	1.3	1	C8X3T1_DESRD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Dret_1794	Desulfohalobium retbaense (strain DSM 5692)	453	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfohalobiaceae, Desulfohalobium, Desulfohalobium retbaense, Desulfohalobium retbaense (strain DSM 5692)	485915	>tr|C8X3T1|C8X3T1_DESRD H(+)-transporting two-sector ATPase OS=Desulfohalobium retbaense (strain DSM 5692) GN=Dret_1794 PE=4 SV=1MRVHISPFAWPIVFFGVAIVLGAVLLHLPLSVTDGAISWTNALFTAVSAVCVTGLIVVDTGSFFSPFGQGVILGLIQIGGLGIMTITS LIFYLWRQRVSLTDHLAVGKSLIHDPRFKLGGFLIRITLLVLVFEALGAVLLRFLAPQGFSWPSAVFHAVSAFCNAGFALQENSLVAWQ GDWAVNGVFMGLIICGGIGFSVLVELGALARRMRRDSLRSVLRATSWYTRVVLSTTAVLLLGGAVLLLVTESTQSGMGVTWPRRLLT ACFQSVTCRTAGFNTVDIGAMTNVSLLIMAGMMFIGGAPGSCAGGVKVTTARTLLAFVRAQLRGGRQRQAVIGRYAVEQGTMDRAL LLLVFALGIVVVAVGVLNMAEGGHLAHAESKGLFLELMFEAVSAFGTVGLSTGLTPSLSAVGKYTLMVLMFVGRLGPILFLTALKDFQK PRHYAWPEHNLLIG

3.4E-51	184	17	1.7E-50	181.4	11.8	1.8	1	A0A024HET7_PSEKB	Trk system potassium uptake protein	PKB_1664	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas knackmussii, Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	1301098	>tr|A0A024HET7|A0A024HET7_PSEKB Trk system potassium uptake protein OS=Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13) GN=PKB_1664 PE=3 SV=1MALPTLRILGYIIGLFLITLAVAMLVPVATLFHYHRAHEISPFLWSSLLTLIAGLGMVLPGRPEQVRLRPRDMYMLTVSSWIIVCFFSALPFILARHMSFTDAIFESMSGITATGSTVLSGLDGMSPGILIWRSLLHWLGGIGFIGMAVAILPMLRIGGMRLFQTESSDRSDKVMPRSHMVAKYIVGVYVGITLLGTLALWWAGMGLFDSLNHAMSAISTGGFSTSDQSLAKWHQPAVHWVAVVLMILGSLPFALYVATLRGHRKALYKDHQVRGFLGLLVFTWLVMGTWYAFNSNLSWPDAFRIVAVNVTSVVTTTGFALGDYSLWGHFSIMVFFYLGFIGGCSGSTAGGLKIFRFQVAFILLRSSLYQLIHPRAVLSQRYNGHRLDEEIVRSILTFSFFFGATVAGLGLALTFLGLDWMTALTGAASTVAGVGPGMGPIIGPSGNFAPLPDAAKWLLSFGMLFGRLEILTVLVLFTPAFWRH
3.6E-51	184	21.9	1.1E-37	139.1	5.2	3.3	3	D8SAE3_SELML	Putative uncharacterized protein (Fragment)	SELMODRAFT_32516	Selaginella moellendorffii (Spikemoss)	492	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8SAE3|D8SAE3_SELML Putative uncharacterized protein (Fragment) OS=Selaginella moellendorffii GN=SELMODRAFT_32516 PE=4 SV=1HLTFFRLHLAYFIAIAIAGTWILWGIGARRHSKISHLKFIDCFYLITSALCITGLASVPIESIPPGGQVVLMLMMILGGQVVTSVVPLFVKKRRYCDVARQVLEQDDRKRPSSSSNPDSDRDLVPNPNAQAPQNREDDATPTSATTPSSSQGPPGSLKRTQSEHSATVSLTWIVVWYYILVHLIGFFITWGCILGDASAKSSLESKNINIGFFALFLTVSSFANAGFVLVDENMTLFSSSTVLLLALAAIILLGNTMFAPSLRGIIWLLHRVDATRREDYEFLLEHPRKCYTHLFPRTTTLWLVLAVTGFNGFECLMFYILDWKSKALEGFGTGDKVVNGIFQSVNTRSAGMNSMNLADLSPSMLFLYCGMMYIAAYPVFLSRQYSRHYEAKEQRASVIVGLDRDDWAYLFLATFFICVSDNKQLKSDPRNFTIFSVIFEVISAYGNVGLTLGYSCSLRIDSAPCTDVPYSFSGKWGVVGKLLLILVMFLGR
3.6E-51	184	32.8	4.8E-51	183.2	22.8	1.1	1	R6M5U9_9CLOT	Potassium uptake protein TrkH family	BN565_01948	Clostridium sp. CAG:253	456	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:253	1262785	>tr|R6M5U9|R6M5U9_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:253 GN=BN565_01948 PE=4 SV=1MFKTLIKKLSTTQIIALGFLGTIFIGAFILCLPFCSSNGTFTPFIDALFTSTTSVCVTGLVVVNTASHWSLFGKIIILILIQLGGLGIVSFVTGIMMIAGSRITLSDRLLLEDALNLSTLKGLVRFLKFIFKGTFIIEITGAICYSFVFIPDYGLIKGLWFSLFHSVSAFCNAGIDLLGENSLEIYASNVWINLITMFLIISGGIGFIVWKDIMDGFKNHFIKGFSFKKCLQKLRLHTKITLITTAILIFGGALLIFLLEYTNSDTIGNMSFSGKIIASFFQSVTLRTAGFATFSQSGLRHGTVLLCYFLMIIGGSSIGTAGGKKTTTAATLFLSTRAVVKNKNNHLFVFRKNIPHQTVTKALAITMVSISFLLASFSLYQAEGGSMVDVVYETTSAIGTVGLTRDFTPKLHLLGKLIIIICMYLGRIGPISMVIFFNNDSRKELVSFPHEDITVG
3.7E-51	184	21.6	2.5E-49	177.5	15	2	1	E0THQ6_PARBH	Trk system potassium uptake protein	PB2503_06432	Parvularcula bermudensis (strain ATCC BAA-594 / HTCC2503 / KCTC 12087)	487	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Parvularculales, Parvularculaceae, Parvularcula, Parvularcula bermudensis, Parvularcula bermudensis (strain ATCC BAA-594 / HTCC2503 / KCTC 12087)	314260	>tr|E0THQ6|E0THQ6_PARBH Trk system potassium uptake protein OS=Parvularcula bermudensis (strain ATCC BAA-594 / HTCC2503 / KCTC 12087) GN=PB2503_06432 PE=3 SV=1MIDLRPVMLIVGIFVMATAALMLIPMVADLLANHRDWRAFAGAALISGSVGAAMAASNWGRVDTITTRQGFLLTGASWLAIVTAAAIPLMLGVRGLSFTDAFFEAMSGLTTTGATVVTGLDTSPPGFLLWRSMLQWIGGVGIVIMAIAILPFLSVGGMQLFRLESSDPSEKLLPGASQIATWIIWIYVTFTATCFVIYWAMGMSGFDAINHAMTTIATGGFSTKDASFGYFLTPESNTGPVDVVATVFMLIGALPFGIYMLALRGNLSRSLSDSQTRFFLAAAFLFSLVIGLRIIVLFDFDIVTGFRLASFNAVSIMTGTGYASTDYSQWGPFAVGFFFCIMFVGGCAGSTSCGLKIFRLQVAVAALFLYIRRLTHPHRVTVARYNGRPLTDEVFLSVLSFFFIYFATFATSAVFLSLYGLDTVTALSAAGTAIANVGPGLGEIVGPAGNFSSLPIAVKWTLSLTMLLGRLELLTILVMLTPSFWSR
3.8E-51	184	18.2	5.3E-51	183	12.6	1.1	1	C7R0B1_JONDD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Jden_0506	Jonesia denitrificans (strain ATCC 14870 / DSM 20603 / CIP 55134) (Listeria denitrificans)	458	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Jonesiaceae, Jonesia, Jonesia denitrificans, Jonesia denitrificans (strain ATCC 14870 / DSM 20603 / CIP 55134) (Listeria denitrificans)	471856	>tr|C7R0B1|C7R0B1_JONDD H(+)-transporting two-sector ATPase OS=Jonesia denitrificans (strain ATCC 14870 / DSM 20603 / CIP 55134) GN=Jden_0506 PE=4 SV=1MFPRFTAALWAGRESADRIARRYPAPLALMVFGFVILTFAALLSLPAATTTGQRADFADALFVATSAVSVTGLTPVDTATYWSLFGQATILLGIQIGGFGVMTLASILGLAVSRKLGLTAKILTASETKTTKLGEVGSLIRVVVITSLTLESVIALLLLPHFIAAEGSTREAVWHAVFYAVSAFNNAGFLPTSEGLLPHWDSPLLIGPIMLGVFIGSLGFPVILNLARARGNKRLWLTHTKLTVVTSTTLVAVGTVWFLIAEWRNVDTIGHMDFGHKILNSLFLAIMPRSGGFSTIDMSAMHESSWLITDAFMFVGGGSASTAGGIKVTTLAVLMLAIVAEARGDRDTDVFHRRIPPDILRLAVAVTFLGATIILISSLVLLELTGMTLDVILFEAISAFATVGLSTGITPVLPDSAKYVLVVLMYVGRVGTMTFGAALALRSRRRVIRLPEERPIVG
3.9E-51	184	16.5	3.3E-50	180.4	11.4	1.9	1	A4XTC4_PSEMY	Trk system potassium uptake protein	Pmen_1826	Pseudomonas mendocina (strain ymp)	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas mendocina, Pseudomonas mendocina (strain ymp)	399739	>tr|A4XTC4|A4XTC4_PSEMY Trk system potassium uptake protein OS=Pseudomonas mendocina (strain ymp) GN=Pmen_1826 PE=3 SV=1MALPTLRIIGFIIGIFLITLAVSMVIPMLTLLVFEHPEDLNAFLWSSMITLIIGLLLVVPGRPENLKLRPRDMYLLTTCSWLVVCLFAAMPMMLLHHISFTDAFFETMSGVTTTGSTVLSGLDDASPALLIWRSMLQWLGGIGFIAMAVAILPLLRVGGMRLFQTESSDWGEKVMPRSHMAAKYIVFVYLTFTILGVIAYWLSGMNWFDAINHSMTSISTAGYSTSDQSMGKFDPASHWVAIVLMVLGSLPFTLYVASLRGHRKALLRDEQVRGFVGMLLITCALFSLWLWLNSEHALIDAIRLASFNIISVATTTGYALGDYTAWGGFAVMAFFYLTFVGGCSGSTTGGLKMFRFQVALTLLHANLKQMVHPRAVIKQQYNGHNLDEEIVRSILTFSFFITMTIGAIALFLALLGLDPLTALSGAATAVCNVGPGLGPIIGPAGNFASLPDAAKWVLAAGMLLGRLEIVTVLVLFTASFWRH
3.9E-51	184	8.4	1E-24	96.3	1.4	2	2	L0JT74_9EURY	Trk-type K+ transport system, membrane component	Natoc_0054	Natronococcus occultus SP4	509	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Natrialbales, Natrialbaceae, Natronococcus, Natronococcus occultus, Natronococcus occultus SP4	694430	>tr|L0JT74|L0JT74_9EURY Trk-type K+ transport system, membrane component OS=Natronococcus occultus SP4 GN=Natoc_0054 PE=4 SV=1MTVRVDWRSSCSLTGTVLKWLAVPLAAPLALAVFDGDDPLPFLVAIVLTGVVGIALETLSEERSLGQREAFLMVAITWLGVAAVGAVPFVLAGLAAGPQSAFYGGLGGPVNALFESMSGLTTTGATVMSGWDFANQSRAILLWRQLIQWLGGLGILIVAIGLLSSLMVGGAQLMETETQTRNVRKLRPHISDTARLIWGLYVGITVLAAATFYALHLAGLGPNMDPFNAVSHALTSVATAGFSPEPGSAGAFSPAVQWAIIPFMILGSTNFVLLYYVTQGGYRRPFESQEFRFYIGALGVFSALVVAILLLDPDVNTGLESTIRHGLFNVTSLVTTTGYASTDFDLWGPGAKHLLLFLCMFIGGMAGSTTCSIKSLRWLVTLKAFRRSLFTSVHPEAIRPLRLGDEVVDEETVRDIYAYILLTLVIFFLLTIFVVVDAARTSDPVGEFEAMGASASIFLNIGPAFERAGPMDNYAGFSVTSRSVMVIMMWIGRIEIIPVLVLLTPAFWKS
4.1E-51	183	28.8	2.1E-49	177.8	20	2.1	1	R5Y8V0_9PROT	Trk system potassium uptake protein	BN575_00270	Acetobacter sp. CAG:267	480	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acetobacter, environmental samples, Acetobacter sp. CAG:267	1262684	>tr|R5Y8V0|R5Y8V0_9PROT Trk system potassium uptake protein OS=Acetobacter sp. CAG:267 GN=BN575_00270 PE=3 SV=1MWQPVLMINGFIIFVLGALMLLPAAALKYYTGSFDAIFIQNSILTMFIGGSLFLANYGKIKNISILQGYLITVICWFSCPLICALPLYGNGDIQTYADALFEATSGLTTTGSTILSNVEAQPKSVLFWRAVLNGISGVGIVIFAVALMPFLGIGGMHIFNKENSDIEEKFLPKIRYIAKDILVYVLLNIICAVLLKWAGMNWFDAICHALATLCTGGLSTKNNSVAYFDSPMIETIIGIFMLLGSLPMTYFVLIAKKRSFASVIENNQVNTFLKLVFWYILISAFYAYTSDIPFVTAFRRASFNMISAMTTTGFSSYDFIQWGTWAVAVFFILFLHGGCTGSTTGSIKIFRWQVIMAFFKKNATNSLSPSQVTVMKAGGKVIDDNIVSSVFVMAFGFLLAIMLFTLIISMTGVDFVTALGAVAGNITNSGLGLTEATGPAGSFTGFTPFVKYILSFVMVLGRLEVIAVFVLLRKIHLM

4.1E-51	183	23.1	9E-51	182.3	16	1.4	1	F2NCK8_DESAR	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Desac_1285	Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	467	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfobacca, Desulfobacca acetoxidans, Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	880072	>tr|F2NCK8|F2NCK8_DESAR H(+)-transporting two-sector ATPase OS=Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2) GN=Desac_1285 PE=4 SV=1MSSGFFRNAAFYLLINRFAPFLRSPQFLLISGFSAVIWVGAVFLWLPWSHQPGKVSFLNALFTSTSSVCVTGLIVVDTSTVYTTF GQVVILLLIQTGGLGVMTFAALTFQMLGRRLSLQSQMVLHDSFFQQDIGSDFRHLFFRILMTTVAIEAVGMMVIGLALFVRTGNWGQS CYSALFHSISAFCNAGFSIYKDSLVDLRDNQIILAAIMLLIIAGGLGHAVLLEFWRRLRPVWNQGHDQTPSRFWSTHARVVWRMTCCLI VIGTLGILFFGLTKDEVGWVERVSGALFQSVTARTAGFNTVNCGALPLSSLMLIIMLMFIGGSPGSCAGGIKTTSFAIWLAEMRSKLRG SQEVKILDRQVPPEILWRNTILIRLAAAWNIFGIFLLLYTETAPGVGMHDVVFEQISAFGTVGLSTGLTEKLSVVGRLWIILTMFIGRVGP LTVAMWIIPERHVMIRYPRGRIMIG
4.2E-51	183	36.3	5.6E-51	183	25.2	1.1	1	W8KNW5_CAMCO	Potassium transporter	YSS_06970	Campylobacter coli RM4661	447	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Campylobacter, Campylobacter coli, Campylobacter coli RM4661	1183379	>tr|W8KNW5|W8KNW5_CAMCO Potassium transporter OS=Campylobacter coli RM4661 GN=YSS_06970 PE=4 SV=1MKQFGLDRRTFKILLAGYIVIALLGAILLHSSWAHTSPISFIDAFFTSTSAVSMTGLIVKNTAVDFTLAGQIIILALVQIGGLGYMGIGL FVYILIRKKVGFSARNLLKESLFYPSMDGLFKFFKKVLLFIFTIELIGAILLAMRFALEMNFKKALWFGIFHSISAFNNSGFTIFEHGLIAYK HDIAINLIITSLIIIGGLGYFVLVELYFFQRKKLQNLSLHTKIVVVASIFLMLSSTLIIFAFEYSNPQTIGHFSFFDKILSSYFIAINYRTAGFNTL DMGHLHDASLFFGSLFMVIGGAPGGTAGGMKVTTVMVLLLYAYWSIRDGRVRIFGHEIPRETISKAFIIAVGSAVYIVIAVILLSLLESKF DFIALLFETSSAFATVGISVGNGGTLSLCALFSDPSKVIIIIMMLSGRIGVFAFLLSVFKQDKSIHLKFPEGKVNL
4.3E-51	183	30.1	3.4E-49	177.1	20.9	2.1	1	Q5E1Q4_VIBF1	Trk system potassium uptake protein	trkH2 VF_2547	Vibrio fischeri (strain ATCC 700601 / ES114)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Aliivibrio, Aliivibrio fischeri (Vibrio fischeri), Vibrio fischeri (strain ATCC 700601 / ES114)	312309	>tr|Q5E1Q4|Q5E1Q4_VIBF1 Trk system potassium uptake protein OS=Vibrio fischeri (strain ATCC 700601 / ES114) GN=trkH2 PE=3 SV=1MVNYKPILFVIGLVLSKLALFMYIPTLVALFTGTGGFIEFGQAVAITHIVAFACLTLGRSKQFKMNVRDMFLITTLVWTIASAFAALP FVFINHISFTDAYFETMSGITTTGSTVLSGLDDMAPSILLWRSTLQWLGGVGFIVMAVAILPMLNVGGMRLFQTESSDWSDKSAPRTK YVAKYIVNVVLSLTLLCFLSYLVTGMTPFEAINHAFTTLSTGGYSTSDSSMNRFSNSTHWVASFFMFAGGLPFLLFIQVLKKRDPKVLF KDAQVVGFLKLVLITSLLVAIWLVIHNDYAIMDALRVSVFNIVSVVTTTGFGLDDFTSWGAFPAIIFAFVMLTGACSGSTAGGIKIFRFQIA STMLNKQMMKLIHPSGIFVQRYNGRPVTDDIARSVVALVFTFLLTIIIISALLGSLGLDPVTSITSAVTAVANVGPGMGHIVGPTGNFATL PDTAKWILSIGMLMGRLEILTVLVLFFPAFWKG
4.4E-51	183	9.8	6.5E-51	182.7	6.8	1.1	1	A0A0F7FS16_9ACTN	H(+)-transporting two-sector ATPase	SXIM_17050	Streptomyces xiamenensis	439	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces xiamenensis	408015	>tr|A0A0F7FS16|A0A0F7FS16_9ACTN H(+)-transporting two-sector ATPase OS=Streptomyces xiamenensis GN=SXIM_17050 PE=4 SV=1MVALGFALAIVVGTTVLALPISRAGDGAAPLLTALFTATSAVCVTGLAVVDTGTYWSGFGEVVILFLIQAGGFGIMTLASLLALLVV GRLRLMTTLQAQAESKIGMGQVRGVLKRVALITVTVEAATALILALRLWLGHGQSPGAAAYSGVFHAVSAFNNAGFGLYGDSLTGYA HDPWVLLPVSAAVILGGLGFPVILELLRQRRAGRRRTRTPRTWSLHLRLTLWLTGALLTAGTALTLLFEWSNPGTLGPLGSEDKALGA FFHSAMLRTAGFNASDISAMEPATLLGSCVLMFIGGGSAGTAGGIKITTFAVLGVAILAEVRGEPGAGIFGRRLAPQVLRQALTVALLG VAAVMASTIALLAMVDARAEIVLFEAVSAFGTVGLTAGLTGELAGPGQLIITALMFLGRVGPITLASALALRHRTQRYRLPEERPIIG
4.4E-51	183	31.6	3.3E-50	180.4	21.9	1.9	1	B8I3Z2_CLOCE	Potassium uptake protein, TrkH family	Ccel_2080	Clostridium cellulolyticum (strain ATCC 35319 / DSM 5812 / JCM 6584 / H10)	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminiclostridium, [Clostridium] cellulolyticum, Clostridium cellulolyticum (strain ATCC 35319 / DSM 5812 / JCM 6584 / H10)	394503	>tr|B8I3Z2|B8I3Z2_CLOCE Potassium uptake protein, TrkH family OS=Clostridium cellulolyticum (strain ATCC 35319 / DSM 5812 / JCM 6584 / H10) GN=Ccel_2080 PE=4 SV=1MLNIAPSKLLVLSFAVLILTGAILLSMPFSSRTGEWTPFINALFTSTSASCITGLITYDTYTYWSTAGQIIILALIQVGALGIITLATFFS LLLKKKVGLKGMLIAQESINSFRYDEVLKLVRRIVTTTLLVEFIGAIVLSLSFVPKFGAFGLYMSIFHSISAFCNAGFDITSGAVNGKFLSIT PFNNDPIVIYTISGLIIFGGLGFTVWRDLYEFRKNKALLFHTKLVLVITSILLIFGTLFFFANEYNNSKTLGPMSLFEKINAAFFQSTAARTA GFNSINLADMKEISKVFSVFLMFVGAAPGSTGGGIKVTTFGVIMFAVFSQIKGSGDVVLFKRKLHQYTVNKALSITGLSATLVILITTVIVT LQSDLHVLDILYEATSAFGTVGLTLGQTPSLNTVSKILIIMTMFLGRVGPLSFAVALTLKSSKRTSDIVYPEAKILVG
4.6E-51	183	30	3E-50	180.6	20.8	1.8	1	B7GK98_ANOFW	Trk-type K+ transport system, membrane component	Aflv_0805	Anoxybacillus flavithermus (strain DSM 21510 / WK1)	442	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Anoxybacillus, Anoxybacillus flavithermus, Anoxybacillus flavithermus (strain DSM 21510 / WK1)	491915	>tr|B7GK98|B7GK98_ANOFW Trk-type K+ transport system, membrane component OS=Anoxybacillus flavithermus (strain DSM 21510 / WK1) GN=Aflv_0805 PE=4 SV=1MRRTMMKPLKLTPPQLLALMFLFLVVVGGVLLKLPIATEKNISWLDAFFLSTSAATVTGLAPIDLGSTFTTFGEIVFMVLIQVGGLG IMTFAVLVVIVLGKKIGMKQRMLMQEALNQPSLGGVIRLARNLLLFSLFMELVGATLLAIDWVPKMGWVKGLYYSLFHTIASFNNAGFA LWPDNLSRFVGDPIVNMTVSLLVIIGGLGFTVVFDVLYQRRWRKWSLHTKLMLVMTLVVNVVAIVAVFFFEQHNPKTLGSLSLREQLW AAYFQGITPRTAGFNTIDIGSLEQPTAMLMIFLMFIGAGSTSTGGGIKLTTFAVIVFAVMSFLKGKEETVIGMRTVRHTTILRALAIASMS MLFIFVVTMMLTLTEDASLLALLFEVVSAFGTVGLSMNVTPHLSTIGKVLIICVMLFGKLGPLTLVYSIAKPKKTNIRYPNGDILTG
4.8E-51	183	31.2	1.5E-49	178.2	21.6	2	1	N8YCG7_9GAMM	Uncharacterized protein	F960_01403	Acinetobacter gerneri DSM 14967 = CIP 107464	446	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter gerneri, Acinetobacter gerneri DSM 14967 = CIP 107464	1120926	>tr|N8YCG7|N8YCG7_9GAMM Uncharacterized protein OS=Acinetobacter gerneri DSM 14967 = CIP 107464 GN=F960_01403 PE=4 SV=1MKQLINKKHKSVNLSPPSLLALGFLSFITIGTLLLKLPFSHIGELSWINAFFTATSAVTITGLSVVNVGDSFTIFGKVIIMLLIQCGGL GFMSFAILAALSLSPKVGLKQQMMAQETIGQTSLAKATLTIKAVFFYSIFFEALGTCILTSAWMEHYDFEHAFFYALFYSVSAFNNAGFS LFPNSLTSFSGQYMVTFTISILYIIGGIGFVVLMDIKQNKRWKKLSTNSKLVLSTITGLNLFAFIIIWLLEANNPLTLAPMSFDDQALNAWF HATVPRSVGFNSIDVGSMTDASSFITMMMLMFIGGGSLSTAGGIKVGTFIITVLSVISFLRREDELTVFNHRIPERTTFKALAVISITSMLIVI GFFSLLILEPHKRFLDLLFETISAACTVGLSRGVTEDLGPYSLMVLACLMFAGRLGPLTLAYLIATPKKSRVSHPDTEIQVG
4.8E-51	183	18	3.4E-49	177.1	12.5	2.1	1	R7I621_9CLOT	Cation transport protein	BN648_00705	Clostridium sp. CAG:411	466	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:411	1262802	>tr|R7I621|R7I621_9CLOT Cation transport protein OS=Clostridium sp. CAG:411 GN=BN648_00705 PE=4 SV=1MIEGVLFLIPCLTALIYLETEGFCYLAVALICILIGWIMRRKKPANNVFYLKEGCVTTALSWIFLSFFGCLPFVFTGEIPFLPDALFETI SGFTTTGASILSDVEALSHCSIIWRSFTHWIGGMGVLVFLLAIIPMSGGSHINLMRAESPGPSVGKLVPKVKSTAQILYIIYFTMTAIEFIF LLLGRMPVFDAINTSFGTAGTGGFGIKNDSMASYSPYIKWVVTIFMILFGVNFNAYYLILFKQFKKAIKMEEVKCYFMIILASILVIFINIVK TYTNVFKAFTDAAFQVGSIITTTGYSTTDFDLWPGTSKTILVMLMFVGACAGSTGGGIKVSRFLIMFKTVVKELRSYIHPKSIQKIKMDD KPVPHEVVRSVNVYGITFITIFAASIFLLSLDGKDLITNFTAVATTLNNIGPGLNLVGPTRNFDLFSPFAKFVLMFDMLAGRLELFPLLILFH PTIWKEHK

4.8E-51	183	17.9	1.1E-50	182	12.4	1.4	1	F9D1U4_PREDD	Trk family K+ transporter, membrane protein (Trk-type K+ transport system, membrane component)	trkH Prede_0958 HMPREF9136_0822	Prevotella dentalis (strain ATCC 49559 / DSM 3688 / JCM 13448 / NCTC 12043 / ES 2772) (Mitsuokella dentalis)	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella dentalis, Prevotella dentalis (strain ATCC 49559 / DSM 3688 / JCM 13448 / NCTC 12043 / ES 2772) (Mitsuokella dentalis)	908937	>tr|F9D1U4|F9D1U4_PREDD Trk family K+ transporter, membrane protein OS=Prevotella dentalis (strain ATCC 49559 / DSM 3688 / JCM 13448 / NCTC 12043 / ES 2772) GN=trkH PE=4 SV=1MINFKIIYKILGSLLFIEASFMLWCLVMALVYEEDDIPTFSISILATAFAGFMLRYMGRNAENRLSRRDSFLVVTLVWVVFSAFGTL PFLLGGYLHNFTDAYFENMSGFTTTGATIIDDVESMPHGILFWRSLTQWIGGLGIVFFTVALLPSLVGGSTKVFAAESTGPIKTKLHPRL SMSARWIWIVYLFITFACMGCYMLFGMDWFQGVNYAMASAATGGFAINNNSTEFFNSPALEYTTIFFCFLSGVNFTLLYFSAAKLKFR ELCRDSEFRFYATIVLGFTAFVMAELILRNHYDLEHAFRSALFQVVSFITTTGLYNDDAARWPHVTWVVLSLCMFIGACSGSTSGGLK CMRGVMLFKVVKNELRQRLHPNAVLPLKVNGNNIPDPQRVSLLAFLTAYLLLMLLMAFVMIAAGIDNTNAITICLSCLGNVGPTLGIEIGP TMSWSILPDFAKWMCSIMMLIGRLEIFTVLVILTPSFWTKN
4.9E-51	183	12.1	6.6E-51	182.7	8.4	1.1	1	D3PW59_STANL	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Snas_1512	Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	454	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Glycomycetales, Glycomycetaceae, Stackebrandtia, Stackebrandtia nassauensis, Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	446470	>tr|D3PW59|D3PW59_STANL H(+)-transporting two-sector ATPase OS=Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21) GN=Snas_1512 PE=4 SV=1MAIRSGVSSSLVLPKLRHPARLVPLSFLAVILVGTVLLALPVSRQGADAAPLLTAAFTAVSAVCVTGLVTVDTGTYWSGFGEVVIT VLIQVGGFGIMTMASLLGLLVAGRLRLRRKLVAQAETKSLGLGDVRKVVVRVALITLSVETVVAVILAARYHFGYGYELGRAAWHGVF HSVAAFNNAGFGLERDNLESFVADPVITIPIAVAVIIGGLGFPVVVELIRKTYRPASWSTHTKLTVLATVVLLLAGFVAYLAIEWNNAKTL GPLGLGDKLLAAFFSGVQPRTAGFNSLPMADLRPETWAVTDILMFIGGGSAGTAGGVKVTTFFLLAFVIWAEVRGEPDVSVFGRTIPH STQRQALTVALLGVGAVGLGTLLILMTDGHPLDQLVFEAISAFGTVGLSTGITADLSATAQIIIMFLMYTGRVGTVAVATALALRVRHRR FRYPEERPIVG
5.1E-51	183	16.5	6.1E-50	179.5	11.5	1.9	1	R4LF61_9ACTN	H(+)-transporting two-sector ATPase	L083_0849	Actinoplanes sp. N902-109	431	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	649831	>tr|R4LF61|R4LF61_9ACTN H(+)-transporting two-sector ATPase OS=Actinoplanes sp. N902-109 GN=L083_0849 PE=4 SV=1MAFLGAIAAGTALMMLPAAKAGGGHAPFVTALFTATSAVCVTGLSVVDTPTYWSGFGLVLLTVLSQIGGFGIVTLATLLSLIVSRR LGLRSRLLAQAESSGLQGGSIGRVLIRVAVVMFVSETLISVVLALRFWLGYDYSFGRAVWEAVFHAVQAFNNAGFALYPDSLVRFVG DWWICVPLALGVLGGSIGFPVWFELAREWRTPAGWSTHTRLTVWGTALLSCAGFLVFLVFEWSNPGTLGPLGVPSKVLAALTQDV MTRSGGFNSINLGDMNTETIAVTNGMMFIGGGSASTAGGIKVTTFFLLAFVIWAELRGEPDVVIKKRRIAEETQRQALTVALLGVALVA GGTLALVALTDHVPFDRALFEVTSAFATVGLSTGITSSLPEPAQLVLVVLMYVGRVGTIAVGTAIALNTRRRLYRYPEERPIVG
5.1E-51	183	41.8	4.9E-30	113.9	13.5	2.1	2	F8E9H6_FLESM	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Flexsi_1657	Flexistipes sinusarabici (strain DSM 4947 / MAS 10)	428	cellular organisms, Bacteria, Deferribacteres, Deferribacteres, Deferribacterales, Deferribacteraceae, Flexistipes, Flexistipes sinusarabici, Flexistipes sinusarabici (strain DSM 4947 / MAS 10)	717231	>tr|F8E9H6|F8E9H6_FLESM H(+)-transporting two-sector ATPase OS=Flexistipes sinusarabici (strain DSM 4947 / MAS 10) GN=Flexsi_1657 PE=4 SV=1MFKFKINPWMYLFITFALFIIAGTFLLKMPFVKHTEGLSYIDALFTATSAVCVTGLIVVDTSGFNFWGQFFIMLMMQVGAIGIMTLT SSLLLFLRGELDFSRKFMVAKISDSLNIQEAEKVLVIVVIYTFVMEFVGFLALSYGFFLDGFALKDAAYYGLFHAVSAFCNAGFSTFDSS LIGSNSIVKVTTMFLIVFGGLGFYVIYNIFMTFVSNERIKVHTKIVVYTTFALIIAGTLLIFMLEKGTMSILDSFFQSITTRTAGFNTVEIGGL HIVTKFLMIVLMIIGASPGSTGGGIKTTAFYIAVVSMYSILRGNKRIVIFNRNIALINILKAYALISMYIFFLVIATLLLLYFGDFTFMDTLFEVT SALGTVGLSLGITAKLGIFGKLIITACMFLGRIGPATLITMLLLKEKTSKLSYPEEKIILG
5.2E-51	183	24.5	7.2E-51	182.6	17	1.1	1	C6CWH3_PAESJ	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Pjdr2_1360	Paenibacillus sp. (strain JDR-2)	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. (strain JDR-2)	324057	>tr|C6CWH3|C6CWH3_PAESJ Potassium uptake protein, TrkH family OS=Paenibacillus sp. (strain JDR-2) GN=Pjdr2_1360 PE=4 SV=1MKNSMLTKISPPQILTAGFIVIILIGSILLSLPYASEDGMHTPFIDAFFTATTAACVTGLVVVDTGTHFSTFGELVILMLMQVGGLGF MTMATLFALAFRKRISLRERLWLQESMSHTSLEGIVRFIRRVLIYAFTIEFVGALLLTLRWSAMMPFDKALYYGVFHSVSMFTNAGLDI MGPIHGPFNSFTNHVDDPIINAVLMLLIFLGGIGFIVLAEVIDYPKIRKLSLHSKVVLYTSGLLFLGGAVLLFIFEYTNTLEPLSFAGKLYSS LFQSISPRSGGANTLNIADMRNASQFLLIILMFIGASPGSAGGGIKVTTFAILIGAVIAMIRGKEDVVFFKRRLAKDRVHKALTITAVSVATI VLFTMILSATEETDFLTVMFEVTSAFGTTGLSMGLTPHLTGIGKILIIIVMFMGRMGPLTLAYTLVPNQSKELYRHPKGKITIG
5.4E-51	183	32	2.7E-50	180.7	22.2	1.8	1	R7BJ95_9FIRM	Potassium uptake protein KtrB	BN803_02549	Firmicutes bacterium CAG:882	446	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:882	1262991	>tr|R7BJ95|R7BJ95_9FIRM Potassium uptake protein KtrB OS=Firmicutes bacterium CAG:882 GN=BN803_02549 PE=4 SV=1MFGKKRISKVQFIALGFLIIILMGTLLLMLPVSSRSGEAAGFLEALFTATSATCVTGLVVVDTFTHWSLFGQIVIICMIQIGGLGFISI GLILAVLLGRKVSLRHRGLMQESVNTLQIGGIVKLTKKMITGTLIFEGIGAVILAIRFSFMMSPWRAIFYGIFHSISAFCNAGFDLLGCYGE YNSLCGFEGDWTINLTISALIIIGGLGFVVWDDISKNGIRIKKYRLHSKIVLAVTTFLLVAGTTLFMIFEWDNTMAGMDVSTRFLASFFSS VTPRTAGMNSVDTGALTPASKLLTMILMFIGGSPGSTSGGAKTTTIFVIVAYLWTTMRGKYGIDVFRRRLKEDVVRKAALVIGVNMILFI TGAMVIFAVQPELGFADVIFEVISGISTVGMTTGITRSLSVVSRIVIIVLMYCGRIGSLSFALSFSENKRVVPLQQPEEEINIG
5.5E-51	183	25.4	1.3E-50	181.7	17.6	1.6	1	M5DPG3_9GAMM	Trk system potassium uptake protein	TOL_1410	Thalassolituus oleivorans MIL-1	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Oceanospirillaceae, Thalassolituus, Thalassolituus oleivorans, Thalassolituus oleivorans MIL-1	1298593	>tr|M5DPG3|M5DPG3_9GAMM Trk system potassium uptake protein OS=Thalassolituus oleivorans MIL-1 GN=TOL_1410 PE=3 SV=1MVHLNITLRLLALPIVWVGIVQLVFAALSEWLFLDHMVVSFLIPSLSMLSVGAILYFKYRTIDLSKASYRDALIYATATWIVSGILAAI PIEIIAGVSFTDAVFESISALTTTGATVLSGLDSMPKTFLMYRQFLQWMGGLGIVIFVVAVLPMLNVGGMKLLKAETPGPVKDDKLSPR VSSTAHYLWGVYIFITLACIMAYYIGGMSLFDAVAHSFTTVSTGGFSTHDTSMGYFNSHTLLWISNLFMVLGAINFGLHFRVFRHRDYS GYFRDEETRVFLIIILVLSILVAGYLFFEDTYTNLFESMSYSTFHIISFITSTGYGASGFTEWPAAATCVLIMTGYLGGCAGSTAGGNKIIR NILTVKIFNRSLKQMIHPHGKFAIKYQRSPVQTEVRSAVMAFMSFSAISTIIITLMLMTTGLDFWSSLSAVAACVNVLGPGFGALGNNFA PVTDAGTWLLSGAMILGRLEYFTVFAIFSPMFWKD

5.7E-51	183	30.9	2.8E-49	177.4	21.4	2	1	R5TN19_9FIRM	Potassium uptake protein KtrB	BN683_01787	Roseburia sp. CAG:50	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:50	1262949	>tr|R5TN19|R5TN19_9FIRM Potassium uptake protein KtrB OS=Roseburia sp. CAG:50 GN=BN683_01787 PE=4 SV=1MFTKLRNNISQMQMIALGFFCIILIGTLLLMTPLASRAGTWTDFLTALFTSTSATCVTGLVVTNTYLHWSLFGQIIIITLIQIGGLGFITFGFGFSMFLRKKITLRQRGLLKESVNVVNTGGIVRLARLILQGTLLFEGIGALILTLCFLRDMPFSQALYYGIFHSISAFCNAGFDLMGAFGMSSFIGYNTNWIVCITLMALIFIGGIGFFVWGDLKEHKLHIRKYALHTKIVLITSLILIIGPSILFLILERHALFADMNTPQAIFNALFCAVTPRTAGFNTTDIASLSQSSQLLTIILMFIGGCPGSTAGGAKVTTITVLILYLRSMLTRTDGVNIFKRRLEDEAVSKAAAVFTTHMLLAVVATFLISMQQDLDLTVIVFDVVSAVSTVGMSTGITPHLVPGAKVILILLMYLGRVGSLSFAMSFTDKKRLAHVRQPKEHISIG
5.7E-51	183	31.3	8.2E-51	182.4	21.7	1.2	1	A5VLS7_LACRD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Lreu_1558	Lactobacillus reuteri (strain DSM 20016)	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus reuteri, Lactobacillus reuteri (strain DSM 20016)	557436	>tr|A5VLS7|A5VLS7_LACRD H(+)-transporting two-sector ATPase OS=Lactobacillus reuteri (strain DSM 20016) GN=Lreu_1558 PE=4 SV=1MIEINKHKYTFPKILTFGFLIVIFMGTILLSLPFATRPGETTNFMTAFFTSTSATCVTGLTLVSTAHHWTLFGQIVIAILMEVGGLGFMTFAVMMSLLIRQRMRMSTRLLTQEALNLDHLSQLNVVYLIIRLSLLIQLAGGIFLFFDFYPCYGLGKGIWFSIFHSISAFCNAGFDLFDNSMANYANDPYMLCVLAVLIVAGSLGFLVWKDILNYPKYHRLSLHTQLALRTGAVLFVVSVVVYFITEKNLAQLSDKLSFSNRILNTIFMAITPRTAGLITFPYTDLSAAGLAFTVILMFIGGTPGSTAGGVKTTTIGLLTIQSFATLRGQRDTTFAHRRFTQENIYRALTLLFVALFILLVSILVLVETQDLPKHDSLAYVTFEAVAAFGTTGISLGITTHLNLLGQFIIMFLMFVGRVGIYTVMFSILNASTAAKNYRYPEESVLIG
5.8E-51	183	9.7	2.8E-50	180.6	6.8	1.8	1	A3CUN7_METMJ	Cation transporter	Memar_1156	Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1)	503	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanomicrobiaceae, Methanoculleus, Methanoculleus marisnigri, Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1)	368407	>tr|A3CUN7|A3CUN7_METMJ Cation transporter OS=Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1) GN=Memar_1156 PE=4 SV=1MHHRKNHFFPEHPGRKALPAAHSQFAIIAPDIGLIFLFIALVSCSPFLVALWYGEESILLPMASAPAGFGIVGVWLAGVPKVEGEARLSVALSAVALIWLAAALIGALPYTFGLNLPYTDSVFEAMSGWTGTGFSLLPSVDATPKTILFWRSLTQWMGGLGIVAFTIALAGRSGLTRFRLYRSEGRSETFMPGVVTTAVEMWRIYLVLTALGIGLVLLSGIPLWDAVNIVMTAISTGGFAVHSAGILYYDSPLLEMLVVPVMIAGALPFKLYFLLYKKKRFQFFSDRQAILLFALIIAGCAAVTLDLATVSALPPAEALREGIFMTVSGITCTGFQNADPRNWYGSTVMILAALMFVGGSAGSTAGGIKLGRVTLGLETLRWWFKRLHTGWRAITPLRHDGRAILEHLPEYEVSKSMLVVVLFALTVAIATLLLLHLAPQDGFDSADIIFEVVSAASSVGLSTGFVNPGISPAAKWLFIIVMWAGRLEIVPVIALVFGAARRL
6.1E-51	183	22.6	1.3E-50	181.8	15.7	1.4	1	E0RWI6_BUTPB	Potassium uptake protein TrkH family	bpr_I1623	Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) (Clostridium proteoclasticum)	456	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, Butyrivibrio proteoclasticus, Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) (Clostridium proteoclasticum)	515622	>tr|E0RWI6|E0RWI6_BUTPB Potassium uptake protein TrkH family OS=Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) GN=bpr_I1623 PE=4 SV=1MKKISLKLSPVQIIPASFLIAIIVGAFLLTLPIASANGQPTGPLTALFTATTSVCVTGLVVVDTYLHWSFVGQLIILILVQIGGLGMITVASMLMVLTRRKFSLTDRMLLRDAFNLNSNSKLLSFLVNMLKGTFLVEGIGAVLYATVFIPEFGVKKGLWCAVFNSVSAFCNAGMDVIGPNSMGNYRSNPMVMTVTMLLIVLGGIGFVVWFDVIARCREGLKKRFSPITVCKRLSEHSKLVLSFSLALIFGGALIFMCFEYNNPDTIGNMGFGAKFVNSLFESITLRTAGFTTIPQDKLTLSSCLVAYIMMFIGGSPIGTAGGIKTVTMFLLIMNLRSYVRHQDAKVIFGRRVSEESMRKASAVAFVGVVAIFILSILLLLVNPVPLEDALFEIVSACGTVGLSRGLTPSLGAGGRVVVIIAMYLGRIGPISLVALFSRSNKEANKLNYSEGIFYVG
6.3E-51	183	20.8	2.2E-49	177.7	14.4	2.1	1	C5BF21_EDWI9	Trk system potassium uptake protein	NT01EI_3564	Edwardsiella ictaluri (strain 93-146)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Edwardsiella, Edwardsiella ictaluri, Edwardsiella ictaluri (strain 93-146)	634503	>tr|C5BF21|C5BF21_EDWI9 Trk system potassium uptake protein OS=Edwardsiella ictaluri (strain 93-146) GN=NT01EI_3564 PE=3 SV=1MLNYRSVLYILGMMLSKVALLMYVPLLYALLTGTGGVYEFLQAVIITHLIALFLIAQGRSQKFYLRIRDMFLTTTLAWLTACCFGALPFVFIKHITFTDAFFETMSGLTTTGSSVLSNLNQMEPSVLLWRSLLQWMGGVGFIVMAVAILPFLDVGGMRLFHTESSDWSEKSSPRMKDVAKSIMAVYAVLTFLCYLGYRYAGMSNFDAVNHAFATISTGGFSTNDKSMAAYSVLAQWNAILFMFLGSLPFLLFVQALRQRSLRTLMRDQQLVGFSRFVLVVGLILTLWLWHKHIFDFEDSLRIAFFNLINILSTTGYSLGNFDQWTPFTTVLFASLMLLGGCSGSTAGGIKMFRVQIGFESLHIEVRKLIHPNAVFPRRYNNRPITNEVSRSVIAFMMAFIAITMLIAAILGLCGVDALSSITGAMSAMANVGPGMGPLIGPSGNFAPLPDVAKWALSLGMLLGRLEVMTMLVLFFPSFWRH
6.3E-51	183	17.5	1.1E-50	181.9	12.1	1.4	1	F0SMI1_RUBBR	Cation transporter	Plabr_0113	Rubinisphaera brasiliensis (strain ATCC 49424 / DSM 5305 / JCM 21570 / NBRC 103401 / IFAM 1448) (Planctomyces brasiliensis)	528	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Rubinisphaera, Rubinisphaera brasiliensis, Rubinisphaera brasiliensis (strain ATCC 49424 / DSM 5305 / JCM 21570 / NBRC 103401 / IFAM 1448) (Planctomyces brasiliensis)	756272	>tr|F0SMI1|F0SMI1_RUBBR Cation transporter OS=Rubinisphaera brasiliensis (strain ATCC 49424 / DSM 5305 / JCM 21570 / NBRC 103401 / IFAM 1448) GN=Plabr_0113 PE=4 SV=1MNWRLLCKLLGMLSLLVGGSMILSLPWAFPVCGVTETFELRGFLGILASTIISLVLGGVLFWVGRGNHGTVLHKEALAIVGLGWLLAGILGALPFLLARVMATPDTPMTVVDAFFESVSGFTTTGASVLTELEDPEMIPKCVMFWRCFTHWLGGMGIIVLFIALLGHLGVGGKALMHREVTGPINETVMPRVVRETAMFMWQIYMGMSVVLAIIFLLQGMSLYDSLCHTFATVATGGFSTYNASAGHFQSVGIETTMLIFMVLAGTNFTLYYVVLFGQRKGQLKNRDARLRDRLSVFYKDTEWRVYMGVLLLSSLALTVNLLLTDEYTSLFEAVRHASFLTVSIMTTTGFGTEDFSQWSEFSKGLLLLLMFVGGCAGSTAGGIKVVRFILFFKIMRLEIEKAFRPKVVRALRLGGESAPESLRHDVVVYFSLILFIVSSWMILNTIEPDTQWQVSTEHREAEKLLDCASAVAATLNNIGPGLGVLGPASNFSGFSPQGKFLLTLLMLLGRLELFAVLVLFFPSFWRNQ
6.5E-51	183	12.7	1.7E-49	178.1	8.8	2	1	G4L1C7_OSCVS	Ktr system potassium uptake protein KtrB	ktrB OBV_19460	Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter valericigenes, Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	693746	>tr|G4L1C7|G4L1C7_OSCVS Ktr system potassium uptake protein KtrB OS=Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20) GN=ktrB PE=4 SV=1METIKKQVSPARVVLLGFLALIGLGTVLLMLPFAARCGRATPFLDALFTATSATCVTGLVVVRDTFTYWAPFGQAVILLLIQIGGMGVVTMAVAAAILSGRRIGLRQRFMMQESIDAPQVGGIVRLTRFIVKTTLAVEGIGAALLALRFVPEYHLGKGLWFAVFHAVSAFCNAGFDLMGEQGPFSSLTGYAADPLVCLTVMVLIFVGGIGFLTWEDFSRNRFHLHAYRLQSKLILTVTAVLLVVPAVCFFAGEFSMPQWQGMPMGQRALAAAFQAVTPRTAGFNTVDYTRMSEPSILLTVFLMLTGGAPGSTAGGYKVTTLATLVMCVRSVYRRKADVRCFGKRLTAETPRSAAALFFLYFALFMLGAGLLGTLDGVPLTAALFESASAIGTVGLTMGVTPTLGAASRLVLIALMYFGRVGGLTLIYAAAGSRVTPPSQLPQEKITIG
6.6E-51	183	20.6	1.8E-50	181.3	14.3	1.6	1	Q2SJ19_HAHCH	Trk system potassium uptake protein	HCH_02555	Hahella chejuensis (strain KCTC 2396)	467	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Hahellaceae, Hahella, Hahella chejuensis, Hahella chejuensis (strain KCTC 2396)	349521	>tr|Q2SJ19|Q2SJ19_HAHCH Trk system potassium uptake protein OS=Hahella chejuensis (strain KCTC 2396) GN=HCH_02555 PE=3 SV=1MGGVQLIFGALSVALFRDNVQQAFMAPGVTMLAASYLFWSRYRKSDLTKIGYRDSLLFASLTWMCSGVLGAIPIILITGVSFTDGVFESISALTTTGATVLSGLDSLPKTFLLYRQFLQWLGGLGVVIFVVAVLPMLNVGGMKLLKAETPGPVKDDKLSPRVANTAHYLWIVYIAITLLCALSYFVAGMSFYDAVAHSFTTVSTGGFSTHDASMGYFQSHLILAVSDVFMLLGAISFGLHFKVFRARNPFVYLKDEETRTFLLIVAGLSLLLCIMLLKAQQYHDPLTALSDSAFHLISFITSTGFGAAGFTDWPEVAAMLLVFAGYLGGCAGSTAGGNKIIRNIISIKSINLELKRIVHPRGVFVMKYQGRSVGADVTSATAAFMSFAAGSTLILTLALMATGLEFWSSFTAVAACLNVLGPAFAELGSNFAPVSDTGAWVLSFAMILGRLEYFTLLAIFLPHFWRR

6.6E-51	183	23.3	6.8E-49	176.1	16.2	2.1	1	R6VFM7_9BACT	Trk-type K+ transport systems membrane components	BN576_02061	Alistipes sp. CAG:268	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes sp. CAG:268	1262693	>tr|R6VFM7|R6VFM7_9BACT Trk-type K+ transport systems membrane components OS=Alistipes sp. CAG:268 GN=BN576_02061 PE=4 SV=1MRVDVVLRYVGVVMLFIAGFMLLSAGISCLNGVDSAFYPLLLSALLTTLLGAFPLIFVGKRDQITNKEGFCIVVGSWLLSCVVGMF PYLIWGGEFSLVNAWFESVSGFTTTGASVLTDVEALPRGLQFWRFSTTWIGGMGVVMFALVVLPTMGRSKMTLSNVELSSLAKDNY RYRTQVIVHILLVVYVGLTALSTVMLRLAGMNWFDSLCHAMSACATSGFSTKNASMAFYNNAWIDTVLIFTMGVAGMHFGLIYATVTG KRNNIFRSEVTRWYMGILLVCSVLIAISLYAAEIYPTITASFRHAAFQFFSLMTTTGFASADSSVWPPFAVILLMFGSIVCACAGSTTGG MKTNRLVLAGKMIRAQLRRQQHPNAVIRIRLDGVMQDDSAIYGVMIFIVTYMLALLVGTVFATLCGVDLLTGFSSTVACLGNVGPGFG DVYSMGNYAGMPAALKTFDALLMLLGRLEIFGLIQLFFIKWWR
6.6E-51	183	34.2	8.8E-51	182.3	23.7	1.1	1	R5EMV9_9CLOT	H(+)-transporting two-sector ATPase	BN724_00517	Clostridium sp. CAG:590	453	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:590	1262825	>tr|R5EMV9|R5EMV9_9CLOT H(+)-transporting two-sector ATPase OS=Clostridium sp. CAG:590 GN=BN724_00517 PE=4 SV=1MDKKRKRLTTTQLVVLSFAAAIFVGAVLLTMPFSAADGHMTPFIDALFTATTSVCVTGLVVVTTATHWSLLGKIIILLLIQIGGLGVI TLTTTIMMAFGKKISLSNRVLLGDAFNLETLKGLVKFLRRVFLGTFVVEGIGAVCYMLVFIPEYGIGRGIWYSVFHSVSSFCNAGIDIVGA NSFMPYVHNVWVNLVTMTLIVFGGIGFVVWWDVVTAIRKKIAGSKRHLFQLMSLHSKVAITMTLFLILSGTVLFAVFEWNNPRTMGEF SGWQKWLAALFQSVTTRTAGIATISQKGLSVPSVITSMFLMFTGGSSVGTAGGVKVTTVAVVILSVAATVRGNSDVTCYGRRISDAIV RKSVAIIFISFMASVLAIVAMRLLEGGESVDIIFEVYSALGTVGLSRDYTATVGIAGKIVLCICMFLGRIGPITMVIAFAMRDKKTALRLPEG KITVG
6.6E-51	183	24.9	9.1E-28	106.4	7.4	2	2	R7H3U1_9FIRM	V-type sodium ATP synthase subunit J	BN645_00413	Ruminococcus sp. CAG:403	435	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:403	1262958	>tr|R7H3U1|R7H3U1_9FIRM V-type sodium ATP synthase subunit J OS=Ruminococcus sp. CAG:403 GN=BN645_00413 PE=4 SV=1MKLLGRRRRFTPVRIIACGFASMIALGTLLLSLPIAQKPGAAVSVLDALFTATSAVCVTGLVAVDVADHFTVFGQTVVGILIQIGGL GVTSIGLGLIALSGRRVRLQDQVLIKEALNSPNLKNILALIRTVLITTFSIECIGAVGSFLVFRKQYTVWHAIGLSLFHSVASFNNAGFDLL GGGQSLAAYRSNVPFLLLTSILVIAGGIGFMVIRDLWQNHGRLLRCTLHTKVVLLMTVLLLAGGTVLLKCGDSSLNWLDAFFYSVSART AGFATVPLAQFSSSATLVMLILMFVGGSPGSTAGGIKTTTLFVFLRTVFVYPSRKNITVFHRQLPKDVMEQAFVLVGMGACVVGGVSL LIGILEPLTLSQILVEVVSAFGTVGLSTGVTGALSAPAKLLLIGTMFIGRLGPWTVVSLWIQKTRCNVSLPEERISIG
6.8E-51	183	17.2	2.7E-48	174.1	11.9	2.2	1	R7FSX1_9FIRM	Cation transport protein	BN797_00164	Eubacterium sp. CAG:841	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:841	1262894	>tr|R7FSX1|R7FSX1_9FIRM Cation transport protein OS=Eubacterium sp. CAG:841 GN=BN797_00164 PE=4 SV=1MNYKIIGKIISQILAIEAVLMLPAVVISVCDGEMNAAKAFLVTMGITFVFSGIFALFSRNAKKGFYAREGLICVGLGWVFLSIFGCLP FVISGEIPHFIDALFETVSGFTTTGSSILENVELLTRGMLYWRSFSHWLGGMGVLVFILAVLPKSKNSGGFSLHLLKAESPGPDVGKLM PKLGQTALTLYSIYIGLTALNFIALIIAKMHWFDALCTAFGTAGTGGFGIKADSIASYSPAIQIITTVFMLLFGVNFNCYYWLLLRNFKSVF KNEELRLYLGSFVAATALITINTLKMFSSVGEGLRHAAFQVASIMTTTGFATTDFNLWPAFSKAIILLLMIMGACAGSTGGGFKCARVLIL FKNLRRSIKKMLHPQSVQTIRTDGEPLRENVVEGTNVYLIAYAFIAVASFLIVSIDGFSVETNLSAVISCFNNIGPGFDVVGPMGNFAGF GVVSKLVLILDMLAGRLEIFPILVLFSGRTWKAH
6.9E-51	183	18.4	3.4E-50	180.4	12.8	1.8	1	A0A0A2DVF0_9PORP	Potassium transporter	JT26_03570	Porphyromonas sp. COT-108 OH1349	493	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, Porphyromonas sp. COT-108 OH1349	1537504	>tr|A0A0A2DVF0|A0A0A2DVF0_9PORP Potassium transporter OS=Porphyromonas sp. COT-108 OH1349 GN=JT26_03570 PE=4 SV=1MHLFDNIRRKVNYRFVARMLGFLCLLEIPFLILSLSVGLFYDKSIVWSFLSAIVAMAAVGGTLLVAGREAKHYKSGRKEAMLTVSL AWVTLSLLGMLPYIISGYIPNPADAFFETMSGFTTTGATILDNIEALPKGLLLWRSITQWQGGIGIVVFALALLPVFGGSGSLVYNCEAS GVLHEKFMPRAGIMAKKVTNIYLILTFACVLLFWIGPMDLFDAVCHALTCVCSGGFSTRTDSLSYYNSAYTDVVAMLFMFLAATNFSLI YFAFTGKPKKLIQDTEFRWFLSIVVIVGFASSVWIYMKGIIDAPLEALRHGFFQVISLISTTGYYTVDYDGWLSFFALLALCIMFVAGCTG STSGGLKVGRFLILVKNLLNEIRKRTHPNAVLPVRADNIVIPTRFVGQVGTFFFAYSMLILLCILFLTVEGIKLDSAVSVAVACISNSGPAL ESFGPTESYAALGSVSKIVMSLMMMIGRLEIFTVLAVFHGGFWKD
7.1E-51	183	24.7	1E-50	182.1	17.1	1.1	1	R5TWH8_9FIRM	Uncharacterized protein	BN481_00492	Ruminococcus gnavus CAG:126	469	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	1263106	>tr|R5TWH8|R5TWH8_9FIRM Uncharacterized protein OS=Ruminococcus gnavus CAG:126 GN=BN481_00492 PE=4 SV=1MKTDWQNVHSKIQEKRKKVTFSTMQIIAFGFLGVILIGSILLFLPISNQEPIAYLDALFVSVSAVCVTGLVTVFPAAQFTLFGKVVLL GLIQIGGLGVIACTMAVFLAIRKKITMKSRVMIQQTYNLETLSGMVRFIIRILKGTVLVEGIGAVLFAFRFVPEYGFIKGVAYGIFHSVSAF CNAGIDVLGTSSFMEYVSSPLVSLTTMFLIVAGGLGFTVWHDVRMNLQDVAGQKRPLKRLFTRLHLQSKMVIVMTAGLIMIGTLGYFLL EYHNDATIGKLGFGEKLLASGFQSVTTRTAGFATVSQAELTSASKLFGCILMFIGGSPGGTAGGIKTTTMAILLLTCAAVIRGRKSTECF GRRLAETNVRSGIAIVFLTFAIWLVGLFGIAILEPDERFIDLIYEATSAIGTVGLSADLTPALTRGSHVILMILMYVGRIGPITMALVFSGRE DMQAKFRDLPEKRIMLG
7.2E-51	183	30.4	3.7E-50	180.2	21.1	1.8	1	Q6LLI9_PHOPR	Trk system potassium uptake protein	SO0028 PBPRA3583	Photobacterium profundum (Photobacterium sp. (strain SS9))	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium profundum (Photobacterium sp. (strain SS9))	74109	>tr|Q6LLI9|Q6LLI9_PHOPR Trk system potassium uptake protein OS=Photobacterium profundum (strain SS9) GN=SO0028 PE=3 SV=1MVNFRPIMFVIGLVLSKIALFMYIPTLVAFFTGTGGFIDFATAVIITHTVAFLCLTFGKTKEFKLGVREMFLITTLVWTISSAFAALPF VFINHISFTDAYFETMSGITTTGSTVLSGLDDMAPSILLWRSTLQWLGGIGFIVMGVAILPMLNVGGMRLFQTESSDWSEKSSPRTKS VAKNIVNVYITLTILCIIGFVMTGMNTFDAINHAFTTLSTGGYSTSDGSMNNFSHSTHWVATFFMFAGGLPFLLFVQALRKRSPGALFA DAQVRGFTLLVLSAGFVVALWLTWKLDYNFLDALRVSLFNIISVVTTTGFGLDDFTSWGPLPSIIFAFIMLVGGCSGSTSGGIKIFRFQV AFALLRKQMMQLVHPSGVFIQRYNGRPVTDGIVRSVVAFALTFILTIVVIAAILGILGLDPVTSITGAVTAVANVGPGMGNIIGPTGNFAS LPDMAKWTLSIGMLMGRLEILTVLVVFFPAFWHD
7.4E-51	183	30.2	9.7E-51	182.2	20.9	1	1	A4VX86_STRSY	Potassium uptake protein, Trk family	SSU05_1759	Streptococcus suis (strain 05ZYH33)	455	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus suis, Streptococcus suis (strain 05ZYH33)	391295	>tr|A4VX86|A4VX86_STRSY Potassium uptake protein, Trk family OS=Streptococcus suis (strain 05ZYH33) GN=SSU05_1759 PE=4 SV=1MRKGRIMSPFRIKLSPSQRIIISFLFVILTGSILLSLPISQISTSTASYWDHLFTSVSMVCVTGLFTKAVAETYSTFGQIICMMLIQIGG LSLIGFIGLFALRGGRKMNFINMATLQEALNRSDTKYFRNFLKSAFGFTLAVEAFGALLLSFHFVPEFGWARGLFTSIFVAISAFCNAGF DNFGATSIMRYVDNPLINITLASLIIMGGLGFSVWFDLQTQIGQKRSLRKLGFHTKIVLGLTAIILTLGTLTTLLTEWNNPSTIGQLSFGHK LLASFFQTVTMRTAGFASIDYTKAEPITLLLYIFQMMLGGAPGGTAGGIKITAFLTLVLYARSEILGLPHTNFMGRTIDNLSIRKAFATFSV FLLMFIIGLFALALTDDRQPLLFLMFEVMSALATVGVTANLTPSLTMAGQAVIMALMFFGRIGPLSILASLSVRKLSKTESLQYAKSSMLV
7.6E-51	183	23.6	5.6E-50	179.7	16.4	1.9	1	R7G2C4_9FIRM	Cation transport protein	BN651_00919	Dorea longicatena CAG:42	481	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea longicatena CAG:42	1263074	>tr|R7G2C4|R7G2C4_9FIRM Cation transport protein OS=Dorea longicatena CAG:42 GN=BN651_00919 PE=4 SV=1MNTKMIRYILCRMLGVESVLLMIPVIVAALYQEMSGIAFLIPAGILLLLFFLAGVKKPEQSHIYGKEGMVIVALAWILWSLFGAMPFT ISGFIPNYMDAFFETVSGFTTTGSSILRDVEALPQCLLFWRSLTHWIGGMGVLVFVLVLTSLDKKNSMYLMRAEVPGPEKDKLVPKAM STARILYGMYLIMTVVEIIFLMLGGVNLFDSMIFSFGSAGTGGFSNYADSVAHFHSAYIDGVITTFCALFGVNFSLFYFMLLGDFKSVRK NEELRTYIMLIVGATALITLNIHSMFPSMIKAFRYAIFQVVTVITTTGYATTDFAKWPMFSKSILMMLTVVGACASSTGGGIKVSRLLVGIK CIKREIVQLAHPKSVGIIRIGGKKVGSDILRTIYIYFIAYVGILIVSVMLVSLDNFDFETTFSAVLTTLGNVGPGMAKVGPMGNFADFSILSK LVLCFDMLAGRLEIFPFLVLFTAPAWRRKF

7.7E-51	183	34.2	1E-50	182.1	23.7	1.1	1	Q46HU2_PROMT	Trk-type K+ transport system, membrane component	PMN2A_1448	Prochlorococcus marinus (strain NATL2A)	461	cellular organisms, Bacteria, Cyanobacteria, Prochlorales, Prochlorococcaceae, Prochlorococcus, Prochlorococcus marinus, Prochlorococcus marinus (strain NATL2A)	59920	>tr|Q46HU2|Q46HU2_PROMT Trk-type K+ transport system, membrane component OS=Prochlorococcus marinus (strain NATL2A) GN=PMN2A_1448 PE=4 SV=1MSIRQETYRRLTVPQFTVVTGLLVIAFGTLLLATPFCSNANVGLWEALFTATSAVTVTGLSIIDIGIDLTFFGQVILAIMLLTGGLGLMAITTFLQGFIVSGTELKTRLDRGKTLDEFGVGGVGTTFKGIAITASILIFLGSITLYFFGFKNITSSSERIWASIFHSISAYNNAGFSLWSSSLQDYRGNWVVNFVLITLIILGGFGWRVTNDIWINRRSLKLRNLSLHTRLVIRSSFILIALGFFGLIFTESLARGSFFSLINFDDRILTALFTSVSSRTAGFTNLPISIESVSDSGLLLIMFLMFIGASPGGTGGGIKTTTIAALMAATRATLRGQNEIIIRNRQISDKVILKAVGITVGSFLFVLIMALLLSLSNGFNSGENFSFLEMLFTCISAFATVGFDLGVTSKLGHVGQLILIIGMFVGRLGILLFLSAVWQALNKSKIQHRNRIGYPKEDLYV
7.8E-51	183	28.5	1.8E-49	178	19.8	2.1	1	I3YR70_ALIFI	Trk-type K+ transport system, membrane component	Alfi_3260	Alistipes finegoldii (strain DSM 17242 / JCM 16770 / AHN 2437 / CCUG 46020 / CIP 107999)	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, Alistipes finegoldii, Alistipes finegoldii (strain DSM 17242 / JCM 16770 / AHN 2437 / CCUG 46020 / CIP 107999)	679935	>tr|I3YR70|I3YR70_ALIFI Trk-type K+ transport system, membrane component OS=Alistipes finegoldii (strain DSM 17242 / JCM 16770 / AHN 2437 / CCUG 46020 / CIP 107999) GN=Alfi_3260 PE=4 SV=1MRVDVVLRYVGVVMLFIALFMLLSAGISFVSGMDSAFYPLLLASLLTALLGAFPLIFVERTQQITNKEGFCIVVGSWLVACLVGMFPYLIWGGEFSLVNAWFESVSGFTTTGSTILNDIEVLPRGLQFWRMSSTWIGGMGVVMFALLILPSLGRNKMTLSSVELSTLAKDNYRYRTQIIVQILLVVYVGLTVLTTVLLKMAGMNWFDSLCHAMSACATSGFSTKNASIAYFNSPMIDTILIFAMATAGIHFGLIYATVTGKRNNIFRSEVTRWYLVMLLGGGLLIAVSLFAANIYPTFSAAFHHALFQFVSLVTTTGFATADSNQWTSFAVILLIFGSIVCACAGSTAGGIKTNRLVLAMKMMRTRLRQQQHPNAIIRIKLDGVIQENEALHSVMIFIVAYLMLILAGTVLGTMFGVDLMTSFSGSVASIGNVGPGFGQVGAMDNFSSVPGVFKISSSLLMLLGRLEIFGLIQLFFIKWWR
7.8E-51	183	28.5	1.8E-49	178	19.8	2.1	1	R5NBT0_9BACT	Trk-type K+ transport system membrane component	BN471_00275	Paraprevotella clara CAG:116	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Paraprevotella, environmental samples, Paraprevotella clara CAG:116	1263095	>tr|R5NBT0|R5NBT0_9BACT Trk-type K+ transport system membrane component OS=Paraprevotella clara CAG:116 GN=BN471_00275 PE=4 SV=1MRVDVVLRYVGVVMLFIALFMLLSAGISFVSGMDSAFYPLLLASLLTALLGAFPLIFVERTQQITNKEGFCIVVGSWLVACLVGMFPYLIWGGEFSLVNAWFESVSGFTTTGSTILNDIEVLPRGLQFWRMSSTWIGGMGVVMFALLILPSLGRNKMTLSSVELSTLAKDNYRYRTQIIVQILLVVYVGLTVLTTVLLKMAGMNWFDSLCHAMSACATSGFSTKNASIAYFNSPMIDTILIFAMATAGIHFGLIYATVTGKRNNIFRSEVTRWYLVMLLGGGLLIAVSLFAANIYPTFSAAFHHALFQFVSLVTTTGFATADSNQWTSFAVILLIFGSIVCACAGSTAGGIKTNRLVLAMKMMRTRLRQQQHPNAIIRIKLDGVIQENEALHSVMIFIVAYLMLILAGTVLGTMFGVDLMTSFSGSVASIGNVGPGFGQVGAMDNFSSVPGVFKISSSLLMLLGRLEIFGLIQLFFIKWWR
7.8E-51	183	15.5	4.2E-49	176.8	10.7	2.2	1	S6AGY1_PSERE	Trk system potassium uptake protein	trkH PCA10_39400	Pseudomonas resinovorans NBRC 106553	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas resinovorans, Pseudomonas resinovorans NBRC 106553	1245471	>tr|S6AGY1|S6AGY1_PSERE Trk system potassium uptake protein OS=Pseudomonas resinovorans NBRC 106553 GN=trkH PE=3 SV=1MSLPTLRILGFIIGLFLITLAVSMVIPMLTLLLFERTDDLFAFLWSSLITAIVGLALVGPGRPTNAQLRPRDMYMLTTASWVIVCGFAALPMVLIQHISYTDSFFETMSGITTTGSTVLTGLDHASPGLLIWRSMLHWLGGIGFIGMAVAILPLLRVGGMRLFQTESSDWGEKVMPRSHMVAKYIVVIYTGLTVLGTLAFWLAGMTPFEAANHAMSLISTGGFSTSDASLANWRQPAVHWVAVVVMILGSLPFTLFVATLRGNRTALLRDHQVHGFVGFLVITWLLVGTWLWAHSDNAWLDAVRIVAVNVTSVVTTTGVALGDYTLWGSFAVLLFFYLTFVGGCSGSTAGGLKIFRFQVAWQLLKANLQQLVHPRAVIKQQYNGHNLDDEIVRSLITFSFFFTTTIAVIALGLCLLGLDWVTALTGAATAVCNVGPGLGPIIGPVGNFSTLPDSAKWLLTIGMLLGRLEILTVLVLFTPKFWKH
7.8E-51	183	32.8	1.5E-50	181.5	22.8	1.4	1	F9Z846_ODOSD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Odosp_1976	Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) (Bacteroides splanchnicus)	608	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, Odoribacter splanchnicus, Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) (Bacteroides splanchnicus)	709991	>tr|F9Z846|F9Z846_ODOSD V(+)-transporting two-sector ATPase OS=Odoribacter splanchnicus (strain ATCC 29572 / DSM 20712 / JCM 15291 / NCTC 10825 / 1651/6) GN=Odosp_1976 PE=4 SV=1MKLYHKAFLYRHKWIQPYLQKVLGGIDAVTFLAALALIGGVVYEHGFIISEGAEADLGVLYRTVWGVFLVQTTMHIGLAYRETLKKYRTFTWVLNILLYLTLIPVIFFEPESGALKYFWLFLNNRIFQLILLLLLSLLRLSSGVIGLLGKRTNPSLILAGSFFLIICIGTGLLMLPRCTVDGISWVNALFVSTSAVCVTGLVPVDVATTFTSLGQLVIIILIQIGGLGVMTLTCFFAMFFMGNTSVYNQLAVRDMISSDSLSSLLSTVIYILFFTLVIEGAGMLVLFLSIHGTLGMTVQQEMVFAAFHSISAFCNAGFSTLSENLGNPLVMQHHNLLYITISVLIILGGIGFPILVNFKHIAGYHLKRLFYFIRTGKRDRQRIRHLYNLNTKIVLLTTLILLTGGTIAILLFEWNGAFAGMSMPDKWVQAFFNATCPRTAGFTSIGLTSFSLQSLLLMLLLMFIGGAAQSTAGGVKVNAFAAAVLSLFAVIRGKSRVEVFRRQLSVDSIRRSNATLVMYLMILFLGVFVLSVLEPHASLLALVFECTSALSTVGSSLGLTPALGEAGKLFVSLLMFIGRVGVITIVLGFVPPQKHTKYKYPDDNLIIN
8.5E-51	182	29.1	8.5E-51	182.4	20.1	1.5	1	E4RWX0_LEAB4	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Lbys_1462	Leadbetterella byssophila (strain DSM 17132 / KACC 11308 / 4M15)	591	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Leadbetterella, Leadbetterella byssophila, Leadbetterella byssophila (strain DSM 17132 / KACC 11308 / 4M15)	649349	>tr|E4RWX0|E4RWX0_LEAB4 V(+)-transporting two-sector ATPase OS=Leadbetterella byssophila (strain DSM 17132 / KACC 11308 / 4M15) GN=Lbys_1462 PE=4 SV=1MIRIKEKFFILKDSLARKMDKSIFVVMLLGFLLVLYQISFPKEEIIKDWINDALRQIPRILMSIYLFKWFITVFLSEKKGIFHKEHNLEFILFILLLLFNFFKKESQLLSSDYFLYLLITSLFFLRFMEFSSQIKTSLMNPAVLFAISFLVLIFWGTAMLLMPHATYGKFKFVDAAFMATSAVCVTGLSTVDLATKFTDLGAEILFVLFQIGGLGLMTFTNFFAVLFRGGMSLRNQLMLSNIVELDEPGSLFSVLKRILFYAFFVELAGAVCIYLAIGGENNAKTWFFSIFHSVAAFCGAGFSIIHDGLHNANYRFNYPLLWIISLLVIFGGMGFPVVNDLYNAIKHFAKGIVRYVFFRERFQYQARLLTVHSALVLCATAVLLVLGTLAFYFLEGNHTLAEHKSWGGKFTLSFFGSVVPRSAGFNAVNMGAITQGTILIYLLLMWIGGAPNSTAGGIKVTTFSLALLNVVSLAKGRERVEIFNREITRSSIQRSYVVIFLSFLIMGIGVFLVSIFDPHVSLQRVAFECFSAYGTVGLSLNLTPQLSDNSKWVIIVLMYLGRVGLFTILFGLFSKDRSVNYKYPKESVQVL
9.2E-51	182	32.7	2.5E-50	180.8	22.7	1.6	1	M4U2J5_9GAMM	Potassium uptake integral membrane protein KtrB	PCNPT3_03355	Psychromonas sp. CNPT3	455	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Psychromonadaceae, Psychromonas, Psychromonas sp. CNPT3	314282	>tr|M4U2J5|M4U2J5_9GAMM Potassium uptake integral membrane protein KtrB OS=Psychromonas sp. CNPT3 GN=PCNPT3_03355 PE=4 SV=1MSVLYKKSGVLHLKNKKGKKRWSEPRVILVSFLAILLPFALLLTTPFFSVSGLSFIDALFTATSAISVTGLGVVDTGSHFSVSGKILLMLLMQIGGLGQMTLSAILLYMFGLRISLRQQSITKEALGQNNSVNLRRLVKHIIVFACVAELIGMIFLSFRFVPVLGWREGVFSALFHAVSAFNNAGFSLFSDSMTSFVGDPTVNFTIAGLFILGGLGFTVISDLHGNRLRGFNHLQLHSKIMLIATPCLLLVGTLLFWFLEKDNMSTLGILSTGEQWLAAFFQSATARTAGFNSISVENLTHPALLVLMVLMMIGAGSTSTGGGIKVSTFVVAMISTWSFLRQNDKVVILKRSVPWSTVTKCLAIIVVSFMVLIGAMFALMISEDADPMSMVMFETISAFATVGLTSGLTAQLSEPGKVIMIVVMIIGRIGPLTLAYMLARPKPTLLKYPEGHVFAG
9.2E-51	182	2.8	3.2E-50	180.4	1.9	1.6	1	E8UBJ2_DEIML	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Deima_2802	Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	448	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus maricopensis, Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	709986	>tr|E8UBJ2|E8UBJ2_DEIML Potassium uptake protein, TrkH family OS=Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34) GN=Deima_2802 PE=4 SV=1MARRPPLRLTAPQLVAATFALGILIGALLLSLPFAHTPGHALTPLQAAFMATSALSVTGLAVVDPGTSLSPFGQVVLLLLVQIGGLGIITFGTLLALLAGRRLYFTDRVRLAQHFSALDVGGVLPLIRRILLTTLAIELLGTLLLWARFAPEQGAGRGLYSAAFHAINAFNNAGFALYPDNLARYATDPFVTLVLSALIILGGLGFLVQLSVVAHLRNPREHRLGVHVKIALSVTAALLLVGIAGFALTEWTNPRTLGPLSPLGKLTASVFQGVTPRTSGLHTLPYDAMRPATLLLTTLLMFIGANPGSTGGGIKTTTFYVVLRGVWNYARGRGEPVTHHRRLDRDLITRAMTIALLGIGVLHAALLLLLLTNPSVPPMNALFETVSALSTAGLSMNTTPHLNAAGHLLLIVLMYLGRVGPLMLATSLSARASRDTVRYPPERDILLG

9.5E-51	182	12.2	2.4E-49	177.6	8.4	2	1	A8ILF0_AZOC5	Trk system potassium uptake protein	trkH AZC_4025	Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	498	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Azorhizobium, Azorhizobium caulinodans, Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	438753	>tr|A8ILF0|A8ILF0_AZOC5 Trk system potassium uptake protein OS=Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571) GN=trkH PE=3 SV=1MSLANAARVQRGSTPALDLRPLAATIGTLLAILGASMVLPALADLRAGVAGESAFVGSAAVTIFVGVLMIVSGRSAGPMRLDLRQAFLLTTSVWVVLALFAALPLAWGPSGLSPVKALFESMSGLTTTGASVMSGLDAMAPGVLLWRNMLHWFGGIGIVVIAIAVLPALSIGGMQLFRTESSDRSEKFLPRAGSVAKGLLAAYGVLTLLCAIGYGLAGMRPFDAVTLAMSTVSSGGFANSDSSLAVFANPAVDYVAIVFMLAAALPFPLYVRAFSGDVRKLFRNPEVRLFLGLVAVFTVASFLQQTFQGIASGEPALRGALFTVASLMSTTGFMAVDYTNWGPLSDAIFFIAMFLGGCTGSTSGGLKSLRILIALKAVRQHLKRISYRNGQFPIRYGGAPVSDDVVASVLGFIFLYVASFVVISVILSMLGLDLRTALSAAIACLANVGPGLGPLVGPASNYGGLSEPAIAVLTLAMLLGRLEIVTVLVLVVPRFWWR
9.7E-51	182	30.7	3.6E-50	180.3	21.2	1.7	1	A0A0F2R9X6_9RHOB	Ktr system potassium transporter B	VR74_19020	Hyphomonas sp. BRH_c22	429	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hyphomonas, Hyphomonas sp. BRH_c22	1629710	>tr|A0A0F2R9X6|A0A0F2R9X6_9RHOB Ktr system potassium transporter B OS=Hyphomonas sp. BRH_c22 GN=VR74_19020 PE=4 SV=1MLVLVYLSWIAIGAALLMLPISSTHGISLSDALFTSTSAVTVTGLVVVDTGSAYTMFGQGVVMLLIQLGGMGLMTFAVMVLSSLGLRIGMTHRRYLREEMGLASFSGLIDLVWTIFRIVLVCELLGMMLMSIVFVPEFGWREGLWQAAFHSISAFNNAGFSLFPDSLMGYVDNPIIIFTVSVQFIIGGLGFAVLSDILLFRKWRRFSLHTRLMLVGTLVLICGTCVIYGLLEWSNPETLGGLHSLQSKLQAIWFESVTPRTAGFNSMNTAGMHDSTALFTMVLMVIGAGSTSTAGGIKVTTAVVLLMATIAFFKNSGRMRAFGYSVGLEQGLKVMALLTVSLFVILIGLFILVGTHHHINFLDAAFEVTSAFGTVGLSRGATGELNDIGRLVICTIMFLGRLGPLTLGFFLASKTPPRVKYPEGEVYLG
1E-50	182	22.5	1.8E-50	181.3	15.6	1.3	1	F0RJ04_DEIPM	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Deipr_0239	Deinococcus proteolyticus (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703 / MRP)	463	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus proteolyticus, Deinococcus proteolyticus (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703 / MRP)	693977	>tr|F0RJ04|F0RJ04_DEIPM Potassium uptake protein, TrkH family OS=Deinococcus proteolyticus (strain ATCC 35074 / DSM 20540 / JCM 6276 / NBRC 101906 / NCIMB 13154 / VKM Ac-1939 / CCM 2703 / MRP) GN=Deipr_0239 PE=4 SV=1MPLISRPAPVRQPEPRRSWYARLQPPQLIALVYFIGILLATAALHLPGVVRPGADMTSVDLLFTATSALTITGLVVADTGETFTRYGQVILMVLFLLGGLGILSFGTLFAFLTGRRVNFSERQHLQAQISGLDTGSVVRLLRTIFTYALGLQLAGAVLLALRFVPQFGLGEGLFQAAFHSISAFNNAGFVVVPGGMPQYVSDPLVSLTISGLVILGALGFIVQFNVVNWLQRPREHRLTVYSLLTLFTTAALLLLGFFAVLLLEWNNHATLEPLPWHGRLLASFFQSMTPRSGGFNTVDIESMRTATIMVLIVLMYIGGGSGSTGGGIKTSTFAILTGSAWNMVMGRGELIAFGRRVEKDNVVRATTVAMLYTMMVATAFFLMLLTNPHMDFTHLLFETVSAAATVGLSLNTTSHINDAGLVILSVLMYLGRIGPLTFAVAFSLRTQQRRGVRYPPERDILVG
1.1E-50	182	16.7	3.5E-48	173.7	11.6	2.1	1	R5HWU1_9FIRM	Uncharacterized protein	BN501_00143	Roseburia inulinivorans CAG:15	479	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia inulinivorans CAG:15	1263105	>tr|R5HWU1|R5HWU1_9FIRM Uncharacterized protein OS=Roseburia inulinivorans CAG:15 GN=BN501_00143 PE=4 SV=1MKYSTIGYILGQVLKFEGIFMLLPFLTGMIYHENEAYSYLIIGIICFVLGCLITLKKVKHPQIFNREGFVAVALSWIVLSIFGAIPFVITGEIPSYVDALFETISGFTTTGASILSNVEALTHTSLMWRSFTHWVGGMGVLVFIMSFLPLMGGSTINLMKAESPGPSVSRLVPHVKDTAKILYRIYLVITIIEIVLLCIFGMPMFDSLTLTFGTVGTGGFGIHNDSIAGYSPVLQNIITVFMILSGVNYVAYFYIMTKQLKEIFKVEEIRVVYFGIILGAGTFIALNIRSLYGSLGEAFRHAFFQVGSIITTCGYATTDFDLWPETSKMILVLLMFIGACAGSTGGGFKISRLLILCKAIPKQLSLVIHPREVKVIRMDGKPIDHNTLRSTNVYLAIYFFILLISTLLISVDNFNLTTNFTAVASTLNNIGPGLDGVGPTRNFGMYSDFSKFVLMFDMLAGRLELYPLLILFMPSLWRRK
1.1E-50	182	8	2.5E-26	101.7	1.7	2	2	D7BBC1_MEISD	Cation transporter	Mesil_0768	Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	473	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Meiothermus, Meiothermus silvanus, Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	526227	>tr|D7BBC1|D7BBC1_MEISD Cation transporter OS=Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) GN=Mesil_0768 PE=4 SV=1MTGVVFVGLGAVMILLGILDAVYRENAIGFLVGGLLGIALGLALRRLGNPHAEPRRAEALFTVALLWILVPALGAIPFWISGNLAPLDALFESVSGFTTTGASVLADFSTWGYGLFLWRSLIQWFGGIGILLIFIVVLPQLAVAGRQLFFAEVTGVQKEKITPKLRQTAAMILRIYVVLTVVCFTVYMATGQPFFEAICNALSTVPAGGLSPSAESFAAYSPVSQWSGTLFMFLAGIGFLLQYRLFFGREVHTLLRDAEFRAYGAIIGVSGMALAGYFFFSGTYGLEPALRHAFFQVTSIVTTTGFASTDFGQWALPAQMLLIILMFIGGTSGSAAGGIKVIRWLIAWALVKRELQRSLHPQAVLPLRVGNKVVSEDALRSVAAFITLYILLFAVGMGVIGIAENNFFYGFTASAAFIGNTGPAYGEFGPFGHYGSLHLASKVVAIIQMWAGRIELIPLMILLLPEFWRRLRS
1.1E-50	182	25.7	1.9E-49	177.9	17.8	2	1	A4GAD8_HERAR	Putative potassium uptake protein (TrkH)	HEAR3373	Herminiimonas arsenicoxydans	457	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herminiimonas, Herminiimonas arsenicoxydans	204773	>tr|A4GAD8|A4GAD8_HERAR Putative potassium uptake protein (TrkH) OS=Herminiimonas arsenicoxydans GN=HEAR3373 PE=4 SV=2MRRGYQPPLLYRQVKRQVRRRVLHLTPPQALILSFIGLSLLGAVLLKLPMASHAHTTWMQALFTAVSASTITGLTVLDVGSHFTLFGQWIVLGLIQLGGIGLLTFGVLIIHLTSGRLTLRNRAAMQDAFNQSGSIDLQHLLRVLFGFIVLTELLGTLLLATQWVPEMGWGKGLFYSFFHAVSAFNNAGFGLASHSLAAYVDNPLINLVIPFLFISGGIGFAVIADLRAKKRFHELTLHTRLMIGTLAINLIAMLVLLLLEYGNPDTLGALHGWGAKLWASWFQAVAPRSSGFTTMDTAALRPVSAFFIMMLMFIGAGSGSTGGGIKLTTFIILLVATRAFLRQQKTPVVLGRSIEANTIVRALAITIIAVLCVVAGTFILMLTEDGLFIDLAFEVISAVSTTGLSRGVTPGLSIAGQCTMMVLMLIGRVGPLTLAFMLANPRGRAIEYPTGRVNIG
1.2E-50	182	30.6	3.7E-49	176.9	21.2	2	1	R6JYJ4_9FIRM	Uncharacterized protein	BN564_00159	Eubacterium sp. CAG:252	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:252	1262887	>tr|R6JYJ4|R6JYJ4_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:252 GN=BN564_00159 PE=4 SV=1MSLFSKIRRRLSHAQIMALGFLTVIIIGTVLLMLPVSSRTGQWTPFIKALFTSVSSTCVTGLVVVDTFSYWTLFGQIVILIMIQIGGLGFISIGVVFALFFNRNIGLANRTLIQESMNSNMLRGIVRLMRNVIVGTAIFEAIGAAVLSLRFIPRMGVARGIYNSIFHSITAFCNAGFDLMGRYEPYSSLTGYYNDYVVNITIMALILIGGLGFTVWADLKHNKLYFKKYTLHTKIVVVSSIVLVVVPTILFMYFERDGVEAGMPFADRFITSLFAAVTPRTAGYNTVDLGAMTQASKLLTIILMFIGGCPGSTAGGVKTTSIVIIMVYIWSNLRNASGCNIYGRRLADEDIKKASMVIGLNLIMAVAALLIISGMQSFDFEDLCLEVFSAVGTVGLSTGITRQLNVASQIVIILLMFCGRIGTVTFASTFAYNRKQVKLLNPEEHVNVG
1.3E-50	182	26	1.8E-50	181.3	18	1.2	1	R6WJ21_9CLOT	Potassium uptake protein TrkH family	BN619_00294	Clostridium sp. CAG:349	465	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:349	1262797	>tr|R6WJ21|R6WJ21_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:349 GN=BN619_00294 PE=4 SV=1MKEKTEQLFNAVGKKIKNLMTPARYIVLGFLGVIAVGTILLLLPFSSASGKTIGFVPALFTSTTAVCVTGLTVIDPATQLSIFGQIVVLLLIQIGGLGFMTTTTFMFMLVGKKISLKERMTIQESLDQDSLKGVVKLTKRILAFTFIFEGFGTLMLMTRLVPALGARGIYVSLFTAVSSFCNAGIDIMGKDYGAFSSISAFSHDPVVLITIMVLIISGGLGFLVFNDILRKKRNRPLRLHTRVSLSMTAILLVVGAAVILGIEWNNPGTLGPMDWGDKVLNAFFQSTTARTAGWTSINQANLTDGAKVATMVLMFVGACPASTGGGVKTTTIFVMVMLFASVFRGRDEVVVGKETINTRTIKRAAVVTTAYFLGSFAQALIIWATEAAYGVQLSVIDSMYEAFSAFGTVGVSAGITTSLHTPALITLCFSMFIGRLGPLTIGTALLNTKKQSANIKYPDAKILIG

1.3E-50	182	35.5	1.7E-50	181.4	24.6	1.1	1	R6P5J2_9FIRM	Potassium uptake protein integral membrane component KtrB	BN582_00345	Eubacterium sp. CAG:274	465	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:274	1262888	>tr|R6P5J2|R6P5J2_9FIRM Potassium uptake protein integral membrane component KtrB OS=Eubacterium sp. CAG:274 GN=BN582_00345 PE=4 SV=1MSKFLHLLRQLDSSQIITLGFLTVILFGAVILSLPICSADFTFTPFVDSLFTATSAVCITGLTAVSTAYHWNILGKLIILMLIQIGGIGFM SMVTMLFIAVGKKITLKERIVIQESFNLSQRHGLVSFTIYIFKFSFVVELIGAFFLSLRFIPQYGFVRGIFYGIFHSVSAFCNAGFDILGDNS LIPFSGDVIVNITVMCLIVVGGLGFPVYSDFTTHLKFAKEHKLHINYVVKKLRLHSKIALITTAVLIIFGGLFFFIAEYFNPYTIGNFSFFHKIM ASLFQSVTLRTAGFDSMGQGNMTYASKVISIVLMYIGGSPASTAGGVKTVTSAILFLAVWAVIRGRESINVFHKNIPFYTLQKALAVVM MMVTITIGASVIMTWTEARTPIHMEYLDILFEVVSAQCTVGLTTGITHFLSNGGKIVLILCMYMGRLGPISVAIALTKNKKHNKNYIHFPED KLLVG
1.3E-50	182	27.8	4.7E-50	179.9	19.3	1.7	1	R5BX74_9FIRM	Cation transport protein	BN814_00676	Veillonella sp. CAG:933	502	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Veillonella, environmental samples, Veillonella sp. CAG:933	1262980	>tr|R5BX74|R5BX74_9FIRM Cation transport protein OS=Veillonella sp. CAG:933 GN=BN814_00676 PE=4 SV=1MRIQIVMRLVGQLILIVAGIMWVPFIYGLTVGESYFSFIGASIMAAVTGSLLYYYGQPSTSYSLRDGFLTVSSIWILVSFFASLPFYF GGVLPTFIDSLFESVSGITATGASVVEELDSLPKSFVLWRSLTHWLGGMGIVVLVLAFLKNLGADSAHLFNAEASVPRPGVVLPRIRSM AFKLWTIYLLFTAVCFSALVIAGMSYFDAINMTFTTIATGGYIPNDGVVDIYTENWAIRWILIFFMILAGGNFTVYYAVFQRGLKAVWQD FEYRMYLLILFIGSIIVMYALYMADNFSSGTSFNRAVFMIVSMQTGSGLVLGNYDVWSPLAQMMLFMSMFFGGCSGSTTGGIKIIRIIILI KSSIIYLRKAIHPDMVQTITINGKSMPQKWVQMTQQPFFLYMTVFAISALGIAATGLSFGESLQCVAGILGNVGLAFGKLGPQGSFAVL HPMAKIICVIDMLLGRLELFTLLVLLHPDFWQGYFLKRRKRSYKVLQPVGTHRRG
1.4E-50	182	24.6	3.5E-50	180.3	17	1.6	1	E7AAE7_HELFC	Putative K+ uptake protein, TrkH family	ktrB Hfelis_05850	Helicobacter felis (strain ATCC 49179 / NCTC 12436 / CS1)	441	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter, Helicobacter felis, Helicobacter felis (strain ATCC 49179 / NCTC 12436 / CS1)	936155	>tr|E7AAE7|E7AAE7_HELFC Putative K+ uptake protein, TrkH family OS=Helicobacter felis (strain ATCC 49179 / NCTC 12436 / CS1) GN=ktrB PE=4 SV=1MNKTFSTIVISYVLLALLGAFLLSLEPMRTKAIPFLDLFFTTASSVCLTGLITANPASDFSIYGQIVILTLIQAGGFGYMGLAGLLFLFI GKKVDFKNRMLLKESLDYPNMQGIIRYLKQILFFTLAIESVGALILTLHFLSHMPWHRALWAGVFHAVSAFNNAGFSIFESNLSDYRDDI VVNLTICALIILGGLGFLALRECYSYRHSPRLSVHTRIVLIATVVCLVVGVAVLLIFEWDNPKSVGHLDWPHKILSTFFISVNLRTAGFNSI DMAGLHDQSLFFSSLLMVIGAAPGSTAGGIKITTVTVLLFYAYCTLKDREVVLFQRTIPASIVKKSFLIGIIATFYIVFSAMILSATDDTQNK HFLPLLFEICSAFGTVGASTGNGGNLSFVATFSNFGKLYIIVLMFMGRVGVLVFSMALVRKGKKSSVRYPEEGVVL
1.6E-50	182	18.3	3E-50	180.6	12.7	1.3	1	G1UW82_9DELT	Uncharacterized protein	HMPREF1022_02855	Desulfovibrio sp. 6_1_46AFAA	454	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio sp. 6_1_46AFAA	665942	>tr|G1UW82|G1UW82_9DELT Uncharacterized protein OS=Desulfovibrio sp. 6_1_46AFAA GN=HMPREF1022_02855 PE=4 SV=1MQCKRLFSPLTWPVFSFLGAIALGTVLLCLPPSWHPGRELQTLDACFLATSAVCVTGLTPVDISSVLSPFGQGVLLFLIQLGGLG VMTYTSIIFLLWRNNVPFTNREAVSQALLGGDFNLAAFVRQVLALVFSIEAIAAMLLYLHDPRFFHPFSAVFHAVSSFCNAGFALSPDNL MPFRDDPVVNLVIAGSVILGGIGFGVLREFLGLLSGGRFGAPVHRLSRFSRLVVKTSLFLIVAGTVLIFCIEFFRAGNEQSVGDGFDLAIT SFFQSVIARTAGFNSVDMAALSEASLMVLMALMFIGAGPGSCAGGIKVVTFRVLTGYVAAQFRGDRQIVLEGRGVTRGNVTRALTLFF LYSMLIAVSTFLLSITENGILHRTGREGVSMLRLLFETVSALGTVGLSVNLTPDLSAEGKMIIIFNMFAGRVGLLSLLMAVQSLQPKKAYT VAEAQLPIG
1.6E-50	181	17.6	2.5E-48	174.2	12.2	2	1	D4K5J7_9FIRM	Trk-type K+ transport systems, membrane components	FPR_27430	Faecalibacterium prausnitzii SL3/3	445	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii SL3/3	657322	>tr|D4K5J7|D4K5J7_9FIRM Trk-type K+ transport systems, membrane components OS=Faecalibacterium prausnitzii SL3/3 GN=FPR_27430 PE=4 SV=1MIQYPRYRQHRFSSFQVIIAGFAAVDLVGALLLMLPIAAQQRCVTPFHEALFTSTSALCVTGLVVQDTGSYWSAFGQSVILLLIQI GGLGVITVGAAFALLSGRKISLKQRSTMQEATAAPQMGGIVRLTGFILRITALFELAGAALLLPTFCADYGLRGIWYALFHSISAFCNAG FDLLGTEDAKFVSLTRYAGNPLLTTVIAALIVFGGLGFLTWEDICTYRLDFHRYRMQSKVILVTTAFLLVLPTLYFYCFEFTAGSARQRIL LSMFQSVTPRTAGFNTADLAAMGSTSQALMVVLMLLGGSPGSTAGGMKTTTFAVLLANMWATFRRREDAEFFGRRIDSSAVKNAAT IAGMYLTLFFLGAFVIATAEQLPMSVCLYETASAVATVGLTLGITPQLGILSQGVLIALMFLGRVGGLTLIYAAFGSSPAHSRLPQEKIAIG
1.7E-50	181	17.8	4.9E-50	179.9	12.3	1.7	1	A0A0A2EYQ6_9PORP	Potassium transporter	HQ41_06005	Porphyromonas sp. COT-290 OH860	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Porphyromonas, Porphyromonas sp. COT-290 OH860	1515615	>tr|A0A0A2EYQ6|A0A0A2EYQ6_9PORP Potassium transporter OS=Porphyromonas sp. COT-290 OH860 GN=HQ41_06005 PE=4 SV=1MKTINFRFISRVLGLMSLVQCVMMLICVGISLYFGEVIMPFVIGVLAYAGVGGVLFGLGRDLKDQRVGRREGMLTVTSTWLLLSL LSTIPMMLSGATPRFVDAFLECISGFTTTGATVFSRVEHLPHGILFMRSLMQWQGGIGIVVFTVALVPMFGGGASQIFNAETTGITHER FLPRIADVAQRLCIVYVVETLVLIVLLVLGPMGLFDAVCHSLSCVSTGGYSTRDAGIAAYDSVYIEYVLSLFMYIGALNLTLIYFAFAGSPL KLLRDEEFRWFNIFIGATVIVTAIWLYSQGFYQDLEEAIRKSLFQVISLGSSTGFLTADITEWRPFFWMLGLQIMFINGCAGSTSGGLKV ARFVLLMKNLYTEFKKQIYPHLFTPVKLNGKQLSISTVHQVLAFCVVYLMLIFAGSLLFMLDGNGFISSLSIACSAASNSGPGIGEYMSTI GPAGDFSKYLMAFLMLTGRLEVFTVLGILTPHFWKR
1.8E-50	181	25	1.5E-25	99.1	6.3	2.1	2	L0KA09_HALHC	Trk-type K+ transport system, membrane component	Halha_1920	Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	491	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Halobacteroides, Halobacteroides halobius, Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1)	748449	>tr|L0KA09|L0KA09_HALHC Trk-type K+ transport system, membrane component OS=Halobacteroides halobius (strain ATCC 35273 / DSM 5150 / MD-1) GN=Halha_1920 PE=4 SV=1MFNQKLTTVISLIGSLLIVLGCTLLLPIVVGFIYGEELVYAFIIPALLSLGLGFITQFKFKKGKINLTTGMLVCALGWITISFVGALPFYL KLDYTYLDTLFETVSGFTTTGITVFTDLSNLPKSIQFWRCLIQWLGGLGFLTFFLVVTFRGQAGLFQLFTAESHKINQSRPVPNIFKTVKI LWGIYALFTLLEIILLKILGVSLFDAITHSFTTLSTGGFTNYDASIAYFKQTGYQYYKLIEYVTILFMTLGGINFLVHYKVLTGEINALWDKIE MKYFWAIISGVSSLIILDHYLAFPFKWSGLERTIRYTLFQVVSILTTTGFATEGIITSFYPALAKQFFLLLMFIGGCVGSTAGGIKIIRVAILN KLLQREVKKIYYPKHAVLPVVVDGNKISDQEIFKTVALVFGWLILIVIGGAITAISSNLSAWQAFSGIFSALGNIGPFYFSVEKMQSLSAGI KITYIIGMLAGRLEILPIFVLFSKQAWRR
1.9E-50	181	33.4	3.1E-50	180.5	23.1	1.2	1	Q89YR6_BACTN	K+ uptake protein	BT_4665	Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides thetaiotaomicron, Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	226186	>tr|Q89YR6|Q89YR6_BACTN K+ uptake protein OS=Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482) GN=BT_4665 PE=4 SV=1MKIYHKFLLYQNKLLKPYVRILLGLVEALTYLASLLLIVGVVYEHGFPLSPVEVQQIQILYKAVWIIFLIDVTLHISLEYRNTKKQYRR LAWILSVLLYLTLVPVIFHRPEEEGAILQVWEFLHGKFYHLILLLVFSLLNLSNGLVRLLGRRTNPSLILAVSFMAIILIGTGLLMLPRCTVN GITWVDSLFTATSAVCVTGLVPVDVSTTFTTSGLVVIILLIQIGGLGVMTLTSFFAMFFMGNTSIYNQLVVRDMVSSNSLGSLLSTLLYIL GFTLVIEGIGMVSIWFSIHDTLGMNLEEELAFAAFHSISAFCNAGFSTLSGNLGNSMVMTNHNWLFISVSLLIILGGIGFPILVNFKDIVLY HLRHVWTFVRTRKLERHKMPHLYNLNTKIVLIMTFLLLLIGTLAILAFEWNASFAGMSVADKWTQAFFNATCPRTAGFSSVDLASLSVQ TLLVYLFLMWVGGGSQSTAGGVKVNAFAVVVLNLVAVLRGSERVEVFGRELSHDSIRRSNATVVMSLGVLFLFIFILSILEPKASLLALT FECVSALSTVGSSLNLTPQLCDASKLLVSLLMFIGRVGLITLMLGIVKQKKNTKYRYPSDNIIIN

2E-50	181	21.2	8.6E-50	179	14.7	1.8	1	R6X075_9PORP	Potassium uptake protein TrkH family	BN675_00130	Parabacteroides merdae CAG:48	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides merdae CAG:48	1263094	>tr|R6X075|R6X075_9PORP Potassium uptake protein TrkH family OS=Parabacteroides merdae CAG:48 GN=BN675_00130 PE=4 SV=1MLNIRFIIKMLGMMFILETLFMLAATAVAFLYEGNDFYPLLQSSGIMFGTGVLFMLIGLRANEHTAGRREGMLTVTLTWALFSLLG MLPFYLGGYIDNVTDAYFETMSGFTTTGSTILTDIEALPHGILFWRSLTQWQGGIGMIVFTVALMPIIGGGATQMFNAETPGITHERFR PRVTQVAKRLWGVYLFLTIILIGLLWAGPMDLYDAVNHALTCISTGGYSTKNASIAYWDSAYIEYIITIFMFIGATNITLIYFFFNGRPKKLF ADEETRWFFWFVLIITAISTVWIMYKGIVDDFGTAFRQTVFQVVTLVSTCGFATVDYIPWGPFFWLLALVLMVVCGCAGSTCGGLKM GRFVILTKNLFNEFKKQTHPHAIIPVRMNGHAVSGDIVHRVLAFAFAYIALIFVSCMVLMIDGVGFEETIGATISSISNVGPGLGSLGPVG NYADVPVVSKWFLSFLMMVGRLEIFTVLTILLPGFWKQ
2.1E-50	181	29.6	1.4E-48	175	20.5	2	1	A0A090KEC5_9GAMM	Trk system potassium uptake protein	trkH MVIS_4341	Moritella viscosa	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Moritellaceae, Moritella, Moritella viscosa	80854	>tr|A0A090KEC5|A0A090KEC5_9GAMM Trk system potassium uptake protein OS=Moritella viscosa GN=trkH PE=3 SV=1MVNFKPVLFMASVVLRALALFMIAPLVLALSTDGHGAPEFFKSIIITTIASGLFWHKGRSKVFRLGIREMFLLTTCVWIIASAFAALP LMLIQHISYTDAYFETMSGITTTGSTVLSNLDATAHSVLLWRSILQWLGGVGFVVMGVAVLPYLNVGGMRLFQTESSDWSDKNTAKT QHTAAYVMYVYLSLTVLCYFGYLAAGMTSFEAVNHAMTTLSTGGYSTSDQSMAHFSNSAQWNGSFFMFLGGLPFLLLISAIHRRDIK VLINDAQIIGFGKLILVMTIMMSLYLWQKGVFELTDAIRISMFNIISVVTTTGFGLTDFGTWGEFTTVLFAGLMFTGACSGSTSGGIKIFR FQIAFTLFRKQMSQLVHPSGVFRQHYNGRNVNDVIVRSVVAFGSAFIATVSILAAILSIIGLDPVTSITGAITAVANVGPGLGPVIGPSGN FASLPDTAKWALSLGMLMGRLEIMTVLVLVTPAFWKS
2.2E-50	181	24.4	4.2E-49	176.8	16.9	2	1	R5HXU1_9BACT	Uncharacterized protein	BN796_01397	Alistipes sp. CAG:831	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes sp. CAG:831	1262698	>tr|R5HXU1|R5HXU1_9BACT Uncharacterized protein OS=Alistipes sp. CAG:831 GN=BN796_01397 PE=4 SV=1MNIKLIARYIGIALLFNALFMFISLGVSALNGFDSSFSPLLLSGLITAMVGCFPLIFVRGQDDVNLREGFAITIFSWILSCIFGMLPYV MWGGEFTLPNAWYESVSGYTTTGGTVLQNVEALPKGLLFWRSSTHFIGGMGVMVFMLLVLPSMSTFRMRISKIEISSISKDNYRYRS KETVRVIASTYIGITVAGTIALMVAGMSFFDAVNHAMSIVSTGGFSTRNLSIMYYDSLPIEIVCIVFMYVSTLHFGMVYALVVKRSTALLK SPVFRYFMGFCLVMSLLIGLDLKASGQIATYGEAMRQGFFQYASIVSSTGFATADTSVWPLFSIFLLLFAMFHGGCSGSTCGGVKADR MWIFYKVLKNNIFKQVHPNAVIPVKVGDHTIDPSVIRSSILYIVAFTLIFIVGAMLISLTGPDFEESFSASLTSMGNVGPGFGASGSMGNF SHFSPFAKLVMTLEMLLGRLEIYTLLMLFFIFKKV
2.3E-50	181	33.8	6.8E-49	176.1	23.5	2	1	F9VEZ6_LACGL	Potassium transporter protein	LCGL_1437	Lactococcus garvieae (strain Lg2) (Enterococcus seriolicida)	445	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Lactococcus (lactic streptococci), Lactococcus garvieae, Lactococcus garvieae (strain Lg2) (Enterococcus seriolicida)	420890	>tr|F9VEZ6|F9VEZ6_LACGL Potassium transporter protein OS=Lactococcus garvieae (strain Lg2) GN=LCGL_1437 PE=4 SV=1MKNFFIKRMIKNLTDLQIIFLSFLFVVILGGSILSLPISSKAGEYTSFVDSLFTAISATCVTGLAVLDTSTYWSFFGQVIILILQVGGL GFMTLVASIFLLLNQKVSMKSRTALQKTYSVSHLGFKKSLVLGILFISLSAEFIGTVLLSFIFIPEYGWLKGVWFSIFHSVSAYCNAGFDL FGNSLVSYDHSPYTMLVISLLIVCGSLGFIVIMDLIGYKKRHKLSLHSKLALIVTGILILFGMLLFFITRFSFYKSDFLVYFVQSLFFAITPRT AGFAIQDYSSLSQASLFLTIILMTIGGTSGSTAGGIKTTTIGVFILNIRAVIRREKHTRFGNRTIPQNLVKQSYESIFLYFSLVIISTFLLLVLE PNLKLDQVLFEVVSALSTVGLSMNVTPELSSASKGLIGLLMFIGRVGIFTIIYSLNTKNREEALYKYPEENVMVG
2.6E-50	181	31	1.5E-47	171.7	21.5	2.1	1	F0RRX3_SPHGB	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	SpiBuddy_2769	Sphaerochaeta globosa (strain ATCC BAA-1886 / DSM 22777 / Buddy) (Spirochaeta sp. (strain Buddy))	445	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Sphaerochaeta, Sphaerochaeta globosa, Sphaerochaeta globosa (strain ATCC BAA-1886 / DSM 22777 / Buddy) (Spirochaeta sp. (strain Buddy))	158189	>tr|F0RRX3|F0RRX3_SPHGB H(+)-transporting two-sector ATPase OS=Sphaerochaeta globosa (strain ATCC BAA-1886 / DSM 22777 / Buddy) GN=SpiBuddy_2769 PE=4 SV=1MHINILRSRLCFIMKKPLSKRMQPNHLLLVGFLLIILFGSLLLSLPIAHNPGIDLAYIDALFISASAVCVTGLVTVDVALTFSLFGRTVI AVLILLGGLGFAAIVISFSLLLGMNVNLSKRLFIKEAYNLSSMKGTLGIVRAVLISSFLIQGVGTVVEYFVFRQAYSPLDAFGHALFNTISA FNNAGFDLMGGYRSLTVYQDNLVMNLTTALLIILGGSGFFVLADCVRNRKWSTLSMHSRIVILMNASLITLGLLFFMAVEHLSPLAAFF QSVTTRTAGFNTVDIAAFSQAGLFFAMILMFIGASPGSTGGGIKTTTTFALLLSLGSLMFRREPAAFKRKVNSDSILKAFQVLLLSFLVV VLGSMTLVLIEGGNFDFLAVLFETVSAFATVGLSCGITPSLSTVSKVVLSLIMFAGRVGPITIATSLKAKPSHLGYIEEQVFIG
2.6E-50	181	22.2	9.7E-49	175.6	15.4	2	1	R6C784_9CLOT	Uncharacterized protein	BN687_00901	Clostridium sp. CAG:510	451	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:510	1262816	>tr|R6C784|R6C784_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:510 GN=BN687_00901 PE=4 SV=1MDADIMNEEIIKRKKRLSSFQIIILGFAGVILLGALLLMLPIATKERVVTPFHETLFTATSATCVTGLVVQDTGSYWSVFGQAILLFLI QIGGLGVVTVAAAFTMLSGKKISLMQRSTMQEAISAPQVGGIVRLTGFILKGTFLIELVGALCLMPLFVKDFGVKGIWYAFFHSVSAFC NGGFDLLGTADNRFVSLTGYAGNVPVNVIIMLLILLGGLGFLTWEDIYTKKIHFKKYRLQSKIILAASIFLLVMPAAFFFAFEFTDMPLKER LLCSLFQTVTPRTAGFNTADLTGMQGASKAVMIVLMLIGGAPGSTAGGMKITTLAVLVTNMRSVFRQKEDMQFFGRRIEDGAVKTAA AVLSLYLTLFAGGAIAISMAEGLPLGDCLFETASAVATVGVTLGITPGLGIFSQIILIMLMFMGRVGCLTLIYAAVSGGNKNFSRLPQEKV MVG
2.7E-50	181	30.2	1.5E-48	175	20.9	2	1	Q5QZ85_IDILO	K+ uptake system component	IL0201	Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	456	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Idiomarinaceae, Idiomarina, Idiomarina loihiensis, Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	283942	>tr|Q5QZ85|Q5QZ85_IDILO K+ uptake system component OS=Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) GN=IL0201 PE=4 SV=1MKQWAPSIAWLYRRPGRKRRRAFKASPPVILSGGFACLILLGTLLLKLPFSTEQPITWLESLFTATSAVTVTGLVVVDTGATYTP FGMSVLALLIQAGGLGFMTFAVLAAISIGGHVGIQHQVLAKEAMQQTSLASIGRTAKAVVSLALIVEAIAVVGLTITWWQEKGFVDAFA ESIFYAISAFNSAGFVLSPNGIVDYADSIPVNLIISILFVIGGLGFSVITNIYEKRRWYKFSVYTRAILWATLIINVLSVAIIWLLEMNNPATFA NLSFGDQAMAAWFQATTPRSAGFNTVDTGAMTEASAVYTMLLMLIGGGSMSTAGGIKLGTFIVLLVATYAFLRRREYVTLLNRTVPQ ELVMKALAVTLVTLTLMFLGIFILMILNPLPFIDITFEVLSASATVGLSRGITAEVTGASQLVLVFLMFAGRVGPLTLAYFLATPRKRHIRFP ETDIQVG
2.8E-50	181	34.9	6.1E-50	179.5	24.2	1.4	1	R5RMR3_9FIRM	Uncharacterized protein	BN747_00215	Firmicutes bacterium CAG:646	461	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	1262995	>tr|R5RMR3|R5RMR3_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:646 GN=BN747_00215 PE=4 SV=1MEKMKNRIKQTKGEVASKLRHTSSAKIIPAVFFAIILAGALLLMLPISQKGEGGASFTDALFTATSATCVTGLVRFDTYTHWTTFG QLVILSMIQIGGLGFMTIAVWIMSFTGYKIGLNSRFVVQNSLSAPQVGGMVKLTRFILLGTAVVEGLGAVLLAGIFIPRYGWGEGIYFSIF HSISAFCNAGFDLMGGEEPFSSLTLMGDSWYLNLIIMALIIIGGLGFMVWKDLLQCRFRFKKLRLHTKIVVVMTAFLIISGTVVIFFMEYG ETGTEGKSVSEQFLNALFQSVTVRTAGFNTVDLTKMTEPSIFLMSILMLIGGSPGSTAGGIKTTTFAVLCISIISVFRRKKTEEAFGRRM EEGIMRTAACVFMIYLFLAGSSAMIISKLEGVSMLTAFFETSSAVGTVGLTLGITPGVGMISKLLLTLLMFVGRVGSITILMSFSSERKMV ASKLPLEKVQIG
2.8E-50	181	19.2	2.5E-48	174.2	13.3	2	1	G8AN53_AZOBR	Trk system potassium uptake protein	AZOBR_150083	Azospirillum brasilense Sp245	456	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum brasilense, Azospirillum brasilense Sp245	1064539	>tr|G8AN53|G8AN53_AZOBR Trk system potassium uptake protein OS=Azospirillum brasilense Sp245 GN=AZOBR_150083 PE=3 SV=1MPAVGNSDWTAFVGSSAATLAVSGGMVLATSSKEHARFTVKQHFLLTTLSWCVLATFGALPFMISAAHLSFTDAYYEAMSGLS TTGGTVIVGLDDAPPGVLLWRSLLNWFGGVGIIVMAIAVLPILRVGGMQLFRTESSDKGDKPFATVQDTAGAIAMIYLALTILSAVAYHL AGMTWFDAINHAMASIATGGFSTKDASLGWFDSHAVLWVATFSMISGALPLTWYIRLLRGQRNAPVFGDSQVNALLAILLVAGVAMT LWAFAVVGLPFRDALSHSAVNVTSIITGTGFVSTDYSTWGSFAVVAFFFYFIGGCTGSTAGSIKVFRWQVLALSMLNQMQRMLKPN RVLVPLYQGKVLDEDVVGSVINLAFAFMAAFGILSLLVAAMGVDYLSAASAVASALANAGPGLGPVVGPSGTMAPLPDAAKWVLSFA MLLGRLEVFTVLVLILPSFWRD

2.9E-50	181	25.8	7.9E-49	175.9	17.9	2	1	I4BW87_ANAMD	Trk-type K+ transport system, membrane component	Anamo_0909	Anaerobaculum mobile (strain ATCC BAA-54 / DSM 13181 / NGA)	424	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Anaerobaculum, Anaerobaculum mobile, Anaerobaculum mobile (strain ATCC BAA-54 / DSM 13181 / NGA)	891968	>tr|I4BW87|I4BW87_ANAMD Trk-type K+ transport system, membrane component OS=Anaerobaculum mobile (strain ATCC BAA-54 / DSM 13181 / NGA) GN=Anamo_0909 PE=4 SV=1MLGFLSLIAVGTFLIWLLNLEEKPISLINALFTATSAVCVTGLSVVDTGGDLTFASQVVLMSLIQLGGLGIMTAMTIVPLLVGQRIGLRQRFYFAKEKGLDYPSGAVKLLIHIIKVTMLFEAIGFVPLFLSFAREMPVGRAFFAAIFHSISAFCNAGFSLFSNNLEGYSNTFIVPGTIMFLIVFGGLGYPFYMELTSRVKTERKLTPYIKLVVLATVSLILFGTLSLLLVEWNRSLAGFSPLLKIWNALFMSITPRTAGFDTIAPASLSKAGYVITILLMIIGASPSSTGGGIKTTTAGVLWCTVKSNLRGKPPSVFAQSISIDLIVSATTLVMLYLATIFVSVIFLSIIEPFSFEQLLFEVVSSLGTVGLSLGITPQLSETGKLVLVILMFWGRVGLVTFMYSVFRKREKENVVLPRAYIPIG
2.9E-50	181	11.2	2.4E-49	177.5	7.8	1.9	1	Q2JHH8_SYNJB	K+ transporter, Trk family	CYB_1338	Synechococcus sp. (strain JA-2-3B'a(2-13)) (Cyanobacteria bacterium Yellowstone B-Prime)	490	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain JA-2-3B'a(2-13)) (Cyanobacteria bacterium Yellowstone B-Prime)	321332	>tr|Q2JHH8|Q2JHH8_SYNJB K+ transporter, Trk family OS=Synechococcus sp. (strain JA-2-3B'a(2-13)) GN=CYB_1338 PE=4 SV=1MREGSVPLPPEEGSERLVPPVPSRARHLPTPGSALSQSSRAFGNRLQWFFGGDRRRPLPPPLRLVTGLGLLAVVGTLVLMLPGIGRGDPLSWNEALFTAMSALSVTGLSTIVAAEDLTLLGQIVLLILIQIGGVGFMVLAVVVFQLIGRRISLLNRLALCNSLGLIDPGAILELTRRVLLGVTLIELGGALLLWVHWRDLYGPERAVFLAIFHAVSAFCNAGFDLFGREGIPTDGLSLAILAGLIFIGGLGIPVLSDLLTWPRGHRPSLHTRITLGVVVVLLCTGGIGLFLGESLPGGSLLEVSWPHRLGLTFFQSVSARTAGFAGIPIEDLTPASQLLLMALMFIGAAPASMGGGMTTGTLAVLVLALWGYARGLPSAQIAGRSLDPSMVRKAAAVLTVSLFVVLLAAWLILLTHSNSRLDPVLFEVISAFATCGLSTGFTGELNWFGQLIIVLVMFWGRLGALTIVLALAQQQPRPLVTYPEESILIG
3E-50	181	16.7	8.3E-30	113.1	3	2.1	2	D2RIQ8_ACIFV	Cation transporter	Acfer_0561	Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4)	480	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Acidaminococcaceae, Acidaminococcus, Acidaminococcus fermentans, Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4)	591001	>tr|D2RIQ8|D2RIQ8_ACIFV Cation transporter OS=Acidaminococcus fermentans (strain ATCC 25085 / DSM 20731 / VR4) GN=Acfer_0561 PE=4 SV=1MNYPVIGRVLSWILCTEGALLLLPSLISLIYREDQGMIYFALALLALAIGYVTSRRKIRNRAIYQREGFVSVGLSWVLLSLYGAIPFVLTGEIPSYVDAVFEIVSGFTTTGSSILSDVEALSHTSLFWRSFSHWIGGMGVLVFILMLMPTNRGGTQMNLMKAESPGPDVSKFVPRVRNTAIVLYKIYLGMTLLMIALLALTGMNWFHNLCITFGTAGTGGFGILNDSCASYTPIQQWIITLFMIAFGVNFGFYYLSLIFRFREALAMEEVRAYVGIILASGLAITWQIRDRFDTLEQALRSAFFQVGSIMTTTGFSTVDFDLWPSFSKTILVLLMVVGACAGSTGGGVKVSRVVLTCKSIFLELGQVLHPHGVQRMRMDGKSVDSKMLNSIYIFLITYFLIFFLSILAVSLDGFNFETNFTAVAATLNNIGPGLAGVGPTRNFGDYSLPSKLVLIFDMLAGRLELLPMLILFYPRTWMKH
3.1E-50	181	20.3	1.2E-28	109.3	1.5	2.2	2	F8L741_SIMNZ	Cation transport protein	SNE_A06790	Simkania negevensis (strain ATCC VR-1471 / Z)	513	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Simkaniaceae, Simkania, Simkania negevensis, Simkania negevensis (strain ATCC VR-1471 / Z)	331113	>tr|F8L741|F8L741_SIMNZ Cation transport protein OS=Simkania negevensis (strain ATCC VR-1471 / Z) GN=SNE_A06790 PE=4 SV=1MSLFDQKIHWKSIWSQTGLLLHVPAAMAAVSLIICVIYQEWFALIPLISVAVFGFGVGQLLYRLFLKEENNAHLWDAMIIAANGWLMCSILAAVPFFWIATERLYAGVISDNLVIFSHPINALFEAFSGYTSTGLTMLQKTGPFPNTLYWWRSFLEWTGGLGLVVFILSLTHLNKMGFQLYYAEARTEQMSNNITQTAHWMWAIYVFYTCIAIFLFWLFGMTPWEAINHAFTTLSTGGFTLGHESFANFSPLIQGTAIFMMILASMSFLVHFRLIRDKKWEILLKSQQTRLLIFFLLGGWLIVVGLNYWNETKIQWMSSFFDWTSALTTCGFSSTKLSTFSPMTKLFLIMGMFVGGATGSTCGGIKLLRRLIYLLGGVMLRLKTLTQKKEKQITDHYRSTKDPLNSEPPGVDLPKTEQSERLYTAGVLFFLWTFSLLIGWFLILKWTPSGQALDALFEVTSAMSNVGLTSGLLTPEFSSFGKCIFMLMMWIGRLEIIPAIILLLSIPMTLKQKD
3.2E-50	181	25.1	2E-49	177.8	17.4	1.8	1	R5MKL1_9FIRM	Uncharacterized protein	BN519_01249	Eubacterium sp. CAG:180	454	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:180	1262882	>tr|R5MKL1|R5MKL1_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:180 GN=BN519_01249 PE=4 SV=1METKKKEKKRKFKLSPMKKIILGYITIIFLGAFILTLPISSRDGIHTSFENALFTSTSATCVTGLVVQDTATYWSLFGQIVILCLIEIGGLGFMTLAVCAMTFTKKNIGLQSRYTLLESINAPQMAGIVKMARFTIRGAFLIEGIGALLLATRFVPRFGVLKGLYFSVFHSVSAFCNAGFDIMGTPGNEYTSLTEYSADIVVNIAVMLLIVIGGLGFFVWADLINTRFIFRRLKLHSKIVLVTTAMLIVGGAGLILIFDIKSDAFKGFSVPHKIIAAFFQSVTARTAGFNTVDLTKLSDASVITMTALMLIGGSPSSTAGGFKTTTLAVLIASIFSELKHKKDVEIFKRRIAPDALRHVVCLIFLYMALFSASGAAITWIDGITMKEALFETASAIGTVGVTLGVTPFLRGYSHLILICLMFFGRVGGLTLLLSLRESKAPDISRYPEEQITIG
3.2E-50	181	27.6	9.8E-50	178.9	19.1	1.7	1	A0A060RDW0_9BACT	Potassium uptake protein TrkH	BN938_2091	Mucinivorans hirudinis	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Mucinivorans, Mucinivorans hirudinis	1433126	>tr|A0A060RDW0|A0A060RDW0_9BACT Potassium uptake protein TrkH OS=Mucinivorans hirudinis GN=BN938_2091 PE=4 SV=1MKTPVVLRYVGEVLMLNAFFMFVSALIALFNDFDTGFYPLFLSFLFTTILGYFPLIFVPADQNMSAKEGYLIVVISWILSPLVGMLPYLIWGGEFTITNSWFESMSGYTTTGATILQDVEALPKSLLFWRCTTHWIGGVGVVLFALVILPAIGKTKMTLSSVELSTIAKENFRYTTRTILRIILFTYCGLTFAETILLKIAGMDWFDAVCHSFSTLATGGFSTKNLSIMYYDNVWIEIVIMVFMVAGGTHFGLIYSSIVGKRNNLWRSEVVRYYYILLIACSILVAANLISNNIYTTIPEALRYSTFQVISYSSTTGFASANDAMWPSLSILIMTFLAIQCAMAGSTSGGMKADRVILLFKSLRAKVLTLQHPKAVVRIKLSGTAQEDTAVNGAILLITFYILCLFVSTLFLTFWDLDILTSFTTTVAAIGNVGPGFGRVSNLENMSFFNDIQKLWITFIMLFGRLELFGLIHLFFLRSWK
3.3E-50	180	30.8	1.2E-24	96.1	8.2	2.2	2	F6BCY4_METIK	Cation transporter	Metig_0800	Methanotorris igneus (strain DSM 5666 / JCM 11834 / Kol 5)	470	cellular organisms, Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanotorris, Methanotorris igneus (Methanococcus igneus), Methanotorris igneus (strain DSM 5666 / JCM 11834 / Kol 5)	880724	>tr|F6BCY4|F6BCY4_METIK Cation transporter OS=Methanotorris igneus (strain DSM 5666 / JCM 11834 / Kol 5) GN=Metig_0800 PE=4 SV=1MKLFKREDIIGIVHELGYLMMIVGFLMIVPIFVGIYYNENYENFIFSAAFSIFVGALLRGLTKPIEIKLKHAMVISAVTWLMASLLGALPFYFGIDYFSYVDAVFESMSAWTTTGFSLINNVEAMPHTILFWRSLEQWIGGVGVLVMMIGILMRSGTAAALFYKAEAREEKILPSTVNTVKTIWWIYLLYTILGICGLYLSGLSLWEAVNLTMCGICTGGMSVNNLSFPYNTMAKVIMILIMVIGGVISFSIHHKILTGKSFRDIQTDFAVKIFIVASIIVAISSNTDIIDALFTVVSAMTSTGYTTIDIKGLDNLSIAILIFLMAIGGGAGTTTGGIKIIRFLVMVKTFYYELKEIFFPPSAVIHEKLGNVVLDYKVIRESFVIGFVFVMHYIFTAMVFIALGYDPYKSIFEAVSLTSNIGMSMGIVNINMPLIGKIVGILAMWIGRLEILPIYVFVLLPIVNKIKKLK
3.3E-50	180	18.4	5.5E-50	179.7	12.7	1.2	1	I0II27_PHYMF	Cation transporter	PSMK_27560	Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	608	cellular organisms, Bacteria, Planctomycetes, Phycisphaerae, Phycisphaerales, Phycisphaeraceae, Phycisphaera, Phycisphaera mikurensis, Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	1142394	>tr|I0II27|I0II27_PHYMF Cation transporter OS=Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01) GN=PSMK_27560 PE=4 SV=1MLSRLRGWRRWWRRLRPLGDAPAGREVWLATRRLVVALIGATIVGLGLVMVVAPGPALIVVPLGLFVLGFEFVWALRLQRRLVATAAGAADAARRWRLPRISGTPDAEIPRNGRPPDRPPLRSVPTMRYATGRLLVAGRRVSPVKVLFLGYLSYVLLGWGLLCIPAAQAPGPDGGGVGVLDNLFIATSAMSTTGLVTVNTPLAYSFWGELVVLLLIQAGGIGYMTFGSFIVLAARTGMSKWREGMARSAFTLPEGFQAGAFVRNVVIFTLLVEAVGAALLFWAFSAAGVGERAIAGGIGASGVGVAHVAWQSIFHSVSAFCTAGFSLFPDSLEAYPTNPWINGIISALALFGAIGFIVMSDVFWRATGRRPHLTFTTRIILVFTGWIVVGGAVLLFIADPAIAALPGEERVLVAWFQSMTAATTVGFNTYPIGRLGQATVLLMVLLMVIGASPSGTGGGLKSTSLSAIIATLKSTIRGRHTVVTFFGARIPLDRLHTAFAALAMYASVLLIGGYLLLLTETRPLAAGALGGTPWAFEDLLFEAASALGTVGLSRGVTGDLTDLGKLVVIALMFIGRLSPLTFGLALFGPGAGDHPAPDAPEAAVADVAV

3.3E-50	180	25.3	4.2E-50	180.1	17.6	1.1	1	D1BNQ6_VEIPT	Cation transporter	Vpar_1335	Veillonella parvula (strain ATCC 10790 / DSM 2008 / JCM 12972 / Te3) (Veillonella alcalescens)	453	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Veillonella, Veillonella parvula, Veillonella parvula (strain ATCC 10790 / DSM 2008 / JCM 12972 / Te3) (Veillonella alcalescens)	479436	>tr|D1BNQ6|D1BNQ6_VEIPT Cation transporter OS=Veillonella parvula (strain ATCC 10790 / DSM 2008 / JCM 12972 / Te3) GN=Vpar_1335 PE=4 SV=1MWHDISHSHVQRYMQQNPYRLLAFSFLGVMIIGTILLMLPMASAQGQTTALVDAAFTAVSCVSVTGLTTVDTYYHWSLFGKIVM VILIQLGGLGIVSFTTIIALLLGKRVGLKNRVLLSEDVGQEGMTGLLHITKKLTLYTFAIEIVGGIIYTIQLYPYIGQAALYSGIMQAISTFCNA GFVFFDNDLPYAMVGDILFNINTAVLIVIGGFGYLAAFDIWSHRKVRRVVDLKLHTKIMLVGTAIILLLGTIIFLGVEWSNPKTFGTLPIWN KIMASLFQSITPRTAGIATVDYNALHPITLFVTIILMFIGAGPNSTGGGVKISTVAVTILASRTLFNNRPDTEIFERRISLVTVLKANGIIFLSL LLIIAATCYLAWDEPYDFIRLLFEVTSAFGTVGLTTGITSDLSESSKWVLMLVMFTGRVGVMTVIGTWALRTSPTKPIGYAEENVLL
3.4E-50	180	26.6	9.3E-49	175.6	18.4	2	1	R6FLY8_9FIRM	Potassium uptake protein TrkH family	BN525_00921	Eubacterium sp. CAG:192	363	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:192	1262883	>tr|R6FLY8|R6FLY8_9FIRM Potassium uptake protein TrkH family OS=Eubacterium sp. CAG:192 GN=BN525_00921 PE=4 SV=1MGVITIALLLTRMSGRKIGLRQRTLMQEAISAHKMGGIVRLTGFIVKMMLIFELAGAVLMYPEFAKQFGIIKGIWYSLFHSISAFCN AGFDLMGVREHYSSLTTFSSSVLINVVIMLLIIIGGIGFVTWDDIKKHKLHFGRYRMQSKVILGVTSILIIVPVLYFYFFEFGKATWNFDSE KDRLLASLFQAVSPRTAGFNTVDLNQLSGVGQLITIILMLIGAAPGSTAGGMKVTTVAVLFSTAVAVFRKRQDAHLFKRRLSNEVARSA SATLLMYTFLFMFGGIVISIADNIPIMKSLFETASAVGTVGLSLGITPSLSMVSKIVLIVLMFLGRVGGLTVIFATLSNKNYNVSRLPEEKIM VG
3.5E-50	180	19.2	4.6E-50	179.9	13.3	1.2	1	I6Z6J1_MYCWM	Potassium uptake protein KTRB	WEN_02120	Mycoplasma wenyonii (strain Massachusetts) (Eperythrozoon wenyonii)	500	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma wenyonii, Mycoplasma wenyonii (strain Massachusetts) (Eperythrozoon wenyonii)	1197325	>tr|I6Z6J1|I6Z6J1_MYCWM Potassium uptake protein KTRB OS=Mycoplasma wenyonii (strain Massachusetts) GN=WEN_02120 PE=4 SV=1MRRRVTKASAKELVSKWFFGASVAQRIARIYVLIILAGFGALNLPWVQTHKGENTKDDTWFSKLFTSVSAFTTTGLLSGSSLKCS FNFAGQLIVLILIQIGGLGIVTIWMILKQTFLKNKKYSIEDRLNIYSERGGGGMSEGSSYVVIKSALISLLGFELFVAALLTFFFYFIGSIPQA QAGTKNQFLASLWAGIFHSISAVNNAGLDILDKSSISSFSRGWGTILSIVFAVCSMVGGIGYPALYEFKEWLQKKRNKEKTKNIFSLFTK ISILMLYLSITLLASGGIILAEYTDNNWTQSDCDKGCGKLQTIEKIWQLVYLVISSRSAGFYGIDPICLHEKSQWILLILMFIGASPASTAGGI RSITLFLMLGKIWVTMRGRRTLSIFSRSISDQTIESAYIVFFVSSALITLCSLGIPNPGEQQEKKGLRHASLFEAASAFGTAGLSLGVSNK TPWYGKLLLMFLMFVGQLGIPNSLIYYNKPRVSKQKFSYPEEKLRIA
3.6E-50	180	22.2	2.3E-25	98.5	6.3	2.2	2	E1SUM8_FERBD	Trk system potassium uptake protein	Fbal_0019	Ferrimonas balearica (strain DSM 9799 / CCM 4581 / PAT)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Ferrimonadaceae, Ferrimonas, Ferrimonas balearica, Ferrimonas balearica (strain DSM 9799 / CCM 4581 / PAT)	550540	>tr|E1SUM8|E1SUM8_FERBD Trk system potassium uptake protein OS=Ferrimonas balearica (strain DSM 9799 / CCM 4581 / PAT) GN=Fbal_0019 PE=3 SV=1MINVRPLLLLLGLFLAVLAGLMLVPVGFSLYHNEGLVQDFMLSAALTGGVAFVALGSSWGCKVTLHTRDFYLFTTLTWFVVAMF AALPFTFFHAISYTDAFFETMSGITTTGSTVLTGLDSAPWSILIWRSLLQWMGGIGFIAVGVAILPLLNVGGMRLFRTESSDWSDKSMP RTKEIGRALVKVYLLLTLLCGVGYYLSGMTVFEAINHAMTTVSTGGYSTSDSSMTHFSVAAHWNGTLFMFLSGLPMLLYVQSLYRRS WAPWRDQQVIGFTRFVIVASVVLGIWLAREQDMAFFPALTLAAFNLVSVVTTTGFASTDYSQWGPAANIIFFLLMFVGACSGSTSGAI KIFRFQIAGAVVFKALRQHIHPHAVVPQRYNRRPINEDILRSLVAFTMLFMATIAVLALFLVLVGVDPVSSLTGAVTAVTNVGPGLGEVIG PAGNFASLPDAAKWALSVGMLLGRLEIVTVAVLFLRTFWGY
3.7E-50	180	39.8	9.6E-50	178.9	27.6	1.5	1	D1B310_SULD5	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Sdel_1462	Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175)	443	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Sulfurospirillum, Sulfurospirillum deleyianum, Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175)	525898	>tr|D1B310|D1B310_SULD5 Potassium uptake protein, TrkH family OS=Sulfurospirillum deleyianum (strain ATCC 51133 / DSM 6946 / 5175) GN=Sdel_1462 PE=4 SV=1MNQKTLRIIFFSYLTVVFVGAILLMLPIAHIGKLTFIDALFTSTSATCVTGLVVKITAQDFTFFGQFVILLLMQVGGVGYMSIVTLFFL FMKKNLNIHEKNMAKDSLNYSSNLDIQNFLQKVFIFTIIIESLGAFILTLRFATHMPLNQAFWQGIFHSVAAFNNAGFSLFRDNLVGYQTD ATVLVTIGLLIIFGGLGYLVLVELHAKATHKRFMISAHTKITLVGTLILIISGMLLFLVIEWDNKGIFKSMSLYHSLLNSFFLSVNFRTSGFNS LDLANLSDASLFCSTIYMMTGGGAGSTAGGIKITTVAVLIIATIHTIKISNQSPHAFKRTITQEIINRSSAIILVASFISITATVILVETQHTHFM RTLFEVVSAFCTVGVSVGNGDVLSLSATFSSFGKSLVIALMLIGRMGIFAFGFLIIGKEKIKHIQYPEGRILL
4.3E-50	180	13	1E-49	178.8	9	1.5	1	D2B6N5_STRRD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Sros_2842	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	446	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	479432	>tr|D2B6N5|D2B6N5_STRRD H(+)-transporting two-sector ATPase OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_2842 PE=4 SV=1MKNLVRQINTPSRVVVAAFLAVVLSGTALLSLPIAVEAGREASLTSALFTATSAVCVTGLAVQDTAAHWTFFGEMVILVLMQIGG FGIMSLASILAVVVSGRLGLRARLNTQAETKTLGPGDVRRVLVGVAKVTLAVETLIAVALTARFVIGYGEPFGRAAYHGVFHAVSAFTN AGFALWPDSIMRFVTDPWVCLPLALGVVAGGLGFPVYAVLRQNWRHPARWSLHAKITLGMTAILLFGGATAITVTEWNNPGTLGPLS PGLRILAGFFHSAMTRSGGLNSVDISQMNENSWLISDVLMFIGAGSASTGGGIKVTTFALLAYVILAELRGEPDVTAGRRRIPEQLQRQ TLTIALLSVASVATGTFVMMMVTPFKLDRVLFEVVSAFGTVGLSTGITPDVGTSGHLVLTALMFIGRLGPVTLGAALALHIQTRRFRYPE ERPLVG
4.4E-50	180	23.5	2.9E-49	177.3	16.3	1.9	1	R6I7B2_9FIRM	Uncharacterized protein	BN517_00609	Ruminococcus sp. CAG:177	485	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:177	1262952	>tr|R6I7B2|R6I7B2_9FIRM Uncharacterized protein OS=Ruminococcus sp. CAG:177 GN=BN517_00609 PE=4 SV=1MNYKLIANYIGNILRIEGLFMIPALLVSLYHNEFKCVLAFGISIAALLVIGQLMHMIKPKKRNVFVREGFAIVSLSWLAISLFGALPFFI SREIPNFIDCFFETVSGFTTTGSSILSNVEALSKGLLYWRSFSHWLGGMGVLVFLLAVVPNGKDNDAQSLYILRAESPGPTFGKLVSK MRQTAQILYIIYIALTIIEIILLFAGGMPLFDSVLNSFATAGTGGFGIKNASIGAYDSYYLQGVIAVFMLMFGVNFNIYYLLLARDFKLVFKN EELRFYIITVLVSVTVIAINIRSMFSSWFDAFHHSFFQVSSIITTTGFSTTDFSLWPELSRYILVVLMLMGACAGSTGGGLKVSRVLILFKA LRNEMQRVVHPRSVKVLRIDGKVQNEALVRNVSMYLVAYVIVMIASTLLVSIDDFSFTTNVTAVISCMNNIGPGIDIVGPMGNFSGFSW FSKLVLSADMIIGRLEIFPVLALFSPSLWKRCN
4.4E-50	180	14.6	1.6E-49	178.1	10.1	1.7	1	A4FBN1_SACEN	Cation transporter	SACE_2150	Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	440	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharopolyspora, Saccharopolyspora erythraea (Streptomyces erythraeus), Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	405948	>tr|A4FBN1|A4FBN1_SACEN Cation transporter OS=Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338) GN=SACE_2150 PE=4 SV=1MRRRPAVLIVGGFGALTGTGTALLMLPGAAAGDESADFMTALFTSVSAVCVTGLYVVDTPMYWSVFGQVVVLCLMQLGGLGI MTMASVLSLLVLRRFGLRMQLTAQAETKTLGLGEVRRVLGLIVLVTALFESVVMLALTARLFAGYDRPLGRAAYEGAFYAVSAFNNGG FVLHSDNMMGFVADPWFCLPIIFAVIAGGLGFPVLLELGRRLRVPRRWSLHTKITVAGTAVLLVCGCGAITVAEWTNPATLGPLSPQT KLLAGFFAAVMPRSAGFNTVDIGSMYPATLLVQDVLMFIGGGSAGTAGGIKITTFALLAFVIHAEIRGEPTVHVMGRRLPEGVQRQALT IALLGVALVMTCTLVLLVITPFGLDQVLFEVVSAFATVGLSTGITPDIGVAGQALLVALMFIGRLGPITLASALALRERPRRYELPEERPIV G
4.6E-50	180	42.1	9.9E-50	178.8	29.2	1.4	1	G2SQJ2_LACRR	Cation transporter	trkLRC_02140	Lactobacillus ruminis (strain ATCC 27782 / RF3)	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Lactobacillaceae, Lactobacillus, Lactobacillus ruminis, Lactobacillus ruminis (strain ATCC 27782 / RF3)	1069534	>tr|G2SQJ2|G2SQJ2_LACRR Cation transporter OS=Lactobacillus ruminis (strain ATCC 27782 / RF3) GN=trkLRC_02140 PE=4 SV=1MIHKLKELYRGATPIQSLVTYYALATVAAFILLSLPCFKNPGAKISFLDTLFMAVSTISVTGLTTFPIEQVYNQGGVVLLEFLFQVGG FGITMLSTVALVIAGKRISLHQRQLIQFDMNQPRLSGMVRLVTSVFGLMIFVQIVFGVIFAAYFKATGVWTTWPTAFFHGIYVSVSSVTN AGFDVTGNSIIPFRHHYGFLFIVMILIIIGSIGYPVLIECENWAFYKFSRQTTKRKFRFSLFAKMAVFFAVFFFIVGTILIYFSEMRGTLSRQ DWFDKLMTAMFYSVSSRNAGLQINDMAEFNTTTILILAILMFIGASPSSVGGGVRTTTVGIFILYMFSFIRGHNSINVFNRRIGRDDVQK AIVVVGLSTVLCVGAILILSITEDASLLSIVFEVASAFGTTGLSLGITSSLTLVGKIVIMVLMFVGRIGMLYTLLFFIPKRNRDLSYELPTEKIII G

4.6E-50	180	27.1	2.1E-47	171.1	18.8	2	1	A9KHL0_CLOPH	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Cphy_1927	Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) (Lachnoclostridium phytofermentans)	430	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Lachnoclostridium phytofermentans, Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) (Lachnoclostridium phytofermentans)	357809	>tr|A9KHL0|A9KHL0_CLOPH H(+)-transporting two-sector ATPase OS=Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) GN=Cphy_1927 PE=4 SV=1MKLLKRVSPGRLISLGFASVILIGAIILWLPISANDGVNVRFIDALFTSTSAVCVTGLIAVDTADTFNIFGRTVVGFLIQIGGLGVTSIGVAILLFAGKKVGIKGRVLMRDSMNLNSLKGIMQLVKAVLFTTLCFEVVGTILSFIVFVKDYSPVKALGISLFHSVASFNNSGFDVLGHFQNLLNYKDNVLLNLTTAGLIIFGGMGFIVTKELVEKRSLRKLSLHTKVVLMMTGILLTVGTVLLYLTEDITWLGAFFMSTSARTAGFSTYNSGNFTNAGLFVLIILMFIGASPGSTGGGIKTTTFFTLIKSLYSTAKNKHCTAFKRRVVPNDVISRSFVIFLLAMGLVCLNTLLMCFIEPDNSFIQNLYEITSAFGTVGLSTGITPYLKDLSKLILILTMFVGRLGPMTIATLWSHKDKPSVSYSEESLIIG
4.7E-50	180	17.9	7.3E-50	179.3	12.4	1.2	1	R5A6R4_9CLOT	Potassium uptake protein TrkH family	BN452_00439	Clostridium sp. CAG:1013	462	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:1013	1262769	>tr|R5A6R4|R5A6R4_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:1013 GN=BN452_00439 PE=4 SV=1MPDLSDLQQRFNDKLKTMPPARIIVISFLMLILAGTLLLMLPIASKRGGFRPLDALFTATSATCVTGLVVGDTYTLWTPFGQGVILALIQLGGLGLSTLTIGFSLFIRRKLGIREMKLATESSGGSFLDIVGLLRLAIGFTFICEAVGACLLAIRFVPSYGLKGIWPSIFCAVSAYCNAGFDVLGFIEGNSSVSAFAGDPLVSLTISFLIIIGGLGFIVVQDIYLCKIQPLFRHKDTLRLNFHSQICLRVTVALLLFGTLGFYIFEFDNTMAHLNVFEKLNCAFFQSTNTRTAGFASVDIGAQLEFTKILSVLLMFIGACPGSTGGGIKTTTFMVLAVTVISTIRGKDEAVVFRHRFSVPTVYKALTVTIVAFFLVFVDAGVISALNPDISYMDCLYEATSAFGTVGLSANVTPRLDAISRLILIFTMFIGRVGPLSFGLSILMRHRGKGNSIYPEGRMLIG
4.9E-50	180	28.8	2.4E-48	174.3	19.9	2.1	1	R5S1B7_9BACE	Uncharacterized protein	BN702_00766	Bacteroides sp. CAG:545	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:545	1262742	>tr|R5S1B7|R5S1B7_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:545 GN=BN702_00766 PE=4 SV=1MNLKVISRNVGFALLASAFFMFLSILVSLAEGNDSALAAMIISFTITFIVGVFPFIFVRKSSNITLKDGYMIIVLSWLLSFVFGMLPYLLWGGPFSVINALFEAVSGYTTTGATILTDVEQLPDSLLFWRSSTHFIGGLGVVVFLLLIIPSSSPMRLRLTNMEVSSLSKEGYRTRTNKTVWVFAAVYLGITISAFICYWLAGMSAFDAINHAFSVVATGGFSTKNLSIASFDSNAINIITIVFMFLASVHFGLIFVVFATRSLKPLKSPVLKFYALMIVIASVMMAISLKMKGSEFSWGDSIMNGIFHVVSSISTTGFAISDNNTWPAFAAVLMVIISVPCGMAGSTTGGVKADRIYLMLKTIGQQVKKALHPASINQVHVGNHILTNEEVYPHLVYIALYFVTIAISVALSIVSGVTIDASVAACISALSNVGPALGDWGTLGSFNSAPVMAKFIFVVDMFLGRVEIYPILAVVAMAFSKRNK
5.2E-50	180	20.4	6.4E-26	100.3	4.2	2.1	2	F7YW18_9THEM	Cation transporter	Theth_0410	Pseudothermotoga thermarum DSM 5069	492	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Thermotogaceae, Pseudothermotoga, Pseudothermotoga thermarum, Pseudothermotoga thermarum DSM 5069	688269	>tr|F7YW18|F7YW18_9THEM Cation transporter OS=Pseudothermotoga thermarum DSM 5069 GN=Theth_0410 PE=4 SV=1MTIVQSYTIVLHLLSKLLKLFCFVLLLPAVFSVFAKEFFFCGWAFVVSTFISYMFSVILSRIVKRPEDAPEVITIREGAIMVFLSWVCVIFLSALPYTFARVLTFDRALFESVSGWTTTGLTVMPDIDSACKTILLWRSITQFLGGAGFAIIVMGAIIGPTGFGLYHAEGRVDNIVPNVRRSARIIMIIYLSYALAGAIALWLSGLNLFDAVNHSLTALATGGFSTRNDSIAAFNNLAAEVVLLIILMFLGATSFGIHYAFWQRNWTALKKNSEPKQMIFLILVSSTLILISASNDQNFANLGLRTILFQVVSALTGTGFSTTDLKSWTTFHVGHFVLVILMLLGGCMDSTSGGIKQYRLTVLGKTLHASFKKFFLPRGSVFDVEIWKGTTKKYLDADLIREAFLVSSLYILTYVVGSTALMLQGYSLEESMFEFASALAGVGLSCGVTNYHMPKSTLWTLMVGMFLGRLEFLVVIYALSKMAKDILHSIFGE
5.3E-50	180	36.7	5.3E-50	179.7	25.4	1.6	1	A0A0E3ZE28_9BACT	ATPase	PKOR_10825	Pontibacter korlensis	599	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Pontibacter, Pontibacter korlensis	400092	>tr|A0A0E3ZE28|A0A0E3ZE28_9BACT ATPase OS=Pontibacter korlensis GN=PKOR_10825 PE=4 SV=1MNTETLNRVLYDSKLTAYKIMRWTTYSLTILAIGLLVLAHGVVEDPTQLRMLFYAIDGILAIFVIIYFLRILYTFERVKFLKRTWFEGILMFIVFLNQVFTYVLGIPLIYNIFEGLGIPLSVEWYRVLVSMYMLVFLIVELLETKVHLKTVQLKPSITFLLSFVFLILLGTGLFMLPKMTNSPDGIRFLDALFMATSASCVTGLAVVDPGTYFTLAGQVVLLLLIQMGGLGILTFATFFASLMRQGIGVKQHVAMHELLESESLFSTKGLMRKLILLTLTIEGIGAVMIFMSWGQEAQFTNLGSKIFFSVFHSISAFCNAGFSLYPEGLYTQPIRFSYILHLTVSLLIFGGLGFPAIIDIFSPAAMRARLKAPWRNWKMMTRVIVYTSAALLALGTVGFFLLEYFNTLSHMSFAEALITSFFQSVTTRTAGFNTVDISALNVPTLLMFIFLMFIGASPGSTGGGIKTTTFTVILFAVATTVRNRRNMEIGHRTIPHSVAYKAFTVFTFAAVFNITFIFILSISDAQFDIIQLAFEQVSAFATVGLSTGITAGLSDVGKSVIILSMYLGRVGTLTLALALSTHAKSTAYKYPASHLAVG
5.4E-50	180	35.7	2E-49	177.8	24.8	1.7	1	C7M447_CAPOD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Coch_0013	Capnocytophaga ochracea (strain ATCC 27872 / DSM 7271 / JCM 12966 / NCTC 12371 / VPI 2845) (Bacteroides ochraceus)	442	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Capnocytophaga, Capnocytophaga ochracea, Capnocytophaga ochracea (strain ATCC 27872 / DSM 7271 / JCM 12966 / NCTC 12371 / VPI 2845) (Bacteroides ochraceus)	521097	>tr|C7M447|C7M447_CAPOD H(+)-transporting two-sector ATPase OS=Capnocytophaga ochracea (strain ATCC 27872 / DSM 7271 / JCM 12966 / NCTC 12371 / VPI 2845) GN=Coch_0013 PE=4 SV=1MLKKISPYNLIMLSFIGLIVVGALLLMMPFAHTPQKDISFLEALFTATSAVTVTGLSVIDIGATFTIYGKLILLVLIQFGGLGVLTISSVLVLLIAKRIGFYTKKIVAEGLNHNKSYDIYAVAKRVVYITLLFEATGALCLFISFIQEFPFGKALFFSVFHSVSAFCNAGVSLFPHSFEGYTYNVFVNIIIAFLVIFGGLGFTTIIQSYEYLRKKRRRLDINSQFSILMTIILLVAGTFLFFILEYKNYHTLYGKSFFGQMLISFFHSVSLRTAGFDTIPLEHLSSATILFCVTFMFIGASPNSTGSGVKTTTIGILFLGIKTALLNKNYIEFSKRRISWKLFNKASALVFIAMMYVITMIVILTVLEPDLEFTKIAFELISAFSTCGLSTGITSQLGNSSKFILIFTMFLGRVGPLTIALALSRPRAEGNYKYPKENILIG
5.6E-50	180	13.8	3.6E-49	177	9.6	1.8	1	A5UV17_ROSS1	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	RoseRS_2088	Roseiflexus sp. (strain RS-1)	453	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Chloroflexales, Roseiflexineae, Roseiflexaceae, Roseiflexus, Roseiflexus sp. (strain RS-1)	357808	>tr|A5UV17|A5UV17_ROSS1 H(+)-transporting two-sector ATPase OS=Roseiflexus sp. (strain RS-1) GN=RoseRS_2088 PE=4 SV=1MRLAPRPSVRSPARPRPMPAALRLVIGLAVLVAAGTSILMLPWMGTERPLTWNEALFTAVSALSVTGLSIITPVHDLSLAGQIVLLLIQIGGVGFMVVAVIVFQVLGRRITLTDRLALTDSMGLLVPGAIVQLVRRVLLTVLLLEAIGAALLWIHWRDMLGPERALLYAIFHAVSAFCNAGFDLFTGLPDYPYGIPNDSITLAILGSLIFLGGLGIPVLAELLTFWRIRFSLHTRITLTVVIILVSIGAGGLFLTEQQSGHLLEREPLDRQIALALFQSISTRTAGFSALQPLDELSPAGRLLTIVLMFIGCAPASMGGGITTGTFAVLMLAVGAYARGLASPQIGGRTLAPQTVRKAAAILTVSLLVVLTATWLILATHEATLDDALFEVVSAFATCGLSLTLTSELNLFGQLVICVMMFWGRLGALTLVVALANQRPQLVAYPEEQVLIG
5.7E-50	180	27.2	5.3E-48	173.1	18.8	2.2	1	B5IA11_ACIB4	Cation transport protein (Cation transporter)	Aboo_0543 ABOONEI_1665	Aciduliprofundum boonei (strain DSM 19572 / T469)	467	cellular organisms, Archaea, Euryarchaeota, unclassified Euryarchaeota, Aciduliprofundum, Aciduliprofundum boonei, Aciduliprofundum boonei (strain DSM 19572 / T469)	439481	>tr|B5IA11|B5IA11_ACIB4 Cation transport protein OS=Aciduliprofundum boonei (strain DSM 19572 / T469) GN=Aboo_0543 PE=4 SV=1MNKILYFSLKLLTYISIFMLIDAVYALIVDRSVVITLAFLFPASWILFLWVPFMKEPVPQNLSLRESFKVAAIGWLLMSFFGAIPFILSGYLNPLDAWFESMSGFTATGLTMFTDVESLPKSILLWRSLTEWIGGVGVIALFLSVMYRTSRVVQSLYFAEGRSDKTEPTIVGTVRKIWGIYLFYTLLFALIFYLLKVPLFDAINISMTALATGGFAVTNNSIAAYSPYVAIAMIFAMAIGGISFVSHINLFKGRVREFFSIELKAMVIIIVLFSTIMLLHLAWLGESWNEAALQTFFHVTSALTGTGFSISDLANLTSFDKTFLILSMIFGGAYGSTSSALKLIRVVVLVYGIVWYVKVRLYPKSAIIPFKIGKKVFESTEVRDVSIYTTTYLFMLLLGAMIFMAYGNSLVNSLFEVASAEGNVGLTVGITSPFMPWVEKLTLILEMWFGRLEIFPILILLADIVKK

5.7E-50	180	5.5	1.6E-46	168.2	0.1	2	2	R8BSY0_TOGMI	Putative cation transporter protein	UCRPA7_2102	Togninia minima (strain UCR-PA7) (Esca disease fungus) (Phaeoacremonium aleophilum)	398	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Calosphaeriales, Calosphaeriaceae, Togninia, Togninia minima, Togninia minima (strain UCR-PA7) (Esca disease fungus) (Phaeoacremonium aleophilum)	1286976	>tr|R8BSY0|R8BSY0_TOGMI Putative cation transporter protein OS=Togninia minima (strain UCR-PA7) GN=UCRPA7_2102 PE=4 SV=1MSRWRPRWWNGFVGEHPWVASCLSRARSALPPVNFITIHYAYFIVVCLAASVVFWGSSNPSRSITYVDSLFVVVSAMTEAGLN TVNLSQMTTWQQIMLCLLIMLGSSIWVSIWTVAARLHVFEQRFAAIVKAERE KNKRPIPLLQRFSTFRKSVTTPAGDSKLPGTGTRMP QTIASDNFLTGRAAGRNGQFHDLTTEEREHLGGCEYRALKVLAVIVPLYFFLWQLLGCVGLGAWMAYNQPNTARENGINPWWLGIF NGVSAFNNSGMSLLDANMIPFQKAYYVLITMGLMILAGNTAYPLFLRLIFWSMLKVLDRTTAEETLGDFKETIKFILKYPRRVYTNLFPS RQTWWLCFMVVLLNSIDWVAFELLNLGNPVIEAIPTGSRVLDGLFQALGTT
6.1E-50	180	24.7	1.3E-49	178.5	17.2	1.4	1	C0G7C5_9RHIZ	Trk system potassium uptake protein	BCETI_4000077	Brucella ceti str. Cudo	466	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Brucella, Brucella ceti, Brucella ceti str. Cudo	595497	>tr|C0G7C5|C0G7C5_9RHIZ Trk system potassium uptake protein OS=Brucella ceti str. Cudo GN=BCETI_4000077 PE=3 SV=1MAAAMLLPAAIDLRDGSDDWSVFVRSAAATGALSALIFLATQNQTMRFTPRLGFLLTACLWLTAAFLGSIPLYFSHLPISYATAFF EAMSGVTSTGATALTGLDNMQRGILLWRSLLCWIGGVGFIGLALLMLPSLRAGGLALFHMENSDKSEKILPRMNQIALGIMAAYLSLTA ACTVAYFAVGMSVFDAINHSLTTIATAGFSTHDSSIGFYQGNRMLLVVSTIFMALSALPFVLYIKAFMPRRMELLTDPQVKLFFTIIIAFSF ILAIVLRLSTNIPFGDALISASFHFVSVITTTGYATEDYSLWGPPAIGIFFLASFLGGCAGSTSGGIKMNRLIILWSLTQANLARLIMPHAVI KIRYGSSEVSGDIAQNVLLYLFLYSASLIIGAVLLASFGLDFVSAFTGSLTALSNVGPGLGDKIGPAGNFSTVRDQALWVLSFLMLAGRL ELVTIFILFTRSFWVR
6.1E-50	180	24.7	1.3E-49	178.5	17.2	1.4	1	C9VUB4_BRUAO	Trk system potassium uptake protein	BARG_02849DK53_1462	Brucella abortus bv. 9 str. C68	466	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Brucella, Brucella abortus, Brucella abortus bv. 9, Brucella abortus bv. 9 str. C68	520455	>tr|C9VUB4|C9VUB4_BRUAO Trk system potassium uptake protein OS=Brucella abortus bv. 9 str. C68 GN=BARG_02849 PE=3 SV=1MAAAMLLPAAIDLRDGSDDWSVFVRSAAATGALSALIFLATQNQTMRFTPRLGFLLTACLWLTAAFLGSIPLYFSHLPISYATAFF EAMSGVTSTGATALTGLDNMQRGILLWRSLLCWIGGVGFIGLALLMLPSLRAGGLALFHMENSDKSEKILPRMNQIALGIMAAYLSLTA ACTVAYFAVGMSVFDAINHSLTTIATAGFSTHDSSIGFYQGNRMLLVVSTIFMALSALPFVLYIKAFMPRRMELLTDPQVKLFFTIIIAFSF ILAIVLRLSTNIPFGDALISASFHFVSVITTTGYATEDYSLWGPPAIGIFFLASFLGGCAGSTSGGIKMNRLIILWSLTQANLARLIMPHAVI KIRYGSSEVSGDIAQNVLLYLFLYSASLIIGAVLLASFGLDFVSAFTGSLTALSNVGPGLGDKIGPAGNFSTVRDQALWVLSFLMLAGRL ELVTIFILFTRSFWVR
6.1E-50	180	24.7	1.3E-49	178.5	17.2	1.4	1	Q2YRP2_BRUA2	Trk system potassium uptake protein	BAB1_1519	Brucella abortus (strain 2308)	466	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Brucella, Brucella abortus, Brucella abortus (strain 2308)	359391	>tr|Q2YRP2|Q2YRP2_BRUA2 Trk system potassium uptake protein OS=Brucella abortus (strain 2308) GN=BAB1_1519 PE=3 SV=1MAAAMLLPAAIDLRDGSDDWSVFVRSAAATGALSALIFLATQNQTMRFTPRLGFLLTACLWLTAAFLGSIPLYFSHLPISYATAFF EAMSGVTSTGATALTGLDNMQRGILLWRSLLCWIGGVGFIGLALLMLPSLRAGGLALFHMENSDKSEKILPRMNQIALGIMAAYLSLTA ACTVAYFAVGMSVFDAINHSLTTIATAGFSTHDSSIGFYQGNRMLLVVSTIFMALSALPFVLYIKAFMPRRMELLTDPQVKLFFTIIIAFSF ILAIVLRLSTNIPFGDALISASFHFVSVITTTGYATEDYSLWGPPAIGIFFLASFLGGCAGSTSGGIKMNRLIILWSLTQANLARLIMPHAVI KIRYGSSEVSGDIAQNVLLYLFLYSASLIIGAVLLASFGLDFVSAFTGSLTALSNVGPGLGDKIGPAGNFSTVRDQALWVLSFLMLAGRL ELVTIFILFTRSFWVR
6.3E-50	180	28.4	8.2E-50	179.1	19.7	1	1	G5KHR1_9STRE	Cation transport protein	STRUR_0274	Streptococcus urinalis 2285-97	458	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus urinalis, Streptococcus urinalis 2285-97	764291	>tr|G5KHR1|G5KHR1_9STRE Cation transport protein OS=Streptococcus urinalis 2285-97 GN=STRUR_0274 PE=4 SV=1MNRFFGRSWSVTQRLTFSFAIVIIVGSILLSLPITHYHDAPQTTYLDHLFNVVSMVCVTGLSVVSISDVYNGFGQIIAMFLMQIGGL GLVTLIAISTFALKRKMDLREHSLLQSALNRGDSHGLQGYLYYVYKFTFTVEFIAALVIMTDFIPRFGVGHGIFNSIFLAISAFCNAGFDNF VTGSLKGFVLDPVINFTVAFCIISGGLGFAVWFEIVNGLKKFFIDKPKYRFSGFRRMTNQSRLVLSTTGIILLLGTVLTWFLEKDNPKTIG HYSFLAQGMISFFQTVTMRTAGFATLSYLHTKEPTNILYMIQMIIGGAPGGTAGGIKVTTIAITYLLFKSELSGQTEVTYRKRIISNKTIKQ TMTVLIFFFATLVTGYLLLLYFEPHHNSIALLFEAISAIATVGVSMDLTPHLSSLGRIVIIALMFIGRVGPITVLLSLLQRKEKTIHYATNDITV G
6.3E-50	180	19.2	2.2E-47	171.1	13.3	2.1	1	R6CWJ8_9CLOT	Cation transport protein	BN687_01612	Clostridium sp. CAG:510	478	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:510	1262816	>tr|R6CWJ8|R6CWJ8_9CLOT Cation transport protein OS=Clostridium sp. CAG:510 GN=BN687_01612 PE=4 SV=1MNHSIIRYTLVSVLEFAGFFLLIPYFVGLFYGEKERYAFLLIAAACLLIGFAGRLFKPKSKVFYAREGFVTVSLSWIILSLIGAVPFVL TGEIPSYVDAVFETASGFTTTGATILTDVEALARCTQFFRLSTHWVGGMGVLVFILSIVPLSGSYNMHLVRAESPGPSVGKLVPRVKNT ARILYIIYIAITVAEIICLLIAGMPLFDSVTMTFSTVGTGGYSILNTGTATYSRAVQAIIMIFMFLCGINFSMYYLLIAKKPGDVLKNTELKAYV GIVAGATLLIAVNVRGYFANFGEALFQSAFHVTSIITTTGLSGRDFNLWPSFSKMILFLLMIVGASAGSTGGGFKVSRLVVLVKSVKNEI QKVIHPRSIKKLHMDGRAFPEDLIRSILVYTGIYVLLSFASILIVSLDNFSFETNVSAVMATLNNIGPGLDVVGPTGNFSAFSDVSKVVMIF DMLAGRLELIPILVLFSPQTWKK
6.6E-50	179	39.6	1.2E-49	178.6	27.4	1.3	1	E4TRM9_MARTH	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Ftrac_1762	Marivirga tractuosa (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43) (Microscilla tractuosa) (Flexibacter tractuosus)	607	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Flammeovirgaceae, Marivirga, Marivirga tractuosa, Marivirga tractuosa (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43) (Microscilla tractuosa) (Flexibacter tractuosus)	643867	>tr|E4TRM9|E4TRM9_MARTH H(+)-transporting two-sector ATPase OS=Marivirga tractuosa (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43) GN=Ftrac_1762 PE=4 SV=1MKISRFKNTIIELLNNAIYKSKKPVLTTVRSVKVFLWIAASVILLYEFGFDVNKEELEQVFLALDIILFFYFLSFLIRWLYSFRRLEFLQ SHKLEFILVIIILVNSISYYAFDNRIVYFLQDFFEFNSYADAYQTLLAFYFIILISYEGVKASVILSQLKTKPARTFIISFIILIFFGTGVLMFPEM SVENETMPFMDALFTAVSASCVTGLIVVDTATYFSLKGQFVIMILMQFGGLGIITFASFLASLLKTGVGIKQQLMLQDFLESDSLFSAKG LLSKIFFITFLVEFIAFVLIFFSWGQDVHFNTVGQKVFFSAFHSISAFCNAGFSLFTNGLFEQGVATSYILHIIIAITLILGGIGFSSLQDLFSL SNLRDRFRNPWKEWKLSTKIAVYTSLVLLITGMIAFYFIERDNTLADMNFMEALITSFFQSATARTAGFNTVDFSALKIPALVLISFLMFV GASSGSVGGGIKTSTFYLLIKSVVATLNNRAKIEIDRKFIPKELLYKALSVFFFAATMNLMAIFALTITDGDITLERLIFEQVSAFGTVGLST GITADLSLGGRIIIILSMFIGRVGTLTFALALSNRATSTTHKYPRAHLMVG
6.7E-50	179	17.5	4.5E-27	104.1	1.9	2.2	2	A0A0D5LRR5_9RHIZ	Trk system potassium uptake protein	TM49_13400	Martelella endophytica	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	1486262	>tr|A0A0D5LRR5|A0A0D5LRR5_9RHIZ Trk system potassium uptake protein OS=Martelella endophytica GN=TM49_13400 PE=3 SV=1MNATLLRSAFYIAAICGLYLAAAMFVPAMADLYYNNKDWEVFAVCGIMVGGISGVTAVAMRGNPPPFSRRLGFFLVNLLWVTFA VVGAVPIYLARADLSFAQALFESVSAITTTGSTVLTGLDHAAPGLLIWRSLLQWMGGIGIVALGLFILPFLRIGGMAFFKMESSDTGDKP FARMASFTRAFLAIYVGITVLCAIGYGTSGMSHFDAVNHALTTVATGGFSTHDASFGYFHDTRLLWIAGFFMTICSLPFSILILFIVRGRL DTLRDPQIMLFLGYLGIAVFALALYISLNGEMTFPMALSESFFNVSSILSTTGYASTDYTLWGSFAVVLVFFLTFMGGCSGSTAGGIKAY RFLILFNMLKTGMKKLIYPNAVYSIRYGQLTVDPETQRAVSMFFSAYILLWAVGSVALAALGYDIVTATTAVLTALSNVGPGLGDIIGPA GNFSSFADPELYLLSLMMLLGRLEILTIVVILMPMYWRG
6.8E-50	179	15.1	2.9E-48	174	10.5	2	1	R7JVU7_9FIRM	Trk system potassium uptake protein TrkH	BN630_01815	Blautia sp. CAG:37	480	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:37	1262757	>tr|R7JVU7|R7JVU7_9FIRM Trk system potassium uptake protein TrkH OS=Blautia sp. CAG:37 GN=BN630_01815 PE=4 SV=1MNYKMIRFVISWVLKVEGMLMLLPALVGAMYQEKAGFAYLIWGLLCVAAGLILCFRKPSNMEIYSRDGFVCVSLSWVVLGVFGA VPFVITGEIPFYINALFEIVSGFTTTGASILSDVEALSHASLFWRSFSHWIGGMGVLVFILALLPMKGGSVMNLMKAESPGPTVSKFVPR VRGTAKILYQIYLGMTLFTIAALLLSGMKTFDSVTLAMGAAGTGGFAVLNSGCAVYTPLQQWILTIAMIAFGVNFNFYYLMLCKKGKAAI SSQEVRAYILIILLAGGVISWNTYPMYHSIGETVRTAFFQVGSIITTTGYSTTFDFDLWPELSKCILVMLMFIGACAGSTGGGIKVSRILILL KTVKKELGSIVHPRSIKRIRFDDHPVEHEVLRAINVFLIVYLVIYSFSMLIISVDGFSFETNFTAVAATLNNIGPGLDLVGPTSNFFGYGPV SKLILIFDMLAGRLELFPMLILFYPSTWKKRG

6.8E-50	179	30.5	8.7E-25	96.6	8.1	2.1	2	Y1485_METJA	Uncharacterized cation transporter MJ1485	MJ1485	Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) (Methanococcus jannaschii)	474	cellular organisms, Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus, Methanocaldococcus jannaschii, Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) (Methanococcus jannaschii)	243232	>sp|Q58880|Y1485_METJA Uncharacterized cation transporter MJ1485 OS=Methanocaldococcus jannaschii (strain ATCC 43067 / DSM 2661 / JAL-1 / JCM 10045 / NBRC 100440) GN=MJ1485 PE=3 SV=1MGICRLTKKDIEGILHILGGIIQIIGIFTLVPCIVSVYYNENTFLNFLIPGLFFSIFGFVLKRATKPKNLKLHHTMVASALAWLIASFIGAI PLYLSIDYFSYVDAVYESMSAWTTTGMTLIPNVEVLPKSILFWRSFQQWIGGVGILVLSALVLARSGTVAYLLYTSEARQERIMPSAIGT IKTIIWIYILYTILGVLLLYLSGLSFWDALNLTMTGISTGGMSISNYSFPYNDFAKIVMIGIMMVGGVMSFSIHHKLLTGKYFNDIQTKYALI VTAFISIIISIKDKVPIIDSLFTVVSAMTSTGFTTINVGNLSSLSLFLIIFLMLIGGGAGTTTGGVKIIRFLVILKALLYEIKEIIYPKSAVIHEHLD DMDLNYRIIREAFVVFFLYCLSSFLTALIFIALGYNPYDSIFDAVSFTSNIGISLGVVTLKTPVIGKIAGIIAMWIGRLEIIPVLVLFATLYFKTL RLLKK	
7.1E-50	179	42	1.2E-49	178.6	29.1	1.2	1	F4AZ80_DOKS4	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Krodi_1051	Dokdonia sp. (strain 4H-3-7-5) (Krokinobacter sp. (strain 4H-3-7-5))	451	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Dokdonia, Dokdonia sp. (strain 4H-3-7-5) (Krokinobacter sp. (strain 4H-3-7-5))	983548	>tr|F4AZ80|F4AZ80_DOKS4 H(+)-transporting two-sector ATPase OS=Dokdonia sp. (strain 4H-3-7-5) GN=Krodi_1051 PE=4 SV=1MRTFYNKLSLRYTALKRSWTPQQNLFYGFLTYVLVGTLLLSLPWLQKTSASILDHLFIATSAVSTTGLVTMSIFDSYNVGGQFVIM ALFQLGGIGYLTFTTFMLLSTTHKITPWHKSILNTEFTLPVTIRIKDFLKSVVLYTVIMEVLGAILFFIAFKSDGMGTGEAIWSSIFHSISAF CTAGFSLFNSGFTPYVVDNGLINFTISMLAICGSLGFIVITDVGLWIKNRTHSLSFTTKIVTIGSLILLAFGYLFFYFLEPSISSLSGSARVSA AFFQSMTAMTTVGFNTVDFGTFILPMLLVTIFLMYIGASPSGTAGGMKITTLTAVFAIMKSRLKGSKNITFLGKRIPYERLYVATSSFIFY TTLIFVGTFVLTFSEDFDFENILFEVASALGTVGVSTGITGDLSSIGKIIIIILMFIGRLGVLTFGLAIWSKSITNEDREILKEDIAV	
7.2E-50	179	34.7	1.3E-49	178.5	24.1	1.3	1	B9DJI7_STACT	Putative cation transport protein of TrkH family	Sca_0441	Staphylococcus carnosus (strain TM300)	434	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus carnosus, Staphylococcus carnosus subsp. carnosus, Staphylococcus carnosus (strain TM300)	396513	>tr|B9DJI7|B9DJI7_STACT Putative cation transport protein of TrkH family OS=Staphylococcus carnosus (strain TM300) GN=Sca_0441 PE=4 SV=1MDFLKKPLSVYLLLFLTTTLIGAFLLYLPITGKQPTPFIDAFFVASSAFTVTGLSTVDITTQFNWLGDLIIMLLIQIGGLGIVTITTLTLII ANRRISLHDRRLIMVTWNVEEPGGMVRFIRQLVIYSFTSELIGMLLLSLSFIPRYGFGKGVYISLFTSVSAFNNAGFALFSKNMIGFNND PVVNIVIPLLIILGGLGPLIMLDLLKTRRLSKLKLHTKVVMSTTLVLIIGGAILYYILEFNNTLKHFNIWGQVGTAFFQSVTTRTAGFQSVDL GLIHTPTAILMMILMFIGGAPFSAAGGIKVTTFMVLIMFVYSTLKNENSTVIFHRTIQPKTISKAVAITAVSGIFVLFITFIVSLLNETTPFIKVI FEVVSAFGTVGLSMDFTTEYHAATKAIIILVMICGKIGVATVLALFIPNKKRLYQYAKGNIYL	
7.3E-50	179	19.7	1.1E-49	178.8	13.7	1.1	1	R6MYV0_9CLOT	Potassium uptake protein TrkH family	BN578_00480	Clostridium leptum CAG:27	462	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium leptum CAG:27	1263068	>tr|R6MYV0|R6MYV0_9CLOT Potassium uptake protein TrkH family OS=Clostridium leptum CAG:27 GN=BN578_00480 PE=4 SV=1METGEKKSLIRRLKDVPPVRLIVSSFFIIIVIGAVLLALPISARDRQATDLLSSFFTSTSATCVTGLVVFDTWTHWSAFGQVVILGLI QLGGLGLVTFTSGFTLFLRRRLDLRDMQIAKEYTNGSTLDLPRLLRTIMFFTFVCEAFGSFLLMLRFVPMFGGKGIWISVFLSVSAYCN AGFDILGFLKPDASLELFVGDPLVCLTICCLIILGGIGFIVTVDLYNWGRKRVRKEERRPHLTLHTRIVLVSTASLLVLGTVLTLGLEYDHT LKDLNFWEKLNASFFQSVTARTAGYATIPQGELGDATKLVTIILMFIGASPSSTGGGIKTTTFVVLVATVVSISRGRDETVINKRRVDKS VVYRAMTIVAMAFLVIAITSGVIMVTTPPEVSAIDAVYEAVSAFGTVGLTTGLTPDLSIVAKILVMLTMFIGRVGPISLVLALTMKHSGGPG KILPEGKVIVG	
7.5E-50	179	28.2	2.7E-49	177.4	19.6	1.7	1	L0HFH1_METFS	Trk-type K+ transport system, membrane component	Metfor_0769	Methanoregula formicica (strain DSM 22288 / NBRC 105244 / SMSP)	485	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula formicica, Methanoregula formicica (strain DSM 22288 / NBRC 105244 / SMSP)	593750	>tr|L0HFH1|L0HFH1_METFS Trk-type K+ transport system, membrane component OS=Methanoregula formicica (strain DSM 22288 / NBRC 105244 / SMSP) GN=Metfor_0769 PE=4 SV=1MRRLEHLSTTLADLGDIFTFIAPVTCLPLLVCIIFSEWEMFLPMASVPAVFLVAGLFFRQLPRSTKGSRLSMAMCSVALFWFACA VVSGIPFMLGLHMSFTDAVFEGMAGWTGTAFSMIRSVDTAPYTLLFWRSYMQWIGGIGIIAFTVALASSTGLFRSRIFRDESRDESLM PAVAAAGRSLWKIYAVLTFCAIGLILFTGLSLWESVNLALSAISTGGFTLHGGGILYYDSVVLQLLLIPIMIAGALPFKLYFLILEHRRLSLF GDEQVRIFFLLLLAGTAVLVYDMVLFSDTGLPAAILQGLFMSASALTTTGFQTVNLQTWAGVTILFLAMLTFIGGAAGSTAGGIKLDRVA FGVRALLWWFRRLFVSGKVLVPFRIEGRVIPRDTAELETAKNMLVILLSVIIIFIASLAVLQYHLTTFSLTEIVFQVVSAFSTCGINTGYVM PDMPVISKWIFILVMWIGRLEVIPVIILFLSLVRGPE	
8.2E-50	179	29.5	8E-33	123.1	9.6	2	2	D4W4D6_9FIRM	Potassium uptake protein, TrkH family	CUW_1826	Turicibacter sanguinis PC909	431	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Turicibacter, Turicibacter sanguinis, Turicibacter sanguinis PC909	702450	>tr|D4W4D6|D4W4D6_9FIRM Potassium uptake protein, TrkH family OS=Turicibacter sanguinis PC909 GN=CUW_1826 PE=4 SV=1MLRTKRLGPTQYVALGFMSVILIGSVLLALPIAHMPGTYVSYIDALFTSASAVTVTGLIAIETAEQFNAFGRLVIALLIQIGGLGVTSV GAIFILVMQRKFGVYHRLLLMEGLNFNSLSGVVRLVKSVLQLTLVIELVGMILSFFTFIQHYPFWEALGISAFHAIASFNNAGFDILGGGQ NLIPYRHHYVLLLTTATLIGLGGIGFVTMLDIYHKRNFKKCSMNTKIVMVTTASLLIIGTILLKLSEGFSWFDAFFHSISARTAGFSTIPIDD FSQAGLLILMVLMFIGASPGSTGGGIKTTTLFTIIKTIKSFATNRPVTAFYRRIPAESIIKAFSVFLLAISVVFVGTFFILLIQPELSLQSILFEV IAATGTVGLSTGIIPSLNIANKLILCIIMFIGRLGPFSIACLWAYQTAAPRFNYPEEQITIG	
8.3E-50	179	19	2E-49	177.8	13.2	1.5	1	W6K6K5_9PROT	Trk system potassium uptake protein	trkH MGMAQ_0279	Magnetospira sp. QH-2	468	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospira, Magnetospira sp. QH-2	1288970	>tr|W6K6K5|W6K6K5_9PROT Trk system potassium uptake protein OS=Magnetospira sp. QH-2 GN=trkH PE=3 SV=1MSILALGMCVPAVVDAALGHPDWQVFAVSAAVTLFVGISLVLAFGVGGTDMNVRQAFIMTTVAWTVLTTFAALPFAFCELELSIT DAFFESMSGITTTGSTVIVGLDNAPPGILLWRGLLQWLGGVGIIVMAIAILPMLRVGGMQLFQMESADASEKAMPRAYQIALGITGIYIL FTAACTVAYWGAGMDGFEAVIHAMTTIATGGYSTSDASMAHFDSMLIDFIAVGGMVAGSLPFLLYLKALQGDVVSLARDEQVRWFLA IGGAAVIIASILLWINQGLDPVQALRYGSFNVISIMTGTGYATTDYGLWGAFANPMFYFLMFVGGCAGSTSCGIKIFRFQVLFAAARTQ FHHLVHPHGVFIPYYNRRPIPDEVITSVLSFFFVFGVCFALLSIALAMLGLDFITAVSSAATAIANVGPGLGPIVGPAGNFQTLPDAAKWL MSGGMLLGRLELFTILILFTRHFWKG	
9.2E-50	179	20.6	1.7E-48	174.8	14.3	2	1	R6AJH1_9CLOT	Trk system potassium uptake protein TrkH	BN491_00342	Clostridium sp. CAG:138	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:138	1262775	>tr|R6AJH1|R6AJH1_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:138 GN=BN491_00342 PE=4 SV=1MNFRLVLNMLGKILLIMAALMLLPAVVSVCSGGTDLLAILASAAITAAVGGGMLLVKPKDTTFFAKEGFVVVALAWVVMSLLGALP FMFGGIFTNYMDAVFETASGFTTTGATVLSGGISAIPHGIGFWRCFIIFIGGMGVLVFVMAVLPLSKERSMYLMRAEVPGPSVGKLVAK AKDTALILYSIYFALMVLMAVMLLFGGMNVYEAFTTALSTAGTGGFMVYDAGFIGLSPYLQTVTTVFMLLFAVNFNLYYYILMRRIGDVT HNEELRWFLGIFFAAVLTMTVANIGQFGSFGESLHHTAFNAASVYSTTGFASVNFDKWPTISKCIMLLLMVCGGCTGSTAGGIKTSRV AILVKNAFNELRRFAHPKYVRSLKLDGKVVSEPVVRSVTVYFSVIIGIIVSIILVSANGFDFESSLSAVFACIFNIGPGFHAFGPTASFTPL SNFSKLVLTFDMLAGRLELWPLLLLFVPSTWKKRAVYK	

9.7E-50	179	18.7	3.1E-47	170.6	13	2.1	1	A6V6V8_PSEA7	Trk system potassium uptake protein	PSPA7_3433	Pseudomonas aeruginosa (strain PA7)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	381754	>tr|A6V6V8|A6V6V8_PSEA7 Trk system potassium uptake protein OS=Pseudomonas aeruginosa (strain PA7) GN=PSPA7_3433 PE=3 SV=1MSLSLLRLVGFVLGLFLLTLAASMLIPLLTLVLFQRYDDFDAFLWSSLLTAAAGLALLLPGRPAQVHFRARHMYFLTTASWVVVC AFAALPMVMARHISYTDAFFETMSGITTTGSTVFSGLDQMSPGILIWRSLLHWLGGIGFIGMAVAILPLLRVGGMRLFQTESSDWGEK VMPRSHMAAQYILAVYVALTLLGVLCFWWAGMTPFEALNHSMAALSTGGFSTSDASLAHWPQPAVHWVAVLFMILGSLPFTLYVAT LRGHRMALLKDHQVHGFIGFLGVTWLVIACWLWMNSDYGWWDALRLVAVNVTSVVTTTGFALTDYTTWGTFAVMLFFYLTFVGGC SGSTAGGLKIFRFQVAFVLLKANLQNLVHPRATIRQSYNGHPLDEEIVRSLITFSFFFTITIGVIALGLTMLGLDWISALTGAATAVCNVG PGLGPIIGPAGNFSSLPDMAKWLLTVGMLLGRLEILTVLVLCTRAFWRF
1E-49	179	26.2	9.5E-48	172.3	18.2	2.1	1	R7BTQ9_9FIRM	Uncharacterized protein	BN674_00375	Firmicutes bacterium CAG:475	491	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:475	1263026	>tr|R7BTQ9|R7BTQ9_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:475 GN=BN674_00375 PE=4 SV=1MNLRLLAFVLGEIAVIIGALMSIPLFMAIGYGEDTTILAFGIAIGVCLLMGVIGIIVRPPKAKRDMRSTSGFAMCALFWIFIALVSAIPF RVSGYIPNYIDALFETISGYTTTGSSILTNVEALPKSLLFWRSLTQFIGGMGVLVFVIVFIPQNDKMSTALAKAEIPGPSFGKIVSKLRFTS LILYAIYIVMTFILAGILCALKMPVFDSFCHAFSTASTGGFSVKAASIAAYNSVGIEVTLTVFMALFSINFNVYFLMLVGHFVKALKNEEVF WFLGIFVSAIAIIVANLMASGTYTDFATALRAASFNVSSLISTSGFGTADYTTWPVLSRITLFAVMCIGGCAGSTAGGLKVSRVIMLSKS SVINVKKTLSPRSVYTVKMDGRPVDDATIRNVKSFFIIYMFIILVSVMLISIENNDFGRYSAFETNFSAVLACFNNIGPGSGAVGPTGNFA SYSIFAKLVLCFDMLLGRLEILPILLLFNVKSWKRA
1E-49	179	16.5	2.8E-48	174	11.4	2	1	R5EH77_9BURK	Trk system potassium uptake protein	BN548_02057	Parasutterella excrementihominis CAG:233	493	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Sutterellaceae, Parasutterella, environmental samples, Parasutterella excrementihominis CAG:233	1263099	>tr|R5EH77|R5EH77_9BURK Trk system potassium uptake protein OS=Parasutterella excrementihominis CAG:233 GN=BN548_02057 PE=3 SV=1MQLLPPVLRLMLLPVLNVLGPIIIGFSLSMLIPLALSLWKKDGASAGFEIAFICTFFTGLLMWLLTRRYKRELIPRDGFLLVTMAWV LLALAATIPLYVNIEGISFVHAFFEATSGITTTCGTILSGLDRLPLSVNFWRCFLAWMGGIGILVMAVAVLPLLGVGGSQIFRAESSGPMK EGRLTPRIADTAKAFYNIYLAISVACAVCYHFAGMDWDDAIMHTFTTVSLGGYSSHDAGFAYWPGRAVDWVCVVFLLIGGINFSMHFI AWRKLSLKVYLKDVETCGWIGTAALISIFASFMLVYSKTYTNVYDAIYYGVTNTVFVISTGGFANTNYGEWPLVVQLMILFGSCFATCA GSTGGGFKMIRAIALVKQGNLEFKRILHPRMVRPLIIGNKVIDKQIIFSVMAFLMLYTVIALISTIVFLLSGLDGLTSFSAALACLNNLGPAL GSLGPSYNFTSLSDFQVLFCCFLMVIGRLELFTVLVLFTRGFWRA
1.1E-49	179	20.1	8E-49	175.8	14	1.9	1	A4VMA8_PSEU5	Trk system potassium uptake protein	trkH PST_2457	Pseudomonas stutzeri (strain A1501)	510	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas stutzeri group, Pseudomonas stutzeri subgroup, Pseudomonas stutzeri (Pseudomonas perfectomarina), Pseudomonas stutzeri (strain A1501)	379731	>tr|A4VMA8|A4VMA8_PSEU5 Trk system potassium uptake protein OS=Pseudomonas stutzeri (strain A1501) GN=trkH PE=3 SV=1MNRRAVYCHRDASRMSAPLSPVPSTFYMALPTLRIIGFILGIFLITLAVSMIIPMLTLAYERTDDLQAFIWGSLITFSCGFALVAPG KPANTHLRPRDMYFLTTISWVVVCCFAALPLMLIQHISYSDAFFETMSGITTTGATVLSGLDSASPGLLMWRSLLHWLGGIGFIGMAIAI LPLLRVGGMRLFQTESSDWSEKVMPRSHVAGQYLLVIYVTFTIAAFIAFLLTGMGAFDAINHAMSTVATGGFSTSDASMGKFGPSAH WVAVFFMIVGSLPFTLYVMTLRGHRTALFRDQQVRGFVLMLAITSVLFSGWYWLNNDVPALDALRIVTFSVVSVVTTTGFAVDDYTQ WGGFAVMAFFYLTFIGGCSGSTSGGLKMFRFQVAYSLLRANFKQLIHPRAVIRQQYNGHNLDEEIVRSILTFSFFITMTIGVLALCLALL GLDPITALTGAATAVCNVGPGLGEIIGPAGNFSTLPDTAKWLLSIGMLLGRLEIITVLVLLTPAFWRH
1.1E-49	179	23.9	5.6E-48	173.1	16.5	2	1	E6X1F4_NITSE	Trk system potassium uptake protein	Nitsa_0619	Nitratifractor salsuginis (strain DSM 16511 / JCM 12458 / E9I37-1)	480	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, unclassified Campylobacterales, Nitratifractor, Nitratifractor salsuginis, Nitratifractor salsuginis (strain DSM 16511 / JCM 12458 / E9I37-1)	749222	>tr|E6X1F4|E6X1F4_NITSE Trk system potassium uptake protein OS=Nitratifractor salsuginis (strain DSM 16511 / JCM 12458 / E9I37-1) GN=Nitsa_0619 PE=3 SV=1MDFKSIFKVLALIGMAVGAFFATEIPVAIYYEEPVDKLMLFLTIFFLINAGIFFILKNHKVDLKIRESILSVNLLWILLGIGGGIPLWLYT YVSPASAFFEAVSGFTTTGATVYSDIESLPHFILFHRSLMHWMGGMGIIVLGVGLLSMINPSGSLSLFKAESTGIQIEKLRPKIKDTALSL WGIYLGLTILDMLLLKFLGMNWFDALNHAFSTLSTGGFSTKNDSLGGFHSDAIIWVTTVFMLLAGINFLAHLRLLYRDFSGYKSEEVRW YLIVFFVLSIFLTLTHEIDDSAQLWFSATHSFFTVASVMTTTGFASTNYGVWGHPAIALIFLAMLVGGNAGSTAGGVKVIRYVVIIKTLFA ELKRILHPRALIAVYVDGNKLKENVIASTFGFFILYIFTNVLLSLYLYGRGFDAMTSISGALAIVGNIGPGFAQVGPADNFGFFSDIDKIILSI GMIIGRLECYTVYVLLSLSFWKKF
1.2E-49	179	34.2	3.7E-48	173.6	23.7	2	1	N8S3E4_ACIGI	Uncharacterized protein	F981_02022	Acinetobacter guillouiae CIP 63.46	450	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter guillouiae (Acinetobacter genomosp. 11), Acinetobacter guillouiae CIP 63.46	1217655	>tr|N8S3E4|N8S3E4_ACIGI Uncharacterized protein OS=Acinetobacter guillouiae CIP 63.46 GN=F981_02022 PE=4 SV=1MRLSKKELINKKHNSINLSPPSLLALGFLSFIIIGTLLLKLPFANQGNLTWLEALFTAISAVTITGLSVVNIGDSLTTFGQVVVMILIQ CGGLGFMTFAILAALSLSSKVGIRQQVMAQETIGQTSLAKATFTVKGVFLYSLFFEAIGTGILTMAWSHHYDLEHAFFYALFYSISAFNN GGFSLFPNSLMSFSDQYMVTFTISMLYIIGGIGFVVLMDIKRAKRWKKLSTNSKLILSTIAGLNLFAFIVIWAIEASNPLTLAPMSVGDQAL NAWFHATVPRSSGFNSLEVSSMTNASTLITMVLMFIGGGSLSTAGGIKVGTFIIMILSVITFLKRSDEITIFGHSVSHQATFKAMAVISITS LLILIGFFTLLILEPDKKFLDLLFEAVSAACTVGLSRGITENLHAGSQIALICLMFAGRLGPLTLAYLIATPNKSRVRHPNTEIQVG
1.2E-49	179	25.2	2.4E-49	177.6	17.4	1.4	1	F8KS94_HELBC	Potassium uptake protein, integral membrane component, KtrB	HBZC1_06710	Helicobacter bizzozeronii (strain CIII-1)	454	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter, Helicobacter bizzozeronii, Helicobacter bizzozeronii (strain CIII-1)	1002804	>tr|F8KS94|F8KS94_HELBC Potassium uptake protein, integral membrane component, KtrB OS=Helicobacter bizzozeronii (strain CIII-1) GN=HBZC1_06710 PE=4 SV=1MLASEGSSNKASSVNKTFGTIVISYVLLALLGALLLSLSPMRLKPIPFIDLFFTSVSAVCLTGLITFNPATDLTIYGQAVIMGLIQAGG FGYMGLAGFLFLLLGKRMDFKGRMLLKESLDYPNMQGIIRYLKKILLFTLCIEGLGALILTLYFLSNMPFKQALWAGIFHAISAFNNAGFS VFESNLVNYRNDVVVNLTICLLIILGGLGFLVLSECYDYRNKSRWSVHTRIVLIATAICIVLGMAVLLLFEWDNPKSFGESNWFEKILGVF FISVNLRTAGFNTIDMSGLHDQSLFFSSLLMVVGAAPGGTAGGIKITTMTLLLVYAYCTLKDREMVLFQRTIPQALVKKSFLVFIITMFYIII SVMILSATDDTQNKHFLHLLFEICSAFGTVGASTGDGGTLSFAATFSNFGKLYLAVLMFMGRAGVLMFSMALIGKSKTRHIKYPEEGVLL
1.2E-49	179	19.6	2.5E-47	170.9	13.6	2	1	M1P486_DESSD	Trk system potassium uptake protein	UWK_01745	Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	485	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfocapsa, Desulfocapsa sulfexigens, Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	1167006	>tr|M1P486|M1P486_DESSD Trk system potassium uptake protein OS=Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1) GN=UWK_01745 PE=3 SV=1MNFASIAHVIGILLIVTGCSMSLPIACSILYQENDLLPLLYSFAITTGAGIPLFIAFRKNNDLQIKDGFFIAVVGWVVVSAFSAIPYMIH GSIPSFTDAFFEMISGYTTTGATILNDIEAVPHGLLFWRSQTHLLGGMGFLTLAIIFLPHGMGGLRLFRAESSPGQVITKDKFKPRNRDT MVMLWWIYIGLNCIQIILLALGGMPLFDSLCTAFGTVSTSGYSTRNASIGAYNNAYFDWIIILFMFLGGLSFVLIYQVLRGDTNALKINTEL RWYLGFLFFFCGAITLILWTKGTYHNISDALRYGTFQIVSLLTTTGFGTADYELWPHSAQMLLFVVCFVGACAGSTTSGIKVVHYVIICK YMYASIRKIFFQPMAVVSLRLNGRTIDDDIISLALCYFIINIFMVLVGGFVMTLTDNMNYSSAISSVIAALMNIGPGFGAVGPSHNFAFISDI GKWFLSWNMLVGRLEMFSALVLFFPSFWEK

1.3E-49	179	19.9	7.3E-49	176	13.8	1.9	1	A0LDP4_MAGMM	Cation transporter	Mmc1_3602	Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1)	457	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Magnetococcales, Magnetococcaceae, Magnetococcus, Magnetococcus marinus, Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1)	156889	>tr|A0LDP4|A0LDP4_MAGMM Cation transporter OS=Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1) GN=Mmc1_3602 PE=4 SV=1MLIRNEVDGVRLVVQSFAMVIIIGALLLFTPWSAADPAGHPVSWLDALFTSTSAVCVTGLVTLDTGQDFSFLGQAVILALIQVGGLGFLTFTNFFIAIQGGRLDFMRRAMLATTHGTLPGEVHPGALLRHIVLFTFALEGVGAVLLTGRFALEMPFTEALWMGIFYSISAFCNAGFGLLSDSLMPYRDDPLVNLTIMGLIVTGGLGFVVFTDLSHRLVLWRRGQPGRLSLHSRMVLIMTGILVPLGTVLFFLLEQGGTAAGENGVSSALSALFLSITSRTAGFNTIDTARLTAPTLYLVILFMAVGGSPGSTAGGMKTTTVGIMAAMLMSRLRNREGVEFLDRTIPAQAVLTAMLTFAAFAVLAVAGFLALLISETGLQAYDPAHDRSLALLFETVSALATVGLSTGVTAGLSAIGKVIIIVLMFVGRLGPLVLGLTLMGRRPRERYKLPDESVNVG
1.4E-49	178	22.8	2.7E-29	111.4	4.1	2	2	R6CHJ8_9FIRM	Trk system potassium uptake protein TrkH	BN708_02044	Firmicutes bacterium CAG:56	484	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:56	1263031	>tr|R6CHJ8|R6CHJ8_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:56 GN=BN708_02044 PE=4 SV=1MNYGMIFYILGMASGFEALFLLLPILVSLIYGESVLSSYLISCGICALFCGVSTLRKPKKITLYTKEGLVAVALVWIWFSVFGAVPFMLTEEIPNFFDAFFEVSSGFTTTGASILTNVEALSRASLFWRSFTHWVGGMGILVFILAFIPNKGNGTIVHLMKAESPGPNVSKLVPKIRYTAAILYAIYFGMTLIQIILLLISKMPLFDTLCITFGTAGTGGFSIKSDGCAGYTMLQQGIITTFMILFGVNFTFYFCILKKKIRQVSSMTEVLAYLAIIAASILAITFNISGGFSSLFQAFHHAAFQVGSIITTTGFSTVDFNQWPGFSRTILVTLMFVGACAGSTGGGIKVSRILLLLKGIGREISLALHPRSVKRVRMEGRTVETEVIRSVNAYLALYMIIFVASVLIVSLDEKDLVTNFTAVAATLNNVGPGLGLVGPAGNFSGFSNLSKLVLSFDMLAGRLELIPMLMIFVPSVWSVKRKKK
1.5E-49	178	20	9.5E-49	175.6	13.9	1.9	1	A0A0F2QQK0_9PSED	Trk system potassium uptake protein	VR76_09470	Pseudomonas sp. BRH_c35	483	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. BRH_c35	1629711	>tr|A0A0F2QQK0|A0A0F2QQK0_9PSED Trk system potassium uptake protein OS=Pseudomonas sp. BRH_c35 GN=VR76_09470 PE=3 SV=1MALPTLRIIGFILGIFLITLAVSMIIPMLTLLAFERTDDLQAFIWGSLITFSCGFALVAPGRPANTNLRPRDMYFLTTISWVVVCCFAALPLMLIQHISYSDAFFETMSGITTTGATVLSGLDSASPGLLMWRSLLHWLGGIGFIGMAIAILPLLRVGGMRLFQTESSDWSEKVMPRSHVAGQYLLVIYVTFTVAAFLAFLLTGMSMFDAINHAMSTVATGGFSTSDASMGKFGPSAHWVAVFFMLLGSLPFTLYVMTLRGHRTALLKDQQVRGFVLMLTITSVLFSGWYWLNNDIPALDALRIVTFSVVSVVTTTGFAVDDYTQWGGFAVMAFFYLTFVGGCSGSTSGGLKMFRFQVAYSLLRANFKQLIHPRAVIRQQYNGHNLDEEIVRSILTFSFFITMTIGVLALCLALLGLDPITALTGAATAVCNVGPGLGEIIGPAGNFSTLPDTAKWLLSIGMLLGRLEIITVLVLLTPAFWRH
1.5E-49	178	33.8	1.4E-48	175	23.4	1.9	1	A0A0F2PI58_9FIRM	Uncharacterized protein	VR67_05560	Peptococcaceae bacterium BRH_c8a	435	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c8a	1629715	>tr|A0A0F2PI58|A0A0F2PI58_9FIRM Uncharacterized protein OS=Peptococcaceae bacterium BRH_c8a GN=VR67_05560 PE=4 SV=1MNRRIKPGHLLIISYALVDLVGTILLLLPIASHKPTTLLEAWFTATSALTVTGLTVVTTATHWNLFGQTVILILMQIGGLGLMVLATIILTMLGMRIQLGHRYLVTQDRNYFDLTGVVRLVRGILILTLTLEVIGGILMAILLPEAWSNGPLWGLFFITFHAVSAFNGAGFDITGHSLESFSHHTGFVLVVIVMIQLGSLGFVVLQELFLNRNWRRLSLHSRLVLSVTGAITVVGTLFFFLSAFKNSLADFSVVDKMVQSLFQATTRTAGFTTLSISGWTEPFLFLMILMMFVGASPGSVGGGIKTTTFGTVLLAIWAIVRGKKEVVLFEREIDPDSVTKAFTVTVMAGLLAAASTLTLMVTEGLPFMPVLFEVVSAMATVGLSMGITRELSGFGQILIGLLMFVGRIGILSVIIILAGKERRRLHYMKEDILIG
1.5E-49	178	27	1.5E-49	178.2	18.7	2	1	I0XWG8_9LEPT	Cation transport protein	LEP1GSC185_1632	Leptospira licerasiae serovar Varillal str. VAR 010	600	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira licerasiae, Leptospira licerasiae serovar Varillal, Leptospira licerasiae serovar Varillal str. VAR 010	1049972	>tr|I0XWG8|I0XWG8_9LEPT Cation transport protein OS=Leptospira licerasiae serovar Varillal str. VAR 010 GN=LEP1GSC185_1632 PE=4 SV=1MNSFLDPDLRTKLVSEWGRISLFFEENIKPFLRFIFGVLGIVSLFILIFLYGFYYPPQWIHPLRLVTMTIVWYLVIYECLSFLFTLTPYRSYLKFHKIEAIVVLVVLLQFFLEEKIESILSQQRTEEVILLFLSLSQLTLAFGGFAHFLRRARLSLGKISPSLVMTGSFAILIFLGTAALCLPRAEARPIQLVDLFFTAVSAVCVTGLSTIDVSQDLTGTGQVILMVLVQLGGLGLMTLTVFFALVLEGQVSVTEKLIVKDLFSQESIGRAGSILKQVAYQTFAIEGIGSVFLYLTFPKELGFSQKELIFQSIFHSITGFCNAGFALFSKGLAEPYFRESYSFLSTLMILVFGGLGFPTVNQLLKKIRFNGESFRYRFSLGSKLILIMTLSLLIFGWISYWVLERNFSLKDLSWYDQAFHSLFYSVTTRTAGFNTLDTSTMGIPMVFVSLFLMWVGASPNSTGGGIKTSTLALAFLQFYQFFTGKERVDVFGRTVAENSLSRASVAIVLSMFIIFLGIFFIVCFEKPFPFLDICYEVVSAYGTTGLSRGITSKFETPGKLLLLCFVMFVGRVGVLTVLLAFVPKRKPRRYWYPEEYVVVG
1.6E-49	178	27.3	4.6E-49	176.6	18.9	1.6	1	R6W553_9BACT	Cation transport protein	BN725_01299	Prevotella sp. CAG:592	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:592	1262931	>tr|R6W553|R6W553_9BACT Cation transport protein OS=Prevotella sp. CAG:592 GN=BN725_01299 PE=4 SV=1MLNFKLIYKILGQLLFLEALLMSLCLAMALFYREDDAMAFAISIAIIVGAGFMLKYKGRMAENSMNRRDAYLLVTLTWALFSFFGAFPFTISGYISDYTDAFFETMSGFTTTGATIIDDVEALPHGLLFWRSMTQWIGGLGIAFFTIAILPSLVPGSIRVFAAESTGPIKSKVHPRISSSAKSIWLVYLLLTLSCSVCLYLGGMNLFDCTNYSMSITATGGFAPYNDSTGHFHSAFIDYTTIAFMFLSGTNFTLLYLTFFKRKFLSLFQNSEFKLYVLVVSLATMGIMYFLIRFNGYDMANALRSALFQVVSFITTTGVFNDDAGKWPHITWVILSICMFIGACAGSTSGGFKSVRGVILFKVVRNELRRILHPKAVLPVRVNGNLVSSSAQVTLLVFFALYMALCIFAYFCLICMGVDSTNSITIAMSCASNVGPTLGLEIGPTVSWNILPAVGKWICSVLMLMGRLEIFSVVVLFTRGFWKDR
1.6E-49	178	33.4	3E-49	177.3	23.1	1.3	1	F9YU52_CAPCC	Ktr system potassium uptake protein B	Ccan_20540	Capnocytophaga canimorsus (strain 5)	579	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Capnocytophaga, Capnocytophaga canimorsus, Capnocytophaga canimorsus (strain 5)	860228	>tr|F9YU52|F9YU52_CAPCC Ktr system potassium uptake protein B OS=Capnocytophaga canimorsus (strain 5) GN=Ccan_20540 PE=4 SV=1MKFLIDKSKLKAFFSVLYIVLVVVLIIDYGYSLPLWLDYCFLAFYTFSLVINISFHAFKLYRSEERHFRIDLLDGLSTVFVIICLYEQFIDDGTTLVVSDWMRWATILILIRGANLPKINYKRSVLNPAQLFIISFVGLIGIGTFLLLLPNSTRTGISVTDALFTSTSAVCVTGLNIADTGSYFTRFGQTIIMLLIQAGGLGILTVASYFSYFFKEGATYENQIALSDISNSNKIGEVFTTLKRILVITFTVELMGAFLIFINLPPRIIPDFWERIYFSIFHAVASFCNAGFSTLHNGLMQEGFVTNYRFQLTIIALFVFGGLGFPIVINTLRYLKHFIKRNVLFFISGKDNYIPWILTLSSKLNLITTSILIVAGTTIIYLKEYEHTLSAHQGFGRLVTALFTATTPRTAGFNTIDFNQMQLSSIIVVMLLMWIGASPASTGGGIKTSTFAIGTLNVLSLAKGKSKIEIFRREIAEISIRRAFAVMSLSLIVIGVGTFFISQLDKQMSLLDISFECFSAYSTTGLSLGITHRLSDASKLVLVAIMFVGRVSMLTILIAIFKKTRTFTYRYPKDEILIN
1.6E-49	178	28	6.7E-49	176.1	19.4	1.8	1	A0A0F5V8I6_9GAMM	Trk system potassium uptake protein	KY46_18630	Photobacterium halotolerans	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	265726	>tr|A0A0F5V8I6|A0A0F5V8I6_9GAMM Trk system potassium uptake protein OS=Photobacterium halotolerans GN=KY46_18630 PE=3 SV=1MVNLRPIIFVIGLVLSKIALFMYLPTLLAFLTGTGGFIDFATAVIITHIVAFACLTFGKVTDFKLGVRDMFLLTTLVWTVASAFAALPFMLINHISFTDAYFETMSGITTTGSTVLSGLDDMAPSILLWRSTLQWLGGIGFIVMGVAILPMLNVGGMRLFQTESSDWSEKSSPRTKNVATNIVIVYLSLTAMCILGFMAAGMNTFDAVNHAFTTLSTGGYSTSDGSMNHFPPAAHWVAIVFMFAGGLPFLLFVQVLRKKQPASLLRDAQVRGYTVTILIVSLMVALWLCWQNGYDFSHAIRVAMFNIISVVTTTGFGLEDFTAWGAFPTVVFAFMMLVGGCSGSTAGGFKVFRFQVAIALLRKQLMQLIHPSGVFIQRYNQRPVTDAIVRSVVAFALTFIMTIIIIAALLAMLGLDPITSISGSVTAVANVGPGMGTIIGPTGNFAALPDAAKWILSLGMLMGRLEILTVLVLAFPAFWKN

1.7E-49	178	28.3	5.6E-47	169.8	19.6	2.1	1	R6INI7_9PROT	Trk system potassium uptake protein	BN570_01575	Azospirillum sp. CAG:260	480	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, environmental samples, Azospirillum sp. CAG:260	1262706	>tr|R6INI7|R6INI7_9PROT Trk system potassium uptake protein OS=Azospirillum sp. CAG:260 GN=BN570_01575 PE=3 SV=1MWQPVLMINGYLISVLGLAMLIPAFLDMYWTRAGWSHFLSSSIICLFIGLSLFLANRMNIKKITLQQGYLITVCGWVSLTLLGTLPF LLYGSIPHFADALFETMSGLSTTGATILPDVEIMPKAILLWRSILSSLGGLGIVMFAVAMLPFLGIGGMQIFQRENSDIDDKFMPKFNYIA KRIMLVYILLTAACTVSLYGVGMSWFDAANHAMSAIATCGLGIKNASVGFYDSVSVEVVLSLFMVLGALPMTFYIMLVQNQDLHSFRT QQVITFLKVLAVYILFTSCWLVFEGVYGFWEALRYSSFNIISIVTTTGFASTDYMQWGAFAGTLFIIFALTGGCTGSTSGSIKIFRWQVIL AFLRKSLTIATDPNRVLPIKVGSLTVSNAVVSSVFVFFAGYMLSIAALSVLVALSGLSFETAFSAVIACITNSGPGVGPIVGPAGNFSSLP DAAKYVLAFAMLLGRLEVVTILVVFTKNFWRK
1.7E-49	178	24	2.8E-49	177.4	16.6	1.2	1	C6BZ44_DESAD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Desal_0802	Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763)	453	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio salexigens, Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763)	526222	>tr|C6BZ44|C6BZ44_DESAD H(+)-transporting two-sector ATPase OS=Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763) GN=Desal_0802 PE=4 SV=1MNSKATSPFWVPIYAFLATILIGGMLLKLDICHPGKELSFLDAIFTATSAVCVTGLAVVDTGTFFSRTGQSVILFLIQLGGLGIMTYA SLVIYLLGKKVSASDRIAVSQTLIHDPSFNIGKFIVGVVTAVLSIEALGALLLNRMDPDGFYPFSAVFHSISAFCNAGFSLYSDSLTTWKN HLGINTVFMALIIMGGLGFYVMTELWHKFMNFVRRRKGEISAHTLSWHTRIVLETSLFLIVVGGLAIFFAESFKVHVVEGAVVNEIAALF QSVTCRTAGFNTVDISGLTNISLLVMIGLMLIGGSPGSCAGGLKTTTFRTWVGFIISKVKGHSQVKVGWYALTEESVNRALTLLTIASVI LGSAIIMLSITEGSHLPHSEVRGHFIEITFEAISAFATVGLSTGVTPDLSGPGKSIIIALMFVGRLGPVWLLTAINSWQKEPRYRLPEDDLP LG
1.8E-49	178	16.3	1.7E-48	174.8	11.3	1.9	1	D7CY25_TRURR	Cation transporter	Trad_0245	Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24)	488	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Trueperaceae, Truepera, Truepera radiovictrix, Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24)	649638	>tr|D7CY25|D7CY25_TRURR Cation transporter OS=Truepera radiovictrix (strain DSM 17093 / CIP 108686 / LMG 22925 / RQ-24) GN=Trad_0245 PE=4 SV=1MRGRFTPFVVGVGLLGALLNLVFALYALLIGDPTLGFVWTVAFALLVGAPLTVIGRQDARPARREALIGVSLLWLSLTFVGAVP YVVNGGMGWIDAFFESSSGFTATGATALNVFEGFAPSMFMYRAVSQWLGGVGIILLFIAVLPQLAIAGRQLFFAELPGPTEEKLTPRL SQTASAVLFIYLSLTLLCTLAYRGAGMGWFDALAHTFTTVSAAGFSPYANSFEGFDAPVEWVAIVFMFFAGISFALYQRLLQGRTWFF WHDVELRAYVAIIAAVSALVTLGLLELYEPLEAVRYATFQVLSILTTTGYASADFAAWPERTQALLVMLMFVGGSAGSAAGGVKIVRW LMVGQSTVREIRRTLHPRVVMPIYLGRVTIPEEVMRAVSAFVALFFGTVGFSTLVLAWLGADLVTAFTASVACLGNVGPGLAGVGPM SDFSHLHPVSRVLLSLMMIAGRLELLTMLVIFDRRFWILPRRRPRGRATHSW
1.8E-49	178	19.9	8.3E-47	169.2	13.8	2.2	1	F5YKX5_TREPZ	Trk system potassium uptake protein TrkH	TREPR_3241	Treponema primitia (strain ATCC BAA-887 / DSM 12427 / ZAS-2)	481	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Treponema, Treponema primitia, Treponema primitia (strain ATCC BAA-887 / DSM 12427 / ZAS-2)	545694	>tr|F5YKX5|F5YKX5_TREPZ Trk system potassium uptake protein TrkH OS=Treponema primitia (strain ATCC BAA-887 / DSM 12427 / ZAS-2) GN=TREPR_3241 PE=4 SV=1MRTLTLLRILVILLGVGALIMLIPLALALILGEQRMIWALGLPAGIIIAAALPAFFSYRKNPLRFRARDGFLLVFLTWVGMSLLGAMPF YLSAREFSFTNAFFESACGFATTGATTITDVEALPKSLLLWRSISHWVGGMGIVLLTVALMPLLGVGGFQLIKAEVSGPEKERITPKITA TAKVMWFTYCILTAVLVILFRIGGMEWLDAFCHSFTTMASGGISTKNSGLSWYNSAFIDHVTMVFMLLAGLNFNLYFRLARGKFKDIIT NTEARVYLGIFLISAAAITFTLIPVYGSLSASWRFGAFHAASILSTTGAVIADYSVWPAFAQAILFALMFVGGCSSSTAGGIKVIRHVVLW KQTGNELRRILFPQGVFSIQLNKKVGRKDVVYGVSAFVFLYAAVVTIVALITAASGVDIFSSFSTALSVISNIGVGFGAIGPGHNFGAFPD QLKWLYSFAMIAGRLELWTVLILFTPEYWRR
2E-49	178	32.5	2.6E-46	167.5	22.5	2	1	G8QS01_SPHPG	Trk-type K+ transport system, membrane component	SpiGrapes_2223	Sphaerochaeta pleomorpha (strain ATCC BAA-1885 / DSM 22778 / Grapes)	432	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Sphaerochaeta, Sphaerochaeta pleomorpha, Sphaerochaeta pleomorpha (strain ATCC BAA-1885 / DSM 22778 / Grapes)	158190	>tr|G8QS01|G8QS01_SPHPG Trk-type K+ transport system, membrane component OS=Sphaerochaeta pleomorpha (strain ATCC BAA-1885 / DSM 22778 / Grapes) GN=SpiGrapes_2223 PE=4 SV=1MKMEPKKSILPNQYLIIGFCSIITLGSFLLFLPISQRSGIHIHYLDALFTSASAVCVTGLVTLDVAATFNLFGRTVIALLILLGGLGFAS FVMSFSMLLGWNIGISKRSVVREAYNLGSLKGTLQVVKTVTYASLIFEVGGTLIEFFIFRKTYPPLQALGHAAFNAISAFNNAGFDLMG GYRSLTGFRGNILMNLTTALLIIIGGTGFFVLSDIARNRRWKKLSMHSRIVILMNLALIVTGTLGIIILEHTDLLSSFFQSVTARTAGFNTIDI GKMSEPGQFLMMVLMFIGASPGSTGGGIKTTTTFAMIISLGSMIFRREPAVFQRRISNESILKAFQVFLLALLVVILGVFLIAVSEAGRFS FLQISFEGVSAFATVGLSTGITPFLGSFSKVVLMIIMFIGRLGPFTIASSLRARESVLKYVEEQVFIG
2E-49	178	31.6	4.9E-48	173.3	21.9	2	1	F4H9T6_GALAU	Trk system potassium uptake protein	UMN179_01221	Gallibacterium anatis (strain UMN179) (Pasteurella anatis)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales, Pasteurellaceae, Gallibacterium, Gallibacterium anatis, Gallibacterium anatis (strain UMN179) (Pasteurella anatis)	1005058	>tr|F4H9T6|F4H9T6_GALAU Trk system potassium uptake protein OS=Gallibacterium anatis (strain UMN179) GN=UMN179_01221 PE=3 SV=1MFNRPFILYILGSVLSKIAWLMIIPLIVTFFHNGDGLIGFLICIGITHFVSFILTRKKPQDMRLRVKDMLLLTTLIWVISCVFSALPFIVIS DFSFTDAYFETVSGLTTTGSSIIVDVSDTSPALLMWRSTMQWLGGLGFIVMAVAVLPFLNVGGMTLFRTESSDKSDKILPQARDIAKSII QIYLSLTVICLFCYMWSEMDFFDAINHAFTTIATGGFSTRSGSMSEFNSNTQWICTVFMFIGSLPFLLMVQAIHRRNILVLFRDQQLMG FTLFVFIVALFTAAWLNYENVFNWQDSLRYAFFNLINIMSTCGFSLGNFDTWTATTTMIFTVAFILGGCSGSTTGGIKIFRFQIMFQVLK HQILRLIHPNSISAVHYNRHTVSNETVFGIVGFIFSYFMIMAVLAVLMAISGMNFESAWSAAATAISNVGPGFGNEVGASGSFANIPTVA KWLMILGMLLGRLEIMTILILLFPNFWKK
2E-49	178	25.3	3.8E-49	176.9	17.5	1.3	1	T0TSK2_9STRE	Potassium uptake protein, integral membrane component, KtrB	HSISM1_2028	Streptococcus sp. HSISM1	460	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus sp. HSISM1	1316408	>tr|T0TSK2|T0TSK2_9STRE Potassium uptake protein, integral membrane component, KtrB OS=Streptococcus sp. HSISM1 GN=HSISM1_2028 PE=4 SV=1MLVKLFFKQWQAKIKSLSPARRIFLSFALVILVGSLLLSLPFLQQASSKAGYIDHLFTAVSMVCVTGLFTQSVASTYNGLGQLICM LLIQIGGLGILTFIGLFFMEGRQKLSYKDRQTIRDSFSFSNNQSLARFVRSIFITTFTIEGVGALLLMTRFIPRFGWGNGIFNSIFVAVSAF CNAGFDNFGGDSMMSFQTDWLVNLTLSALIITGGLGFMVWFDLATKARNQSGRRTLRFHTKVVLWLTAAILLFGTVTSLLTEFNNPAT IGSLPLGEKILVSFFQTVSMRTAGFASLDYTAVRPVTLFIYLLQMFLGGAPGGTAGGMKITTFLVLILLARKELLGLPHTNLGKRTIAPDL VQRSLGTAVIFQLTFLLGLFGLCLVTPDGQRFLYLVFEAVSALATVGVTANVTSTLNGAGLGIIMVLMFIGRIGPLTLMVSLNNYKAKKA DALQYAKADIIIG
2E-49	178	23.2	1.4E-48	175	16.1	2	1	G8PR69_PSEUV	Trk system potassium uptake protein	PSE_3992	Pseudovibrio sp. (strain FO-BEG1)	473	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Pseudovibrio, Pseudovibrio sp. (strain FO-BEG1)	911045	>tr|G8PR69|G8PR69_PSEUV Trk system potassium uptake protein OS=Pseudovibrio sp. (strain FO-BEG1) GN=PSE_3992 PE=3 SV=1MLGYLYVGLAAAMLIPAFVDVVSRNADWQAFIISALITGLVGMLLIVAMGGALRDGLDTRQTFILTTLCWVSLPAFGALPFLWLGI AYVDAAFEAVSGFTTTGSTVLTGLDSLPPGLLVWRSLMQWMGGVGIVVMAIVLLPFLRVGGMQLFQTESSDQSEKIVSRSIELIRLISM TYLLLTSLCIVLYWFSGMTMFDAFNHGLTTIATGGYSTHDNSFGYFTNPVTGWIAVVFMIVGALPFVLIIQALRGQPMLLWRDPQVRAF LWLVGLISLALTIYLGTSGNADSFGSAILQSAFNVISVVTGTGYAMGDYTSWGAPVIGLAFLLKFVGGCTGSTTGGIKVFRFLVFFGTVI AHMRRMVRPNRVISVSYGNTHLTPELTFSVLAFLVVYIGTVGILTLILSLFHLDLVTAVSAAATSVGNVGPGLGTMIGPAGNFAPLPDPV KWILCAAMLLGRLELFTVLILLDPDFWSK

2E-49	178	20.8	1.6E-47	171.6	14.4	2	1	A0A0F4RKL9_9RHOB	Trk system potassium uptake protein	TW80_06835	Loktanella sp. S4079	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Loktanella, Loktanella sp. S4079	579483	>tr|A0A0F4RKL9|A0A0F4RKL9_9RHOB Trk system potassium uptake protein OS=Loktanella sp. S4079 GN=TW80_06835 PE=3 SV=1MLDLRPVGYVVGLLVAALGATMLVSLFADVLAQNGHWPVFFESAVITILTGGLTAIACSNGVGHGLNLRQTFLLTSLVWLTLPVFGALPLMLGAPNASFTNAFFEAMSGLTTTGSTTFEGLEALPEGIKLWRATLQWLGGVGIIVVAMVFLPELRVGGMQIFRSEAFDTMGKILPRAGEIASSISVIYIWLTVACALAYGASGMGPFDALVHAMTTVSTGGMANYDSSFGEFGAVAHYVGTVFMILAALPFVRFVQLMAGTAKPLIHDTQIHVFLSVITICVLLITAWVWGREGEFTELAFREALFNVVSVMSGTGYSSADYMTWGTFPVVIFFFVGLVGGCAGSTACSVKIFRYQILFASIKAQVRQIHSPHGIFTPRFEGRAISEDVMNSVMAFFVAFILLLGVTAVLLGMTGLDFITSVSGAATAIANIGPGLGPEIGPAGNFAHINDTAKWILSIAMFIGRLEIMVVLTILSVKFWRT	
2.1E-49	178	19.1	2.6E-28	108.2	4.4	2	2	R5F3T1_9CLOT	Uncharacterized protein	BN723_00339	Clostridium bolteae CAG:59	430	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	1263064	>tr|R5F3T1|R5F3T1_9CLOT Uncharacterized protein OS=Clostridium bolteae CAG:59 GN=BN723_00339 PE=4 SV=1MKYLERQSPARIIAIGFLAVILTGSFLLMLPVCVKPGVRLHYVDALFTSTSAVCVTGLIAVDTADTYTALGQTVVALLIQIGGLGVTSVGVGVILALGKRVNLKERLLVKEALNLDSGRGIVCLVRNVLITTLCFEGVGAVLSFLVFSRDYPPLKAVGISLFHSVAAFNNSGFDILGGLKNLTGYQDNVLLNLTTAGLIIFGGLGFLVIMDLIKNRSFKKLCLHSKAVIVTTLILLASGTILWLTEDITWLGAFFTSVSARTAGFSTFPLGEFTSAGLLSVSVLMFIGASPGSTGGGIKTSTLFTLFHTIKGAACNEEPHAFHYRIPQEAFYKAAIVTALSALVVCLGTFFMCILEPGIPFEDILFEITSAFGTVGLSTGITPGLSSLSKLLEVLVMYIGRLGPLTIVTIWVFKPTKSVSYAEGSISIG	
2.1E-49	178	26.1	6.4E-24	93.7	9.3	2.1	2	R9SMU3_9EURY	Potassium uptake protein, TrkH family	Abm4_1600	Methanobrevibacter sp. AbM4	479	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobrevibacter, Methanobrevibacter sp. AbM4	224719	>tr|R9SMU3|R9SMU3_9EURY Potassium uptake protein, TrkH family OS=Methanobrevibacter sp. AbM4 GN=Abm4_1600 PE=4 SV=1MQALGAAFLVPIIISILYLETNCIIGFAITSALSLIMGTSLNKAFKDTDNIRLKHAMAVSALAWLWASILGAIAMKLILNFPLINGLFENMSTWTGTGLTMFTNVEVLPKSIQFLRSFEGWLGGLGVVIIGIGVLIRSGTAAAKLYKSEARDERIKPSIVNTMQKTIEIYVIYTIFGVVLYLLAGLPPFDAINLCFAMICTGGMSIKNANIGFYNNEIIYIISMIIMILGSISFPVHYKVFKTKGKAILDDVQFKVIILLIVVCTTLIFFSCKILPTDALFMVISATTSTGANCISSNQMMGWNSVGIIIILLLMFIGGSSGSTSGGIKVIRILTTIKGFEKTIMEILSPEGRIFKLKIQNKEITDRNVKESSSYIVIAATLILISWIILIANGYNGLDLSLFDVISACGNSGLSSGVTGPDMPIIVKLTLTFDMWLGRLEIIPVLVMLRGTLELFKPSKKQRQFINNIISKVNPYSKKI	
2.2E-49	178	19.4	5.2E-48	173.2	13.4	2.2	1	R6XTC3_9FIRM	Trk system potassium uptake protein TrkH	BN602_01265	Firmicutes bacterium CAG:313	519	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:313	1263017	>tr|R6XTC3|R6XTC3_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:313 GN=BN602_01265 PE=4 SV=1MNMKVIGKIIGKIMILEGILMCFPLIVSFIYLESYIYKLAFIIPIAILLIGGYLLQLLKPKRNGLYQKEGFAVCALVWIVMTIFGALPFMISGEIKNFINAIFETMSGLTTTGASILDGVEELNVTDLSHSILFWRSFTHWIGGMGILVFILIFIPESDDGSALHLLKAESPGPQVGKMTSKLKITTRILYLIYLGMTIIEVAILLFDRGNVVDGVTYKMDLFNALLTTFGSAGTGGFGFVANSMEFFSPYAQYVTATFLILFGINFTLYYLILIGKFKEVIKSEELKTYFGLIFSAIVIIMISVLRTRVSTIKELTPTLFEETFRATYFQVTSIITSTGYTTANFDTWPVVARTMLIVLMFCGAMAGSTGGGMKISRIVIVFKGMGTKIRKLINPRYVGKTKFDGKTLDDETINDVFGFVAMYFIIVIIVTLILGLDPSNGLITIIDGHEVKHDFLTNFSATLSCLSNIGPGLEAVGPYASFACYNNFSTLLLTLTMLVGRLEILPVLILFNPKTWRK	
2.2E-49	178	39.5	4.2E-49	176.8	27.4	1.5	1	Q2FWN5_STAA8	Cation transport protein, putative	SAOUHSC_02247	Staphylococcus aureus (strain NCTC 8325)	435	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus aureus, Staphylococcus aureus subsp. aureus, Staphylococcus aureus (strain NCTC 8325)	93061	>tr|Q2FWN5|Q2FWN5_STAA8 Cation transport protein, putative OS=Staphylococcus aureus (strain NCTC 8325) GN=SAOUHSC_02247 PE=4 SV=1MNKVHKPLYFYLMLFFSTTIIGALLLYLPFTGKKPISFLDALFIASSAFTVTGLSPVDIGSQFNILGEIVILLLIQIGGLGIVTVTLLTLVFLNRKISMKNRFLIMVTWNIDEPGGVIKLIKHLAIYSLVTELIGMICLCLSFIPKFGIGKGLFLSLFTSVSAFNNAGFALFKNNLIDYSSDPIVIITISILIIFGGIGHFVVIDFINCKKLSKLSLHSKLVLVTTTSILIIIGAITFFLLEQFNTMQHMGLVEKIGNSFFQSVTTRTAGFNSIDIASINKSTALMLMLLMFIGGAPLSAAGGIKITTFAVAFIFVVNYIRKENNVSVFNKEISDKHIKLSIVTINISFLFISIITFILSIINPNISLIKLLFEVVSAFGTVGLSMNLTTEYHGITKIIIIFVMLCGKVGLLTLLRTFIPPKSPKNYRYTKGQIYL	
2.3E-49	178	30.5	3.6E-49	177	21.1	1.3	1	A0A0C3NE01_9PORP	Uncharacterized protein	BA92_08970	Sanguibacteroides justesenii	604	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Sanguibacteroides, Sanguibacteroides justesenii	1547597	>tr|A0A0C3NE01|A0A0C3NE01_9PORP Uncharacterized protein OS=Sanguibacteroides justesenii GN=BA92_08970 PE=4 SV=1MFSTEIQYQFRKFYRITKTILEGAGRVVLFMASFVAIFLVVYKFGFKGASAYQEEIYSMYKGITNLFFIFLTIRFLLNFKLLREEKGFWLEVFFLIVLLGLIIAEYRFSIPEVITRNPVLYRLNRIVTYTVVLILSTIYLSKEFFVVLKSNVRPEMMFVISFLMLILIGTFLLKLPTATYEKISFIDALFTATSAVCVTGLTVLDTAKVFTPTGDVILLLIQLGGIGVMTFTSFFAMSFLGKTTFRDQLALKNLLNESSLNNIFRTLFYTVTTTLLIEAVGVYIVYLQIQDVEGIQDKFFFSLFHAVSAFCNAGFSTLPGNLYDPLVRNVYGLQVWLGLLIVFGGLGFPILFNYGSYFKYKIRCFLVYLFHGKRKVEYRAHIVSTTTRIVLPTTLVLLVLGMVFFLFFEDGNTLEGLSWQGKLATSFMASVTTRTAGFNNVDMAALHQATIFLILLMWIGASPMSTGGGIKTTTFVIALKNVIAILRGEDRVEIGKRQLTRLNVNRAQAIIFLSLAWTALAVMLLSILEPQGRFVQIVFEVFSALGTVGLSLNFTPAMSDAGKIIISLTMFVGRVGLITLLSGVVKQRQEKLYRYADDTVIL	
2.3E-49	178	27.6	4.3E-48	173.4	19.2	2	1	R5FEC9_9BACT	Trk family K+ transporter membrane protein	BN812_00200	Prevotella sp. CAG:924	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:924	1262938	>tr|R5FEC9|R5FEC9_9BACT Trk family K+ transporter membrane protein OS=Prevotella sp. CAG:924 GN=BN812_00200 PE=4 SV=1MINHKIVYKIIGSLLFIEAALMSGSLLVSLIYKEDDIFAFIVSIIVTTFFGFILKFMGRNAENRLSRRDSFLVVTLSWALFSLFGTIPFLTGGYLHSFTDAYFETMSGFTTTGATIIDNVEVMPHGILFWRSLTHWIGGLGIVFFTIALLPSLVDGSIKVFSAEATGPFKSKLHPKLSMSAKWIWVYLAISVTCMVAYKVCGMGWFDAINYSMSSVATGGFSTHNQSTATFHSAAIDYVTIFFCFLAGANFTLLYFSVAKLKIRQLWHDSEFKLYTIVVLAFTAFITYQLMAHKGYGLEHAFRSSLFQVIAFITTTGLFNEDVGLWPHITWVILSICMFIGACSGSTSGGFKCIRAVMVLKIVRNELRQRLHPNAVLSVKVSGQNVPDHNRVSLLAFLAAYILLVIIFSIVMICLGLDSTNAVTLTLSSIGNVGPTMGSQIGPTMSWSVVPDLGKWCCSLLMLIGRLEIFTVLVIFTPAYWQEN	
2.4E-49	178	23.2	1.5E-46	168.4	16.1	2	1	R5SXQ3_9CLOT	Potassium uptake protein KtrB	BN544_01837	Clostridium hathewayi CAG:224	431	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	1263067	>tr|R5SXQ3|R5SXQ3_9CLOT Potassium uptake protein KtrB OS=Clostridium hathewayi CAG:224 GN=BN544_01837 PE=4 SV=1MTEHLRKLSPGRIVVLGFAFVILTGSLILWLPISANEGVDVSYIDALFTSTSAVCVTGLIAVDTADTFNVFGRTVVALLIQVGGLGVTCVGVGVILLAGKKIGIHGRVLIRDSMNLTTVKGVVRLVEAILFMTLLFEGAGALLSFLVFSKDYPPLDALGISVFHSVAAFNNSGFDILGGLKNLIPYQSNVLLNLTTCGLIIFGGLGFLVIREIWEKHSWRKFSLHTKVVIATTIALLAAGTVLLKMTEDITWLGALFQSTSARTAGFSTYPIGAFSNAGLFVLAVLMFLGASPGSTGGGIKTTTTFVLMKSMFSAATNRHCSAFKRRIPTEVVSQAFLIAILALAVVCVQTFLMCIAEPELDFMKLLFETVSAFGTVGLSTGITPDLNAGAKLILITTMFIGRLGPLTMATVWSFKPKAAAWYSEESITIG	
2.6E-49	178	14.2	1.4E-48	175.1	9.9	1.8	1	E8RB55_DESPD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Despr_1545	Desulfobulbus propionicus (strain ATCC 33891 / DSM 2032 / 1pr3)	672	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfobulbus, Desulfobulbus propionicus, Desulfobulbus propionicus (strain ATCC 33891 / DSM 2032 / 1pr3)	577650	>tr|E8RB55|E8RB55_DESPD H(+)-transporting two-sector ATPase OS=Desulfobulbus propionicus (strain ATCC 33891 / DSM 2032 / 1pr3) GN=Despr_1545 PE=4 SV=1MELIVASRPSRAKAGIEGILLSLVPLPPLLTCLVGTAGSPPWSRAAALVAALACLAAALLLSRQFRLGKLFGFLALVGCALAGFPAFATEPLSALIGAVVVMQAGYFLSELAPHNLVEQRGHAVYRRLQRARSAVWTSLLLTLASFALNPARLWIGDAAVAGSTILTQLVVLHWIWTAHRGPARLSWALLPLTALAVSGIGLYSGCGQLVTLCLGLATLFFLPGATSGLEPREQWWEPFLNHPARVLITTFFVLCLAGALLLQLPWATTEQSITLVDAAFTSVSAVCVTGLTVLDTPRDFTLLGQGCILLLIQLGGFGIMTLTTVALHAMGKRLSLRQERLLTTLTETSHQDLIDSLLTIVRFTLLTELAGAVLLSLCFLDTADSLPQALWQGLFTSISAFCNAGFALQSANLVPYQSQPLVLHTVAALIVLGGLAPATCLLLPQWVRGKKIALAPRIALVTTTALLLTGTLCFLMFEWHNALDGLSLPDKLHNAWFQSVTLRTAGFNSIDLGNVLSPTLLIMLSFMFIGGSPGGTAGGIKTTTVGILAMTFWACITGRDEVIAQNRRIPQSVINRGITVLASGAMIWLVMVVMALVLTQPLPARALIFEATSALGTVGLSLGVTPHLDEIGKIIVMLTMFIGRIGPMTLFTLLSGDLQATGSRCPDARITLT	

2.7E-49	177	10.8	3.8E-49	176.9	7.5	1.1	1	F6FUT1_ISOV2	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Isova_0549	Isoptericola variabilis (strain 225)	461	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Promicromonosporaceae, Isoptericola, Isoptericola variabilis, Isoptericola variabilis (strain 225)	743718	>tr|F6FUT1|F6FUT1_ISOV2 H(+)-transporting two-sector ATPase OS=Isoptericola variabilis (strain 225) GN=Isova_0549 PE=4 SV=1MTVRWRRGRTLSEWADQAAREYPARLAMAVFAAVVAIFTLLLSLPFATASGERAPFADALFTATSAVCITGLTVVDTGSYWSD FGRVVILTGIKVGGLGVMTIASLLGLAVSKRIGLTQRLLTASEVKASKLGDVGTLLRIIILTATAIEVAIALVLLPRFLVLGHDLGEAVWHSV FYGISAFNNAGFVPTTDGLAPYAADWLVVVPIGVGVFIGSLGFPVIHNLLQTRGSGRRWFASWSLHSKLTITTSVALVAAAMVLIGALE WSNERTMGSQDFWHRLLTVFFTAVNPRSGGFSTVDAGALRQETWLVTDALMFVGGGSASTAGGIRVTTLAVMLLAILAEARGDRDI DVFGRRIPRDTLRLAIAVVFMGATAVLVSCIALLQLTDHDLGPVLFEVISAFATVGLSTGITPGLPDAAKYWLCALMYVGRVGLISLLGAL ALRDRRRIVRFPEERPIVG
2.9E-49	177	33.1	4.7E-49	176.6	23	1.2	1	R5UVF0_9BACE	Uncharacterized protein	BN535_01286	Bacteroides caccae CAG:21	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides caccae CAG:21	1263037	>tr|R5UVF0|R5UVF0_9BACE Uncharacterized protein OS=Bacteroides caccae CAG:21 GN=BN535_01286 PE=4 SV=1MKIYHKFLLYQNKLLKPYVRILLGLVEALTYLASLLLIVGVIYEHGFPLSVDEVAKIQVLYKAVWIIFLVDVTLHISLEYRSTKKQYRR LAWILSGLLLYLTLIPVIFHRPEEEGAILQFWEFLDGKFYHLVLLLIFSFLNLSNGLVRLLGRRTNPSLILAVSFLAIILGTGLLMLPRCTVNG ITWVDSLFTATSAVCVTGLVPVDVSTTFTTGGLVVIILLIQVGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLGSLLSTLLYIL GFTLVIEGIGMISIWFSIHGTLGMTLEGELAFAAFHSISAFCNAGFSTLSGNLGNSMVMTNHNWLFISVSFLIILGGIGFPILVNFKDIVLY HLRHFWKFVRTRKLERHKVSHLYNLNTRIVLIMTFLLLVTGTLAIAAFEWNASFAGMPVADKWTQAFFNATCPRTAGFSSVDLASLSV QTLLVYLVLMWIGGGAQSTAGGVKVNAFAVVVLNLVAVLRGSERVEVFGRELSHDSIRRSNATVVMSLGVLFLFIFILSILEPQASLMA LTFECVSALSTVGSSLNLTPNLCDASKLLVALLMFIGRVGLITLMLGIIKQKKNTKYRYPSDNIIIN
3.1E-49	177	20.8	2.7E-48	174.1	14.4	2	1	G8ULD9_TANFA	Potassium uptake protein, TrkH family	BFO_0519	Tannerella forsythia (strain ATCC 43037 / JCM 10827 / FDC 338) (Bacteroides forsythus)	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, Tannerella forsythia (Bacteroides forsythus), Tannerella forsythia (strain ATCC 43037 / JCM 10827 / FDC 338) (Bacteroides forsythus)	203275	>tr|G8ULD9|G8ULD9_TANFA Potassium uptake protein, TrkH family OS=Tannerella forsythia (strain ATCC 43037 / JCM 10827 / FDC 338) GN=BFO_0519 PE=4 SV=1MFKLNVRYIVKLLGMTHLLESFFMLAATGVAFGYGGCDFYPLLISTGIMSGTGLLLYLIGRKGNDYRSGRREGMLSVSFMWTMF SFLGMLPYLISGYIDNVTDAFFETMSGFTTTGATILTDIEALPKGLLFWRSLTQWQGGIGIIVFTVALMPIFGGTASQLFDAETPSITHER FLPRITQVAKRLFGIYLLITGVVFGLLWIGPMNAYDAINHALTTVSTGGYSTKNEGVAYWQSAYTEYIICFGMCLGATNITLLYFSLRRH WHKLVRDEELHWFYGVIATATVIVTIWLLVHQHETSIEKAFRQSLFQVASLISTTGYLTADYSTWGAFFTFIMLFISVVAGCAGSTSGG LKMGRFVILIKNMLNEFKKQTHPNAVLPIRMSGQIIPSHIVQRVSTFAFVYMGLILLGGVVLVLDGLNFEEALGISVSAVGNVGPALGQY TDGNFSALSAFPKWILSFLMMIGRLEIFTVLTILLPGFWKR
3.3E-49	177	29.8	7E-24	93.6	9.7	2.1	2	D7DQL9_METV3	Cation transporter	Mvol_1491	Methanococcus voltae (strain ATCC BAA-1334 / A3)	482	cellular organisms, Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanococcaceae, Methanococcus, Methanococcus voltae, Methanococcus voltae (strain ATCC BAA-1334 / A3)	456320	>tr|D7DQL9|D7DQL9_METV3 Cation transporter OS=Methanococcus voltae (strain ATCC BAA-1334 / A3) GN=Mvol_1491 PE=4 SV=1MKIFKKTDATGIMHELGLLMMFIGSLMIIPGIFAVYYSENWFIFVIPALAFILLGYLVNRFTKSISIKLKHAMVISALAWLMASMIGAV PLMLSIDYFGYIDGVFESMSAWTTTGFSIINDVESLPRSVQIWRSLQQWVGGVGVLVMVISILSKAGASAYYRAEAREEKILPSTLGTV KKIWHIYILYTVLGICMLYISGLNLWDAINICMCGISTGGMSVSNSSFPYGDVAKLIMVAIMYIGGVVSFSVHHNLLTGKDVHDIQTKASL PILSVSALILVLSSGISPIDALFTMVSAMTSTGFSTVSMNGLSNISLAVIIFVMIIGGATGTTTGGIKLMRFLIMGKAFYYKLKESVLPTGSV VYKKIGKNVMSGNLITDAFIIGFGYVVHYIAASMMLIFLGYDPYKSMFEAVSMVANMGLSVNIVDSAMHPLAKLTGIISMWVGRLEIIPVY VLLILPAYLKLKDMGNNSKNEVICQKNRR
3.4E-49	177	32.4	4.9E-49	176.5	22.4	1.1	1	A0A0C2TSV3_BACBA	Potassium uptake protein, integral membrane component, KtrB	SD77_3590	Bacillus badius	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus badius	1455	>tr|A0A0C2TSV3|A0A0C2TSV3_BACBA Potassium uptake protein, integral membrane component, KtrB OS=Bacillus badius GN=SD77_3590 PE=4 SV=1MKDPGKIKALKLSTFQLIVMLYLTGALFSTGLLLLPVAHKPGVDISLIDAAFVAVSALSVTGLSPVSVVDTFSTVGYFFILFILQVGG VGIMTLSSIIWILFGKRIGMRERQLIMADQNRTDLSGLVKLMIEIFLLILSIEAVGALILSIYFLQYYPTVSEAFLHGVFASISATTNGGFDIT GNSLIVFANDYFVQFINMVLIVLGAIGFPVLVEVKDFLTYRGPLKFHFSLFTKLTTTVYAILAVLGTILIYLIERNHFFIDKAWHESFFYSAF QSIAARSAGLTSMDLNEFSMATLLLLSTLMFIGASPSSVGGGLRTTTFAIAILSVYFYARGKNTIKIFNREVHPVDVQRAFVVITTGFFIW GGSIIFLSSLEPELPIVKIIFEVSSAFGTTGSSLGITGELSSAAKCLLITLMFIGRIGLFSLLFIIRGKEIKDGYHFPKERILIG
3.6E-49	177	22	4.9E-49	176.5	15.3	1.2	1	V9RAV3_9MOLU	Potassium transporter KtrB	OVS_01600	Mycoplasma ovis str. Michigan	484	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma ovis, Mycoplasma ovis str. Michigan	1415773	>tr|V9RAV3|V9RAV3_9MOLU Potassium transporter KtrB OS=Mycoplasma ovis str. Michigan GN=OVS_01600 PE=4 SV=1MFGSTVSQRIARIYILIILAGFGALNLPWVKTTNGQNGSDNWFSKLFTSVSAVTTTGLLSGSSLNCSFNFAGQLIVLILIQIGGLGL VTIWTILKQTFLKNKKYSIEDRINIHSERGGVIQGSSYVVTKSALITLLWIELFVASSLTFFFYFVDTNSDSQKTNLKGNFLSSFWAGIFH SISAINNAGLDTLDKTSISSYSRGWGVVLSIVFAACSMVGGIGYSALYEIKEWLHRKRNREKTKNILSLFTKISILMYLSITLLAGGGVVLT ELLANGAQTTSNGACSDNCTKLKKSEKIWQWIYLVISSRSAGFYGIDPKCLHEKSQWILLILMFIGASPASTAGGIRSITLFLMMGKIWT TMRGRRTLSIFSRSVEDQTIDNSYMVFFVSSALITLCSLGITHSEAGQGKGGFSHASLFEASSAFGTAGLSLGVSSKTTWVGHILLMFL MFIGQLGVPNSLVYYNKPRAARQNFSYPEEKLRIA
4E-49	177	41.1	7.6E-49	175.9	28.4	1.4	1	K8E5C1_CARML	Cation transport family protein (EC 3.6.3.14)	ntpJ BN424_2425	Carnobacterium maltaromaticum LMA28	457	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium maltaromaticum (Carnobacterium piscicola), Carnobacterium maltaromaticum LMA28	1234679	>tr|K8E5C1|K8E5C1_CARML Cation transport family protein OS=Carnobacterium maltaromaticum LMA28 GN=ntpJ PE=4 SV=2MQKLKKIMRQLVGRFSSIQMIVIFYFIAVVVAAILLSLPIFRIPGQELSFLDLMFTAVSTVSVTGLTTIDLGSTYNRAGVGLLMVLFQ LGSLGIMMISTSFFILSKRKISLKQRQLIMVDMNQPNLSGIVRLIRNALAIIIWFQLIGGLILSVYFYYNYYTIHDALFYGFYTAVSAVTNSG ADITGTSLIDFSQDYFIQTIVMFLIVVGGIGFPVLIELKAFFNYKKKKHDLPFRFSLFAKLSMWAFLILFVVGSVLIWLLEFDDFFKGMNFT ESAFYSMFFSVSTRNAGLLTTPLGNFSDGTLLLFAALMFVGASPSSVGGGIRTTTLAIVVLYLFSFIRSRENINIFGRRIHNDDVKKSIVV LNLSIALCFFSVLVLSVTEKHSLVSLVVEVASAFGTTGLSMGITPSLSIFGKIMIMILMFIGRVGMLYMLMLLVPKEKRDANYLYPTEKIIIG
4E-49	177	31.1	6.8E-49	176.1	21.6	1.2	1	R6RYJ6_9BACE	Potassium uptake protein KtrB	BN532_00619	Bacteroides finegoldii CAG:203	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides finegoldii CAG:203	1263045	>tr|R6RYJ6|R6RYJ6_9BACE Potassium uptake protein KtrB OS=Bacteroides finegoldii CAG:203 GN=BN532_00619 PE=4 SV=1MKIYHKFLLYQNKLLKPYIRIILGLVEALTYLASLTLIVGVIYEHGFPLSVDEIAKIQVLYKAVWIIFLIDVTLHISLEYRSTKKQYRKLA WILSGLLYLTLIPVIFHRPEEEGAILQFWEFLDGKFYHLILLLVFSLLNLSNGLVRLLGRRTNPSLILAVSFLAIILGTGLLMLPKCTVNGIT WVDSLFTATSAVCVTGLVPVDVSTTFTTGGLVVIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLGSLLSTLLYILGF TLVIEGIGMVSIWFSIHGTLGMNLDEELAFAAFHSISAFCNAGFSTLSGNLGNPMVMTNHNWLFVSVSFLIILGGIGFPILVNFKDIVLYH LRHFWRFIRTRKLERHKVHHLYNLNTKIVLIMTFLLLVIGTLAIAAFEWNASFAGMPVADKWTQAFFNATCPRTAGFNSVDLASLSVQT LLVYLVLMWIGGGAQSTAGGVKVNAFAVVVLNLVAVLRGTERVEVFGRELSHDSIRRSNATVVMSLSVLFLFIFILSMLEPQASLMALT FECVSALSTVGSSLNLTPSLCDASKLLVALLMFIGRVGLITLMLGIVKQKKNTKYRYPSDNIIIN

4E-49	177	11.8	1.1E-48	175.5	8.2	1.5	1	D2B520_STRRD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Sros_4696	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	452	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	479432	>tr|D2B520|D2B520_STRRD H(+)-transporting two-sector ATPase OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_4696 PE=4 SV=1MMRRSVSQALLDRFQHPAQVIVTAFATAAAVGAGLLATPLAAESGTATRLIDALFTAVSAVCVTGLVTVDTASHWSAFGEAVILV LIQAGGLGIMTLATLFAMMISGRIGLRARMWAQAETKAPQMSDLRRVIGNVVLFTLACEALTAVALAARFAVGYGEPPGRAAYLGLFH AISAFNNAGFGLWPDNLVRFATDGWICLPIAAAVIVGGLGYPVVFELRRSWRHPKRWSVLTRITVATTLVLLLLGFLVFTITEWSNPKT LGPMDAPGKLLAGFFTGVMPRTAGFNSLDVAGMYPTSWLTTDVLMFIGGGSAGTAGGIKVTTFAVLAYVLWAELRGETHVNAGHRR LAATVQRQALAIALLGVALVIISTYALLALTPHSLDQVLFEVISAAATVGLSTGITADLTAAGQILIALLMFAGRVGPATLFSALALRARRRR YELPEEKVIVG
4.1E-49	177	27	1.1E-47	172.1	18.7	2	1	F7YQB0_VIBA7	Trk system potassium uptake protein	VAA_01773	Vibrio anguillarum (strain ATCC 68554 / 775) (Listonella anguillarum)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio anguillarum (Listonella anguillarum), Listonella anguillarum serovar O1, Vibrio anguillarum (strain ATCC 68554 / 775) (Listonella anguillarum)	882102	>tr|F7YQB0|F7YQB0_VIBA7 Trk system potassium uptake protein OS=Vibrio anguillarum (strain ATCC 68554 / 775) GN=VAA_01773 PE=3 SV=1MLNLRPISFVIGLVLSKLALFMYVPTLVAFFTGTGGFLDFAQAVIITHIVAFICLSLGRTAHFKLSVRDMFLITSLVWTVASAFAALP FVFINHISFTDAYFETMSGLTTTGSTVLSGLDNMPPSILLWRSILQWLGGVGFIVMAVAVLPMLNVGGMKLFQTESSDWSDKSSPRAK TVAKNIVLVYLVLTLLCLIGYILTGMTLFEAINHSFTTLSTGGYSTSDGSMNHFSNGAHWVATLFMFLGGLPFLLFVAAARKQNIKVIIKD AQVRGFAYLFLIASLIIALWLNLKLGYYWLDALRVSMFNIVSVVTTTGFGLEDFTAWGALPSTLFIFLMAAGACSGSTSGGIKVFRFQIA MTLLNKQIMKLVHPSGIFVQRYNHRPVNDDIVRSVVAFGLTFFITVIAIAGALSAMGLDPVTSISGSITAVANVGPGMGSVIGPTGNFAP LPDAAKWVLSLGMLMGRLEILTIIVLFFPAFWRR
4.1E-49	177	34.5	7.2E-49	176	23.9	1.3	1	T2KQM3_9FLAO	Potassium uptake protein, integral membrane component, KtrB	BN863_34250	Formosa agariphila KMM 3901	580	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Formosa, Formosa agariphila, Formosa agariphila KMM 3901	1347342	>tr|T2KQM3|T2KQM3_9FLAO Potassium uptake protein, integral membrane component, KtrB OS=Formosa agariphila KMM 3901 GN=BN863_34250 PE=4 SV=1MKLKTLQNLYRFTDILILFFLIFDFGFTLEDEYKPLRVPVYTSILLLLITFNTFKFFQYSKSDPIRKTVKFNIGILVTTLVAASTAYYLN QHLPPIEQLMRPKVIFELGLFFYLLMRLTFLIKYIYKIYFNPAILFAGSFFLLILMGALLLMLPKVTVNGISFLDALFTATSAICVTGLAVLDT GKDFTQLGQTLIVILIQIGGLGILTFTSFFAYFFKENSSFRESMYLKDYTSTENLQDVFKIGAQIVGITLGIELIGAILYTSIDSITTIENKVFF SIFHSISAFCNAGFSTSSSSFYEPSLRYDYSLQWVLMLLIIIGGIGYSFIFNSYSYLKRSFLNLFRTKNKVSRTVRVFTLNSKITIVTTSVLLI FGFIFFYFAETNFSLQDHDSVFGKITTAMFSSVTPRTAGFNTVDYGQIATPSLLIVIFLMWIGASPGSTGGGIKTSTFAIASLNIFATARG KKRIEINTREISSSTVNRAFSIIFISLMTIGTAILLLLFFEPEKDLLAIAFECFSAYSTSGLSMNLTPTLSDPSKYVIIAVMFVGRIGLLNLLFG MLGQVEQKFYQYPQENILIN
4.3E-49	177	22.1	5.7E-49	176.3	15.3	1	1	R6EV28_9FIRM	Uncharacterized protein	BN538_02250	Lachnospiraceae bacterium CAG:215	461	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	1262985	>tr|R6EV28|R6EV28_9FIRM Uncharacterized protein OS=Lachnospiraceae bacterium CAG:215 GN=BN538_02250 PE=4 SV=1MSKEKKSDGRLSLNTMQMIALGFLGVILLGGVLLWLPFSNQEPIAFADALFTSVSAVCVTGLLTIVPATQFTVAGKVILLLLIQIGG LGVIACTVAFFLILRKKITMKERVIIQQTYGLDTLSGLVKYMLLILKGTFLVEGIGACCYAFRFVPEFGVVKGIAYSIFQSISAFCNAGIDILG DQSYKGYATSPIVNFTTMALIVLSGLGFLVWHDIGKNVFRVWKQKLPKKRMWTRLRVQSKIVLVMTGFLIFFGMIGFFFLEYHNPETM GTMSAGEKLMASAFQSVTSRTAGFAAVSQGDLTPASKLLGCILMFIGGSPGGTAGGVKTTTVALLLLVCISVLRGSKDAECFGRKIAS AVVRSAVTIILVTFLIWVGGIAVITILEPNVDFLDIMYEATSAIATVGLSADLTPLLGRGSQAVLMFLMYAGRIGPVTMALVFAGKARKSS QLRELPEKHIMIG
4.6E-49	177	16.7	6.3E-46	166.3	11.6	2	1	R5GWM0_9FIRM	Uncharacterized protein	BN555_01488	Firmicutes bacterium CAG:24	434	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:24	1263012	>tr|R5GWM0|R5GWM0_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:24 GN=BN555_01488 PE=4 SV=1MPLTTFLKKLSPGRIIALGFLFCILLGSLLLMLPCSLQPDIALPYLDALYTATSAVCVTGLNVIDPGSTFSPFGQFVLGCLIQIGGLG VASIGVGIMLAMGKKINLKERRVIRDAMNLDSGKGLIRFVKAIFYTTLLIELLGTFLSFPVFFRDYPLPRAIGLSLFHSVASFNNSGFDVLG NGTSLIPYQKDVLLNLVTCALVIAGGIGFPVIFELPLKHFSRERLSMHTRVVLSTTFALLLFGTLLLKLTESISWLGAFFYSVSARTAGFST YNLGDFSTAGLLVVSGLMFIGASPASTGGGIKTTTFFVLLSGIYSAATNHSERAFHNAIPKDAFRKASVISILAAFLVMTASYLMLIFDPQ LSLRDVLFEMISAFSTSGLSTGITPQLSAQSRILSIIMMYIGRLGPLTVASLWYFTIGERVRYPEGTIAIG
4.7E-49	177	20.9	2.3E-48	174.3	14.5	1.8	1	L7VKS8_CLOSH	Trk system potassium uptake protein TrkH	trkH Cst_c02450	Clostridium stercorarium subsp. stercorarium (strain ATCC 35414 / DSM 8532 / NCIMB 11754)	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminiclostridium, Clostridium stercorarium, [Clostridium] stercorarium subsp. stercorarium, Clostridium stercorarium subsp. stercorarium (strain ATCC 35414 / DSM 8532 / NCIMB 11754)	1121335	>tr|L7VKS8|L7VKS8_CLOSH Trk system potassium uptake protein TrkH OS=Clostridium stercorarium subsp. stercorarium (strain ATCC 35414 / DSM 8532 / NCIMB 11754) GN=trkH PE=4 SV=1MNIRMILRIVGIVLLIEGTGMVPSFIVSLIYAQGDAIAFLISILITAASGFLLYRIPVRNGKFYARDGFAAVALGWTAISLFGSMPFVIS GAIPSFIDAFFETVSGFTTTGSSILKDIESLPKGILFWRSFTNFMGGMGVLVFTLAVIPSIAPGSIHIMNAESTGPSKEKLVPKLKETVRIL YTIYVVMATCQIILLLIAGIPLYDSLVHAFASAGTGGFSNRNLSVGAYGNVYAEVIITVFTILFGVNFGLYYRLINGDIRGFFKDEEFRFYIG TILVSITLITIDLYTHRFFTLGQSLRHSSFQVGTIITTTGFSTTDFNLWPTFSKIILVMLMLFGACAGSTGGGIKCIRILLLLKTARREIARIIH PRAVHTVKVSNRVIDENTVNKTLSYFFIYMSLFFISVLLISLDGKDLVTSATAVLATLSNIGPGFEAVGPTGNFSDFSAFSKLVFSFDMLA GRLEFYPIFVLISPEAWKRGNI
5E-49	177	43.9	5E-49	176.5	30.4	2	1	G8LR03_9FLAO	K uptake transporter subunit KtrB	ktrB BLBCPU_536	Blattabacterium sp. (Cryptocercus punctulatus) str. Cpu	584	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Blattabacteriaceae, Blattabacterium, Blattabacterium punctulatus, Blattabacterium sp. (Cryptocercus punctulatus) str. Cpu	1075399	>tr|G8LR03|G8LR03_9FLAO K uptake transporter subunit KtrB OS=Blattabacterium sp. (Cryptocercus punctulatus) str. Cpu GN=ktrB PE=4 SV=1MIQINFRKLLPFLTPIIFLYIIISLGWKTSINTFINVVILIVMMLILSFFHFFILFEKKLDKGYQSMIFLSFFVFIPSILFSMGKFFFFSHETI TDVRGVLLTSLTIYILIRITYFMRKIYVKINNPIFIFITSFVFLSFLGSLFLMLPSSTVKKISFIDALFTSTSAVCVTGLGVLDTSKDFTYLGKIII LTLIELGGLGILTVTSFFSYFFRDGFSFREGVYISNFLNTKTTNNVLFLAVKVVLLTLIVEIVGTLLIYLSIKNERSIIEYDSPLFFSIFHSISAF CNGGFSTLNRGFYSESVRFNYLFQFIIACLLILGGIGFNILFNFFTYIWLTLKKYFYKIFKDEYFRCPVHIFTLNTKIVLFTTFSLLFFGTIFY YISEYHYSLSEHSSIFGKWIISFFSSATSRTAGFQVLNMEKWTPLTILFTIFLMWIGASPASTGGGIKTSTFALALMNIISLSIGKDRLEIQ KKEISSKSVRLAFAIIILSLIIIYISIFIILFLDPKKDILSISFEAFSAFSTVGLSLGITPNLSNGSKLVLITLMLLGRIGVFNIMIGLLKRNRINSSY YYQYPQGNILIN
5E-49	177	26.6	6.3E-49	176.2	17.7	1.7	1	B1KCW0_SHEWM	Trk system potassium uptake protein	Swoo_0034	Shewanella woodyi (strain ATCC 51908 / MS32)	480	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella woodyi, Shewanella woodyi (strain ATCC 51908 / MS32)	392500	>tr|B1KCW0|B1KCW0_SHEWM Trk system potassium uptake protein OS=Shewanella woodyi (strain ATCC 51908 / MS32) GN=Swoo_0034 PE=3 SV=1MLNLRPLLFILGIFLSTLTVFMFIPLIFALFYGEETVGAFMISSLFTGTCASACIHQGRSRNLHLNIRDMFLLTSLTWLIVSFFAAMPF TLYHGINYTDAFFETMSGITTTGSTVLSGLDSMDHSILIWRSLLQWMGGIGFIVMAVAVLPFLNVGGMRLFRTESSDWSDKAIPRTQD MAKHLFYIYILLTVLCGIAYHLSGMNWFQAINHAMTTLSTGGYSTSDSSMAAFSNQAHWVGVVFMAAGGLPLLMFVNSIQQRSLWV WNDAQVKGFILFISLVSMSLAFWLWLGHEMSPLDALRLASFNVVSVVTTTGYGLTDYTAWGALANIAFLFLMFAGSCSGSTSGGIKIF RFQIAGAIMREQLKQQFHPSGVFKERYNNRIISDDIVRSLVTFILLFAFVIVLLSIILVLTGLDPMTSFTGAITAVTNVGPGLGDVIGPAGNF STLPDVAKWALAIGMLLGRLEILTVAVLFHPSFWKY

5.3E-49	176	30.9	9.9E-49	175.5	21.4	1.4	1	A0A0C7P483_9BACT	Cation transporter	DTL3_1380	Defluviitoga tunisiensis	516	cellular organisms, Bacteria, Thermotogae, Thermotogae, Petrotogales, Petrotogaceae, Defluviitoga, Defluviitoga tunisiensis	1006576	>tr|A0A0C7P483|A0A0C7P483_9BACT Cation transporter OS=Defluviitoga tunisiensis GN=DTL3_1380 PE=4 SV=1MSSYREFLILRYKAIFRNVGNITIGLSLLILAISFFALINDGNKLFFSFFIPAILTFLTGLFFRIISRGERKKELSIHDATVTVFLVWSLAI FLSSLPFIFANYLNFTQAIFESTSGWTGTGLSMFLDVEILPKSILLWRSVTQYVGGAGFAIITVIIAGSVGAGIYQAEGRSDNLVPNLRES AKIILRIYIIWAIIGTILLMTIGKLPFFDSFNHTLTALATGGFSTKNLSIGAYNSLSVEIIIMILMIMGATGFGIHYAAILMVKNFFRYRKELKKG VLTKLEFKEKIRSEPFLKNPEPRLMFVILLIFSTLLFLFSLLQMYGIKEGIINSIFQSISSLTGTGFSTVSFINWNSFGLLILTLLMIFGGMMD STSSGLKLYRIYIAFELVLNQIKSFFKPSGTTFYLEVYKGISRKKIDVDAIKNVIVVFTAYFVTYFVGVFVLLGYGYSLPNVLFELASTVSN VGLSVGITGPQAPLGVLWTEIIVMYLGRLEFFVIINSCIKIIRDLREVTTF	
5.4E-49	176	14.5	5E-47	169.9	10.1	2	1	F2IZB3_POLGS	Trk system potassium uptake protein	trkSL003B_0097	Polymorphum gilvum (strain LMG 25793 / CGMCC 1.9160 / SL003B-26A1)	480	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, unclassified Alphaproteobacteria, Polymorphum, Polymorphum gilvum, Polymorphum gilvum (strain LMG 25793 / CGMCC 1.9160 / SL003B-26A1)	991905	>tr|F2IZB3|F2IZB3_POLGS Trk system potassium uptake protein OS=Polymorphum gilvum (strain LMG 25793 / CGMCC 1.9160 / SL003B-26A1) GN=trk PE=3 SV=1MDFRAVALPIGRLLIVVAAFMMIPAGADLVARNPDWVVFATSALVSGCIGALLSAALARRAFPFRPRETFLFVNAAWFTFSFAGA IPLYASGLDISFADAFFEAASGLTTTGSTILTGLDGLPPGILLWRSLLQWIGGIGIVVIGIWLLPGLRVGGSQLFAIESSEKTAKPYGRIEP FLFRLLGLYLVLTLSCGLLYYLAGMTAFQAINHAMTTISTGGFSTSDSSMGQFSSLAILWIAIVYMLASGMPFLFLIKLAERREVPHPEQ VRVYLLFVAGASFLAFLSMHATTEDTPFRQFTHSVFNIVSVVTTTGYATTDYLQWGNFAIALFFVLTFFGGCSGSTSGGFKIFRVAILLS SIRAILKRIVHPHRIIEPRFGGAKVTPGVMEGVLIFSVLYAGTFAVFAAVYAALGLDLATALSASATALANVGPGVGPIIGPAGTFQSLSD PVKWLLAVQMILGRLELIGGILVLTPDFWTET	
5.5E-49	176	13.6	6.8E-48	172.8	9.4	2	1	A0A0F2QMN1_9RHOB	Trk system potassium uptake protein	VR75_05580	Hyphomonadaceae bacterium BRH_c29	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, unclassified Hyphomonadaceae, Hyphomonadaceae bacterium BRH_c29	1629720	>tr|A0A0F2QMN1|A0A0F2QMN1_9RHOB Trk system potassium uptake protein OS=Hyphomonadaceae bacterium BRH_c29 GN=VR75_05580 PE=3 SV=1MQLRPLLLAIGIMTVLLGVAMLPCALIDWADKRPEAHVFAVSSFGAVFIGACLWVLSRGEVERTGQREGFLLTVMVWTILPLVAA IPFIASGMSFTDAVFESVSGLTTTGSTVLTGLDSLPRGLLLWRAIIHWFGGIGIIVTAIAILPQLRVGGMQLFQLENSDRSGKFLPRVTDI ATYLGLTYLIVSVACALSYYVCGMTWFDAICHAMATMSAGGFSTHDASFGYYNDTAAPWAAIIFMLIAGLPFSLMAMLVLQGRVMQFV HDPQPRLYFALAIIFSALISFLYFANTSGLLDEGVIGGLKLSIFNTVAVMTGTGFATAPYDTWGIPVQALILGITFVGGCAGSAACGLKIFR LEIAGKALFAYSRRMVQPHRRAPIKYGGKTVDEDTLQSVMVFMFLYFATFLISAALLGLDGLDAMTAITGAATTLSNVGPGLGPINGPS GTFQGFSDFATWICTINMLLGRLEFVVVFVVLTRRFWRG	
5.9E-49	176	22.7	2.8E-47	170.8	15.8	2	1	Q6AQC1_DESPS	Trk system potassium uptake protein	DP0723	Desulfotalea psychrophila (strain LSv54 / DSM 12343)	485	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfotalea, Desulfotalea psychrophila, Desulfotalea psychrophila (strain LSv54 / DSM 12343)	177439	>tr|Q6AQC1|Q6AQC1_DESPS Trk system potassium uptake protein OS=Desulfotalea psychrophila (strain LSv54 / DSM 12343) GN=DP0723 PE=3 SV=1MNPASIANVFGALLLVTGGSMLLPIICALCYNDGDVKALSISALIIVAVGLPLKRVFRNHDTLSIRDGLFIACFGWVVISAFSALPFMI HGTIPSFCDAFFEMMSGYTTTGSTILTDIEKVPHGLLFWRSQTHLLGGMGFLTLTIIFLPHGVGGARIFRAESSPGQVITGDRFMARNR DTMVFLWAIYLGLNILQTLLLYLGDMSLFDSLCHAFGTISTSGYSTMNDSVGAFHSSYIDWVTIVFMILGGVTFVLFYEALRGNWRSVID NTEFRYYLAVLLFFCLSVSWILYVDGIYDSFPDALRYGTFQVVSILTTTGFATANYLTWPQSTQLFLVIVCFIGACAGSTTSGIKIVHYVLI FKHMYVSIKRIFLQPMYVSTTRLNGKPVDASVVDLAVCYFIVNILMVFFGGMVMILLEDITAVTAFSSVVATLMNIGPGFGQVGPVDNFA FFSDTGKWFLAWNMLVGRLEMFSVLVIFYPAFWKR	
6.1E-49	176	30.9	8.1E-49	175.8	21.4	1.1	1	A0A0F5I037_9BACI	Potassium uptake protein, integral membrane component, KtrB	QY95_02454	Bacillaceae bacterium MTCC 8252	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, unclassified Bacillaceae, Bacillaceae bacterium MTCC 8252	1123719	>tr|A0A0F5I037|A0A0F5I037_9BACI Potassium uptake protein, integral membrane component, KtrB OS=Bacillaceae bacterium MTCC 8252 GN=QY95_02454 PE=4 SV=1MKESKKIRLSKLSSFQLIVLLYLVGALFSTVLLMLPIAHKPGVDISFIDTMFVAVSALSVTGLTPVSIVNTFSTTGYVFILFILQVGGV GVMTFSSVVWIIFGKKIGIRERQLIMADQNRTDLAGLVKLMKEIFLLILAIEAVGAIILGVYFLPYYPSASEAFLHGLFGSISATTNGGFDIT GQSLVIFADDYFVQFINMILIILGAIGFPVLVEVKNYLTYRGPIKFHFSLFTKLTTIVYAILAVFGAISIYLLERSHFFADKSWHESFFYSTFQ SVAARSGGLTTLDLNEFSTATLLLLAILMFIGASPSSMGGGLRTTTFAIAILGVYFYARGKDTIKLFHREVHPIDLRRASVVMTTGFVIWFI SIILLAFFEPDLPILKIVFEISSAFGTTGFSLGITDDLSTPSKLLIMTLMFIGRIGLFSLLFIIRGKTIKDTYHFPREREIFIG	
6.1E-49	176	34.4	2.4E-48	174.3	23.8	1.8	1	Q4FP56_PELUB	Trk system potassium uptake protein	trkHSAR11_0211	Pelagibacter ubique (strain HTCC1062)	481	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Pelagibacterales, Pelagibacteraceae, Candidatus Pelagibacter, Pelagibacter ubique, Pelagibacter ubique (strain HTCC1062)	335992	>tr|Q4FP56|Q4FP56_PELUB Trk system potassium uptake protein OS=Pelagibacter ubique (strain HTCC1062) GN=trkH PE=3 SV=1MSNYKTVFFTLGVLQIILGISMMIPIAQLIYSEIDSSFIGGSIISIIFGVLFFLTNLNHDKKLNLQQAFLLTALSWLSIAIFGSLPFIFSTL ELSITDSFFESMSGITTTGSTIISNLESAPRSILLWRAMLQWLGGIGIIVMAITLMPIMNVGGMQLFKISSNDSSEKLLPKSKEISLRLIYVY LGLTVLCASTYKIFGMNIFDSLTHSMTTIATGGFSNYNESIGYFNSLPIEISSMVFIILGSLPFIAYIKFLNGDRKILISDVQIKSFLKIIIFSIIIL FIYLLFHNKDFSQINIRTICFNVSISILSGTGYVTGEFDGWGNFPLIFFLTLMFIGGCAGSTTCGIKIFRIQILYLFIINQLKKIIYPKGIFIIKYDK NNVDDKFMASIISFIFLYLVIFFLITAFLSLSGLDFVTSISGAATSISNVGPGLGSTIGPNGNFSSLPEISKWILSLGMILGRLELFAILVLFLP SFWRN	
6.1E-49	176	32.1	6.1E-49	176.2	22.3	1.5	1	Q5LG26_BACFN	Putative transmembrane K+/Na+ uptake protein	ktrBBF9343_1134	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	611	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides fragilis, Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	272559	>tr|Q5LG26|Q5LG26_BACFN Putative transmembrane K+/Na+ uptake protein OS=Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343) GN=ktrB PE=4 SV=1MKIYHKFFLYQNKLLQPYVRLLLRLMAIITYLASIMLIVGVIYEHGFTLSAHEVTKIHLLYKTVWIIFLIDVTLHILLEYRDTKKNFRKLA WILSWLLYLTLIPVIFHRPEEGGAILHLWEFLHGYFYHIVLLLLFSLLNLSNGLVRLLGRRTNPSLILAASFLVIIILGAGLLMLPRCTVDGV TLSWVDALFTSTSAVCVTGLVPVDVSATFTPAGLTVIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLGSLLSTTLYIL GFTLVIEGVGMLSIWFSIHGTLGMDVQDELAFSAFHSISAFCNAGFSTLPGNLGNPMVMTNHNWLYITVSLLIFGGIGFPILVNFKDIIV YHARRFWRLIRTRQWDNHRVHHLFNLNTKIVLIMTVLLLVFGTVAIAIFEWNHSFAGMSIADKWTQAFFNATCPRTAGFSSVDLTSLSI QTIMLYIVLMWIGGAAQSTAGGVKVNAFAVASLNLIAVLRGTERVEVFGRELSHDSIRRSNAAVVVSLGILFVFIFILSILEPKMSIMTLTF ECVSALSTVGSSLNATPLLCDESKLLVSLLMFIGRVGFITLVLGIVKQKKNTKYRYPSDNIIIN	
6.3E-49	176	30.8	7.7E-49	175.9	21.4	1.1	1	Q891T4_CLOTE	Potassium transport protein	CTC_02281	Clostridium tetani (strain Massachusetts / E88)	387	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium tetani, Clostridium tetani (strain Massachusetts / E88)	212717	>tr|Q891T4|Q891T4_CLOTE Potassium transport protein OS=Clostridium tetani (strain Massachusetts / E88) GN=CTC_02281 PE=4 SV=1MVTVDTGTHWNYFGKTVIMLLIEIGGLGFMSFGTLVALILGKKITLKERLVMQEAYNFFSTQGVVKMVKYILIFTFSAQLGGALILS TQFIPEFGIGKGIYYSIFHSVSAFCNAGFDLIGNYSSITGYYNNSVIILTISLLIIIGGLGFYVWQEIYNFRGFKRLSLHSKICISTTSILIVVGA ILMFLFEFNNPGTMKNMGLKGKMLSSFFASVSPRTAGFNSISTSDMTTAGKFLTIIIFMFIGGSPGSTAGGIKTTTAGLMFMTILCVIKGR EDTEIFQRRVPKDNIYKALAIVVIGFLIVTIVTMLLSITDSAHSFENLLYEATSAFGTVGLTLGITTKLSFAGKIIIALTMYAGRVGPLTLALAL SNKKSSRNIKYPEGKVLVG

6.8E-49	176	11.4	9.3E-49	175.6	7.9	1.1	1	Q47MI5_THEFY	Putative cation transporter	Tfu_2302	Thermobifida fusca (strain YX)	469	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Thermobifida, Thermobifida fusca (Thermomonospora fusca), Thermobifida fusca (strain YX)	269800	>tr|Q47MI5|Q47MI5_THEFY Putative cation transporter OS=Thermobifida fusca (strain YX) GN=Tfu_2302 PE=4 SV=1MGERLRGLRSKAVRLSHRLPFGVLFPRASRILWGKPARILASLFGAVILLGTGLLLLPVAQQTQVSPVEALFTATSALCVAGLSITDPAHDWSFFGQLVILGLIQVGGIGIMTLASLLGMVVIRRFGLRMQLSVQSEQRTLNVGGTREVVWRIAATSVICEAVLALLLIPRMWLGHGLPLPEAVYSGVFHSVSAFNNAGLSLYPDSLTRFAGDPLVLVPIMAATVLGGLGFPVLLELRKHLRTPRRWSLHTKMTVWTSLLLFVGGMVVVTALEWGNPATLGPLPWPHKLLDGAFHGVMPRSGGFNVVPVDAMESHTLLVTIMLMFVGGGSAGTAGGIKVSTFAVIWLVVWAEIRGHPQVHAFGRRLSAGAIRQALSLTFLSMTVIALATVYLTAVSPFSSQEVLFDVVSAFGVVGLSTGVAAGLPQHGQVLLVILMFAGRLGPITFASALALRERTRRYDLPEGRPVIG
6.8E-49	176	28.6	1.1E-47	172	19.8	2.2	1	E1RH54_METP4	Cation transporter	Mpet_0504	Methanolacinia petrolearia (strain DSM 11571 / OCM 486 / SEBR 4847) (Methanoplanus petrolearius)	478	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanomicrobiaceae, Methanolacinia, Methanolacinia petrolearia, Methanolacinia petrolearia (strain DSM 11571 / OCM 486 / SEBR 4847) (Methanoplanus petrolearius)	679926	>tr|E1RH54|E1RH54_METP4 Cation transporter OS=Methanolacinia petrolearia (strain DSM 11571 / OCM 486 / SEBR 4847) GN=Mpet_0504 PE=4 SV=1MYELVSPVDLSVVLKYTGRLMMAIAVVLAVPMAMAIVFMESYTAAVYGLTAVLVACGGFILVKVLPDGELRWKESLVIAAIIFPFIALLNAFPFALSTGMSLSDSFFEAVSGITTTGLSVAPADVGPVFLFARSWLQWVGGIGIVILVLSVLVQPGTSAFRLFSANVGENRIGPNVMATARILVKIYLIITAIAFILLLLSGMPVFDSICHALSAVSTGGFSTGSDSIASFPGFFIPLVIAAGFLMGAIDFGLYTRISGGLSGLKEIISDIQFRYFVVVLVAGFLFLLFTMSEGMSFTEALSASAFQAASALSTAGFSTVDIGALSDSSKAVLTVLMWIGGCTGSTAGGIKIMRLVILFAIVYLVFIRFFLPKEALTPLKVGGDVVEPDQIYHILTYVILYVLVILVSGFIFMLHGIGTGDAFFEVSSALGTVGLSTGITGSGMPDLMKWTLIVDMVLGRIEIIPVCILLFPRTWIRR
6.9E-49	176	24.2	4.7E-48	173.3	16.8	1.8	1	A0A085BY47_9RHOB	Ktr system potassium transporter B	IV89_05455	Sulfitobacter sp. CB2047	428	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Sulfitobacter, Sulfitobacter sp. CB2047	1525218	>tr|A0A085BY47|A0A085BY47_9RHOB Ktr system potassium transporter B OS=Sulfitobacter sp. CB2047 GN=IV89_05455 PE=4 SV=1MLVLIYLTMVVLGGLILWTPLANTAGISLSDALFTSTSAVTVTGLAVVDTGTAFTGFGQAVIALLIQMGGLGLMTFAVLVLSALGIPLGMPQRIILREDLNQPSIYNLTSLVMAILKIAILAELIGAALMAFVFVPEFGLAQGLWHSVFLSISAFNNAGFALFPDSLSNWVSDPIINVVIPALFIIGGIGFIVLADIWEKRSWRRLSLHSKLMLTGTVVLILLAWALFAALEWRNPATLGQFGSLGSKLWASWFQAVTPRTAGFNTLDYAEVHESTALMTMTLMLVGGGSTSTAGGIKVTTLIVLILATVAFFRRSTSLHAFGRSMGPDEVFKVMALTTISILLVLTGIFIMSIKHDGEFIDLAFEATSAFGTVGLSRGATAELDSTGRAMIMLMMFLGRVGPLTIGFFLATQSVPRVRYPEGKVYLG
7E-49	176	27.3	3.1E-26	101.3	5.4	3	3	F4BUL7_METCG	Cation transport protein	MCON_0192	Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) (Methanothrix concilii)	523	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosaetaceae, Methanosaeta, Methanosaeta concilii (Methanothrix soehngenii), Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) (Methanothrix concilii)	990316	>tr|F4BUL7|F4BUL7_METCG Cation transport protein OS=Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) GN=MCON_0192 PE=4 SV=1MLDILGLMLVLLGSLMLIPGIVAAIYKEPAGVMAFGLSSFITISAGLIIRRIGEKGEVTNKEAFVIVALAWLLATIFGSLPFIFLGLDETDSLFETMSGFTTTGATILTESDSHGYWIINSTAADNSLAHNLILTLFKSPEVLLSGIGKISTSDSGFNNYVESTFYGLLFWRAFTQLLGGMSIILLFIAILPHLGVAGRQLYYVDTSREALTPRVRSTAKIFWGIYLGFVALQTILLWSAGMSLYDSLCTSFTTISTAGFSPLSAGIVAYDSVLIEAILIIFMIVGATNFILHYQFIYKNDFLCYFKDPEFRLYLFLQATATALIVLWGGVDGGVLHRIRLAGFHVVSVGTTTGFTNTFDYAHWSSAANMVIIMLMLIGGCAGATAGGIKVLRVLLIKKYARRELMKMLHPKAVIPIKLNDISVSEGVLISVLFFTIIYLIIFFACSLLLTITESGNQNFDLLSAISAVATCMASVGPGLGVVALDFSQVTPVGKMIAIFCMYIGRMEILPVMLLFIPNLWKD
7.1E-49	176	26.1	7.6E-48	172.6	18.1	1.9	1	Q8DY99_STRA5	Cation uptake protein, Trk family	SAG1591	Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R)	475	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus agalactiae, Streptococcus agalactiae serogroup V, Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R)	208435	>tr|Q8DY99|Q8DY99_STRA5 Cation uptake protein, Trk family OS=Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R) GN=SAG1591 PE=4 SV=1MIRFLLSKLLLIEAALLAIPLTVGLIYREPQSVMMSIVITMIILIILGLLGSLFKPKNYHIYTKEGMLIVALCWILWSFFGALPFVISGQIPNIIDAFFEVSSGFTTTGATILDDVSVLSPALLFWMRSFTHLIGGMGVLVFALAIMENSKNSHLEVMRAEVPGPVFGKVVSKLKKTAQILYLLYLLMFAVFAVILYFAGMPFFDSIIIAMGTAGTGGFAVYNDSIAHYNSPLITNLVSIGMLIFGVNFNLYYLLLLRKIKAFFGDEEELKTYLRIVAIATFMIALNVIGMYDNFRQGLEHIFFEVSAIITTTGFGVTDITRWPLFSQVILLFLMFIGGSAGSTAGGFKVMRSLILAKIARNQVLSTLYPNRVMSLHINKSVLDKNTQHGVLKYLTIYLAIFMALVLVLTLDTNDFLVVISAAASCFNNIGPLLGSNETFSFFSPFSKLLLSFAMIAGRLEIYPVLLMFIPKTWSKL
7.2E-49	176	20.4	1.5E-48	175	14.1	1.4	1	E3F2L1_KETVY	K+ transporter Trk	EIO_2085	Ketogulonicigenium vulgare (strain Y25)	447	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Ketogulonicigenium, Ketogulonicigenium vulgare, Ketogulonicigenium vulgare (strain Y25)	880591	>tr|E3F2L1|E3F2L1_KETVY K+ transporter Trk OS=Ketogulonicigenium vulgare (strain Y25) GN=EIO_2085 PE=4 SV=1MKTAVKGWAARFLSLPPPLVVAGIYIATITMGASLMMLPMAQAMPMRWSDAFFMATSAVTVGLAVVDVGSHLSLLGQAVLVTLVQLGGLGLMTFAVLILEIVGRPVGLMGEAYLREDLKQNALWRVGRLVRRIAVVVFAIEAVGIAILCLSFIPDLGFWPGLWAAIFHGIGAFNNAGFSIFRTGLMEYVADPIVNLVIPALFITGGIGYFVLHDLIYKRRWRYWSLNTRIMLAGTAVLIPWSVLMFAALEWTNPATLGGLDGIWPRIAASWFQGVTPRTAGFNTLDISGIHDSTAMLFISLMLIGGGATSTAGGIKVTTFVVMILATIAFFRRQTQLHIFGRGIGPDEVLKVMAIVAVSLVLVFCGVFLLSLSHDGHFLDIAFEVASAFSTTGLSRNYTPELNDFGRCVIMVIMFIGRLGPLTLGFFLATQLSPRVRYPQERIHIG
7.7E-49	176	26.9	3.3E-48	173.8	18.7	1.8	1	Q7MGK2_VIBVY	Trk system potassium uptake protein	VV3229	Vibrio vulnificus (strain YJ016)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio vulnificus, Vibrio vulnificus (strain YJ016)	196600	>tr|Q7MGK2|Q7MGK2_VIBVY Trk system potassium uptake protein OS=Vibrio vulnificus (strain YJ016) GN=VV3229 PE=3 SV=1MVNFRPVLFVIGLVLSKLALFMYVPTLVAFFTGTGGFLDFGQAVLITHFAAFICLSIGRTAHFKLSVRDMFLITSLVWTIASAFAALPFMFINHISFTDAYFETMSGITTTGSTVLSGLDNMAPSILLWRSILQWLGGIGFIVMAVAVLPMLNVGGMKLFQTESSDWSDKSSPRAKTVAKNIVVVYLVLTGLCLIGYLLTGMNLFDAINHSFTTLSTGGYSTDGSMNHFSNGAHWVATLFMFLGGLPFLLFVSAMRKRRLDALIKDAQVRGFTYLFLGTSLVISAWLVIRDGYTIADALRVAMFNIVSVVTTTGFGLEDFTAWGALPTTLFAFLMMAGACSGSTSGGIKIFRFQIAMTLLNKQIMKLIHPSGIFVQRYNQRPVNDDIVRSVVAFGLMFFITIIAIAGGLSAMGLDPVTSISGSITAVANVGPGMGSIIGPTGNFAPLPDAAKWLLSFGMLMGRLEILTLLVLFFPAFWRR
7.7E-49	176	31.7	1.2E-48	175.3	22	1.3	1	H1Z7J3_MYROD	Cation transporter	Myrod_0794	Myroides odoratus DSM 2801	596	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Myroides, Myroides odoratus (Flavobacterium odoratum), Myroides odoratus DSM 2801	929704	>tr|H1Z7J3|H1Z7J3_MYROD Cation transporter OS=Myroides odoratus DSM 2801 GN=Myrod_0794 PE=4 SV=1MPLFYLKDVVVNKIKYFLVRLPFLLSFISLFVLIFDLGFNTLNDYHSHLHHLYNVCLTFGMVIIIYRYYSAFQKKKFPSLGVKIFDVFSVLLFLTLVVVRWQPEHTIRFFDSNAVIFFAVFIMLVREFSMLQLNLKKTKLTPPQLFIVSFLLIIFIGAFMLSFPKATVTPGSLRYIDALFTATSAVCVTGLSTVDIGSQFTLFGKTVMIFLMECGGLGIMTIASYFSYFFRGKASYGNQLVLKDVSSIDKLGDVFGTLKRIMIISGIIQLIGMIAIFISIRNQVFDSIYERIFFAIFHGVSAFCNAGFSTLPENLYTLEYRFNYPLQLIIAGLFIMGGLGFPIVYNVYKYVKHLIVNRILPFSLKEASVYVVPRVINLSTKIILITTAGLIVGGTVLVYLLEYNNTLSEHHGIGKVVVAFFTATSPRTAGFASVDNNLFTVPTFLILMLLMWIGASPISTGGGIKTTTFAIALLNIWTLMKGKTRIEVNRREVDESAVRRAFAIIFLSLFSIGIALFALTFFEPKIDIIRLAYEAFSAYSTAGLSTGITAKLADPSKVTLIMLMFVGRVSILTILIAISKKETITNYRYPTEEILIN

7.8E-49	176	32.5	2.5E-46	167.6	22.5	2.1	1	A0A061AAT3_9MOLU	Potassium uptake protein, integral membrane component TrkH	trkH Aocu_04310	Acholeplasma oculi	434	cellular organisms, Bacteria, Tenericutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Acholeplasma, Acholeplasma oculi	35623	>tr|A0A061AAT3|A0A061AAT3_9MOLU Potassium uptake protein, integral membrane component TrkH OS=Acholeplasma oculi GN=trkH PE=4 SV=1MKKLTPYAVIILSFFSIVLTGSILLVLPISKSGVGALSYVDALFISTSAVTITGLSPVSNLSILLSPFGKVVLAALIQIGGLSVVTISVFV MYLIGAKIGIGNRVLIKESLNQNNMSGMVKLVKRIVVFTLVIELVGFIINMFVFLPDYELMDAIGISAFHAISSFNNAGFDILGDQSLQAYN GHVLLNLSTAILIMLGGLGFIVLNDLFEKRSYKRLMIHSKVVLMMNLVLWVSGILIFKFSQNHQESLTWLEAFFLSVTARTAGFTTINMQ ELSGITTLILMVLMFIGASPASTGGGIKTTTVYTLFVGARSYARGTQTTTHQRLIGHETRHKASILLTVSILIIIVSTSILLSVENISLDEALFE SISAFANVGLTINITAGLNDISKIMLSIVMFIGRVGPLTMISLLNTNWYRKDLQSLEYIEEKMMIG
8.2E-49	176	28.5	2.6E-48	174.2	19.8	1.7	1	Q6F1V1_MESFL	K+, Na+ uptake protein bound cytoplasmic subunit	Mfl166	Mesoplasma florum (strain ATCC 33453 / NBRC 100688 / NCTC 11704 / L1) (Acholeplasma florum)	564	cellular organisms, Bacteria, Tenericutes, Mollicutes, Entomoplasmatales, Entomoplasmataceae, Mesoplasma, Mesoplasma florum (Acholeplasma florum), Mesoplasma florum (strain ATCC 33453 / NBRC 100688 / NCTC 11704 / L1) (Acholeplasma florum)	265311	>tr|Q6F1V1|Q6F1V1_MESFL K+, Na+ uptake protein bound cytoplasmic subunit OS=Mesoplasma florum (strain ATCC 33453 / NBRC 100688 / NCTC 11704 / L1) GN=Mfl166 PE=4 SV=1MNGGNQMSTNTNKSNKSKWLHFKKNKEQKNKFDPHKAFLKLKTWWPLSKVSGRIFLIYLFIVLFGGFLLCIPGIVVNNDLNGYD FRWDYLTGIFTASSAFSDTGINIIDPSHDYTFWGQLILLILIEMGGIGVLTLKIILFISINKKISLSDTVVAQSERGNDVKSSTIELIKDGFIFLT FIQLIAAGVLFFLFFFSEPATQSLNGTELNVVSPYHNFIKSIWFAIFHSTSAINNAGYDLLSTNSLQPYNIEGHQAYAIQIVFLLEWVIGGL GYPTFHDIKRKMRARRVGQKVKFSLFTKLNFWVYSTLFVVGPLLIFLSEYSNQTNSLIFNYYTYDVDPLTQMPINVIVTEAKPTFVVAM DIIFNTTACRNAGFSTVPINDFNASSKTILSSLMFIGSAPSSTAGGIRTTTFAIILLSTWAIIRNKSYTSAFKKVIPAETVRRSFSVFFISVFIL TIVIILIYFDSNGFLTPGIENGVAGELVQNQGDASIVQILTLITSAYGTVGMNPFTQHQMYNFGVLTKLLIILCMFLGQLGISNTLLAFIKPS RKTNFKYLEEDVTIG
8.9E-49	176	21.2	2.6E-47	170.9	14.7	2.1	1	R6Q818_9CLOT	K+ transporter TrkH	BN597_00932	Clostridium sp. CAG:306	483	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:306	1262794	>tr|R6Q818|R6Q818_9CLOT K+ transporter TrkH OS=Clostridium sp. CAG:306 GN=BN597_00932 PE=4 SV=1MRLTYIFTSLALVLRCIALVILAPAAVAVYYKDWHSIIPFVGASLLSFVLSFLFTRKSDTFESLNDIKKSEALCVVTLSWLSFSIIGML PYIYFGLSPLNSLFESVSGITTTGATILTSFDYPKAMFFWRSMSQWLGGMGIIVLFIAILPQFAVAGRQMFFAEAPGPTEDKITPRIRHT ASAVWTIYLLVTLMEIILLRLAGMPLFDAFCNSFSTLAGGGLSPNPLSIMGYGSNLINWIMIFFMFIAGVNFALIYKVYLNKKPSLLFQDEE FRTYTGIIFVFSLLIAGALYLNNTYNIFEAITSGFFQTTSIIITAGFASVDFQQWHLSAELLLFCLFFIGACAGSAGGGMKVVVRWLFLFKYL RRELAKILHPNAVYPIKINKTIVPVEVIQQIIAFIFFYFLIFGISAFFIAILENNTLLGVTGSITTLGNVGPAFGALGPMGSFDVLHPFSKIICIF NMLIGRLELIPFLAMLHPDFWNIK
9.1E-49	176	15.5	2.1E-48	174.4	10.7	1.5	1	M9X4R8_MEIRD	Cation transporter	K649_04950	Meiothermus ruber (strain ATCC 35948 / DSM 1279 / VKM B-1258 / 21) (Thermus ruber)	473	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Thermales, Thermaceae, Meiothermus, Meiothermus ruber, Meiothermus ruber (strain ATCC 35948 / DSM 1279 / VKM B-1258 / 21) (Thermus ruber)	504728	>tr|M9X4R8|M9X4R8_MEIRD Cation transporter OS=Meiothermus ruber (strain ATCC 35948 / DSM 1279 / VKM B-1258 / 21) GN=K649_04950 PE=4 SV=1MTGTVYVALGGVMGLLGLVDALLGEDARGFFVGAGLGLSLGMLLRRLGSPQAEPRRAEALLTVAGLWIMVPLLGAIPFWISGG LSYLDALFEATSGFSTTGATILADFNQFSYGLFFWRSLSQWFGGMGILLLFIVVLPHLALAGRQMFFAETTGVQKQQLTPKLHQTASYI LRVYLLLTFVTLAAYLVTGVPLFEAITNTFSSVSAGGFSPNPQSFASYTPLTQWIAAGVMFLTGVNLLLQYRAIFGREYTALLRDPEFRA YALIVLVVGLLMATVLYARHDYDLEPALRHAFFQTTSIITGTGFASADFAQWVIPAQTLLVMLMFIGGSAGSVGGSIKVIRWLIIGALVRR ELQRALHPQAVLPLRVGNKNIGEDVMRSVAAFITLYVSLFALGVLVMGILEEDFVVAFSASAAAIGNVGPGLGAVGPMAHYGDLHPISK AVMIFQMWAGRIELIAVFSLFTPELWRRLRA
9.7E-49	176	16.4	5.5E-48	173.1	11.4	1.8	1	F8A371_CELGA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Celgi_2565	Cellvibrio gilvus (strain ATCC 13127 / NRRL B-14078)	457	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Cellulomonadaceae, Cellulomonas, [Cellvibrio] gilvus, Cellvibrio gilvus (strain ATCC 13127 / NRRL B-14078)	593907	>tr|F8A371|F8A371_CELGA H(+)-transporting two-sector ATPase OS=Cellvibrio gilvus (strain ATCC 13127 / NRRL B-14078) GN=Celgi_2565 PE=4 SV=1MAAGAGVLWRARELVDRSARQSPARLALGVFAAVIALITVLLEAPWATAHGESAPFIDALFTATSATTVTGLVVVPTGEYWSTW GLVVILVAIKIGGLGVMTLASLLGMAVSRRIGLTQRLLVSSETKVTRLGEVGSLVRTVIVTSTILEVAIAIVLLPRFHMYDEDWGTAAWHA IFYGVSSFNNAGFVPTPEGLSPFVSDWWVLLPIIVGVFIGSLGFPVILNVARSLREPRRWSLHAKLTITTSLGLVVAGSVLVAAFEWTN GGTFKDLDPSGTALASLFAGVMPRSGGFSTVDVGQMHESTWLLMDALMFVGGGSASTAGGIKVTTLAVMLLAIVAEARGDRDVEAY GRRIPRDALQVAIAVSLISATFVLVSSLLLLAMTGERLDTILFEVISAFATCGLSTGITPELPDGAKYVLTILMFIGRTGTMTLAAALALRNR RRVIRLPEERPIIG
1E-48	176	31.4	1.6E-48	174.9	21.8	1.2	1	A9BID6_PETMO	Cation transporter	Pmob_1921	Petrotoga mobilis (strain DSM 10674 / SJ95)	514	cellular organisms, Bacteria, Thermotogae, Thermotogae, Petrotogales, Petrotogaceae, Petrotoga, Petrotoga mobilis, Petrotoga mobilis (strain DSM 10674 / SJ95)	403833	>tr|A9BID6|A9BID6_PETMO Cation transporter OS=Petrotoga mobilis (strain DSM 10674 / SJ95) GN=Pmob_1921 PE=4 SV=1MPSYTYFLKLRYKAIFRNTGNIIIGLSVLILLVGSTAFIYDSFKDFLPFLITGILSFLSGGMFRFIGSGEKRKELNTQDAVVTVFFVWT LAIFLSSLPFIFSGELNFSQAVFESTSGWTTTGLSMFSDVEVLPRSILIWRSVMQFIGGAGFAIITVIAGTMGVGIYQAEGRSDNLVPNL RESARIILRIYLSWAVIGVLLLMFVGKLSFFDAFNHTLTGLATGGFSTKNFSIGSFGSLKVEIIIMLLMIMGGTGFGVHYAGLLMIRNFIRN RRDYRSKKISLLELREKIKSEPFLKNPEIKTMFIILVISFLLLFAFTTVEIYGVGNGLVHSAFQSISALTGTGFSTVAFSNWNYFGLLILTILM ILGGMMDSTSGGLKLFRVYIAFKLIINQIKEFFKPSGTTFYIEVYKGVSRKKIDLNSIKNVLVVFTMYFITYFIGVFILLAYGYPLHNALFEY ASTLSAVGLSTGITSNQAPVGVIWTQTLGMYLGRLEFFVIINALIKLFKDLRDIF
1E-48	176	23.3	7.8E-47	169.3	16.2	2.1	1	D5E7D5_METMS	Cation transporter	Mmah_1577	Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP)	477	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanohalophilus, Methanohalophilus mahii, Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP)	547558	>tr|D5E7D5|D5E7D5_METMS Cation transporter OS=Methanohalophilus mahii (strain ATCC 35705 / DSM 5219 / SLP) GN=Mmah_1577 PE=4 SV=1MYELVSPINTYAVAKYIGYLLMIFALVLTVPVGAALLLGDFSSAYYYALTSIITGMLGFAIYKVLPEYELETKDAIVLAALAFPLISVVS SIPMSLTTGMPFIDAFFESVSATTTTGLSVAPTDAGPVFLFSRAWSQWVGGIGIILIALSVFVNPGASAFRIYKAYSGEKPIKPTVVSTT RLIGKIYVAITVIATAILLLSGMSLFDAIAHGLSSVSTGGFSTRPGSVGEFGHILVPLTIAIACIMGAINFELYPEVLKNPKKIAENLELRYFFI IAGIGTLIFTFSILQDPGIQLGTTEIAFQVISALTTAGFSTLDMSVLPDSSKAALSGLMWIGGSIGSTAGGIKIFRLIVLAGLIRFVFLRFFLP KETVTPFRIRGRIIENDEMYQITVFVALYVVIVIVSTYILMLHGIGTENAIFEVSSALGTVGLSAGVTDATMPSILKLVLCFDMLLGRIEIIPIL ILFMPRTWIQGAR
1.1E-48	175	37.7	1.1E-46	168.8	26.1	2	1	A7GMT3_BACCN	Potassium uptake protein, TrkH family (EC 3.6.3.14)	Bcer98_1115	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cytotoxicus, Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	315749	>tr|A7GMT3|A7GMT3_BACCN Potassium uptake protein, TrkH family OS=Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98) GN=Bcer98_1115 PE=4 SV=1MKAEKKQGVYNRSIRLSPPQILATGFFCLIVVGGILLKLPFATKESISWVDAFFTATSAATVTGLGVVDTASTFTMFGQIVIMFLIQ TGGLGLMTIAILIVWVLGKKIGLRHRLLIGEAFNQTNIGGLVKLVKRVFIFSICIEGIGIIFLSIRFIPEFGFSKGMYYSIFHVIAAYNNAGFAL WPDNLMRYVGDPIINIGICSLIVIGGLGFTVLIDMWYSRSFQKLSLHSKIMIVGTIALNVIGMIAIFILEYNNVKTLGPLSVNEKLWASFFQ GITPRTAGFNTVDYGGMEESSILFTMILMFIGAGSVSTGGGIKLTTFVILITSVISFFRKKEDIVLFQRTIKMATVTRALAIVVASQILIFVAV FLLMLTEKFSFIQLLFETISAFGTVGLTMGITAKLSAVGKCIIMFVMFCGLIGPLTLVFSLARPAKQKIRYPSEDVFTG

1.1E-48	175	28.4	1.6E-48	174.8	19.7	1.3	1	A6LA36_PARD8	K+ uptake protein	BDI_0780	Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	606	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides distasonis, Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	435591	>tr|A6LA36|A6LA36_PARD8 K+ uptake protein OS=Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152) GN=BDI_0780 PE=4 SV=1MNLKNIYFSWLIYWGKMKGLLNGIAEAIILLASLASFFVLIYQFGFVQTPDSVHILERSRPFILLAFFTGITLRYVVRFQEIIQEKMLY LDISIYFLLFAVLSSKIFFKDAIAHSLPYLSFLTKPLFVYVLLLLLSTIHLSRQTFTLMQTRIKPSLLFLLSFVFVILVGAGLLSLPNATTHRIPF IDALFISTTSVCVTGLTTVDVATSFTHIGHIIIMILIQIGGIGVMTFTSFFALSFMGKSSFTSKMMLKDMLNEDRTGGLFRVILNILFVTLFIE GIGAYFIYMDVRGSLPGGTQQELFYAMFHAVSAFCNAGISTLSGNMYDPLVADKYNLHFWIAMLIIFGGLGFPIVFNYLKLLHHLLMNGI KILIGKQKHYIHTPRIINVHTYIVVISTLILLITGTAFYLFFEYDNTLGDLPLRGKLANAFLGAVTPRTAGFNVADMATLAPPTLMLTLILMVI GAAPMSTGGGLKVTTVFVALVTTLNAAREKDKVEVRKREIAPFAIRRAFAIIMMYFMWVAIATWVLSYTEKGAPLFSLLFEVVSALSTV GLSIDYTPHLTPIGKIIIISTMLVGRIGVLAFLVSFCKEYTKKDYTYPQENILM	435591
1.2E-48	175	18.4	1.8E-48	174.7	12.8	1.2	1	R6XY83_9FIRM	Uncharacterized protein	BN815_00931	Firmicutes bacterium CAG:94	462	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:94	1262989	>tr|R6XY83|R6XY83_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:94 GN=BN815_00931 PE=4 SV=1MPGLSELQHRINERIKATPPVRVIVISFVLIILAGTLLLMLPISSKVGGATPIGALFTITSATCVTGLVVGDTFTLWTPFGQGVILACI QLGGLGLSTLAIGFSLLVRRKLGIREMKLASESSGGSGLDIAGLLKLTIIFTFACEAIGACLLAIRFVPMFGVNGIWPSIFCAISAYCNAGF DVLGFVEGNSSMTAFAGDPLVSLTISFLIIIGGLGFIVVQDIYLCKIQPRFHHKDTTRLNFHSQICLRVTIVLLLFGTLGFFLLEFGNTMEG LNLLEKLNCAFFQSTNTRTAGFASVDIAAQYEFTKVLSVLLMFIGACPGSTGGGIKTTTLTVLLFTVICTIRGKDEVVVLRHRFSTPAVYK AFSLTFIAILLVFIDAGVISSLNPDILYIDCLYEATSAFGTVGLSASVTPNLDPISKLILIFTMFIGRVGPLSFGLSILMRHKPKGDSIYPEGR MIIG	1262989
1.2E-48	175	10.8	1.2E-48	175.2	7.5	2.5	1	Q1QVI6_CHRSD	Trk system potassium uptake protein	Csal_2171	Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)	493	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Chromohalobacter, Chromohalobacter salexigens, Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768)	290398	>tr|Q1QVI6|Q1QVI6_CHRSD Trk system potassium uptake protein OS=Chromohalobacter salexigens (strain DSM 3043 / ATCC BAA-138 / NCIMB 13768) GN=Csal_2171 PE=3 SV=1MAVIHPRIMRSLAVSAPVVRILAVLLLVLAVLMVVPLIVLTLEGDPDRMAFLLSIAVVAGAALTMLLITRGVEILLRPRQMFILTTLSW VLVSACASLPLILGAPQLSFTDAVFESISAITTTGSTVLVGIDDLSDGLKLWRGLMQWLGGIGIIVMAIAILPFLKVGGMRLFQTESSDWS DKVLPRAGGIAKASGAIYLGGTLLAMLTYWLAGMTPLDAVVHAMSSMATGGFANSDASFGVYQDRPLILWLASFFMLCGALPFVLFIR ALRDTPQVLWQDQQVRGLLSLLLVVILGLTLYRVVGGVAFFEALTQVAFNVISVVTTTGYASDDYTQWGPLIVAAFFYLTFVGGCSGS TSGGMKIFRFQIGAIMLFTQLRHLVHAQGVFAQRYNGNPLSDEVVRGVIAFSFFFFLTIAGLALGLALLGLDLVTALSGAATAVANVGP GLGPIIGPAGNFAPLPDAAKWLLSLGMLMGRLEILTVLVLLTPTFWRK	290398
1.3E-48	175	20.9	2E-48	174.6	14.5	1.2	1	D1BB90_SANKS	Trk-type K+ transport system, membrane component	Sked_06990	Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	458	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Sanguibacteraceae, Sanguibacter, Sanguibacter keddieii, Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	446469	>tr|D1BB90|D1BB90_SANKS Trk-type K+ transport system, membrane component OS=Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74) GN=Sked_06990 PE=4 SV=1MASGVSGRIWAGRELVDRMARQSPARLAITVFAAVIAVFTGLLSTPFATTSGVRAPFVDAFFTATSAVCVTGLVTVPTGTYWSP FGQAVILVAIKVGGLGVMTLASLLGMAVSRRIGLTQKLLTASETKTTRLGEVGSLIRVVIITSTTIEVLLALLLVPRFLVLRETTGEALWHG IFYAVSVFNNAGFIPTEEGLTPHAGDWLLLVPIIVGAFIGALGFPVILNVARNRRQFRRWSLHAKLTVVTSALLVVFGAVMFIALEWTNA GTFGSMSVGDKLLSGVFMSVMPRSAGFSTVDIGQMHEASWLITDALMFVGGGSASTAGGIKVTTLAVMMIAIVAEARGDRDVEVFG RRIPRDTLRLAVAVVFVGATAVLVSCLLLLEITGWSLDVVLFEVISAFATVGLTTGVTHELPEAGKYVLIALMFIGRTGTMTLAAALARLRD RRRVIRLPEERPIIG	446469
1.3E-48	175	0.6	1.1E-33	125.9	0	3.6	2	Q4WRH0_ASPFU	Potassium transporter, putative	AFUA_1G16340	Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	616	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Neosartorya fumigata (Aspergillus fumigatus), Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) (Aspergillus fumigatus)	330879	>tr|Q4WRH0|Q4WRH0_ASPFU Potassium transporter, putative OS=Neosartorya fumigata (strain ATCC MYA-4609 / Af293 / CBS 101355 / FGSC A1100) GN=AFUA_1G16340 PE=4 SV=1MLHKSGPLSLANWFQVDLSSLNTFQQSIIFALLILGHAILVSITVLFVRKRAFQLKFKTISESSAARNLFRQSALGFLKPAGKTKTH TSQPEEPHSPEGSHVSAIENSPSESPNAVDNDHIRWDNDDQITIGNIQPRHHHHHHNHHHHRVFPMAGVGARLDLNNHPRNVAPTV PLDGEPDEIPRLKGILRDTQKYFASKGFISRNSQFHGLTLEEREKLGGVEYKAVSFLLVIVLLYWATFLIIGIVGVGGWLEVNHPEIPRAN GLSPFWTGAFFAVSAFVNSGMSLLDANMTALQTKEYSLPLLFTIYHLDYEALNGRSAIMGDLEGHFGFYPRPSQKGMHHGVYTNLFP VRHTWYLLGTIIILNGIDWAGFEVLAIGNKEIETLPTGYRILDGLFQALVRLSVPSIGDHEVRLVYVFQCSFTDCHRNTNVYEERSLGIYA SDEPLDAHSSRSPNIVMSLIRHHLLGRQDVSTVESSRSYFVHQQLRSQLSHDVWWIALAVLFITIAESPHYSDNPIAYSTFNIIFEVVSA YGCVGISVGFPGRNYSFCGSWHTISKLILAAVTLRGRHRGLPVAIDQAVMLPNESLAWAEEEDAVLRREQTRTYGSDKMPVGTV	330879
1.3E-48	175	24.5	9.9E-48	172.2	17	1.9	1	S5R663_9STRE	Putative potassium uptake protein TrkH	KE3_16054	Streptococcus lutetiensis 033	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus lutetiensis, Streptococcus lutetiensis 033	1076934	>tr|S5R663|S5R663_9STRE Putative potassium uptake protein TrkH OS=Streptococcus lutetiensis 033 GN=KE3_16054 PE=4 SV=1MNKSMVRYLLSKLLLIEASLMLIPVIVAFIYHEDIRVINSLVITIGMLVIIGLLGVAFKPKNYHVYTKEGLLIVALCWILWSFFGALPFV LSGQIPSIIDAFFEMVSGFTTTGATIVPDVAVLSHSLLFWRSFAHLIGGMGVLVFALAIMENSKNSHLEVMRAEVPGPVFGKVVSKLKE TAQILYVIYLSMFAILVVILMVAGMPAFDSVITAMGCAGTGGFGVYNDSIAHYNSSLITNIVSIAVLLFGINFNLYYFLLLRKFKAFFKDEEL RTYIGIVMIATALIWLNVSGLYPSTGKALENSLFEVANVMTTTGFGVTDLTVWPLFAQVILLFLMFVGGSAGSTAGGIKVMRTLILTKIAR NQVLSTLYPHRIMTIHINEQPLDKEIQHGVLKYLTLYVFLLLGLTLMLSLDNNNFMVVVSAATSTFNNIGPMLGTSQTFAIFSPFSKLLMS FAMIAGRLEIYPMLLLFIPKTWSKY	1076934
1.4E-48	175	30.5	1.4E-43	158.6	20.3	2.8	2	D6YSG8_WADCW	Putative potassium uptake system, Trk family	trkH1 wcw_1669	Waddlia chondrophila (strain ATCC VR-1470 / WSU 86-1044)	492	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Waddliaceae, Waddlia, Waddlia chondrophila, Waddlia chondrophila (strain ATCC VR-1470 / WSU 86-1044)	716544	>tr|D6YSG8|D6YSG8_WADCW Putative potassium uptake system, Trk family OS=Waddlia chondrophila (strain ATCC VR-1470 / WSU 86-1044) GN=trkH1 PE=4 SV=1MLFSAVLYFFGRESQGHLHRRESILTVALIWILTPGISSLPFIFSDTLSNPIQAYFESVSGFTTTGASVLVGKEYNNHGQEKKIQLII EGETPVVYEFFGTVPPVRNKEGQIIAEGIEAVSKAVLFWRSLTQWLGGVGIIVLFIAVLPSLGIGGKQLMSSEIPGPTEISLATRLRETAS ILWKVYLFFTVLQTVLLRLTNPDVTWFDAITISFSTLSTGGFSVKNASIGAFKNPITEWVVILFMIVGSLNFAIWFNIIRKKIYKIFDVEIIIYF LVILLSCLFSTFSILNTDQQLLTGEFVNINSVKDAARFATFQIVSANSSTGFSTVNFDLWPYRVQVLMLVLMYVGGMSGSTCGGIKILRN YILFKITQFKVESIFRPETIKIMRIKHRKISQEVSIKSLVFFVLIISISVMATLLFILDGLDPESALTFVGCSINNTGFSFRAYGPMQSCAFLSN FGMILSCFLMIAGRLEFFALITILIPSFWKKTV	716544
1.5E-48	175	27	2.7E-48	174.1	18.7	1.4	1	B0SJZ1_LEPBP	Cation transporter	LEPBI_I0152	Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris)	605	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira biflexa, Leptospira biflexa serovar Patoc, Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris)	456481	>tr|B0SJZ1|B0SJZ1_LEPBP Cation transporter OS=Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris) GN=LEPBI_I0152 PE=4 SV=1MKFKRILVFLLQIFESLQSKRFEIRKLYMEHLRPMGRMFYIFFGFLSVAILILDFGFYYPVEWKPYVTISIRTLVSFFIGYETLHLIFT NKKWKEYLDLHKIELIILLMLGLEVIYEKNIISVLKSYHISGDDTTLIFLSANQFLFLFSNLAHFFRLSKKRESKKLNPSIVFVGSFAFIILMG VCFLHFPKSTNGDVRTIDILFTTISATCVTGLSTLDISSQFTLTGQLVILLLIQVGGLGLMTLTSFFSIFLTGKGSVSDTLMLKDLLSEETM GRAKDTLKQITLQTLAIEFVGATLLFCSFPKNFPVSFPEKIYYSVFHSISAFCNAGFSLMPNGMATEAFRDSEGFLTILMFLIVFGSLGFP VLYQIRTRLFHPRDQIFRWSLTSKLVFRMSALLLIFGWTSHLLLEWDMSLKEFSMEEKLFHSLFYSVTTRSGGLHTFDLGLMGHPMTF VTFFLMWVGGSPVSTGGGIKTTTFAISILNITNQIRGKSRMEIDYRTIADSTISRAGATIVLSLFVIFIAIFCLLLTENAHFIDLCFEAVSAFS TTGLSRGLTPHLSDSGKIIICVVMFVGRVGILTLLIALSKKVDHIAYEYPKEYVVVG	456481

1.5E-48	175	17.6	6.1E-48	172.9	12.2	1.7	1	E6S9T3_INTC7	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Intca_0578	Intrasporangium calvum (strain ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP)	465	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Intrasporangiaceae, Intrasporangium, Intrasporangium calvum, Intrasporangium calvum (strain ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP)	710696	>tr|E6S9T3|E6S9T3_INTC7 H(+)-transporting two-sector ATPase OS=Intrasporangium calvum (strain ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP) GN=Intca_0578 PE=4 SV=1MPDSVQAMASMEAPVGAWSRVAQALSHPIRVVVVAFLAAILAGTALLMTPLAAASGDETGIVTALFTATSAVCVTGLVLVDTGTYWSGFGQGVILLLIQIGGLGIMTLASVLAVMIGRRIGVRASLLSGAEARRGHGAGMSARDIVVGVVRTSLLFEAVLALVLILRFSLSYDEPPARAAYLGVFHAVSAFNNAGFALWADNLERFALDPVVSLVIAGAIICGGLGFPVLWELRREWRRPRDWSLHTRITMTATVAILVVSTVVITLAEWGNDATIGSFPTPGKLLAGFFHAVNTRTAGFNSVPIGDLRSESLLASDLFMFIGAGSAGTAGGIKVTTFVLMGYIMWAELRGERHVIASRRTVPADVQRQALTVAFFAVTAIIVSTWVLLATSAFSLDVVLFEVVSAFGTVGLSTGITASLPTHGQLLLTVLMFVGRLGPLTVGASLALRTRPRRFEYPEERTIVG
1.6E-48	175	25.8	2E-47	171.3	17.9	1.9	1	D5EYT7_PRER2	Trk system potassium uptake protein TrkH	trkH PRU_2881	Prevotella ruminicola (strain ATCC 19189 / JCM 8958 / 23)	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella ruminicola (Bacteroides ruminicola), Prevotella ruminicola (strain ATCC 19189 / JCM 8958 / 23)	264731	>tr|D5EYT7|D5EYT7_PRER2 Trk system potassium uptake protein TrkH OS=Prevotella ruminicola (strain ATCC 19189 / JCM 8958 / 23) GN=trkH PE=4 SV=1MVNFRIISKIIGSLLLIEALFMSLCALVAFSYHEDDLMAFLISLLITFGSGFTFMYMGRNADNSLSRRDAYLLVTAAWLVFSVFGMFPFLTHGCITNITDAFFESTSGFTTTGASIIDDVEILPHGILFWRSLTQWIGGLGIVFFTIAILPSLVGGSVKVFAAEATGPIKAKMHPRLTTTAKWIWSIYLILTLACVLSYCAAGMNWFEALNYAMTTTATGGFAIHNESTEYFHSPTIDYISITFQFLSGINFTLLYLSIVKMRLKALLTNSEFKLYVSVVIGATLWIMYLLLTRMGYDLEHAFRAALFQVVSFITTTGMFNEDAGTWPHITWVILGVVMYLGACAGSTSGGFKCIRGVMLLKVVRNNFRQILHPNAVLPVKINGMSIPQSKLVALFAFFTLTMLMTLVTATIMIVAGIDNTNAITIALSCVSNVGPTLGTQIGPVMSWSILPEYIKWILCPLMLMGRLEIMTVLVLFTRTFWKEN
1.6E-48	175	36.2	1.6E-48	174.9	25.1	1.4	1	Q6MSL2_MYCMS	Sodium transport protein	MSC_0759	Mycoplasma mycoides subsp. mycoides SC (strain PG1)	539	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma mycoides group, Mycoplasma mycoides, Mycoplasma mycoides subsp. mycoides, Mycoplasma mycoides subsp. mycoides SC, Mycoplasma mycoides subsp. mycoides SC (strain PG1)	272632	>tr|Q6MSL2|Q6MSL2_MYCMS Sodium transport protein OS=Mycoplasma mycoides subsp. mycoides SC (strain PG1) GN=MSC_0759 PE=4 SV=1MKRGGFMFFKKKNNKKHKLKFTSRLFKKTSNFNEEKYKFFRLVKDIWPLSKTSGKIFLIYVAIILLGGLLLSIPNFSLTKSGSKYNWDFLTGIFIASSGFSDTGLTVLDVSHSYTFWGQFILLLIEFGGIGVLTFKIVLFLIINKKISISDTIVAQSERGSATTSLTIVLIKDGFIWLTSVQVISAFILFFLFFFNQPSNNPNLEVVSPYHDFWKSLWFAVFHSTSAVNNAGFDIISPNSLQPYNVDNHRVYAIQVIFMLEWIIGGLGYPTFHDIKRKLKAIKTKEKINFSLFTKINFWVYLVLFIFGPLVVFATEYSNYNHSLIFHYYDENFTVLNAKSNIVVFMDILFNTTASRNAGFSTIDISTFNSGSKAILSILMFIGSAPSSTAGGIRTTTFGILLLSTFKIIKNQKFTSAFRKTIPSETVNRSYAAFFISTFLIFVALFIIYVDSNSVFHTLKNHNSASINTILLITSAFGTVGLSPLAHFQMYQLGVVTKISIILIMFIGQLGVSNTLLIFLKPARDKAYKYLEEDITIG
1.6E-48	175	25	1.5E-47	171.6	17.3	1.9	1	R7I3R8_9CLOT	Potassium uptake protein TrkH family	BN648_00237	Clostridium sp. CAG:411	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:411	1262802	>tr|R7I3R8|R7I3R8_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:411 GN=BN648_00237 PE=4 SV=1MLKKWKKMSQTRLIALSFFCVILAGTFLLTLPWASRTGEWTSPLNALFTATSATCVTGLIVYDTYCHWSLFGQIVIICLIQIGGLGLMTIISLLAVFTKRRIGLGERRLLMISSGNMRMSGVIRLIQKVAVITFVCEGIGALVLACSFVPQMGIVRGCYNAIFHSISAFCNAGFDLMGRFKEGSSLALYEQNVAVMLPLAILIVVGGIGFQVWSDLHENGFHVKKYSLHTKVALLSTGALLFGGWLLYFIFENKYHLNGMTLPEKLLSSGFMSATTRTAGFAGFDLSQLSQSGSMLTIILMLIGGCPGSTAGGIKATTIAVMVMSVIGMSRGDTDITVFKRRLNKELIKHAAVICFVYVSVVLAATMTICTIEHASLASVLFETSSAMGTAGLSQGLTAQAGDVSKVILIVLMYGGRIGGLSLLSVFAERKKEAPHKRPAERIMIG
1.6E-48	175	30.7	3.5E-24	94.6	9.6	2.1	2	R7GE29_9CLOT	Potassium uptake protein TrkH family	BN598_01274	Clostridium sp. CAG:307	446	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:307	1262795	>tr|R7GE29|R7GE29_9CLOT Potassium uptake protein TrkH family OS=Clostridium sp. CAG:307 GN=BN598_01274 PE=4 SV=1MKLKRKIKPQFLIIISFLCVILAGTLCLLLPISTTNRKGLSFLDALFLSTSSTCVTGLSTIAVGPTLSTFGHLIVLILIEIGGLSFLTLVSFIYSLVGAKIGVSSRLLMKETLNQDTSRGIVQLVKKVVPLALIIQAIGALLLFFIFRFKYDYSFLTSLKYGLFHSVSAFNNAGIDMFENELPSLMPYTNDVMLNIIIMVLITLGGLGFIVIIDVLSKRRWYKLQLHTKVVLIVTFIILITGALGYKLFFHLSGDDITWLQAFFQSVTTRTAGFASIDQSRVEACKPAYLLSVIQMFIGASPCSTGGGLKTTSFTILIVSILCFAKGQTPNIFKRKINQQTINKVFILFVVEIAYLAIAILLACAFEAKSSFSLESIAYEVISAFDTVGLSTGITSTLNAATKILIIVTMFIGRLGPLTFISMWTSRTNLIISRDVKYVEGKIIIG
1.7E-48	175	18.3	1.7E-48	174.8	12.7	2.2	1	A0A0F4R207_9GAMM	Trk system potassium uptake protein	TW86_11545	Halomonas sp. S2151	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas sp. S2151	579478	>tr|A0A0F4R207|A0A0F4R207_9GAMM Trk system potassium uptake protein OS=Halomonas sp. S2151 GN=TW86_11545 PE=3 SV=1MLRWCRDWAPVLKVLSVLWLVLALFMLLPWGVLVWEGDADAPAFARSLLVVLATVLMCWWLTWRIPVALKTQQMFVLTTLSWVSISGFASLPLVLGAPHLSLTNAVFESVSAITTTGSTILTDIDQLSDGLKLWRGLMQWLGGIGIIVMGIAILPFLKVGGMRLFQTESSDWSDKVMPRTGGIAKATLGIYALGTLVAILAYGIGGMAPVDAVVHAMSSVSTGGFANSDASFGAYADQPHLLWMGTLFMLLGALPFVLYIRFLRGSPLALWRDEQVRGLVWLLVVVTLILSLYRVWRGEAMFDALTHTAFNVVSVVTTTGYASDDYSQWGPFAAMAFFYLTFVGGCSGSTSGGMKIFRFQVAIKMLLSQLRFLIHTHGVFVSRYNGAPLSDEISRGVVAFSFFFFLTIAGLALALAMLGLDLVTALTGAATAVANVGPGLGDIIGPAGNFSTLPDAAKWLLCVGMLMGRLEILTVLVLLTPMFWRK
1.7E-48	175	30.4	2.4E-48	174.3	21.1	1.1	1	Q7VEB5_PROMA	Trk-type K+ transport system, membrane component	trkG Pro_0098	Prochlorococcus marinus (strain SARG / CCMP1375 / SS120)	467	cellular organisms, Bacteria, Cyanobacteria, Prochlorales, Prochlorococcaceae, Prochlorococcus, Prochlorococcus marinus, Prochlorococcus marinus subsp. marinus, Prochlorococcus marinus (strain SARG / CCMP1375 / SS120)	167539	>tr|Q7VEB5|Q7VEB5_PROMA Trk-type K+ transport system, membrane component OS=Prochlorococcus marinus (strain SARG / CCMP1375 / SS120) GN=trkG PE=4 SV=1MPFSKQVNLKLAWYRKLTVPQFTVLTGLLLIFSCTVLLATPLCSSAEVGIWESFFTATSAVTVTGLTIIDIGKDLTIYGQILLACMLLIGGLGLMAITTFLQGFVVSGTELRTRLDRGKTLDEFGVGGVGRTFRGIALTAFVLIAIGACILFYFGFTDISNLGERAWASIFHSISAYNNAGFGLWSNSMQSYRSNWVVNGVVILLVLLGGLGWRVTSDIWTNRKNLHFRRLSLHTRLVIRTSVFLICLGTFGLFLTESIEKGAFFFTINWHERFLTSLFASISARTAGFTSMPISIETISDSGLLLLMTLMFIGASPGGTGGGIKTTTIAALMAATRSTLRGQDNVVIRHRQISDKVVLKAVGITVGSLLFVLIMALLISMANGFGGQDNFSFLEILFTCISAFATVGFDLGVTQHLSGIGQFILVLGMFVGRLGILLLLSAIWQALNRGGIKDQNRIGYPHEDLYV
1.7E-48	175	37.1	1.4E-46	168.5	25.7	2	1	Q81G21_BACCR	Potassium uptake protein KtrB	BC_1390	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	226900	>tr|Q81G21|Q81G21_BACCR Potassium uptake protein KtrB OS=Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711) GN=BC_1390 PE=4 SV=1MDVTKKQGLYNRLIRLNPPQILALGFFCLIVVGGLLLKLPFATKVHISWVDAFFTATSAATVTGLGVVDTASTFTMFGEIVIMFLIQTGGLGLMTIAILIVWVLGKKIGLRHRLLIGEAFNQTNIGGLVKLVKRVFIFSICIELIGVIFLSFRFIPEFGFGKGLYYSIFHVIASYNNAGFALWPDNLTRYVGDPIINIGICSLIVIGGLGFTVLIDIWYSRSFRKLSLHSKIMIIGTVVLNVIAMIVIFVLEYNNVKTLGNLSLNEKLWASFFQGITPRTAGFNTVDYGGMEESSILFTMILMFIGAGSVSTGGGIKLTTFVILITSVLSFFRKKEEIVLFQRTIKMSTVTRALAIAVASQILILAAVFILMLTENFSFIQLLFETISAFGTVGLTMGITAKLSAFGKCIIMFVMFCGLIGPLTLVFSLARPAKQKIKYPSEDVFTG

2E-48	175	13.6	2E-48	174.5	9.4	1.9	1	D5SQJ7_PLAL2	H(+)-transporting two-sector ATPase	Plim_2635	Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	616	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Planctopirus, Planctopirus limnophila (Planctomyces limnophilus), Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	521674	>tr|D5SQJ7|D5SQJ7_PLAL2 H(+)-transporting two-sector ATPase OS=Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) GN=Plim_2635 PE=4 SV=1MNMPSLPFQFDDSTSLHPRLNRALILLEWLSGLVALVLVLSDQGFVRQKESLPGQELTNSNWWLLGLTAACLALPVVTLPVRY WWSRTRSTFLRSHALLVTITLIWFLGAIAFSIPTATMEVIQEEIAGTHGPGQGMIFWTELFGLLRGISSLIRLIRWSTEAGLSPALVFVAS FLLLIFSGTLLLMLPRCRPEGLPPATWLEALFTATSACCVTGLNVVVDPGTYWSRTGQCVILGLIQAGGLGVMSFGAFIALVVTRNIAAR EAATFRDLLESDRLGDVSGLIKDIIAFTLAIELVGAVAISGLWSHLPLGEQIFYSVFHSVSAFCNAGFCLHAEGLIGRELRPEVWGGIALLI LGGIGFGPLHNLREIASHQFLKIFMPQKISPSIGRMRVSLTTRIVFRVTIALLVGGAVVLFLTELGRPVAGQTIWQQIANAWFHSVTLRT AGFNTMDHSQLTPASKLISIVLMFIGASPGSTGGGIKTTCFAVAILTLRSVLQQKSHIEAGGRTIPQEQILRGLSIVALSLTAIIGCTLILVIV ENKPTLFLDHFYEATSAFATVGVSTGITPSLKPLSQLALIATMFIGRIGAVTLVVALAGSASQVVYRYPDERISLG
2.1E-48	175	25.4	8E-48	172.5	17.6	1.7	1	F9T2F8_9VIBR	Trk system potassium uptake protein	IX91_00160	Vibrio tubiashii ATCC 19109	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio tubiashii, Vibrio tubiashii ATCC 19109	1051646	>tr|F9T2F8|F9T2F8_9VIBR Trk system potassium uptake protein OS=Vibrio tubiashii ATCC 19109 GN=IX91_00160 PE=3 SV=1MVNFRPVLFVIGLVLSKLALFMYVPTLVAFITGTSGFLEFGQAVIITHTAAFACLTIGRTKQFKLSVRDMFLITSLVWTIASAFAALP FVFINHISFTDAYFETMSGITTTGSTVLSGLDNMAPSILLWRSILQWLGGIGFIVMAVAVLPMLNVGGMKLFHTESSDWSDKSSPRAKT VAKNIVAVYLSLTGLCIVGYLLTGMNLFEAINHAFTTLSTGGYSTSDGSMNHFSNGAHWVATLFMFLGGLPFLLFVAAIKKRRLNELVK DAQVRGFSYLFLVSSLIIAAWLVIRDGYAVLDALRVSMFNIVSVVTTTGFGLEDFTAWGALPTTLFAFLMMAGACSGSTAGGIKIFRFQI ALTLLNKQMMKLIHPSGVFVQRYNQRPVNDDIVRSVVAFGLTFFITIIAIAGGLSAMGLDPITSISGSITAVANVGPGMGSVIGPTGNFAP LPDAAKWLLSLGMLMGRLEILTLLVLFFPAFWRR
2.3E-48	174	27.4	2.7E-47	170.8	19	1.9	1	U1YH67_9BURK	Potassium transporter	N879_02570	Alcaligenes sp. EGD-AK7	455	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Alcaligenes, Alcaligenes sp. EGD-AK7	1386079	>tr|U1YH67|U1YH67_9BURK Potassium transporter OS=Alcaligenes sp. EGD-AK7 GN=N879_02570 PE=4 SV=1MRNWLPNSLTRRLEVNPHTRTLSASPPLVLALGFMALIILGAILLSLPQAATPRLGIFQALFMATSAVTVTGLAVIDPATDLTHFGQ IVLALLVQIGGMGFVTFAVIAAITMHKRISVSQQALALEAFNQTSVSRIRSTAFQVFKIAALIELIAAAILFLRWTIDLPWTTALYRALFHAV TAFNNAGFSLFHDSLIPISGDFVSVMTLSGLIILGGIGFTVLADVGQKKRWQTLLPYTKLIIGTLILNLIGFFSLWALEFTNPNTLGMLGL GDQALAAWMQNAATRTAGFTTMDIASLRDSTQLTLIVLMLIGGGSLSTASGIKIGTLIVLLAAVRSYIRQREEVVLMERSVAPETVQKAL ALFLITGALYFISVLLLTLFEDMPITSLLFEAASALSTTGMSHGITHKLSTPSQILIMVLMFAGRLGPLTLIYSLATRKRSRIRYPEGNFQVG
2.3E-48	174	28.1	3.1E-48	173.9	19.5	1.1	1	R6QPF4_9CLOT	Uncharacterized protein	BN618_01494	Clostridium nexile CAG:348	459	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	1263069	>tr|R6QPF4|R6QPF4_9CLOT Uncharacterized protein OS=Clostridium nexile CAG:348 GN=BN618_01494 PE=4 SV=1MEYSSLKKIRFSTMQLLAMGFIATIFLGGILLTLPISNTQPIRFIDALFTATSAVCVTGLVTVVPAVQFTVFGKVILLILIQIGGLGVIAC VTGFFIILKRKITVRERVIIQESYNLNTLSGIVAFVLKIIKGTFLVEGIGALLFAVVFVPEFGALKGIAYAIFHSVSAFCNAGIDILGDGSFTQY VRNPVINLTTMMLIIAGGIGFTVWNDLIGNFKKVKAKKLVWSKFFTRLSLHSKLAITMTVLLIITGTVFVFALEYDNAKTIGNLSFGEKIMA SAFHSVSTRTAGFATVSQDGLTAGSKFLSCILMFIGGSPAGTAGGIKTTTAAMLILTCMTVVYGRRDTECFGRRIPVENFRTGFAVVML ALLFLTAGVTMLTIFEPGKDFLDLLYEAVSAIGTVGLLANLTPSLGFGSKLVVMSLMYVGRIGPITIALVFGGKKNPKEFTRELPEKRIMV G
2.4E-48	174	26.3	2.2E-47	171.1	18.2	2	1	R5CH97_9BACT	Trk system potassium uptake protein TrkH	BN458_02042	Prevotella sp. CAG:1058	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:1058	1262918	>tr|R5CH97|R5CH97_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:1058 GN=BN458_02042 PE=4 SV=1MINFKLVYKVIGSLLFIEAMMMFISLLISAYYGEDDILAFLIAIATVLLAIGLKFKGYGAENSMGRREAYLLVSLIWVVFSALGALPFV ISGYLTSYTDAFLETMSGFTTTGATIIDDVEALPHGLLFWRSLTHWIGGLGIMFFTIAILPSLVGGSVKVFSAEATGPIKSRMHPRLSTTA KWIWAIYLILTVSCAFSFFVLGMGVFDSLNYSMSITATGGFATHNASIAFFNSPAIDYAAIVFMILSGINFSLLYVLIFKGKFRDLVKDTEL RIYLSIILASTLFITFILTTQGGIHVADSFRYALFQVSSFITTTGLFNTDAGLWPHLTWVVLTMCMVCGSCAGSTSGGVKCIRIAMLFRIIR NEFKHILHPRAVIPVRLNNTNIPYQAQATLLVFFALYGITCIVAFFCFKLMGIESTNAITIAISSASNVGPTLGAELGPTMSWSGLPDAAK WICAVLMLMGRLEFISVMVLFTRAFWKKN
2.4E-48	174	35.6	4.8E-48	173.3	24.7	1.4	1	D6XSX7_BACIE	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Bsel_1401	Bacillus selenitireducens (strain ATCC 700615 / DSM 15326 / MLS10)	449	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Sporolactobacillaceae, unclassified Sporolactobacillaceae, [Bacillus] selenitireducens, Bacillus selenitireducens (strain ATCC 700615 / DSM 15326 / MLS10)	439292	>tr|D6XSX7|D6XSX7_BACIE H(+)-transporting two-sector ATPase OS=Bacillus selenitireducens (strain ATCC 700615 / DSM 15326 / MLS10) GN=Bsel_1401 PE=4 SV=1MKLGAARFLSPFRIIVASYVIAMFVFSILLYLPVSTQEGVTVTYSEALFTSVSAVSVTGLTVLNVSETYSPLGIFFLASAIQLGGIGV MTLGTFIWMVMGKKIALSQRMLIMVDHNQISFAGMVKLMRGILFVAFGIELTGALILGTYYTNYFDSVGEAFYQGAFGALSAFTNAGFD VTGQSLIPFADDYFVQLVNILLIFAGAIGFPVLMELKEYFTTKDTQFRFSLFTKIATATYFIVFAIGAVGLWITERTAFYDGMVWHQQLFF SLFNSATARSGGLATMDMNELTMASLMLLSGLMIIGASPSSVGGGIRTTTLAVMFLTIRSFALGRSDVKVFGREIHIEDQQKSFIVLSVF AVGLFAAITGISFLETGQDVALEAIIFEASSAFGTSGLSMGITPDLSQGSQIILMLMLIGRVGLVAFLFSIRARERKKTHYQYPKERIIIG
2.5E-48	174	28.6	1.3E-47	171.8	19.8	1.8	1	D3IEA5_9BACT	TrkH family potassium uptake protein	HMPREF0669_01759	Prevotella sp. oral taxon 299 str. F0039	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella sp. oral taxon 299, Prevotella sp. oral taxon 299 str. F0039	575614	>tr|D3IEA5|D3IEA5_9BACT TrkH family potassium uptake protein OS=Prevotella sp. oral taxon 299 str. F0039 GN=HMPREF0669_01759 PE=4 SV=1MINWKIIFKILGSLLFIETALLLSSVAVSLFYHEFDSLAFIVSSLITLFFAFFFRSLGNEAENSMSRRDAYLVVTLSWIIFSIFGSLPFMI TGAIPHFTDAFFETMSGFTTTGATIIDDVESLPHGLLFWRSMTHWIGGLGIVFFTIALLPSLVGGSVKIFSAEATGPIQSKLHPRLSTNSK WIWSVYLILTIACIASFKLCGMGLFDCINYSMAITATGGFSTHNSSILYFHSSTIEYLSIFFCFASGVNFTLLYMAMAKRRFKTLFHNAEFI FYCFLVLAATAFIMFELIYQNGYALEKAFRSSLFQVVSFITTTGLFSDDAGKWPHVTWVILALCMFFGACSGSTSGGLKCVRGVLILKII SNQFKQILHPNAVLPLKIDGVNINIRKRVTLLAFLAIYLILAVIAAFAMIAAGVDNTNAITIALSSMSNVGPTLGIEIGPTMSWSILPDFAKWI CSALMLVGRLEIFTVLVILTPEFWKRT
2.5E-48	174	27.1	3.1E-46	167.3	18.8	2.2	1	F0RST9_SPHGB	Cation transporter	SpiBuddy_2170	Sphaerochaeta globosa (strain ATCC BAA-1886 / DSM 22777 / Buddy) (Spirochaeta sp. (strain Buddy))	485	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Sphaerochaeta, Sphaerochaeta globosa, Sphaerochaeta globosa (strain ATCC BAA-1886 / DSM 22777 / Buddy) (Spirochaeta sp. (strain Buddy))	158189	>tr|F0RST9|F0RST9_SPHGB Cation transporter OS=Sphaerochaeta globosa (strain ATCC BAA-1886 / DSM 22777 / Buddy) GN=SpiBuddy_2170 PE=4 SV=1MINWKLDLRLLAFIELFIGFLMLIPTALSFRYQEADAMRGFLIAYLGIAIFCSITLILIGKPKTKTMYARDGYLVVTLTWVIATAFSAIP LAASGAYVDYSSAYFEIMSGFTTTGATVLPEIESLPKSILFWRSQTNWLGGMGIVVLFVALLPALGVGSGSLLVGAESVGPTKDKLTPKI KNTAIILWSIYIGFSFLQTILLVFGGLNWYDAITVTFSTMAAAGFCVKNSSIGAFGSAYVDIVVTFFMLVSGANFALYYKALSGKISSVFK DGELRVYLGIWAFVSVFAALQLSFSSTYGSFFESLRYSAFQTASILTTTGFATANYVHWPAFSQALLFLLFFIGGSAGSAGGGVKVIRI VALIKMGRAQLKQRIHPRGVFQVRVGQTTFREDLLVSIATFFGVYILTGVVGAVVISLSGADLITSFSASFLCLGNIGIGFGEVGPTGNF AFLPSWIKWFCSFLMLVGRLELFTVYVLFSKHFWKH

2.5E-48	174	17.3	3.3E-48	173.8	12	1.1	1	K9P6I2_CYAGP	Trk-type K+ transport system, membrane component	Cyagr_1571	Cyanobium gracile (strain ATCC 27147 / PCC 6307)	459	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobium, Cyanobium gracile, Cyanobium gracile (strain ATCC 27147 / PCC 6307)	292564	>tr|K9P6I2|K9P6I2_CYAGP Trk-type K+ transport system, membrane component OS=Cyanobium gracile (strain ATCC 27147 / PCC 6307) GN=Cyagr_1571 PE=4 SV=1MIRRQGWRHRLTVPQFTVVTGVLVITFGTVLLASPLCSSDEVGLWEALFTVTSAITVTGLSIIDVGAELTFAGQVTLAGLILTGGLGLMAITTFLQGFVQGRSGLRQRLDKGRALDDFGVGGIGPTLNQILLIAGIVIGIGTVTLYNFGFTDIPDKGQRLWASLFHCISAYNNAGFGLWRDNLVGYRSQPVVNAVIGLLIVMGGIGWRVTNDIWVNRFRLARIRRLSLHTRLVIRTTIVLIVLGAVGLLFTEHFATEGMVEQLSLWDKLQVTIFQSITTRTAGFNTVPLSLETISDSGLLLMIMLMFIGASPGGTGGGIKTTTFAALIAATRSTLRGHDEVVVRNREIPLKVILKAVGVTLGSGLFILLMALLLGLGNTTAGTPGSEAFTFLEKLFTCVSAFGTVGLDVGVTSQLNRWGQLVLMVGMFVGRIGILLMLSAVYGSRPQNRVGFPREELYI
2.6E-48	174	24.8	1.2E-47	172	17.2	1.8	1	U4K3G8_9VIBR	Trk system potassium uptake protein	trkH VIBNI_A3840	Vibrio nigripulchritudo	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio nigripulchritudo	28173	>tr|U4K3G8|U4K3G8_9VIBR Trk system potassium uptake protein OS=Vibrio nigripulchritudo GN=trkH PE=3 SV=1MVHLRPILFVIGLVLSKLALFMYAPTAVAFFSGTPGFIEFGQSVLILHGVAFVCLTIGRTAEFRLGVRDMFLITSFVWTIASAFAALPFVFINHISFTDAYFETMSGITTTGSTVLSGLDEMAPSILLWRSILQWLGGIGFIVMGVAILPMLNVGGMRLFQTESSDWSDKSAPRTKIVAIHIVYVYLTLTALCLIGYLLTGMSGFDAINHAFTTLSTGGYSTSDGSMNHFSNGAHWVAIAFMFLGGLPFLLFVTALKKKRPMSLWQDAQVKGFAYLVLFTASVVAVWLWFHEDYSMSDAVRVSLFNVISVVTTTGFGLEDFTAWGALPGVIFAFIMMAGACSGSTSGGIKVFRFQIALTLLHKQMMKLIHPSGVFVQKYNQRPVNEDIVRSLVAFGLMFLITIIVIAGALGAMGLDPVTAISGAVTAVANVGPGMGHVIGPTGNFAPLPDAAKWILSLGMLMGRLEILTILVLFFPAFWRR
2.7E-48	174	27.8	3.5E-48	173.7	19.3	1	1	U2KGH8_9STRE	Potassium uptake protein, TrkH family	HMPREF1557_02045	Streptococcus sobrinus W1703	457	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus sobrinus, Streptococcus sobrinus W1703	1227275	>tr|U2KGH8|U2KGH8_9STRE Potassium uptake protein, TrkH family OS=Streptococcus sobrinus W1703 GN=HMPREF1557_02045 PE=4 SV=1MLSFVKHLSIAQRISGSFISVILIGSILLSLPIMHYANAPATSYFDHLFNTVSMVCVTGLSVFSVGAVYNGLGQFVVMCLMQIGGLGLVSLISISYYSINRRMSLRQQEILQSSIGNNSIADLKHYLFRIYKITFAIECIVALILMTDFIPRFGWQNGIFNSLFLAVSAFCNAGFDNLGNNSLINYKLNWTVNLAVAFSIISGGLGFRNLMAIIDLVKCWIKERPHKFGLIKKNLTIQTRLVLTTTAIILIAGTLSAWILEFNNPKTIGNLGIFHQGLVSFFQTVTMRTAGFATIDYTKAGNSANFIFMIQMLIGGAPGGTAGGLKLIVTAITFLIFKAEFLGERRVSVYNRIIPTQLVKRTFTILVFFFIILLVGYVALLELEPNISPFRLLFEACSALATVGVSMDVTTHLTAGGRIVIMALMFFGRVGPITVLLSLRQRSKKTIDYARTDLTLG
3.4E-48	174	28.8	1.2E-25	99.4	8.1	2.2	2	Q6LXC2_METMP	Putative TRK system cation (K+) uptake protein	MMP1430	Methanococcus maripaludis (strain S2 / LL)	478	cellular organisms, Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanococcaceae, Methanococcus, Methanococcus maripaludis (Methanococcus deltae), Methanococcus maripaludis (strain S2 / LL)	267377	>tr|Q6LXC2|Q6LXC2_METMP Putative TRK system cation (K+) uptake protein OS=Methanococcus maripaludis (strain S2 / LL) GN=MMP1430 PE=4 SV=1MKIFKKSDISGIFHELGILISTIGFIMLLPSFIGIYFHEPFFYFLFPSLFFMILGLLINKITKPISVKLKHAMVISALAWLMASLIGAIPFYIGIEYFSYLDGVFESMSAWTTTGFSIVGDVESLPRTLQFWRSFEQWIGGVGVLAMVITILSKAGASAYYRAEAREEKIMPSTIGTIKKIWQIYLLYTTIGICLLYLSGLNLWSALNICMCGISTGGMSISNQSFPFNNFAKIIMTLIMYIGGVVSFSVHHNVLTGRRVDDIQTKTSIPILFFAAFVITLTSGIDPLDSLFTVVSAMTSTGFSSVQISSLTNISIAVLIFVMAIGGATGTTTGGIKLIRLVIMAKGFYYRLKEVVSPGNAIIYKKIGKNQLSDFLILDAFIIAFAYIIHYLFGTLVLISLGYDPFLSVFESVSLVANMGLSVDIVNHSLHPIAKILGVFSMWVGRLEIIPIYVLIILPLYLKLLKDVGKNKISKNRKL
3.4E-48	174	20.2	4.2E-48	173.5	14	1	1	R5QLL6_9FIRM	Uncharacterized protein	BN734_01110	Ruminococcus torques CAG:61	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus torques CAG:61	1263108	>tr|R5QLL6|R5QLL6_9FIRM Uncharacterized protein OS=Ruminococcus torques CAG:61 GN=BN734_01110 PE=4 SV=1MEYICRVWGKQIKIIGWFLEMEKKKKSPRRLKFNTVQTVVIGFFGVILGGGILLSLPICNQKPIEFIDALFTSVSSVCVTGLVTIVPAEQFTLLGKIILLLLIQVGGLGVIACMSAFFLLGKKINMKGRITIQQAYGLDTLSGLVKFVIRILKGTFLVEGIGAVLFSLRFIPEFGFIKGVGYAIFHSVSAFCNAGIDILGSTSFIQYSGSWLINFTTMFLIVMGGLGFPVWHDIAINIKKMTEIKKRPLKWLFTRLCLQSKIVLTMTGLLILCGAVGFFLLEFNNPETMGDMNLLEKMTASLFQSVTTRTAGFATVPQGDLRESSKLLGCMLMFIGGSPAGTAGGVKTTTIAMLLLTVLCVLKNKRDTECFARKIDNNIVRSGITITMITLIFLMSGITALTIFEPGIDFLDLTYEAASAMGTVGLTADLTPILSRGSHVILMILMYVGRIGPLTMALALSGRSDKISKFRELPEENVMLG
3.9E-48	174	36.5	3.9E-48	173.6	25.3	1.5	1	I3YUY5_AEQSU	Trk-type K+ transport system, membrane component	Aeqsu_1310	Aequorivita sublithincola (strain DSM 14238 / LMG 21431 / ACAM 643 / 9-3)	583	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Aequorivita, Aequorivita sublithincola, Aequorivita sublithincola (strain DSM 14238 / LMG 21431 / ACAM 643 / 9-3)	746697	>tr|I3YUY5|I3YUY5_AEQSU Trk-type K+ transport system, membrane component OS=Aequorivita sublithincola (strain DSM 14238 / LMG 21431 / ACAM 643 / 9-3) GN=Aeqsu_1310 PE=4 SV=1MSRWKKTSLTNIVVWFLDLGLLSFLIFDFGFENFKDFRQYKLIVLPLLLLALIAFNFYKFYKYRKDVDVNRSSRISLFILLILIVLEVIMILANYETSVVETFFNARYVIEYGLLFYFFIRLTFLLRKVYSLYFNPAILFVGSFAIIALAGTFLLLLPSATTHEISFTDALFTATSATAVTGLIVLDTAKDFTPFGQTVIMILFQIGGLGMLTFTSFFAYFFKSGASFKESLYMRDILGHDKLNSVMKTVMQIVAFSLILEGIGALFIYHSLAHIDSFKDRGFFAVFHAISAYCNAGFSLASEGLFDSGLRFNYYMQWVVMGLIVFGGLGYHIAYNVIQYLRKFVTNIFQKKERVFISRVINLNTKIVLYTTAILAAGAVFFLFSEQNTNLVPHTTAFGKFTTAMFSSITSRTAGFNTVDMTNFTIPGLLFMIFLMWVGASPASTGGGIKTTTFALATLNVFAIARDKKYIEIGTRRIAIEAVHRAFAIISISLASIGMGILLLLIFNPEFSLIQIAFEVFSAFSTVGISMGITSQLSEYSKYVVILLMFFGRIGLLNLMIGLLKSVGKTDYTYPEENILIN
4.3E-48	174	25	5.7E-46	166.4	17.3	2.1	1	R6JSI3_9PROT	Trk system potassium uptake protein	BN554_01352	Azospirillum sp. CAG:239	481	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, environmental samples, Azospirillum sp. CAG:239	1262705	>tr|R6JSI3|R6JSI3_9PROT Trk system potassium uptake protein OS=Azospirillum sp. CAG:239 GN=BN554_01352 PE=3 SV=1MWQPVLMINGYLISVLGLAMLIPAAVDMLETGRNWSLFVTSSIVSLFIGLSLFLGNRTKIEKITLQQGYLLTAVSWVSLTLLATLPFILSDVTPGFADALFEAMSGLSTTGATVITDLEVLPDSILLWRSMLNGLGGVGIVIFAVALLPFLGIGGMQIFQRENSDLNDKFMPKFNYIAKRIMAVYFILVALCAGCLYFAGMTPLESVNYAMAAIATGGFSTKNASVGFYDSVSIEMILSLFMYLGALPMTFYIVLMQRRDLHSFRTAQVAVFTKVLAFYILLTAVWLAYEGIYDSFWQSLRYATFNIVSITTSTGFVSTDYMKWGPPVGTIFIIFALTGGCTGSTSGSVKIFRWQVVWAYLKQSMIVATEPNRVVPIKIGNLTTSNSIISSVFVFISAFMATLVVLTVLVAWTGLDFSTAFSAVVACITNSGPGIGPVVGPAGTFAPLSDFAKYMLSLAMLLGRLEVLTVIVIFTKSFWRN
4.3E-48	173	30.6	7.4E-48	172.7	21.2	1.3	1	Q4FRA3_PSYA2	K+ uptake transporter, KtrB subunit	ktrB Psyc_1607	Psychrobacter arcticus (strain DSM 17307 / 273-4)	586	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Psychrobacter, Psychrobacter arcticus, Psychrobacter arcticus (strain DSM 17307 / 273-4)	259536	>tr|Q4FRA3|Q4FRA3_PSYA2 K+ uptake transporter, KtrB subunit OS=Psychrobacter arcticus (strain DSM 17307 / 273-4) GN=ktrB PE=4 SV=1MYVGIPYRLLNKFIVVISLIGVGVALIDSGFTLSAWLQQLFHLFYMSIILLSFVTTLRRYIRPKIRLTVNKVAVFDLLTSIAILILLVLHFTELFQSGLSTPADGFIAIKIAVLVTFIREISDNNFSLNRTFLNPGQFFILSFLSVILVGSLLLMMPNATNQPISFIDALFTATSAVCVTGLIVVDTATHFTTFGQVIILGLIQIGGLGILTFVTYFSYFFKGGISYETQLSISEMTYSPRMGDMVTTLKSILYVTFGIEALAAILYISIYDLAGMSVFERLFFSIFHAVSAFCNAGFSTFSAGLYDESLRFNYYPLQIIISITFLFGGMGFLIVVNLLRYLRYRMQRALCRDGQRYAYQPWLLSINSRITLITSGALLLVGLIGVMMFEYHGVLAEHSSWYGKLVAGLFTAATPRTAGFNNIDMNDLAFPTIMLTIFLMWIGASPNSTGGGIKTTSFAIALLNTLSLARGQTKVEVFKREIADNSIRRAFSIMWLSLLVIGLGVTLISYDQPELDLIKVIFECFSAYSTVGLSLNLTTELSTFSKLVVVSFIMFVGRVSMLTIFIALLKNRHERNYRYPTEEITIN

4.4E-48	173	33.3	6.6E-48	172.8	23.1	1.2	1	D6D2T0_9BACE	Trk type K+ transport systems, membrane components	BXY_37730	Bacteroides xylanisolvens XB1A	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides xylanisolvens, Bacteroides xylanisolvens XB1A	657309	>tr|D6D2T0|D6D2T0_9BACE Trk-type K+ transport systems, membrane components OS=Bacteroides xylanisolvens XB1A GN=BXY_37730 PE=4 SV=1MKIYHKFLLYQNKLLKPYVRILLGLIEALTYLASLSLIVGVVYEHGFPLSIDEVANLQTLYKTVWIIFLIDVTLHISLEYRNTKKQYRRL AWILSGLLYLTLVPVIFHRPEEEGAILHIWEFLHGKFYHLLLLLVLSFLNLSNGLVRLLGRRTNPSLILAVSFMAIILIGAGLLMLPRCTVNG ITWVDSLFTATSAVCVTGLVPVDVSTTFTTSGLVVIILLIQIGGLGVMTLTSFFAMFFMGNTSIYNQLVVRDMVSSNSLGSLLSTLLYILG FTLVIEGIGMVSIWFSIHGTLGMTLEGELGFAAFHSISAFCNAGFSTLSGNLGNPMVMTNHNWLFITVSLLIIFGGIGFPILVNFKDIVLYH LRRFWKLIRTRKLDRHKMQHLYNLNTKIVLIMTFLLLLIGTLAIAAFEWNGSFAGMPVADKWTQAFFNATCPRTAGFSSVDLASLSVQT LLVYLFLMWVGGGSQSTAGGVKVNAFAVVVLNLVAVLRGTERVEVFGRELSYDSIRRSNATVVMSLGVLFIFIFTLSILEPGVSIMALTF ECVSALSTVGSSLNLTPHLCDASKLLVSLLMFIGRVGLITLMLGIVKQKKNTKYRYPSDNIIIN
4.4E-48	173	24.2	6.3E-47	169.6	16.8	1.9	1	Q8EQN0_OCEIH	Na(+)-transporting ATP synthase (Divided with OB1663 and OB1664)	OB1664	Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)	289	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Oceanobacillus, Oceanobacillus iheyensis, Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)	221109	>tr|Q8EQN0|Q8EQN0_OCEIH Na(+)-transporting ATP synthase (Divided with OB1663 and OB1664) OS=Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831) GN=OB1664 PE=4 SV=1MDLVGIFTSLFHVVSAFNNAGFSLWSDSLMGYVGDPVVNIIITFLFIVGGIGFTVISDLMMTRKYHQLSLHTKLMIIGTLSINIIATIVI FLLEYTNSETLANLALDEKLWASYFQAVTPRTAGFNSLDIGSMNPATLTLTMFLMFIGAGSASTGSGIKLTTFIVIVLAVNAYLRGKKEA VIFKRSIPGQVVHRALAITVISLLMVITVIFLLTITEDAPYLHIIFEAFSAFGTVGLSMGLTAELSESGKLLLCILMLAGRIGPITLAFALARTS KGNIGYPKDDVFTG
4.8E-48	173	26.3	2.1E-47	171.2	18.2	1.8	1	A0A097QP18_9VIBR	Trk system potassium uptake protein	IX92_15805 JV59_39090	Vibrio coralliilyticus	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio coralliilyticus	190893	>tr|A0A097QP18|A0A097QP18_9VIBR Trk system potassium uptake protein OS=Vibrio coralliilyticus GN=IX92_15805 PE=3 SV=1MVNFRPVLFVIGLVLSKLALFMYVPTLVAFFTGTAGFLEFGQSVVITHLAAFVCLTIGRTKHFKLSARDMFLITSLVWMVASAFAA LPFVFINHISFTDAYFETMSGITTTGSTVLSGLDDMAPSILLWRSILQWLGGIGFIVMAVAVLPMLNVGGMKLFHTESSDWSDKSSPRA KTVAKNIMLVYLILTGLCMVGYLLTGMNLFEAINHSFTTLSTGGYSTSDGSMNHFSKGSHWVATLFMFLGGLPFLLFVAAMRKRRVDE LINDAQVRGFTYLFLITSLIISAWLVIRDGYSVMDALRVSMFNIVSVVTTTGFGLEDFTAWGALPTTLFAFLMMAGACSGSTSGGIKVFR FQIAMTLLNKQMMKLIHPSGVFVQRYNHRPVNDDIVRSVVAFALMFFITIIFIAGCLSALGLDPITSISGSITAVANVGPGMGAVIGPTGN FAPLPDAAKWLLSFGMLMGRLEILTLLVLFFPAFWRR
4.9E-48	173	21.2	3.9E-46	167	14.7	2	1	M4U114_9GAMM	Trk system potassium uptake protein	PCNPT3_00705	Psychromonas sp. CNPT3	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Psychromonadaceae, Psychromonas, Psychromonas sp. CNPT3	314282	>tr|M4U114|M4U114_9GAMM Trk system potassium uptake protein OS=Psychromonas sp. CNPT3 GN=PCNPT3_00705 PE=3 SV=1MVYRPLFFITGLVLSKMAVFMYFPMALAFYNESLGGVEFLAAIIITHIFSFIFIFVGDEKERSRLGVREMFLLTTGVWVLASLFAALP FVFIEHISYSDAFFETMSGITTTGSTVLHDLDSMPHSILLWRSILQWLGGVGFIVMGVAILPFLNVGGMRLFQTESSDWSDKAESKTRQ VALDILAVYLLLSICCFIGYRLTGMNGFEAVNHAMTTISTGGYSTSDGSMGHFSIGAHWNAIIFMFLGGLPFLLLIRAFNRRQPSAIYKDA QVCGFFTLVVVFSSLLTVYLVLTDQFGWLDALRLSLFNVISILTTTGYGLDDFVQWGDFSVVIFLGLLFIGACSGSTAGGIKIFRFQIALR LLNRQLLLLMHPRGIFPQKYNNRIVSDDILRSLIAFVLAYLMTIGLSTLLLSLFGSPAIEAFTASITAVSNVGPGLTPSIGPSGNFAHLADAS KWVLAIGMLMGRLEILTVVVLFTRHFWRR
5E-48	173	37.3	9.3E-48	172.3	25.8	1.4	1	R7NW33_9BACE	K+ uptake protein	BN821_00057	Bacteroides sp. CAG:98	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:98	1262754	>tr|R7NW33|R7NW33_9BACE K+ uptake protein OS=Bacteroides sp. CAG:98 GN=BN821_00057 PE=4 SV=1MERLHKLFIYRKKLVRPYIEQLLKWMDIITYVMSALLIMTLVYEHGFLISFQEIGVINRLYHIVWVVFLVDTTLHLLLNYSDTRRKYR GLAWLLSVMLYLTLIPVVFHEPEIQGGIHTFWAFFNSRLYHVILLTLLSLLQLSNGIVRLLGRRTNPSLIFASSFLIFILIGAALLMLPRATY HGISFIDALFTATSATCVTGLVSVDVSSTFTPEGLFIIIMLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSQSLSSLLSTLLYIL GFTLAIEAAGMGIIFLGIHGTMDMTVREELAFSAFHSISAFCNAGFSTLPGNLGNEMVMHGHNTIYITISFLIILGGIGFPILVNLYETVTYE VKRIWHHYIKGNKRMRRKIHLYNLNTRIVLIMTAILLIVGTVVIVVLEWNNAFAGMSPTDKWVQAFFNATCPRTAGFSSVGMTTFSMQT LLLMVILMMIGGGTQSTAGGVKVNVFAVVMLNLRAILIGADKVTIFNRELSHDSIRRSNATLILYLLVVFAGIFSLSLLEPQASIMALVFEC TSALSTVGSSLDLTPTLGSDSKLIIIILMFVGRVGVLTLMSSIIKQKKITKYRYPSDNIIIN
5.2E-48	173	17.3	7.2E-48	172.7	12	1.1	1	D7AX97_NOCDD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Ndas_0524	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	473	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	446468	>tr|D7AX97|D7AX97_NOCDD H(+)-transporting two-sector ATPase OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_0524 PE=4 SV=1MGLRRLRGSLLPLRAARLSYKLRRELSATREASTWRQPARVFLMAYVIVDLLGTALLMTPLTTPDHRGLGFVEAFFTATSALSV CGLSVVSIGNDLNTFGQGVVLALMQVGGMGIMTLASLLGTAMIRRFGLRMQLTVQTETRSLWVGDVRGLVSRVALIFLICQGLTFLLIT PRMWLGYDMPLGEAAYSGFFHSISAFNNAGLSLYGDSMMRFSGDAFVLVPIALAVILGGIGFPVLLELRRELRTPRLWSLHTKLTVTT TAILFAAGALLVTVMEWHNPQTLGQMHWWAKLVDGFFHGVMPRSGGLNSVDTGEMEDATLLVTIMLMFVGNGSAGTSGGIKVATL AVIFLVVAAEVRGNDKVHVYGRQLSPEVIRQSLSLVFLSATVVAFTTVLLVRTTPFELLPVMFEVVSAVGVVGLSTGITADLAPWAQFLL ALLMVAGRIGPITFVTALAFRDHRRRYDLAEARPIIG
5.4E-48	173	22.4	3.9E-47	170.3	15.5	1.9	1	T0T5H3_9STRE	Potassium uptake protein TrkH	HSISB1_1818	Streptococcus sp. HSISB1	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus sp. HSISB1	1316409	>tr|T0T5H3|T0T5H3_9STRE Potassium uptake protein TrkH OS=Streptococcus sp. HSISB1 GN=HSISB1_1818 PE=4 SV=1MNKSMVRYLLSKLLLIEASLMLVPVIVAFIYKEDFHVIISLGATIGILVILGLLGAAFKPKNYHVYTKEGLLIVALCWILWSFFGALPFV LSGQIPSIIDAFFEMVSGFTTTGATILPDVAVLSHSLLFWRSFAHLIGGMGVLVFALAIMENSKNSHLEVMRAEVPGPVFGKVVSKLKET AQILYIIYLSMFAILMVILMLAGMPAFDSVITAMGCAGTGGFGVYNDSIAHYNSSSLITNIVSIAVLLFGINFNLYYFLLLRKFKAFFKDEELR TYIGIVIAATALIWLNVSGLYPSAGKAFENTLFEVANVITTTGFGVTDLTVWPLFSQVILLFLMFIGGSAGSTAGGIKVMRALILAKISKNQI LSTLYPNRIMTIHINEQPLDKETQHGVLKYLAIYVFLLLGLTLLLSLDNNNFLVAISAASSTFNNIGPMLGTGDTFAIFSPFSKVLMSFAMIA GRLEIYPMLLLFIPKTWSKY
5.4E-48	173	23.3	4.8E-43	156.8	17.2	3	2	F8KWK3_PARAV	Trk system potassium uptake protein TrkG	TrkG PUV_04560	Parachlamydia acanthamoebae (strain UV7)	549	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Parachlamydiaceae, Parachlamydia, Parachlamydia acanthamoebae, Parachlamydia acanthamoebae (strain UV7)	765952	>tr|F8KWK3|F8KWK3_PARAV Trk system potassium uptake protein TrkG OS=Parachlamydia acanthamoebae (strain UV7) GN=TrkG PE=4 SV=1MQFKDLCKILSIFVFGIAGTLLIPLCVACYYKFFLDPALHPQPYAIDAFLESVAICLVLGMWLRYCGRRSNRKMYLKEGIAAVVFL WVLAPALAALPFVLSGTLTNPLQAYFEMASGLTTTGATVMQAKSYDLKTGEEIPITRTFCGSPDVEYTFHGTIEPIRDPHTHEIVLSGIE AVGKGLLFWRSLTQWMGGVGIVVLFVAILPALGAGGRILFQAEVPGPMKDSITPRIKDAAIVLWKIYCFLTLVQIGLLMFTNAQMSLFD AITISFSTLSTGGFSVHSTSIGFYHDSWTEWIVLLFMILGGVNFTLYFYMFKGKFYRIYEPEFLCYLAIILSSTLIAIWKLVGTPKVLIGGIP DGLFSWQEAARYGMFQVVSAQTSTGFATANYDTWPYAMQTLMLILMFVGGMGSGTAGGIKIMRHYMLFRIAQFKVESLFSPERVRT FRVADKEVDASSAIMVLCFFLIIITLSVLGTYIYILDGIDPQTSLGIVGCMVNNVGLGFRMAGPVESFAFLSNFGLMWSSILMIAGRLEFF AVLAVLTPHFWEDH

6.1E-48	173	28.4	1.3E-47	171.9	19.7	1.4	1	Q5E0H2_VIBF1	Potassium uptake protein KtrB	VF_A0404	Vibrio fischeri (strain ATCC 700601 / ES114)	454	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Aliivibrio, Aliivibrio fischeri (Vibrio fischeri), Vibrio fischeri (strain ATCC 700601 / ES114)	312309	>tr|Q5E0H2|Q5E0H2_VIBF1 Potassium uptake protein KtrB OS=Vibrio fischeri (strain ATCC 700601 / ES114) GN=VF_A0404 PE=4 SV=1MSYLPKRGLYPLQHNNEEKGWSEPKIILSSFLAILLPSALLLTLPVFSVTGLSFMDALFTATSAISVTGLGVVDTGTHFTTSGKIVL MFLMQIGGLGQMTLSAVLLYIFGLRLSLRQQALAKEALGQEKKVNLRKLIKGIICFALIAELIGMIVLSFRWVPEFGIAEGLFYAAFHSVS AFNNAGFSLFSDSLMGYVGDPLVIFTLSLLFIGGGLGFTVIVDLVKNGSKGFKRLQLHTKIMLIATPTLLLVGTLFFYILEYQNPNTLGALS SGDKWLAAFFQSASARTAGFNSVDLTLFTQPALLIMILLMLIGAGSTSTGGGLKVSTITVAAVATWTFLRQKKNVVMFKRTIGWPIVTK SLAIIVVSGSLLSIAMFSLMLTEKAGFDKVMFEVISAFATVGLTAGLTAELSEPGKFIMVIVMIIGRIGPLTLAYMLARPEVSRVKYPEENV LTG
6.1E-48	173	26.6	2.3E-47	171.1	18.4	1.7	1	T1ZDG2_STRIT	Cation transport protein	trkG SIR_0382	Streptococcus intermedius B196	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus anginosus group, Streptococcus intermedius, Streptococcus intermedius B196	862967	>tr|T1ZDG2|T1ZDG2_STRIT Cation transport protein OS=Streptococcus intermedius B196 GN=trkG PE=4 SV=1MNRSMIRFLLSKLLIIEAGLLLVPLIVAFIYHEPNDILLSIGATIGILLVVGLLGSTFKPKNHHIYAKEGVLIVALCWILWSFFGALPFVF SGQIPHLIDAFFEISSGFTTTGASILPDVSVLSHSLLFWRSFTHLIGGMGVLVFALAIMENNKNSHLEVMRAEVPGPVFGKVVSKLKDTA QILYLLYLALFVIFVIIYYLAGMPLFDSFIIAMGTAGTGGFAVYNDGIAHYNSSLITYLVSFGVLIFGVNFNLYYFLLLRKFKAFFGDEELRT YLIIVTSATIFICLNVFHIYQNLSQTLEVSLFQVSNIITTTGFGLGDITSWPLFSQFILLILMCIGGSAGSTAGGLKVVRCLILVRIAKNQILST LSPKRVLTLHVNHNVIDKDTQHKILKYLVLYAMMIICLIFIVSLDNNNLMTVVSAVLSCFNNIGPMLGTTDSFAIFGPISKLLLSLAMIAGRL EIYPMILLFMPQTWSKR
6.4E-48	173	25.1	5.2E-46	166.6	17.4	2	1	D5EE60_AMICL	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Amico_0707	Aminobacterium colombiense (strain DSM 12261 / ALA-1)	439	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Aminobacterium, Aminobacterium colombiense, Aminobacterium colombiense (strain DSM 12261 / ALA-1)	572547	>tr|D5EE60|D5EE60_AMICL H(+)-transporting two-sector ATPase OS=Aminobacterium colombiense (strain DSM 12261 / ALA-1) GN=Amico_0707 PE=4 SV=1MKTYSSLRVERTIVAGFLSLIVIGTLLIWAFNLEGEHSIAVVDALFTATSAVCVTGLTVVDTGKDLTLLSQWVVLVLIQLGGLGVMT AATTLLLLFRQKIGIRQRLLFAGGLGLDTPAGAIKLLILILKMTVAIEVAGAVPLFIAFVRDYNPARALYLALFHSISAFCNAGFSPFSTGLQ GYAHTFLVPATIMLLIILGGAGFLVLLGIARYMRRGEPLTPHCHLVIKVTGILIIGGAFLFLISDWNGAFRGLSPTLKVWNALFQSVTPRTA GFDTIRTANFTALGVFVTCLLMIIGASPGSTGGGVKTTTLGLLVYSALCEMRGRNNIVYANRNISFNNVRRALSLSLLYVSTVLLSIVLLS FTETATAPFHTLIFEAFSAMGTVGLSLGITSSLSTMGKIILIMLMFWGRVGILTFMYVVITRETRDNVNYAATNIPVG
6.5E-48	173	15.9	8.7E-48	172.4	11	1.1	1	Q9RTT9_DEIRA	Potassium uptake protein KtrB	DR_1667	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	458	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus radiodurans, Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	243230	>tr|Q9RTT9|Q9RTT9_DEIRA Potassium uptake protein KtrB OS=Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422) GN=DR_1667 PE=4 SV=1MTRNAALPEPAPGRRWRLTPPQLLALVYALGILLGAALLHLPGVQRPGAALNSIDLLFTATSAICITGLTVADTGEAFTRFGQVLII LLVQIGGLGILTFGTVFAFMTGRRVNFTERQHLVAQLNALDVGSVLGLVRTILLYTFVTEALGAALLALRFVPQFGWGEGLYQAAFHAV SAYNNGGFVVLSGGLAPYAQDPLVCLTLAGLVILGGLGFLVQLNVVAHLRNRRRSRLLVYSKLTLLTTAVLLTLGTLVLLGLEWNNPST LARLSAPGKLLAAFFQSMTPRSAGFSTVNIEGLQTASLFTLIGLMYIGAGSGSTGGGIKTSTLAILVGSAWNMVRGRGELILFERRVMN DNLVRAGAITTLYTLLVATAFFAMLATNPKLGFTHLLFETVSAAATVGLSMNTTHKLNDAGLLILTALMYLGRIGPLTFAVAFNLRPTRSR WVKYPPEHDILVG
6.6E-48	173	31	7.8E-47	169.3	21.5	2	1	F6D586_METPW	Cation transporter	MSWAN_1177	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	496	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	868131	>tr|F6D586|F6D586_METPW Cation transporter OS=Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1) GN=MSWAN_1177 PE=4 SV=1MILYSINKLTKKEVYSIFHYTGYISLLLGFLMLIPVLVALIYGETHYIMPFIYSAVLSIAFGFVFYRVFKSKGEMSLKSVMIFATGIWLI GSALAALPFYFSGDLSYLDGYFEAMSGFTTTGFTMYTNLDAVTHTMDFWRGFMQWLGGIGIIVMALTILSSPSVNIMRMYSAEGREE RLVPSIKHTTRIILYIYIGYTIISIALFKLAGMPVFDSIFYAFSALSTGGFGMQNASLGFYNSIWIEIAAIIVMIIGATNFALHYTIIKGNWKEYF KDIETKVAWFLLIVGIFLVTVFLYNTSYYGHNFLLSLRYSIFQVVSALTTTGLQTVPPNEITVQWEGMGIFVLTILMIIGAGACSTGGGIK WLRIGILVKGMWWQVKSLLLPKGAIIPQKIHHVNDVKISEKLLKLTGLFVFSYFAIYLISVIIVLFYYQNVPQVMFEVASALSNVGLGSGL MTATSPVVTKIVFIADFWIGRLEIWPILLFIAIIIQNTIRK
6.6E-48	173	27.9	3.6E-45	163.8	19.3	2	1	R7ILN1_9FIRM	Uncharacterized protein	BN596_00019	Roseburia sp. CAG:303	432	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:303	1262944	>tr|R7ILN1|R7ILN1_9FIRM Uncharacterized protein OS=Roseburia sp. CAG:303 GN=BN596_00019 PE=4 SV=1MVDLIKKQSSARIIALGFALLIFAGSVLLMLPCSRQPGVELHYIDALYTSTSAVCVTGLIAVDAGDTFTVFGQFILALLIQIGGLGVTT IGVGIMLAMGKKVNTKGRMVLKEATNFHSAKGLIRLVHKIFLVTIIFELLGAILSSFVFLKDYPGLRGIWISVFHSIAAFNNAGFDILGNYQ NLLPYQNNVWLNLVTCGLVFFGGIGFYVIWDLWDKKCCWRKLSMHSKVVLSVSLVLTAVGTVVLIKMTESVTWLGAFFHSISARTAGF STYSIGGFSKSGLFLLMILMFIGASPGSTGGGIKTSTFFVLLQGIKAAATNYSEKAFHYAIPKDTFKKAAVITIMGISVIITGTYMMGIMEP GISFLDILFEVTSAFGTVGLSTGITPHLTDGSKILSVVIMYIGRLGPLTIATLWHFSKGERVSYPEGNLNIG
7E-48	173	27.5	3.6E-24	94.5	7.7	2	2	R7DQ96_9FIRM	Trk system potassium uptake protein TrkG	BN794_01028	Coprobacillus sp. CAG:826	439	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:826	1262857	>tr|R7DQ96|R7DQ96_9FIRM Trk system potassium uptake protein TrkG OS=Coprobacillus sp. CAG:826 GN=BN794_01028 PE=4 SV=1MKKRKITPYLLVLVSFATIILLGSFLLSMPWSYKNGSFANYWDALLLSTSAVCVTGLTPYANLSQTLSLFGQIVLILLVQIGGLGFIT LFTFFLSALGVKIGAMDRFVLKEALSLENFASVLKFVKKVVLYTFVVEGIGILLYLFIFIPKYGVSDGIWISIFHSISSFNNAGFDIVGDNSLI SYAGHIPLNIITMLLIVIGGIGFPVIDDVIHHKPKKWSCYTKIVLLSTSILIVFGTAALWLAEYRNGMTFLQALFQSVSCRTAGFATYDMNL LSDPGRLICEFLMFVGASPLSTGGGIKTTTFFTIILAIFSYMHGKKPVVFQRTISQNSITRAMALIFVACAVIIMGYLGIEIIESSHGVNHAS GKIFFEVFSALNTVGYTQSLTPNLFNGSKVILSLLMFLGRVGPITVLSVFSSALNNEREGHVRYIEENLVIG
7.1E-48	173	33.6	7.1E-48	172.7	23.3	2.6	1	I4AKE1_FLELS	Trk type K+ transport system, membrane component	Fleli_2042	Flexibacter litoralis (strain ATCC 23117 / DSM 6794 / NBRC 15988 / NCIMB 1366 / Sio-4)	624	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Flexibacter, Flexibacter litoralis, Flexibacter litoralis (strain ATCC 23117 / DSM 6794 / NBRC 15988 / NCIMB 1366 / Sio-4)	880071	>tr|I4AKE1|I4AKE1_FLELS Trk type K+ transport system, membrane component OS=Flexibacter litoralis (strain ATCC 23117 / DSM 6794 / NBRC 15988 / NCIMB 1366 / Sio-4) GN=Fleli_2042 PE=4 SV=1MKNFKTRFSTYKNTFRERYQNHVYESRDRILLLIKTLSVICSAIALVFLVYRYGFHVDAPIERVIFGTLDIIFFAFAAFFTLRVIYDSH WIDFLRKNWFEALLIAFIILFGAINYILNFRITYYYFELLGFTNPELANQHFLSIYMLLMIGLDLTRITTHLSEINYKPATTFLLSFVLLILMGA GLLMLPTMTPGRTSLDLIDAIFTSTSASCVTGLIVVDTATAFTLKGQIVILVLIQLGGIGMVSFATFFASFLTQGVGIKHQSIIQDYLSSESL VSATKLLRKVVLITLFIEIIGAVCIFYAWDEELWEQSQQFENIGEKIFFSFFHSVSAFCNGGFSLFSGGMADTNYKIDRMYNLHFILVWIV VLGGLGYTTIEDIFSFNNIKERFVKPWKQWNVVTKINVYTTFTLLAIGTIGFLLLEIEKLTDRTIIQAFVTALFQSMTTRTAGFNTMDFEAL NPATIMMCLVLMFIGASSGSTAGGIKITTFVLVFVAAIANIRRQERIVIANRTIPDELIRKAYSIFIFAIAYNIVAIFLLLLVQEPSSPNDTKFIL KIIFEQVSAFATVGISMNLTGELSFWGKVIIIMSMYLGRVGTLTLALALSNAVVTNSYRYPNAHVMVG

7.3E-48	173	28.6	7.3E-48	172.7	19.8	1.6	1	R6WTW3_9PORP	Potassium uptake protein TrkH family	BN675_00466	Parabacteroides merdae CAG:48	606	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides merdae CAG:48	1263094	>tr|R6WTW3|R6WTW3_9PORP Potassium uptake protein TrkH family OS=Parabacteroides merdae CAG:48 GN=BN675_00466 PE=4 SV=1MDIKHLQFSFRMYWANMKGLLNMVAEGIILVASLASLFILVYQFGFKYSAHVTHMLETSRVYLLLAFFTGISLRYILKFKEIIQEKMLYLDIGIYFFLFAVLSGKVFFKEAIHQSLPYLGFLTEPLFVYFLLLLLSAIHLSRQTFTLLQSHIKPSLLFLLSFVFVILVGSGLLMLPNATVHGIHFVDALFISTTSVCVTGLTTVDVATTFTHTGHIIIMFLIQIGGIGVMTFTSFFALSFMGHSSFTSKLVLKDMLNEDRVNGLFRVILNILFVTLFIEGVGAYLIYLDIKGGLPGGTQEEVFYAVFHAVASAFCNAGISTLSGNMYDPLVAQKYNLHVWIALLIVFGGLGFPIVFNYLKLLRHLLVNTFKIVIGQQKHYIHTPRIININTYIVMISTLVLLAGGTFFYYLLEIDNTLAGLPFRGQLANAFLGAVTPRTAGFCVADMGTLTTGTLMLTLILMIIGAAPMSTGGGLKVTTVCVALLTAHNAARGKENVEIRKREISPETIRRAFATIVFYFCWLGAAVWILSITEKDVSVFTLTFEVVSALSTVGLSLNFSPLLSISGKLVIIFTMLVGRIGILAFFISFYKEYKKKNYTYPQENILM	1263094	
8E-48	173	12.4	1.1E-44	162.2	5.6	2.1	2	D8TAD3_SELML	Putative uncharacterized protein (Fragment)	SELMODRAFT_1751	Selaginella moellendorffii (Spikemoss)	422	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Lycopodiidae, Selaginellales (spike mosses), Selaginellaceae, Selaginella, Selaginella moellendorffii (Spikemoss)	88036	>tr|D8TAD3|D8TAD3_SELML Putative uncharacterized protein (Fragment) OS=Selaginella moellendorffii GN=SELMODRAFT_1751 PE=4 SV=1VDCFYGITSALCLSGLTTVPVEDIPPGGQVVLMIMMLLGSQVVTSSVPLLVKKHRYCRVARIAIDPSDHELEHQATIVLIRIIVIYGVVVHLMGFFIAWLSILCGRPYPRNLIRHNKKTNLGFFSLFAVVSAFCNVGYIASNENLMPFNSSLVLLLDMILLIMLGNGIYPPCLRGIIRLLHHFSKGNTKQACEFLLDHPRKCYTHLFPPNTTRWLLISFFGLNGFEICVIYILDWNSTAFDGLDTGEKIVNGIFQCVNTRSGGMNSVAITGLSPTTLFIFAVMMYISAYPVFLSRQATRQKSVDDEGAISHLSARKQRDILDTTLATQFRRLLAQDTAYLFLATFFICVSVNHGLKHDPLNYNIFSVIFEIISAYGGVGLSYGYSCSLRMEPGYCVDEPVSFSGKWGFTPKIIMIVVMLLGR	88036	
8.1E-48	173	30.4	9.2E-47	169.1	21.1	1.9	1	R6NCR1_9FIRM	Uncharacterized protein	BN662_01233	Roseburia sp. CAG:45	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:45	1262947	>tr|R6NCR1|R6NCR1_9FIRM Uncharacterized protein OS=Roseburia sp. CAG:45 GN=BN662_01233 PE=4 SV=1MFGKFEKRMSGTQMIALGFLLLIFIGTILLMLPVSSRNGEWTPFITALFTSTSATCVTGLVLVDTFTHWSIFGQLVLLVLIQIGGLGFITIGVTVSLILRKKIGLKQRGLIKESLNTLEIGGVVVRLVRRVIGGTFLFEMSGAFILTLRFLKDMDVLHAIYYGIFHSISAFCNAGFDLMGRYSPFSSITRFYNDPVVILTISALILIGGIGFFVWNDLREHGLHCRHYALQTKMVLSATAVCLFGGTLLFYLFEHNRLFAGMSFGEQLLNSFFCTVTPRTAGFNAVDNGALSESSKFLSIVFMFIGGAPGSTAGGVKVTTIFVLLLSVRSTLTRTTGTNIFGRRLEESVITKSVVVLMFQLTLALSATLAITAISGYPVIDVAFEAFSALDTVGMSTGITSSLSTSCHIILILLMYLGRLGSLSFALSFTDKKRIAHVMQPVEKINVG	1262947	
8.4E-48	173	27.7	1.3E-46	168.6	19.2	2.1	1	C7NCJ8_LEPBD	Cation transporter	Lebu_1982	Leptotrichia buccalis (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249 / C-1013-b)	481	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Leptotrichiaceae, Leptotrichia, Leptotrichia buccalis, Leptotrichia buccalis (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249 / C-1013-b)	523794	>tr|C7NCJ8|C7NCJ8_LEPBD Cation transporter OS=Leptotrichia buccalis (strain ATCC 14201 / DSM 1135 / JCM 12969 / NCTC 10249 / C-1013-b) GN=Lebu_1982 PE=4 SV=1MNKKMISFITGRILILEAGLMILPLIISFLYNENAKYKIAYGTVILMLLATGFLLSAKTPEETSIQGREGYIIVSLSWILMSMFGALPFVITKEIPSFIDAFFEIVSGFTTTGSSIITDLSKISHSNLFWRSFTHFVGGMGVLVLALAIFPSSATSVHVMKAEVPGPTFGKLVSKLSTTARMLYKIYIVMTIVLIILLMFGGLDLFESSLLAFGTAGTGGFGVRNGSILPYNNPYIEIVLGIGMIVFGVNFNIYYFILIGKVKDVLKNEELRYYLLIVFGAITLIVLNICKTYTSLAHCIRDVFFSVSSVITTTGYSTADFGKWPLFSQVILLILMFFGACAGSTAGGLKISRVVLMIKIYFAEIIQMISPNRVIAIKSDDKPVNVKMQKSIAVYFLIYSLVFGGILLIISYSVDDFMTAFSAVAATFNNIGPGLGKVGPAFSFAELNNFSKIVLSFGMLAGRLEIFPMLILFSPTTWKLK	523794	
8.4E-48	173	41.2	6E-47	169.7	28.7	1.9	1	Q7V3J1_PROMP	Possible sodium transporter, Trk family	PMM0084	Prochlorococcus marinus subsp. pastoris (strain CCMP1986 / MED4)	467	cellular organisms, Bacteria, Cyanobacteria, Prochlorales, Prochlorococcaceae, Prochlorococcus, Prochlorococcus marinus, Prochlorococcus marinus subsp. pastoris, Prochlorococcus marinus subsp. pastoris (strain CCMP1986 / MED4)	59919	>tr|Q7V3J1|Q7V3J1_PROMP Possible sodium transporter, Trk family OS=Prochlorococcus marinus subsp. pastoris (strain CCMP1986 / MED4) GN=PMM0084 PE=4 SV=1MKIKNVVYKLKEIYRKLSVPQFTIVTGLIIIIFGTLILSSPLCSSSDVGLWEAFFTSTSAITVTGLTIIDVGVDLNIFGQIFLALMLLSGGLGLMAITTFLQGFVVKGTQLRTRLDKGKTLDEFGVGGIGRTFQSIAITATSIISFGAIVLYFFGFLEIQNNWQRLWSAIFHSISAYNNAGFSLWSKSLQDYRSNFVVNVVFIFLIVMGGLGWRVIDDIWSNRKNLSYKKLSLHSRLVIRTSFSLIIFGSLGFFITETLLNSQFFSDLNFFEKVLSSIFETVSARTAGFTNFPISLNSISDTGLLLLMTLMFIGASTGGTGGGIKTTTFIALMAATRSTLRGQKDVIISNRLISDKVILKAVGITVGSLLFVLLMAMLLSTTNTFIKKESFTFLEILFTCISAFATVGFDIGLTAKLNHFGQFILIIGMFVGRLGILLLLSALWQALYKSRIERQKRIGYPKADLYV	59919	
8.5E-48	173	34.3	1.4E-47	171.7	23.8	1.3	1	S0GQ97_9PORP	Uncharacterized protein	C803_01731	Parabacteroides goldsteinii dnLKV18	607	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides goldsteinii, Parabacteroides goldsteinii dnLKV18	1235789	>tr|S0GQ97|S0GQ97_9PORP Uncharacterized protein OS=Parabacteroides goldsteinii dnLKV18 GN=C803_01731 PE=4 SV=1MDIKHIQFTCRMYWANMKGILNIFAEGLILLASIASLFVLIYQFGFQQTSETIHHLYLSRIYILLAFFIGITLRYIVRFGEIIQEKLLYLDIGIYFLLFAVLSAKVFFREVIQQSLPYLDFLSKPLFVYTLMLLLSMIHLSRQTFTLMQTRIKPSLLFLLSFIFVILIGAGLLMLPNATTRPIHFVDALFTATTSVCVTGLTTVDVATTFTHIGHVIIMILIQIGGIGVMTFTSFFALSFMGHSSFTSKLVLKDMLNEDRIGGLFRVILNILFVTFFIEGIGAYFIYMDIRGVLPGATTQDNIFFAIFHAVSAFCNAGISTLSGNMCDPIVAHNYNLHVWISLLIIFGGLGFPIVFNYLKLLRHFIVNTFMIAIGQQKHYIHTPRIININHTYIVVISTLVLIVGGMFFYFLFEMNNTLADLPLKGKLADSLLGAVTPRTAGFTVANMDALRPVTLMLTLILMVIGAAPMSTGGGLKVTTVFVAIATALNVSREKEKVEVRKREISPATIRRAFATIVFYFIFASLAVWILSYTEEGTPVFTLTFEVVSALSTVGSSLNFTPMLSMAGKLIIICTMLIGRIGVLTFMVSFMREYKKRDYTYPQENILM	1235789	
8.7E-48	172	27.2	3.1E-47	170.6	18.9	1.6	1	R7K7Q9_9FIRM	Potassium uptake protein TrkH family	BN603_01242	Subdoligranulum sp. CAG:314	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Subdoligranulum, environmental samples, Subdoligranulum sp. CAG:314	1262970	>tr|R7K7Q9|R7K7Q9_9FIRM Potassium uptake protein TrkH family OS=Subdoligranulum sp. CAG:314 GN=BN603_01242 PE=4 SV=1MTKNRNGKKIRLKETQLLILGYLLVILVGSFLLSLPAASRDGEWTNYADALFTATSSTCVTGLVTADTFLKWTGFGQVVILILIQIGGLGFMTVITTTLMVLGRKIGLYERKILMQSAGTMRLSGIVHLVRRITIGTAIFEGAGALLLATRLCPKLGFWEGLYSSVFHSVSAFCNAGYDLMGRYGAFGSLAAFSGDWVVCLTIMGLIFMGGIGFIVWSDVLDCGFNPKKFSLHTKIALYGTTALIFAGALLFWLFEKSNLLVGKSAGESFLICMFMSVTPRTAGFATIDYAAATDSSLLLTMFLMLVGGSSGGTAGGIKVTTFVVIILGVVSSARSDGDIVIGKRRLEKNLVNQALGLLAVYLAAIFAAILIMSAIEPFSLADIGIEVFSAINTVGLSTGITPDLTLTSQIILMLLMLMGRVGALSFTLAFTQNKPILTKYPVEKILIG	1262970	
9.4E-48	172	24.9	2.2E-47	171.1	17.3	1.5	1	D1BM95_VEIPT	Cation transporter	Vpar_0821	Veillonella parvula (strain ATCC 10790 / DSM 2008 / JCM 12972 / Te3) (Veillonella alcalescens)	495	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Veillonella, Veillonella parvula, Veillonella parvula (strain ATCC 10790 / DSM 2008 / JCM 12972 / Te3) (Veillonella alcalescens)	479436	>tr|D1BM95|D1BM95_VEIPT Cation transporter OS=Veillonella parvula (strain ATCC 10790 / DSM 2008 / JCM 12972 / Te3) GN=Vpar_0821 PE=4 SV=1MRIQIVMSLVGRLLYIFGAFTLIPFIYSVVFETAYWSFLITTSLSLVLGTFLSYYGCESQSFSIRDGFLVVSATWIFTVILGSLPFLGSGILTNIFDALFEATSGITATGATIIYSVDELPNTFVLWRGLMHWVGGMGIIVLILSFLKNLGADAAHFFNAEASVPKPGIVMPRIQSMATKLWQLYIAFTALCFLMLWAGGIEPFDALNYAFSIIATGGFAPTSAGAFIYEQSNYICFVFIFFMFLAGGNFSVYYNALQKGIRVLINDFETRMYWLVVFIGIAIVSISLALQSSYSSPLEIVRNAAFNLVSLQTGSGFAISDYDLWPAAAQMMLFICTFFGGCSGSTTGGVKIIRLIILIKSSIIYLRKSIHPDMVQVVRINGKPMPTKWIQMTHQFLFLYLMIYVVSVFLMTCTGLNTYDSMQVVTAFLSNVGLGFGGFGPTDSFNVMPDTAKCIAIVDMLLGRLELFTILVMLHPQFWEGYFIKKEVPKRYRIL	479436	

9.6E-48	172	25.2	3E-46	167.4	17.5	2	1	D9R751_CLOSW	Cation transporter	Closa_2947	Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	492	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	610130	>tr|D9R751|D9R751_CLOSW Cation transporter OS=Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1) GN=Closa_2947 PE=4 SV=1MTRRFSDCSSCGKLMMLVGVLVATPLTVLPFYPEDVIYALSFLIPASGSIFLGTILCLFGRRDGDGGLEWRSSIQRSSLTVLFAWSWGIFIGALPFVISRQLTVLQAFFESVSGWTTTGLSVMDVTITPKIFLFHRSFMQFCGGLGFVMMMVMFVSGKQSMNLYSAEGHPDKLMPNLKKTAQTVFAMYSSFLVVGTAAYRIAGMELFDAIMHTMCALSTGGFSTRLNSIGEYNNFSIEVITIVLMLIGTTNFAVLLLLAKRKWRQFVRVSEIRFMFLLLLLFVPLTAISLSYGLGISLEQGLRKASFDIVSALSTTGYSTMSYTSWPPFAIGVLILMMLIGGGMGSTAGGIKLSRVYIMLRLAALDIRRRLTPARNVEAPYYIKAQGKTPIDASLTADTTGFAVCYLVLFLTGSLLTTVTADCGLTEGMFEFASALGTVGLSIGLTGPATGAGTLIVEMFGMIMGRLEIFIVLIALYSGVSILRQGFHKTED
9.7E-48	172	22.2	2.4E-46	167.6	15.4	2	1	B8HDV7_ARTCA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Achl_2860	Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	460	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter chlorophenolicus, Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	452863	>tr|B8HDV7|B8HDV7_ARTCA H(+)-transporting two-sector ATPase OS=Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6) GN=Achl_2860 PE=4 SV=1MAAQAGTKDGPSRRESVLRRLLSHPVRSLPLAFLAVIIVGAGLLMLPASRTGNGPDAFMAAAFTSVSAVCVTGLATVDTATYWTPFGQAVILGLVQAGGFGIMTLATLLALLVRKSIGLRGQLVAQSETHTLNLGDVRSVLLRVARIMLFFEGLTALVLTVHFWISYGKDPVGAAWHGIFHAVSAFNNAGFALYSNSLIGFAEDPWVIVPICLAIIAGGLGFPVIIQLTGGGVHPRNWTVHLRLTVYGTLFLLAVGMALFAAFEWNRGETLGNLSLTGKLVGSFAGSVFPRTAGFNSIDYGAASPETLMVTNVLMFIGGGSAGTAGGIKITTFLVLGFAIWNEVRGRDTVTIAHRSISSSSQRQALSVALLGIAAVIVGTMMLLMLTDHSLEKVLFESISAFGTVGMSTGITPTLPPAAQWVLMVLMFTGRIGTVTVASALALSARPRLFRLPEERPIIG
9.8E-48	172	23.2	2.4E-47	170.9	16.1	1.5	1	A0A0B4XU97_9PROT	Trk system potassium uptake protein	TH3_00670	Thalassospira xiamenensis M-5 = DSM 17429	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Thalassospira, Thalassospira xiamenensis, Thalassospira xiamenensis M-5 = DSM 17429	1123366	>tr|A0A0B4XU97|A0A0B4XU97_9PROT Trk system potassium uptake protein OS=Thalassospira xiamenensis M-5 = DSM 17429 GN=TH3_00670 PE=3 SV=1MIDFRPILFIIGILLCTLSIGMFIPALVDMYYGQRDWLVFSAASAVSLFIGGALVMMNRTENLKITSRQAFILTTTSWLVLTAVSALPFAFSDLDMSYTDAFFEAMSGISTTGSTVIVGLDTAPPGILLWRALLQWLGGIGIIVMAIAVMPMLRVGGMQLFRMENSDKSDKAFPRATQIAIGIASLYLGFTIIWAFLLWWAGMPGFDSIAHAMTTIATGGFSTKDASVGHFDNAAVDVIITLGMATGALPFILYLQMLRGRTLALFMDGQVRWFVAIASSIILGLTIWHSQTNDVAFLNALRYTSFNIISVMTGTGYATTDYGLWGPFAVTVFFFVMFIGGCAGSTTCGVKIFRLQVLYEIAKVQLSHMLRPHGVFIAYYNRKPLSEDVTESVLSFFFLFVFCFVVLAAALGAMGLDFITAVSSAGTAIANVGPGLGPIVGPSGNFATLPDGAKWLMSIGMLIGRLEVFTVLVLLFPAFWRD
9.9E-48	172	12.9	3.4E-47	170.5	8.9	1.7	1	A0A0F2RDM0_9RHOB	Trk system potassium uptake protein	VR74_11360	Hyphomonas sp. BRH_c22	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hyphomonas, Hyphomonas sp. BRH_c22	1629710	>tr|A0A0F2RDM0|A0A0F2RDM0_9RHOB Trk system potassium uptake protein OS=Hyphomonas sp. BRH_c22 GN=VR74_11360 PE=3 SV=1MQLRPVLLAIGIMTILLGAAMIPCALMDMADNRPEAYVFAVSSFGTIFIGTCLWVLARGGDQRTGQREAFLLTVMAWVFLPAMASIPFLASGMSITDAVFECISGMTTTGSTVLTGLDDLPRGLLLWRAILQWIGGIGIIVAAIAILPQLRVGGMQLFQLESSDISGKFLPRITDIAAYLGFTYLLISSLCALLYFLAGMSWFDAVTHAMTTMSAGGYSTHDASFGYFNETPAAWIAAPFMMFAGLPFALLAMLVLQGRPMPLLKDPQPRFYFGLAAVLTLIVTVYYETVIDTEGAGTILGNLKICLFNVVSVMTGTGYASAPYDTWGQPMLALFLCITFLGGCAGSAAGGLKMFRLEIITAKALVAYSHKMTMPHRRTPVRYGGRTLDEETLQSVMVFLFLFISTFMIAAALLSLCGLGAMEAISASATSVSNVGPGLGPIIGPSGTFQTLPDAAKWICAIAMLLGRLEFISVFVVLTRRFWQG
1E-47	172	32	1E-47	172.2	22.2	2.4	1	Q8EZ85_LEPIN	Potassium uptake transporter	trkG LA_3971	Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	599	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira interrogans, Leptospira interrogans serovar Lai, Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	189518	>tr|Q8EZ85|Q8EZ85_LEPIN Potassium uptake transporter OS=Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) GN=trkG PE=4 SV=1MNSIKDIIFKLSNIRRNVTIFYQTKIYPFLRIYYSICGTISLCLLVLIYGFYYPHEWTHWIRLIVNVIVVSLVVYEALSFIFVENNLFNYLKTHKTEAIVVFLIVFQEIISQEIYEILTLDSLSGEDASLAFLSLSQLFLLFSNFSRLIRKTELLNYRQISPSLVIAVSFGILILLGTLALSLPRAQATSISTIDVFFTVVSAVCVTGLSTISVSTQLTGTGQTILMILIQIGGLGLMTLTVFFAIFLAGQVSVTNKLLIKDLFSQESVGRASSVLKQVAAQTFLIEAIGVLLIFICYPDSNETNLKNKIFYSLFHSVSSFCNAGFSTFPKGFETDWMNLNQKEFLSVVMILIVLGGLGFPTVNHLIQWVFKIGDYPKRMELGVKLILTVTVGLILFGMVSYYVLERKETLSELGIIDGMFHSLFYSISSRTAGFNTLSISKMGTPMIFVSLFLMWVGASPNGTGGGIKTTTLAISVLHLFNHIRGKEELEVFGRRVSSGTTSRASAGILVSLFIFFGIFFLTCTENSAFLDLCYEVVSAFGTAGLSRGITPSLTSAGKVLICLMMFCGRVGMLTILIAFVPKEKKSGLKFPEESVIVG
1E-47	172	33.5	1.3E-47	171.8	23.3	1	1	R6QP41_9FIRM	TrkH family potassium uptake protein	BN583_01720	Anaerostipes sp. CAG:276	452	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, environmental samples, Anaerostipes sp. CAG:276	1262699	>tr|R6QP41|R6QP41_9FIRM TrkH family potassium uptake protein OS=Anaerostipes sp. CAG:276 GN=BN583_01720 PE=4 SV=1MKKIKPVHIILFGFLFVILIGSVLLTLPISSKSGEATPYINALFTSTTSVCVTGLVVETTMTYWSTFGQLVILVLIQLGGLGVITFTTGMFLFLKKKLTMKNRMLIQESFSLNTMSGLIELVRKILKGTFIIEGIGAALFATQFIPEFGVRYGIWASVFNSVSAFCNAGIDIIQTDSLRSYITNPVVNFTVMGLIVLGGLGFIVWRDLLRVFRGLIHREFPLKRAFGKLKLHSKIVLSTTVILIFIGTVFIFIFEFANTKTIGNLSLGNKLMASMFQSVTVRTAGFETVPQAALTEGSSLISMILMFIGGSPVGTAGGVKTVTFVVLVYCVLVTVKQEGAIHIFKRTIPMTVIPKALTIICVNLIVLLSSILVVLVSDSASFMDTCYECVSALGTVGLSKGLTPDLSVIGRLAIIITMYLGRVGPVSLAVGFAVRGKKKVLATYPEEDIILG
1E-47	172	34.4	8.7E-47	169.1	23.9	1.9	1	A0A098C0D5_9PORP	Uncharacterized protein	ING2E5B_1129	Porphyromonadaceae bacterium ING2-E5B	488	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, unclassified Porphyromonadaceae, Porphyromonadaceae bacterium ING2-E5B	1562970	>tr|A0A098C0D5|A0A098C0D5_9PORP Uncharacterized protein OS=Porphyromonadaceae bacterium ING2-E5B GN=ING2E5B_1129 PE=4 SV=1MHRFNYRFVFSSIGLVLMIEALFMLFSALIGEYYNESAVRSIYISSIVTSLSGTFFMFLGRKKNKRSGNITKREVYITVTAVWLVLSVYGTLPYLLSGSIPSFTNAFFESMCGFTTTGSSTLFNIEAFPKSLHFWRSITQWIGGIGIVIFVLSFMTVFGSVSAHFYEVESIGIAEDLFRPRIKEVSKNIALTYVALTIIGFFFLWAGPMDAFDAACHTFSAISTGGFSTKHYSIASFNSPFTEYVITLLMFFGATNFLLISAIFSKFSFKMLKNEEFRWYVSLIMLFTIGITGALLATGQMSDIEETFRTVLFQVVAAITTTGYATVDFLAWGPFYWLLFLVLILFCGCEGSTSGGMKISRLVVLAKNSLLVFKRQVHPNALYMVKINDKVVSNDSISKVIAFVFLYIFVTIMSAVILSLTGMTFEESISVALSTISNYGFGLGSYGPSGTFESATVFAKYFLSFLMLVGRLEIFTVLSLFVPSFWKR
1.1E-47	172	33.8	1.7E-46	168.2	23.4	1.9	1	R4KPI3_9FIRM	Trk-type K+ transport system, membrane component	Desgi_2112	Desulfotomaculum gibsoniae DSM 7213	437	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum gibsoniae, Desulfotomaculum gibsoniae DSM 7213	767817	>tr|R4KPI3|R4KPI3_9FIRM Trk-type K+ transport system, membrane component OS=Desulfotomaculum gibsoniae DSM 7213 GN=Desgi_2112 PE=4 SV=1MYKKLKPGQLLLISYALVDLVGTLLLLLPIASTEPGPANLVQAWFTATSALTVTGLTVVTTATHWTMFGHMVIMILIQIGGLGLMALATIILAMLGLRIHLGHRLLVVQDRNYFSMSGVIRLVLNIFLLTLVLESIGAVILAFLFPGVWDNGLIEGLLFVVFHAVSAFNGAGFDLTGQSLEPFRDYLGINLVMIALIILGSLGFVVLQELFLVRKWHRLSLHSRMVLLVTGAVTLLGSIFFLASEYNHTLAGAPPEDKIVISLFQAATRTAGFTTVPIMSWSEPFIFLMIIMMFIGASPGSVGGGIKTTTFGTVVLAVWSIVRGKKAVVLFEREIAPESVTKAFTVVVMAGMLVAIITLLLMIVEGLPLVPVLFEVVSAMATVGLSTGITSHLSPFGMALIGLVMFVGRIGVLTVVVVLAGKEKRRSHYMKEDILIG

1.1E-47	172	16.8	4E-25	97.7	2.1	2	2	A0A0B5DXP1_9RHOB	Trk system potassium uptake protein	P73_3483	Celeribacter indicus	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Celeribacter, Celeribacter indicus	1208324	>tr|A0A0B5DXP1|A0A0B5DXP1_9RHOB Trk system potassium uptake protein OS=Celeribacter indicus GN=P73_3483 PE=3 SV=1MTDLRPVGYVIGILVALLGLTMAIPMAVDAAAGTDEWVVFFEAGLVTLVTGGSLALASANGQSQRLTIQQMFLLTTLVWLVLPLF GGLPFMLGATGASFTDAFFEAMSGMTTTGSTVLSGLDDLPKGLLLWRSMMQWFGGVGIIVVAMVFLPELKVGGMQVFRSEAFETD GKVLPRAAEIAAKISVIYVWLTVACFLAYLLVGMSTFDALNHALTTLSTGGFSTRDASFGAFQGPAEYVSSLFMILASLPFVRFVQLLAG TARPLWRDTQIHAYLVIILGLTLAFALYRLVANGDHFEHSFREGLFNVTSIISGTGYASVDYQLWGAFPAVAFFFIGLIGGCAGSTACSV KVFRYQLLWASMRAQIRKIHSPHGVFTPRYQGQPVTEDVLSSVMAFFSFFIVTLGISAVLLSATGLDFVTAVSGAATALACVGPGLGEI IGPAGNFASLNDPAKWVLSIVMLIGRLEVMSVFALFTIRFWRA
1.2E-47	172	35.6	1.9E-46	168	24.7	2.5	1	R5J7K8_9FIRM	V-type sodium ATP synthase subunit J	BN738_01380	Peptostreptococcus anaerobius CAG:621	455	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptostreptococcus, environmental samples, Peptostreptococcus anaerobius CAG:621	1263100	>tr|R5J7K8|R5J7K8_9FIRM V-type sodium ATP synthase subunit J OS=Peptostreptococcus anaerobius CAG:621 GN=BN738_01380 PE=4 SV=1MLKKFRNKPTILYWLSPAQIMVFGFGSIILLGAFLLTLPIASNKGVWTPFIDCLFTATSSVCVTGLVVLDTSLHWSLFGKIVIILLIQI GGLGFMTISTLIVLFLGKKVDIRQRVLIKESYNQDHISGTIKMVLAVIKYTFSVEILGSIMLSTVFIPEFGLYKGIGYSVFHSISAFCNAGFD LFGSKYGAFTSISHYYNNPVVVFTIAALIILGGAGFFVGANILSGKSLKKWKLTSKLGVLIMVFLLVLGTVLLFTGEYNHSLSGMTGLEKF EVAFFQSVTARTAGFATIDLTKFRESSLLVMIFLMFIGASPASTGGGIKTTTFAVLLLALRTFLKNESEITVFRRRIGVYTIRKSIGVLVMG MIFLLVGTYLISATQGPKFGLLESSFEVTSAYATVGLSLAGTNNLNGLGRFILIVLMFAGRVGSLTLVSIFIKENKMKNVRYAEESITVG
1.2E-47	172	27.6	3.4E-47	170.5	19	1.8	1	R7J587_9BACT	TrkH family potassium uptake protein	BN799_00148	Prevotella sp. CAG:873	495	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:873	1262936	>tr|R7J587|R7J587_9BACT TrkH family potassium uptake protein OS=Prevotella sp. CAG:873 GN=BN799_00148 PE=4 SV=1MQVLQNIRERRFINFPMLLKTVGWLLMIESVFICVPTIVSLCYGEDDWSIFALTVAITFAVGFILNNCVHATYSRMARREGFLLTGF TWVIFSLFGMLPLIFASSSHLSITDAFFESVSCFTTTGASAYLDAESLSHGVHIWRAIMQWTGGMGIILFTLAVIPMLNSSGGMQMFNA EVTGITHDKVRPRISQTAKALWVTYFVLTACCAILLMIGHMDVFDSICYAFGTLSTGGYSTRASVDFFNSDYIKVVITVFMFLGGVNFAL LVRNAIRNPRRLWDDDVFRWFIIIIIAITAISSITLLSVGVEDTWREAIIDPLFQTVTSTITSTGYVVNSISQWGPFVMGLLMILVFIGGCAGS TSGGVKLDRIIFLFKHIHNELYRCIHPNAVLPVRLNSRVLPPQLVNKVVVFVCLYMLTIIIGGLIMTIFGLNVKDALLSSLMCISNASPNFGL TSFGEEYSMLADGCKWVLAWIMLIGRLEVFTIVIVFTPSFWHK
1.2E-47	172	2	3.6E-44	160.5	0	2	2	J3NI46_GAGT3	Uncharacterized protein	GGTG_00929 GGTG_00929	Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	517	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Sordariomycetidae, Magnaporthales, Magnaporthaceae, Gaeumannomyces, Gaeumannomyces graminis, Gaeumannomyces graminis var. tritici, Gaeumannomyces graminis var. tritici (strain R3-111a-1) (Wheat and barley take-all root rot fungus)	644352	>tr|J3NI46|J3NI46_GAGT3 Uncharacterized protein OS=Gaeumannomyces graminis var. tritici (strain R3-111a-1) GN=GGTG_00929 PE=4 SV=1MRHGDGRVENASFPAGVLRRLQGLLPPLTFITCHYAYFVGMCLVFSLIFWGSSSAVFPVGYVDSLFLVVSAMTGTGLNTVNLSH LNTWQQIMLFLLIMFGGPIWVSVWTFLARKRAFERRFNDVVRAAGERTKSPCHSATSPVAAAVGYLLLPVVPWSRSQSSRPTVKGP QAGCAGDGARRPRSTNGANKPQFDAAVGLGPETGGLAVGDDVALETHTPPGAAANEGRITFADVVNNVPLRKRPPHRTSADPGAP SDKAEGKLPRARESGNGGVREFLDTIPVGCNGQFHDLSSEEREQPGGTEYRALKVLATVVPLYFALWQLAGCLALGAWMAVNMPD VALANGIDPWWLSIFNGVSAFNNSGMSLLDANMIPFGQAAFVLVTMALLILAGNTAYPVFLRLIFWAWLKLLKLATGEGALVDFKATLE FILRYPRRVVTNMFPSRPTWWLLFMVVLLNSIDWAAFELLNLGNPVIESIPKGARVLGGLLQAAVVRSGGFSVVPIAKVSIGLLSVGF
1.2E-47	172	35.7	1.2E-47	171.9	24.2	1.4	1	A0A0B5RPM1_9FLAO	ATPase	MPR_1806	Myroides profundi	533	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Myroides, Myroides profundi	480520	>tr|A0A0B5RPM1|A0A0B5RPM1_9FLAO ATPase OS=Myroides profundi GN=MPR_1806 PE=4 SV=1MLAIVRRYFNKDNHETLGVKIFDCFSIVLFLILIIARWQPEHTIRFFDSNAVISFGLFLMLVREFSVLQLNLKQTRMNPAQLFVVSFL LIIFIGAFMLSFPKATNTPGSMRYIDALFTATSAVCVTGLSTVDIGAQFTIFGKTVMIFLMECGGLGIMTLASYFSFFFRGKASYGNQLVL KDMSYIDKLGDVFATLKRIIIISGIIQFIGMIAIFISIRHQHFESLFDRVFFSIFHAVSAFCNAGFSTLPENLYTFEYRFNYPLHLIAGLFIMGG LGFPIVFNVYKYVKHLIINKLLPFSMKEAKIHIPRVINLSTRIILITTAVLIVGGTAVVYISEYNNTLAEHSGFGKLVTAFFTATSPRTAGFAT VDNNLFTTSTFLVVILLMWIGASPVSTGGGIKTSTFAIAVLNIWALMKGRSRIEVYRREVDQLSVQRAFAIIFLSLFVIGIAIFALSFFEPKT DLLRLAYEAFSAYSTSGLSTGITAQLTDPSKVTLIMLMFIGRVSMLTILIAISKKEKLTNYRYPTEEILIN
1.2E-47	172	19.6	1.1E-28	109.4	3.3	2.1	2	G4Q358_ACIIR	Uncharacterized protein	Acin_1650	Acidaminococcus intestini (strain RyC-MR95)	481	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Acidaminococcaceae, Acidaminococcus, Acidaminococcus intestini, Acidaminococcus intestini (strain RyC-MR95)	568816	>tr|G4Q358|G4Q358_ACIIR Uncharacterized protein OS=Acidaminococcus intestini (strain RyC-MR95) GN=Acin_1650 PE=4 SV=1MNYAVIGRILSWVLRTEGLLMLLPCLIALIYGEWQGLVYLALGVGAIAAGWLLSRKKIANPAIYQREGFVSVGLSWVVLSLYGAIP FVITGEIPVFLDALFEIVSGFTTTGSSILANVEALSHTSLFWRSFSHWIGGMGVLVFILMMIPSGSGGTQINLMKAESPGPDVSKFVPRV KNTAIVLYRIYLGMTLLMIAILAFSGMNWFHNLCITFGTAGTGGFGVLNSSCAEYTPFQQWIITIFMIAFGVNFSFYYLLLTKNFYEAFHL EEVGAYLAIILCAGLAITWQIEPRYGNFEEALRVAYFQVGSIITTTGFSTVDFDLWPSFSKTILVMLMIIGACAGSTGGGVKVSRVVLVM KSIKQELRQIIHPHGVQCVRMDKKTVDRKVLSSLYVYLTSYFFVFGLSVLAISLENFSFTTNFTAVAATLNNIGPGLAEVGPSRNFGVYG DFSKLVLIFDMLAGRLELLPMLLLFYPRTWSSKC
1.3E-47	172	36.6	1.4E-45	165.2	25.4	2	1	Q81T78_BACAN	Ktr system potassium uptake protein B (Potassium uptake protein, TrkH family)	ktrB GBAA_1409 BF27_5568	Bacillus anthracis	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus anthracis	1392	>tr|Q81T78|Q81T78_BACAN Ktr system potassium uptake protein B OS=Bacillus anthracis GN=ktrB PE=4 SV=1MEVTKRQRLYNRFIRLNPPQILALGFFCLIVVGGLLLKLPFATKVHISWVDAFFTATSAATVTGLGVVVDTASTFTMFGEIVIMFLIQ TGGLGLMTIAILIVWVLGKKIGLRHRLLIGEAFNQTNIGGLVKLVKRVFIFSICIEFIGVIFLSFRFIPEFGFGKGIHYSIFHVIASYNNAGFAL WPDNLTRYVGDPIINIGICSLIVIGGLGFTVLIDIWYSRSFRKLSLHSKIMIVGTVALNVIAMIVIFILEYNNVKTLGNLPLNEKLWASFFQGI TPRTAGFNTVDYGGMEESSILFTMVLMFIGAGSVSTGGGIKLTTFVILVTSVLSFFRKKEEIVLFQRTIKMSTVTRALAIAVASQILIFAAV FVLMLTENFSFIQLLFETISAFGTVGLTMGITAKLSAFGKCIIMFVMFCGLIGPLTLVFSLARPAKQKIKYPSEDVFTG
1.3E-47	172	18.6	6.1E-46	166.3	12.9	2	1	D1CF40_THET1	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Tter_0628	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	417	cellular organisms, Bacteria, unclassified Bacteria, Thermobaculum, Thermobaculum terrenum, Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	525904	>tr|D1CF40|D1CF40_THET1 H(+)-transporting two-sector ATPase OS=Thermobaculum terrenum (strain ATCC BAA-798 / YNP1) GN=Tter_0628 PE=4 SV=1MLPVSSNHGWTSPLVALFTSTSAVCVTGLVVVDTGTYWSPFGQLVILLLMEVGGLGFVVGATALVLLGKGRLGFQEREIVRQT GTTLILGGQSSFVTRAVTLALVGQLAGAILLLIRFIPEFGLIRGIWMSIFHSVAAFTNGSFDLFGDYRSLAGYRSDPLVLLTIAMLIAGGT SLLVAEDLWRHRSWRKFTLDTKIIVIGIPTLLILGTVFIMLIESKNPNTLGNRPLGEQLLNSFFHSSAARTAGFTTWNFGLSDDRTLFFVI GLMFIGSAPGSMAGGIKITTMAIILAVAWSNILGRRDTELMRRRVPQEQVGQALTVALLGVLLIVTIALTISLLERARFRDDFIKVLFEVTS AFGTVGLSTGITPELSAPSQILLIITMFVGRLGPVTLATSLSHRSQSKYRFPIESVRIG

1.3E-47	172	19.6	1.7E-47	171.5	13.6	1.1	1	R6RP95_9CLOT	Uncharacterized protein	BN719_00799	Clostridium sp. CAG:58	338	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	1262824	>tr|R6RP95|R6RP95_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:58 GN=BN719_00799 PE=4 SV=1MREAVAAPQVGGIVRMTRFILKGTLLIEGLGAAALALYFCPRLGLFKGLYYSVFHSVSAFCNAGFDLMGAETPFSSLTAEAGNW YLNLVIMALIVIGGLGFFVWLDLLDSRFRFKNLRLHSKIVVFMTAVLLAGGALGLFLLELTGEAYEGMSLGDRILASLFQSVTVRTAGFN TVDLAALREGSIFLMICLMVVGGSTGSTAGGMKTTTAAVLVLSIFSTFRQKKNVECFKRRLEDGITRTASCIFMMYLILIILSTLVLSAAE GIPVLTAMFETTSAIATVGVTLGITPEVSMVSKLVLAFLMIFGRAGSLTMLLAFASDRPPVASKKPLEKIQVG
1.3E-47	172	27.9	3.6E-47	170.4	19.3	1.7	1	R5EG80_9GAMM	Trk system potassium uptake protein	BN779_00454	Succinatimonas sp. CAG:777	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Succinivibrionaceae, Succinatimonas, environmental samples, Succinatimonas sp. CAG:777	1262974	>tr|R5EG80|R5EG80_9GAMM Trk system potassium uptake protein OS=Succinatimonas sp. CAG:777 GN=BN779_00454 PE=3 SV=1MVIDFRLVAKLLAPALFLFGIVAFIPAIYALCNTTHGIGAFVATGIIGLFVSFCCHTLGKKAGQNPSIRVLFLFTTSLWVIVSLIAAIPF YYQLPDLSFSQSLFEACSGLSTTGSTVITHLEQRPQAIILWRAILHYIGGVGFVALAVVILPISAMGGMSIFKTESQSFDDSAKFTPHLKT MVISLFVWYVAILVTCTLFYVVGGFDIFTAITTAMSTVSTGGMTATDASMNGTTPFIQYVTIVFMLISSCPFLLILSSLSGNFFKFFKDQQ VKGFILLNVIVATAVAISLIYMNDYDLEKAFRISFFNVVAVTSTTGYSLEDFTLWNPFASSLFLCILAIGGCSGSTSGGIKTFRIQICLSMFN TQLQKLLHPHIVSEPRFNRKVIDPATLSSVITYLVSYIFIAMLSSIVACSLGLDLGDSITATVSCLSNVGPAMGTTLNPSSNFSQVSNPLCL LFSVDMILGRLEILPVLICFTRMFYKR
1.4E-47	172	4.7	1.1E-46	168.8	3.3	1.8	1	D1AC18_THECD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Tcur_1710	Thermomonospora curvata (strain ATCC 19995 / DSM 43183 / JCM 3096 / NCIMB 10081)	449	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Thermomonosporaceae, Thermomonospora, Thermomonospora curvata, Thermomonospora curvata (strain ATCC 19995 / DSM 43183 / JCM 3096 / NCIMB 10081)	471852	>tr|D1AC18|D1AC18_THECD H(+)-transporting two-sector ATPase OS=Thermomonospora curvata (strain ATCC 19995 / DSM 43183 / JCM 3096 / NCIMB 10081) GN=Tcur_1710 PE=4 SV=1MSPAARLLARFQHPAQIVAVAFAAAIAVGTTLLALPVATAPGESTGALTALFTATTAVCITGLATVDTASHWSPFGQVVILVLMQA GGLGIMTLATLFALLVSGRLGLRARMLAQAETKALQGTGLRRVVRNIVLFSLCSEAVVAAVLGLRLALAYDEPAARAAYLGIFHAVSAF NNGGLALWPDSMMRFVADPWVLLPVALAVVLGGLGFPVVFELVRAWRRPKTWTVLTRITLGVSAALLAGGTLLFTIVEWHNPRTLG PLPDQTKFLAGFFTAVMPRSGGLNAIDISQMRPESWLATDILMFIGAGSAGTGGGIKVTTFGLLAFVMWAELRGEDRVNVGHRRLAG PVQRQALTIALLSVGLVALGTFVLLSLVPYALDRVLLEVVSAFGTVGLSTGITPHLPPGGQLLLVALMFVGRVGPLTVFSALALRERTRR YELPEERPIVG
1.4E-47	172	27.2	2E-46	167.9	18.8	2	1	Q87KD1_VIBPA	Trk system potassium uptake protein	VP3046	Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio harveyi group, Vibrio parahaemolyticus, Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	223926	>tr|Q87KD1|Q87KD1_VIBPA Trk system potassium uptake protein OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VP3046 PE=3 SV=1MVNLRPVLFVIGLVLSKLALFMYVPTLVAFFTGTGGFLDFAQAVVITHLAAFICLTIGRTAKFKLSVRDMFLITSLVWTIASAFAALP FVFINHISFTDAYFETMSGITTTGSTVLSGLDNMAPSILLWRSILQWLGGIGFIVMAVAILPMLNVGGMKLFQTESSDWSDKSSPRAKT VAKNIVLVYLILTGMCIGGYVLTGMNLFEAINHAFTTLSTGGYSTSDSSMNNFSNGAHWVATTFMFLGGLPFLLFVAALRKRSIDILVKD AQVRGFAYLFLFSSLVVAAWLVIRDGYTILDALRVSMFNIVSVVTTTGFGLEDFTAWGALPTTLFAFLMMAGACSGSTAGGIKIFRFQI AMTLLNKQIMKLIHPSGVFVQRYNQRPVNDDIVRSVVAFGLMFFITIIFIAGCLSALGLDPVTSISGSITAVANVGPGMGSVIGPTGNFAP LPDAAKWLLSFGMLMGRLEILTILVLFFPAFWRR
1.4E-47	172	14.3	8.7E-27	103.2	1.1	2.1	2	U5T843_9GAMM	Uncharacterized protein	SPICUR_07320	Spiribacter sp. UAH-SP71	512	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Spiribacter, Spiribacter sp. UAH-SP71	1335757	>tr|U5T843|U5T843_9GAMM Uncharacterized protein OS=Spiribacter sp. UAH-SP71 GN=SPICUR_07320 PE=4 SV=1MPRSACAAGAGSPSASVTWKADSVREVLRGTGFLLHVPGLMALLSLPIAGWAGEWWGAWGLATAAVALISGQLLVWTTRG TDRLYRYQSMLIAGISWLLIAIIGAIPVFVSAHLAPLPTESVLQPFRQPSHAFFESVSGFTSTGLTVVAAASELPHHIQWWRSFSQWIG GIGVILLLLAVVPAERGAINLYFSEARDEKILPTVKSTVQTIWAIYLGYTLGAIALLWIVGEPPWRAVNHGMTAIATGGFTITDDSLMSAP QAVQLAYVPIMLAGAVSFLIHYRLIVERVSPRSLWQLVEVRVLVWVLLGGGLLLWGQRWLTVGGSDTLISSVMVWVSAMTSAGFAAA DLSSWGDAALLLVLTAVLMGGMAGSTSGGVKLLRVGLLLKDLVGQLRSLRATPHEVVVLRYDGAHITPAQMASLGHTALRLVGIFMLL WLLGVFIMLHWLPADTRLAHVFFDTASALFNSGLDTGVVGPDLNAGAAVVLSILMLLGRLEVFPLLLLAAFFMGRR
1.4E-47	172	32.7	2.5E-47	170.9	22.6	1.3	1	R6DAH8_9BACE	Uncharacterized protein	BN772_03193	Bacteroides sp. CAG:754	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:754	1262750	>tr|R6DAH8|R6DAH8_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:754 GN=BN772_03193 PE=4 SV=1MKIYHKFLLYQNKLLKPYIRIVLGLLEALTYLASLTLIIGVIYEHGFPLSVDEVAKIQTLYKAVWIIFLIDVTLHILLEYRSTKKQYRRLA WILSVLLYLTLIPVIFHRPEEEGAILQLWEFLHGKFYHLVLLLIFSLLNLSNGLVRLLGRRTNPSLILAVSFLAIILGTGLLMLPRCTVNGIT WVDSLFTATSAVCVTGLVPVDVSTTFTTGGLVVIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLGSLLSTLLYILGF TLVIEGIGMISIWFSIHGTLGMNFEDELAFSAFHSISAFCNAGFSTLSGNLGNSMVMTNHNGLFISVSLLIILGGIGFPILVNFKDIVLYHLR HFWKFVRTRKLEKHRMLHLYNLNTKIVLIMTFLLLVIGTLAIAAFEWNASFAGMPVADKWTQAFFNATCPRTAGFSSVDLASLSVQTLL VYLVLMWIGGGAQSTAGGVKVNAFAVVVLNLVAVLRGTERVEVFGRELSHDSIRRSNATVVMSLGVLFLFIFILSILEPQASLMALTFE CVSALSTVGSSLNLTPVLCDASKLLVALLMFIGRVGLITLMLGIVKQKKNTKYRYPSDNIIIN
1.4E-47	172	37.7	3.2E-47	170.6	26.1	1.5	1	Q8EUQ4_MYCPE	Trk-type cation transport protein	MYPE8660	Mycoplasma penetrans (strain HF-2)	654	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma penetrans, Mycoplasma penetrans (strain HF-2)	272633	>tr|Q8EUQ4|Q8EUQ4_MYCPE Trk-type cation transport protein OS=Mycoplasma penetrans (strain HF-2) GN=MYPE8660 PE=4 SV=1MKLNVKNIKRKIRKLHFSFKNHHFFFSDKWKNLLMMHWTYPKKIFLGILLIWLVGAILLYTPISFNYESYQYINNEYVFNLKETTID QYMNSATAMHEYHFNFLKAIFTSASAFTNTGLSVIPSAGTYLSFFGQFIVFVLIEIGGFGYISLFYLIGKSLRKITKKDLFGTSLLNIERGG TKVSNSPKMIVRIFFVFIIIQIVFSLIFSGMFYSIPFYEQQSWAHFINTNSWTQIQYNVGGKIIQITPGDGFNEKANDLLSLTFDSNTLVKTY HNYPVSLWYSIFLTGSAVNNAGFDLFGYTSLQFLRNSNGISIQVLMLILIVIGGIGFPILYDLSNQVEWLIKYKIMYKIFKKQEYARFLKPK LSVFSKLCLWSALIVSAVSLAILYLTEYVGSNSYVGFEMNDSNIITGGSFFQNNISLINYPISANVQWSDGSSSLVSFWHGDPSLNKNF SIFFNCIASRSSGFSTVNFQNMTEASIVVLAILMFIGTSPSSTGAGIRTTTLFIMIKSLLSWYRGVEKTSMFKRKIPIKTIKESYMVFLSAVI LVLVCTSIVFITSAHLINGKNLVADEYSSSNKIFNFSSFFFEICSAFGTSGNSMGITGSSSIQWWNLVILVILMYVGQMSMSAANLLFARK VPKKQESFYLEEDIRIG
1.5E-47	172	20.2	6.6E-45	162.9	14	2.1	1	Q88FX4_PSEPK	Trk system potassium uptake protein	PP_3953	Pseudomonas putida (strain KT2440)	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas putida (Arthrobacter siderocapsulatus), Pseudomonas putida (strain KT2440)	160488	>tr|Q88FX4|Q88FX4_PSEPK Trk system potassium uptake protein OS=Pseudomonas putida (strain KT2440) GN=PP_3953 PE=3 SV=1MPLPALRFIAFIIGVFLITLAVSMVIPMLTLLVYDRSDDLGAFVWSSLIVLCVGLLMVARGVPDTPQLRTRDMYLLTTASWVIVCAF AALPMVFIRHISYTDAFFETMSGITTTGSTVLTGLDSASPGLLIWRSLLHWLGGIGFIGMAVAILPLLRVGGMRLFQTESSDWSDKVTP RSHVAAKIILLVYLGLTALGTGALWAAGMTPFEAINHSMSLVSTGGFSTSDASLGHWEQPAVHWVAVVIMILGSLPFTLYVATLRGHR GILLKDHQVRGFIGFLVFVWLTVGTWLCLHSNLAWWDAFRIVAVNVTSVVTTTGIAVGDYTLWGSFAIMLFFYLTFVGGCSGSTAGG LKIFRFQVAAALLVSSLKQLIHPRATISKKYNGHPIDEEIVRSLLTFSFFFTVTIAVIALGLSLIGLDWMTALSGAATAVCNVGPGLGTLIGP AGNFASLPDAAKWLLTVGMLLGRLEILTVLVLVSPVFWRF

1.9E-47	171	20.8	2.6E-47	170.9	14.5	1.2	1	J7LI26_NOCAA	Cation transport family protein	B005_3392	Nocardiopsis alba (strain ATCC BAA-2165 / BE74)	500	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis alba, Nocardiopsis alba (strain ATCC BAA-2165 / BE74)	1205910	>tr|J7LI26|J7LI26_NOCAA Cation transport family protein OS=Nocardiopsis alba (strain ATCC BAA-2165 / BE74) GN=B005_3392 PE=4 SV=1MRGGAGGDGVRRRLGGNERPMNGTGERPLTRWWRSLPWPIRRRSGRFHVTEPGVAQREIGAWRKPARVFLTIFLMVNLAGTLLLMLPVSTTDGRGLDFVPALFTSTTSLAVCGLSVISVGHDLSVFGQVVLMVLMQVGGMGIMTLAAILGTAVIHRFGLRMQLNVQAETRSLWVGEVSGLVRRVAIIFLVVQTCVFLMIAPRMWLAYDMDPLQAAYSALFHAVSSFNNAGLSLYDDSMTRFSGDAFILLPIALAVILGGIGFPVIIELWRSMRRRERWSLHTKLTVTTSAVLIVAGVVLVTLMEWSNPSTLGGLHWWARLTDGFFHGVVPRSGGLNAVPTGEMRDSTLLLTIMLMFVGGGSAGTAGGIKVATLAVLFLVVLSEVRAHDNVHAFGRSLPSTVIRQSLSLVFLSASVVAFGTLLILRTTAFDFMQVLFEVVSAVGVVGLSTGITPDLPPWIQVLLAAFMVAGRIGPITFVTALAFRDRNRHYTFPQARPIIG
1.9E-47	171	16.1	8.4E-47	169.2	11.2	1.7	1	R6TW92_9FIRM	Ktr system potassium uptake protein KtrB	BN503_00332	Oscillibacter sp. CAG:155	457	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, environmental samples, Oscillibacter sp. CAG:155	1262910	>tr|R6TW92|R6TW92_9FIRM Ktr system potassium uptake protein KtrB OS=Oscillibacter sp. CAG:155 GN=BN503_00332 PE=4 SV=1MKLQFGEETPPLWRRGQISPARVIILGFLLLIFGGTLLLMLPWSTRTPGGANFLDALFTSTSATCVTGLVVHDTVGYWSGFGQAVILLLIQGGMGVVTVAVALFIFSGRRIGLKERWVMQESISAPQVGGIIRMTGFILRTALIIEGVGALLLALRFCPQFGLWKGIWYGVFHGVSAFCNAGFDLMGSEVPYSSLTAYGADPLVCVTVALLIIVGGIGFSTWQDIAGNGCRLRQYRLQSKLILLTTFLLLLAGTLYFACYEFRLPQWADMDPGERVLAAFFQSASPRTAGFNTVDLTQMSELGRLVTILLMLTGGSPGSTAGGFKTTTLAVLLLSAWAVFRRRRSSAECFGRRLPEAVLRNASAIFWLYLTLFFLGGALICCIDGVALLDALFESASAIGTVGLSIVGTANLSAPSRLILIFLMYFGRVGGLTMIYAVTAGTLNLSSQYPQESVTVG
1.9E-47	171	25.4	3.2E-27	104.6	9.2	2	2	R6QJ17_9FIRM	Uncharacterized protein	BN606_00280	Butyrivibrio sp. CAG:318	433	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, environmental samples, Butyrivibrio sp. CAG:318	1262761	>tr|R6QJ17|R6QJ17_9FIRM Uncharacterized protein OS=Butyrivibrio sp. CAG:318 GN=BN606_00280 PE=4 SV=1MLQRIFKRLSSARIVAIGFIAIIFIGSGLLMLPVSLKHPGSLHYIDALYTSTSAVCVTGLLSIEAGDTFSTVGQFILGLLIQIGGLGVTSVGAGVILAMRKKVNLKGRAIIKDAMNLDSGKGVVKFVQSVFLTTLAFEAAGAFLTFFVFIRDYPPARAIGLSFFHSIAAFNNSGIDIFGGGRSLSGYQDNVYFNIITMLLIVFGGIGFLLIREVIDKKFCWRRFSMHTKVVLSMSASLIIVGALLLMLTENISVLGAFFQSVSARTAGFYTYPLGKFTNAGRIVIIVLMFIGASPGSTGGGIKTTTFFVLLQGIKSAATNRSEKAFRYSVPVNAFRKASVILLMGLTIVLTGSFIMSALEPGIDMSDILFEITSAFGTTGLSTGITGSLTTGSKILSIIIMYIGRLGPLTIATLWYFDKGERVSFPDGNISIG
1.9E-47	171	17.3	5.4E-47	169.8	12	1.6	1	C5C1A2_BEUC1	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Bcav_3269	Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	456	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Beutenbergiaceae, Beutenbergia, Beutenbergia cavernae, Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	471853	>tr|C5C1A2|C5C1A2_BEUC1 H(+)-transporting two-sector ATPase OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432) GN=Bcav_3269 PE=4 SV=1MEVPAVLQAARDTVDRVARRSPARLALATFASVVAIATALLSLPAATTTGERAPFADAVFTATSAVCVTGLVSVDTATFWSPFGQVVIMIAIQIGGLGVMTLASILGLAVSRRIGLTQRLLTASETKTTRLGEVGSLIRAVIAASLTLEILLALVLVPRFLTLGEELGQAMWHGSFLAVSTFNNAGFVIIEGGMSPYVGDWWMCLPIIVGTFIGAVGFPVILNVAQAWRRPRRFTLHTKLTLTTHAALAATSVLIIGGFEWFNDRTFGGLPVADRILASLFAGIMPRSSGFSTVDVGEMREATWFMTDALMFVGGGSASTAGGIKVSTLAVMLLAIVAEARGDRDVEAFGRRIDRATLRLAVAVSFIGATLVGIATLALLTITDLPLDVILFEVISAFATCGLSTGITPTLPDSAHYVLSALMFAGRTGTMTLAAAALALRSRRRVIRLRPDERPIIG
2.1E-47	171	14.1	5.1E-47	169.9	9.7	1.5	1	I0IDZ2_PHYMF	Trk system potassium uptake protein TrkH	trkH PSMK_13210	Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	521	cellular organisms, Bacteria, Planctomycetes, Phycisphaerae, Phycisphaerales, Phycisphaeraceae, Phycisphaera, Phycisphaera mikurensis, Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	1142394	>tr|I0IDZ2|I0IDZ2_PHYMF Trk system potassium uptake protein TrkH OS=Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01) GN=trkH PE=4 SV=1MNFRRVSRALGLLLLMLSACMAIALVAELCGFGTPDPRWEPVVESFGIALAMGALLGAAFIFGGREPGAPLLDSPNRREALLLVGTGWLLAASVAAIPFYAWSYLQPAVGAEHPFARYAACWFEAMSGLTATGGTVLGEQGNTIEALPSGLLLWRSGVQWLGGLGIVVLFVAVLPLLGAGAKSMLRFETSGPVKKGVQPRISETARELWLIYLGLTCACAALLATVGGMSLFDAVNHTFTAVATAGFSTRNASAGAYDSVAVDTILLCFMVIGGVNFALYHQLLKGRLVSVWRDAEFRTYASLLIGTAIVACCIVGTEVTLLTGEVRVPGVVDSLRYAGFQVASIMTTTGLATADFDQWGFVPKAVLFSLMFVGGCAGSTSGGLKVIRVMVMCRIFAGDLEKVYRPTVIRSVRIGGVTVTDDLRRSVTTFVVTMFALAGLGALCVKLIQGDELDVVSAAMASVACLFNIGPGFRQVGPTQSFAFFSDASLLILGLLMAMGRLEVFALLVLVSPRFWRDSS
2.1E-47	171	22.7	3.1E-45	164	15.8	2	1	J1ARX8_9EURY	Cation transporter	Metli_1854	Methanofollis liminatans DSM 4140	486	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanomicrobiaceae, Methanofollis, Methanofollis liminatans, Methanofollis liminatans DSM 4140	28892	>tr|J1ARX8|J1ARX8_9EURY Cation transporter OS=Methanofollis liminatans DSM 4140 GN=Metli_1854 PE=4 SV=1MDRLEYFSIIAPDIGQIFRFMAVVTSLPLAVTVIYGEWEMFVPMALVPLIFLLVGSLLVRVPHPAREARLSIALTAVALIWFSSALIGSVPFIVGLQMPVTDAIFEAMSGWTDTGLTLLPDVDQTPKTLLFWRSFMQWLGGIGIVAFTVALASRSGLIQRGLYRSEGRSEAFMPSVVGTGMAMWRIYIIITLASIGLVLLSGVPLWDAVNLALTAIATGGFSVHSAGIPYYQNHLLELLLVPVMLAGAMPFKLYYLMYSHRKVSFFGDRQAVALLAFTLIGFLVLTADFIFLMGHDLFTALREGIFMATAGITSTGFQNTSLHVWPAVTTLFLVMFMFIGGSSGSTAGGLKISKVILGLEGLAWWFRRIFVSGKAIVPFRHEGRTVQKNIAEIEVSKNMLVIILYFVSVFFCTIAILHFEAQTTVDSSKVIFEVVSAFCNNGISTGFVNPDMSFGSKWAFIFLMWFGRLEIVPVLVLFMGLIKGFD
2.2E-47	171	33.2	4.6E-47	170	23	1.5	1	R6N370_9BACE	Cation transport protein	BN659_01145	Bacteroides sp. CAG:443	610	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:443	1262739	>tr|R6N370|R6N370_9BACE Cation transport protein OS=Bacteroides sp. CAG:443 GN=BN659_01145 PE=4 SV=1MDSWERLLLYRKKLILPRIYQVLGWVMWVTYFFAILFLATLVYEHGFMISPVEAKVIRGIYQAVWIVFLLSATIQIIFQRDEEGKKNTFWAWIINVLLYLTLLPVVFKQPDAADEGVFWIWTFFHSHYYRIGILLLYSLLQLSSSLVRLLGRRTNPSLILASSFLVIIFIGAGLLMLPRATCHGISWIDALFTATSATCVTGLVSVDVPSTFTLEGQIIIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVGDMISSNSLNSLLSTLLYILGFTLAIEGIGMVVIWFSIHDTLGMTLQEELYFAAFHSVSAFCNAGFSTLPGNLGNPAVMQQHNLLFMTVSFLIILGGIGFPILVNLKETLFYYLRYLKWFCLGRSSRFPKQVHLYNLNTRIVLIMTAILLVFGTLAIALYEWNHAFAGMSVTDKWVHAFFNATCPRTAGFTSVGLTTLSTQTLLLMIALMIIGGGTQSTAGGVKINVFAVILLNLWAVIRGANRVTIFHRELSDDSIRRSNAVLMLYLILLFAAIFVMSLLEPEASIMALTFECVSALSTVGSSLDLTPVLSTAGKSVIILLMFIGRVGAFTLLLGLVKQVKKRNYKYPSDNIIIN
2.2E-47	171	32.4	3.2E-45	163.9	22.4	2.2	1	U4KLD0_9MOLU	Trk system potassium uptake protein TrkG	trkG BN8541520	Acholeplasma palmae	426	cellular organisms, Bacteria, Tenericutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Acholeplasma, Acholeplasma palmae	38986	>tr|U4KLD0|U4KLD0_9MOLU Trk system potassium uptake protein TrkG OS=Acholeplasma palmae GN=trkG PE=4 SV=1MITLSFFVIIMIGTILLLLPISKTGKGSLDFIDAFFVSTSAITITGLSPVSDLSIILSPFGKVVLAVLIQIGGLSVLTISVFIMYIIGAKIGISNRVLIKENLNQNDLSGMVSLVVRIVTFTLCIEFTGFIINLFVFIPQYDTVTAIGISAFHAISAFNNAGFDLLGSISLQNYQAHILLNINTAALIMLGGIGFIVINDLIEKKSYKKLTTHSKIVLKVNLLLWILGMLVFKFSNLGGKSFSWLESFFLSVTARTAGFTTIDISAISAVATLMLIILMFIGASPSSTGGGIKTTTIYTIFKGIPSYAKGKQVITYQRLINNETRHKASTLLAVSLLIIISSTFVVLTFDHVNLEKAVFEIVSAFSNTGLSKNLTPTLSDYSKLTLCILMFIGRLGPLTILSLFNSEWHKKELHNIEYIEEKMMIG
2.2E-47	171	34.4	4.8E-27	104	10.6	2	2	F6D579_METPW	Cation transporter	MSWAN_1170	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	494	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	868131	>tr|F6D579|F6D579_METPW Cation transporter OS=Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1) GN=MSWAN_1170 PE=4 SV=1MYSINKLKKDEAYSILHYTGYTCILLGLSMLIPILVALIYHEYQYIMPFIYSIIISVVFGFLLYHSFRNTNELSLKSAMIFATVIWLIGSALAALPFYFSRDLSYLNSYFEAMSGLTTTGFTMYTNLDIVTHTMNFWRGFMQWFGGIGIIVMGLAILTSPSINIMRMYSAEGREERLAPSIKHTTRIILYIYLIFTVISIILFILAGMPLFDSIFYAFTALSTGGFAMQNASLAYYNSIWIEIAAIIIMLIGATNFALHYTVLKGNWREYFKDIETKVAYPLLIIGTLLVAVFLYNGPYYGHDFLLSIRYSVFQVVSALTTTGLQTASGTQITNQWEGMGIFVLTILMMVGAGACSTGGGMKWLRIGILVKGMWWQVKSLLLPKNAVVPHRIHHVKEITLDNKILKVTGLFVFSYLMIYLVSVIIILFYYQNVSQVMFEVASALSNVGLGSGLMSASAPAVTKIVFIIDFWIGRLEIWPILLVLVILAQNTIRK

2.7E-47	171	12	5.1E-47	169.9	8.3	1.3	1	I0IED9_PHYMF	Trk system potassium uptake protein TrkH	trkH PSMK_14680	Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	567	cellular organisms, Bacteria, Planctomycetes, Phycisphaerae, Phycisphaerales, Phycisphaeraceae, Phycisphaera, Phycisphaera mikurensis, Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	1142394	>tr|I0IED9|I0IED9_PHYMF Trk system potassium uptake protein TrkH OS=Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01) GN=trkH PE=4 SV=1MKFRLIARHLGLLLLVLGGCMLVATLAELLGFGRDGPNVEPVAEAFGAGLATCASLGGGLLFLGRRTATQRQARAAARSRGERYAGPQLTRRDAMAMVAAGWVLGAGVAALPFFSWAWLHTDEVVPAVSAGPDAPAPEEAAGTPVTPAGKVVQAAGFDHPFRSFAACYFEAMSGMTTTGASVLGTAPHDIESLPSGLLLWRSLIQWLGGLGIVVLFVAVLPLLGVGGKTLVQFETTGPVKQGVRPRIADAARELWLIYLGLSAACCGLLVWPGGLSLFDAVNHTFTALATGGFSTRNASAGAYDSVPVDLVLVLFMLLAGVNFGLYHQAINGRWRAVLQDAELRTYLLIVLAATLVIAAMLVGSELTLTTGQPREAGVLESLRHSLFQVVSVMTTTGYATADFDQWGFVPKAILVGLMFVGGCASSTGGGIKVVRILTVFKVFGATLEKVYRPTVVRTVKIGGAPLSEGVKESVLIFVLTMIGLFVAGALVLRLLEPDQLTVVGAATASAATLMNIGPGLQAVGPMNNFGFFGSDSLIVMSLLMALGRLEVFALLVVLTPRFWRNTT	>tr|A0A0F7HK26|A0A0F7HK26_9STAP ATP synthase OS=Salinicoccus halodurans GN=AAT16_03620 PE=4 SV=1MLKWFKEFFYKMSPQRWIFVYYLLALFIATIFLSFPLFYRGIKDIQLIDTVFVAASALSVTGLTPVSISETFNGGGYIVIMLIMNLGGIGIMALGTLIWVFFGRRIGLRERMQIMVDNNQVKMAGAVKLVVEIFKTLIFIEVVGAFIYVIYFMNISGDIGYSLMTGIFLSVSATTNAGMALFDNSLIEYTESYFLQFVVMLQIMSGAIGFPVLIELREYFSRRQKKFRFSLFTKVTTSTYGLLLAVGTFFIFVMESQNYFQNDSWFKTLSNSFFASSTTRSGGLTTVDPAFFADGTQVVMSGLMFIGASPSSAGGGIRTTTFALLILFLIAFSRGRERVNVFNREIAQEDMRRAFAVVSLAVLLVFSGIVSIVVIEDSRFDLIDVIFEVTSAFGTCGLSTGITDDLSAPSKVIIMMFMFIGRIGFISFLFSIGGRQHELPYHYPKERILIG	2.7E-47	171	35.9	4.7E-47	170	24.8	1.3	1	A0A0F7HK26_9STAP	ATP synthase	AAT16_03620	Salinicoccus halodurans	451	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Salinicoccus, Salinicoccus halodurans	407035
2.8E-47	171	19.3	1.8E-46	168.1	13.4	1.8	1	A6WZH5_OCHA4	Trk system potassium uptake protein	Oant_1663	Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	500	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Ochrobactrum, Ochrobactrum anthropi, Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	439375	>tr|A6WZH5|A6WZH5_OCHA4 Trk system potassium uptake protein OS=Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168) GN=Oant_1663 PE=3 SV=1MDRSHAKQGKICLTSEPSAIYKTVANICARFGLLMAVAMLLPAAIDLRDGSDDWLIFVRSAAATGALSALILLATQNQTMRFTPRLGFLLTACLWLTASFLGSIPLYFSHLPISYATAFFEAMSGVTSTGATALTGLDNMQRGILLWRSLLCWIGGIGFIGLALLMLPSLRAGGLALFHMENSDKSEKILPRMNQIALGIVLAYLSLTAACIIAYFAVGMSMFDAINHGFTTIATAGFSTHDSSIGFYQGNRPLLVVSTIFMALSALPFVLYIKAFMPRRMESLVDPQVKLFFTIAISFSFALAVVLRLGSDVPFGDALISASFHFVSVMTTTGYATEDYFLWGPPAIGIFFLASFLGGCAGSTSGGIKMNRLIILWSLTRANLARLIMPHAVIKIRYGSSEVSGEIAQNVLLYLFLYCASLIIGAVLLASLGLDFVSAFTGALTALSNIGPGFGDTIGPVGNFSTIHDPALWVLSFLMLAGRLELVTVYILFTRTFWVR	2.9E-47	171	25.9	2.9E-47	170.7	18	1.8	1	R5HGB9_9SPIR	Sodium transport protein	BN676_00434	Brachyspira sp. CAG:484	489	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Brachyspirales, Brachyspiraceae, Brachyspira, environmental samples, Brachyspira sp. CAG:484	1262759	>tr|R5HGB9|R5HGB9_9SPIR Sodium transport protein OS=Brachyspira sp. CAG:484 GN=BN676_00434 PE=4 SV=1MRLSYLANAISLIMMYIGMVILSPIIIALIYHDFYSVIPFLCASIISSAGGFIIRKLVPQSKELENLNDIKKAEALFIVAVSWIIFGIMCAIPYLFYGLSPLDSLFESVSGITTTGATILTNFDYPKAFFFWRSLTQWLGGLGIIVLFIAILPQFAVAGRQMFFAEAPGPTEDKFTPRIRNTASALWKVYAGLTLLQVILLVLAGMPVFDAVCNSFSTLAAGGFSPNAQSTMGYHSNYITWIILIFMFFAGSSFNLQYKVIMKKNPLLFFKNEEFRAYLIMTLVFSSLIAIVLITENNYSIFGGITHALYQVISIATSTGSASVDFAQWDFTAKVLLFLVMFMGSCSSSAGGGIKMTRWVLVAKSMKAELMRILHPNAVFNIKIDNNNVPPEVVRQIIVFVFFYFLVFALIAVIITLTEQNATIGLTGSITALGNIGPGFGKIVGPMGSFSSIHSISKALMVTGMLVGRLELMPFLVMFQRDFWSFKEN	>tr|A0A0D1LVF8|A0A0D1LVF8_9LACT KtrB protein OS=Weissella cibaria GN=ktrB PE=4 SV=1MRKLLSKMTPPQILTLGFLVIIFAGAGILMLPISQKAGVTVHYMDTLFTAVSATAITGLTVLDTASTWSLFGHIVLLVMIEIGALGFMTFAVLLFAITGQRLDLKARLMAQQALNLGSLADVKSVLSYVFSLSAVIQLIGAVLMMPDFIPRFGASHGIFLSIASSISAFGNAGFTFFDEPVFFLRNDPYILVVWMLLISAGSLGFLVWRDLLLYRKQRRLSLHTRVALHVSAWLTGLAFVFFLFTEKVLTPLAGSTSLWHRIMDTLFLAVVPRTAGLEVVPLRDLTAAGLMIIMLLMFVGGTPGSTSGGIKTTTLGILWLQSMAALRGQEQVNFGGRRFSQKVVIKAMMLAVISIVFVIGVVSLFLSITETIPKGEGLEYIVFEVISAFSTTGFSLGLTPHLTTLGKIVIMMVMFIGRVGLYTVMFSVMNIREKPTSFQYPTEEVIIG	2.9E-47	171	31.6	4.3E-47	170.1	21.9	1.2	1	A0A0D1LVF8_9LACT	KtrB protein	ktrB QX99_00031	Weissella cibaria	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Leuconostocaceae, Weissella, Weissella cibaria	137591
3.1E-47	171	24.4	3.3E-27	104.6	5.1	3.1	2	G7WM05_METH6	Cation transport protein	Mhar_1011	Methanosaeta harundinacea (strain 6Ac)	526	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosaetaceae, Methanosaeta, Methanosaeta harundinacea, Methanosaeta harundinacea (strain 6Ac)	1110509	>tr|G7WM05|G7WM05_METH6 Cation transport protein OS=Methanosaeta harundinacea (strain 6Ac) GN=Mhar_1011 PE=4 SV=1MSARIALHTLGFLMIVLGALMLVPLAVSIIYSEPSGVVAFVLSSLATLAVGYSMRRLGSGGDVGHKDAFLIVTFGWLLAAVFGALPFVLMGVGFIDSLFESMSGFTTTGATILTEYDANGYWIINSTASSGCLASGIVTGLSHQLAGGPTTNAALIGGDIADPTYYGLLFWRSFTQLLGGLGIILLFIAIFPHLGVAGRQLYYVDSARLKKETLTPRVKDTAKIFWGIYLLMVGLETFMLYLAGMPIYDSILTAFATLSTAGYSPQASGIVAYSSLPIEAIVVFFMILGATSYNLHYILLYKGSISVYVRDSEFRFYLLIMASAIVMILLAGGGEGNLLHRLRIVGFQVVTTMTTTGFTNFEYNTWPVASSMIIVALMLIGGCVGSTGGGIKVARILLILKYGRRELIELIHPRAVKPIKITGATVQEEVLRSILFFALLYLLVFFVASLAMALTEAGNPVFDLISTVSAIATCMGAVGPGLGAVAYDFSGVTAAGKMIGVICMFVGRMEILPVMVLFMPNFWRK	3.1E-47	171	13.5	3.1E-46	167.3	9.4	1.9	1	V6F8K4_9PROT	Trk system potassium uptake protein	trkH MGMSRv2__3833	Magnetospirillum gryphiswaldense MSR-1 v2	483	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum gryphiswaldense, Magnetospirillum gryphiswaldense MSR-1, Magnetospirillum gryphiswaldense MSR-1 v2	1430440	>tr|V6F8K4|V6F8K4_9PROT Trk system potassium uptake protein OS=Magnetospirillum gryphiswaldense MSR-1 v2 GN=trkH PE=3 SV=1MIDFRPVLQIIGWILCLLALSMTVPAAIDAMAGSGQWMAFIASAGITLVAGLGLVLGTRTDNRKPLSIRQAYLAAGLGWLVPCLFAALPFSLSSLDLSATDAFFEATSGITTTGSTVLSGLDTLAPGLLLWRGLLQWLGGIGIIVMALAVLPVLNIGGMQMFRVEVVSARERTAPRAARIGSTLISVYVGLTALLALALWAAGMGRFDAITHAMSTIATGGFSNYDRSMAHFDSVTMDLIVLVGMILGGMPFLLFFTLAQGDWRRVLRDQQVHWYLGLMALGSIAITLWLIDVRHFQPLTALRHAAFTVASVMTGTGLVTLDYSDWAGMPVAILFFLTFVGGCAGSTAAGIKVFRFQLLFANAVVQIRQLLRPHAVMVPSFNNKPIPKDVLTSVMGFIFVYALAFATLSMMLAVLGLDFVTALSASASAISNVGPGLGDLIGPGGTFAPLPDLAKILLAGGMLFGRLEMFILLVVFVPSFWRD	3.2E-47	171	36.7	8.4E-27	103.2	9.6	2.2	2	A9NH06_ACHLI	Trk system potassium uptake protein TrkG	trkG ACL_1026	Acholeplasma laidlawii (strain PG-8A)	441	cellular organisms, Bacteria, Tenericutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Acholeplasma, Acholeplasma laidlawii, Acholeplasma laidlawii (strain PG-8A)	441768	>tr|A9NH06|A9NH06_ACHLI Trk system potassium uptake protein TrkG OS=Acholeplasma laidlawii (strain PG-8A) GN=trkG PE=4 SV=1MRKMIIIMKKISPYIIIVLSFLSIILIGGILLILPISKQAQGHLSFVDALFISTSAVTITGLSPVANLSTLLSPFGKVVLGILIQIGGLSVITISVFVMYLIGAKIGLSNRILIKESFNQTSLSGMVKLVKKIIIFTLVIESFGFIANMIVFVPQYELVDAIGLSLFHAVSSFNNAGFDILGDQSLQGYNGHVLLNLSTAILIMLGGLGFIVLNDILTKKSYKKLMIHSKIVLKVNLVLWSLGFGFFLLSKVDGKNLNVLEAFFLSVTARTAGFTTINMGTISSLTALILMVLMFIGASPSSTGGGIKTTTLYALFKSTTSYAKGKTTTTTHNRLITDETRHKASILLTTAIMIVLVATSLIIMMENIDLEKAIFEVISAFANVGLSMNLTPTLSNASKIVLSIVMFIGRVGPITIISIFNTQWYKKGMDSIEYIEEKMMIG	3.2E-47	171	14.4	3.9E-45	163.7	10	2	1	R5CCI9_9FIRM	Trk system potassium uptake protein TrkH	BN785_01852	Firmicutes bacterium CAG:791	481	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:791	1262993	>tr|R5CCI9|R5CCI9_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:791 GN=BN785_01852 PE=4 SV=1MHYPIVCYVQGQILKIEGALLLVPALTGLLYREQAAAAYLLIAAICETIGFLLTLRRPKKLVLYAREGMVSVALAWIVLSLFGALPFVLCGDIPSFSNALFEIISGFTTTGASILEDVEVLSHASLIWRSFSHWVGGMGVIVFMLAIIPMASGYNMQLMKAESPGPSVGKLVPRVKESAKILYLIYVSLTGIQLVLLLLTGMKGFDAVCITFGTAGTGGFGIWNNSCGGYTTLQQGIITIFMLAFGVNFNAYYFLLGKDKKQAFRMEEVRGYFLIVAVSILLITINIRGLFHSLPESFHHAAFQVASIITTTGYSTEDFDLWPMFSKMILILLMFCGACAGSTGGGIKVSRILILLKAVRTEIRHYMHPRAVTTMKMDGKAIDKSIFRGVLVYLAAYAFLFAVSVLILSLDPTQSFATDFTAVAATFNNIGPGLEMVGPAANFNSLTLLSKYVLMFDMLAGRLELFPLLVFFLPSTWKKSA

3.2E-47	171	34.8	3.4E-46	167.2	24.1	2	1	R9TAV4_9EURY	Cation transporter	MMINT_15030	Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1	527	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Methanomassiliicoccales, Methanomassiliicoccaceae, Methanomassiliicoccus, Candidatus Methanomassiliicoccus intestinalis, Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1	1295009	>tr|R9TAV4|R9TAV4_9EURY Cation transporter OS=Candidatus Methanomassiliicoccus intestinalis Issoire-Mx1 GN=MMINT_15030 PE=4 SV=1MELTKPSQNSQIAPVKKKSFFKRHGVDKYTITKKVSRRENTVLYLFGTLVFYVGLALIVPLICSYIFNDPYDPWIITMLICFLFSIPLLMRFKSAEHTRSTETLFVITTSWILVTIFGSLPFILSGMDVIDALFESMSGFTTTGSTIMGGGGVAPIEEWSKSILLWRSMMQWLGGAGIIMIFVTILPMMGATGRSLVTLELAGTDTQNITQRMQEESRKFHYIYLSLTLLMIVMLLLTGLGVYDSATIALSSISTGGLSPYSDSISHFNSRIVEWIVIIFMFLGGTNFFLQFRAMSRGGYKELIKNSEFRAYVLIVIIASLILFAFLGPEVAGMSTFDRFTASTFQIISAMTSTGYTTISLGGLVNIASLILIIAMIIGGSSGSTAGGIKIVRFVILRKFLSATLYRTIHPKAVVPIKINEKTVEEKTVSSLMALLVCYFGTAVVCIFILMMLGVDTMGSVCSTIASLSNAGLGMGDVASSYGGLPDLAKLVLMFAMWAGRLEFISVFVILSPVFWKEFLRFHKRYS
3.2E-47	171	22.7	4E-47	170.2	15.8	1	1	A0A0A7KPN7_9DEIO	Potassium transporter KtrB	QR90_13205	Deinococcus swuensis	461	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus swuensis	1182571	>tr|A0A0A7KPN7|A0A0A7KPN7_9DEIO Potassium transporter KtrB OS=Deinococcus swuensis GN=QR90_13205 PE=4 SV=1MPSPVSRPDPLPRRALSARLTPAQLLALVYAAGILIGTGLLHLPGVQRAGAQALTSIDLLFTATSAICITGLVVADTGEAFTRLGQVIIIILVQIGGLGILTFGTLFAFLTGRRLNFSERQGLVAQLNALSVGGVLPLLRAILTYTLVTELVGAVLLSFRFVPQYGLGEGLYQAVFHAVSAYNNGGFVVLAGGMAPYAQDPLVSLTLAVLVILGGLGFLVQLNYVSHLFSPRKNRLLVYSRLTVLTTAILLALGTLVILLVEWQNTKTLGALSTPGKFLAAFFQSVTPRSAGFSTVNIEAMNTATIFTMIGLMFIGANSGSTGGGIKTSTFAILVGSAWNMVRGRGELIVFQRRVLNENVVRAGSITTLYTLLVATAFFALLATNPKLGFTHLLFETVSAAATVGLSMNTTHLLNDPGLLILTALMYLGRIGPLTFAVAFSLRSTQKRNIKYPPERDILVG
3.3E-47	171	20.7	1.1E-46	168.7	14.3	1.7	1	R7JCB3_9PORP	Potassium uptake protein TrkH family	BN646_01692	Parabacteroides sp. CAG:409	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides sp. CAG:409	1262913	>tr|R7JCB3|R7JCB3_9PORP Potassium uptake protein TrkH family OS=Parabacteroides sp. CAG:409 GN=BN646_01692 PE=4 SV=1MLNVRFIFKMLGLMFILETLFMLMALAVAFIYQGDDVEPLALSSGILFGFGVLFYLIGIRANEHSAGRREGMLIVTLTWTLLSLFGMLPFYLGGYVNSIADAYFETMSGFTTTGSTILTDIEALPKGVLFWRSLTQWQGGMGMIVFTVALMPIFGGGASQMFDAETPGITHERFRPRITQVAKRLWGIYLFITLLLTGLLWIGPMDLYDAVNHAMTCMATGGYSTKNASIAYWDSAYIEYVISIFMCIGSTNMTLIYFFMNGRFGKLLKDEETRWFYSIVAISTMIVMAWVYFKGIITDPEEAFRESLFQVTTLISTCGYATVDFIPWGPFFWMIALMLMVVCGCAGSTCGGFKTGRVVILAKNVVNAFKKQTHPHAVLPVRVNGHVVSTDIVNRVLAFAFIYITLIFATAFFLMLDGTGFEEAVGTATSAVSNTGPGLGIYGPVGNFSSYSDLSKWVLSFVMMTGRLEIFTVLTILLPGFWKQ
3.4E-47	171	21.7	1.7E-28	108.8	5.4	2.1	2	Q9X0H4_THEMA	TRK system potassium uptake protein TrkH	TM_1089	Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)	495	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Thermotogaceae, Thermotoga, Thermotoga maritima, Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)	243274	>tr|Q9X0H4|Q9X0H4_THEMA TRK system potassium uptake protein TrkH OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=TM_1089 PE=4 SV=1MTSTKYRLKVIFWYVGQLLIWFPAILLLPTIFVIFYPEEWIYIESFLVPSIISFASGVVLKKVSKLNETRVVGYQEGAVIVVTTWCAAVVLSALPFVIEGLLNFHQAVFEATSGWTTTGLTMFPDVESLPHVFLVWRSVMQFIGGAGFAVIMLATLIGPLGASLYSSEGRVDNILPNVTHSTKVIMVIYVAYAAAGMFFLHMAGMPWFDAFNHSLTALATGGFSVKNASIGYYGSVSIEVITIVLMLLGGTGFGIHYTLWKGNFKAFVKNGEPWIMGSTIVIASLFLLRPAEKVFHEKALRYVVFQVVSAITGTGFSNADLVPWVTLFPIGVYLLTVIMMLGGMMDSTAGGLKQFRVFVTLKLIYRSIINFMGPRRKVEKIIVWKGENRKTIDDGIIKDMFVFFGVYALTYLVGTLILMSYGYDPLVSMFEFSSAMNGVGLSVGLTSPNLPVGVIWTMTVGMFLGRLEFLVVFYAIVRIIRDVKILLEERGGVNS
3.6E-47	170	17.6	1.6E-45	165	12.2	2.3	1	R5EZ34_9FIRM	Cation transporter	BN466_00280	Firmicutes bacterium CAG:110	489	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:110	1263000	>tr|R5EZ34|R5EZ34_9FIRM Cation transporter OS=Firmicutes bacterium CAG:110 GN=BN466_00280 PE=4 SV=1MNYPLLRYLFGMILLIVAAFLVLPLAVAVIYGESSGIYFLYTMIAAGLLGFLLTRFKPAKRDMYAREGFVFTALAWVVISLIGAAPFTLSGQIPSYLDAVFETVSGFTTTGASILTDVEALDNGMLFWRSFTHWLGGMGILVFMLSLVNMGGQANHLLRAESPGPTVSKMVPNMRKSAAILYGIYIVMTAVEVVLLIGGMPLFDSLCTAFGTAGTGGXXXGTAGTGGFGIKNSSMGYYNSYYLQGVVSVFMALFGVNFNVYFFLLMKKYAMAWRNTEVRAYFAIIAGSTLIITLNILGMFPTAFDAFHHAFFAVSSVITTTGFSTTDFDLWPQLSRCILVLLMIVGACAGSTGGGVKVSRLVILCKALGSELRKLLHPRSVRVLTVDGKPVSRETVQGVQSYMTLYFLVTLVSVLLVALDNLDFVTTFTAVLATLNNIGPGLGLVGPTGCFAAFSPLAKIVLTADMLFGRLELFPMLILLMPSTWRKY
4.1E-47	170	18.5	8.6E-45	162.5	12.8	2.1	1	G4RCL3_PELHB	Trk system potassium uptake protein	KKY_646	Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	479	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Pelagibacterium, Pelagibacterium halotolerans, Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	1082931	>tr|G4RCL3|G4RCL3_PELHB Trk system potassium uptake protein OS=Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2) GN=KKY_646 PE=3 SV=1MLGATAYVTAFFTLVLSGMMLVPMLADLSVGNPDWQAFLISSLTAGVPSGFLVLATRREMPPFSLKFGFLLVNMIWASTSIVAALPLFLSGLSISFTDAVFEATSGITTTGSTILAGLDDMPPGLLLWRSMTQWFGGLGIIAMGLLLLPFLRVGGMQIYKLESSAQADSPFARFTKFSWAMVGLYLTLSLACALAYWFAGMSSFDAINHAMATVSTGGYSTHDASMGHFGLPVLVVGIVFMIGGALPFIAILRAVTTGRISAAFEAQVPVLLSILAVLSFVVFLSALVHWPSDPGALGVHSAFNIVSVVTTTGFASTDYTLWGSFVNVVFLLATFLGGAAGSTSGGIKTYRLIIIYQSLRNGLKELIYPNGIFVVRYEGREVPWQAIKSVYHFIGAFLVLLLAVTLVLGFTGLDVLTAFTGALTALTNVGPGLGEIIGPAGNFSSLEPLAKWALILAMLAGRLEILAILVLFSPAFWRR
4.3E-47	170	37.6	4.9E-45	163.4	26	2	1	C2WZ69_BACCE	Potassium/sodium uptake protein	bcere0024_12360	Bacillus cereus Rock4-18	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus Rock4-18	526988	>tr|C2WZ69|C2WZ69_BACCE Potassium/sodium uptake protein OS=Bacillus cereus Rock4-18 GN=bcere0024_12360 PE=4 SV=1MKVTKRQSLYNRFIQLNPPQILALGFFCLIVAGGLLLKLPFATKVHISWVDAFFTATSAATVTGLGVVDTASTFTMFGEIVIMFLIQTGGLGLMTIAILIVWVLGKKIGLRHRLLIGEAFNQTNIGGLVKLVKRVFIFSICIEFIGVIFLSFRFIPEFGFGKGLYYSIFHVIASYNNAGFALWPDNLTRYVGDPIINIGICSLIVIGGLGFTVLIDIWYSRSFRKLSLHSKIMIIGTVALNVIAMIVFVLEYNNVKTLGNLSLNEKLWASFFQGITPRTAGFNTVDYGGMEESSILFTMVLMFIGAGSVSTGGGIKLTTFVILITSVLSFFRKKEEIVLFQRTIKMSTVTRALAIVVASQILIFTAVFVLMLTEDFSFIQLLFETISAFGTVGLTMGITAKLSAFGKCIIMFVMFCGLIGPLTLVFSLARPAKQKIKYPSEDVFTG
4.4E-47	170	29.9	1E-25	99.6	7.2	2.1	2	R6E0X2_9BACE	Uncharacterized protein	BN760_01994	Bacteroides sp. CAG:709	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:709	1262748	>tr|R6E0X2|R6E0X2_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:709 GN=BN760_01994 PE=4 SV=1MNLKVISRNVGFALLASAFFMFLSILVSISNGNDSALAALIISFTITFIVGIFPFIFVRKSPNISLKDGYMIIVLSWTLSFIFGMLPYVLWGGPFSVINALFEAVSGYTTTGGTVLANVEQLPDSLLFWRSSTHFIGGLGVVVFLLLIIPSSSPVRLRLTNMEVSSLSREGYKTRTNKTVWVFTAVYFGIAICAFLCYWLAGMSPFDAINHAFAVTATGGFSTKNLSIASFGSPLINIVTIFFMFISSIHFGIIYMVFASRSFKPLNNPVLKFYAGTILVAALLVAFSLKMSSAGFTWGESFMTGFFQVVSSISTTGFAISDNNTWPLFACIITVLITVPCGMAGSTTGGIKMDRMLLMFKSVGQQVKSSMHPSSINQVHIGNHMLGNNEIYPHVVFIGLYFITIAASMALTILSGMDVQNAMAASMSCLSNVGPAMESVGTMGNYSGVPVLAKIVFIVDMFLGRVEIYPVLAVVTMAFSGRK
4.5E-47	170	53.8	1.7E-46	168.2	32.6	1.7	2	F0RBX3_CELLC	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Celly_1784	Cellulophaga lytica (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy l20)	450	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Cellulophaga, Cellulophaga lytica (Cytophaga lytica), Cellulophaga lytica (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy l20)	867900	>tr|F0RBX3|F0RBX3_CELLC H(+)-transporting two-sector ATPase OS=Cellulophaga lytica (strain ATCC 23178 / DSM 7489 / JCM 8516 / NBRC 14961 / NCIMB 1423 / VKM B-1433 / Cy l20) GN=Celly_1784 PE=4 SV=1MKNKTYKKISNWYRKFQISKSPQMNLVWGFFLYTLIGFILLSIPFFHKTDISVLDNLFISTSAISTTGLVTISVFDSYNFFGQFVIMALIQIGGIGYMTLTTYYLIFTTKKITHWHSKLIGTEFTLPNTIQIKDFIKSVIVFTLIMETIGAILFYFAFTNSGMGSLKAIWFSIFHSISSFCTAGFGLFNDGFESYQDNTFINTIISVLAISGSLGFIVITDLWYRIRGKSKEISFTTKIIVYGFLFLLFLGTLLIYTTESSSILGSNSSLMTSFFQAMSAMTTVGFNTIPIGELSLPILLLVTFLMYIGASPSGTAGGMKITTLTAMLSILKSRLFGQKKITFLNRLIPFERIYVATSTFMLYTSLIFLFSFLLSYFENFSFESILFEVASALGTVGLSTGITGDLSNIGKTLIIILMFIGRVGVLTFGFALLQQKDNDSKKIRADDLAV

4.5E-47	170	21.6	6.1E-46	166.3	14.9	2	1	R5Q29 0_9BA CT	Trk family potassium uptake protein TrkB	BN679_ 02057	Prevotella sp. CAG:487	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:487	1262928	>tr|R5Q290|R5Q290_9BACT Trk family potassium uptake protein TrkB OS=Prevotella sp. CAG:487 GN=BN679_02057 PE=4 SV=1MINLKVIYKIIGSLLFIEAALMSVCLIMAMAYGEDDMYAFLYAVGITAACGAVLRYMGRNSGNMLSRRDAYLVVSLAWVLFSLFGT LPFVTGGYIKSFTDAYFETMSGFTTTGATIIDDVECLPHAILFWRSLTHWIGGLGIVFFTIALLPSLIGGSVKIFAAESTGPIKMKLHPKIST NSKWIGSVYIILTLACALSYMFFGMDWFDAINYSMSTTGTGGFATHNASIAHFQSPGIEYSAILFCFLSGTNFTLLYFTMAKLRFRELFM NSEFRLYFILVAAFSLFIACELVVHNGYDVEHALRSSLFQVTAFITTTGFFSDNAGLWPHVTWVVLSFCMFIGACSGSTSGGLKCVRG VMLLRIVRNEFRQILHPNAVLPLKIDSTNVPNNKRVTLLAFLTVDLILILVCSFIFIVQGIESTNAVTVTLSSLGNVGPALGSDIGPTMSWS SLPDNVKWICTLLMLVGRLEIFSVLVIFTSAFWKDN
4.6E-47	170	14.4	2.2E-46	167.8	10	1.8	1	R6LLD 4_9FIR M	Trk system potassium uptake protein TrkH	BN515_ 00924	Firmicutes bacterium CAG:170	481	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:170	1263006	>tr|R6LLD4|R6LLD4_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:170 GN=BN515_00924 PE=4 SV=1MNKRMISFILGTLLILEAVILLLPALVALIYAERAGWYYLFTALGAALAGLALRLISRPTRKTIYARDGLLCVALGWVVLSLAGALPFT LCGDIPSYLDAVFEMVSGFTTTGSSILPNVEVLNRCSLFWRSFSHWIGGMGILVFMLAIVNMEGGQGIHLLRAESPGPTVSKMVPRMV DSSKILYGIYFGLTVIQMIFYLAGGMPLFDTLCNAFATAGTGGFAIKADSFAGYSYYHQTVTTVFMALFGVNFSIYFFILRRKFDLVWKN TELRWYLAIIFLSIAAITLNILPMYPRACDALHHAAFSVSSVITTTGFGTENFGLWPEFSRVILVLLMLIGACAGSTGGGLKISRLVILVKTV QREVRLLLLHPRTVKVMTIDGKPLSNDTVRGVSAYFLTYVFLIVISILLVSLDGFDGSTTITAVFATVNNIGPGLGMVDPAGSYAAFSPLAK VVLTLDMLFGRLELYPMLILMLPTTWTRRR
4.7E-47	170	42.8	1.2E-46	168.7	29.7	1.6	1	E4TRN 0_MAR TH	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Ftrac_1 763	Marivirga tractuosa (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43) (Microscilla tractuosa) (Flexibacter tractuosus)	606	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Flammeovirgaceae, Marivirga, Marivirga tractuosa, Marivirga tractuosa (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43) (Microscilla tractuosa) (Flexibacter tractuosus)	643867	>tr|E4TRN0|E4TRN0_MARTH H(+)-transporting two-sector ATPase OS=Marivirga tractuosa (strain ATCC 23168 / DSM 4126 / NBRC 15989 / NCIMB 1408 / VKM B-1430 / H-43) GN=Ftrac_1763 PE=4 SV=1MKFSKLKNAFAEWLNNLLYSSRTQVLNTLVSLKAFIWLTATILLLYVFGFETEQDELEQVFLGLDVVLIIYFSTFLIRLLYEFRRTEFI KNNKLETFLVLIIIVNTISHLFLDNKIMGFFIENFEFESYEDAYLALITFFFIILILYELVNASDIFSRLKASPSHSFIVSFIILILFGTGMLMLPA MTVQEGSMKFMDALFTSVSACCVTGLIVVDTATFFTLKGQIVIMMLVQIGALGIISFAAFFANIMKSGVGIKQQLFLQDYLISESLFSAKG LLRKIIFITISLELITFVLIYFTWGDGVVFNSQAQKLFFTAFHAVSAFCNAGFSLFTNGLAEHGVATSYILHIVVAVSMIFGTIGFSTIQDIFN VQRLRDRYQNPWKDWNLSTKVAVYTTAFLIVFGMLVFYLLERDYILSDKNFIEATITSFFQSVTRTAGFNTVDIGALRTPTLILLAFLMFI GASSGSVGGGIKTSTFYLILVSVFATIRGRLKIEIDKRFIPKELLFKALSIFFFAASINLIGVFILTLTDSNFSFVQIIFEQVSAFGTVGLSTGI TSELSTAGRTVIILSMFVGRVGTLTFAFALSSRQTTQNYKYPKAHLMVG
4.7E-47	170	23	2.4E-46	167.7	15.9	1.8	1	X5MM7 2_9PR OT	Trk system potassium uptake protein	BN1012 _Phect 1912	Candidatus Phaeomarinobacter ectocarpi	485	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, unclassified Alphaproteobacteria, Candidatus Phaeomarinobacter, Candidatus Phaeomarinobacter ectocarpi	1458461	>tr|X5MM72|X5MM72_9PROT Trk system potassium uptake protein OS=Candidatus Phaeomarinobacter ectocarpi GN=BN1012_Phect1912 PE=3 SV=1MALFDARPIFLVVGILLVTLGIAMVLPALYDAAVSNPDWRVFLASAVVTTFFGVTFALMNWGSAGDMTLKQAFVLVPAVWLSLVI FGALPFAFSELNLSYTDAFFESMSGLTTTGSTIIVGLDTVAPGLLLWRSLLQWLGGIGIIVMAVSILPILQVGGMQLFKVEAFDTPDKVL PSAAGLAGTITTVYVIFTVVTAFALWAAGMSFFDGINHAMTTIATGGYSTRDASVGHFDSALIHYIIIAGMIAGSLPFVLYIQAFRGKAMP FLQDTQVRVFLSLLGIATLAMIVYQMARGLEGTFEAQIRYAAFNVVSVMTGTGYATQDYGAWGPFAIALFFTLMFIGGCSGSTSCGLKI FRVQVIAATCVSHLRRMIYPHGIFIPHYNRRAIPESVSASVMSFFFLYIACFGGLALLLTFSGLEPLTALSSAATSIANVGPGLGPEVGPS ANFSGIPDTAKWLMALGMLIGRLELFTVLILFSRIFWRS
4.8E-47	170	27.2	6.3E-47	169.6	18.9	1	1	E1VYI8 _ARTA R	Trk system potassium uptake protein TrkH	trkH AARI_2 4710	Arthrobacter arilaitensis (strain DSM 16368 / CIP 108037 / JCM 13566 / Re117)	477	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter arilaitensis, Arthrobacter arilaitensis (strain DSM 16368 / CIP 108037 / JCM 13566 / Re117)	861360	>tr|E1VYI8|E1VYI8_ARTAR Trk system potassium uptake protein TrkH OS=Arthrobacter arilaitensis (strain DSM 16368 / CIP 108037 / JCM 13566 / Re117) GN=trkH PE=4 SV=1MSTASASSPSARAAEMREQRRKKWLAVRIAVADFTVRSPARLTLGAFLLAITIFTSLLAAPFSSATGEATALHDALFTAVSAVCVT GLTTVSTAVHWSFVGQLIMLVATFMGGLGILTLASIMSLAVSRKLGVRAKLMAQNSMNSSGASALGEISSLLRIVILTAVSLQAVIALFLI PRFYILGESVLSSIWHGLFYAVSSFNNAGFTPHSDGLVPYETDLWILGPLMAAVFTGSLGFPVIMVLLAHKFNVKKWNLHTKLTVLTTTI LLFAGSLLWMIFEWANPKTIGGLSFGDKVIHGFFASTMTRSGGFNLVDQNDIHQVTVLLSDALMFAGGGSASTAGGIKVTTIAVMFLAI LAEVRGDVDARAFGRRIPQGTMRVAISVVAMGASLVMLATGALVTIDEEIGFSRALFESISAFATVGLSSGVSQELPPAGKYVLSALMF AGRIGSITLASALTMRHRNTLFRLPEERPLIG
4.8E-47	170	31	5.7E-47	169.7	21.5	1	1	R5JJP 1_9FIR M	TrkH family potassium uptake protein	BN781_ 00984	Coprococcus sp. CAG:782	453	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus sp. CAG:782	1262863	>tr|R5JJP1|R5JJP1_9FIRM TrkH family potassium uptake protein OS=Coprococcus sp. CAG:782 GN=BN781_00984 PE=4 SV=1MKKKFHFKLSTTQTTMLSFFLAILVGSVLLALPISSANGEAVPYIDALFTATTAICVTGLVTLPTVSTWSLFGQVVILILIQIGGLGVI TIMSGLMISLHRKIGIKDRMLIQDAFNLNTLSGIVKFIKKVLVGTFVVEGTGAILYMTVFVPEYGAKGIWISIFNSISAFCNAGIDIISENSLC DYALNPMINIVTSALIILGGIGYIVWWDVIRALKDIRNKKLKFFSNLTLHSKIALSATGVLIVVGAVFFFIFEYNNPLTMKDYSLFDKIQASLF QSVTTRTAGFATIPQQNLTNASATVSLLLMFIGGSPVGTAGGIKTVTIAVLIFAAFSTIKNKEDVVLFQRTIPKQAVSKAVAVVCMSFMIM FISTLLLSAVTNANALDIAYETVSATATVGLTRNLTPILNIWGKLIIIVTMYLGRVGPISLVIAFNTTKEKKNIIKEPTEEISIG
4.8E-47	170	13.4	6.7E-46	166.2	9.3	2	1	R5IT45 _9FIR M	Cation transporter	BN480_ 01257	Firmicutes bacterium CAG:124	481	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:124	1263002	>tr|R5IT45|R5IT45_9FIRM Cation transporter OS=Firmicutes bacterium CAG:124 GN=BN480_01257 PE=4 SV=1MNKRVIVYVLGAVLLIEAALMLLPLLVAVIYREKNGWYFLWVLLGAAVLGALALGLGGRKRSAMYAKEGLIAVALSWIVLSLVGAL PFTLSGQIPFYLDAVFEMISGFTTTGSSILPAVESLDRCMLFWRSLSHWIGGMGILVFMLAIVRMDGGQAIHLLRAESPGPTVSKMVPR MVDSSKILYGIYFGLTVVQIILYLAGGDPLFDSLCNAFGTAGTGGFAIRNDSFASYSAYTQTVTTVFMALFGVNFSIYFFLLRRKFDLAW KNTELRWYVSIIVISTLLITFNIKSLYHGDFGYSLHHAAFTVSSVITTTGYGTENFDLWPEFSRVILVLLMIVGASAGSTGGGLKVSRVVIL MRAAKAELRKILHPHTVKVITVDGKPVSGETVRAVSTYFILYVLIAAASVLLVSLDGYDGSTTLTAVLATFNNIGPGLGLCGPAGNFAFF SPLAKVVLCIDMLLGRLELYPMLVLLMPSTWRKK
4.8E-47	170	20.2	3.6E-46	167.1	14	1.9	1	F0JHI1 _DESD E	H(+)-transporting two-sector ATPase	DND13 2_0826	Desulfovibrio desulfuricans ND132	454	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio desulfuricans, Desulfovibrio desulfuricans ND132	641491	>tr|F0JHI1|F0JHI1_DESDE H(+)-transporting two-sector ATPase OS=Desulfovibrio desulfuricans ND132 GN=DND132_0826 PE=4 SV=1MRTKVFSPYWMPVWFFAGAILIGTLILHLDVSHPGGPLSFVDALFTATSAMCVTGLAVVDTGTYFSTLGLDVILVLIQLGGLGIMT FTTLIIHLLGHHVSLTDRLAVGQSLLHDPSFSLPRFLMRVVAWAFSFEALGALCLWFLDPVGFGPYSAVFHSVSAFCNAGFSLYPDSLT RWAGDGGVNSVFIVLITAGGLGFYVLNECGILIWNALFKRGGRKSGRPRMSWHTAIVLKTSLALVVAGTVVIFVAEGAAGNAPDNFLE HFWNALFQSVTCRTAGFNTVDIGGMTNVSLAFMMVLMFIGGSPGSCAGGIKTTSFRALVGFIWAEFRGWEQVRIGRFALDQKAMNK VVSLVTMSLLLVGVGTMILTSLESGDSSYLMARGEFIADMFESISAFATVGLSTGMTPLLDDFERVTLIVLMFVGRLGPIWMLSALQSW QTERRFKVPTATLPFG
5.2E-47	170	37.2	1.8E-45	164.8	25.8	2	1	R6UJD 5_9CL OT	Uncharacterized protein	BN818_ 01536	Clostridium sp. CAG:964	428	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:964	1262848	>tr|R6UJD5|R6UJD5_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:964 GN=BN818_01536 PE=4 SV=1MIITLGAVLLSLPVSSRSGEYTNFLDSFFTSTSATCVTGLIRFDTYTHWSWFGKVVILCLIQIGGLGFMTMAISIVALTKMKISIATR VIMQNSISAPQIGGIVRLTKKIFLSTAIIEAVGAFMLSFYFVPRLGVFRGIVYSIFHSVSAFCNAGFDLMGYEKPFSSVTYQAGDWYFNIII MALIILGGLGFIVWFDLLTNRFKFKKLKLQSKLVLTVSLSLIVIGTVAIFIFEQKGVLFKNMPLNEQILTSMFQSVSARTAGFNSLNLAAMT EPSLCMIICLMFIGGSTGSTAGGLKTTTFSVLVLSILSTIRHRKDIEAFGRRLESGLGRTAACIFTLYILIVALASMTISSIESVPILHAVFEC VSAIATVGTTLGITTQLQPASEIILILLMMIGRIGSVTILLALFSDKGKTVSKHAQEKLQIG

5.2E-47	170	30.2	5.5E-46	166.5	20.9	1.9	1	D4JWG5_9FIRM	Trk-type K+ transport systems, membrane components	EUS_24760	[Eubacterium] siraeum 70/3	444	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminiclostridium, [Eubacterium] siraeum, [Eubacterium] siraeum 70/3	657319	>tr|D4JWG5|D4JWG5_9FIRM Trk-type K+ transport systems, membrane components OS=[Eubacterium] siraeum 70/3 GN=EUS_24760 PE=4 SV=1MQPSRMLVLGFSIIILAGATLLFLPISSKSGQFSSFIDCLFTATSATCVTGITVLDTFNYFNGFGQGVILALIQVGGLGFLTLVTFINLILGKKLGWSTVKIAASDLTDNALETTPKRLFYEIVLYSFAIEFVGAVILAFVFVPDFGALGIFEAIFLSVSAFCNAGFDLLTATPGAVGLSEYTNNPLVMITLIVLITTGGLGFIVWRNIRHYSKAKRLLLHTKLVLIMAAVMLLVGAAIIFIVEFSNQDTLGQMPIGEKILTSIFLSASSRTAGFPCFDMNDLMPFTKIIITILMFIGAAPASTAGGIKITTVALVVCTVISVLKGREDTYLMGHRIKRDAIYKTFTVIVLSLTLIAVSFTGILMCCEGMSLQKTIFEVVSAFSTTGFSVGASAEMNVPAKLIMVFTMLAGRIGPVTLMTSLIIRKNHNSDKNRILPEGNILVG
5.4E-47	170	33	1.3E-45	165.2	22.4	2.5	1	Q6APM2_DESPS	Related to V-type sodium ATP synthase, subunit J	DP0973	Desulfotalea psychrophila (strain LSv54 / DSM 12343)	670	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfotalea, Desulfotalea psychrophila, Desulfotalea psychrophila (strain LSv54 / DSM 12343)	177439	>tr|Q6APM2|Q6APM2_DESPS Related to V-type sodium ATP synthase, subunit J OS=Desulfotalea psychrophila (strain LSv54 / DSM 12343) GN=DP0973 PE=4 SV=1MKVAEHFYSSLSRFGLEGASLVLFPLPLLLFDRAEMIGGNWRFYLALLASCSSLICAFSLHRRPLLGKFFGLICSAAILALIFFHVLADPFVALPAAIIYIGIVFFLLDFRGDGGVNLYPEAFVRYTQRAWWASFVVMFLVLLDLLMPASVGGPYLYIVLFSFAMAQLLLFLAALSKRSTSYLCFTLFTGLSVALSACFFGMGNIATLILFLNILTLVVLPRGNFLGGRRELWWEVLFDHPARILLVSFLSLSVFGTFLLSFPFATEAGGVGLLDAAFTSVSAVCVTGLTVLDTATDFSLWGQIAILLLIQFGGLGIMSITAVALHAMGRRLSLKQERILTSIADSGSQGLLESLSTILKFTFVVEGVGASLLALVFYCTGDTPLLAIWRGIFTAISAFCNAGFALQSDSLVSYQTNPFVLHLVAILILGGLAPATSLIIPSWLRGKAISIPARIALITSLALLFTGTFFILAFEWNGALAGLSIFDKINNAWFQSASLRTAGFNSIEFAHLCSSSFLVMLFLMFIGGSPGSTAGGVKTVSIGILAITFWRNITNRHHHVIFQGRVISPSTIFRAITVIISGMIVWFFLVLMLTTTQQIFARDIVFEVTSALSTVGLTLGATPLLDGMGKVIVMLAMFIGRIGPTTIFMLLSSDEERSSQRRPEVKISLT
5.5E-47	170	17.2	1.4E-46	168.5	11.9	1.5	1	D3LVT5_9FIRM	Cation transport protein	HMPREF0889_1092	Megasphaera genomosp. type_1 str. 28L	484	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megasphaera, Megasphaera genomosp. type_1, Megasphaera genomosp. type_1 str. 28L	699218	>tr|D3LVT5|D3LVT5_9FIRM Cation transport protein OS=Megasphaera genomosp. type_1 str. 28L GN=HMPREF0889_1092 PE=4 SV=1MDSKVISYILGKLSWAVALALLLPLGAAIGSGEQALAPFLTAIAAAGVTGSLLRRYGRAATADLTVREGLAITTLGWILVTFLGMLPYTVGGYLSILDGILESISGLSGTGATVFNDLTYVPAGILLWRAETHWLGGLGIIVIFIALFPQMGRGTIHLFNAESTGPSSARALPRIKEMARALFRVYVGLTMLAFAALKCCGLSFLAALEHAFSTIATGGFSPYNDSAAHFHSPLIEGVLIVFMLLSSANFGIYVAVRQRGIRVLLQDTEFRCYLGIVVAAAIAITLNLIWQMGMAPPTALRQAAFQAVSLSSSTGFVSADFDTWPSFSKLVILGLMFIGGCGGSTAGGFKVTRVMLLCHMIREAVRQKIHPGVVVQVRSNHSEVSSDLILGVARFFFVYVMLDLLWTILLTWNGVPLFAALGVSISTMGSCGPAFGIFGATCTYAALPAFGKVIVCVSMLMGRLESFTVLALLMPSFWQRRKGW
5.5E-47	170	32.9	6E-46	166.4	22.8	1.9	1	E4RMG5_HALHG	Cation transporter	Halsa_1058	Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	494	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	656519	>tr|E4RMG5|E4RMG5_HALHG Cation transporter OS=Halanaerobium hydrogeniformans (strain sapolanicus) GN=Halsa_1058 PE=4 SV=1MKYKKLLISRYYLISKYTGIIIIFAGAAILSPLLFLLAYPEESMLAPHFLLAGGLSILTGLILFIYGSKYQTENVELSLNEGSIIVIFSWLGAIFFSAIPFVTILNMSWTHSIFEVVSGWTTTGLSLVDVTTAPKLILIWRSIMQFFGGASLAVIALSSLLPVHGMGLYIAEARSDKLLPHVKRSTMMIMKIYTFYTAAGIFLYYIAGMPLFDSINHSMAVISTGGFSTQVDSIGHYNSLSIEVVTIVLMFLGTINFATHYTLIKGKIKTFFKNAEIRLMITLFTLLTPILMFFSLNALYPRLSENFRITFFQIITALSTTGFSTIAFAGWPVFAIFIIVLIMLVGGGTGSTAGGIKQYRIYLIFKSIYWEIKEQFLPRRSVSSNYLWRGENKFYVKDQHVKDVANYIILYLFTFFVGVAIHTAYGYSLLESMFEFGSALGTVGLSIGLISPEAPTGIIWTQTIGMFLGRLEFFIILYAGIKLFKDGIYISKHK
5.9E-47	170	28.2	5.8E-46	166.4	19.5	1.9	1	B7VMX5_VIBTL	Trk system potassium uptake protein	VS_3131	Vibrio tasmaniensis (strain LGP32) (Vibrio splendidus (strain Mel32))	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio tasmaniensis, Vibrio tasmaniensis (strain LGP32) (Vibrio splendidus (strain Mel32))	575788	>tr|B7VMX5|B7VMX5_VIBTL Trk system potassium uptake protein OS=Vibrio tasmaniensis (strain LGP32) GN=VS_3131 PE=3 SV=1MVNFRPILLVIGLVLSKLALFMYIPTLVAFFTGTGGFLEFGQSVVITHIVAFICLSLGRSAKFRLGVRDMFLITSLVWTIASAFAALPFVFINHISFTDAYFETMSGITTTGSTVLSGLDSMAPSILLWRSILQWLGGIGFIVMAVAVLPMLNVGGMRLFQTESSDWSDKSSPRAKTVAKNIVAVYLVLTGLCIISYLFAGMGIFDAINHAFTTLSTGGYSTSDGSMNHFSNSAHWVGTLFMFLGGLPFLLFVSALRGRKLSILYKDAQVRGFTYLFLVTSAVISTWLVVRDGYTVMDAMRVSMFNIVSVVTTTGFGLEDFTAWGALPTTLFAFLMMAGACSGSTSGGIKIFRFQIAMTMLHKQMMKLIHPSGVFVQRYNQRPVNDDIVRSLVAFGLMFFITIILIAGGLSAMGLDPITSISGAITAVANVGPGMGSVIGPTGNFAPLPDAAKWLLSLGMLMGRLEILTLIVLFFPAFWRR
6.5E-47	170	26.3	3.6E-29	111	5.9	2.2	2	G8QUT1_SPHPG	Trk-type K+ transport system, membrane component	SpiGrapes_2628	Sphaerochaeta pleomorpha (strain ATCC BAA-1885 / DSM 22778 / Grapes)	485	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Spirochaetaceae, Sphaerochaeta, Sphaerochaeta pleomorpha, Sphaerochaeta pleomorpha (strain ATCC BAA-1885 / DSM 22778 / Grapes)	158190	>tr|G8QUT1|G8QUT1_SPHPG Trk-type K+ transport system, membrane component OS=Sphaerochaeta pleomorpha (strain ATCC BAA-1885 / DSM 22778 / Grapes) GN=SpiGrapes_2628 PE=4 SV=1MINWKQDATLLAKILIILALFMGIPTCLALYYGETTALHGFLVTYGAVFLFSAAIFLITRNNTNTHLNARDGYLFVSSTWIIATAFSAIPLVVSGSYVDYSSAYFEIMSGFTTTGATVLPEIESLPKSILFWRSETNWLGGMGIVVLFVALLPALGVSGTMLVGAESVGPTKDKLTPKIKTTASILWTIYVLFSLLETILLKFGGLSLYEAVTVTFSTMAAAGFCVKNASIGTFQSAYVDIVVTVFMMIAGANFALYYKAISGHLRSVWKDGELRAYLGIWGIISIISAISLSYNGTYDGFWQSLRFSAFQNASIITTTGFATANYINWPSLPQMLLFLLVFVGGCAGSAGGGIKVIRVVVTLMKMAFVNIKQRIHPNGIFHVRVGQNSVKNEILLSISTFFGVYIATGLIGAVLISFSGADILTCFSSSFLCLGNIGIGFSEVGPTGNFAFYPSWIKWVCSFLMLAGRLELFTVYSLFSKVFWKR
6.6E-47	170	28.2	9.3E-47	169	19.6	1.1	1	R6ED39_9FIRM	TrkH family potassium uptake protein	BN749_01378	Firmicutes bacterium CAG:65	453	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:65	1262994	>tr|R6ED39|R6ED39_9FIRM TrkH family potassium uptake protein OS=Firmicutes bacterium CAG:65 GN=BN749_01378 PE=4 SV=1MNSKKIIQLSTTQKIMLSFLCAILVGSFLLALPISSATGEAVPYIDALFTATTSICVTGLVTVPTYSTWSVWGQIVILFLIQLGGLGVITVMYGVMMGLHRRLGLGNRWMLQDVFNLNNISGIVRFLRKVLIGTLVVEGCGALLYMTVFVPEYGLRGIWISIFNAVSAFCNAGMDIMAEDSLCGYVFQPMVNLVTMLLIILGGLGYIVWWDVLRVLKNIRSQKLKCFRLLTLHSKIALTVTGILIVVGAAAFYIFECNNPLTMQDYTVPQRIWASLFQAVTTRTAGFATIPQEDLTNTSAIISVLLMLIGGSPVGTAGGMKTVTIAVLLVSMFATIGNKEDAELFGRNIPKQAVNKSVAVVSMFFIIASLSTILLSVVTDADVIDIVYETVSATATVGLSRNLTSMLNLWGKLIIIVTMYLGRVGPISLVVAFSTQKKNKNIVKNPTEEISVG
6.6E-47	170	31.7	1.4E-46	168.5	22	1.5	1	R5VLM0_9PORP	TrkH family potassium uptake protein	BN709_00851	Odoribacter laneus CAG:561	603	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter laneus CAG:561	1263089	>tr|R5VLM0|R5VLM0_9PORP TrkH family potassium uptake protein OS=Odoribacter laneus CAG:561 GN=BN709_00851 PE=4 SV=1MTPHTELKYKIRQYYQKFQSFVKLSTDIIAFLTSFITLCLLIYEIGFHEDGKIHLFLLETYKVILRIFLYTGLARVLSDPQGVKKERGFWFEVVLLIALVFIIILEAWPAFKDALVSKHFIEVATYLLLSTISVIEFSKQIVTTLQRYVKPEMMFVYSFLFIILVGTFLLLLPNAHTYHLDFIDAFFTSTSAVCITGLTVVDTSTAFTFTGLIILVSLIQIGGIGVMTFTSFFAMSFFSQVSFRDQLSLKNILNENSLSNIFRTLFYIILTTFLIEGFGAYVIYNQIQDIPQHILPDKLFFSIFHAVSSFCNAGFSTLPGNLYNPAVRNLYGFQSWIACLVILGGIGFPILFNFGKLFIHYFHNALSRLKGNPIAHYGQFHIISLTTRIVLPITLILIIGGTFAFLFLENHHILQDVPLSGKIALAFMNAVTPRTAGFNNVEMTSLLPSTLFLILLLLMWIGASPMSTGGGIKTTTFVVAFKNIVSIIREKKTVEIARRTISPTSIRRANAIILLSLLWIGGATLLLLITNPQAPFLQALFEVVSALSTVGLSLGLTPELNISGKIIISITMFAGRVGILTLLTGMIRQQPTQPYQYPEENVIL

6.7E-47	170	25	1.1E-27	106.1	5.5	3.2	2	D3BGN2_POLPA	Transmembrane protein	PPL_07684	Polysphondylium pallidum (Cellular slime mold)	502	cellular organisms, Eukaryota, Amoebozoa, Mycetozoa, Dictyosteliida (dictyostelid cellular slime molds), Polysphondylium, Polysphondylium pallidum (Cellular slime mold)	13642	>tr|D3BGN2|D3BGN2_POLPA Transmembrane protein OS=Polysphondylium pallidum GN=PPL_07684 PE=4 SV=1MLTLAVVLIRRYYLRRAYSNRHGHFSINLEDASSIQQQLQQQQELQQQQQKDVGNSGRSEDSLSPSSLSGNSDTLTTSSLVTTSSTSTMTTLTLRENSPNVVNNKIVQPNAGGVIINSDSNTNSHDSDNNAQIHHFEHQHDLSLISEDEKEKSVGDDEYDISPDALFILEMNIEYRSLGKLLYIIPIYQVTVYLTGFIVLLLVSNTGGTVETIIKTNKVNTFWWSFFNTISAFNNVGITLLNDNMIQLNRSSFVLFVISILIVMGNTLFPVILRFIIFILRKISKDPDPYEHLLNNPRSVSLMAILEANEKAFAGMSSGDTFVNYLFHSISTRTGGFNSIDISLLSNSVLLLFIGLMFVSSYPFVISLKGSAVNGKYAAEEKTREVMKDLLIRDIFILYICILLIGIFEETRLRDIPDNSFTVFHVMFEVVSAFGTVGLTMGNPKIQSSFSTLLGVTSKLIIIIVMLLGKHRSLPDSVDNAVAIQDKDILSKFLRRKYRQYKY	13642	>tr|D3BGN2|D3BGN2_POLPA Transmembrane protein OS=Polysphondylium pallidum GN=PPL_07684 PE=4 SV=1MLTLAVVLIRRYYLRRAYSNRHGHFSINLEDASSIQQQLQQQQELQQQQQKDVGNSGRSEDSLSPSSLSGNSDTLTTSSLVTTSSTSTMTTLTLRENSPNVVNNKIVQPNAGGVIINSDSNTNSHDSDNNAQIHHFEHQHDLSLISEDEKEKSVGDDEYDISPDALFILEMNIEYRSLGKLLYIIPIYQVTVYLTGFIVLLLVSNTGGTVETIIKTNKVNTFWWSFFNTISAFNNVGITLLNDNMIQLNRSSFVLFVISILIVMGNTLFPVILRFIIFILRKISKDPDPYEHLLNNPRSVSLMAILEANEKAFAGMSSGDTFVNYLFHSISTRTGGFNSIDISLLSNSVLLLFIGLMFVSSYPFVISLKGSAVNGKYAAEEKTREVMKDLLIRDIFILYICILLIGIFEETRLRDIPDNSFTVFHVMFEVVSAFGTVGLTMGNPKIQSSFSTLLGVTSKLIIIIVMLLGKHRSLPDSVDNAVAIQDKDILSKFLRRKYRQYKY
6.9E-47	170	14.8	2E-46	167.9	10.2	1.6	1	D1BVW5_XYLCX	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Xcel_0429	Xylanimonas cellulosilytica (strain DSM 15894 / CECT 5975 / LMG 20990 / XIL07)	461	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Promicromonosporaceae, Xylanimonas, Xylanimonas cellulosilytica, Xylanimonas cellulosilytica (strain DSM 15894 / CECT 5975 / LMG 20990 / XIL07)	446471	>tr|D1BVW5|D1BVW5_XYLCX H(+)-transporting two-sector ATPase OS=Xylanimonas cellulosilytica (strain DSM 15894 / CECT 5975 / LMG 20990 / XIL07) GN=Xcel_0429 PE=4 SV=1MAQVKRNLLGLRELVDRVARRSPARLALAVFLGVCVLVTLLLSAPWATASGHRAPFVDALFTAVSAVCVTGLTVVDTATYWSTWGLVSILVAIKVGGFGVMTLASILGLAVSRRIGLTQRLLTASETRTDRLGEVGSLVRVVIVTTTTLELVVAAMLLPRFLALHESVGTAVWHSVFYGVSAFNNAGFVPTSEGLTPHVGDWLLDLPIILGVFVGALGFPVVLNIMNTRRKGYRGWNRWSLHTKLTIVTSLALVALGWLLMAVLEWNNPATFGPLPTNEKVLASLFAGVMPRSAGFSAVDVGAMHEGTWVVTDALMFVGGGSASTGGGIKVTTLAVMLLAIRAEARGDRDIEAFGRRIPSDTLRVAIAVVFLGATAVLVTTIALMEITGLPLDRVLFEVISAFATCGLSTGITADLPDAGKYLLSALMFVGRTGTMTFAAALALRDRRRIVRFPEERPIIG	446471
7.4E-47	169	20	1.6E-45	165	13.8	2	1	E2SFR8_9ACTN	Potassium uptake protein, TrkH family	HMPREF0063_12877	Aeromicrobium marinum DSM 15272	440	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Aeromicrobium, Aeromicrobium marinum, Aeromicrobium marinum DSM 15272	585531	>tr|E2SFR8|E2SFR8_9ACTN Potassium uptake protein, TrkH family OS=Aeromicrobium marinum DSM 15272 GN=HMPREF0063_12877 PE=4 SV=1MNRWLTPVRVVPAAFLVTITIGTVLLSLPMSTTGRGRGDLLDALFTSVSAVCVTGLTSVDTATYWTPTGQAIILALIQVGGFGIMTLASVLLLTIGRNLGLRNGLIAQTETHAVDLGDVRSLVRRLAVIVLVVETVIIAILVPRFRLVYDDDLPTAVWHAVFHGISAFNNAGFALYSDNLVGFVDDPWIMLPLCLAVVIGGLGFPVVGEIVRRGRRRWSVHTRITVYGSLMLLVVGVVGFGIAEWSNPATIGGLDTGGKLIASVTGGVMPRTAGFNSIDYSAATSESLMLTNMLMFIGGGSAGTAGGIKVSTFILLGVVIWSELRGEQSVGIYGRAMPSSLQRQALTVALLAVGVVMAGTMAMMITTDYTFEPLLFESVSAFATVGLSTGITFDLPASGEIVLILLMFVGRVGVVTVGAALALSHRHRRYTLPEEHIIVG	585531
8.4E-47	169	13.5	1.5E-45	165.1	9.4	2	1	R5UNL3_9FIRM	Uncharacterized protein	BN518_00918	Roseburia sp. CAG:18	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:18	1262941	>tr|R5UNL3|R5UNL3_9FIRM Uncharacterized protein OS=Roseburia sp. CAG:18 GN=BN518_00918 PE=4 SV=1MNYKMMGKFLSQILIVEAGFMVPALLISLYTGSRAAVYGFGLSILITAGVGALMYYFCRNSTRRFFAREGMVCVAGSWIAISFFGCLPFVFSREIPNFVDALFEIVSGFTTTGSSILGDVEALSPGIMYWRSFSHWLGGMGVLVFLLALSPNGERGKGYTMHLLRAESPGPNVNKLVPKMRTTARILYVIYMVLTFINFLFLLLGKMPVFDAVCTAFGTAGTGGFGIQNDSIAGYSPYIQNVCTVFMFLFGINFSCYYLLLVRHVKEVLKDQELRLYIIIFVVSILLITFNVRGLYGSWEETIRHAAFQVSSIMTTTGFASTDFDLWPGFSKALLLCLMFVGACAGSTAGGLKMGRLLLILKNLRRNIRRILSPQRVEVVRMNGNRIGEDVLNNTNTYLAAYGVILVGSFLLISIDGLSMTTNVSAVAACFNNIGPGFDVVGPTCNFSVYSWFSKLVLIFDMLAGRLEIFPMLVLFSRSTWRHK	1262941
8.6E-47	169	35.8	8.6E-47	169.1	24.8	1.6	1	E6XBU8_CELAD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Celal_1641	Cellulophaga algicola (strain DSM 14237 / IC166 / ACAM 630)	582	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Cellulophaga, Cellulophaga algicola, Cellulophaga algicola (strain DSM 14237 / IC166 / ACAM 630)	688270	>tr|E6XBU8|E6XBU8_CELAD H(+)-transporting two-sector ATPase OS=Cellulophaga algicola (strain DSM 14237 / IC166 / ACAM 630) GN=Celal_1641 PE=4 SV=1MWNKVRLSSLAVLFLDLGLVIFLIYDFGFKDYQDLRQYKLIVLPTLVLALIVFNLYKYRLFKRQRVSSISPKINLYYLSILVIVEIVTIISDFEISLFDSFFNVRYVIEYGLLIYFFIRISFLVRKIYAIYFNPAILFVGSFAIIALGGTFLLMLPASTLHGISFIDALFTATSATSVTGLIVVDTAKDFTPFGQTIILFLFQLGGLGMLTFTSFFAYFFKSGSSFRESLYMKDIMGNNDELGGIMKKVMQVVAFSLIIEFLGALLIYTSLPEVDKIPNQIFFSIFHAISAYCNAGFSLESMGLHDINLRHNYYLQWVVMALIIFGGLGYHIAYNVIQYLKRFTTNLFRSKNKIFISRVILLNTKIVLYTSLILIVAGTGFFLISEKHTNLLEHTTWFGKLTTALFSSVTARTAGFNTVDYADFSIPGILFMIFLMWIGASPASTGGGIKTTTFAIATLNVFFVAKDQPYIEIGTRRIAAQSVRRAFAIMAISLASIGTGILFLLIFNPEFTLIQIAFEVFSAFSTVGVSMGITASLSSASKIVLIILMFLGRIGLLNLMIGLLKNVSQADYSYPEENILIN	688270
9.1E-47	169	28.8	1.3E-46	168.6	20	1.1	1	D4MUB1_ANAHA	Trk-type K+ transport systems, membrane components	CL2_21020	Anaerostipes hadrus	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, Anaerostipes hadrus	649756	>tr|D4MUB1|D4MUB1_ANAHA Trk-type K+ transport systems, membrane components OS=Anaerostipes hadrus GN=CL2_21020 PE=4 SV=1MKELRPVQVILLGFLITIFAGSILLTLPIATQSGQATPYIDALFTATTSVCVTGLIVETTMTHWSIFGQAVIILLVQIGGLGVITITTGMFFMLRKRITLGNRMLIQESMGLNTMTGLVPLVKKILIGTGIIEGIGAVLYATQYVPEFGIGYGIWAAIFNSISAFCNAGMDIVRDDSLRSYVTNPVMNFTTMGLIILGGLGFVVWKDLWQGFKKIIKDKVPVKRMIQQWRLQTKIVLSITSFLILFGTILIFLFEYHNPATMESLSLPQKIQASLFQSVTTRTAGFETVAQGALTDASSLVSMFLMIIGGSPTGTAGGVKTVTFAILVFCVLSVAKQEESITLFKRRVPQNLLAKALAIIVINLIVLMTSVLLLLVFDHGTFMDSCYECVSALATVGLTKGLTPNLTIAGKVIIIITMYLGRVGPISMAIGFSQKNKKKMVMYPEQDLIL	649756
9.2E-47	169	29.7	1.2E-46	168.7	20.6	1	1	R5P0H2_9FIRM	Potassium uptake protein TrkH family	BN730_02169	Eubacterium sp. CAG:603	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:603	1262891	>tr|R5P0H2|R5P0H2_9FIRM Potassium uptake protein TrkH family OS=Eubacterium sp. CAG:603 GN=BN730_02169 PE=4 SV=1MSLSNPKHKLQLSTTQMIALGFLLTVVGGSLLLMLPVSSADGTYTPFVDALFTSTTSVCVTGLVVVNTFEHWSLFGQIVILFLIQCGGLGIITFTTSLMLLLHKKVTLKGRMLLQDAFNLDSLSGLVRFTHKVLIGTFTIEFIGAFFYSFTFIPDFGLAKGIWISVFTSISAFCNAGIDLIGPSSLAEYATNVNVNLTTMFLITMGGLGFIVWFDILKNIRAIRNKEMPHTAFFNRLCLHTKIVLTVSISLIIIGAVIVFAFEYNNPATIGNMSVPHKILASFFQSVTTRTAGFFTFSQKGMRDATTLFCLILMFIGGSPVGTAGGVKTTTLALIIIAAMSAVKGSEYGTAYGRRIPNRTMRKALAVVLASLCFLFTSIIILSTYTGGDLLDIVFESTSAIGTVGLTRDYTATLDLSGKVIIIICMYAGRLGPMTLPIIFSSRKSKYGLAMFPREDITVG	1262891
9.4E-47	169	15.6	5.7E-46	166.4	10.8	1.8	1	F6FVZ0_ISOV2	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Isova_1710	Isoptericola variabilis (strain 225)	475	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Promicromonosporaceae, Isoptericola, Isoptericola variabilis, Isoptericola variabilis (strain 225)	743718	>tr|F6FVZ0|F6FVZ0_ISOV2 H(+)-transporting two-sector ATPase OS=Isoptericola variabilis (strain 225) GN=Isova_1710 PE=4 SV=1MRFPRPQPDVVRHDGRPTPRASGPSPASLRRRPAQLVTLGFVGAIAVGTLLLSLPVASTGRRATFVEALFTTTSAVCVTGLVVVDTETFWTPFGQVVILALIQVGGFGVMTVASLLGVLLTRRLGLSTRLVAAESTHTVGLGDVRRVLLGALRLTVVAEALVASVVAARLMVSYDESPAHAAWSGAFHAVSAFNNAGFSLYSDSLVRFVADPWVCLPICAAVIVGGLGFPVLLELWRLHRSGDGHLLRPRWWSIHSRITVGTTAVLLTVGTLVFLLAEWGNPRTFGPLDVPGKLLAAFTQAVMPRTAGFNSVPTSELNNGTWFFTDILMFIGAGSAGTGGGIKVGTFAALAFVIWSELRGDPDVEVFDRRLAVTTQRQALTVALLGVAAVVVPTFVMTVTTTTFALDAILFEVVSAFSTTGLSTGITASLPAWDQLILVVLMFVGRLGPITLGTSLALRERRRLYRRPESAMIIG	743718

9.5E-47	169	38.5	9.5E-47	169	26.7	1.4	1	A0A0C5WBT6_9FLAO	Potassium transporter	AW14_03275	Siansivirga zeaxanthinifaciens CC-SAMT-1	580	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Siansivirga, Siansivirga zeaxanthinifaciens, Siansivirga zeaxanthinifaciens CC-SAMT-1	1454006	>tr|A0A0C5WBT6|A0A0C5WBT6_9FLAO Potassium transporter OS=Siansivirga zeaxanthinifaciens CC-SAMT-1 GN=AW14_03275 PE=4 SV=1MKRESILNYVYRFFDIIVLFFIVFDFGYDYAENFTTPHVLGLLILTGFLLSFNTAKYFIYKYKTNKRVAFVNIIIISALLILSLIISIVYSEHSYHYILQKIKPILEGGLILYFLLRLLILVRHIYDVYFNPAIVFVGSFLILALSGAFLLMLPSATTNGISFTNALFTATSSVCVTGLAVLDTSQDFTTVGQSIILVLIQLGGIGILTFTSFFAFFFRGSSSFKEGLNTKDFLAHEGLRDVFRVALNVVVVFTLTVELVGSLFIYFSLGNNKEIENKFFFSMFHSISAFCNAGFSIFSNGLFNQSIRFNYAFQWIIMTLVVFGGLGHNIVFNFFHYLKTLVLELFNKKLIHKQIPVITVNTKLVVYTTLILLTAGWVFLFVSEYTNTLLEHKTLFGKITNAAFGSVSPRTAGFNVVDYSEMTVPSLLFVIFLMWIGASPASTGGGVKTSTFAIATLNIFAIARGKSRIEIFGRRLSAETTLRAFAILCISLIVIGMAIMALLILEPKDTPLLTVVFECFSAYSTVGLSLNFTPTLSEASKYVIIAVMFIGRIGMLNLMVGLLRQINHQFYEYPKENILIN
9.9E-47	169	30.6	9.9E-47	168.9	21.2	1.6	1	R6GBD6_9BACE	Uncharacterized protein	BN744_02791	Bacteroides sp. CAG:633	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:633	1262744	>tr|R6GBD6|R6GBD6_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:633 GN=BN744_02791 PE=4 SV=1MKIYHKYLLYQNKWIHPYVRIVLNIFTSLTYLASLLLIIGVVYEHGFTITAEEAQQVNRLYHGVWIVFLVDVTLHILLEYKDTRRTFSKLTWVLTGLLYLTLVPVIFHRPEVEGGILDFWNFLHGKGYRLVLLLLLSLLTLSNGMVRLLGRRTNPSLILAVSFLIIVLIGTGLLMLPRCTVDGISWVDSLFISTSAVCVTGLTSVDVASTFTPAGFVVIIILIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSDSLNSLLTTLVYILGFTLVIEGVGMLAIWSDIHGTLGMSLKEELAFSAFHSISAFCNAGFSTLPGNLGNPVLMSGHNSLYLYISFLIILGGIGFPILVNFKDILLHYVRRFWHFVRTREWDARRFYHLYNLNTKIVLILTLLLLVVGTVAIAVLEWNGAFAEMPVGDKLTHAFFNAVCPRTAGFVSVDLTTLGVQSLLIYMLLMWVGGGSQSTAGGIKVNAFAVVVLNLVAVLRGTERVEVFGRELSSDSIRRSNATVVLSFTVLFLFVFVISLIEPEHSLMAIAFECVSALSTVGSSLNLTPLLHDSSKLLIVVLMFVGRVGLITLMLGIVKQKKNTKYRFPNGQIIIN
1E-46	169	22.9	3.5E-45	163.8	15.8	2	1	W8X9C2_CASDE	Potassium uptake protein, integral membrane component, KtrB	BN940_10551	Castellaniella defragrans 65Phen	454	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Castellaniella, Castellaniella defragrans (Alcaligenes defragrans), Castellaniella defragrans 65Phen	1437824	>tr|W8X9C2|W8X9C2_CASDE Potassium uptake protein, integral membrane component, KtrB OS=Castellaniella defragrans 65Phen GN=BN940_10551 PE=4 SV=1MARINIHPLQAYRQARRTGQLQASPPAVLAGSFLILILVGTVLLSLPVAQRHPFGMFEALFTATSAVTVTGLMLIDPATDLSFFGQAVLLALVQIGGIGFVTFAIIATLTLGRRVSLKYQALALEAFNQTSVARIRQTALTVLKFSLVIEGAAILILTLWWWRHDSLEHAFLLAGFHAVSAFNNAGLSLFPGSLAGFAQDPVTTFVITGCVILGGLGFSVLADIQQKRSWTTLAYYTRLMLIGTLVLNLAGFALFWLIEARNPNTLGALPAAGQGLAAWTQVVAARTAGFASVDVDQLYDSSRFLLTGLMFIGGGSLSTASGIKLATFIVLLAVVRAYILQRKEVVLMHRTIAPETIHKALALMMVSGLLVCLGIFLVSLFEDMPFIAVVMEVMSAFSTTGISPDLTRVLSLPSQIVLMLLMFVGRLGPLTLVYSLGTQRRSRVRYPETVVQIG
1E-46	169	21.8	1.4E-44	161.8	15.1	2.1	1	D5U282_THEAM	Cation transporter	Tagg_0962	Thermosphaera aggregans (strain DSM 11486 / M11TL)	500	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Thermosphaera, Thermosphaera aggregans, Thermosphaera aggregans (strain DSM 11486 / M11TL)	633148	>tr|D5U282|D5U282_THEAM Cation transporter OS=Thermosphaera aggregans (strain DSM 11486 / M11TL) GN=Tagg_0962 PE=4 SV=1MFFTITVIIYEWLAHMVELRGLNVLKTMGALTSLLGVLMISVPLIDLGTGQQVSTGFLAFSVVLMVGGFLLSRLKSQEGLSFTEAVLSSTLAWTLLPAISAIPLSMELSIPFYDAFFESVSGFTGTGLTVLTGLESLKPSILFWRALMQWVGELGFVVFAMVLFPFFYKYGLLMYGVERPVRIEASMYRTAKRLFNIYIVLTLAGALMLYYSGMNIFDAITHSMTGIATGGMSNYDANYDVIYRAVPLTSIPLIIIMVLGATNFLLLDKLLRGDVGEVARNEEFKLYLILLLFFSTITPISILVSNNSSSNIPEIIASGVFNSISAMTTTGFNIGVIGQLPYATKLTLTFSMLIGGMTFATVGGIKVLRFLIILKKLKASSINVVTGGRAETKIRLGGNILDDSETASALLLALIHFTAVFTGAMLIKLMLPGFDYADALFEATSAASCVGLSTGITSAMAPPGVKAVLIILMILGRLEYLPLLMLIGWVLGRKTIKLLR
1E-46	169	19	1.9E-46	168	13.2	1.3	1	B2GK13_KOCRD	Putative Ktr system potassium uptake protein KtrB	ktrB KRH_15110	Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)	466	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Kocuria, Kocuria rhizophila, Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)	378753	>tr|B2GK13|B2GK13_KOCRD Putative Ktr system potassium uptake protein KtrB OS=Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201) GN=ktrB PE=4 SV=1MQTHRSRIRRTVPMMKSRPDPFHLHELTPARSARLIVLAFLLALLTGTGLLMLPPATAAPGGTDLLTAAFTATSALCVTGLVTVDTATYWTPFGQVVIVCLIQVGGLGVMTFTTMLGILLARKFGLSTRLLANAETKSRGGARQVVARIVLTTLVIECTAAAVLFLRFLLHYHYPPGLALAHGVFHAVSAFNNAGFALYSLNVVDFAADPVVLLTSAAVILGGLGYPVLNELRRHLTLPRRWSMNTRLVLLATPVLLLGGTLFLALLEWNNPATLGPQAPAVKVLNAFFQSTISRTAGFNSIDISQMHPVSWLGMDILMFIGGGPAGTAGGLKVTTFGVLFFIALTEIKGGAAVPVLGKQLSRSVQREAITVVVLATGAVIGGSMLIMLTDTSLGLDRVLYEAVSAFSTVGLSTGITATIAPFAQCVLIVLMVMGRLGPVTVAASIAFGRRPPAYELPKERPLIG
1E-46	169	11.2	4.3E-42	153.6	2.2	3.1	3	A9SBR9_PHYPA	Na+ transporter	hkt1 PHYPADRAFT_77216	Physcomitrella patens subsp. patens (Moss)	706	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Bryophyta, Bryophytina, Bryopsida, Funariidae, Funariales, Funariaceae, Physcomitrella, Physcomitrella patens subsp. patens (Moss)	3218	>tr|A9SBR9|A9SBR9_PHYPA Na+ transporter OS=Physcomitrella patens subsp. patens GN=hkt1 PE=4 SV=1MGRLTVTVVSVVKPWVGSSCSVIDCQVKCVETMFYRAWYCHGFGKSWGLARSKTLTDGQQLTEAPPHPRNSNSASNIGHSKRFKTPREFMQSLSMSWIKSPFNSDMMRRRVESSKQRLKRIVCGSHTFFWLHVAYYGVLTIVGTMSLWWCRERNSISFLDCIFTVVSMVTTTGLTSVLLRDFNTTGLFTLMVLMLLGSSVFVSLLPIYVRRLRILRYNRALDTSNAANVSSSQLSSYNSSDCHHSRATGMSPISNHTLQIVAEVDAQSHDSGTGFGRHPHINSDPVVINIANRFNDLSDEQEVAQQSDDLRIARWLEDQALRSLSWIIPTYIVVLLTFGFLAVVWNNSFNSKEASKIRSLFDAQGINPTLAAIFMSISAFSNTGSSPLDENFVPFATSSLVLVSLTVLFLGGNTLFPPILRFIIWGLRTLKRTDDPQKDVYNFLLRYPRRCSTHLFPHMQSLWIIATVLGFNTVDLIAFCALEWKSAALAALPDRSAWIKLMDGLFQSLNTRSSGMNVLTLSTLSPSLLVLYSAMMCIAVYPVYLSRQHTRLTHTDFNQLHLFSTSDLCDPEKHKSTADGADDNRLSTQYKQLLTRDSASLFVLVFLVCTLEMRNTNSDPLNYSVFNIVFEVISAYGNVGLSLGYSCEQWQRASSNSSTSQLADECKNVSYSFSGKWSSGSKLLLICCMILGKHRSLPNDDDSTIS
1.1E-46	169	23.5	1.1E-45	165.5	16.3	1.9	1	Q9KVU7_VIBCH	Trk system potassium uptake protein	VC_0042	Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio cholerae, Vibrio cholerae O1, Vibrio cholerae O1 biovar El Tor, Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	243277	>tr|Q9KVU7|Q9KVU7_VIBCH Trk system potassium uptake protein OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) GN=VC_0042 PE=3 SV=1MLNLRPITFIIGLVLSKLALFMYVPTLVAFFTGSGGFLDFAQAVIITHLVAFLCLSIGRTEHFRLNVRDMFLITSLVWTIASAFAALPFVFINHISFTDAYFETMSGLTTTGSTVLSGLDDMPPSILLWRSILQWLGGVGFIVMAVALPMLNVGGMKLFQTESSDWSDKSSPRAKTVAKNIVAVYLVLTGLCFLSYIATGMTPFEAINHAFTTLSTGGYSTSDSSMNRFSHGAHWVGTLFMFLGGLPFLLFVQALRKQSARALLKDEQVRGFFWLFMISSLLVAGWLWLKNDYAILDALRVSMFNIVSVVTTTGYGLDDFTAWGALPSTIFAFLLMAGACSGSTSGGIKVFRFQIAMALLKKQLLNLIHPSGIFIQRYNKRPVNEEIIRSVVAFGLTFFITIVVLAGALSAMGLDSVTSISGAVTAVANVGPGMGSIIGPTGNFAPLPDAAKWLLSFGMLMGRLEILTILVLFFPAFWRH
1.1E-46	169	17.2	7.1E-46	166.1	11.9	1.9	1	I7DSJ2_PHAIB	Trk system potassium uptake protein	PGA1_c23520	Phaeobacter inhibens (strain ATCC 700781 / DSM 17395 / CIP 105210 / NBRC 16654 / BS107)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Phaeobacter, Phaeobacter inhibens, Phaeobacter inhibens (strain ATCC 700781 / DSM 17395 / CIP 105210 / NBRC 16654 / BS107)	391619	>tr|I7DSJ2|I7DSJ2_PHAIB Trk system potassium uptake protein OS=Phaeobacter inhibens (strain ATCC 700781 / DSM 17395 / CIP 105210 / NBRC 16654 / BS107) GN=PGA1_c23520 PE=3 SV=1MLDLRPVGYVIGLLVAILGATMVFPLAVDLYDGQGEWPVFLESAVITILGGGLIALSCANGVREGLTIQQTFLLTTLVWVALPLFGAIPLMLGATELRFVDAFFEAMSGLTTTGSTVISGLDDLPRGLLLWRGILQWLGGIGIIVVAMVFLPELRVGGMQIFRSEAFDTMGKILPRAQAIAKQISLIYVGLTVACMVVYMLLGMEPFDALVHALTTCSTGGFSNYDASFGTFTGAPEYAASVFMILAALPFVRYVQMINGHSKPLFRDSQIQAFLATIALLVVVTACVLVYVFPHHPEQAVREALFNITSIISGTGYASVDYMQWGSFLVMLFFFIGLIGGCAGSTACSVKIFRYQLLFASIRVQIQRIHSPHGVFVPRYQGRAVDTEVLSSVISFFMFFVVTLGIVAWALALTGLDFVTAVSGAATAVANIGPGLGDRIGPAGNFATLNDGAKWILSAAMLIGRLELMAVYAILTIRFWRN

1.1E-46	169	28.8	4.9E-46	166.7	20	1.7	1	F0LQ32_VIBFN	Trk system potassium uptake protein	vfu_A00276	Vibrio furnissii (strain DSM 14383 / NCTC 11218)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio furnissii, Vibrio furnissii (strain DSM 14383 / NCTC 11218)	903510	>tr|F0LQ32|F0LQ32_VIBFN Trk system potassium uptake protein OS=Vibrio furnissii (strain DSM 14383 / NCTC 11218) GN=vfu_A00276 PE=3 SV=1MLNLRPIMFVIGLVLSKLALFMYVPTLVAFFTGTGGFLDFAQAVIITHIAAFICLSIGRTSNFRLSVRDMFLITSLVWTIASAFAALPFVFINHISFTDAYFETMSGITTTGSTVLSGLDTMAPSILLWRSILQWLGGVGFIVMAVAVLPMLNVGGMRLFQTESSDWSDKSSPRAKTVAKNIVAVYLVLTGLCIVGYMLTGMRLFDAINHAFTTLSTGGYSTSDGSMNHFSNGSHWVATLFMFLGGLPFLLFVTALRKRRPQELFKDAQVQGFFLLFIISSLIVAFWLHFNNGYAMLDALRVSMFNIVSVVTTTGFGLDDFTAWGALPSTLFAFLMMAGACSGSTSGGIKIFRFQICFALLKNQMMCLIHPSGVFVQRYNQRPVNEDIVRSVVAFGVTFIITIILIAGALSVMGLDPTTSITGAITAVANVGPGMGSVIGPTGNFAPLPDAAKWILSFGMLMGRLEILTILVLFFPAFWRR
1.2E-46	169	21	6.9E-45	162.9	14.6	2.1	1	R7J4F2_9FUSO	K+ transporter TrkH	BN657_01220	Fusobacterium sp. CAG:439	489	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Fusobacterium, environmental samples, Fusobacterium sp. CAG:439	1262899	>tr|R7J4F2|R7J4F2_9FUSO K+ transporter TrkH OS=Fusobacterium sp. CAG:439 GN=BN657_01220 PE=4 SV=1MRLNYLANAIGLTMIYIGLVTLTPIIAALYYHDFSSIMPFLTAGIISAGLGYVFRKVVPNSTTLENLNDIKKAEALFIVAVSWVIFGIIAGIPYLFYGISPLDALFESVSGITTTGATILTNFDYPQAFFFWRSLTQWLGGLGIIVLFIAILPQFAVAGRQMFFAEAPGPTEDKITPRIRNTASALWGVYAGLTILQIILLMVGGMHGFDAVCNSLSTLAAGGFSPNPESLMGYHSNYLTWVTLIFMFLAGASFNVQYRAIVQKNPMVLFKNEEFKLYFSLVMLMAVLITISLIINTHSTVFQGFTDALYQVISITTSTGSASVDFINWDYTSKLLLFMVMFMGSCAGSAGGGIKMVRWLIVYRSMKSELLRILHPNAIVNIKVDNKTVPAEVSRQIVVYVFYYFLIFGVTSVIISIVEHNSAIGLSSSITALGNIGPGFAKLTGPMANFDCLHDSSKALMVFNMLVGRLELIPFLVMLQKDFWTLKDN
1.2E-46	169	27.7	4.3E-45	163.5	19.2	2	1	D4IK16_9BACT	Trk-type K+ transport systems, membrane components	AL1_06790	Alistipes shahii WAL 8301	468	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, Alistipes shahii, Alistipes shahii WAL 8301	717959	>tr|D4IK16|D4IK16_9BACT Trk-type K+ transport systems, membrane components OS=Alistipes shahii WAL 8301 GN=AL1_06790 PE=4 SV=1MLFIAMFMLLSAGISYLSGMDSAFYPLLLSSLLTALLGAFPLIFVGKREQITNKEGFCIVVGAWLVACVVSMFPYLIWGGEFSLVNAWFESVSGLTTTGSTILNDVEALPRGLQFWRMSSTWIGGMGVVMFALVVLPSMGRSKMMLSNVELSTMAKDNYRYRSQIIVQILLVVYVGLTVLSTVLLKMAGMNWFDALCHAMSACATSGFSTKNASIAYFNSPAIDTILIFAMATAGVHFGLIYATVTGKRSNIFRSEVTCWYFGMLLAGGVLIAVSLFAADIYPTLTASFRYAMFQFVSVVTTTGFATADSNTWTSFAVILLIFGSIVCACAGSTAGGIKVNRLVLAGKMMRTRLRQQQHPNAIIRIRLDGVIQENEALHAVMIFIVTYLMFILAGTVFGTMLGVDLTTSFTGAVASMGNVGPGFGEVGSMDNFSAMPAAFKVSNSLLMLLGRLEIFGLIQIFFIKWWR
1.2E-46	169	12.8	1.8E-25	98.8	1.4	2	2	R7F7C4_9BACT	TrkH family potassium uptake protein	BN677_00763	Prevotella sp. CAG:485	486	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:485	1262927	>tr|R7F7C4|R7F7C4_9BACT TrkH family potassium uptake protein OS=Prevotella sp. CAG:485 GN=BN677_00763 PE=4 SV=1MHGALNYKAVARVMGRLVGVEGLLLSIPLAVALFGREADWPGFAVATAAALAVFALTELTTRRIRLIRAREGFALTALVWIIFSVIGLIPFVMGPAPLSFTDALFETISGFTTTGASVYADVDGLERGILLWRALMQWIGGLGIIFFMLAAIPALNRDEGISMFHAEATGIYHTKLHPRIRQTVLSLWRVYSALTLCCILLLWAGPMSLFDAVCQTFTAISTGGFTTHNAGLAYWHSEYADWVLTIFMAVGGVNFMLLYGAIHRRFHDLAANAVARCYFGVILAFWALMALATWLQGNVEPTFRNLGLNTLEHTVSAITSTGFTVPGANQWGPAAMTLTVLLMIAGSCAGSTSGGVKIDRLMALRSNLRNNLLRTIHPHRAFVVRIGPEVLKAPVMHRIAAFFTIYMLLIALTVLVAVFCGYDFADSVFLSASAVGCNGLGYGITAAGFGSLHDVLKYVMMFDMLAGRLELFAFLTLFTPAFWRH
1.2E-46	169	14.6	3E-46	167.4	10.1	1.5	1	C5CB56_MICLC	Potassium uptake protein, TrkH family	Mlut_14850	Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) (Micrococcus lysodeikticus)	431	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Micrococcus, Micrococcus luteus (Micrococcus lysodeikticus), Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) (Micrococcus lysodeikticus)	465515	>tr|C5CB56|C5CB56_MICLC Potassium uptake protein, TrkH family OS=Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) GN=Mlut_14850 PE=4 SV=1MVGSFLVVIVTGTGALLLPASYQGRAPTPLEAAFTATSATTVTGLGVVDTQTFWTPLGQVVILALIKLGGLGVMTFTSLLGLVILRRLGLTQRLDAAASTRAEGIGDLPRVLRALILYSTAVEASVALLLSLRFWLGAGMSPGQALWQGVFHAVSAFNNAGFALFSDNLMGFVSDPFICLPIAAAIILGGLGLPVVLTLRRDLRRPERWNLTVRLVLVGTAVLLVGGTLMYLVLEWSNPRTLGGLDPASRVLAAFFQSVTTRTAGFNTLDYGQMHPVTLFGTDVLMFIGGGPAGTASGVKITTASVLLFIVLAEIRGEGAVHAFGRRLSRTTHREAITVIMLSATAIAVATMALMGLLSSFTTDQILFECVSAFGTVGLSTGITAQLPPAAQGILMLLMFVGRIGPATVAGSLALTDRTRHFEYPKERPLIG
1.2E-46	169	18.4	1.2E-46	168.6	12.7	1.9	1	Q1GF98_RUEST	Trk system potassium uptake protein	TM1040_1935	Ruegeria sp. (strain TM1040) (Silicibacter sp.)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Ruegeria, Ruegeria sp. (strain TM1040) (Silicibacter sp.)	292414	>tr|Q1GF98|Q1GF98_RUEST Trk system potassium uptake protein OS=Ruegeria sp. (strain TM1040) GN=TM1040_1935 PE=3 SV=1MLDLRPVGYVIGLLVVILGGTMVFPLLLDLYDGKGEWPVFLESALFCFLVGGVLALTCANGVGRGLSIRQTFLLTTLVWVVLPIFGALPLMLGATELSFTDAFFEAMSGLTTTGSTVISGLDDLPRGLLLWRGILQWLGGIGIIVVAMVFLPELRVGGMQIFKSEAFDTMGKILPRAQEIAKQISVIYLVLTLVCALVYTVLGMGLFDAVVHAMTTMSTGGFSNYDASFGTFSGPAEYAAAIFMVVAALPFVRYVQMVNGKTLPLFQDSQVRAFMATILLLVAITAGVLVTIFPHHPEQAVREALFNIISIMSGTGYASVDYMAWGPFLIMIFFFIGLIGGCAGSTACSVKIFRYQLLFASIRVQVQRIRSPNGVFVPRYEGRPVTPDVLSSVISFFMFFVITLGIVAWALALTGLDFITAISGAATAVANIGPGLGDIIGPAGNFAPLNDTAKWILAIAMLIGRLELMAVYAILTVRFWRS
1.2E-46	169	27.8	3.4E-46	167.2	19.2	1.5	1	R5BI55_9FIRM	Cation transport protein	BN814_02150	Veillonella sp. CAG:933	457	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Veillonella, environmental samples, Veillonella sp. CAG:933	1262980	>tr|R5BI55|R5BI55_9FIRM Cation transport protein OS=Veillonella sp. CAG:933 GN=BN814_02150 PE=4 SV=1MILGPNFTRRPLTWQEKVRNSLMTNPQRLLALSFAVLMLFGGYLLTLPWATLDGSRTPFIDALFVAVSCVSVTGLTTVDTFHHWSIFGQTIMILLIQIGGLGTMTFTTFIFIVLRRRVGLENKLLLQEDIGQDNISVQTVLKQIAILTFGFEFIGGVAYTLDLYPYLGYSAIYYGFYQAISTFCNAGFVFFDNDLPYKMVGDWGFTLITCSLILIGGFGYMASFDIWNNRQRGFAQLTLHTKVMLVGELILVVAGTLSILGLEWTQTLAGLPFTTKIQGALFQAITPRTAGIPTLNYADLHPITVFITVVLMFIGAGPNSTGGGIKISTMAVLWATSRSLFTNTRRVEIFERSLSQSVIYKAVGIVFFSSMLVVLATFVLAGVESFPFLDLLFEVTSAFATVGLTIGITPELSTISKLTLIIVMYTGRIGVLTLIGAFFLKRRATTTAYYPEDNVLL
1.7E-46	168	25.6	8.4E-46	165.9	17.8	1.9	1	R5SY65_9CLOT	TRK system potassium uptake protein TrkH	BN544_02011	Clostridium hathewayi CAG:224	526	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	1263067	>tr|R5SY65|R5SY65_9CLOT TRK system potassium uptake protein TrkH OS=Clostridium hathewayi CAG:224 GN=BN544_02011 PE=4 SV=1MNDHMILWETLGAENHHERHVLKGYRLIAGYMGIVMILAGIITLLPLFTLFFYPEEMGQAQYFVAPGVSSILAGYLLSLVLRGRRAGNLEKNQEMIVVLGTWVIVIFVTAIPFVLSGTYSVTQAVFETTSGLSTTGLSVVDVSTAPHIFLIHRTILLFFGGIGLVLVMTSVLSDVYGMRLYHAEGHSDRLLPNLIESARLIIGIYSGYILGGTFLYILFGMSPFDAINHAVAALSTGGFSTRAESIGYYNSTAIEMVTVILMLLGSTNFFVHLLLLKGKFKEFISHCEVRLMLFLLALFVPILTVLLMNGVYSNVPVSLRAALFQAVSALTTTGFQTVESFAAWTPAMMFLMILLMLIGGAGSTAGGLKIYRVYVVMLKEIWWKLVRDAHPDRVVVFTEQINRGGKKEVITDREKNRINAFVFFYLLLFAVGSFVFCCYGYSIQDSMFEFASAISTVGLSVGITSYGASPVIHWTAIAGMFLGRLEIYVVLIAAARMASDGKNYLHEKQMKRKRHRNRNRKRDHYEK

1.8E-46	168	24.5	2.5E-46	167.6	17	1.1	1	D7BM87_ARCHD	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Arch_0278	Arcanobacterium haemolyticum (strain ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018)	481	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Arcanobacterium, Arcanobacterium haemolyticum (Corynebacterium haemolyticum), Arcanobacterium haemolyticum (strain ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018)	644284	>tr|D7BM87|D7BM87_ARCHD H(+)-transporting two-sector ATPase OS=Arcanobacterium haemolyticum (strain ATCC 9345 / DSM 20595 / NBRC 15585 / NCTC 8452 / 11018) GN=Arch_0278 PE=4 SV=1MAHGVPPRSSSAGRGRFDVRMSLGPDSDSGVHGHSLRNYINSLARRSPARLAMLVFGALIFAVTLLLMVPFSSTTPGSSSFTD ALFTATSAVCVTGLTVVDTATHWTAFGHIVLALGIQIGGLGVMVIASILALAVSRHLGLTQRMLAATETKSRLGDVGALLKAVIATSLVAE SVLTLVFLGSFVGIDPSFVSALGHSLFMAVSTFNNAGFVILEDGLGQFVGDWAVSLPIIIGTIIGAVGFPVTLNVAQNLRHPRNWTLHSK LTLVTYGILLGISIVMIALLEWNNPATLGGLNGAERTLATLFHATTPRSSGLSTLDVGDMNQSTWFFIDMMMFIGGGSASTGGGIKVTT FAVLALAILAEARGDRDTEAFGKRIPADVVRLAISATFLGAFMVGAATLIIMQLTDFSLSHVLFEVISAFATCGLSTGITSALPESAKIVLIV LMYLGRVGTMTLAAALALRNRRRVIRLPQERPVIG
1.9E-46	168	26.9	3.8E-46	167	18.6	1.4	1	R5AV99_9BACE	Cation transport protein	BN813_00508	Bacteroides sp. CAG:927	621	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:927	1262753	>tr|R5AV99|R5AV99_9BACE Cation transport protein OS=Bacteroides sp. CAG:927 GN=BN813_00508 PE=4 SV=1MFQLGNIILRIRKRLRTIGVSVHRFKVHSAATLRFTGFAVELLAVLASVACIVCMLVLMGYDQSMAHREELKYIVRCCQVMFVVNV AYHMIFEFHQTCRSNKPIKWILDTAIMISVVPLVWHQPDHPWIPWLSDLLYSRWFIYPVLLAYSVITLSYSIIKAIGKRTNPSLLLSGSFIVI ILAGSLLLQLPRCTYAPLEYCDALFVSTSAVCITGLTPVDVYSTFTPLGQLILLVLIQVGCLGLMTFTSFFALFFSGSTSIYSQLMLKDIIYS RSMNALIPTLRYIFAFTVMVEAIGAGLVYLSVEGTMGMSHADELWFSVFHSVSSFCNAGFSVIPHGLSNPLLMKGNISIYWVTSLMIVA GAIGFPILTNFKDTLIEHIRKFWHRLSGRGAGQRIVHNYNMNTRIVLTTFGLLFAFGSVAFFVLEYNNTLSGMSLVEKITQSVFNSATPR SAGFSSVNPAGFLPATLIVVMFLMWIGGGSQSTAGGIKVNTFAAICLNLRSIVSGRSSVTAFSRTIAVGSIRRANAVVALSIISYFLFSVT LVLLEPHLPTKDLLFEALSALFTVGSSLGITPRLGAASEVLLCFAMFLGRVGIISLLIGITPQQHDGGAKFPNDVIIIS
1.9E-46	168	38.1	9.7E-46	165.7	26.4	1.9	1	Q49US0_STAS1	Putative Trk-type K+ transport system membrane component	SSP2353	Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229)	434	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus saprophyticus, Staphylococcus saprophyticus subsp. saprophyticus, Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229)	342451	>tr|Q49US0|Q49US0_STAS1 Putative Trk-type K+ transport system membrane component OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229) GN=SSP2353 PE=4 SV=1MKQLTKPLYFYLLLFITTTLIGALLLYLPITGKHPIDFVDAFFIAASAFTVTGLATIDVSTQFNWLGDTIIMSLIQIGGLGIVTVTLLTFIL INKRISNKSRYLVVMAMWNIDTPGGIICLILQFVLYSLVTKLVGALCIALSFIPKYGLGQGVFLSIFTSVSAFNNAGFALFKDNLISAVNDPII TITVPLLIIMGGIGPLVFLDLVTTQKLTKLKLKLHSKIVLSTTFILIIVGSISFFILEYPSTLNHLSLIEKIGASFFQSVTTRTAGFNTVDIGQISTPT SMMMMLFMFIGGAPISSAGGIKVTSLVLTLLFIKSTLRNESHPAIFKKSIPERTLKIAVTITLLATIFVLSISFIVSVLNPHTSYTTVLFEVISA FGTVGLSMNFTTDYGTVTKIIIIVTMLIGKIGILTFVQLFISEKKQLFHYAKDNVQL
2E-46	168	18.9	1E-44	162.3	13.1	2	1	I5AT87_EUBCE	Trk-type K+ transport system, membrane component	EubceDRAFT1_1193	[Eubacterium] cellulosolvens 6	484	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium cellulosolvens, [Eubacterium] cellulosolvens 6	633697	>tr|I5AT87|I5AT87_EUBCE Trk-type K+ transport system, membrane component OS=[Eubacterium] cellulosolvens 6 GN=EubceDRAFT1_1193 PE=4 SV=1MNYRVIGWVLAWVLKVEGSLMLVPCFIALIYRDRQGLIYLALALLAIVAGNILARRKPANMEIYQKEGYVSVGLSWILISLYGAIPF VLTGEIPNFVDAVFEVASGVTTTGSSILTDVEALCHTSLFWRSFTHWSGGMGVLVFLLMLIPAGGGSHMNLMKAESPGYEVSKFVPR VRNNAITLYKIYLALTVATFAALLLTGMYWFDSICIAFGAAGTGGFGILNSSCAAYTATQQWIITFAMIAFGVNFTFYYLCLIHHSRDAFR MEEVRAYLLIILGAGLLITWNIHQALPQQFTSWGEALRHAFFQVGTIITTTGFSTVDFDVWPAFSKMILFLLMICGACAGSTGGGVKVS RILIILKSTRQELYSIVHPRSVRKIRMDDNSISDRTLRSLYIYMMTYFMIFGISVLLITMDGFDFETNVSAIAATLNNIGPGFSKVGPACNYS MFSNFSKIVMIFDMWIGRLEILPILILLYPRTWKRRG
2E-46	168	12.2	2.4E-45	164.4	8.5	2	1	E1QE32_DESB2	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Deba_0445	Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	454	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfarculales, Desulfarculaceae, Desulfarculus, Desulfarculus baarsii (Desulfovibrio baarsii), Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	644282	>tr|E1QE32|E1QE32_DESB2 H(+)-transporting two-sector ATPase OS=Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14) GN=Deba_0445 PE=4 SV=1MPASQATTWSSPFRLLVGSFAGLILLGAALLGLPWCQAAEAVGWLDCLFTSASAVCVTGLITVDTATAWSPWGQALIAVLIQLG GLGIMTFSVGLLYLTGRRPGMASRMALRGALGAAPPRELGLLLRDVIGYTLLIESIGAALLFARFVFDHPPHLALGLAVFHAVSAFCNA GFSMFGDSLVGYAKDPLINLTVMGLIFLGGIGFIILRELRLRLLDHTRRHPRLNLSARMALVTSLWLIVGGATAIGLFELLAEGGPDFFGH LWEILFTSVTARTAGFNTIDLNLLCNSSLFVVMMLMFVGASPGSCGGGVKTTTLAVLWAMARSRLGGRPTTEAGGRTVPEAQVGVA LALVLLALSVLSVATVTLMSVGLAEPFLGHQRGDFLVLAFEAVSAFATVGLSMGATPLLTPAGKWVIIILMFIGRLGPLTLVYALAQRGR AIGYSLAEEQVSLG
2.1E-46	168	27.9	2.2E-45	164.5	19.3	2	1	Q8DSR2_STRMU	Putative potassium uptake protein TrkH	trkH SMU_1709	Streptococcus mutans serotype c (strain ATCC 700610 / UA159)	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus mutans, Streptococcus mutans serotype c (strain ATCC 700610 / UA159)	210007	>tr|Q8DSR2|Q8DSR2_STRMU Putative potassium uptake protein TrkH OS=Streptococcus mutans serotype c (strain ATCC 700610 / UA159) GN=trkH PE=4 SV=1MNKSMVRFLLSKLLLIEAALLLVPLIVAFIYQESFTIIFSILATMAILILLGSIGIIFKPKNYHIYTKEGLLIVALCWVLWSFFGALPFIFTG QIPNIIDAFFEVSSGFTTTGATILPDVSVLSHSLLFWRSFTHLIGGMGVLVFALAIMENSKNSHLEVMRAEVPGPVFGKVVSKLKNTAQI LYIIYLIMFAVFAIILWGVGMPLYDSLVTAMGTAGTGGFTVFNDGIAHYHSSLITNLVSIGMLLFGVNFNLYYLLLIRKFKTFFGDEELRTYI GIALLATLLIWLNVGGQFATAKEGLEISFFQVSTTMTTTGFGITNLTTWPLFSQFILLLLMFLGGSAGSTAGGFKVMRVLILSKIAKNQVL SSLYPNRVISLHINQQSLDKRTQHSVLKYLAIYLLIFISLVLILTLDNNNLMIVTSAAASAFNNIGPILGTDKTFAIFSPFSKLVLSFAMIAGRL EIYPMLLLFIPKTWSKT
2.2E-46	168	34.1	3.1E-46	167.3	23.6	1.1	1	R5Y300_9FIRM	Potassium uptake protein KtrB	BN537_00883	Firmicutes bacterium CAG:212	463	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:212	1263009	>tr|R5Y300|R5Y300_9FIRM Potassium uptake protein KtrB OS=Firmicutes bacterium CAG:212 GN=BN537_00883 PE=4 SV=1MRKKTIKERLQEGSFNTVRVIGLGFLVILIGAVLLWMPFSVTTSMKFTDALFTSVTAVCVTGLVTVTPAVQFTVVGKVILLFLIQI GGLGIIACVVAFMILAGQRISLRRRVMIQESYGLDTLSGMVQYIIRIIKGTFFVEGIGALAYSFYFVPKYGVLKGIAYAIFHAVSAFCNAGI DILGSSSYMHMVTSPIINFTTIFLVVSGGLGFVVWYDILNNIKQVRSIKDVRRNFFHRLSLQSKIVLTMTAGLLLFGMFAFLLLEYHNPVT MGKLTFWQKVQASLFQSVSTRTAGFATVSQSGLTAASKAIGCMLMMIGGSSGGTAGGVKTTTVALLLLTCLSVVRGSRDIECYGRKI PLSQVKSAVTILFLTIMFWMSGTIIITIIDPQVNFLRIVYETTSAIATVGLSADLTPSLSRASQYVLMVIMYIGRIGPVTMAMIFAGKGKNEE QYRELPEKQIMIG
2.3E-46	168	20.7	6.1E-46	166.3	14.3	1.6	1	B8IYE2_DESDA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Ddes_0629	Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	457	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio desulfuricans, Desulfovibrio desulfuricans subsp. desulfuricans, Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	525146	>tr|B8IYE2|B8IYE2_DESDA H(+)-transporting two-sector ATPase OS=Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949) GN=Ddes_0629 PE=4 SV=1MGGMQRNRFFSPLTWPVFSFLVVIAVGAVLLHMPASLQEGQSLSPIDAAFIATSAVCVTGLTPVDISAVLSPAGVMVLLFLVQLG GLGVMTYTSIIFLLWRNHVPFTSREAVSQALLGDDFNLKGFLLQVLALVFSIELVTGLLLYWHDPVFFHPISAAFHAVSAFCNAGFSLSP NSLMNFRDDVTVNCIITASVFLGSIGFGVLREALGIISGGRMGIPVRRFSRFSRLVLKTTVFLIVVGAALGFVIEFWRVGNEQALGDGFD LALTAFFQAAVARTAGFNTVNMSSLSEATLLVLMALMFVGGGPGSCAGGIKVVTFRVLVGYIAAQFRGDRQIVLEGRGVPAENVSRAL TLFFFYSMLVGFSTFLLSITEYGILHGTGVEGPSFLRILFEEVSALGTVGLSMNLTPELSAEGKGVIIVNMFAGRVGLLSLLMAVQSLQP RKAYTVAETQLPIG

2.6E-46	168	23	3.4E-46	167.2	16	1	1	F6EG07_AMYSD	Putative cation transporter	AS9A_0249	Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1)	458	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Amycolicicoccus, Amycolicicoccus subflavus, Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1)	443218	>tr|F6EG07|F6EG07_AMYSD Putative cation transporter OS=Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1) GN=AS9A_0249 PE=4 SV=1MSRAAGAFVKYPARVIVAGYLAVILFGTFLLSLPIATAGSGRATFVEALFTATSAACITGLVVVDTGSFWSPFGHWVIVGLFQLG GLGIMTVASLLGLLVARRMGMRMQLIAHTEQKNLRLGEISRVVAGVIRMSLLIEFITAIFLVTRYYIAYADSFGEAAYWGIFHAISAFNSA GFALQSDSMMQYVGDPLILFPVIIAFTLGAIGFPVIFEVSRHFRQQVREARGAEHTARHWTIHTKVTVLTHGVLGVIGIASVIMFEWANP STMGPLSTLQKLMAGAVQGLTPRSSGFNAIETGEMNAATILITDVLMFIGGGSAGTAGGIKVTTFALLGFVILAELRGQPTVHVMGRKL ADSVQRQALTVALLSIAAVMGGTIIISTFSEHALDHVLFEVISAFCTVGLSMGITEDLRPLAQLILVVLMFAGRIGPIILASALALQERPRRY ELPEERPIVG
2.7E-46	168	29.2	7.5E-24	93.5	6	2.3	2	Q2GFA5_EHRCR	Trk system potassium uptake protein	ECH_1093	Ehrlichia chaffeensis (strain ATCC CRL-10679 / Arkansas)	486	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Anaplasmataceae, Ehrlichia, canis group, Ehrlichia chaffeensis, Ehrlichia chaffeensis (strain ATCC CRL-10679 / Arkansas)	205920	>tr|Q2GFA5|Q2GFA5_EHRCR Trk system potassium uptake protein OS=Ehrlichia chaffeensis (strain ATCC CRL-10679 / Arkansas) GN=ECH_1093 PE=3 SV=1MYKSLRSIIFIIGVFCLIFSLLMFIPVAVDYCTGYIWQNFFCACLFTLFFSLICISIGRLSNLKKTEVFIVTTVVWIVLSVIAAVPFVFED KIAYIDAFFESVSGLTTTGATILTNLQNQSPGILIWRSLLNAIGGLGIIVSGIFLLPCLKVVSLHELYRSESSDQSRKFKYGIVRSSMYIFAIY CLLIILCSMLYWIAGMSWFDAICHAMSTVSTGGFSNYDDSLQHFNNVYIEVIAIIFMLLSSCPLILYVKVITKQCFYDEQVIFFGIILFLFIIIS AINCYFDEITAGYSLPNVLRYSAFSVVSLSTSTGFINYDYSNWHFFSVFGVFIMLIGGCSGSTNSGIKVYRIMLLLKAFNAYISDLLHHSR TSTIRYNRRYVSKNFIGDIGLFFFLYVFVLFIGCILISSSGVNFITAFSTVAAAFSNTGPGMGDIVGPSANYYHMLPLVKVFLSCLMLMGR LEIIPFFACAYLIVNGLFDSKSKC
2.8E-46	167	17.9	4.5E-45	163.5	12.4	1.9	1	H0UKB7_9BACT	Trk-type K+ transport system, membrane component	JonanDRAFT_0746	Jonquetella anthropi DSM 22815	440	cellular organisms, Bacteria, Synergistetes, Synergistia, Synergistales, Synergistaceae, Jonquetella, Jonquetella anthropi, Jonquetella anthropi DSM 22815	885272	>tr|H0UKB7|H0UKB7_9BACT Trk-type K+ transport system, membrane component OS=Jonquetella anthropi DSM 22815 GN=JonanDRAFT_0746 PE=4 SV=1MKAYSSRPIERTIIGGFLLVILTGALLLFFFGASAGRPISPVDALFTATSAVCVTGLTVVGTDQLPLASQITILILIQLGGLGVMTAVT ASFLLTGRRVGHYQRLLFTSSIGLDSQAGAVRLVRWIIASVFIIEGIGACCLWILFCGELPPGHALWNAVFHSVSAFCNAGFSLFPDNL ASWHGSGVVPVVIACLIVIGGMGFIVLLDVALRLLRRRKTLSAHSRMVLWTTAVLLAGGSLLLWASSWSSGASWSANLKRLPEAMFM SVSARTAGFNIAPMTNVTSVGAFILCLLMLVGASPGSTGGGLKTTTVAVLAMTAIRETQGVRQVTVGRGGIPQSTINLSITLAVLYLSSI GTGIIVLGLVEPLPLKNIVFDAFSALGTVGLSLGDVGRYSPAGKLVLTLLMFWGRVGLLTFAYGLFRKSVSETGVTYPDASIPIG
2.9E-46	167	24.5	3.7E-46	167.1	17	1.1	1	A0A0A1D4S7_9MICC	Potassium uptake protein	ART_3082	Arthrobacter sp. PAMC25486	498	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. PAMC25486	1494608	>tr|A0A0A1D4S7|A0A0A1D4S7_9MICC Potassium uptake protein OS=Arthrobacter sp. PAMC25486 GN=ART_3082 PE=4 SV=1MTSITGYRSPATFAVSVATPTVHGRKGSTALSANSTLSQRLPQWPLRVVVRIRDFVDKVANSSPARLALIVFALVILAFTLTLCLP AASRDGQATAFHDALFTAVSAVCVTGLTTVSTALHWSFFGQLVILIGIFVGGLGILTLASLMSLMVSKRLGVRGKLIAQEAMNAGRLGE VGTLLRIVISTSVAIEVLLALALAPRFLILGESLPQAIWHATFYSISSFNNAGFTPHSDGVVPYEADLWILTPLMIGGFIGSLGFPVLMVLL AVGFRFKKWTLHAKLTIQVSLMLLVAGTILWGAMEWTNPDTIGGMSVGDKLTHSVFASIMTRSLGFNLVDMNAMNSSTMLLTDALMF VGGGSASTAGGIKVTTLAVMFLAIVAEARGDNDVKIYGRTIPQGTMRVAISVIMMGATFVMIACGLLLAISGESLDRVLFETISAFATVGL STGLSGELPPSGKYVLSAMMFFGRVGSITLAAALALRQRRQLFHYPEERPIIG
2.9E-46	167	35.4	5.3E-46	166.5	24.5	1.3	1	Q4L3A1_STAHJ	Staphylococcus haemolyticus JCSC1435 DNA, complete genome	SH2567	Staphylococcus haemolyticus (strain JCSC1435)	435	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus haemolyticus, Staphylococcus haemolyticus (strain JCSC1435)	279808	>tr|Q4L3A1|Q4L3A1_STAHJ Staphylococcus haemolyticus JCSC1435 DNA, complete genome OS=Staphylococcus haemolyticus (strain JCSC1435) GN=SH2567 PE=4 SV=1MSKANKSLYFYLMLFFSTTLVGAILLYLPYTGKKPITFIDALFIASSAFTVTGLSPVDIGAQFNLLGEVVILLLIQIGGLGIVTVTMLIF VFLNKKVSLQNRFLIMVTWNIDEAGGVVKLIKHLAIYSFITELIGAFCLSLSFIPKFGIGQGLFISLFTAVSAFNNAGFALFKNNLIDFSNDP VVIITVPFLIVLGGLGHFVLVDLINCKKLNKLSFHSKVVLSTTFILIIFGAILFFLLEQSNTLNNMGLIEKIGNALFQSVTTRTAGFNSIDMGNI KTPTALLLMALMFIGGAPLSAAGGIKVTTFAIVFIFVLNAICKENTVSLFNREISDKYIKLSIVTITISIIFIFVITFLLTIINPSIPLVKILFEVISAF GTVGLTMDLTSEYNGLTELIIVIVMLFGKVGLLTMARAFIPPRSPRKYHYSKGHIHI
3.2E-46	167	4	7.6E-37	136.3	0	3.2	3	K1XQC1_MARBU	Cation transporter	MBM_06985	Marssonina brunnea f. sp. multigermtubi (strain MB_m1) (Marssonina leaf spot fungus)	545	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Dermateaceae, Marssonina, Marssonina brunnea, Marssonina brunnea f. sp. 'multigermtubi', Marssonina brunnea f. sp. multigermtubi (strain MB_m1) (Marssonina leaf spot fungus)	1072389	>tr|K1XQC1|K1XQC1_MARBU Cation transporter OS=Marssonina brunnea f. sp. multigermtubi (strain MB_m1) GN=MBM_06985 PE=4 SV=1MTMLLYVCSIPHGSVSFVNCLYLAVTALTCTGMAPINLSTLNTAQQVLLGISFFIGSAPTVSLAVLEIRMRAFHTAFAARSKKKGS QEQGGTAGPESRPLVAGQVGGESFPGNDSEPMNHPTPEDTEKPLQSSSWRRAQQFLSKRTVGRNCAFHDLTREEQKSLFTVEIFG AISVAAYLAVYRADTCRENGANPISRDGRSTGIFISVAAFNNAGMSLLDQSMLADLPPNDHIAYGSLSLLPKTLHNTLRRHTKHAQIYSQ LPPPCIYPYVSNEGNMLVAFEIFTQHDAEVMAVPRIDRIIDGVFQAFSVRCSGFTIVSIGALNSGLQSLYVGMMYVSAYPITIVMRNSNV YEERSLGIFSDNTPPVRGDSSGEEGDAPHTSSNSREDRLFFVKQQPPSQTTPIAAMATLNSSSPTVEALLGYDLWALVVAMTLIAFLE NQKYEHDPLGYSLFNIIFEVFSAYATIGLSIGTPGQYYALSGSWTTVSKVIVIGLMLRGRHRSLPVDIDRAVQLPGEDDDGRHEEDGEE EQQRVREREGDREQVEK
3.3E-46	167	32.1	7.2E-46	166.1	22.2	1.5	1	F8I0P2_WEIKK	TrkH family potassium uptake protein	WKK_03535	Weissella koreensis (strain KACC 15510)	447	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Leuconostocaceae, Weissella, Weissella koreensis, Weissella koreensis (strain KACC 15510)	1045854	>tr|F8I0P2|F8I0P2_WEIKK TrkH family potassium uptake protein OS=Weissella koreensis (strain KACC 15510) GN=WKK_03535 PE=4 SV=1MKKIAKKMTPPQILTLGFLLIIFMGSLLLTLPWMHHSHTHVPLIDAIFTAVSATTITGLNTLPTATTWTLPGQIIILMMIEVGALGFMT FAVLLITLTGRRLDLRSRMLAQQALNLKSFSDVHSILEYVLRLSTIIQALGAVLLAFDFIPRFGWMKGIYYSIAHSISAFANAGFVFFDAPF GQFKSDSYVLIVTMLLILAGSLGFLVWRDIISKRKRHNFSLHTRLTLTVSAWLIGIGFVGFLISDTLTGTFNQANGWFNQIIDTLFVAITPR TAGFEIVPMNTISNAGFMTFVFLMFIVGTPGSTSGGIKTTTAGILIAQVWASLRGQESVRFRDRQFSKKTVNKALMLAIVAIIFIFLASFFL SITETLPKGRGTEYYVFEVVSAFSTAGLTLGLTPNLSSVGKVIIMTVMFIGRVGLYTVMFSVLNVHAQDIHIEYPEEEVLIG
3.3E-46	167	37.4	1.2E-45	165.4	25.9	1.7	1	A0A0D6DXN2_9LACT	Trk system potassium uptake protein B KtrB	ktrB1_LACPI_1323	Lactococcus piscium MKFS47	446	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Lactococcus (lactic streptococci), Lactococcus piscium, Lactococcus piscium MKFS47	297352	>tr|A0A0D6DXN2|A0A0D6DXN2_9LACT Trk system potassium uptake protein B KtrB OS=Lactococcus piscium MKFS47 GN=ktrB1 PE=4 SV=1MFVPRFVKNMKPPQLIIFVFLTVILIGSIFLALPISDQNGQATSYLDSLFMAVSATCVTGLAVVNTADHWNTFGQVVILIMVEVGGL GFMSFLVLLLNMTGQHPSFKSKMMIRDAYSFTSINGGVNLVKSVIKLSLMTQMIGALLLSVDFIPRFGWAKGIWFSVFHAISAHSNAGF DLFETSLFQFKDNPYVLFVMSLLILSGSFGFIVWFDLINFRSIKKITLHSRLALTMTTVLVVAGTLLYSLLNLKSFDGHILSYMAQNFFLSIT PRSGGFTFSNYNATSYASLVLTMILMFIGGTSGSTAGGVKTTTFGILILNIKAIFTNRNSTIYHERRIPRRIISRVYEIVFIYIGIIFTSAFILLIT EHLPKNNGIKYVFFEVISALATVGLSLGLTPELTAIGKVTIMILMFIGRIGIMTVIYAVGSHAKIDEELIQYPDEEIVVG

3.6E-46	167	32	9.8E-46	165.7	22.2	1.6	1	Q5HQT9_STAEQ	Sodium transport family protein	SERP0458	Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	435	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus epidermidis, Staphylococcus epidermidis (strain ATCC 35984 / RP62A)	176279	>tr|Q5HQT9|Q5HQT9_STAEQ Sodium transport family protein OS=Staphylococcus epidermidis (strain ATCC 35984 / RP62A) GN=SERP0458 PE=4 SV=1MSKVNKPLYFYLMLFLLTTLIGAFLLYLPYTGKKPINFIDALFVASSAFTVTGLSPVDVGTQFNIFGEIIILLLIQIGGLGIVTVAMLTLIFLNKKISINNRILFMITWNIDEPGGVIKLIKHLAIYSIATELFGTLCLCLSFIPKFGIGKGLFLSLFTSVSAFNNAGFALFKNNLIDFSNDPVIIITIPILIILGGLGHLVVVDLWNAKSFRKLSLHSKLVLTTTGLLILIGTVFFFLLENQNSMLHMGLIEKIGNAFFQSVTTRTAGFNTIDVGNIKTPTALLLMALMFIGGAPLSAAGGIKVTTFVIATIAIFNTIRKEKNNSIFNREISERYIQLSFVTILISIAFIGMVTFILTIINSNIPLIKILFEVVSAFGTVGLTMDLTSEYYNWTEFIIIIVMLCGKIGLLNISRALVPPKDPKNYRYTKGHIHL
3.7E-46	167	26	4.3E-22	87.7	4.7	2.1	2	D3E0F0_METRM	Potassium uptake protein TrkH family	mru_2024	Methanobrevibacter ruminantium (strain ATCC 35063 / DSM 1093 / JCM 13430 / OCM 146 / M1) (Methanobacterium ruminantium)	496	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobrevibacter, Methanobrevibacter ruminantium, Methanobrevibacter ruminantium (strain ATCC 35063 / DSM 1093 / JCM 13430 / OCM 146 / M1) (Methanobacterium ruminantium)	634498	>tr|D3E0F0|D3E0F0_METRM Potassium uptake protein TrkH family OS=Methanobrevibacter ruminantium (strain ATCC 35063 / DSM 1093 / JCM 13430 / OCM 146 / M1) GN=mru_2024 PE=4 SV=1MKRKYITKADLFIVLHYLGYIMQGLGVVLIVPTLVALIYGEYDPIAPFMIPCFVSFVLGTAFSKKFKDYTKLRLKHGMLISSFAWLWASLIGASIMVLSLGIPFVDAIFENMSAWTGSGMTFFVNVEVLPKSILFLRSLEQWLGGLGIVIIFIGILIRAGTAASRLYKSEAREEKIKPNITNTLRKALEIYLIYTAVGIFLFILAGLPIFDAINITFTSISTGGMSIKNANVGFYQDSTTWYSIYLISMFLMILGATSFTIHYKIVKTKGKALFKDVQFQLLITLIIVAGAFFIATNKMVPIEELFTIVSAVTTTGANVVDPHVLATWNGSTLIVLMVLMLIGGSSGSTGGGLKLIRIITVLKGMNLTVTNLVSPEGRVVNTRIGGKKINEREIKEASAYIVTFLMFLVFGWIIMTMYGYDPFTALFDVISIQSNNGLSTGIVYGGLPLPLKLTLIFLMWIGRLEIIPVLVLFRTFYGLVNPKRRIKQMKKTNGNDKKTN
3.8E-46	167	19.9	1.4E-45	165.1	13.8	1.7	1	B8IPL6_METNO	Cation transporter (EC 3.6.3.14)	Mnod_7572	Methylobacterium nodulans (strain ORS2060 / LMG 21967)	444	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium nodulans, Methylobacterium nodulans (strain ORS2060 / LMG 21967)	460265	>tr|B8IPL6|B8IPL6_METNO Cation transporter OS=Methylobacterium nodulans (strain ORS2060 / LMG 21967) GN=Mnod_7572 PE=4 SV=1MRKTRLSHPGRIIPLAFLLVIALGTVVLMLPAARAAPGHAPFIVALFTATSAVCVTGLAATDTATYWSAFGQATILILAQIGGLGIMTGATLLGLLVSRRLGLATRLIAQAETRSLRLGDVTTVLRLILTVTLVMEATTMAALTLRFRYAYDQTWGEALWHGLCHAVFAFNHAGFSTYSDNLMRFARDPFVLTPIMLTVMIGSLGFPVIHELAYGARRPSRWSVHGKMTLFGSALLLLVGFVAVAAYEWDNTATIGALAWPEKLFNAAFHSVMTRSAGFNAVDVGKMKLTTLMVSDALMLIGGGSAGTAGGIKITTFLILGFVVWAEIRGEEDTTAFRRRISQQAQRQALSVVLLAVGIIAIGVLIMLSLTDFAFETVLFEVVSAFATTGLSTGITPQLPAPALAVLTCLMFLGRVGTITVASVLALKERRSAFRYPEERPIVG
4.1E-46	167	25.7	1.5E-45	165.1	17.8	1.7	1	D2YTG3_VIBMI	Trk system potassium uptake protein	VMD_30470	Vibrio mimicus VM573	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio mimicus, Vibrio mimicus VM573	671076	>tr|D2YTG3|D2YTG3_VIBMI Trk system potassium uptake protein OS=Vibrio mimicus VM573 GN=VMD_30470 PE=3 SV=1MLNLRPITFIIGLVLSKLALFMYVPTLVAFFTGSGGFLDFAQAVIITHLVAFICLSIGRTESFRLNVRDMFLITSLVWTISSAFAALPFVFINHISFTDAYFETMSGLTTTGSTVLSGLDDMPPSILLWRSILQWLGGVGFIVMAVAVLPMLNVGGMKLFQTESSDWSDKSSPRAKTVAKNIVAVYLVLTGLCFLSYIATGMTPFEAINHAFTTLSTGGYSTSDSSMNRFSHGAHWVATLFMFLGGLPFLLFVQALRKQSPRALLKDEQVRGFFWLFMISSLIVATWLWLRDDYEIMDALRVSMFNIVSVVTTTGFGLDDFTSWGALPSTIFAFLLMAGACSGSTSGGIKVFRFFQIAMALLKKQLLNLVHPSGIFIQRYNQRPVNEEIIRSVVAFGLTFFITIVVLAGALSAMGLDSITSISGAVTAVANVGPGMGSVIGPTGNFAALPDAAKWLLSLGMLMGRLEILTILVLFFPAFWRH
4.3E-46	167	28.9	1.6E-44	161.7	20	2.1	1	R6FKK6_9FIRM	Uncharacterized protein	BN497_01960	Firmicutes bacterium CAG:145	491	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:145	1263005	>tr|R6FKK6|R6FKK6_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:145 GN=BN497_01960 PE=4 SV=1MGLNFRAIIKVLGILTLIEGLFMLPAVVAGLYYEEWKAAGSLFTISLICISVGFVILTQFRFDKIALRSREGFFIAFVSWIYCSLLGALPLYLSGQNFSFMSCLFESVAGFSTTGCSVLDVSSVPLCMLMWRALCHWLGGMGILVLLISIFPLWGINNQSLAMAETPSSESSKMEAKSSDMGKFLYSSYLLLSTLEFILLIAGPMDWYNALLTTCSSISTAGLIITPDAAWMYDTLYVKIVVMIFSILSSLNYAVYFLASRRKWREIFKNNEIKAFFKIMGIATVLIALSLRFSGTYDNIWHAVKDGLFQVVSFISTSGYFVCDYTTWPAFTTTILMIILFIGGCSFSTSGSLKVMRVTVLFKLIRRGFMQQIHPHMVKAVMLDDNTPVSAKAASSIVSHTLLFFVIFFLGCVLLSFNNLDMETTVTTSIGLFSNTGMALGLPGCSGYFGMFDDFSKLVMCFLMIAGRLEMYSLVIVFAKSFWKPDKAVII
4.3E-46	167	27.1	2E-22	88.7	6.9	2.2	2	D3DZA4_METRM	Potassium uptake protein TrkH family	mru_0207	Methanobrevibacter ruminantium (strain ATCC 35063 / DSM 1093 / JCM 13430 / OCM 146 / M1) (Methanobacterium ruminantium)	492	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobrevibacter, Methanobrevibacter ruminantium, Methanobrevibacter ruminantium (strain ATCC 35063 / DSM 1093 / JCM 13430 / OCM 146 / M1) (Methanobacterium ruminantium)	634498	>tr|D3DZA4|D3DZA4_METRM Potassium uptake protein TrkH family OS=Methanobrevibacter ruminantium (strain ATCC 35063 / DSM 1093 / JCM 13430 / OCM 146 / M1) GN=mru_0207 PE=4 SV=1MRIKYLSKQDIKIILHYLGYIMIGIGAILLFPLPIDLFYREFNYVYGVIPPLISIILGVIFSQGFREYDKLKFKHGMIISSISWLWAGLVGAIIMMLILDVSFVDAFFENISAWTGSGLTMFSDVESLPMSILFLRSVEQWIGGLGVVIIFISLLIKPGTSAFKLYKSEAREDRIKPNIKNTLKKTMQIYAIYTVIGVILYLIAGLPLFDSINLTFTTISAGGMSIKNANIGFYQNDIVYIITIFLMILGATSFTVHYKMAKTKGKAILKDIQFQLLIVSIILSAIAIAIITKLAPMDVVFHVVSAITTTGANIAPPSEMAAWAPPALIIIIVLMLMGGSSGSTVGAIKLVRVITLLKSTHLAVTNIVSPGRFVKIKIISGKSINEGEMKEASSYMAVYIFFLAISWIIMTYYTNDPFNTLFDVVSTLGNVGLSTGIISGELGTIPKVVLIFLMWLGRLEIIPILLTIQIGFETFNQSLRFVKRRMMRKIKPN
4.4E-46	167	40.8	9.3E-46	165.7	28.3	1.4	1	A0A0G0I6F3_9BACT	Potassium uptake protein, TrkH family	US32_C0004G0028	candidate division TM6 bacterium GW2011_GWA2_36_9	441	cellular organisms, Bacteria, unclassified Bacteria, candidate division TM6, unclassified candidate division TM6, candidate division TM6 bacterium GW2011_GWA2_36_9	1619072	>tr|A0A0G0I6F3|A0A0G0I6F3_9BACT Potassium uptake protein, TrkH family OS=candidate division TM6 bacterium GW2011_GWA2_36_9 GN=US32_C0004G0028 PE=4 SV=1MAKRLIHRYPGRIILATLLLTILIGTLLLKLPFCQAIPMGWFDLFFTATSATTVTGLLTVPVTNFTPFGHLVILILIQIGGLGLITMTLFFLSLFIDIGLTTKLMATEILEVESIKDIRHIVKFIVTTTLVCELTGAIITYLTIHNQYHFKEALFKSIFHAVSSFCNAGITLFPNGMADFVYNPIMLITTSLLAFLGGLGFLVIYEIIRYFFYRKYPRKLNLHSRVVLWTSFFIAIISFILFWILEHNNTLSTMSLPYQWLNAFFNSMCMRSTGYLSVNFNNLQLATIFLIMCVSFIGSSPGSTGSGIRTTTFAIFLATARAIITGRTFVHIQNRKIKTIQVFRATTIISIALAWIALVTFLLLITEKNFSFLAIFFETVASFTDLGITSGITPLLTTIGKMFIMTTMIIGRIGSLTMILAFAKSPDEKDFSYPEERVMLS
4.5E-46	167	13.9	3.6E-23	91.2	4.2	2.1	2	A0A0E3NV30_9EURY	Potassium uptake protein TrkH	MSMTP_1063	Methanosarcina sp. MTP4	480	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina sp. MTP4	1434100	>tr|A0A0E3NV30|A0A0E3NV30_9EURY Potassium uptake protein TrkH OS=Methanosarcina sp. MTP4 GN=MSMTP_1063 PE=4 SV=1MYELVSPVNPVAVLRYTGHLLLVFAGVLLVPMFAALVLGETDAVSIYGVTVLISAVIGIGLYKALPDYELEVKEAVILAAITFPLCSFVSAVPMALSAGMPFLDAYFECVSGLTTTGLSLAPASPTRLFFFTRSWLQWVGGIGIIVLVGLVLIRPGTTAFRLYRVNFGESRIRPSVVATARALGAVYLGLTLLSLLLLLFSGMPFYDALCHTLSAISTGGFSTRPESIGAYGGILIPFLITISCFMGAISFSLYPEILRDRKTLTRDSQVRYMFWLALLGTPVFAFALSGGSVGLELLRMLPDAAFQTASALTGTGFSTIDLAPVSDASKGFLSTFMCIGGSIGSTTGGIKLFRLIVIVQLVRLVFYRFFLPREAVTPLKVGAQVVDSEEIYRIMTYVLLYSGVLVFSAFIFMLYGIDSGDAIFETSSALATAGLSVGVTNPAMPGLLKLVLCADMLLGRVEVIPLCILLLPRTWLESRR
4.6E-46	167	18.8	8.4E-45	162.6	13	2	1	A0A099T7F0_9RHOB	Trk system potassium uptake protein	PM04_10710	Thalassobacter sp. 16PALIMAR09	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Thalassobacter, Thalassobacter sp. 16PALIMAR09	1225651	>tr|A0A099T7F0|A0A099T7F0_9RHOB Trk system potassium uptake protein OS=Thalassobacter sp. 16PALIMAR09 GN=PM04_10710 PE=3 SV=1MVDVRPVGYVIGQLLAVFGLAMLAPMMLDLWEENGHWIVFLESATVTFLIGVGMALACANAQRARLSLQQTFLLTTGVWFVLPIFAALPFWMGATEARIVDAFFEAMSGLTTTGSTVFTGLEALPRGLLLWRGMLQWFGGIGVIVVAMVFLPELKIGGMQIFRSEGFDTFGKILPRATQIAGSISVIYLGITAACALAYAAAGMEPFDAIVHAMTTVATGGFANTDASFSAFGPLVQYVAVVFMALAALPFVRFVQLAAGTAQPLLQDSQVRLFFGIAGVLVAVMVGVRLLDQGQLSEAAFRAALFNSVSILTGTGYASADYMQWGSLAVVILFFAGLIGGCAGSTACSIKVFRYQLLFKAIVMQIRQIHSPHGIFAIRYDGRRVGPDVLSSVMAFFVVFVVSIGVLSVLLGMTGLDFTTSLSGAATALANVGPGLGDTIGPAGSFASINDTAKWLLAAGMLVGRLELMVVYALFTLQFWRR

4.7E-46	167	20.4	9.9E-46	165.6	14.1	1.4	1	A0K1F9_ARTS2	Cation transporter	Arth_3754	Arthrobacter sp. (strain FB24)	464	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. (strain FB24)	290399	>tr|A0K1F9|A0K1F9_ARTS2 Cation transporter OS=Arthrobacter sp. (strain FB24) GN=Arth_3754 PE=4 SV=1MAAQLSGSAKAGTDIRPGDSRIRRLLLHPVRSVPVAFLAVIMLGAGLLLLPASHYPTDSDTAMPALFTSVSAVCVTGLITVDTATF WTPFGQAVILGLIQVGGFGIMTLATLLALLVRKNLGLRGQLVAQSETHTLNFGDVRSVLVRVAKIMAAIEGSTAAVLTLRFWFAYDANP ATALWHGIFHAVSAFNNAGFSLYSDNLVGLAEDPWIIIPICAAVVAGGLGFPVIIALMGGGFRFKEWTVHVRLTVYGTLMLLAAGFVLF AAFEWNRPETLGSLSTGGKFLGALAGSVFPRTAGFNSIDYGAATPETLMVTNILMFIGGGSAGTAGGIKITTFLILGFAIWNEVRGREQ VTIAHRSISSSAQRQALSVALLGVAAVIAGTLLLLMFTDYSLEKVLFESISAFATVGVSTGITYHLPASAEWVLMALMFIGRIGTITVASAL ALSAHPRLYHLPEERPIIG
4.8E-46	167	23.6	2.5E-44	161	16.3	2.3	1	E4RL14_HALHG	Cation transporter	Halsa_1351	Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	496	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	656519	>tr|E4RL14|E4RL14_HALHG Cation transporter OS=Halanaerobium hydrogeniformans GN=Halsa_1351 PE=4 SV=1MIKSTKYNTIFYYLSSLSFILAIMIVIPLVVSFYYQDGRQIYQAFYYSIISFAAGILLKLPTDKEKTYIDLTTAMLLCALGWILVSILGSL PFMIGIEKSFIDALFETVSGFTTTGITVFTGLELMPRSILFWRSLIQLLGGLGILTFFLLVSTRAKGETWQLFSAESHKINVSRPVPNVFKT VKILWSIYLGFMLLQTLLLIILGLSPFDALTHSFTTLSTGGFSSYDASVAHFAANNYSNYILIEYVITFFMFLGGVNFLLHYRLFQKDFESIK NNSEFRTMVKIIIYSTIFLSLVIITLETAPGISVEEVFRRTIFQVTSILTTTGYATKDINSAFFPAAARQLFLAFMLIGGCVGSTSGGIKIMRL NILRALFKREVKKIYLPNHAVLPVTVDRKIIRKDELNKLTGIFTFWLVLIVVGGIITSLFSHLDGWQAYSGMFSAMGNIGPFFFSVEEMSN ISPVVKTTYIIGMLAGRLEILPVIILFSKKAWQN
4.9E-46	167	30.6	7.8E-46	166	21.2	1.2	1	R5J4K7_9BACE	Uncharacterized protein	BN523_01066	Bacteroides sp. CAG:189	611	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:189	1262737	>tr|R5J4K7|R5J4K7_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:189 GN=BN523_01066 PE=4 SV=1MKIYHKILLYQNKLLQPYVRILLRMMAVLTYMASLLLIVGVVYEHGFPLSATDISHLKILYKAVWIIFLIDVTLHIFLEYKGTKKNFRKL AWILSWLLYLTLVPVIFHRPDEEGAILYVWDFLGSKLYHIPLLLLFSFLNLSNGLVRLLGRRTNPSLILAVSFFVIILIGTGLLLLPRCTVEG VVLSWVDALFTSTSAVCVTGLVPVDVSATFTPMGLTVIILLIQVGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLGSLLSTLL YILGFTMVIEGAGMVSIWLGIHGTLGMSLEEELAFSAFHSISAFCNAGFSTLPGNLGNPMVMTGHNSLYISVSLLIILGGIGFPILVNFKDI VLYHLRRFWKFVRTLKLDRHKKQHLYNLNTKIVLIVTLLLLVLGTLAVAAFEWNGSFAGMSVADKWTQAFFNATCPRTAGFSSVDLTS LSVQTILIYIFLMWIGGAAQSTAGGVKVNAFAVVVLNLIAVLRGTERVEVFGRELSHDSIRRSNATVVMSLGVLFLFIFVLSILEPKMSVM TLTFECVSALSTVGSSLNATPLLRDESKLLVALLMFVGRVGLITLMLGIVKQKKNTKYRYPSDDIIIN
5.2E-46	167	27.3	6.5E-46	166.2	18.9	1.1	1	A9WTC9_RENSM	Potassium uptake protein	ktrB RSal33209_2725	Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	467	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Renibacterium, Renibacterium salmoninarum, Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	288705	>tr|A9WTC9|A9WTC9_RENSM Potassium uptake protein OS=Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235) GN=ktrB PE=4 SV=1MAKGQPGWHPPTERGRFAFIGVLRDFIDSVANSSPARLALIVFALVIMFFTTLLTLPISSAKGQVTALHDALFTAVSAVCVTGLTT VSTALHWSFFGQLVILIAIFVGGLGILTLASLMALMVSKRLGVRGKLIAQEAMNASKLGEVGTLLRIVITTSVAIEVLLALVLAPRFMILGE SFWQAIWHAAFYSISAFNNAGFTPHSDGLVPYEADPWILTPLMVGVFLGSLGFPVMMVLLSKGFRISRWNLHTKLTMQVSIILVVVGM LGFAAFEWSNTIGGLSFGDKLLHSVFASIMTRSGGFNLVDMNSMEPVSRLFTDALMFAGGGSASTAGGIKVTTLAVMFLAIVAEARGD SDVKAYDRTIPQGTMRVAISVIVMGATFVLLATGALIMISGAPLDKVLFESISAFATVGLSTGLSSNLPPAGVYVLSLLMFAGRVGTITLA AALALRQRRQLFHYPEERPIIG
5.4E-46	167	31.1	3.7E-45	163.8	21.6	1.8	1	R6YWZ6_9FIRM	Potassium uptake protein TrkH family	BN600_00177	Roseburia sp. CAG:309	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:309	1262945	>tr|R6YWZ6|R6YWZ6_9FIRM Potassium uptake protein TrkH family OS=Roseburia sp. CAG:309 GN=BN600_00177 PE=4 SV=1MLGKWSRKLGPSRLIALSFVILILTGTFLLCLPVSARDGNFTSPLDALFTATSATCVTGLIVADTFTKWSLFGQIVILILIQIGGIGLM SFISMFFIFMKRKLSLHERMLLMQAAGNTQLSGMVKLVRRIVSGTFLIEGCGALLLALRFIPRMGFGQGLYYAIFHAVSAFCNAGFDLM GRYEAFSSLTGYASDVLVNITVMLLIIIGIGIFLVWDDILKYRLSFKNYSLHSKIVLVTTPVLLVGGAFGYFVFEQNYTLQGNGIGEQILKS FFASTTMRTAGFNTIDYASMSPSASLLSDVLMMIGGSPGSTAGGMKITTITLVFLSMVSMLRGQSDTVIGKRRVSTILIKQAAVIILVYAV YILAGTMLICHIEGLPMSNVLFEVISAVCTVGVTTGITPHLCAMSHIILIILMYGGRIGGFTLMLILGKQNKQPPLRRPKENILIG
5.7E-46	166	14.4	8.4E-37	136.2	5	4	3	G7WQ94_METH6	Cation transporter	Mhar_1930	Methanosaeta harundinacea (strain 6Ac)	660	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosaetaceae, Methanosaeta, Methanosaeta harundinacea, Methanosaeta harundinacea (strain 6Ac)	1110509	>tr|G7WQ94|G7WQ94_METH6 Cation transporter OS=Methanosaeta harundinacea (strain 6Ac) GN=Mhar_1930 PE=4 SV=1MRWVRIRVFLRVFGTLLKLLGGLMLLPAGVSFLYGEVEGVIAFVLPALFTFAIGLLMAILGEEEVLTNREGFALVAFGWLGAAAT GALPYILLGLSPIDALFESMSGFTTTGASILSEVGADGLWAMNATAASYGLAASIAHNAFSDLSISPTFDPAGFVGSNISALNDTVLNAT LNGSLVGVEANASSGLVGPTYRGLLFWRCFTQWLGGMGIIVLFIAILPNLGVAGRQLFKAEVPGPSEDLIRPRIRETAKILWGVYYMVIT AAEFLLLMLARMPAYDAVCTTFSTVSTGGFSPRADSIAYYGGPDYNAPFIEVIVIVFMFISGASFALHYRTMYVNRTSLIEDPEFRFYSL LVGAVILIVVLIGGVDGSFLGDSPEAEGVGLAGQRLRAAAFQTVSIVTSTGFATADYDLWSSPAKLILLFLMFTGACAGSTSGGMKLVR VLLSVRYCRRELFRTLHPKAVMAVKLKASPVREDVLHSIMVFMALYILIFAVGSVLFASVTSLPGEAATSEEIVCFVSGDGEKVVCFGP DGWNGSRELLGSDPKVSGGVACFFPAENGTRRIEVDRRPINLSEIYSKGGGLVSFGSGFSSDMDVISAASAVASALGNVGPAFHRY GPTDNYSEVPGIGKLILIVCMWIGRLELLTVLVLLVPDFWKD
5.8E-46	166	36.8	9.7E-46	165.7	25.5	1.2	1	A6L334_BACV8	K+ uptake protein	BVU_2440	Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	615	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides vulgatus, Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	435590	>tr|A6L334|A6L334_BACV8 K+ uptake protein OS=Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154) GN=BVU_2440 PE=4 SV=1MQDDIDMEPLHKLFIYRKKLVKPYIERLLKWMDGITYMMSALFILTLVYEHGFLISFEEMEMINTLYHFVWIVFLVDISLHLLLNYSD TKRKYRGLAWILSLMLYLTLIPVIFHEPEVQGGIHDFWSFFHSRLYHVVLLTLLSLLQLSNGIVRLLGRRTNPSLIFASSFLIFILIGAALLM LPRATYHGISFIDALFTATSAICVTGLVSVDVSSTFTSEGLFIIIMLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSQSLSSLLS TLLYILGFTLVIEAAGMGVIFLSIHGTMGMDIEEELAFSAFHSISAFCNAGFSTLYGNLGNELVLHNHNLLYITISFLVILGGIGFPILVNLYE TVSYESKRLYHRYVKKNKRTIRKIHLYNLNTRIVLIMTAILLVTGTVAIVVFEWNHAFAGMTATEKWVQGFFNATCPRTAGFSSVSMTT FSVQTLLLMVVLMMIGGGTQSTAGGVKVNVFAVVMLNLRAILIGADKVNIFNRELSHDSIRRSNATLILYLLIVFAGIFGLSILEPQASVMA LVFECTSALSTVGSSLDLTPTLGSDSKLIVIVLMFIGRVGVLTLISSLIKQKKITKYKYPSDNIIIN
5.8E-46	166	15.8	3.1E-45	164	11	1.8	1	D5UJJ4_CELFN	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Cfla_2746	Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134)	457	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Cellulomonadaceae, Cellulomonas, Cellulomonas flavigena, Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134)	446466	>tr|D5UJJ4|D5UJJ4_CELFN H(+)-transporting two-sector ATPase OS=Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134) GN=Cfla_2746 PE=4 SV=1MAAGPGLLWRAREYVDRSARQSPARLALGVFALVIAIITALLSAPWATAHGGRAPFVDALFTATSATTVTGLVVVPTGEYWSW WGLLVILVAIKIGGLGVMTLASLLGMAVSRRIGLTQRLLVSSETKVTRLGEVGSLVRTVIVTSTALEVAIAIVLFPRLLVHGEPVGTAAWH ATFYAISAFNNAGFVPTPRGLDPFVSDWWMLLPIIVGVFIGSLGFPVILDVAHHLRAPRRWKLHSKLTIATSVGLVVFGSVVVAAFEWT NPGTFRPLDPGGTALASLFAGVMPRSGGFSTVDVGEMHEGTWLLLDALMFVGGGSASTAGGIKVTTLAVMLLAIVAEGRGDRDVEA FGRRIPRETLQLAIAVGFISATIVLVASLLLLAMTGLTLDRILFEVISAFATCGLSTGITAELPAPAKYVLVVLMFIGRTGTMTLAAALALRN RRRVIRYPEERPIIG

5.9E-46	166	22.1	4.9E-44	160.1	15.3	2.1	1	R6DNT2_9FIRM	Trk system potassium uptake protein TrkH	BN710_00436	Ruminococcus sp. CAG:563	482	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:563	1262961	>tr|R6DNT2|R6DNT2_9FIRM Trk system potassium uptake protein TrkH OS=Ruminococcus sp. CAG:563 GN=BN710_00436 PE=4 SV=1MNKKMITYVLGILLITEGALLLLPTLIGLYYKEDVVPFLITIAATVISGFVMIRFKPHDKTIVSMDGFAIVSLGWIFISLFGALPFFISKEIPNYLDAVFEVVSGFTTTGSSILTNVEALSKGMLFWRSFTHWIGGMGALAFIMAILPLAKGGGNLQLMKAESPGPDVEKLVPKSKSTARILYGIYVIMTIVQILLLRCGGLSFFESTTLSFGTAGTGGFAIVNSSIADYSLYTQIIIGVFMMLFGINFNFYFLLFCGKLKAAFRNVEVKSYIGIMATSIILIALNIRHMFGSFFEALHQSAFQVSSVMTTTGYATTDFDKWPVFSKTVMLIVMCVGACAGSTGGGFKVSRIIILAKSAKRELKRLAHPRSVVSVITMDGKRVSDEVVTGTNVFFFSYIVIFVVSLLIVSTDGQDMVTNISGVIATLNNIGPGLGKVGPKGNFSDFSWYSKVVFILDMLLGRLEIFPFLMLFTPKLKRSKIIK
5.9E-46	166	17.1	3.9E-43	157.1	11.9	2	1	A0A0F0CFL4_9CLOT	Ktr system potassium uptake protein B	ktrB CLFS41_32950	Clostridium sp. FS41	430	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. FS41	1609975	>tr|A0A0F0CFL4|A0A0F0CFL4_9CLOT Ktr system potassium uptake protein B OS=Clostridium sp. FS41 GN=ktrB PE=4 SV=1MKSIEKQTPARIIALGFMAVILTGSFLLMLPVCVKPGVNLHYVDALFTSTSAVCVTGLIAVDTADTYTALGQAIVAFLIQVGGLGVTSVGVGVILALGRRVNLKERLLIKEAMNLDSGKGIVCIVKNVLKTTLCFEGAGAVLSYLVFSRDYPPLKALGISLFHSVAAFNNSGFDILGGLQNLTGYKDNILLNLTTSGLIIFGGLGFLVIMDIAGKRSFKKLCLHSKAVIVTTLILLAVGTVLLRLTEDITWLGAFFTSVSARTAGFTTFPLSDFTTAGLLTVTVLMFIGASPGSTGGGIKTSTLFTLFHTIKGAATNTQPHAFHYKIPQEAFYKAAIVTALSSLVVISGILCMCVLEPGLPFEDIMLEITSAFGTVGLSTGITPGLSPLSKLLEVLIMYIGRLGPLTIVTIWIFKPDTSVSFPEGSISIG
6.1E-46	166	15.8	6.6E-45	162.9	11	2	1	S5Y1S6_PARAH	Trk system potassium uptake protein	JCM7686_2607	Paracoccus aminophilus JCM 7686	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus aminophilus, Paracoccus aminophilus JCM 7686	1367847	>tr|S5Y1S6|S5Y1S6_PARAH Trk system potassium uptake protein OS=Paracoccus aminophilus JCM 7686 GN=JCM7686_2607 PE=3 SV=1MIDIRPVANTIGKLVVTLGAAMSLPMLVDYAHDDPNWKSFLESGILCAVIGSLIVFATRSNEKSLNLQQAFLLTNGLWIVLPLFGALPFFLGAPHVGFTDAFFESMSGLSTTGTTAFPSLDTLPKGTHLWRGQLQWLGGLGIIVVAMIFLPVMKVGGMQFFRSEGFDTLGKILPRAFDIARETTLVYVFITVACAVTFIMLGMNGFDAVFHALTTCSTGGFSNYDASFGAYPGAPQLAASFFTILAALPFIRMVQLVRGDAMPLFEDVQVRAFLRWLFYAIAIVILYRLVWLGAENPFHVMRETVFNVVTLTAGSGFGTGDVTQWGSFPFAILIMMGMIGGCTGSTTCSIKVFRYLVLFKAVRAQIRRMHSPHRVFPVMLEGRPLDREVVGSVMAYFTTFMLSFGLLIVALALTGLHPRTALTGAWATIANIGPIWGPEVSANGAVDQFPTASKWLMVIGMFLGRLEVLSVLVVLHPRFWRQ
6.6E-46	166	34	8.8E-45	162.5	23.6	2.1	1	F0TCK4_METLA	Cation transporter	Metbo_1034	Methanobacterium lacus (strain AL-21)	494	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium lacus (strain AL-21)	877455	>tr|F0TCK4|F0TCK4_METLA Cation transporter OS=Methanobacterium lacus (strain AL-21) GN=Metbo_1034 PE=4 SV=1MHSMSKFRRSEIYSLLHYTGYISVLLGIVMLVPIIVAFIYHEPHYVLPFIYSSITSLVFGVVLYKCFSSGSEISLKVAMLFSTLIWLIGSAIGALPFYLSGDLSYLNSYFEAMSGFTTTGFSMYSNLDTVSYTMDFWKGFMQWLGGIGIIVMALTVLSSSNVSIMRLYSAEGRDERLVPSIKHTTRIILYIYLAYTAVSILLFIVAGMPIFDSIFYAFTALSTGGFAMQNASIGYYYHSIWIEIVAMIIMMGATNFALHYTVLKGNWKEYFKDIETRVSWPLIILGTIIGTIFLFNTSVYGHDMLISLRYSIFQVVSALTTTGLQTATPSDITSQWEGLGIFILTLLMIVGAGACSTGGGIKWIRIGILIKGMWWEIKSLILPESAVISKKIHHINDVKIDTKLLKITGLFVFSYLVIYFVSVIIVLFYYPNVSQTLFEVASALSNVGLGSGLITATSPFVVKIVFIIDFWIGRLEIWPILLLVALLIQNSIRK
6.9E-46	166	31.9	1.3E-45	165.3	22.1	1.5	1	R6ZQU4_9BACE	Uncharacterized protein	BN762_00588	Bacteroides sp. CAG:714	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:714	1262749	>tr|R6ZQU4|R6ZQU4_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:714 GN=BN762_00588 PE=4 SV=1MDYWDRLFLYRQKHFLPRVHQLVTWMMGITYLCAFAFILAIVYEYGFMISPEERSGVEVIYRAVWVVMLICTTVQIIFREDGTSYKFTVWTWILDILLYLTLVPVIFHRPEHGGGVEWVWTVLHSTYYRNGILLLLSLSQLSSSLVRLLGRRTNPSLILASSFFIFILIGAGLLMLPRATYHGISWIDALFTATSATCVTGLVTVDVPSTFTLEGQIIIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVGDMISSNSLNSLLSTLLYILGFTLAIEGVGMLLIWWNIHGTLGMSLHQELYFSAFHSISAFCNAGFSTLPGGMGNPMVMQNHNLLYIILGLLIALGGIGFPILVNFYETLSYHIGYLRWKILRPSRHFAKKVHLYNLNTKIVLIMTVLLLVVGTVVIVIFEWNHAFAGMPVIDKWVHAFFNSSCPRTAGFASVGLTTLSKQTLLLMLVLMMIGGGTQSTAGGLKINVFAVILINLWAVIRGSEHTVILKRELSVDSIRRSHAALISYLVIVFIGIFAMSICEPQASVMAIAFECFSALSTVGSSLDLSPTLSNTGKFIDILLMFIGRVGTFTLIAGLVKQEKKRNYKYPSDNIIIN
7E-46	166	26.7	4.2E-22	87.7	8.5	2.1	2	B8D5N5_DESK1	Cation transporter	DKAM_1090	Desulfurococcus kamchatkensis (strain 1221n / DSM 18924)	484	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Desulfurococcus, Desulfurococcus kamchatkensis, Desulfurococcus kamchatkensis (strain 1221n / DSM 18924)	490899	>tr|B8D5N5|B8D5N5_DESK1 Cation transporter OS=Desulfurococcus kamchatkensis (strain 1221n / DSM 18924) GN=DKAM_1090 PE=4 SV=1MKMVSIATGLLSLLLIVGLMILSVPIVDLLSGEPVSMNFLFFSILYISTGFSGVIVLTRFGSVREMGFLEAYIVSTASWLVIPFLAALPLMREINISFIDALFESISGFTGTGFAVLNDIDHLKKSINWWRALMQWSGELGFVVFAMLIIPFFWKFGYTLYGLERPVRVMRTLRSTARRIIEIYMVFTLAGIVLLYYSGVDFYDAVIHTMTAIATGGMSNYSMNYEALYDYAPFSVIPAIFIMVIGGMNFLALSQLLDFRFKDVLRSDEVKYYFISLCILSLLATLVFMLHNEGLTYSILLGFFNTISAMTTTGFNIGNVAGFPNGVKIILVVAMIIGGMTFSTAGGIKVYRLIVLLRKLSSYSTSTLLRERVNLHVVIDGKTLEEEEVSGALLIILLHLITVFLIASVTKIVLPGTDFLDAIFEAASATGCVGLSTGIISSSTPLLVKIALMAGMYLGKTEYLPLIVLTSYLVHRGMIKSFTS
7.2E-46	166	25.8	8.3E-45	162.6	17.9	2	1	B2A4T2_NATTJ	Cation transporter	Nther_0255	Natranaerobius thermophilus (strain ATCC BAA-1301 / DSM 18059 / JW/NM-WN-LF)	497	cellular organisms, Bacteria, Firmicutes, Clostridia, Natranaerobiales, Natranaerobiaceae, Natranaerobius, Natranaerobius thermophilus, Natranaerobius thermophilus (strain ATCC BAA-1301 / DSM 18059 / JW/NM-WN-LF)	457570	>tr|B2A4T2|B2A4T2_NATTJ Cation transporter OS=Natranaerobius thermophilus (strain ATCC BAA-1301 / DSM 18059 / JW/NM-WN-LF) GN=Nther_0255 PE=4 SV=1MISMKYKEILIRKYNYIIGYIGVILLGLSIALLLPLIFLFIFGEESILVRSFLIPAVFSALLGFIMSTPIRKGNNDSHLTLHEGGVIVVLSWLMVTFISAFPFLLSGELNFTQALFESVSGWTTTGLSVVDESEIANTLIFWRSLMQYLGGAGIAVTLLAAIIGPSGGMGLYSAEGRSDKLLPNVFKSIKLIIIIYLGYTFSGIILYMIVGMPWFDSIIHSFSALSTGGFSSRPESIGAFDSLAIELVTIILMILGTTNFAAHHVFLRGKIKEFFKIGEIKFMFILMGITIPVVIFVALFPLYGNFAESLRFGTFELISSITTTGYSTGVDYDSWGSFAVFVIIVLMIFGGGAGSTAGGVKLIRIYVLFKSVVWHIQEHFLPKNIVRENYILKPGEKFYVYQRHITQFANFLLLYLATYILVGLVIFLAHGFQLEDSMFEFASTLGTVGLSVGLTSPDAPLFILWTQIFGMLLGRLELYIIFFAFIRIIKDIKQLVLK
7.3E-46	166	23.7	1.1E-45	165.5	16	1.4	1	R5IK69_9FIRM	Potassium uptake protein TrkH family	BN480_00346	Firmicutes bacterium CAG:124	456	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:124	1263002	>tr|R5IK69|R5IK69_9FIRM Potassium uptake protein TrkH family OS=Firmicutes bacterium CAG:124 GN=BN480_00346 PE=4 SV=1MLLSFFQRLGRPFRTMRPGRLIVLVFLFIILLGAGLLCLPAASRSGEPTPFLTSLFTATSATCVTGLIRVDTGTHWAMFGQVVILLLIQIGGLGFMTIACLFFFALRRKIGLRERMVLAQALGSDSYSGIVSLVRNILRGTAAVEGAGALILFFRFLPEFGFGKALWYGVFHSISAFCNAGFDVLADTDVGGSLCRYATDPVVNFTIMALIIIGGLGFAVWGDIRHNRRFSRMSVVTRLVILITTVLIFGGAGIFAALEWNNPGTLGGLTPSQKLMAADFLMLVGGSSGSTAGGVKTVTVGVILLAAWSTARGRTSVQIMKRRIPQQAVANASALFILVLLLSGLGAAFLSIADHVSLENALYETISALCTVGLTTGITSSLCAASQIVLIIFMFFGRLGIMTISVGFMAADRAEERVSYAETKIMIG
7.5E-46	166	11.5	1.1E-44	162.1	8	1.9	1	U2RAM4_9FIRM	Potassium uptake protein, TrkH family	HMPREF1546_01174	Oscillibacter sp. KLE 1745	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	1226323	>tr|U2RAM4|U2RAM4_9FIRM Potassium uptake protein, TrkH family OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_01174 PE=4 SV=1MRRKNHMAPARIILIGFALLILAGALLLTLPISTRDGQGAAFFDALFTATSATCVTGLVVQDTALYWSGFGQAVILMLIQIGGMGVVTAAAAISMLAGRRIGLKERWVMQESISAPQVGGIVRRTRFILAVTLVLEGTGTLLLALRFCPEMGLFRGLWYAVFHAVSSFCNAGFDLMGAAGTPFVSLTGYAGDPLVNFTVMGLIVLGGIGFLTWGDVREHKWHLRAYCLQSKLVLAVTAALILLPALFFLLYELRLPQWQTLTLGEKVQGALFQAVTPRTAGYNTLDLSQLSEPSRLLITLLMLVGGSPGSTAGGFKVTTLAVFVLAARAVFRRRADLQCFGRRLPTETLRSAAAVLMMYLGLFLLGGMAICCVEDISLEAALFETASALGTVGLTLGVTPGLGGVSRLILIFLMYFGRVGGLTLIYAVLPDSGAAPAQLPQERVTVG

8E-46	166	26.4	1.2E-44	162.1	18.3	1.9	1	D4KZ03_9FIRM	Potassium uptake protein, TrkH family	RO1_20580	Roseburia intestinalis XB6B4	447	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, Roseburia intestinalis, Roseburia intestinalis XB6B4	718255	>tr|D4KZ03|D4KZ03_9FIRM Potassium uptake protein, TrkH family OS=Roseburia intestinalis XB6B4 GN=RO1_20580 PE=4 SV=1MLPKKLKRLSDMQLIALGFLLLILGGTCLLMLPCSSRTGEFTPFITALFTATSATCVTGLILVDTYTHWSFFGQLVLLLIQIGGLGFITIGTAVSLVLRRKIGLKERGWIKESFNVLDIGGVVRLIKRVLKGTVLFEGIGALLLFTRFYPEMGFFNGLYYSIFHSISAFCNAGFDIMGKYKPYSSFTAYYDDPIVNFTLSALILIGGIGFIVWSDIIDHKWHFKKYALQTKMVLSFSAVLVFGGALLFYLLERNNLYADMSTTGIICSSFFSVITPRTAGFNTLDIGSLTEGGKLLTIILMFIGGGSGSTAGGVKMATIFVLLLHLRSTLLRTTGTNIFGRRIEDDTITKATALLCTYLFAGLAATLAICGMQGFPLGDTLFEVISAICTAGMTTGLTGQLNFISRLIIIFLMYIGRLGSLSFALSFTDHKKLTHIMQPVERINIG
9.4E-46	166	17.4	2.6E-45	164.3	12.1	1.6	1	Q168P3_ROSDO	Trk system potassium uptake protein	trkH-1 RD1_1942	Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)	496	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseobacter, Roseobacter denitrificans, Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)	375451	>tr|Q168P3|Q168P3_ROSDO Trk system potassium uptake protein OS=Roseobacter denitrificans (strain ATCC 33942 / OCh 114) GN=trkH-1 PE=3 SV=1MRLTPAERRANPAHMLDLRPVGYVIGLLVAVLGAAMVLPMMIDIAEGRAHWPVFLQSALFTVLAGGLIAVACSNGVKEGLTIQQTFILTTGVWVALPLFGAIPFVLGATEARFVDAFFEAMSGLTTTGSTVFTGLETLPKGLLLWRGILQWLGGIGIIVVAMVFLPELRVGGMQIFKSEAFDTMGKILPRATQIASQISSIYLGLTMACALCYLALGLDAFDATVHALTTVSTGGFANYDASFGTFSGPPEYVASLFMILAALPFVRYVQMINGHTEPLWRDSQVRVFLITLMIIVLAIAIALTQIFPKDAETAFREALFNVTSIMTGTGYSSADYMQWGPLLISLFFFIGLIGGCAGSTTCSIKIFRYQLLFASIRLQLRKIRSPNGVFIVRYEKRAVDEEVLSSVMSFFMFFVLTLGLLAVALSLTGLDFITSLSGAATALSNVGPGLGDEIGPAGNFAGLNDTAKWLLSLGMLLGRLELLAVYAMLTLSFWRD
9.4E-46	166	27.8	9.4E-46	165.7	19.3	1.6	1	R7EH50_9BACE	Uncharacterized protein	BN594_02605	Bacteroides uniformis CAG:3	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides uniformis CAG:3	1263055	>tr|R7EH50|R7EH50_9BACE Uncharacterized protein OS=Bacteroides uniformis CAG:3 GN=BN594_02605 PE=4 SV=1MKIYHKFLLYQNKWIHPYVRMTVGVMTSITYLASILLIVGVVYEHGFTISEVEAHQLQRLYHGVWIVFLVDVTLRILLEYKDTRRTFSKLTWILTILLYLTLIPVIFHRPEEEGAILQFWEFLHGKAYHLVLLLVFSFFSLSNGLVRLLGRRTNPSLILAASFLIIIMIGTGLLMLPRCTVNGISWVDSLFISTSAVCVTGLTSVDVASTFTPTGFVVIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLNSLLSTLVYILAFTLVIEGIGMLAIWGDIHGTMGMDLQEELAFSAFHAISAFCNAGFSTLPGNLGNPLVMTGHNPFFIYISLLIILGGIGFPILVNFKDIILYHLRRLWHFLRTWHWDGKRFYHLYNLNTKIVLIVTFLLLVLGTVGIAVFEWNAAFAGMSVADKWTQAFFNATCPRTAGFTSVDLAGLGVQTLLIYLFLMWVGGGSQSTAGGIKVNAFAVVVLNLVAVLRGTERVEVFGRELSHDSIRRSNATVVMSFGVLLLFVFIISMLEPGTSLLAITFECVSALSTVGSSLNLTPRLGDDSKLLVALLMFVGRVGLITLMLGIIKQKKHTKYQYPSGQIIIN
9.7E-46	166	26	1.8E-45	164.8	18	1.3	1	E3GNL5_EUBLK	Potassium uptake protein	ELI_2217	Eubacterium limosum (strain KIST612)	460	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium limosum, Eubacterium limosum (strain KIST612)	903814	>tr|E3GNL5|E3GNL5_EUBLK Potassium uptake protein OS=Eubacterium limosum (strain KIST612) GN=ELI_2217 PE=4 SV=1MINIVKKGGRMTTFMRHRRSPAEILMFGFAAVIFLGAVILNLPVSSASGQSPGFLNCLFTATSSVCVTGLVVVDTGTYWSLFGQIVIILLIQIGGLGFMSLMTIFFVLAGKRITIKNRLLIQSSVNSDRVQGVVKFTKYIVFSCLVIEGIGALLLSFVFVPDYGLGKGIYFGIWHSISSFCNGGFDLIGGFQSFTGYANNFLLNFTVCALIVVGGLGFAVTSEIVSYRTTRRLSMHSKIVLSITAILVVGGAVLFYIFEHANPETMGNLPWYGKIYAAFYQSVTPRTAGSNTISQTGLNPVSKVLTIVLMFIGGSPGSTAGGVKTTAVAMMAITLFTELMGRKDVTCFKRRIPEITIKRAACVLTIGISIIIVIIMVLMVCEPGADPMAITFEVFSAYSTVGLTCDLTPHLHALSKVALIITMFIGRVGPLTIAYVITRKERKELENKGQFKLPEGNVLIG
1E-45	166	19.7	1.4E-27	105.8	4.9	2.1	2	Q8TNS3_METAC	Trk potassium uptake system protein, transmembrane component H	trkH MA_2209	Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A)	492	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina acetivorans, Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A)	188937	>tr|Q8TNS3|Q8TNS3_METAC Trk potassium uptake system protein, transmembrane component H OS=Methanosarcina acetivorans (strain ATCC 35395 / DSM 2834 / JCM 12185 / C2A) GN=trkH PE=4 SV=1MYELVSPVNPLAVLRYIGHLLLVFSAVLLVPVLAAFVLGETDAAVIYGSSALVTAGTGFLLQKVLPDFELEIKEALILAALTFPLCSLVSAVPMAFSTGMPFLDAYFECVSGLTTTGLSLAPPSPTRLFFFTRSWLQWIGGIGIIVLVLGILIRPGTTAFRLYRVNFGESRIRPSVITTARTLGTVYLVLTLLSLLLLLFSGMPFYDAVCHTLSSISTGGFSTQAGSIGAYGGFLIPFLITVSCIMGAISFSLYPEVLKEPGTLIRDPQVRYLFGLSLLGTALFVLTLSGGEGGPELFHMMPDAVFQVVSALTGTGFSTIDLAPLSDASKGFLSAIMCIGGSIGSTTGGIKLFRLIVIVQLIKLVFYRFFLPREAITPLKVKSQVVDPDDFYRIMTYVLLYLAVLVFSAFIFMFYGINSADAIFETSSALATAGLSTGVTTPGMPSLLLKLVLCADMLLGRVEIVPLFILLLPRTWFEINRNTGEKRSSKDTA
1.1E-45	166	25.9	2E-45	164.6	18	1.4	1	A9WC68_CHLAA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Caur_0208	Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl)	458	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Chloroflexales, Chloroflexineae, Chloroflexaceae (filamentous anoxygenic phototrophic bacteria), Chloroflexus, Chloroflexus aurantiacus, Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl)	324602	>tr|A9WC68|A9WC68_CHLAA H(+)-transporting two-sector ATPase OS=Chloroflexus aurantiacus (strain ATCC 29366 / DSM 635 / J-10-fl) GN=Caur_0208 PE=4 SV=1MTALVTGRNLARLRRKPIPPPLRLVGGLALLIVIGTLLLLLPISSTRPLTFMEALFTAASALSVTGLSVITPVQDLSLVGQILLMLLIQIGGVGFMVVAVIIFRLLGRRISFTDRIALSDSLGLLSPAAIVTLTRRVLITVVTIEAIGAMLLYIHWRTDPRLSEGQAFFYALFHAVSAFCNAGFDLFTGTPGFENGIPRDSITLFIMGMLILTGGLGIPVIADLISYANERKLSLHTRITLLVVSFLVGIGTFGLWLSEGFDADGTLHGQPLDRQLIVTTFQSISARTAGFSGMDSFESLTPASQLLLIALMFIGCAPASMGGGITTGTFAVLSISLWSYARGLPTAQFAGRSLATGMVRRAAAVLTISLFVVLLASWLIVATHDATLDQVVFEVVSAFATCGLTLGFTSELNTFGQLIIIAVMFWGRLGALTIITAIARQSATPQQITYPEEQILIG
1.3E-45	165	19.6	8.6E-24	93.3	4.3	2	2	C6XMA6_HIRBI	Trk system potassium uptake protein	Hbal_0347	Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hirschia, Hirschia baltica, Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418)	582402	>tr|C6XMA6|C6XMA6_HIRBI Trk system potassium uptake protein OS=Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418) GN=Hbal_0347 PE=3 SV=1MKLRPLLYAMGLMTLGLGLFMLPCVVADLEADRDEWRIFFLLSIASITLGGVMALSARVEKVPIRTHDAFVLTVLLWVVLVFVASGPFFIGFGMSFTDAVFESMSGLTTTGATIMTGIENYPPSLHLWRSLLHWIGGIGIIVTAIAILPSLRLGGMQLFHLESSDTSEKFLPRIGEIALQTTYVYLGLTVICAGLYRLTGMSGFVSITMAMSTVSTGGFAVTDASFAPYVEGHADIVAMIFMSICSMPFALMVIALHGKWKLVIKDPQPLVWCCFAIAGSVIMAMYIAYHQEVEVGPEGTLRMVAFNVISILSGTGFGTEDFNTWGPFPATIFILMMFLGGTAGSASCGLKTFRVHIAFKAMISYTKQMIRPNQISPVRYAGKRVEETTLQSIMIFVFLFLASFAVLTCGLAMTGLDPLTAISAAAATICNVGPGLGEIVGPAGTFQPLPDAAKWMCITAMLLGRLELISIFVILSPSFWRN
1.3E-45	165	15.2	1.3E-45	165.2	10.6	2.5	1	TRKI_HALED	Trk system potassium uptake protein TrkI	trkI HELO_1450	Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9)	492	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas elongata, Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9)	768066	>sp|E1V0R4|TRKI_HALED Trk system potassium uptake protein TrkI OS=Halomonas elongata (strain ATCC 33173 / DSM 2581 / NBRC 15536 / NCIMB 2198 / 1H9) GN=trkI PE=1 SV=1MADTRRVTDTLRRWAPILKVLAVLWLVLAIFMAIPLLVLIVESEPDALAFGLSIAIVLAAATLSWIVTWRIPVSLKPWQMFVLTTLSWVTISSFASLPLVLGAPQLSLTNAVFESVSAITTTGSTILVHIEDLSDGLKLWRGIMQWLGGIGIIVMGIAILPFLKVGGMRLFHTESSDWSDKVMPRTGGIAKATLSIYCGFTLLAAMAYYLGGMSPLDAVVHAMTSLATGGFANSDASFGAYAEQPQLLWMGSLFMLCGALPFVLYIRFLRGSRMALLRDQQVQGLLLLLLVILALTIWRVSQGTPAFTSLTQVTFNVVSVVTTTGYASDDYSAWGATAYVAFFYLTFVGGCSGSTSGGMKIFRFQVAMLLLRDQLRYLIHASGVFVSRYNNQPLTDDITRGVVAFSFFFFLTVAGLALGLSLLGLDFTTALSGAATAVANVGPGLGETIGPAGNFAPLPDAAKWLLCVGMLMGRLEILTVLVLLTPMFWRQ

1.4E-45	165	21.8	3E-45	164	15.1	1.4	1	C1CZV3_DEIDV	Putative K+ uptake transporter (Trk family) putative membrane protein	Deide_03830	Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	458	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus deserti, Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	546414	>tr|C1CZV3|C1CZV3_DEIDV Putative K+ uptake transporter (Trk family) putative membrane protein OS=Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923) GN=Deide_03830 PE=4 SV=1MTLTPLSPRPQRTLISRLQPPQLIALVYIVGIVVGTLLLHLPGVTTPGAKLNSIDLLFTATSAICITGLVVADTAEVFTRTGQVIIILLS QIGGLGIIAFGTLFALLAGRRVNFTERQHLVQQINALNVGSVLSLVRTIFLYTMVAEAAGAALLALRFVPQFGWGEGLYHAVFHSISAYN NAGFVVMPGGMAQYAQDPLVSGVIALQIILGGLGFLVQLNVLAHWRSPRRNRLLVYSKLTLSTTAALLVGTLALLLLEWHNTRTLGDL GMGGRLLTAFFQSVTPRSGGFATVDIESLTNASLFLMIALMFIGANSGSTGGGIKTSTFAILLGSAWNLVSGRTELITFKRRILPENVVR AGTITTIYTLLVFTAFFAMLVTNPELGFTHLLFETVSAAATVGLTMNTTHLVNDPGLLILTVLMYLGRIGPVTFALALNQRQQRRNAIKYP AEQDILVG
1.5E-45	165	25.8	4.9E-45	163.4	17.9	1.7	1	A4A4V4_9GAMM	Trk-type K+ transport system, membrane component	KT71_09367	Congregibacter litoralis KT71	466	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, OMG group, OM60 clade, Congregibacter, Congregibacter litoralis, Congregibacter litoralis KT71	314285	>tr|A4A4V4|A4A4V4_9GAMM Trk-type K+ transport system, membrane component OS=Congregibacter litoralis KT71 GN=KT71_09367 PE=4 SV=1MSGKAPKHSSGAKAPVMGLGRLLSGMLRRIPPVWSIVIGYAAYMVVLFAFLSLPTAQSTYPATGLDHAFVAVSAVSTTGLSTVD VGNTYSFWGELAILLAIQAGGLGYMTLGSFVLLTMGNGLSANRIRIGRLAFHLPPTFALRLFLIRVVAYTVLIELIGAIILWTQFSEVTGTF DRAWAAAFHSISAFCTAGFSIFPNSLEQYRSNYVVNAVVICLSLAGALGFILFNDVWSKIKDWSNHHFSLTSKVILMSTLISILLATMVLY VFENALFNLPAEEHLAVALFQATSALTTVGFDTYPVSRFAHSGLFLLMLLMTLGASPAGTGGGLKSTTWMTGIGTLTTALSHRRPGQV FAFGREIPTRRVIAAFAAITLYVLFLFVGTFTLLSVEPSIAIADLSFEAASALGTVGLSTGITADLGSAGRWTIMILMFIGRVGPLTVALALS SMLPESDHEGQPEEDLAL
1.5E-45	165	28	1E-43	159	19.4	2	1	G9WN11_9FIRM	Uncharacterized protein	HMPREF9625_00744	Oribacterium parvum ACB1	440	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Oribacterium, Oribacterium parvum, Oribacterium parvum ACB1	796943	>tr|G9WN11|G9WN11_9FIRM Uncharacterized protein OS=Oribacterium parvum ACB1 GN=HMPREF9625_00744 PE=4 SV=1MRFFRLNYFQKIILGFAALILFGAFLLMLPISSNERVYTPFLNALFTSTSASCVTGLIVYDTAVHWSFFGQVVILILIQIGGLGVAVAV SSVILLSGKRIGYSQRNTLANSISINSQGGIMKMLIFLLKWTGMIEFFFAILLATQFIPEFGWRRGLWYSIFHSVSAFCNAGFDLMGIKSP YSSLTDYAENPIVNLSIMALILLGGLGFMTWQDIAKNKGNLHRYRLQSKIILSTTIFLVLLPALFYFFVEFGEMPMESRILASFFTAVTPRT AGFNTVDFSKFSDSGIFLQTLLMLVGAAPGSTGGGMKITTMTVLFLTSVAIFRNNSRTEAFGRTIPGEVIRNATTIAFMYICLCVLSGMFI SLHENLPLLTTSFETASAIATVGLTLGITPKLSPVSRVVLISLMYIGRVGGLCLIYAVFPNANPNKGRLVEENVIVG
1.7E-45	165	32.4	3.1E-45	164	22.5	1.3	1	R6K7Z3_9BACE	Uncharacterized protein	BN506_02580	Bacteroides cellulosilyticus CAG:158	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides cellulosilyticus CAG:158	1263038	>tr|R6K7Z3|R6K7Z3_9BACE Uncharacterized protein OS=Bacteroides cellulosilyticus CAG:158 GN=BN506_02580 PE=4 SV=1MKIYHKFLLYQNKWIHPYTRIILGGVTYIAYLASILLIMGVVYEHGFTISEHEASQLQTLYRFVWGVFLSEVTLRLLLEYRDTKRTFK KLTWILIALLYLTLIPVIFHRPEEEGAILHFWEILNGKPYHIVLLLIFSFLNLSNGLVRVLGRRTNPSLILAGSFLIIILIGTGLLMLPRCTVSGI SWVDSLFISTSAVCVTGLTSVDVASTFTTPGFVVIILLIQIGGLGVMTLTSFFAMFFMGNTSFYNQLVVRDMVSSNSLNSLLSTLLYILGF TLAIEGIGMLAIWSDIHGTMGMTFEEEVAFSAFHAISAFCNAGFSTLPGNLGNPLVMTGHNPFLIYISLLIILGGIGFPILVNFKDIVLHHLR RIWKFLHTWEWDRHRFYHLYNLNTRIVLIMTFLLLVFGTVLIAVFEWNHAFAGMSVADKWTQAFFNATCPRTAGFTSVDLASLGVQS VLVYIFLMWVGGAAQSTAGGIKVNAFAVVVLNLVAVLRGTERVEVFGRELSYDSIRRSNATVVMSISVLFVFVFILTIWEPQASVMALL FECVSALSTVGSSLNLTPTLGDNSKLLVAFLMFIGRVGLITLMLGIIKQKKHTKYQYPSGQIIIN
1.9E-45	165	27	3.5E-25	97.9	9.8	2.1	2	A3DNI4_STAMF	Cation transporter	Smar_1098	Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1)	477	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Staphylothermus, Staphylothermus marinus, Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1)	399550	>tr|A3DNI4|A3DNI4_STAMF Cation transporter OS=Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1) GN=Smar_1098 PE=4 SV=1MNWRGIAKIIGALEIVVGLLMLSVPLIDLLTLKPLTLSFTFFALFLIFIGYYLQQIEAKPIGLLDGIVATSIAWPLISFEASIPLMLSLNIS LVDAWFESISGFTGTGFTVLTGLDYMKPSIVTWRSIMQWSGELGVVVFAMVLFPYFYRLGASAYGVERPLKIEASFYMTARKLIRIYLV LTIAGIVSYVYAGMNFYEAFNHVLTTVATGGMSTYDAGYNVIFERAPFTYIPVMVFMFLGGMNFVLLDKLLRGDLGRVWRSEEFKTYL YTMLVLVFLTIISYYFVDHYNLYYSLIAGSFNLVSAMTTTGFSIGSISDLSATTKLVLIASMYFGGMVFSTAGGIKSFRLLLILKKFKYSSIS TILGGKVEKTLRVDGKPIDEAEVSQALLFSFIHLLAIFIGATFMTIYGYSFVDTLFEATSAAGCVGLSVGVVSPTAPLGVKLTIMTLMLLG RVEYVQVITIFGYIAGRKAVKILK
2.3E-45	164	22.5	3.6E-45	163.8	15.6	1.3	1	E3H087_ROTDC	Potassium uptake protein, TrkH family	HMPREF0733_10436	Rothia dentocariosa (strain ATCC 17931 / CDC X599 / XDIA)	505	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Rothia, Rothia dentocariosa, Rothia dentocariosa (strain ATCC 17931 / CDC X599 / XDIA)	762948	>tr|E3H087|E3H087_ROTDC Potassium uptake protein, TrkH family OS=Rothia dentocariosa (strain ATCC 17931 / CDC X599 / XDIA) GN=HMPREF0733_10436 PE=4 SV=1MGRYLRRLRAHQRKRVRDFSEGRISTAIGKVPPTSPMMYEQEEVTRRFNPFDIRSYEKLRNLIDTTVFSSPSRTAIASFFLVIVFF TVTLSLPISSVTGEPAPFHHAFFTATSAVTVTGLTTVSTAAQWSVFGQVMILLACQIGGLGALTMTSLLALAIGRKMGLRSKLIAQEELS IGRLGEVGSVLRTVAYTSIGIESTIALVLTPRFLLLGENLPTSLWHGIFYAISSFNNAGFTPHSDGLVPYGHDFFVLAPVSIAVFLGALGF PVLMTIQQKPFRPRDWTLTTKLTVTTTSILFVLGALLVGIAEWANPRTIGNYGAGEKILSSIFASIMTRSGGFNLVDMNDIRPVTGLITD VLMFIGGGSASTAGGVKVTTIAVIMLAIIAEARGDQFVMTFGRTIPVSALRIAISVTMMSTGIVLVGTGVLLAITDQPLVRVLFEVISAYAT CGLSNGLSTELPPSGIYVLSLLMFIGRIGTITAATGLALRSRRRLYKYPEERPVIG
2.5E-45	164	22.3	3.4E-24	94.6	5.5	2.3	2	A8ZYR9_DESOH	Trk system potassium uptake protein	Dole_1370	Desulfococcus oleovorans (strain DSM 6200 / Hxd3)	479	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobacteraceae, Desulfococcus, Desulfococcus oleovorans, Desulfococcus oleovorans (strain DSM 6200 / Hxd3)	96561	>tr|A8ZYR9|A8ZYR9_DESOH Trk system potassium uptake protein OS=Desulfococcus oleovorans (strain DSM 6200 / Hxd3) GN=Dole_1370 PE=3 SV=1MRAQVILRYVGFVLLFNATFLLISALFSLAGGDSALSPLLFSTVVCALFGLFPLLFVPATTDISNREGLFIVVCSWLASCLVGTLPYL LWGGGFTFTNAWFESVSGFTTTGATILANVEGLAPGLLFWRAATHWMGGVGIIIFVLAVIPSMGAASMVLYRSEVSPLVKESFHYRT KKTLTILLYVYIGLTAAETLLLMIEGMSLFDAVTHAFSTIATGGFSTKNASIAHFASPGMETTIILFMVLSGVHFGLLYQAVTGNPKDLFQS TVFRYYMIAILVLGVVLVTINIHGPVYGQWVDALRYAAFQVVSIGTSTGFANADSSVWPPFAQLAILFFTLQCACSGSTSGGIKADRIVLL WKAAARRLVRLRHPKSVVVVKVNQAAVDDEVVETALTYILIYLGVLLVSTLAITGFGVDIMTAFSGAAAAMGNVGPGFGTVGSMGNYS HLPDLVKWILTADMLVGRLEIFGLILFVTIHRWR
2.6E-45	164	31.3	4.8E-45	163.4	21.5	1.3	1	B5Y9D7_COPPD	KtrB	COPRO5265_1073	Coprothermobacter proteolyticus (strain ATCC 35245 / DSM 5265 / BT)	449	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermodesulfobiaceae, Coprothermobacter, Coprothermobacter proteolyticus, Coprothermobacter proteolyticus (strain ATCC 35245 / DSM 5265 / BT)	309798	>tr|B5Y9D7|B5Y9D7_COPPD KtrB OS=Coprothermobacter proteolyticus (strain ATCC 35245 / DSM 5265 / BT) GN=COPRO5265_1073 PE=4 SV=1MEAAIKARRLIVRSFAAVILVGAVLLALPITSRGGGFTNFVDALFTSTSAVCVTGLIVKDTWDYWNFAGQFIIMLLIQFGGLSYLTIT TFTLLLLTGARIGLRTRITLASQWNVNSLQGVVKLLGFTVRFALLVELIGALLLSITFIPYYLNSRGLAGGIWASVFDAVSAFNNAGFDIH GGFKSLSEFAQDPVVNLTIMGLIIAGGLGFVVWSEIFQKVRQKKFYFSLHTRIVLGVTLALIVLGALLIGIFEWNNPKTLGPLSIQGKILAA FFQSVTPRTAGFATINHGYATLPTLLITMLLMFIGGSPGGTAGGIKTTTFFSVFQYIKAVLTGSSRVHVAHRTIKWSILDTANAILILNMTI AVISIVLLSVFEPALHLHQIAFEVFSALGTVGLTTGITPNLSVASKIVLILTMFVGRVGVFTILTGYIFRPELPSYTYPEEDIIVG

2.9E-45	164	37.8	4.7E-44	160.1	26.2	2	1	R6MG60_9FIRM	Potassium uptake protein integral membrane component KtrB	BN647_02030	Firmicutes bacterium CAG:41	450	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:41	1263021	>tr|R6MG60|R6MG60_9FIRM Potassium uptake protein integral membrane component KtrB OS=Firmicutes bacterium CAG:41 GN=BN647_02030 PE=4 SV=1MNIIRKILFHKRINTARRISFGFALIILVGALLLMLPISSKERVVTPFLSALFTTTSATCVTGLTIINVGAYFSLFGQAVILFLIQLGGLG FMTILCIVFIVSNRQIGLRNRMLIAQAMGTESLEGIVKLAKHVLYITGIIELLGAIVLSIRFVPKYGFFKGMWFSIFHSVSAFCNAGFDIIGD GNSMLSYRHDPLVLCTLAILVAIGGLGFIVWEDIIAKKSWKKLNVYSKVIILAQIFFIVVGTFVYFILEYGNINTIGAESVGQKILASFFQSV TTRTAGFDALIQNNLTDLSKAWGTVLMMIGGASGSTAGGVKLGTAVLVIMTLISVLRGKSDVVIHGRRIAHTTILQAMALLVLWLVVV GGSVLISYIDNQDLINSIYEVASAYSTVGLSVGVSGSASTFTKILLIVYMFFGRVGIMTISVVFMTRIRKTNDIRYPECNFIVG
3.1E-45	164	21.9	1.1E-43	158.9	15.2	2	1	R5PP97_9BACT	Trk system potassium uptake protein TrkH	BN465_01060	Prevotella sp. CAG:1092	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:1092	1262919	>tr|R5PP97|R5PP97_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:1092 GN=BN465_01060 PE=4 SV=1MINTKIIYKILGSLLFIEVALMMTCLGVALVYDEDDVFSFLVSIVVTLVAGILCRLKGYKADNNLSRRDAYLVVTVAWVVFSLFGTM PYMVGGYIDNFTDAFFETMSGFTTTGATIINDVECLPHGILFWRSLTQWIGGLGIVFFTIALLPSMVGGSTKIFAAEATGPIKSKLHPRLS TSAKWLWAVFLTITLSAMGCYMLCGMDSFEAINYAMTSAATGGFAIYNDSVTHFHSPMLDYVVTFFCFISGVNFTLLYASVAKLKFKN LMKNAEFRFYLFSVFASTAAVMLALIFKNGYGIEHAFRNSLFEVVTALTTTGFANDNAGNWAHITWVVLIVCMFLGANSGSTSGGFKSI RSVMVIKIIKNEFRQMLHPNAIVPLKLDSINVPMQKRVTLLAFLASYMLILAISIFLMSLAGVESVDCVSISFSSLGNVGPAFGNEIGPNDS WAILPDTCKWISSILMLIGRLEIFSVLIIFTPAYWREN
3.2E-45	164	21.7	1.4E-44	161.8	15	1.8	1	V9VRI3_9RHOB	Trk system potassium uptake protein	METH_05715	Leisingera methylohalidivorans DSM 14336	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Leisingera, Leisingera methylohalidivorans, Leisingera methylohalidivorans DSM 14336	999552	>tr|V9VRI3|V9VRI3_9RHOB Trk system potassium uptake protein OS=Leisingera methylohalidivorans DSM 14336 GN=METH_05715 PE=3 SV=1MFDLRPVGYVIGLLVVILGAMMLFPLLVDLMDGRGEWHVFLESALFTILVGGILALSCANGVREGLSIRQTFLLTTMVWVALPLF GAIPLMLGATELRFVDAFFEAMSGLTTTGSTVISGLDDLPRGLLLWRGILQWLGGIGIIVVAMVFLPELRVGGMQIFRSEAFETMGKILP RAQAIAKQISIIYAVLTLFCMIVYLMLGMQGFDALVHALTTVSTGGFSNYDASFGTFSGSAEYAASVFMILAALPFVRYVQLVNGHAEPL LRDSQIRVFLIVILLLVGVTSAVLVYVFPHHPEQAFREALFNITSIISGTGYASVDYMEWGSFLIIVFFFIGLIGGCAGSTTCSVKIFRYQLL FSAIRVQIQRIRSPHGIFVPRFDGRAVGADVLSSVISFFMFFVVTLGIVAWLLALTGLDFVTSVSGAATAVANIGPGLGDVIGPAGNFST LNDPAKWILSAAMLIGRLELMAVYAMLTVRFWRS
3.3E-45	164	22.7	3.5E-42	153.9	15.8	2.2	1	A5UM72_METS3	Trk-type potassium transport system, membrane component, TrkH	Msm_1095	Methanobrevibacter smithii (strain PS / ATCC 35061 / DSM 861)	478	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobrevibacter, Methanobrevibacter smithii, Methanobrevibacter smithii (strain PS / ATCC 35061 / DSM 861)	420247	>tr|A5UM72|A5UM72_METS3 Trk-type potassium transport system, membrane component, TrkH OS=Methanobrevibacter smithii (strain PS / ATCC 35061 / DSM 861) GN=Msm_1095 PE=4 SV=1MMKYITKTDLCIVTRYSGVVMICVGLMCLSPLLIDLIYFEFNYSCFIIPGVFSVILGYICMKTLDKYSRSKMKLKHGMMISSIAWMW ACIVGGVVISLATGTDFLNGIFESTSALTGTGITMFDNVEILPHSILFFRAFEQWVGGLGVVVMVIGVLTRPGTATAKLYQSEAREERLK PSVKTTLKKTIEIYLIYTIVGIILYHLAGMPTFDSICNTFCMIATGGMSVKNANIGYYHNDLIYLISIVLMILGATSFLAHYKIIKTKGKSLIQDL QFKTLICIITFVTIILYLASHIVPIDLLFTVTSSITTTGANVQLASTMAGWPSFILVILMILMLMGGSSGSTVGAIKLYRVITYVKAIYRHIKEIL SPDGRVIPIKISGRRVSEKEIGKTGNFITLYLVIIAITWIIFCFYGYPPFDSLFSIISLQGNNGLDIGVLNNTLNPVLKIVSVLNMWVGRLEIY PVLVLFRAIFEIFKK
3.4E-45	164	17.8	2.8E-44	160.8	12.3	1.9	1	D6ZGD8_MOBCV	Cation transport protein	HMPREF0573_11377	Mobiluncus curtisii (strain ATCC 43063 / DSM 2711 / V125) (Falcivibrio vaginalis)	470	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Mobiluncus, Mobiluncus curtisii, Mobiluncus curtisii (strain ATCC 43063 / DSM 2711 / V125) (Falcivibrio vaginalis)	548479	>tr|D6ZGD8|D6ZGD8_MOBCV Cation transport protein OS=Mobiluncus curtisii (strain ATCC 43063 / DSM 2711 / V125) GN=HMPREF0573_11377 PE=4 SV=1MARISEFNPGRKISAAFLITILVGTVLLMLPASRSGAAVATSFDVVAPHAIPTGVPVFGPSFADGAPLSIALFTAASATSVTGLIVVD TGSYWSAFGQAVIFLLIELGGIGTMTMVTLFASALRKRATFEDRAIAKVWFGLTPREVRHSVGQIVVASLLLQLGFAFLNSLYLWFSHH ATSPLQAMAHGVFLTGSAFNNAGFAPYQDSLMSFSTEPFLLLSLGALIVIGGLGFPVWLMLYRNGWHWWKWGMTTRIMLLGTAAAI VFGWVAITVLEWHNPHTFGAMPVPERLLNGLFSSISPRTAGFNSVDISQQYPETWLITDGLMLIGGGPAGTAGGLKITTAIVVMATLW GEIRGAHAINILGWRLARSAQRQALAVLSLFFGLVAVGAFLLMLFTPFNLNQCLFEICSALGTVGLSTGITPLLPVAAQFMVIIFMILGRIG PLTLAAALATRRRPVAYELPRDHPLIG
3.4E-45	164	20.3	6.8E-45	162.9	14.1	1.3	1	D2NRB0_ROTMD	Trk-type K+ transport system, membrane component	RMDY18_03540	Rothia mucilaginosa (strain DY-18) (Stomatococcus mucilaginosus)	539	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Rothia, Rothia mucilaginosa, Rothia mucilaginosa (strain DY-18) (Stomatococcus mucilaginosus)	680646	>tr|D2NRB0|D2NRB0_ROTMD Trk-type K+ transport system, membrane component OS=Rothia mucilaginosa (strain DY-18) GN=RMDY18_03540 PE=4 SV=1MGRILRRTRRRHHHPQGQLNRRWDTLSGATSEPQKQQVRRSRRDRLEAEKLSILTSVPGIDLDRLPTLRDHEDPKTQRKRTPL EFNQKTLERFRDFIDSSVLASPSRTAIGAFFLVIIFFTIMLSLPISSADGQRVALHHAVFTSTSAVTVTGLTTVSTADQWSTFGQAMILLA CQVGGLGTLTITSLLALAIGRKMGLRTKLIAQEDLNISRLGEVGGIVKAVAYASFSIEAFIAMLLTPRFLALGEAPHEALWHGIFYSVSAF NNAGFTPHSDGIVPYGHDLFLLVPICIAVFLGSLGFPVFIAIQRNPFRPSHWQLTAKLTIVTTLFFFGFGAFFWGAFEWNNPATIGSYSP GDKILNAIFASVMMRSGGFNLVDMDAITPVSTLLTDTLMFIGGGSGSTAGGVKVTTIAVIALSILAEARGDQKVVAFNRTIPESSLRIAIS VIVMGATVVAVGAASILIISGADLKEVIFEVISAFATCGLSNGLSASLPPAGVYVLSGLMLIGRVGTTTAATGLALRSRRRLYKFPEERPTI G
3.5E-45	164	2.7	5.3E-45	163.2	1.9	1.2	1	Q1AWJ0_RUBXD	Cation transporter	Rxyl_1274	Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)	442	cellular organisms, Bacteria, Actinobacteria, Rubrobacteria, Rubrobacterales, Rubrobacterineae, Rubrobacteraceae, Rubrobacter, Rubrobacter xylanophilus, Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)	266117	>tr|Q1AWJ0|Q1AWJ0_RUBXD Cation transporter OS=Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129) GN=Rxyl_1274 PE=4 SV=1MLPRPSAARAIALAFAALIAAGTGLLKLPAANNGLSWEDALFMSVSAVTVTSLQSVDPATALTPLGQALLAGLVQVGGLGIMTVT TVAALLVGYRLGFRELLLLREELASPEAPRNVLRLAGQVALITALVELSGLLVLAGRFLLLGYGPAEALGYATFNAIAAFCNAGFNVFEE GLSPFAGDWAVNLALVYLIVAGGLGFPVLANLYRYRRMRRLTLQSRLVLTTSALLVAAGALSVALLEWDNPQTLGGRPLHTRLLMSLL QGVTPRTAGYATVDYAEMRDPTLAIQTALMFVGTGPVSTGGGIKVTTLALLFLIVLAQVRGREEVSAFGRTVGRTVISRSLALLSLAAL LVGGSSVALMILEGVPFLPAVFEVTSAFGTVGLSLGPPPGLSSELGWSGKLLLELVMFAGRLGPVTVALAFSERSRPRRYGYPEEDIAI G

3.5E-45	164	26	3E-44	160.7	18	1.9	1	Q5M618_STRT2	K+ transporter (Trk), membrane-spanning protein	trkH1 stu0264	Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311)	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus thermophilus, Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311)	264199	>tr|Q5M618|Q5M618_STRT2 K+ transporter (Trk), membrane-spanning protein OS=Streptococcus thermophilus (strain ATCC BAA-250 / LMG 18311) GN=trkH1 PE=4 SV=1MNRSIVRFLISKLLLIEAGLLVVPLIVALIYQEDAKVFTSILGTMAILLFIGVLGTLFKPKNYRIYTKEGMLIVALCWVLWSFFGGLPFVFAGQIPSVIDAFFEMSSGFTTTGATILTDTGVLTHSLLFWRSFAHLIGGMGVLVFALAIMNNSKNVHHEVMRAEVPGPVFGKVVAKLKNTAQILYILGMFVIFAMILWICGMPLFDSIVIAMGGAGTGGFAVYNDSIAHYNSDLITYVVTVGTLLFGVNFNLYFYILLRKIRFFFQDEELRTYLTIVAVSTSLIILNIFGIYHSLANSFKYSFFEVSTIITTTGFGLTDITKWPLFSQYILLLLMFIGGSAGSTAGGFKVIRAMIIAKIARNQTLASLYPNRILSLHINGSVLDKETQHSVLKYLAVYVLIILSLVTILSLDNQNFLIVTSAAASTFNNIGPLLGTTDSFAIFSPLSKLIMGFAMIAGRLEIYPLLILSLVTILSLDNQNFLIVTSAAASTFNNIGPLLGTTDSFAIFSPLSKLIMGFAMIAGRLEIYPLLILSLVTILSLDNQNFLIVTSAAASTFNNIGPLLGTTDSFAIFSPLSKLIMGFAMIAGRLEIYPLLLLFLPKTWSKI
3.7E-45	164	19.8	2.1E-44	161.3	13.7	1.9	1	A0A085BW18_9RHOB	Trk system potassium uptake protein	IV89_15625	Sulfitobacter sp. CB2047	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Sulfitobacter, Sulfitobacter sp. CB2047	1525218	>tr|A0A085BW18|A0A085BW18_9RHOB Trk system potassium uptake protein OS=Sulfitobacter sp. CB2047 GN=IV89_15625 PE=3 SV=1MLDLRPVGYVIGLLVSVLGIAMIVPMLVDIAEGRGHWPVFVEAGLITMLGGSMIALACANGVREGLTIQQTFLLTTAVWLMLPLFGALPFMLGATEARFVDAVFEAMSGMTTTGSTVFSGLDDLPKGLLLWRAILQWLGGIGIIVVAMVFLPELRVGGMQIFKSEAFDTFGKILPRAGQIASQISVIYVWLTFACALTYLTLGMNVFDATVHALTTVSTGGFSNYDASFGTFSGNAEYAASIFMVLAALPFVRYVQLLNGNPLALHRDPQVKGFLLTIAVLVGLIFISIQSVFPHHWEQSLREALFNITSIISGTGFASVDYMTWGPFPVALFFFTGLIGGCAGSTACSIKIFRYQLLFASIRAQLQRIRSPHGIFTPRYDGRPISGDVMISVMSFFMFFTLTLGLVAVALSMTGLDFVTSISGAGAALGNIGPGLGKIIGPAGNFSTLNDTAKWILTAAMLVGRLELMAVYVILTFKFWRA
4.1E-45	164	31.2	1.2E-25	99.4	5.4	2.2	2	E0USS5_SULAO	Trk system potassium uptake protein	Saut_0053	Sulfurimonas autotrophica (strain ATCC BAA-671 / DSM 16294 / JCM 11897 / OK10)	480	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Sulfurimonas, Sulfurimonas autotrophica, Sulfurimonas autotrophica (strain ATCC BAA-671 / DSM 16294 / JCM 11897 / OK10)	563040	>tr|E0USS5|E0USS5_SULAO Trk system potassium uptake protein OS=Sulfurimonas autotrophica (strain ATCC BAA-671 / DSM 16294 / JCM 11897 / OK10) GN=Saut_0053 PE=3 SV=1MNYKNVLKILSLIGITVSVIFLLDALIGIIYKEQYENFLLYDGLFFLVNLAVWQWLRNHEFDLKIKESILVVNLLWVLLGVAGAIPLFLYTDISFASSFFEAISGFTTTGATVYTDIEALPHLILFHRSLMHWLGGLGVIVLGVGLLSVINPTGSLSLFKAESTGVVLEKLTPKIKDTALSLWIVYTLLTLVDMMLLKFFGMSWFDAINHAFSTISTGGFSTKNDSLGYFTNDGIIWTTTIFMMLAGINFLAHLKLYYKDAGGYKTEEVKWYFIIFIVLSILLSLVHVDISGDSFYDALKHSSFTIASVMTTTGFATIDYGSWSHLAIAIIFIGLLMGGNAGSTAGGIKIIRHVIIFKTLASELKRILHPNMIISVFIDGVKQKERILSSTFGFFTLFMITVAIVTVYIYARGYDAMTSISGAFAIVGNVGPGFSMVGPADNFSFFSDFDKIFLSVAMIIGRLECYTVFVLLSSSFWKKF
4.2E-45	164	18.4	3.4E-36	134.2	4.2	4.5	3	G7WQ95_METH6	Cation transporter	Mhar_1931	Methanosaeta harundinacea (strain 6Ac)	618	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosaetaceae, Methanosaeta, Methanosaeta harundinacea, Methanosaeta harundinacea (strain 6Ac)	1110509	>tr|G7WQ95|G7WQ95_METH6 Cation transporter OS=Methanosaeta harundinacea (strain 6Ac) GN=Mhar_1931 PE=4 SV=1MRVRVFLRVFGTLLKLLGGLMLLPAGVSLLYGEVEGVIAFLLPALFTFAIGLLMAILGEEEVLTNKEGFALVAFGWLGAAATGALPFVLLGLSPMDALFESMSGFTTTGASILSESGADGLFLINATAASSSLAVALVQIASNQSFMPSAVGPSTFLASNASALNDTILNAAFPGGLSGSGTNLTSNLIEPTYRGLLFWRCFTNWIGGMGIIVLFIAILPNLGVAGRQLFNAEVPGPTEDLIRPRIKQTAKILWGVYMVLTAAEFLLLMLAKMPAYDAICTTFSTVATGGFSPRAESIAYYSGPDYNGPLIEVVVILFMFVCGANFALHYRTMYVSRKSLIKDAEFKFYSLIVLASILVITLIGGIDESLPPEGPDLEGFDLASHRLRTAAFQTVSIITTTGFATADYDLWSSPAKLILLFLMFTGGCAGSTAGAMKVVRILLALQCCRRELFRTLHPKAVMAVKLKGAPVREDVLRSILIFMAIYILIFAIGSALFASVCTLAEEEETGAEDRIYFVSGAGVGLEVVGGISGGWAGAEGPGDGICSGRGVGGIDMISACSAVATCLGNVGPGLHRFGPTDNFSEVPGIGKLILILLCMWMGRLEVLTVLVLLIPDFWKG
4.8E-45	163	11.7	2.6E-43	157.7	8.1	2.1	1	W8SSU1_9RHOB	Trk system potassium uptake protein	roselon_03337	Roseibacterium elongatum DSM 19469	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseibacterium, Roseibacterium elongatum, Roseibacterium elongatum DSM 19469	1294273	>tr|W8SSU1|W8SSU1_9RHOB Trk system potassium uptake protein OS=Roseibacterium elongatum DSM 19469 GN=roselon_03337 PE=3 SV=1MFDLRPVVHVLGLLVFSLGATMIVPLAFDLVVGNGHWGAFAEATAITMVIGLMMTLSCANGVSQGLSVQQTFLLTTGVWLVLPVFGALPFVLGATEARYVDAFFEAMSGLTTTGATVFSGLDDLPAGLNLWRGLLQWFGGIGIIVVAMVFLPELRVGGMQIFRSEAFDTMGKILPRATEIAARISVIYLALTVACALTYAALGMPGFDALMHALTTISTGGFSNRDASFGAYQGPLEYVAAVFIILASLPFVRYIQLVAGTARPILRDSQIRAYLVTILALTVLLALYRVIANGDHWEQGFREGIFNITSIISGTGYASTDYQLWGPVPVAIFFFVGLIGGCAGSTSCSIKVFRYQLLFASVSTQVRRLYAPHGVFEPRYEGRPIAEEVLSSVMAFFVLFFVTLGITAVLLGLTGLDFVTSVSGAAAALGNIGPGLGDTIGPAGNFATLNDTAKWILSAAMLIGRLELMAVFVLLTTAFWRT
4.9E-45	163	36.4	9.1E-45	162.5	25.2	1.3	1	A0A0G0BWD1_9BACT	Trk system potassium uptake protein B	UR26_C0004G0029	candidate division TM6 bacterium GW2011_GWF2_32_72	453	cellular organisms, Bacteria, unclassified Bacteria, candidate division TM6, unclassified candidate division TM6, candidate division TM6 bacterium GW2011_GWF2_32_72	1619079	>tr|A0A0G0BWD1|A0A0G0BWD1_9BACT Trk system potassium uptake protein B OS=candidate division TM6 bacterium GW2011_GWF2_32_72 GN=UR26_C0004G0029 PE=4 SV=1MNSESQLKRKRGFLSKFAPGQIILLSIFIIILIGAIILALPISQKEPISLLNIYFVATSVTCVTSLSPVPLTQFSDFGQLIILIMMQIGGLGLITLTLFTMYLLMDLGLRTQLIAGKLLEMESWPKVRELLFFIIGLTFTCEAIGAFFIFPTIANKFTLGRAIFLSIFHSVSSFCNAGFCLFPDGIPAFNENIPFLLITSLLMFMGSLGFITWHEISKFLREFRTKKHFSWSLHTRLIATTTIALLIFSTCFFWMLERDNSLITLSPFKQFLNSLFNAIANRNTGFLSVDIIGLHTATLFMIMIMAFIGAAPGSTGSGIKIATFAILIATLRATILDKKHITIKGRTIADDQIYKALSIIGLSLIWITIMTFLLLITESTFNFLDVVFEVFSAFATLGLSTGVTPFLSTTGKMLIMLTMIAGRVGSLTIILALKQRSGTQFEFEYPEERIAIN
4.9E-45	163	13.2	7.1E-44	159.5	8.6	2.2	1	F3Z3E6_DESAF	Cation transporter	Desaf_3192	Desulfovibrio africanus str. Walvis Bay	498	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio africanus, Desulfovibrio africanus str. Walvis Bay	690850	>tr|F3Z3E6|F3Z3E6_DESAF Cation transporter OS=Desulfovibrio africanus str. Walvis Bay GN=Desaf_3192 PE=4 SV=1MGYLPGPALRLRTMFSYAGFIWTLVGLLMLASLAVLPFADGEAAWSWAFLYPASALLLGGLTTWRMARPRTYVTLTLQDGGVVVLLGWIVCCLAATWPFLSILDLTFTQALFETVSGFTTTGLSVVDVTTAPKVVLLWRSLMQLAGGAGLAIIMLAAIAGPAGTSLSGAEGRSDQLAPHVRSSATLVLVIYSAYALAGSLAYRIAGMEWFDAVNHAFAAISTGGFSTRPESIGYWNSSEIELVTVVLMILGNLNFVTAYLLLTGKWRSVLKNGELRFSLLLFLAAAGLLFWFVAHHGYTGLGKQVRVALFEAVTAATTTGFSTVGYTGWPAIGWLVMLLLMLVGGGTGSTAGGIKQYRVVYLLIKSVWWEIKRALLPRGSVPAESIWMGERPKFIDDSDLRRATCFVTLYLVCFTLGVGIMVAYGYPLRESLFEYASSIGTVGLSIGITSADAPPAVLWTQIMGMFLGRLEFFIVFIAALHAGKIVLPIISRRKRPARS
5.5E-45	163	19.2	2E-44	161.4	13.3	1.7	1	F8AWJ7_FRADG	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	FsymDg_1896	Frankia symbiont subsp. Datisca glomerata	446	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia symbiont subsp. Datisca glomerata	656024	>tr|F8AWJ7|F8AWJ7_FRADG H(+)-transporting two-sector ATPase OS=Frankia symbiont subsp. Datisca glomerata GN=FsymDg_1896 PE=4 SV=1MTRSDGGRRGPALYVVAAFAAAIVVGTLALMVPYARAGHGGAPPLVALFTATSAVCLTGHVVVDTSSYWTPFGQTMIVLLVQVGGFGIMTAASLLALLVSRRLGLRGRLLAASETKTLGLGSVRRVVVGVVVLSVIVEAGVAVVLTLRFWTAYDTALHSAAWQGIFHAVSAFNNAGFALFPNNLTSFVTDPVISLVVLVAFVLGGLGFPVLFELRRTVWRRPRRLSLHSKITLWVTAVLAAIGVVGAQLVLEWTNPATLGPLAVPQKALAGLFQGMTPRTAGFNTLDFGAMNETTWLVTDALMFIGTGSAGTGGGIKVTTFAILGFMIIAEARGANDVDVAGRRVAPAAQRQALAVALLGVGVSFLGTLLLLATSGIALDRVLFEAVSAFGTVGLSTGITAELPGPAQAALIVLMFIGRIGPVTAASALALRQQVRFYRLPEERPIVG

5.8E-45	163	16.8	6E-44	159.8	11.6	2	1	R6BQL2_9CLOT	Potassium uptake protein	BN513_00724	Clostridium sp. CAG:169	386	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:169	1262778	>tr|R6BQL2|R6BQL2_9CLOT Potassium uptake protein OS=Clostridium sp. CAG:169 GN=BN513_00724 PE=4 SV=1MSYCSLFWRSFTHWIGGMGVLVFLLTILPLSGGSHINLMRAESPGPSVGKLVPKVKHTARILYIIYLGMTVIEILLLLLGDMPLFDALTTAFGTAGTGGFGIKNTSMMDYSPYLQWVVTIFMVLFGVNFNAYYLMLFGKFRRAFAMEEVRWYLIIIAFATGVIFLQILGNSAGVFDALTHSSFQVASIITTTGFSTIDFDLWPQTSRTILVLLMFIGACAGSTGGGIKVSRCVVMVKTVAKELNSYIHPRSVRKIKLEGKPIDHEVLRSINVYFCTYLLIFCGSIFLLSLEGKDLVTNFTAVAATFNNIGPGLELVGPTRNFGGFSHFSKYVLIFDMLAGRLELFPLLILFHPAVWKQALSKKVEEGQVHPLPQDDFTTFWYDSKY
6E-45	163	16.6	3.1E-28	107.9	7.4	2	2	R6SSB9_9CLOT	Uncharacterized protein	BN660_00681	Clostridium sp. CAG:448	434	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:448	1262808	>tr|R6SSB9|R6SSB9_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:448 GN=BN660_00681 PE=4 SV=1MRNLFRKMTPVRIIALGFALTVLIGAGLLLLPCSVRPGVSLSLIDALYTSTSAVCVTGLIAVDAHDTFTPLGQCILGLLIQIGGLGVTAVGAGVILAIRKRISIKGRTLLREAMNLDSGKGIVHFLKSVLLTTLTIELAGACLSFPVFVRDYSVPQAIGISLFHSVAAFNNSGFDILGGMRNLTPYRDDVLLNLVTSALIILGGIGFLVIREVLEKRFCWKRFSMHTKVVLSVSAVLTLAGTLLLKLTERGNISWLGAFFQSVTARTAGFSTYPLGGFSNAGLVAMMVLMFIGASPGSTGGGIKTTTFFAVLQGIRSAATNRSEKAFRYTLPADAFRKASVIASIGLFLVAGSTFVLLLLEPQLALRDALFEMVSAFGTVGLSTGITPGLGVAAKLLSIVMMYIGRLGPMTIATVWYFSRGERVRFPEGNIAIG
6.1E-45	163	22.2	2.2E-44	161.2	15.4	1.8	1	Q5LTR0_RUEPO	Trk system potassium uptake protein	trkH-1 SPO1353	Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) (Silicibacter pomeroyi)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Ruegeria, Ruegeria pomeroyi, Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) (Silicibacter pomeroyi)	246200	>tr|Q5LTR0|Q5LTR0_RUEPO Trk system potassium uptake protein OS=Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) GN=trkH-1 PE=3 SV=1MLDMRPVGYVIGLLVAILGATMVFPLAADLIEGRGEWPVFLQSGVITVLTGAILALSCANGVREGLTIQQTFLLTTLVWVALPLFGALPFMFGATELRFVDAFFEAMSGLTTTGSTVISGLDGLPRGLLLWRGVLQWLGGIGIIVVAMVFLPELRVGGMQIFRSEGFDTMGKILPRAQEIAGQITVIYVALTFACALVYGALGMSFFDALVHSLTTISTGGFSNYDASFGTFSGLPEYAASVFMILAALPFVRYVQMVNGHSAPLFQDSQVHVFLIVIALLVGVTTVVLTTVFPHHVEQAFREALFNITSIISGTGYASVDYMGWGGFLVTMFFVIGLIGGCAGSTACSVKIFRYQLLFASIKVQLQRIRTPHGVFLPRFQGRPIGPDVLGSVMSFFVFFIVTLGVLAWGLALTGLDFITALSGAATAIANVGPGLGEQIGPAGNFAGLNDAAKWMLSVGMLIGRLEVMSVYVLFTVQFWRA
6.3E-45	163	27.6	3.8E-43	157.1	19.2	2	1	A1SR41_PSYIN	Trk system potassium uptake protein	trkH Ping_0082	Psychromonas ingrahamii (strain 37)	481	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Psychromonadaceae, Psychromonas, Psychromonas ingrahamii, Psychromonas ingrahamii (strain 37)	357804	>tr|A1SR41|A1SR41_PSYIN Trk system potassium uptake protein OS=Psychromonas ingrahamii (strain 37) GN=trkH PE=3 SV=1MVTRPLLFITGLVLSKMAIFMYPPMVFAFYNNTLGGVEFLSSIIITHLASALFIFMGKEKEFSRLGVREMFLLTTGVWVLASMFAALPFVLIEHINFSNAFFETMSGITTTGSTVLNNLDTMHPSILLWRSILQWLGGVGFIVMGVAILPFLNVGGMRLFQTESSDWSDKAESKTRSVAIDILLVYIFLSVCCFVGYRLAGMGSFDAINHAMTTISTGGYSTSDRSMGNFSNAAHWNAIIFMFLGGLPFLLLIRAFNQHSLVTLFRDAQVLGFIKVVLFFTLSLTAYLVFSDQFSPANALRLSLFNVVSVVTTTGFGLDDFISWGDFSLVVFWGLMFSGACSGSTSGGIKIFRFQIATSMLKRQLMILIHPRGIFPQRYNNRTVSDDILRSLIAFILAYMGTIAVSTLLLALFGSTAIVALSASITAVSNVGPGLDPSIGPSGNFSALSDPSKWVLAIGMLMGRLEILTVVVLFLPHFWRR
7.1E-45	163	20.4	4E-44	160.4	14.2	1.8	1	R7KKT5_9BURK	Trk system potassium uptake protein	BN692_00111	Sutterella sp. CAG:521	490	cellular organisms, Bacteria, Proteobacteria, Burkholderiales, Sutterellaceae, Sutterella, environmental samples, Sutterella sp. CAG:521	1262977	>tr|R7KKT5|R7KKT5_9BURK Trk system potassium uptake protein OS=Sutterella sp. CAG:521 GN=BN692_00111 PE=3 SV=1MLRTLKRLLFPVLNALGPLLIILAAAQLLPIAIAYRDGENVLSEFFTSAAISLFVGLLFLFSTKRFKRELEPRDGFLLVTLSWFTAAVFGSIPLVLLLPEVPYYYRLFFEAVSCLTTTGATALTNLADLPLSLNYWRCLLSWLGGMGIIVLAVAILPLLGVGGAQLFKVENSNLFKDDRLTPRIADTAKALYGIYILASAACVTAYHWAGMNWDDAVMFMFTTMSLSGITPYDQSIGYFNSPAIEMVAVAFIVFSGFNFSLHFTAWRQRSISAYFTDIEARSWLFVLLIGISIVFGVLTFNHVYPTWEITLRHAVFNVASLFSTTGYTTENYELWPSSLGFLLLIGSLFASCSGSTGGGVKMIRMLIFVKQAILCLHTLLRPRDFLPLRLGKHTISNNLAANVSAFFALHVSVVLVCTLLIMFSGVNLTEAFSTVLACIANTGPGLGSVGPAGNYASCNPMHLWVGSFCMFVGRLELFTVFVIFTRSFWRS
7.2E-45	163	21.5	1E-44	162.3	14.9	1.1	1	F6EL21_AMYSD	Putative cation transporter	AS9A_4251	Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1)	446	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Amycolicicoccus, Amycolicicoccus subflavus, Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1)	443218	>tr|F6EL21|F6EL21_AMYSD Putative cation transporter OS=Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1) GN=AS9A_4251 PE=4 SV=1MVVGGFTGAITVGTVLLMLPLASAKAEWTDPVSALFTATSAVCVTGLVVVDTGSYWSVFGQVVIVCLFQVGGLGIMTVASLLGMLVARRMGMRMELIAHTETKNLRIGDVRRVVIGVVRLSLLIEIVIAVLIGVRYYVTYTDSAAAAAGFAVFHAVSAFNNAGFALQADSVMQFVGDPFILMPLMLGFTLGALGFPVLFEVGRYFRQQVIAAQKGRGRMQHRQWTLHTKITILAHAALAVVGIVAVMGFEWANPATLGQLTLGEKLLGGVFQGLAPRTVGFNSLEVGDMNSATVLITNVLMFIGGGSAGTAGGIKVTTFALLGYVIFAELRGHPTVHVMGRKLAESVQRQALTVALLGVAAVVSATVAILAVTDHETDVVMFEVISAFGTVGLSMGITDDLPVIAHLILVVLMLLGRVGPIMLASALALQERPRRYELPEERPIVG
8.1E-45	163	24.3	2.1E-43	158	16.7	2.2	1	I4Z975_9BACT	Trk-type K+ transport system, membrane component	PrebiDRAFT_1037	Prevotella bivia DSM 20514	485	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella bivia, Prevotella bivia DSM 20514	868129	>tr|I4Z975|I4Z975_9BACT Trk-type K+ transport system, membrane component OS=Prevotella bivia DSM 20514 GN=PrebiDRAFT_1037 PE=4 SV=1MLNIKLISKIIGALLGIEAMLMLVCLVVAIGYHSADIYPFVWSVLITTVAGIVFRLYGVNADNNLSRKDAYFVVSIIWVLFSTFATLPFLISGYLHSFTDAFFEMMSGFTTTGATIIDYPEKFPQGLLFWRSLTHWIGGLGIVFFTVAILPSLVGGSVKVFAAEATGPIKSKLHPRLTTSSKWIWIVYLVLTVTCVLSYKICGMGWFDACNYSMATTATGGFGTSSTSIMGFNKPALDYTAALFCFLSGINFSILYASITGLDIKVLIKNSEIKFYTVVVLSFSCFIAYQLVHVNQYDVEHAIRSALFHVCSIITTTGSFNDDAGLWPHITWVVLATCMVIGGCSGSTSGGVKSIRIVMLFKVIRNEFRQILHPNAVLPLKVNGVNISMKQRVTLVSFIGIYIGIVLISSFIMILIGLDNTNAITITLSSIGNVGPTFGREIGPTQSWAILPDAVKWMCSILMLLGRLELFSVLVLFTPDFWKNN
8.3E-45	163	29.6	3.5E-44	160.5	20.5	1.7	1	R6A8J3_9FIRM	Uncharacterized protein	BN678_01259	Dialister sp. CAG:486	449	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Dialister, environmental samples, Dialister sp. CAG:486	1262870	>tr|R6A8J3|R6A8J3_9FIRM Uncharacterized protein OS=Dialister sp. CAG:486 GN=BN678_01259 PE=4 SV=1MMRKLFNALSQLHRGVLICGGFAAFMLFGALLLMLPISQTGTKEVSFLDALFMSVSISVSVTGMSMFDLKTDFTIFGQLVVLFLMQVGGLGIMTMMAMVGISRGRKIRLQERLLIRDSFNLQTPSGMVMLVRKIILMTLSIEFCAGTILAAYFFTQNGWIGIYQGYWHAVSAFTNCGMDIMGNDVGFAGMAANPLVSTVVCISMFLGGVGFIALDDLLRHHSWSALTLNSKFILVMEMILIPLGVIVYFLLEGNNPATLGHLSTAEKWQSAFFMSISSRMAGFTLFDIHAMNNATGLIIMLFMFIGAAPVSTAGGIRTTTIGLLLLSLWSWIRGRKDVVIFHKRVDPECLVKASNVFTLATVLTFLTAMMVFLLEPASHFDFEDALFEAVSAFSTVGFSMGLTTEWNIPCKIVIMIAMFIGRIGVMTLAVTFAGRPKSQIKYPKENIVIG
9E-45	163	20.3	1.2E-44	162	14.1	1	1	C7MFK8_BRAFD	Trk-type K+ transport system, membrane component	Bfae_24340	Brachybacterium faecium (strain ATCC 43885 / DSM 4810 / NCIB 9860)	471	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Dermabacteraceae, Brachybacterium, Brachybacterium faecium, Brachybacterium faecium (strain ATCC 43885 / DSM 4810 / NCIB 9860)	446465	>tr|C7MFK8|C7MFK8_BRAFD Trk-type K+ transport system, membrane component OS=Brachybacterium faecium (strain ATCC 43885 / DSM 4810 / NCIB 9860) GN=Bfae_24340 PE=4 SV=1MSTPGRRAVPQRSSPLGASRRPPEWRAALSSLAKPTPARLALGVFTLLIGVFTALLSLPAATADGQRTALTDALFTSVSAICVTGLVTVDTGAHWSTFGLTVIMVAIKLGGLGLMTVASLLSLSVMHRLGLAQRVITAQETRAERLAEVGGVLRIILITSTLFEVLTFVALTPYMVITEHGIGQSLFLGLFYAISAFNNAGFFPEAAGTAQYMADPFFTIPIALAVFVGSLGFPVILVVVRKLRTPRKWSVHAKLTLTTTALLFVLGFVGFLALEWSNPATFGDRPFGTKVLGAVFAAVMPRSGGFATIDVGQMTAESRLLTDLLMFIGGGSGSTAGGIRVTTFALLMLAIFAEVRGNPDVEVFGRRIPHGTIRQAIGVLVMSATTVFLAAFLLLRMTPHSLDQTLFEVLSAFGTVGLSTGITAALPAEAKWVLIGCMYVGRLGPMTLGAALAVRSRLRMIQYPYERPIVG

9.8E-45	162	37.9	2.9E-44	160.8	26.3	1.6	1	A1R0E8_BORT9	Potassium uptake protein KtrB	BT0724	Borrelia turicatae (strain 91E135)	441	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Spirochaetales, Borreliaceae, Borrelia, Borrelia turicatae, Borrelia turicatae (strain 91E135)	314724	>tr|A1R0E8|A1R0E8_BORT9 Potassium uptake protein KtrB OS=Borrelia turicatae (strain 91E135) GN=BT0724 PE=4 SV=1MFMLKFEFSDRFFLFSYFILIMFLGSLLLSLPIAWNGEKKLEYIDVLFTSVSAVSITGLVTVKMENFSTFGFIIIMLLIQFGGLGFITIA TFYLLIPKRKLNLTDARIIKQYSLSNIEYNPVKILKSILFVTFLIELIGVLLILVCFRLRGVNISLLEALFTTISAFCNAGFSMHSESIYAWRDV PEAIVVIAILIICGGLGFMVYRDITNTIKYRKKLSLHAKIVFLLSFFLIILGTILFFFSEMHKLKEGYSLGTLIFNSIFYSISTRTAGFNYLDNALI TSRTQMLSLPFMFIGGAPGSTAGGIKITTFFLIILAVIKSQDGNGYIIGSYKVSIDSIRFALLFFVRAVFILCFSFFVLLAAESGGKWRVIDL GYEVFSAFGTVGLSVGVTQDLSFLGKVIIIFTMFAGRIGLFSMAIFVSRRSRFEEFTRPRQDILVG
1.2E-44	162	20.6	2.6E-42	154.4	14.1	2.1	1	A0A0E3S692_9EURY	Potassium uptake protein TrkH	MSLAZ_1237	Methanosarcina lacustris Z-7289	499	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina lacustris, Methanosarcina lacustris Z-7289	1434111	>tr|A0A0E3S692|A0A0E3S692_9EURY Potassium uptake protein TrkH OS=Methanosarcina lacustris Z-7289 GN=MSLAZ_1237 PE=4 SV=1MYELVSPVNPLAVLRYVGHLLLVFSAVLLVPMLAAFVLGETTAAIIYGSSALITAGTGVILQKVLPDFELEIKEALILAAITFPLCSLVS AVPMALFTGMPFLDAFFECVSGLTTTGLSLAPLSPTKLFFFTRSWLQWVGGIGIIVLVLGILIRPGTTAFRLYRVNFGESRIRPSVIATAR TLGTVYFVLTLLSLTLLLLSGMPFYDAVCHALCAISTGGFSTQTASIGAYKGFLIPFLITVSCIMGAISFSLYPEVLKDPGALIRDPQVRYM LGLSVLGTALFALTLSGGAGWLELLHTLPDAAFQVVSALTGTGFSTIDIAPLSDASKSFLSAIMCIGGSIGSTTGGIKLFRLIVIVQLIRLVF YRFFLPREAITPLKVKSQVLDSEEVYHIMTYVLLYSAVLVLSAFIFMLYGINSADAIFETSSALATAGLSTGVTAPGMPSLLKLVLCADML LGRVEIIPLLILLLPRTWLERRSKTEENRVKAEDKRVQEDTA
1.2E-44	162	31.2	1.2E-44	162.1	21.7	2	1	R5PFT9_9PORP	TrkH family potassium uptake protein	BN783_02975	Odoribacter sp. CAG:788	602	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter sp. CAG:788	1262909	>tr|R5PFT9|R5PFT9_9PORP TrkH family potassium uptake protein OS=Odoribacter sp. CAG:788 GN=BN783_02975 PE=4 SV=1MRLAELKYKTRLFLRTGRAIVRISATVISFIASFCTLCLLIYEIGFQEDPETKYYILETYKILLRIFFYTALGRILSDIKGFRREKAFWLD SIILAFILLTVILDSRPAAHLSAFMHHAITIMTYILLSVVSLIQLSKQIVTTLQRNLKPEMMFAYSFLFIILTGTFLLLLPNAHHGHLQFIDALFT STSAVCVTGLTVVETSSTFTFTGLIILATLIQIGGIGVMTFTSFFAMSFFCQVSFRDQLSLKNILNENSLSDIFRTLFYILLTTFIIETIGAYLI YDQIRSVPATEIPDKLFFAVFHSVSGFCNAGFSTLPGNLYDPTVRHLYGLQCWIALLVILGGIGFPILFNFGRLFNYHFRNAVNRIKRNP STYNRQLHIISLTTRIVIPMTLILVIGGTCLFLGLEYNNTLKDLPFSGKLAISFMSAVTPRTAGFSSIDMASLLPPTIFVTMLLMWIGASPMS TGGGIKTTTFTIAIKNIFSVIRNKNNVEIARRQIPSENVRRAHAIILLSVLWIGIATLLLLLTENHVSVTEATFEVISAISTVGLTLGLTPELSIA GKIIISLTMFVGRVGLITLLTGIARQQLSQPYRYPEERVIL
1.3E-44	162	2.1	4.5E-42	153.6	0.1	2.8	2	A6QRR8_AJECN	Putative uncharacterized protein	HCAG_00074	Ajellomyces capsulatus (strain NAm1 / WU24) (Darling's disease fungus) (Histoplasma capsulatum)	526	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain NAm1 / WU24) (Darling's disease fungus) (Histoplasma capsulatum)	339724	>tr|A6QRR8|A6QRR8_AJECN Putative uncharacterized protein OS=Ajellomyces capsulatus (strain NAm1 / WU24) GN=HCAG_00074 PE=4 SV=1MWKPPLNFITIHYAYIVTLSIFSLVVLYPYGNLKAIDAYFFGASSCTESGLNTYDVKDLKTYQQLFIYVIPIISHHAFINIAVVLVRLH WFRKRLDEIGNMAHYRFGISPSQAPTQVRHRHDVEAKAYKPLENGKKYTSNDQHITDATALNVISTGEHTNETDKPQAQTAEPTGRS ISFAADVRGYDKSKALYVPPPQERDRGRPMVEIDEIFSDDDEITKTNDSNYTSSAFTSLARYVCFVGSYIRIRNIGSIYKSALSPLCGVP KTSPLKEQLNFLLKHPRRCYTHLFPSGTTWALFAVLFVMNFVDIILMITLDLHNPAVNDLPWGKRILASLFQAASTRHTGTASFNLANV NPAVQVSILVMMYIAIFPIALSTRASNTYEQRALGIYPQDRELDEYHGKTYILAHIKNQLTFDLCKYSGFFFPSLFPSRNDISPFLTKITQV ETSASVSVSPASTHPYPEKFSAFGKLIMCAMMLRGRHRGLPSQLDRAVMLPSDRLVDGDEKENTIEIRNSTKIKRHHTH
1.4E-44	162	32.3	2.6E-44	161	22.4	1.3	1	R6MBL0_9BACE	Cation transport protein	BN507_00518	Bacteroides clarus CAG:160	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides clarus CAG:160	1263039	>tr|R6MBL0|R6MBL0_9BACE Cation transport protein OS=Bacteroides clarus CAG:160 GN=BN507_00518 PE=4 SV=1MKIYHKFLLYQNKWIHPYIRVALGVMTTLTYLASILLIVGLVYEHGFTISVAEAHQLQRLYHGVWIVFLSDISLRIALEYKDTRQTFS KLTWILTFLLYLTLVPVVFHRPEVEGAIQAVWDFLNGRMYHLALLLMLSFLNLSYGLVRLLGRRTNPSLILAVSFLIIILGTGLLMLPRSTV AGISWVDSLFISTSAVCVTGLTSVDVASTFTTTGFVIIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLNSLLSTLVYIL GFTLAIEGAGMLAIWSDIHGTMGMDIHEELAFSAFHSISAFCNAGFSTLPGNLGNPLLMSGHNPFYIYISLLIILGGIGFPILVNFKDIILYHI RRFWRFLRTWEWDGRRFYHLYNLNTRIVLIVTFLLLVVGTAGIALFEWNASFAGMSVADKWTQAFFNASCPRTAGFSSVDLAGLSV QTLLIYLILMWIGGGSQSTAGGIKVNAFAVVVLNLVAVLRGTERVEVFGRELSYDSIRRSNATVVMSFGVLFVFIFIISILEPNLSLLTVTF ECVSAISTVGSSLNATPLLGSDSKLLVALLMFVGRVGLITLMLGIIKQKKNTKYQYPSGQIIIN
1.7E-44	162	42.5	3.6E-44	160.5	29.5	1.4	1	L7WFF4_NONDD	Na+-transporting ATP synthase	DDD_2506	Nonlabens dokdonensis (strain DSM 17205 / KCTC 12402 / DSW-6) (Donghaeana dokdonensis)	451	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Nonlabens, Nonlabens dokdonensis, Nonlabens dokdonensis (strain DSM 17205 / KCTC 12402 / DSW-6) (Donghaeana dokdonensis)	592029	>tr|L7WFF4|L7WFF4_NONDD Na+-transporting ATP synthase OS=Nonlabens dokdonensis (strain DSM 17205 / KCTC 12402 / DSW-6) GN=DDD_2506 PE=4 SV=1MKTYFKKFNLRYRKFKLGLSPQQNLFYGFLTYVLVGFILLSLPWLQKTDTSLIDNLFIATSAVSTTGLVTVSVFDSYNFAGQFVVM SLFQVGGIGYLTFTTFMLLSTTRRITHWHKRLLNTEFTLPATIKIKDFLKSVVIFTIVMETIGAILFFIAFYSDGMPVGEAIWNAVFHSVSA FCTAGFSLFNSGFTEYVDDGFVNFIIAFLAIAGSLGFIVVTDLVMWIKDRTHKLSFTSKIIFIGFAFLLSTGFLFMYLFEPTITALSGSERLY AAFFQTMSAMTTVGFNTVDFGAYSLPIILVTIFLMYVGASPSGTAGGIKITTLTAVFSIMKSRLQGSKNITFLGRKIPFERLYIATSSFIFYT SLIFLFTLAMTFTDDFGLEKTLFEVSSALGTVGLSMGITGDLSIWGKSIIVLIMFIGRLGVLTFGLAIWSKSTIQDNVPILEDDIAV
1.8E-44	162	32	7E-25	96.9	8.5	2.1	2	A6LMF8_THEM4	Cation transporter	Tmel_1260	Thermosipho melanesiensis (strain DSM 12029 / CIP 104789 / BI429)	493	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Fervidobacteriaceae, Thermosipho, Thermosipho melanesiensis, Thermosipho melanesiensis (strain DSM 12029 / CIP 104789 / BI429)	391009	>tr|A6LMF8|A6LMF8_THEM4 Cation transporter OS=Thermosipho melanesiensis (strain DSM 12029 / CIP 104789 / BI429) GN=Tmel_1260 PE=4 SV=1MPKKKEQYKVIIHNLGLILMYYTLLLLFPTFLVFFYPNEAKNAFAFIFAAILSFIIGYFLFKLSNIKSSQTVTVREGAVIVLFTWLSVVLI GAIPFMIIEHLTFSQAVFESTSGFTTTGLTMFTDVTTVSKLILVWRSFMQFIGGAGFALIMMGSVIGPKGFGLYHAEGRVDNIAPNIKRS ARIISFIYVTYAIIGTILLDVFGMPLFDAFNHSLTALATGGFSVRNGSIGEYNNLSLEIIVIILMFLGGTGFGVHYTLWKGNFKAFIKNGEPW LMLSTVFITSTLISINIGIKGIFKNNFSDGFRQAIFQTSSAITGTGFSTVDLTNPIWISFGLAMFILTSLMIAGGGMDSTAGGLKQYRIWITIKV VLHSIKEFLLPSKSVTKIFAWKGQNKNTITNDDVKEIFLIFSMYLFTFFLGSIILSAYGYDLTSSMFEFASAMNGVGLSVGITKPTMPLGA MWTLTVAMFTGRLEFLVIIYAIAKLINDLKEKIKK
1.8E-44	162	24.5	3.6E-24	94.5	10.5	2.1	2	R7FC14_9FIRM	H(+)-transporting two-sector ATPase	BN611_00117	Ruminococcus sp. CAG:330	432	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:330	1262954	>tr|R7FC14|R7FC14_9FIRM H(+)-transporting two-sector ATPase OS=Ruminococcus sp. CAG:330 GN=BN611_00117 PE=4 SV=1MKWNKTLTPGRVIILCFAVLIAFGAVLLALPIAYKNRTPLSPLDVCFTSFSAVCTVGLTVAPTYETFSAFGQGVLLFLIQVGGVGIT SIGVGVMLLAGKRIGLRERILIKETLNYPTFGGVVKLLRSLLLVTFGIEGVGAICCFPIFYADFPLGRAIWLSVFHSVSTFNHAGFDIIGDA GMQEYTHHASLLVITALLTIFGGLGFFVIRDVARNRRFRKFSLHTKVVLTMTAILLVGGTLLMKLSEGELRWLQAFFYSAISRTSGFSIY SLAAFSNASLFMVFLMFIGASTGSTSGGIKDTTLFVCVWSAIAYTRNRQPTIFHRRISQTVRDKAVMILLMGLGVVMVSTFLMSVFEP DVSLIRLLFEVVSAFSTTGLSTDLTSQLCSGSKIVLMLTMYIGRLGPLTVATLWMMQGRNKNAIQRPEGTISVG
1.9E-44	161	26.3	5.2E-22	87.4	6.1	2.2	2	R7JJF7_9BACT	Cation transport protein	BN752_00393	Alistipes putredinis CAG:67	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes putredinis CAG:67	1263036	>tr|R7JJF7|R7JJF7_9BACT Cation transport protein OS=Alistipes putredinis CAG:67 GN=BN752_00393 PE=4 SV=1MRVNVILRYVGMIMLLLAFFMFVSAGISYVNYMDSAFYPLLLSALLTALLGGFPLIFVEKQDRITNKEGFCIVVGSWLLACVVGMF PYLIWGGEFSVINAWFETVSGFTTTGSSILQNVEALPRGLQFWRMSSTWVGGMGVVMFALVILPALGTSKMMLSSVEMSTLARDNY RYRAQMVVQILLFVYVGLTIFFTFMLKFAGMNWFDAVCHSMSACATSGFGTKNTSVAFYDSAMIDTVLIFAMGISGIHFGLIYATVTGK RNNIFRSEVTLFYLGMLILGSLLIALSLYIADIYPTFWSSLRFASFQFVSVTSTSGFATADSNLWTPFAIILLILGSLICACAGSTSGGMKA NRALMALKMLYIRVKQQQHPNAVIRLKMDGVIQEAGVLHTVSLFIVAYLLLILGTILCTLFGVDLMTSFSGCVASIGNVGPGFGGVNSM ANYGDLPAIVKFIFTALMLLGRLEIFGLLQFLLIRWWK

1.9E-44	161	29.9	5E-42	153.4	20.7	2.2	1	R5QM S3_9P ROT	Trk system potassium uptake protein	BN682_01518	Proteobacteria bacterium CAG:495	478	cellular organisms, Bacteria, Proteobacteria, environmental samples, Proteobacteria bacterium CAG:495	1262987	>tr|R5QM S3|R5QM S3_9PROT Trk system potassium uptake protein OS=Proteobacteria bacterium CAG:495 GN=BN682_01518 PE=3 SV=1MWQPVLMISGYFISVLGLAMLFPAALDIYYSHAKWSLFITSSIVSVFIGLSLFLANNSKIKNISLQQAYLLTVISWFSVTLLAAIPFMLYGISGADAVFEAASGISTTGATVFADIEALPRSFLLWRAILNGLGGVGIVIFAIAMLPFLGIGGMQIFQRENSDVNEKFMPKISYIAKRIILVYVILIMACLAALHLAGMNWFDALCHSLATVATGGLSTKNASVGYFNSAAIDWIITLFMILGAIPLTFYHSLLATRDIHSLRSSQVAMFLKVLAVYIVFMACWLTYNGTYNFLTALRYAAFNVTSIVTSTGFVSTDLYLLWGPFAATAFVVFALTGGCTGSTSGSIKIFRWQVVFAQLKRAFITTTEPNRMVPLKIGHSNISAQVAGSIFIFLTAFSLSTIVLTLCIALTGIDFTTAFSGVVACLSNSGPGISQLIGPSGNYSSLPETAKWLLAFTMLLGRLEVMTILVIFTKSFWRQ
2.1E-44	161	26.1	1.3E-43	158.7	18.1	1.8	1	T0VBJ9_9STRE	Potassium uptake protein TrkH	HSISM1_1882	Streptococcus sp. HSISM1	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus sp. HSISM1	1316408	>tr|T0VBJ9|T0VBJ9_9STRE Potassium uptake protein TrkH OS=Streptococcus sp. HSISM1 GN=HSISM1_1882 PE=4 SV=1MNRSMIRYLLSKLLLIEAGLLIVPLVVAAIYREPAKVFVSIGATMAILLAFGLLGSFHKPKDFHIYAKEGVLIVALCWILWSFFGALPFVFSGQIPNIIDAFFEVSSGFTTTGATILDDVGVLSHSLLFWRSFTHLIGGMGVLVFALAIMDNNKNSHLEVMKAEVPGPVFGKVVSKLKNTAQILYFLYLGLFFLFVILYFLAGMPLYDSFVIAMGTAGTGGFTVFNDGIAHYNSSLITYLVSIGVLVFGVNFNLYYFLMIRKFKAFFKDEELRTYITIVILSSVLIAYNCLHLYANVAKSFEISFFQVSNIITTTGFGYGTTEKWPLFSQFILLMLMVIGGSAGSTAGGLKVIRCLTLWRIAKNQVLSTLSPNRVLTLHVNDTVLDKDTQHQILKYFTIYSFITIGLLFVVSLDNNNFMTVVSAVFSCFNNIGPMIGTGQTFSIFSPISKLLLSLAMIAGRLEIYPMILLFLPKTWSKR
2.3E-44	161	30.2	7.2E-44	159.5	20.9	1.7	1	E8JY73_9STRE	Cation transport protein (EC 3.6.3.14)	ktrB HMPREF9423_0239	Streptococcus infantis ATCC 700779	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus infantis, Streptococcus infantis ATCC 700779	889204	>tr|E8JY73|E8JY73_9STRE Cation transport protein OS=Streptococcus infantis ATCC 700779 GN=ktrB PE=4 SV=1MNRSMVRFLLAKLLLIEAGLLLVPVSIALYYRESSQVFTALFSTIGILVVLGLLGIISKPKKQRIYAKEGVLIVALCWILWSFFGALPFVFSGQIPNMIDAFFEISSGFTTTGATILNDVSVLSRSLLFWRSFTHLIGGMGVLVFALAIMDNAKNSHLEVMKAEVPGPVFGKVVSKLKNTAQILYILYLAMFALFVIIYYLAGMPLYDSFVIAMGTAGTGGFTVYNDGIAHYHSSLITYLTSVGVLMFGVNFNLYYYLMLRRVKEFFFDEELRAYLLIVVVSTGLITLNLTLHLYSGVSQSFEMAFFQVSNIITTTGFGYGNITNWPLFSQYILLMLMAIGGSAGSTAGGLKVMRGVILAKIAKNQFLSTISPHRVLTLHVNQTVIDKDTQHKILKYFVVYVMILLSLMFIISLDADNLMIVTSAVFSCFNNIGPILGTTASFSIFSPFSKLLLSFAMIAGRLEIYPIILLFMKRTWSKR
2.3E-44	161	41.9	3.1E-44	160.7	29.1	1.1	1	A0A0F9XX78_9BACT	Potassium uptake protein, TrkH family	SZ59_C0003G0068	candidate division TM6 bacterium GW2011_GWF2_28_16	450	cellular organisms, Bacteria, unclassified Bacteria, candidate division TM6, unclassified candidate division TM6, candidate division TM6 bacterium GW2011_GWF2_28_16	1619077	>tr|A0A0F9XX78|A0A0F9XX78_9BACT Potassium uptake protein, TrkH family OS=candidate division TM6 bacterium GW2011_GWF2_28_16 GN=SZ59_C0003G0068 PE=4 SV=1MSALRILDISPARILIGSFLFVILAGTFLLSLPVSRLVDMHLIDLFFTATTSTCVTGLFTVPMSYFSFFGQCVILALIQIGGLGLMTLSIFLVSLVLNLSLTTKFLAGQILDFAFSGKLKTFLKTIIGFTIFTEIIGALILYKSFIKILPRDKAIFYSIFHSVSAFCNSGASLFEPGISNLAQDSLSLLTMAVLIFLGGIGFIVWYEAVSNLVNYIKNWWNEEPKKLTMSLHTKIVLITSSTLIFLGSLLFFILERTNTLAGLSTWHQIVNSIFISVTARTAGFENVDMSNLGLPILLILIILMFIGASSSSTGGGVKVTTFTVFVATIAATIRGKNNVEIFGRTISPEQIFKTTAIIALSLSFVLATTFILLITDPEFSFMQILFEAVSAFATVGLSTGITPYFSIFGKIVLMLAMLLGRVGALTLVLALRKGQETQLYKYPEERVLLG
2.5E-44	161	18.4	4.7E-44	160.1	12.8	1.3	1	C5CCT4_MICLC	Trk-type K+ transport system, membrane component	Mlut_18030	Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) (Micrococcus lysodeikticus)	491	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Micrococcus, Micrococcus luteus (Micrococcus lysodeikticus), Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) (Micrococcus lysodeikticus)	465515	>tr|C5CCT4|C5CCT4_MICLC Trk-type K+ transport system, membrane component OS=Micrococcus luteus (strain ATCC 4698 / DSM 20030 / JCM 1464 / NBRC 3333 / NCIMB 9278 / NCTC 2665 / VKM Ac-2230) GN=Mlut_18030 PE=4 SV=1MAGPRPTPHAHRRGGVRRPGGLPRPGQASTLESSTDLRTALRRSGRAVSSVVGGSPARAALSAFALMALVFTGLLALPWAAADGHATPLHDAMFTAVSAFSVTGLTTVNTAVHWSPAGQVIILVAIQIGGLGILSMASLLTLAVSRHLGLRSKLATQQAGMTSGSLGEVGQLLRVVVLTVLTAEAALALVLVPRFAAISGSWLTGLWHGVFYSVVSAFNNAGFTLHVDGLPEIMHDPVIITVLGVGVFLGALGFPVVMVLLEKGWRFFQWNLHTKLTVEVTLTLLVLGAVALFFFEADNPATQAGMGFWQRVGHSLFGSVMTRSGGFAIDDTNAHQPESLLLMDALMFVGGGSASTAGGIKVTTLAIMFLAIVAEARGDREVTAHGRTIAPESLRVAIAVLALGATLVLVATLALVHITDESIQRPLFEVISAFGTCGLSVGVSAESPPTGKYVLTAMMFAGRVGTITFAAALALRQRRVLYRYPVERPVIG
3.1E-44	161	28.3	2E-43	158	19.3	2.1	1	D3HB04_STRM6	Potassium uptake protein	trkG2smi_1814	Streptococcus mitis (strain B6)	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus mitis, Streptococcus mitis (strain B6)	365659	>tr|D3HB04|D3HB04_STRM6 Potassium uptake protein OS=Streptococcus mitis (strain B6) GN=trkG2 PE=4 SV=1MNKSMIRYLLSKLLLIEAALLLVPVAVAIYYRESIQVFTALFTTIGILVLLGGSGILQKPKNQRIYAKEGILIVALCWILWSFFGGLPFVFAGQIPSVIDAFFEISSGFTTTGATILNDVSVLSRSLLFWRSFTHLIGGMGVLVFALAIMDNAKNSHLEVMKAEVPGPVFGKVVSKLKNTAQILYLLYLALFSLFVIIYYLAGMPLFDSFVIAMGTAGTGGFTVYNDGIAHYGSSLITYLVSIGVLVFGVNFNLYYYLMLRRIKAFFGDEELRAYLVIVLLSTGLISLNTLYLYPGFSKSFEMAFFQVSNIITTTGFGYGDITNWPLFSQFILLFLMAIGGSAGSTAGGLKVIRGLILSKIAKNQILSILSPHRVLTLHVNKTVIDKDTQHKILKYFVIYAMILLALIFIVSLDSNDFLVVTSAVFSCFNNIGPILGTTSSFSIFSPISKILLSFAMIAGRLEIYPILLLFMKRTWSKR
3.2E-44	161	16.2	8.2E-42	152.7	11.3	2.1	1	Q2RVB0_RHORT	Trk system potassium uptake protein	Rru_A1134	Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	498	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum rubrum, Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	269796	>tr|Q2RVB0|Q2RVB0_RHORT Trk system potassium uptake protein OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1) GN=Rru_A1134 PE=3 SV=1MSLRGSQLGTSRGLMLGGIDLAPVLMVLGLLLSGLGLSMLAPALVDLVVENRDWRAFLGSSVITLFCGMMLTLANWRMPLRFNIRQGFLMTALAWLTMSLFGSMPFMLATTGLDFAGAFFESVSGLTTTGATVISGLEHQPPGILFWRCLLHWIGGIGIIGMAIALLPALRVGGMQLFRTESSDTSEKGMNRIGELGLAITAVYLTLTVVIALGYIAVGMSVFDAICHAFGTVSTGGFSNWDTSLGHLDAAGLWMSTVGMMLGAMPFVLYVQAVARGRPMDVVRDPQVQALTGFLVACWLVMALWQSLENGRPFLDALTASAFNITSVVTTTGYASEDYTLWGGFPQLFFFMITFAGGCTGSTSGGIKMFRYQVAYKVLSANIRRRYMPNAVIVSTYGGRAIDEDVAVSVVLFFFATGATTAIIALALTMVGLDWVTALTGTAAAIANVGPGLGTIVGPAGNYATLPDSAKWLLSLAMLMGRLEFFTLLVLFSRDFWKS
3.5E-44	161	0.2	8.3E-23	90	0.1	2	2	K2SIU3_MACPH	Cation transporter	MPH_00250	Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	246	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Macrophomina, Macrophomina phaseolina, Macrophomina phaseolina (strain MS6) (Charcoal rot fungus)	1126212	>tr|K2SIU3|K2SIU3_MACPH Cation transporter OS=Macrophomina phaseolina (strain MS6) GN=MPH_00250 PE=4 SV=1MVPSRGFYSAQSMGSNLGFTLTLDSMITSQDATLPLFVMSFLAYAGNKLYPCLSRLVIWTMAKPAPRHSVMQEPLNFLLEHPRRCYTLLFPSRTTWILFGIIFVVNFIDTPLVLVLGLQNPAVNNLPVQPAAHDVHLCLPVATTVRASNTYEDRSLGMYAPDPEVDEITPGNTTSYLLNHLPNQLGFDLWSISLGILCITIAEADRIIDQADSVFQVFPVFFEVVSAYGNIGLSLGYHTVLTSLTG
3.7E-44	160	10.1	1.5E-43	158.4	7	1.7	1	Q2S0A6_SALRD	TrkH potassium uptake protein	trkH2SRU_2271	Salinibacter ruber (strain DSM 13855 / M31)	499	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidetes Order II. Incertae sedis, Rhodothermaceae, Salinibacter, Salinibacter ruber, Salinibacter ruber (strain DSM 13855 / M31)	309807	>tr|Q2S0A6|Q2S0A6_SALRD TrkH potassium uptake protein OS=Salinibacter ruber (strain DSM 13855 / M31) GN=trkH2 PE=4 SV=1MIAARRLRRVSSVLGPVLKWFSAVFSVPIATALYHGTSVVPFLVPLGLSFGAGALAEWIGGDSELTVQDGFLLVTLTWVLVSLLGSVPYLLSGTGSFATPINAIFESFSGFSATGSTILLDISIEKHGAALMLWRQLTQWIAGMGILALAVAVLPRLSAGGAQFLDAEVPGPRLERLTPHIAETARRLWLLYIGCSVVLLVLLLGVHYAGLAPRMTPYQALAHVFTTIPSGGFSPQARSIEAFGPAVQWILVPFMFVAAMNFTLLWQAIVSTPTAPARDTEFRVYLSVFAVGSLLVSAMLWGNGQFAGLEETLRHGTFQTATLLTTTGYASTDFAVWSEEVLVVLLLLMFASGCVGSTSGGLKLMRWTVGFKVIGRELFQMIHPSSVRPMWLGRRTVKEPVVRGILIVILTYLLLVVGGTGFIAVDAHRVGIDLSISEALSGTLVVLGNIGPGFGAVGPMGGFEALPVPTKVFMCLLMVAGRLEVMTFLVVLSPSYWRG

4.3E-44	160	21.8	7.2E-43	156.2	15.1	2	1	R6V2V6_9FIRM	Uncharacterized protein	BN746_00933	Erysipelotrichaceae bacterium CAG:64	500	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, environmental samples, Erysipelotrichaceae bacterium CAG:64	1262981	>tr|R6V2V6|R6V2V6_9FIRM Uncharacterized protein OS=Erysipelotrichaceae bacterium CAG:64 GN=BN746_00933 PE=4 SV=1MKERLLLKQHEVTGFELMLGYIGVLLMLIGGIVLLPLLTLLWYPEEAYEAKYFILPGIGSILLGYLLFYNIRGRETGRLQRNQDAVIVVTCWILAIMICALPFLLSGNYTFTQAVFETTSAWSTTGLSVVDVEHTSHLFLMHRSTILFFGGIGLVLVMLSVLSDTYGMRLYAAEGHNDHLLPNLLKSARIILTMYLCYILSGVALYCLFGMPLFDALIHSIGALSTGGFSSHAQSIGYYDNIWIEMITIVLMLLGNINFLAHLFLIRGKLRNFFQYCEIRFSFLVIALAVPVLGFLLCAGMGTALPHALRTALFQVVSALTTTGFQTVDTFVTLPSAALLLLIVLQLIGGGIGSTAGGIKQYRIYALCKGIWWNIESQLRCGNVIRSHKINRVDKKEAISPTELSQMGLYVVLYFCLFLLGSFILCCYGHPIAYSMFEFSSALGTVGLSAGIMTCDAPSLVLWTGTIGMFIGRLEIYVVLLAAARLGKDIRSRVRRRKTA														

6.7E-44	160	22.1	5.6E-43	156.6	15.3	1.9	1	E0QMK3_9ACTO	Cation transport protein (EC 3.6.3.14)	trkB HMPREF0580_0117	Mobiluncus mulieris ATCC 35239	470	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Mobiluncus, Mobiluncus mulieris, Mobiluncus mulieris ATCC 35239	871571	>tr|E0QMK3|E0QMK3_9ACTO Cation transport protein OS=Mobiluncus mulieris ATCC 35239 GN=trkB PE=4 SV=1MGKPEAVSRVRQDKVRFWQTLRETTQKWWSDFARKKPARFTLLVFFCIIALVTGLLMLPISTADSRPASFVDALFNGTSAVCVTGLTTVPTDSYWSTFGLVVLMFGIKIGGLGVMTLASILSLAVSRHIGLSARLLAAGENNSKLGEVGSLIKMVVLVSITVELSMAVLFFPQFMAMKYGIGQSAWYAIFMAISVFNNCGMVVIPGGMQQFASNFGIFFPLTVGAAVGALGFPVALDVTRNWKHPRKFSLHTKLTLTTYGALTVVGGAIVAILEWDNPATFGRLEPMGKFLATVLHGVNARSLGISNVDFSEVTQATWFIDDIMMFIGGGSASTGGGIKVTTFAVMVLAILAEIRGDRDIEVFGRRIGPSTVRLAVAVVALGAVIVGAATTIMLEITGLPLSEVLLEVISAFGTVGLSTGITDNLPDSAKILLSLLMFTGRLGTMTFGAALAMRTRRKVIRFPEETPSIG
6.8E-44	160	12.2	2.9E-22	88.2	1.3	2.2	2	Q9YE55_AERPE	Trk system potassium uptake protein TrkH	trkH APE_0715.1	Aeropyrum pernix (strain ATCC 700893 / DSM 11879 / JCM 9820 / NBRC 100138 / K1)	503	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Aeropyrum, Aeropyrum pernix, Aeropyrum pernix (strain ATCC 700893 / DSM 11879 / JCM 9820 / NBRC 100138 / K1)	272557	>tr|Q9YE55|Q9YE55_AERPE Trk system potassium uptake protein TrkH OS=Aeropyrum pernix (strain ATCC 700893 / DSM 11879 / JCM 9820 / NBRC 100138 / K1) GN=trkH PE=4 SV=2MPVRRRRQTLFTALQYLGLILMVTSLPFTASGLVGLLLWSGRSMAEFRVASELLASGVVLVLVGLLLSRAPGGLLGKGDAVFITVATWLSVPLFSAALMSEILDIPYVDALLETVAGWTTTGLSILTGAESSSGGYVPSVDEIPESVKLWRSMLQWVGGVGIVVFTVAFLARPGISAAALYIAEGRFERLEASLKASAIRMTLVYMVYTLLGALIIYLSGMSLSDAIQHSMTAISTAGFSTHADSVGFYKGDYAVYASTLLVSFLGALSFVDLDNIMRLRLGRVLRSVEFRVIAGLTALSAAAAAAVWYIDPVMRSSYTLADTIYNSVSGYITVGFSTASLEGASDSYKLLIAALGLIGGSAFSTAGGIKVLRLAIALKTLDVETTRILKPSSYVPKNLIGGRRLTEDMVKRSLAVIIAFATVEILLGLTAVALYSDIYPTVDIIFDVTSALANIGLSTGVTSPEAPTGLKVILIAGMLLGRLEILPYIVAAKYLVESVRART
7.6E-44	159	32.7	4.4E-42	153.6	22.7	2.1	1	R6SUP0_9BACE	Uncharacterized protein	BN777_01532	Bacteroides sp. CAG:770	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:770	1262751	>tr|R6SUP0|R6SUP0_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:770 GN=BN777_01532 PE=4 SV=1MNLKVISRNVGFALLASAFFMFLSILVSIGNGNDSALAALLISFTLTFTVGIFPFIFVRKPLTISLKDGYMIIFLSWMLSFIFGMLPYVLWGGPFSVINALFETVSGYTTTGGTILTDVEVLPDSLLFWRSSTHFIGGLGVVVFLLLIIPSSSPMRLRLTNMEVSSLSREGYKSRTNKTVWIFAAVYLGLAVVSFLSYWAAGMSAFDAINHAFSVISTGGFSTKNLSIASFDSNLINILTIIFMFFSSVHFGLIYMVFATRSLRPLNNPVLKFYVLTILIASLLVALSLKMSSAGFTWGDSFMTGIFQAVSFISTTGFAISDNNTWPLFACFITVLISIPCGMAGSTTGGVKSDRMFLIFKTIGQQIKNSIHPSSINQVHVGNHIMGSNEIYPHFVYFGLYFITIAASIVLTVLSGMDIQNAFASSVSFLSNVGPALEAQGTLGNYNAVPVFAKVVFIIDMFMGRVEIYPILAVVMMIFTGKKK
7.6E-44	159	20.7	4.1E-25	97.6	6.8	2	2	R6WLC5_9FIRM	H(/)-transporting two-sector ATPase	BN636_00383	Ruminococcus sp. CAG:382	428	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:382	1262957	>tr|R6WLC5|R6WLC5_9FIRM H(/)-transporting two-sector ATPase OS=Ruminococcus sp. CAG:382 GN=BN636_00383 PE=4 SV=1MRRLTPARIIALGFALVILFGSLLLSLPFSIRDGVSLSYADALYTATSAVCVTGLVVVDIADTFTLFGQMVVLLLMQVGGLGVAAVGTGIILAIGRKVDLKGRTLIREAMNLGSDKGTVGFLRYVLLTTLIFEIAGAVLTYPVFAGDYPPLRALFISIFHSVAAFNNSGFDVLGGMRSLTPYSGNIMLNIVTMILITAGGIGFFVIRELWEKRFRWRRLSMHTRVVITVSAVLTFGGALLLCLTEDIPFLGALFSSVSARTAGFSSYPLGGFSNAGLIVMGTLMFVGASPGSTGGGVKTTTLFALVQGVKASATNRGEKAFHYSLPKDAFRKAVIIVAIGAFVVLTGTYLLSVFDPGVSFRDSFFEIVSAFGTVGLSTGITSGLSLPSKILSILIMYTGRLGPMTIATLWYFSGGERVSYPTGNISIG
9.3E-44	159	20.6	1.1E-41	152.3	14.3	2	1	I2F5D7_9BACT	Trk-type K+ transport system, membrane component	Theba_1454	Mesotoga prima MesG1.Ag.4.2	494	cellular organisms, Bacteria, Thermotogae, Thermotogae, Kosmotogales, Kosmotogaceae, Mesotoga, Mesotoga prima, Mesotoga prima MesG1.Ag.4.2	660470	>tr|I2F5D7|I2F5D7_9BACT Trk-type K+ transport system, membrane component OS=Mesotoga prima MesG1.Ag.4.2 GN=Theba_1454 PE=4 SV=1MFLNLLKQRYRLVFGYLGNLFVFFPIVLLIPLLYCIWNPEDFLQSLAFVEAASISFVIGMTLKLTMKVRPGSPISVQEGAIVVLFSWVMAIILSALPFIFAGYFNFTQAIFESTSGWTTTGLTLADVETIPGTFLLWRSMMQYLGGAGIAIIMMSAILGPAGLGLYKAEGRMDNLVPNIKSSTRTITTIYGSYAVAGIIMYRIAGMNLFDAINHSLTALATGGFSTKAGSIAEFNSVSVEIVTIVLMLLGATGFGIHYTIWKRNFRAFWKNGEPKLMFVILAIFTPLLMTGTLSIFYSSGAEQFRHSVFQAVSALTGTGFSTVDLVPWNHFGIYLVILLMIFGGDLDSTSGGLKQYRLFALLKILWLEIRRYFLPKDAILKEEIWKGETKRYIDNSLVKEILLVFSLYFLTYAIGTGVLMAYGHSMAFSAFEYASALSTVGLSVGITAPNAPAGLIWAETIGMFLGRLEFLVVIYAITKLMRDGRILLRRRRNA
1.4E-43	159	33.9	1.3E-42	155.4	21.8	2.3	1	E3DRW5_HALPG	Cation transporter	Hprae_0935	Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL)	496	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium praevalens, Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL)	572479	>tr|E3DRW5|E3DRW5_HALPG Cation transporter OS=Halanaerobium praevalens (strain ATCC 33744 / DSM 2228 / GSL) GN=Hprae_0935 PE=4 SV=1MIKSTKYNTILYFLSILAFIMAFIIVAPLILAFINQAGTVIYKAFYYTIIISLLTGTLLKLPTDANNIYIDLTTAMLLCSLGWLIVSILGAIPFMIGIEKSFIDSLFEAVSGFTTTGITVFTGLDKMPQSIIFWRSLMQLLGGLGILTFFLLISTRAQGETWQLFSAESHKINVSRPVPNVFKTVKILWIIYLGFMFLETVILISLGLSPFDAITHSFTTLSTGGFSSYDASIAYFANSGYQNYILIEYVITFFMFLGGVNFLLHFRFFTKDFESIKKNSEFKTFIKLILYSTIFISFLIISLNTAGNFKLEAVFRKTIFQVTSIITTTGFGTHDINSSFFPAAARQIFLVFMLIGGSVGSTSGGIKVMRLNILGGLFKREIKKIYLPNHAVLPVTLDKKIIKSDEINKLTGLFSFWLILIVIGGIITSIFSDLNGWQSFSGMFSAMGNIGPFFFSVEKMASLSPIIKLTYIIGMLAGRLEIIPIIILLNKNAWKN
1.4E-43	159	10.1	1.3E-42	155.4	7	1.9	1	A1AZF4_PARDP	Trk system potassium uptake protein	Pden_0536	Paracoccus denitrificans (strain Pd 1222)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus denitrificans, Paracoccus denitrificans (strain Pd 1222)	318586	>tr|A1AZF4|A1AZF4_PARDP Trk system potassium uptake protein OS=Paracoccus denitrificans (strain Pd 1222) GN=Pden_0536 PE=3 SV=1MIDIRPVANIVGKVVVTLGAAMALPMLVDWWHGDPHWLIFLECGILTTLAGGLVALSTRQVDKSLTIQQVFLLTAMLWLVVPVAGALPFMLGAPHVGFTDAYFEAMSGVTTTGTTAFPDLDNLPKGTNLWRAFLNWAGGLGIIVVAMIFLPAMKVGGMQFFRSEGFDTLGKILPRAFDIAREMTGVYIAMTASCMVVYILLGMKGFDALVLALSTCSTGGFSNYDASFAPFIGPAEYAAAFFMILASIPFIRMVQLIRGSAEPIWRDIQVRAYLRWTFYAIAVVVLYRLLWLEAKNPLDVIRETTFNVVSTFSGTGFASTDVTQWGHFPFVILIVVGLIGGCTGSTSCSVKVFRYLVLFQAVKAQLRRMQSPHRVFPLLYGGRPLEEDVVDSVMAFFTLFILSFGLLIVGLALTGLHPRTALTAAWTAIANVGVVWGPELTPEGAVTDFPTASKWLMIWGMYLGRLELISVLVLFLPRFWRS
1.4E-43	159	22.7	1.5E-41	151.9	15.8	2	1	W8TLW2_EUBAC	Trk-type K+ transport system, membrane component	EAL2_c18760	Eubacterium acidaminophilum DSM 3953	493	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium acidaminophilum, Eubacterium acidaminophilum DSM 3953	1286171	>tr|W8TLW2|W8TLW2_EUBAC Trk-type K+ transport system, membrane component OS=Eubacterium acidaminophilum DSM 3953 GN=EAL2_c18760 PE=4 SV=1MIDLTYSDVMQQRRRLIWGYAGKILMGSSLIYLLPLLLIPFYPEESANAAGFLIPAALALIIGFIFNSKGDGKDEILTTKEGGVIVIITWSLTVLISGLPFMISGGMNFTQAIFESVSGWTTTGLSVVADVKNTSKLLLLWRSITQFLGGAGLAVIMISAIIGPHGFGFYSAEGREDVVPNVVKSAKSIMIIYISYYIIGAAFYIEAGMPFFEAINHSACAIATGGFTTRPGSIGSYDSKRIELITIMLMLLGNINFGTHYMLVKGEARRFFKLGEIRLLAFILSLFIPLVFLFSTSRIYNSAEMAARASFFELISALTGTGYTIVDYNRWDDFGILVVIMLMIIGGGTCSTSGGIKQYRVLLLFKAIYWSMRRYFAPKNEIRHEYIERAEGQYEISSEHIVSTACFAIMYMSVYIAGIIVFVINGYSLRDSMFEFASAIGTVGFSIGITSPSAPGIILWTEIAGMFLGRLEFFVVFFGFINLVKLLRVQKRA

1.7E-43	158	38.4	8E-43	156.1	26.6	1.7	1	D4KDH3_9FIRM	Trk-type K+ transport systems, membrane components	MHY_16050	Megamonas hypermegale ART12/1	414	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	657316	>tr|D4KDH3|D4KDH3_9FIRM Trk-type K+ transport systems, membrane components OS=Megamonas hypermegale ART12/1 GN=MHY_16050 PE=4 SV=1MLPITVVDIEPLSFVDALFMSASAVCVSGVSIFSLGDNFSVFGQIIIIILVQIGALGIMTITTILAVVMGKRIQLRDRLLIQESLQRWSV AGVVRLVISIVKMTVAFEFIGGVILTIIFCQDYSVGTAIYFGFWHSVSAFCNAGFDILGGSNFADYIFHPFFNLILLIEVVCGGLGFAVLLDI YQKRKWQKLSINSKLVLVTTGFLILIGSVLIFILEYGNKNTLGDLGLFDKVMVSTFMASMARTSGFSMLDIGSLTEPSLLLIMFLMFIGGS PASTGGGIKTTTIAVIFAAIWSLIRGREDVVIFERTVPPIVIFRAMSIFFVSAIVVFLMSMFLCLTEDIALSKILFESVSMFATVGLPTGTINE MDASSRIVIIFVMLMGRIGIISFAMALVIRKKKNKIRYPEDKFIIG
1.8E-43	158	17.9	3.1E-42	154.1	12.4	2	1	R5D700_9FIRM	Cation transport protein	BN705_00063	Firmicutes bacterium CAG:555	480	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:555	1263030	>tr|R5D700|R5D700_9FIRM Cation transport protein OS=Firmicutes bacterium CAG:555 GN=BN705_00063 PE=4 SV=1MNFKTIRKTVGTILCMEAVFMLAPLLLAFADGDRAAMHGFAIAIAAVLVVGLPLALVNRSSMSLGSRDGCVTVALAWIVISVFGAI PFYVSGVITAPGDAIFETVSGFSTTGATILDDVEAAPRAILLWRSITNWVGGMGVLVFMLAIVPAAREGSSMFLLRAEFPGPMAGKLVP RMQKSAKLLYEIYILLTAAQVLLLVLGDIPLFDSVNIALSTVSTGGFAIKNGSLVSYGSYVQTVTLVFMTLCSMSFSIFYCLIARELLRIKRN HELRVFGVLVLGMALVIGISSAAQFATAGEDIRHSLFQVISIISTTCYVSVDTGLWSPFVWSLLLVLMITGPMSGSTGGGMKLSRVMILA KSTYRAIAKAITPGSVHLIRVDDEVVDEETVSSVNSFAVAYLMALVITAVILSLDGLDFGKGIVVAISSIGNIGYGIDANTFTYGVSGLSVP SKLALCFDMFLGRLEIFPLLIMFAPATWRK
1.9E-43	158	17.4	2.1E-20	82.1	4.9	2.1	2	R6F780_9BACT	Cation transport protein	BN691_02137	Prevotella sp. CAG:520	483	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:520	1262929	>tr|R6F780|R6F780_9BACT Cation transport protein OS=Prevotella sp. CAG:520 GN=BN691_02137 PE=4 SV=1MINLKLLYKIIGSLLFIETTMFLVCLGVAIGYEEEDIFPFACSVIISASVGLTMRLLGRKCENSLSRRDAYLVVTLTWVVFSLFGTLPF LIGGYLQSFTDAFFETMSGFTTTGASIIDDVSTLPHGILFWRSFMQWIGGLGIVFFTIALLPSFVGGSVKVFAAEATGPIKTKLHPRLSTN AKWIWVVYLCITLLCIGSLMLAGMTPFRSINYSMATAATGGFAVDSDYSVFTPAVQYILTFFCFVSGVNFTLLYISVSKRKLSTLLKSAE CRLYFSMVLGCAAFIAFELMWKNDYALEPAVRSSLFHVVSFITSTGLLADDPAKWAHVTWVVLAVCMFLGPCSGSTGGGFKCIRGV MLLKVIKNEFRQMLHPNAVLPVKIDGVNVPQSKRVTLLAFLTSYLILCLICSFSMIAMGIDNTNAITITLSTLGNVGPTLGLEIGPTMSWSI LPDTAKWICSILMLIGRLEIFTVLVIFTPQFWKEN
1.9E-43	158	19.2	4.1E-43	157	13.3	1.4	1	Q5YXZ6_NOCFA	Putative cation transporter	NFA_20990	Nocardia farcinica (strain IFM 10152)	476	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia farcinica, Nocardia farcinica (strain IFM 10152)	247156	>tr|Q5YXZ6|Q5YXZ6_NOCFA Putative cation transporter OS=Nocardia farcinica (strain IFM 10152) GN=NFA_20990 PE=4 SV=1MVDRPRPRWALIGAPGRARRSFAAPAPHALPAPRHPARLVVCGFAAATALGTLLLMLPVAAESRTVTAPVTALFTAVSAVCVTG LVVVDTESHWSLFGELVILGLVQVGALGIMTVASLFGLLVARRMGLRMQLIAQTETKTVRLGEIRRVVIGVLRMSLLVEAVVATALTARF LFGYDEPWGRATYLGIFHAVSAYTNAGFVLFADSLVGFAADPWIMVPITVAFVVGGLGFPVVLEVGRSLRRGARRGVAHWSLHTRIT LVTYGVLAVAGILAITLLEWTNPATLGPLGLPDKLLVGGFHGLSPRTSGFNAVDVGAMHSATLLITDALMFIGGGSAGTAGGIKVTTFAL LAFVIVAEIRGEPTVHVMNRRLAAEVQRQAITVALLGVGTVVAGTVTLLTITGMALDAVLFEVVSAFGTVGLSTGITAELSDPARMVVIV LMFIGRLGPITLATALALRTRRRRYELPEERPIVG
1.9E-43	158	18.2	3.7E-42	153.9	12.6	2	1	E1QH83_DESB2	Cation transporter	Deba_1558	Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	505	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfarculales, Desulfarculaceae, Desulfarculus, Desulfarculus baarsii (Desulfovibrio baarsii), Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	644282	>tr|E1QH83|E1QH83_DESB2 Cation transporter OS=Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14) GN=Deba_1558 PE=4 SV=1MREKQYLLQRYAAIASSIGLILLLTGALMFTPLLVLPWRPEELGQAWAFVLPAVCQCSLGLVLWRAFGGRARDALTVQEGGVIV VLGWALVILFSAWPFTAVLGLPFSRAVFESVSGWTTTGLSVVDVTRAGWMILLWRSVIQLAGGAGLAIIMLSAIVGPVGAGVTSAEGR GDQLAPHVRRSARLVLVIYGCYAIAGTVAYWLVGMSFFDALNHSFAAVSTGGFSTRVESIGYWDSAVIEAVTIPLMILGNLSFVTAWLL WRGRLRLVALNGEARLMAVLIPLCAAAVFLLTSRALYPTLEKSLRVALFETVTALTTTGFSTVGYGDWNAFGLMALIVLMIIGGGTCST AGGVKQFRVYLLWRMLCWEIKRGLVPKSVVLERPLWEGEARVFVDDGRVRQAAVFVFLYLATYMLGVMVLCACGYDLSQALFEFAS AMGTVGLSIGVTSAQMPDVALWAETLAMFLGRLELIVVVVSLLKLGVDGRKMLARRRGGRTRSLHWAAR
1.9E-43	158	25.3	3.5E-23	91.3	7.8	2.1	2	U5Q4W0_9BACT	Trk system potassium uptake protein trkH	trkH BRDCF_p909	Bacteroidales bacterium CF	481	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, unclassified Bacteroidales, unclassified Bacteroidales (miscellaneous), Bacteroidales bacterium CF	1400053	>tr|U5Q4W0|U5Q4W0_9BACT Trk system potassium uptake protein trkH OS=Bacteroidales bacterium CF GN=trkH PE=4 SV=1MNYSIVSRYIGMALFLNAIFMLISAMVSAMNGYDASFSPLMMSAIITFVCGAFPLIFVSSKYEINIKEGFVIVVFAWIFSCIFGMLPYI LYGGEFSIANAWYESVSGYTTTGATILQNVEGIPKGLHFWRASTHWLGGVGVVLFMLLILPTVGSFRMKISKMEISDLSKENFRYKAR QTIAIITTVYVGLTLVETVLLMFGGMSLYEAVIHSFSTIATGGFSTRNLSVKAFDSFYIELIIMIFMLLSGLHFGLLFSAVSGRSKQLFKSPI VRLYVGSILVGGFVVGLNLFFSGTYDSLATCLRHSYFQVISCGTATGFASEDSSIWPGFSMLVIVYFTLSCACSGSTTGGIKVDRIWIFF RSVKSQIVKQLHPNAIVSIKVGNNALEPDIVHSVNLFIALYLFVVFVVALLLSLMGVGLTEAISGSIANMANCGPGFGAVGSLGNYSSLP DMGKFLLGIEMLLGRLEIYPFILVLSVNRWR
2E-43	158	14	4.9E-42	153.5	9.7	2	1	Q28R86_JANSC	Trk system potassium uptake protein	Jann_1859	Jannaschia sp. (strain CCS1)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Jannaschia, Jannaschia sp. (strain CCS1)	290400	>tr|Q28R86|Q28R86_JANSC Trk system potassium uptake protein OS=Jannaschia sp. (strain CCS1) GN=Jann_1859 PE=3 SV=1MFDLRPVGYVLGLLVFTLGVTMVIPLGADVWAGNGHWGAFAEAAAVTIVTGIFLTLACANGVTEGLSIQQTFFLTTGVWLVLPLF GALPFIFGEPGARVVDAVFEAMSAMTTTGSTVITDLDNLPVGVNLWRGLMQWFGGIGIIVVAMVFLPELRVGGMQIFRSESFDTMGKI LPRAGEIASRITVIYLGLTIACGLAYLAVGMAPFDAAMHALTTLSTGGFSNYNASFGAFQGPAEYVAAVFMILASLPFVRYIQLVAGTAK PILVDTQIRAYLGIIVLLTIVFTVYRLVVSGDSIEHGVREGVFNVTSIISGTGYSSTNYELWGPAAPVMFFFIGLIGGCAGSTSCSIKVFRY QLLFASISTQVRRIYAPHGIFEPKFEGRPVAEEVISSVMAFFVLFFVLLGIIAVLLGLTGLDVVTSISGAATALGNIGPGLGDIIGPSGNFAP LNDTAKWILTAAMLVGRLELMAVLVLFTATFWRA
2.1E-43	158	25.5	8.8E-25	96.5	4.8	2.2	2	A7HNN9_FERNB	Cation transporter	Fnod_1687	Fervidobacterium nodosum (strain ATCC 35602 / DSM 5306 / Rt17-B1)	498	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Fervidobacteriaceae, Fervidobacterium, Fervidobacterium nodosum, Fervidobacterium nodosum (strain ATCC 35602 / DSM 5306 / Rt17-B1)	381764	>tr|A7HNN9|A7HNN9_FERNB Cation transporter OS=Fervidobacterium nodosum (strain ATCC 35602 / DSM 5306 / Rt17-B1) GN=Fnod_1687 PE=4 SV=1MLKRYTKIYKAFSIIMIQYAFMALVPLIFCFFYPEELNHINGFIVTAITALCLYLSGYLIKGEDIGSINYKEDAVLTIFTWIMVALLSAIP HMLEGHLNFSQAVFESVSGLTTTGLTMYTDVTKISKLILFWRSFTQYVGGAGFALLMLSMVIGPKGVGFYKAEGRVDNLVPNIRRSTQ IILQIYVAYTIAGTLALKLAGLNWFEALNHTMTALATGGFSTRNGSVGEFNNLAVEIIIMVLMFLGATGFAIHYAFWKRNWKAVVKNGEP WLMIISITVFSIITAVNGIGKYFKDFNQAIRYTTFQIMSAISGTGFQTLPLSEEKWFSFSPLILSLIVLMIAGGDMDSTSGGIKQFRVWVILN TILESIKGFLLPKNRVKTRIIYKGEQQIVLSNENVREALIILFLYIIAFIIGSFALTLHGYDLELSLFEFASAMDGVGLSVGITSPNMPLTAMW TLTIGMFTGRFEFLIIIYAISKLASDFRMTFKKTKKRRDVVA
2.4E-43	158	26.2	2.9E-25	98.1	10.2	2.1	2	R5E4S2_9FIRM	Uncharacterized protein	BN798_00220	Eubacterium sp. CAG:86	432	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:86	1262895	>tr|R5E4S2|R5E4S2_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:86 GN=BN798_00220 PE=4 SV=1MFMLLKKLSTSRIIALGFALAILTGSILLMLPCSVRPGVHLEYIDSLYTSTSAVCVTGLVSVDAKDTFTPLGQFFLAMLIQIGGLGVT AIGAGIIIAMGKKVNMKGRSLIRDALNVDSGKGMIIFIRDIFMTTVFFELVGAMLSYIVFSKDYPPVEALGISLFHSIAAFNNSGFDILGNYR SLTGYYDNFTLNIITCVLIFFGGIGFLVIRELRIKHFHWKKLSMHSRVVISMSLFLIVSGTLLIKATENISWLGAFFLSFSTRTAGFSTYPLG NFSSAGLLVVIILMFIGASPGSTGGGIKTSTFFVLLQGIKSAATNKSEKAFHYAVPKNAFSKAAIITAIGAAIVLTGTYIMLVLQPELSFIDV FFEVTSAFSTSGLSTGITQQLGMGAKLLSIIIMYAGRLGPLTIVTVWYFSKGERVSYPEGNISVG

2.5E-43	158	13.1	7.6E-24	93.4	1.4	2.1	2	A0A0B5DZE4_9RHOB	Trk system potassium uptake protein	P73_0862	Celeribacter indicus	475	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Celeribacter, Celeribacter indicus	1208324	>tr|A0A0B5DZE4|A0A0B5DZE4_9RHOB Trk system potassium uptake protein OS=Celeribacter indicus GN=P73_0862 PE=3 SV=1MSFVIFINGLVMVAFAVLMGGVAVGFPATAPVFEEPGFLFGFLGGALVLAATPRAEHLRPLHTFLLTSSVWMTAAICGAGPLYFY GLPLTDAFFEAMSGITTTGSTVMTGLDRVPHGVILWRAILQAVGGVGFIVTGIALLPILKVGGMQLFRSESSETGERELRNATMFASAT LQIYFALIFLCGLLYLLGGMSPFDAATHAMTTLSTGGYSGYDASFGHFTSPFLQWVCTLFMLAGALPFSWYIRGIRRRVWQSEQVVA MLRSLGVTILVLTLWLILRQERAPFEALRLVAFNVVVSVVTTTGYATTDYTLWGPFAVATFVVLTAVGGSTGSTAGGAKAMRWLVAGR AMIAQIRQSHAPHRVTFVKYQGRRVDPDALSGVISFFVLFAATFGVLASLLSFLGLDMETATSGALTALANVGPGVGDIIGPAGNFATL DTAPKLVLIFGMYVGRLEMATVYALLAPLFWRELVASR
2.5E-43	158	34.7	2.5E-43	157.7	24.1	1.9	1	F0NXB3_WEEVC	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Weevi_0163	Weeksella virosa (strain ATCC 43766 / DSM 16922 / JCM 21250 / NBRC 16016 / NCTC 11634 / CL345/78)	581	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Weeksella, Weeksella virosa, Weeksella virosa (strain ATCC 43766 / DSM 16922 / JCM 21250 / NBRC 16016 / NCTC 11634 / CL345/78)	865938	>tr|F0NXB3|F0NXB3_WEEVC H(+)-transporting two-sector ATPase OS=Weeksella virosa (strain ATCC 43766 / DSM 16922 / JCM 21250 / NBRC 16016 / NCTC 11634 / CL345/78) GN=Weevi_0163 PE=4 SV=1MYNKIAKITQNRVLGKVLSATYILAIVILIAMLGFGFPKIYYQYVNYFFITILLIGVVRTSFNNIIFAEKLITRVFIFDLISIAIVLYCIYRQL NEYSFFYVSKYLQLAIVLKLIREIAIPQLNIRKSKITPPQLFIISFLILVFGGSGLLMLPKATTQSISYLDALFTATSAVCVTGLTVVDTASTFT PFGHFLLMLLIQAGGLGILTFAGYIAYFFKGQSTYENQIALGNIANHDTISEVFDFVKRILLLTFGIELLGAIFIFFSVDNINFTFFDQLFFSIF HSVSAFCNAGFSTLPNNVMNDKLIFNYPFQSALIFLIFLGGIGFPILINLLKYFRYFIQKTIFRFIQKTPNNKTWVFTLSSKVNLVTTLCILIIS TIILFFEEYYQTLAPHKGFGKLISAIFLSTTPRTAGFNHIDFTELHFSSTLIIIFLMWIGASPAGTGGGIKTSTFAIAVVNFLNIARGKTKIEIY KRELSPVNVQKAFAVMTLSFLVIGLGIFLMTRFDSHLHLINVAFEAFSAYSTVGLSRNTTPYLSSESKIVVISMMFIGRVSMITILMAFFKK TTSENYRYPTDEILI
2.7E-43	158	25.8	1.5E-41	151.9	17.9	2.1	1	Q12YF1_METBU	Trk-type K+ transport systems membrane subunit	Mbur_0548	Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M)	485	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanococcoides, Methanococcoides burtonii, Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M)	259564	>tr|Q12YF1|Q12YF1_METBU Trk-type K+ transport systems membrane subunit OS=Methanococcoides burtonii (strain DSM 6242 / NBRC 107633 / OCM 468 / ACE-M) GN=Mbur_0548 PE=4 SV=1MYELHTPVNHKAVAKYIGYYLIAFTFVLVVPTIAALVLGNVDAAIDYGSTAVAVFIIGSLIYRALPDYDLETKEALIIVALVFPISAFLS AVPMSLTTGMPFIDAYFESVSAVTTTGLSVAPADVGPVFLFARSWGQWVGGIGIILVVLSVLIRPGTTASRMYKANYGDMKIKPTVIST TRTLGKVYIIITLISLILLLMSGMSLFDSICHALSCVSTGGFSTRPEGIRAYQGSLIPTAISISCLLGAVSFVLYPHLFKKPEKIFKNLELRYFL AFIAIGSIVFAFTLERGNTDYDLIQDSLFQIINAITTAGFSTIDLSILSEASKAVLIFMMWIGGNVGSTAGGIKVLKVILLLKVVHNVLLRLFLP RETITPIKIEDHVIESDEIYNLVTFMLLYTLILIVSSFIFMLYGTNMSSSVFEVSSALSTVGLSAGATSASMPVVLKLVLIIDMLFGRIEIIPLIL LFMPGTWIKRKWANKRNVKT
2.8E-43	158	25.1	4E-42	153.7	17.4	2.1	1	D9QQU1_ACEAZ	Cation transporter	Acear_1369	Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	492	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halobacteroidaceae, Acetohalobium, Acetohalobium arabaticum, Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288)	574087	>tr|D9QQU1|D9QQU1_ACEAZ Cation transporter OS=Acetohalobium arabaticum (strain ATCC 49924 / DSM 5501 / Z-7288) GN=Acear_1369 PE=4 SV=1MRYKEMIIQRYKLLLKYIGILTIGIGVILLLPLLVLPFYPQNIMYSTSFLIPSFLYMILGGVIWKLIQSENNFTLSLKEGGIIVLASWILAII ASALPFIIAGKLNFTQAVFEATSGWTTTGLSVVNEAKTPNIFLLWRSIMQFFGGAGLIVVMLSSILHPYGFGLYNAEGRSDQLLPHVKQ SAKAIMLIYSGYTIGGIILYILAGMGVFDAVNHSIAALSTGGFSTRQASIGYWNSISVEIVTWVLMLLGTTNFATHFALLKGKFKIFFKNGE VRLLGVLIAVFTPLISYFTLTELYNYLPDLLRRGIFETITAISTTGFSLDTFNNWNSFGMLSMILLMLIGGGTGSTAGGIKLYRIYLMFKSLI WQFEGYFLPQNAVRENYIWRGETKLYIKLEYIRETANYIYLYMGTYFIGVFIYLAYGYDLTNSMFEFASALGTVGLSIGITAADAPTGIL WLETVGMFLGRLEFLVIFFAVAKIIKDLKFNLENK
3.1E-43	157	22.5	1.6E-42	155	15.6	1.9	1	A0A076K3Q0_9RHOB	Trk system potassium uptake protein	RCA23_c27470	Planktomarina temperata RCA23	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Planktomarina, Planktomarina temperata, Planktomarina temperata RCA23	666509	>tr|A0A076K3Q0|A0A076K3Q0_9RHOB Trk system potassium uptake protein OS=Planktomarina temperata RCA23 GN=RCA23_c27470 PE=3 SV=1MFDVRPVFNVIGLLVSCLGLTMMFPMALDMSRGNGHAGVFLESALITCLTGSMMYLATRREAARGLTLQQTFLLTSGVWLALPI FGALPFALGATDSSFTDAFFEAMSGLTTTGATVISGLDYLPDGLLLWRSILQWLGGIGIIVVAMVFLPELRVGGMQIFKSEGFDTFGKIL PRATEIAAQVAWLYVGLTGACAVIYIATGMRSFDAVLHAMTTIATGGFSTYDSSFVKFGASTEYAAVVFMCLAALPFVRYVQLINGAPG SLFHDSQVRVFFIVLLVTVGFLTLVLWQGYQFSGELGFRKALFNVVSITTGTGYASADYSTWGPVALVVFFYAGLVGGCAGSTSCSV KVFRYQLLVSAIHMQLRKIHSPSGVFNLRYQGRIVGTDVINSVISFFVIFFVSLGVSAMALALTGLDLLTAFSGAAAALANIGPGLGEVIG PSGNYSTLSDSAKWILAFTMLLGRLELLAVYTLFTLRFWRN
3.1E-43	157	28.3	7.1E-43	156.2	15.5	2.6	1	R5AYN0_9BACE	TrkH family potassium uptake protein	BN813_00561	Bacteroides sp. CAG:927	490	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:927	1262753	>tr|R5AYN0|R5AYN0_9BACE TrkH family potassium uptake protein OS=Bacteroides sp. CAG:927 GN=BN813_00561 PE=4 SV=1MRYIKRSHINFAAVLRVIGMLLTIEAFFMLVPLITCIAYGEGDAQAFGITVAITLVAGCALAFGLKPSNPDMGKRDGFLLTALVWVF FSLFGMLPFMIGDAGMNMSDAFFEAMSGFTTTGASVIGSIDELSRGAVMWRSLMQWLGGMGIILFTLAVIPMLNHSGGMQMFNAEV TGITHDKLRPRISQTAKGLWGIYCVLTVLLAALLWVGPMDFYTALCYTFSTISTGGFTTTNSGLTEYGTLYVKIVLTVFMFLGGVSFSLM FRWWNGDHGSLWRNDVFRAYVRIILVCLMLFIITILAIGAYTGIESVSIDPLFQIISTLTSTGFMVEGARNWGPFVISLLFVLMFFGACAG STSGGAKIDRMLFLIKNANNEVYRCVHPNTILGVRINGVTASYDTVNKVIAFLCIYMMLIVGGGIALTALDIPIVDAFFSSFACLSNTGLDV NITGYGDNYMALPAAGKWVLSLEMLIGRLEIFTVLLLFTKGFWK
3.2E-43	157	13.7	5.2E-43	156.7	9.5	1.2	1	E0QPM8_9ACTO	Cation transport protein (EC 3.6.3.14)	trkB2HMPREF0580_0995	Mobiluncus mulieris ATCC 35239	509	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Mobiluncus, Mobiluncus mulieris, Mobiluncus mulieris ATCC 35239	871571	>tr|E0QPM8|E0QPM8_9ACTO Cation transport protein OS=Mobiluncus mulieris ATCC 35239 GN=trkB2 PE=4 SV=1MIKDGTGSLQPSRIVILAFLLTMLAGTVLLCLPVARTGAGENLILDQSPALPAAANSGIAPHEPPTKTVPSLGPALPAAANSGIAPH EPPTKTVPSLGPALPGGAPLSVALFTAASATCVTGLIVVDTGTYWSPFGQTVLLGLMELGGIGTMTVVSLVSLALGRATSDTREVAAH SLRGIPLGGIKHTVAAILGFSLVAQMIFGVILAWRLGASGKVPGGAMGVFHGFFLAASAFNNAGFAPWTDSVTGFNHDPVVLGSLAVL ILVGGLGFPVWAVLWVKGPHWWRLNLNVRIMLVGTAVLVAGGTVLMAALEWNNPATLGAHHPGEKLLNAFFAAVSPRTAGFNAIDI GAQYPATWLVTDGLMLVGGGSAGTAGGLKVTTTAVVLATLWGEVRGAGAINILGLRLARAAQRQALAVFSLFIGLVGISVFLMVLTTP WGLSRSLFEVCSALATVGLSTGITPSLPVANQALLIALMLVGRLGPLTIATAWGARKRRLVYELPKDYPLIG
3.4E-43	157	27.1	2.8E-42	154.2	18.8	1.9	1	Q8DQY9_STRR6	Trk transporter membrane-spanning protein-K+ transport	trkHspr0426	Streptococcus pneumoniae (strain ATCC BAA-255 / R6)	479	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pneumoniae, Streptococcus pneumoniae (strain ATCC BAA-255 / R6)	171101	>tr|Q8DQY9|Q8DQY9_STRR6 Trk transporter membrane-spanning protein-K+ transport OS=Streptococcus pneumoniae (strain ATCC BAA-255 / R6) GN=trkH PE=4 SV=1MNKSMIRYLLSKLLLIEAVLLLVPVAIAVYYRESSQVFTALFSTIGILVLLGGSGNLQKPKNQRIYAKEGVLIVALCWILWSFFGGLP FVFSGQIPSLIDAFFEISSGFTTTGASILNDVSVLSRSLLFWRSFTHLIGGMGVLVFALAIMDNAKNSHLEVMKAEVPGPVFGKVVSKLK NTAQILYLLLYLALFSLFVIIYYLAGMPLYDSFVIAMGTAGTGGFTVYNDGIAHYGSSLITYLVSIGVLVFGVNFNLYYYLMLRRIKAFFGDE ELRAYLVIVLVSTGLISLNTLYLYPGFSKSFEMTFFQVSNIITTTGFGYGDITNWPLFSQFILLFLMAIGGSAGSTAGGLKIIRGLILSIKIAK NQILSILSPHRVLTLHVNQTVIDKDTQHKILKYFVIYAMILLALIFIVSLDSNDFLVVTSAVFSCFNNIGPILGTTSSFSIFSPISKILLSFAMIA GRLEIYPILLLFMKRTWSKR

5.2E-43	157	25	1.4E-42	155.2	17.3	1.6	1	L0HES1_METFS	Trk-type K+ transport system, membrane component	Metfor_1491	Methanoregula formicica (strain DSM 22288 / NBRC 105244 / SMSP)	498	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula formicica, Methanoregula formicica (strain DSM 22288 / NBRC 105244 / SMSP)	593750	>tr|L0HES1|L0HES1_METFS Trk-type K+ transport system, membrane component OS=Methanoregula formicica (strain DSM 22288 / NBRC 105244 / SMSP) GN=Metfor_1491 PE=4 SV=1MKRTRHLAMIAHDMGLIFEFLGIVSLLPFLILVIFGEWDLLLPMATAPFVFLATGFLISHIPHEDIEPSLSATLSAVALSWLAIAFVGA LPFVFGLGMSYTDAVFEAMAGWTGTAFSMIPSLDQTPDTLLFWRSFMQWVGGIGVIVFGISLRTKTRVSLFRMYRAEGREDALVSAT TSSSRRLWMIYLVLTFGFTGLVMLTGIPLWDSLNLVMTTIATGGFTLHDTGLAYYNNAALEAVLIPVMFAGSIPFKVLFLFLYHGKVMGIF RDQTVRILLLIAVIGAALISLDLSIFSNLSPLSAVRQGTFTAVSGLTTCGLQNTSLHHWATVPLAILAMMVFIGGAMGSTAGGIKVNRLAL VFEGVKWWFRRFFVSSRVLVPLRVGGRTLSVERSNLAVSKNLLVIVIYVLTIFLATVIALHLYITSFRLDEVVFEIVSALSNSGLSVGFIGP ESPLSMKWLFITLMWLGRIEIAPVLIIAMGIFREIRDDLAKDVSETRYQ
5.6E-43	157	27.4	1.3E-23	92.7	2.3	2.5	2	A0A060BF55_9GAMM	Trk system potassium uptake protein	FF32_12950	Halomonas campaniensis	495	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas campaniensis	213554	>tr|A0A060BF55|A0A060BF55_9GAMM Trk system potassium uptake protein OS=Halomonas campaniensis GN=FF32_12950 PE=3 SV=1MTIFPSGIYYRDTYRNWAQIFKIMAVLWLVLAMFMTLPWIVLVIEKDPDAPAFGMSLLIILSATLTTWLLTRRVSLELKPWQMFILT AGSWISISCFASLPLILGAPQLSVTNAVFESVSAITTTGSTILSGIEDLSDGLKLWRGLMQWMGGIGIIVMGIAILPFLKVGGMRLFHTES SDWSDKVMPRTGGIAKATLTIYVGLTLLAMLSYWVGGMLPLDAVVHGMTSLATGGFANSDASFGAYSEQPWLVWMGSFFMLSGAL PFVLYIRFIRTSRSALWKDQQVRGLLKLLLTAILILSAWRVLQGDDWFVSLTHVTFNVVSVVTTTGYASDDYTLWGSLPIAAFFYLTFM GGCSGSTSGGMKIFRFQIAMLMLRNQLRYLIHANGVFTTRYNQQPVTNDISRSVVAFSFFFFITIAVLALSLSALGLDLVTALSGAATAV ANVGPGLGDIIGPAGNFATLPDAAKWLLCLGMLMGRLEILTVVVLLTPMFWRR
9E-43	156	26.9	7.8E-41	149.5	18.6	2.1	1	H2J632_MARPK	Trk-type K+ transport system, membrane component	Marpi_0655	Marinitoga piezophila (strain DSM 14283 / JCM 11233 / KA3)	501	cellular organisms, Bacteria, Thermotogae, Thermotogae, Petrotogales, Petrotogaceae, Marinitoga, Marinitoga piezophila, Marinitoga piezophila (strain DSM 14283 / JCM 11233 / KA3)	443254	>tr|H2J632|H2J632_MARPK Trk-type K+ transport system, membrane component OS=Marinitoga piezophila (strain DSM 14283 / JCM 11233 / KA3) GN=Marpi_0655 PE=4 SV=1MPKYLSNLKHRYKLIFKNTGTMLIYFGIALMLFGTLAIILYKDLPSFYSFFETGLITVFTGAFFILLSWGTENAPINIQDAIVIIFLVWTL SIFFSALPFVFSGILNIHHAIFESTSGWTTTGLTLVDVTKIPKIFLIWRSLMQYFGGAGFALIMVIATGALGVGLYQAEGRTDNVVPNLRD SAKIIFGIYLSWAGIGIILLTILAHMSFFDAFNHTLTALATGGFSTKIDSVGEFNNPVAEIIIMVLMIAGGTGFGVHYAALRRGDLFKKNPEP KTMFFILLFSIPMIAYFTTDKLYGPLNGIRHSAFQAISALTGTGFSTVTFNNWNNMGLLIMTILMILGGMMDSTSGGLKLFRVFVIWKIIVH QIKTYFKPEGSIFHIEVYKGISKKRISYDTLKDVIAVVFMYFIVYTIGVMVLLGYGYSMEDSLFEYASALSAVGLSIGITTPDSPLGVIWIET IGMYLGRLEFFVIYFAIIKMIRDIKDIIEIKIQEFRGGESF
1E-42	156	23.5	3.2E-39	144.2	16.3	2	1	R6I8J5_9FIRM	Uncharacterized protein	BN517_01777	Ruminococcus sp. CAG:177	432	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:177	1262952	>tr|R6I8J5|R6I8J5_9FIRM Uncharacterized protein OS=Ruminococcus sp. CAG:177 GN=BN517_01777 PE=4 SV=1MRKLLKRMSPARIIALGFAAAIFIGSGLLMLPCSVQNGVDLKYIDALYTSASAVCVTGLVTVDIGDTFTAFGQFVVAALIQIGGLGV ASMGAGVILAVGKRINLKGRRVLRDAMNLDSGKGIVKFIKSVFLTTAAFELVGAALSFIVFVRDYPPLKALGISLFHSVAAFNNSGFDILG NFQSLSAYKEDVFLNLVTCLLIFFGGIGFLVIREIVEKRFRWRRFSMHTKVVLTMSVALTVGGAVIFRITENMPWIGALFNSVTARTAGF STYSLGEFSNAGLLAMIFLMFVGASPGSTGGGIKTSTLFALIQGIKTAATNTSGKAFHYSVPHGVFRKASVIAVMGISVIAVGTFMLCAF EPDIAIRDALFEMTSAFGTVGLTTGITTGLCTASKLTSIVMMYIGRLGPLTIATLWYFTNGDRIKYPDGNIAIG
1.3E-42	155	28.3	2E-42	154.7	19.6	1.2	1	E6SNK5_BACT6	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Bache_1769	Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	609	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides helcogenes, Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	693979	>tr|E6SNK5|E6SNK5_BACT6 H(+)-transporting two-sector ATPase OS=Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108) GN=Bache_1769 PE=4 SV=1MKIYHKFLLYQNKWIDPYVRMAGGVMAFITYLASILIAGVVYEHGFTVSAAEARQLQRLYHGVWIVFLAAVTLRILLRYKDTRRT FGRVAWILTALLYLTLVPVVFHRPEQEGAVLQFWEFLHGKPYHLVLLLIFSFLSLSNGMVRLLGRRTNPSILAVSFLIIILVGTGLLMLPR CTVAGISWIDSLFISTSAVCVTGLTSVDVASTFTPTGFAVIILLIQIGGLGVMTLTSFFAMFFMGNTSLYNQLVVRDMVSSNSLNSLLSTL VYILAFTLAIEGAGTLAIWGDIHGTMGMNIQEELAFSAFHSISAFCNAGFSTLPGNLGNPLVMAGHNPFYIYISLLIILGGIGFPILVNFKDI VLYHLRRLWGFLRTWHWDRNRFSHLYNLNTKIVLIVTFMLLLGGTVGIAAIEWNGVFAGMSVADKWTQAFFNAACPRTAGFSSVDLT GLGVQTLLIYLFLMWVGGGSQSTAGGIKVNAFAVVVLNLVAVLRGTERVEAFGRELSHDSIRRSNATVVMSFGILFLSVFVISILEPGAS LTAITFECVSALSTVGSSLNFTPTLGGDSKLLLAALMFIGRVGLITLMLGIIRQKKHTKYQYPSGQIIIN
1.5E-42	155	28.4	2.4E-42	154.5	19.7	1.3	1	R5AMZ9_9BACT	K+ uptake protein	BN456_00971	Prevotella sp. CAG:1031	612	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:1031	1262917	>tr|R5AMZ9|R5AMZ9_9BACT K+ uptake protein OS=Prevotella sp. CAG:1031 GN=BN456_00971 PE=4 SV=1MIFRNLAYRLRLTRMSLQRFSHRFASTVRLLDITVDVLTVTAALVCSVGMLIYVGFDHSAREFAILEQIIHCGQQGIFLFNIVYGLLLT SPRRRTLFQWIIDIAVVLTIFPLIFPHTGSYLWQLLCSNRVTFAIIAVYSVVQLSYAIMRLPGKRTNPSLILTSSFMLFIIVGTLALMLPKST YNGISFVDSLFVATSAVSITGLTPVDVASTFTPLGLTILGVLIEVGALGVITFTCFFAMFFTGNTSIYSQLIVRDIIYSKSMSSLLPTMLYVL TTTLTVQLIGAVALYFSVPDSLQFDTEQRIGFAAFHSVSAFCNAGFSSLPDGLSNPALMNSGGLIYWMFSLIIIAGAIGFPIIINFRDALAD LLGFHRHRRRSRFMTPFVDDKKVHLFNMNTKIVLTTTGTLFAIGAIGFFILEYDRSLAGMSLCDKITQSVFNSVTPRSAGFSSIAPAQFA APTLIMILFMMWVGGSAQSTAGGVKVNTLAAIVLNLRSIVKGQSRVVAFRRTIATASIRRANAMVSVSLITYTLLSVIILILEPGLPPRAVL FETCSALFTVGSSLGITAELGPAAETVLCVAMLLGRVGIVSLLSGILSHRRAQPHYPTDNIIIN
1.5E-42	155	30.2	2.2E-41	151.3	20.9	2	1	R6DS05_9FIRM	Uncharacterized protein	BN553_01413	Firmicutes bacterium CAG:238	490	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:238	1263011	>tr|R6DS05|R6DS05_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:238 GN=BN553_01413 PE=4 SV=1MNINFRVLIKILGVLALIEGLFLLPCAAVGIVFKEWGSAGALFEVGIFSVCIGFVILTQYHFDKIKLHSHEGYLIACLSWLFCSMIGAL PFYFSGQGYPMVQSFFESVAGFTTTGCSVFDLATMPRSLLLWKSVSNWLGGMGILVLLVSIFPALGISGQVIASAEATGPTLEKIGGGR FSDTGRVLYLTYLFFSFAEFVLLALGPLSIFDALISTFSSISTAGLVITPANAAAFDTVYVRAVIMIFTLLSSLNYTLFYFMLRGDFKTVLQN VETKIFAIIIIGATLAIAVSLKISGTYASLWQAVKDALCQVVAFISTSGYFVCDYTQWPTFAVIVLFSLLFVGGCCMSTSGSLKIMRVIVFLK LIKRGIFRQIHPRAVKAVVIDGRAIPADKVSAITTHILLFFAFFFFSALVLGLNNFDLETTISTSIGLFSNTGMALGEAGASGYFGMFNSFS QFYMCFMMIAGRLEIYAVLLLFSKSFWKIDSVSSI
1.6E-42	155	20.1	2.4E-41	151.2	14	1.9	1	F4H0Q6_CELFA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Celf_0892	Cellulomonas fimi (strain ATCC 484 / DSM 20113 / JCM 1341 / NBRC 15513 / NCIMB 8980 / NCTC 7547)	458	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Cellulomonadaceae, Cellulomonas, Cellulomonas fimi, Cellulomonas fimi (strain ATCC 484 / DSM 20113 / JCM 1341 / NBRC 15513 / NCIMB 8980 / NCTC 7547)	590998	>tr|F4H0Q6|F4H0Q6_CELFA H(+)-transporting two-sector ATPase OS=Cellulomonas fimi (strain ATCC 484 / DSM 20113 / JCM 1341 / NBRC 15513 / NCIMB 8980 / NCTC 7547) GN=Celf_0892 PE=4 SV=1MARLGPGVRYHVRELVDRAARQSPARLALGVFGTVIAVITLLLYAPWATVSGEQAPFADALFTATSATTVTGLVTVPTGEYWST WGLVVILVAIKIGGLGVMTLASLLGLAVSRRLGLTQRLLVSSETKFTRLGEVGSLVNTVIITSTAFEVAIALVLLPRFHMYDESWGEAAW HAIFYGVSSFNSAGFVPTPEGLFPYASDWWVLMPIIVGVFVGSLGFPVILNVAGSLRRPGRWNLHSKLTLTTSVALVVFGSLIVAAFE WTNPDTFGGLGPSATALASLFAGVMPRSGGFTTFDIAEMHEGTWLLMDALMFVGGGSASTAGGIKVTTLAVMLLAIVAEARGDKDV EAYGRRIPREALQVAIAVSFISATFVLVASLLLLAITGEALDVILFETISAFATCGLSTGITMDMPDAGKYVLTVLMFIGRTGTMTLAAALA LRNRRRVIRLPEERPIIG

2E-42	155	52.8	1.6E-24	95.7	12.5	2.9	3	R7J4Y3_9FUSO	Trk-type K+ transport system membrane component	BN657_01247	Fusobacterium sp. CAG:439	434	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Fusobacterium, environmental samples, Fusobacterium sp. CAG:439	1262899	>tr|R7J4Y3|R7J4Y3_9FUSO Trk-type K+ transport system membrane component OS=Fusobacterium sp. CAG:439 GN=BN657_01247 PE=4 SV=1MKFIYNLEKRLAKLESYQVIILGFLTYIICGMIAISLPFAQKMHVGVVDNLFNITSALSTTGLTTGNISELYTPFGKLVLLIMIQLGAIGYMTITSFFILSSGNNLSKYRTKILSTEFTMPENFNIREFVRNIIIYTFAVELFGTFLLALEFHKLGYAKPLWSALFHCVSAFSTAGFSIYGQGLTLFRDDLSVNLIIAFLCYAGAIGFIIPMDIYKKVVDKNNHITFTTKVILFITALVCVGGTALYLVKSDHNVLAAFFQVMSASTTAGFNTVNIGALSTTSLSVLIAAMVIGASPSGTGGGIKTTSISVLLGVVQSVMRGQFKQICFLNRTIPFNRVFTSIAAATTYIFTLIIVVYLLTLTEPFSFLELCFEAASALGTVGLSMGITADLSMWGKIILSIAMFLGRVGPLSLGIAIFKSQSNVIPCKSDLAT
2.4E-42	155	18.5	1.2E-40	148.9	12.9	2.6	1	G0ED01_PYRF1	Cation transporter	Pyrfu_1868	Pyrolobus fumarii (strain DSM 11204 / 1A)	536	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Pyrodictiaceae, Pyrolobus, Pyrolobus fumarii, Pyrolobus fumarii (strain DSM 11204 / 1A)	694429	>tr|G0ED01|G0ED01_PYRF1 Cation transporter OS=Pyrolobus fumarii (strain DSM 11204 / 1A) GN=Pyrfu_1868 PE=4 SV=1MPWREQGFEVLEEYGVRKRLALHPLIYYLGFVWIVAAATLIVPALYGLIFHYHEPREYTVSIELLEYGTVFMVLGLLSTRLTMPSRRMRREEALLLVVITWVLIPLVVAWPIADVLGIPFVDAWFESVSGFTTTGLTMFTGSVDPVTGTYVPAVEELPRTVLFWRSFIQWVGGVGIVVVAVSIIARPGSAARLLYVAEGRSERIEPSVIATAKKVLFVYTIVTVIDTILLYVAGMDWFDAVNHAMTGIATGGFSTKNNSIAEYHSIAIELAAMFAMFSGAVSFSDWHSLIIKWRLKRFFSSPELKALLTLMAIGTIAATAALVRNGFGIIEALRYASFQIVTTITGTGFQNTGLGDKPEIFKALLTTYCLLGGAAFSTTGGIKMLRLIIAVKSTLWEAEALSAPRGYTLRRRLAWIVLDDESARRALTIIFAFSLTMVVGTFIAMLILPDRSFADVALETASALGNVGVSTGITGADSPLALKLLYIALMTLGRLEIVPYFYAVHVMYSKVVHAVRARRGRRKLLRETRVAREAPL
2.4E-42	155	18	1.6E-40	148.4	12.5	2.1	1	G8QC85_PSEFL	Trk system potassium uptake protein	trkH2 PSF113_2435	Pseudomonas fluorescens F113	484	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens F113	1114970	>tr|G8QC85|G8QC85_PSEFL Trk system potassium uptake protein OS=Pseudomonas fluorescens F113 GN=trkH2 PE=3 SV=1MSIAVLRLIGFILGIFLITLAISMAIPLFTLMLYERNDDLSAFLWSSLITFVCGIALVARGRPEHVQMRPREMYLLTTASWVFVCAFAALPMVFIQHISYTDAFFETMSGITTTGSTILTGLDTASPGLLIWRSMLHWLGGIGFIGMAVAILPLLRVGGMRLFQTESSDWSEKVTPRSHVAANYILWIYIGLTALATLALWLAGMTPFEAINHAMSLISTGGFSTSDASLAHWPQPAIHWVSVVVMMAGSLPFTLYVATLRGNRRALLKDQQVRGFIGFLVITWLVVGTWLSLNSDHEWWDAVRIVAVNVTSVVTTTGVALGDYTLWGSFALLLFFYLTFVGGCSGSTAGGLKVFRFQVAGALLMGSLKQLIHPRAVIRKKYNNHPIDEEIVRSLLTFSFFFTITIGAIALGLALIGLDWTTALTGAATAVCNVGPGLGTIIGPAGNFSTLPDSAKWLLTIGMLLGRLEILTVLVLFTPVFWKY
2.7E-42	154	30.3	1.6E-41	151.8	16.4	2.8	3	D6YSZ8_WADCW	Potassium uptake system, Trk family	trkH2 wcw_1854	Waddlia chondrophila (strain ATCC VR-1470 / WSU 86-1044)	550	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Waddliaceae, Waddlia, Waddlia chondrophila, Waddlia chondrophila (strain ATCC VR-1470 / WSU 86-1044)	716544	>tr|D6YSZ8|D6YSZ8_WADCW Potassium uptake system, Trk family OS=Waddlia chondrophila (strain ATCC VR-1470 / WSU 86-1044) GN=trkH2 PE=4 SV=1MLYRDICKILGYYLLGLAVVLVVPLLLAAYYQWIADPMMHPQPHVTHAFFWSAASCLAISFCCYQYGKHSIGHLYRREGLVAVVLIWFLTPVFAGLPFYLSGTLENPCHAFFEAASGFSTAGATTMQAKKYDPRTGQEIPIERVFGGQQKTIYSYYGTIKPVVDPVTGKVLYEGIEAVGKALLFWRSFTQWLGGMGIVVLFVAILPALGIGGKRLFQAEIPGPIKDSLTPRIKETALQLWKIYLGLTAILAGLLLVTNHEMSWLEVATVTLSTISTGGFTTRNASIGAFDNPFTDWIVMIFMVLGSINFSLYFFLLKGKFYRIYVEPEFFLFIAILILGCGVVSWQLVGNPLVLLSGEKLGLMSIHDAIRYGSFQFISAMTTAGFATVDYDHWPYFVQVLMLIVMFIGGMSGSTAGGMKVIRQLMVFRIVQYKCESLFRPETLRFFKLGEKEVGSGASIMVLCYFVIVIAMMAFSTIFYVWDGIDPQTSLSLSTMMINNIGMGFRMASPMESCAFLSDFALLFSSLLMIFGRLFEFLAVLAVMVPAFWQKSK
3.4E-42	154	25.1	1.1E-22	89.7	5.1	2.1	2	C5CDT1_KOSOT	Cation transporter	Kole_0375	Kosmotoga olearia (strain TBF 19.5.1)	502	cellular organisms, Bacteria, Thermotogae, Thermotogae, Kosmotogales, Kosmotogaceae, Kosmotoga, Kosmotoga olearia, Kosmotoga olearia (strain TBF 19.5.1)	521045	>tr|C5CDT1|C5CDT1_KOSOT Cation transporter OS=Kosmotoga olearia (strain TBF 19.5.1) GN=Kole_0375 PE=4 SV=1MYPKALKKRYKVIFGYIGELFVYFSVALLTPLIIGIWHPEEFSNAEPFIYAALISFLFGMAFKLWLKVKPGTPLSVQEGAIIVVFVWIFGIVFSALPFVFGNILNFSQAIFESTSGWTTTGLTLVDVTKIPRVYLVWRSLMQFLGGAGFAIIMMSAILGPGGFGLYHAEGRIDNLVPNIKSSVRRILLIYFTYAIGGIIAYKIAGMNWFDAFNHSLTALATGGFSTRAGSIGEFNSVAIETVTIVLMILGTTGFGIHYTLWKGNFKAFAKNGEPKLMGLILLFFTPMLMSTTFNMLAASSSSSFRLAVFQAVSALTGTGFSTVDFTNWASKGLFTGLYLLTLLMIFGGDMDSTSGGLKQYRLYALIKLIGLEIKKFFLPKNAVAVTEIWKGEKKRYIDSNLVKEILIVFTMYFLTYTIGTGIISAYGYSLADSAFEFASALSTVGLSVGITRPDAPLGIIWTETIGMFLGRLEFLVVIFGITKMFKDAFYIATVRKRKATEV
3.9E-42	154	27.3	1E-41	152.4	18.9	1.6	1	U2KSU4_9STRE	Cation transport protein	HMPREF1557_00489	Streptococcus sobrinus W1703	475	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus sobrinus, Streptococcus sobrinus W1703	1227275	>tr|U2KSU4|U2KSU4_9STRE Cation transport protein OS=Streptococcus sobrinus W1703 GN=HMPREF1557_00489 PE=4 SV=1MVRYLLAKLLLIEAGLLAVPLFVALIYHEHWRVFASLLATMGILTFLGLAGSILKPKNYRIYTKEGMLIVALCWILWSFFGALPFVFSGQIPSLIDAFFEVSSGFTTTGATILSDLAVLSHALLFWRSFTHLIGGMGVLVFALAIMENSKNAHLEVMRAEVPGPVFGKVVSKLKDTAQILYIIYLVMFAIFAAILWVCGMPFFDSLVTAMGGAGTGGFAVYNDSIAHYHSSLITIVVSVGTLIFGVNFNLYYFLLIRKFKVFFGDEELRTYLSIVVVAATGLIFLNILHLYGSWSQSLQYSFFEVSTIITTTGFGITDLTKWPLFSQTVLLILMIIGGSAGSTAGGFKVMRSLIVSKITKNQILKTLYPNRVMSLHVNHRPLDKATQHGILKYLAVYAMIFLGLILVISLDNNNFMIVVSAVASTFNNIGPLLGTADTFAIFSPWAKFLMSLAMIAGRLEIYPVLLLFIPKTWSKY
4E-42	154	19.2	2.8E-41	150.9	13.3	1.9	1	R5Q046_9PROT	Trk system potassium uptake protein	BN820_00897	Acetobacter sp. CAG:977	527	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acetobacter, environmental samples, Acetobacter sp. CAG:977	1262685	>tr|R5Q046|R5Q046_9PROT Trk system potassium uptake protein OS=Acetobacter sp. CAG:977 GN=BN820_00897 PE=3 SV=1MRLGIPLFVSGVILLIFGVAMLIPAALDFADGNTNSALGFCHAAAVTCFCSLLFIATFYNTWKKLSVREMYLTTSVVWMSVCCFCALPFFFSSHPLSYTDAFFEAMSGLTTMGATVISGLDNMPRGILLWRAMLHWVGGLGIIVIALAILPLLKIGGMQLFSTESSDKSGKTMPKTSQIIGTLMIVYLLSTIACIVCLKISGMSSFNALAYSMATVPTGGFAPTDSSAMNLPAAQQQWILTLFMFTSGLPLFYLFFIYKKDWQKVKSDMQVKTYAAFVLIVSLTLTAWLLAKFPDRNIEEALRASFFQVISAVTSTGFVSENYETWGDFGMLVILLLIPVGACCGSTSGGVKMFRFDILFLSSLHYLRSKILPHGVFVPKYNDTPLNDDVVSGVIVFMTIFFASFLLSALALAAMGIDLITALSAAASAIGNTGLGLGKVGPTAGKSRSYRQLCRFARRRKMDFVRRYDVGTSGVYDRLRLAVAFGLAKGKEKKYRLYLLDSEEETVISCPHFSINFFWRSFNVITLR
5.2E-42	153	32.3	9.9E-42	152.4	22.4	1.3	1	R7CU88_9FIRM	Uncharacterized protein	BN625_00565	Dialister sp. CAG:357	448	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Dialister, environmental samples, Dialister sp. CAG:357	1262869	>tr|R7CU88|R7CU88_9FIRM Uncharacterized protein OS=Dialister sp. CAG:357 GN=BN625_00565 PE=4 SV=1MFRYIVSALSQLHRGVLICGGFALFMAFGALLLMLPFSTTGNAEVSFVDALFMSVSVVSVTGMSMFDVRTDFTIFGQLVILFLMQVGGLGIMTIMAMVGISTGRKIRLQERLLIRDSFNLQTPSGMVMLVRKIIFMTLLVEFISGTLLAVYFYFKFGPMGIYLGYWHAVSAFTNCGLDIMGANAGFAKMAADPFVSTVIVVTMFLGGVGFMAADDFLRHRSWSGLSLNSKLIFLMEAILIPLGTIIFYNLEGNNPETLGGLSTMEKWQSAVLMSVSSRLGGFAVFDIHSMLDQTVLLVMMFMFIGAAPVSTGGGIRTTTIGLLFLSLYAWIRGKKDVVIFHKHVDPDCLVKASNVFTLAVVITFITAFLVFAFEPMSFDFEDVMFEAVSAFSTVGFSMGLTGEWNTPCKIVLMIAMYIGRIGVMTLAITFASHHSRQLKYPKENIIVG
5.2E-42	153	20.8	1.9E-29	112	11.7	2.9	2	Q3JAN5_NITOC	Cation transporter	Noc_1639	Nitrosococcus oceani (strain ATCC 19707 / NCIMB 11848)	469	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Nitrosococcus, Nitrosococcus oceani, Nitrosococcus oceani (strain ATCC 19707 / NCIMB 11848)	323261	>tr|Q3JAN5|Q3JAN5_NITOC Cation transporter OS=Nitrosococcus oceani (strain ATCC 19707 / NCIMB 11848) GN=Noc_1639 PE=4 SV=1MLAILTLAPLGASIIFNEYALSIRYLAIVLVLSFLAIPLARLSVPVQVQVNEALVVVVLTFILAPLVMSFALMGEGLSFLDAFFEAVSAITTTGLSTLASVEDKSQTFLFARAWMQWYGGLGIVVLSVALLMGQHIAARRLTEPMGGADDGWVTTARAHARRMLVVYGVLTGWGLWVLWMVEGDFSWALNYALSAVSTGGFSPSDKSLLGLDTSFARWAIILLALAGAIPLPLYYLIYHFGWRQALGKRGLRIFDMELRALVLIGLAGSGVLAWLLCSSLGLPWMESVFQGLLLGFSAQTTAGFSSLEVAELDSGSKLLLIGMMGIGGGVGSTAGGIKILRLLIFLRLVQFLIQGTALPPQAVHKPKLAGRILQEEEIRQVLLLILLFGMVVWCSWFLLVLFGALPLDAFFEVVSATGTVGLSTGITAPDDLHPLLKLLLCLDMLFGRLEIIALLVLCYPHTWIGRRTGS

															>tr|X4QWH5|X4QWH5_9ACTO Potassium transporter Trk OS=Trueperella pyogenes GN=CQ11_09860 PE=4 SV=1
5.5E-42	153	27	4.2E-41	150.4	19	1.9	1	X4QWH5_9ACTO	Potassium transporter Trk	CQ11_09860	Trueperella pyogenes	460	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Trueperella, Trueperella pyogenes	1661	MALEPFQVKVARRGSSIRDRVDHFARHSPARLALIVFAIIIILLITSLLLMPFAKAGPGSATFLEALFTATSAVCVTGLTVVDTASYW TSFGHVVIAIGIQIGGLGVMTLASILGLAVSRHIGLTQRILAATETKSRLGDVGGLLQAVLITSLTVEAILAVVLFPSVMAVEGTFLGALGH SIFMSLSTFNNAGFLITKAGLTPFVGNWAISLPIIFGTMAGAIGFPVILNISRNLRSPKRWSLHTKLTLVVYAALWASAVLLIGAFEWNGA FAGLATDERILASLFQGTTPRSSGLSTVDIGSMSESTWFIIDILMFIGAGSASTGGGIKVTTFAVLFLAIVAEARGDRDTEAFGKRIPPDV IRLAISAAFLGAFLVGISTLIILQISDLPLSRVLFDVISAFATCGLSTGITPMLPDSAKVILVILMYLGRIGTMTFAAALALRSRRRVIRLPEDR PIIG
									>tr|G4TN64|G4TN64_PIRID Related to potassium transporter TRK-1 (Fragment) OS=Piriformospora indica (strain DSM 11827) GN=PIIN_06700 PE=4 SV=1						
6.2E-42	153	0	7.3E-42	152.9	0	1.1	1	G4TN64_PIRID	Related to potassium transporter TRK-1 (Fragment)	PIIN_06700	Piriformospora indica (strain DSM 11827)	219	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Sebacinales, Sebacinales group B, Piriformospora, Piriformospora indica, Piriformospora indica (strain DSM 11827)	1109443	ATSVRCAGVASVSLAAVAPATQVLYVIMMYIAPFPIALAIRSSNTYLDRSLGIYEQDSDSDDEEMEARFEKDKRPRHRVWGSYLA WHAKRQLEYDIWWLVMAWLVVTIFERGKIWNPATKQFDLFGILFELVSAYSSVGLSIGLSNANYSLSGAWSVPSKLMLILVMIRGRSR GLPVAIDRAVMLPKEFWSKTISQTPTMAPPASEKPRLETIHEKQSQ
									>tr|R5EIB4|R5EIB4_9BURK Cation transport protein OS=Parasutterella excrementihominis CAG:233 GN=BN548_00269 PE=4 SV=1						
6.5E-42	153	33.4	9.9E-42	152.4	23.2	1.2	1	R5EIB4_9BURK	Cation transport protein	BN548_00269	Parasutterella excrementihominis CAG:233	615	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Sutterellaceae, Parasutterella, environmental samples, Parasutterella excrementihominis CAG:233	1263099	MPNNLPRLEKAIKRIIWEQKHKAPNESQNYVQWLQKIDVFFTGLTAIASVGSLLGIAFYYGLNNSTNEASGFLVGLHAALFLFTVN ILLGICFAFNRFVLHAGILKWIVNLLILISAAAYFFPAASNWFGYISSKEFLFFSLASYSLVFLSAKALDLANSYRMNPSLILASSFIVVIFIGT FLLMLPKSTKEPIDLIDAFFISTSAVCVTGLSPIDISQIFTNFGLLVLSVLIQIGGLGLIAFTSVFAIFYAGSTSVYNQLLIRDMIYSKSMDALL PTLLYILGFTLSIETIGAFLIYVTVPSSLFTTLSDKLIFSAFHSMSAFCNAGFSNLKDGLSNEVLLKGNQFFYLVICALMFLGSIGFPILNLK DKLFWKLKNQLFLSTEEQTNFIRFDLNTKLVLITSSILVAAGTVLFLIFEYDGTLKDMSFFTKIVQSLFNAILPRTTGFASVNPADFQPSTI LLVCLLMWIGGSSQSMAGGVKVNTVAVLFLNLKGIITGSDQTGAFHRAISEKAVLRAYAVAFIATVCVFVFSFILILLEPGQPIRSIIFEVM SALFTVGSSLGLTPVLSGESKFVLCIAMFLGRVGLLSILIGLLGHRGAKGCSFPNEHIIIN
									>tr|N1RHU4|N1RHU4_FUSC4 Low-affinity potassium transport protein OS=Fusarium oxysporum f. sp. cubense (strain race 4) GN=FOC4_g10010473 PE=4 SV=1						
7.9E-42	153	0.2	2.1E-18	75.5	0	2.4	2	N1RHU4_FUSC4	Low-affinity potassium transport protein	FOC4_g10010473	Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	849	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Hypocreales, Nectriaceae, Fusarium, Fusarium oxysporum species complex, Fusarium oxysporum (Fusarium vascular wilt), Fusarium oxysporum f. cubense, Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)	1229665	MAHPGSPLSLFLGFCLRIFLNVTKVTNGLLFSLEDMLDETRASVWARLKAVKPPFMSKKPHFNFISVHYTWIIGATLLASVIIYGA GRGQTSYVDSLMFASGANTQAGLNPIDVNLLNTFQQIVVYLFTITSNPITLHTSVVFLRLYWFEKRFQGWVTDARQRRATLSKAKTRP RNEREAEEGVNGRHITVVPYQGRPPRITNDGILLDGNDVIQSQAIADDDDDENLPHKPPPASSDESDTVSAGRSNSIELSPLEKPDQG FGDGREANEGQSRSQNAPTGIKFAETVKRSDGVDDDLTKFPQRRSHAEHIAILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQ DGDDDNNTIAMTRTVESRPDHATLDSRAPTGRRPTIVIAEPKRPLKHELTDDAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMG RAFRTRTIDTIKSALSNDHTKDMPYLSYTPTMGRNSNFVGLTLEQREELGGIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEKYGR IVEGNAISRTWWGFWTANSGRSNSIELSPLEKPDQGFGDGREANEGQSRSQNAPTGIKFAETVKRSDGVDDDLTKFPQRRSHAEHI AILERQRNQDNEILRIPGPRETERGMGPRRLDNDDTQDGDDDNNTIAMTRTVESRPDHATLDSRAPTGRRPTIVIAEPKRPLKHELTD DAKAVGGTLNALRVRKPRVFNRGQKEVHDDNESTMGRAFRTRTIDTIKSALSNDHTKDMPYLSYTPTMGRNSNFVGLTLEQREELG GIEYRSLRTLALILLSYFWGFQLIAVTFLLPFILHNEKYGRIVEGNAISRTWWGFWTANSAL
									>tr|Q8F982|Q8F982_LEPIN Potassium uptake transporter OS=Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) GN=trkG PE=4 SV=1						
9E-42	153	31.9	8.9E-36	132.8	18.2	3	2	Q8F982_LEPIN	Potassium uptake transporter	trkG LA_0314	Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	539	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira interrogans, Leptospira interrogans serovar Lai, Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	189518	MQPLKFIKRNVNRIAKAFLLLSVARTLCLGFTITILIGSFGIYISESGRLSYTVSLYLATSSICVTGLSPVLLSELQRSTQLIMMFLIQI GGLGIITFTVLIGVLVVRGLSRSTRLASFVYEATDAHLAKRMRDKKLEQQSAVISPGKKKTEAEASYVRRMLISLFNITLSIEAVGATLLF FCMPETDRLPGTPNRFFLSIFTSISAFNNAGFSIVDDLSFLSKDPLCLLIVQFLIVMGGIGFPVIIFIEKSILEIIQKFMGKVEAVTETFMMR RTVLLGEDPPAWYIFVIATSVRLEGRLEIYRKELFGDANRMQMAIIVLGSLILIHIGGIAILLIEYNNVETIGKMVFSEKLFNSFFLSVSSRT AGFNTFDIAEIESATYVLLCALMFIGGGPQGAAGGIKITTFFILILYLKNVIRPQARVQAWGEDVSKNSVAISTRIYFLATISLVVFMFLITL ANGNRHGIETIFFEVMSAFGTVGLSLGMTAYTNDLEKFLYIALMFMGRVGTFTLLIAFTGHSGLGDLGGKDDDGLKIQVG
									>tr|A0A0F0KZ77|A0A0F0KZ77_9MICO Ktr system potassium uptake protein B OS=Microbacterium azadirachtae GN=ktrB PE=4 SV=1						
9.3E-42	153	19.2	2.2E-41	151.3	13.3	1.5	1	A0A0F0KZ77_9MICO	Ktr system potassium uptake protein B	ktrB RL72_01483	Microbacterium azadirachtae	476	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium azadirachtae	582680	MARSTPARSFSDVARRTVRVAKTLTTSSPSRFAIVVFSALILITTALLSLPIATTDRTVTPLADALFTAVSTICVTGLSTVDMATHW SGFGRAVIFIGVNIGGLGVLTLASVMGLAISKRLGLRAKLIAAGDTNPMRAHGGPVNESQTVRLGEVGALLRTVAISAFAIEAGLMVLLY PALLTAGVDPLTALWEAPFYAAMAFTNTGFTPNPGGLAPFAQNYYVLTVLMLGVFLGSLGFPVIYTLARQRWHVRRWSLHTKLTMIT TIVLFVVGAGVFLLLEFDNPKTFGSMDAADTTFQAFFLSAMTRSGGFNVVDMGDLNGSSMLAASMLMFVGGGSASTAGGIKVTTLAV LALAVVSEAKGRPSVQAFGRRIPSDVQRVALSVVAWGSTIVAVSTIAISQITKFPVDEVLFDVVSAFGTVGLSTGVTGNLPDPATYILAA TIFMGRVGTVTLAAAVAATNRTQLYSLPVERPIVG
									>tr|A1R9W2|A1R9W2_ARTAT Trk-type K+ transport system, membrane component OS=Arthrobacter aurescens (strain TC1) GN=trkB PE=4 SV=1						
1E-41	152	24.4	1.4E-41	152	16.9	1.1	1	A1R9W2_ARTAT	Trk-type K+ transport system, membrane component	trkB AAur_3328	Arthrobacter aurescens (strain TC1)	477	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter aurescens, Arthrobacter aurescens (strain TC1)	290340	MSQSQSRSTSPTNWQPNQQEREGLWIFTRVRDFVDNIANTSPARLALTVFAVVILIFTGLLSLPAASTAGTVTPLHQSMFTAVS AVCVTGLTVVSTATHWTFFGQLVILVGIFVGGLGTLTLASLLALMVSKRLGVRGKLIAQEAMNNAGRLGEVGTLLRIVIVTSVVIEAALAL ALIPRFILLGEDFWQSVWHGVFYAISSFNNAGFTPHSDGIVPYETDLWILIPLMLGVFLGSLGFPVVMVLQQNGLNWKKWNLHTKLTI QVSFILLAAGTVLWALMEWDNVRTIGHMDMGDKVIHSLFASVMTRSGGFNLVDQNHMESTTMLLTDALMFAGGGSASTAGGIKVTTI AVMFLAIMAEARGDADVKVYGRTIPQGTMRVAISVIVAGATLVSVAAFLLLSISGASLDRVLFESISAFATVGLSTNLSAELPPSGVYVLT ALMFAGRVGTVTLAAGLALRQRSQLYHYPEERPIIG
									>tr|R7EJL6|R7EJL6_9FIRM H(/)-transporting two-sector ATPase OS=Anaerotruncus sp. CAG:390 GN=BN640_00514 PE=4 SV=1						
1E-41	152	19.7	2E-39	144.8	13.6	2	1	R7EJL6_9FIRM	H(/)-transporting two-sector ATPase	BN640_00514	Anaerotruncus sp. CAG:390	438	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Anaerotruncus, environmental samples, Anaerotruncus sp. CAG:390	1262703	MKNAFSGFIKRQSPARIIAFGFAAVILIGSGILMLPCSVREGVALRYIDALYTSTSAVCVTGLIAADAGDTFTAFGQTVLAALIQIGG LGVTAIGAGVILATGRRMNLKERTVVREALNFDSGSGVVRLLRSIFLTTVVIELAGAALSYPVFARDHTPLHAVGISLFHSIAAFNNAGF DILGGGTNLIPYRDSITLNLVSAMLTVLGGIGFLVIREVLSKRFRRRRFSMHTHVVLSMSAVLLAAGTLLLKFTEGDNISWLGAFFFSAS ARTSGFSTYPLSGFSNAGLIVLNVLMFIGASPGSTGGGIKTSTFFALLQGIRSAATNKSEKAFRYSVPKSAFRKAAVITAIGISVVLTGTF FMALMEPDIPLRDIVTEVVSAFATVGLSTGITPGLSVGSKLLSVLIMYIGRLGPMTIVTLWYFSRGERVSYPEGNLVIG

1.2E-41	152	14.2	7.1E-41	149.6	9.8	2	1	A0A0D6TGK8_9RHOB	Trk system potassium uptake protein	SY26_04590	Paracoccus sp. 361	483	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 361	1603292	>tr|A0A0D6TGK8|A0A0D6TGK8_9RHOB Trk system potassium uptake protein OS=Paracoccus sp. 361 GN=SY26_04590 PE=3 SV=1MIDIRPVAHPIGKILTAIGGMMLAPMMVDWWHGDPHWMVFLQSAVITMAAGVFVAVATAGRYDHLSLHQAFLLTSGIWLVLPLF GALPFMLGAPNATFTDAMFESMSGFTTTGTTVLPQLDSLARGIHLWRAILHWAGGLGIVVVAMVFLPVMKVGGMQFFRSEGFDTLG KVLPRAGQIATEMTQLYLILTGACIITYLILGLTGFDAVVQAFSTISTGGFSNYDASFGAFLGPAEWASSVFMVLASIPFIRMVQLMRGQ AKPLWRDIQVRAYLRWIGYACVIILLYRVLWLGQTGHPEEMLRETVFNVISTFSGTGFASTDVTQWGHLPLMILVICGLIGGCTGSTGC SVKVFRYLVLFEAVRAQIRRMHSPHRVYPLRYDGQPLEQDVVDSVMAFFTLFFLTFGLLIVGLSLTGLHPRTALTAAWTAIANIGPVWG PEVTRNGSIAEFPTSAKWLMTVGMFLGRLELVSVLVLLLPRFWRD
1.3E-41	152	14	1.6E-40	148.5	9.7	1.9	1	A0A099GH73_9RHOB	Trk system potassium uptake protein	IX56_09610	Paracoccus sp. 5503	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 5503	1545044	>tr|A0A099GH73|A0A099GH73_9RHOB Trk system potassium uptake protein OS=Paracoccus sp. 5503 GN=IX56_09610 PE=3 SV=1MIDVRPVIHAISKLAIVMGVMMAAPAAVDWSAGAASWRIFAATGAGTALVAWMVMLATRHEGRTLTLEQAFLLTSGLWLVLPVI GAMPIRAAVAGAGFTDAMFEAMSGLSTTGATAFPELGALSDGVHLWRGLLQWSGGLGIVVVAMVFLPVMRVGGMQFFRSEGFDTM GKVMPRAGSIAAEMTELYLGITILCAMIYAGLGMSGFDAVMHALTTCSTGGFSNLDASFGAFIGAPEVAATVFMILASLPFVRMVQAM HGDFAPLWRDSQIWTFLAIIAVVCTLIVIYQSLWLDVPPSLGLLREVAFNVVTIMTGTGYASVDVTQWGHLPFVLLITVGLIGGCTGSTC CSVKVFRYQVLFQALTAQLAQMRSPNRVRLLSLQGRRLDPEVVNSVMALFTLFVLTFGVLIVGLALTGLHPRTALTAAWTAIANVGPA WGPEVSGNGSVANFPTTAKWLMIVGMYLGRLELITVFVVLMPRFWRQ
1.5E-41	152	18.5	5.4E-41	150	12.8	1.8	1	A8LS49_DINSH	Trk system potassium uptake protein	trkG Dshi_2406	Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Dinoroseobacter, Dinoroseobacter shibae, Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12)	398580	>tr|A8LS49|A8LS49_DINSH Trk system potassium uptake protein OS=Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12) GN=trkG PE=3 SV=1MFDLRPVGYVIGLLVAALGASMLVPMALDLIAGNGHWPAFLESAILSGLVGGLTAIACANGVGDRLNIQQTFLLTTGVWLALPVF AALPFVFGATEARYVDAFFEAMSGLTTTGSTVFTGLETLPPGLLLWRGMMQWFGGVGIIVVAMVFLPELRIGGMQIFRSEGFDTIGKI LPRATQIASRISVIYLGLTGACALTYLILGMTGFDAVVHAMTTVATGGFANSDASFGAFPAAMEYAATLFMLLAALPFVRYVQLVAGTA RPLLHDPQVRAFFATVAVIVLIIATWKMIAIDTPGEESLRKSLFNTVSIITGTGYASADYMLWGAFPVVVLFFAGLIGGCAGSTACSIKVF RYQLLIASIVAQIRRIHSPHGMFTPRYGGKPVTEDVLSSVMAFFVMFTVSLGILSVLLALTGLDFITSVSGAATALGNIGPGLGDQIGPA GNFAGLNDTAKWILSAAMLIGRLELMVVFALFTVRFWRA
1.5E-41	152	24.8	2.2E-41	151.3	17.2	1.1	1	B8HFD7_ARTCA	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Achl_3144	Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	477	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter chlorophenolicus, Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	452863	>tr|B8HFD7|B8HFD7_ARTCA H(+)-transporting two-sector ATPase OS=Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6) GN=Achl_3144 PE=4 SV=1MTQSQSRPRTPASWHPPAQEREGLWIFTRLRDFIDDIANTSPARLALSAFAGVCLVFTFLLSLPVSSASGTATPIHQALFTAVSA VCVTGLTVVSTAVHWSFFGQLVILVGIFIGGLGTLTLASLLALMVSKRLGVRGKIIAAESMNNAGRLGEVGTLLRIVITTSVVIEGILALTLI PRFLTLGEPFWQSVWHGIFYSISAFNNAGFTPHSDGIVPYETDLWILIPLMVGVFLGSLGFPVVMVLQQNGLNWKKWNLHTKLTIQVS FILLAAGAFLWALMEWDNARTIGPMGFGDKITHSLFASVMTRSGGFNLVDQNHMESTTKLLTDALMFAGGGSASTAGGIKVTTIAVM FLAIIAEARGDADVKVYGRTIPQGTMRVAISVIVAGATLVSVSAFLLLQISGASLDRVLFETISAFATVGLSTGLSAEVAPEGVYVLTALM FAGRVGTVTLAAALALRQRSQLYHYPEERPIIG
1.8E-41	152	30.7	1.8E-41	151.6	21.3	2.4	1	E0SRK9_IGNAA	Cation transporter	Igag_0446	Ignisphaera aggregans (strain DSM 17230 / JCM 13409 / AQ1.S1)	492	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Ignisphaera, Ignisphaera aggregans, Ignisphaera aggregans (strain DSM 17230 / JCM 13409 / AQ1.S1)	583356	>tr|E0SRK9|E0SRK9_IGNAA Cation transporter OS=Ignisphaera aggregans (strain DSM 17230 / JCM 13409 / AQ1.S1) GN=Igag_0446 PE=4 SV=1MSKRLKAIIFSVSILVTTILFIALLLGVIFFLYSSYTGIEIEKLSSIRLIEISLVMILIFLIPTYLCRGEPITEIIDAFIVVVLSWLIIPCVSAIIYR YTIDLDIFDAFFESISGFTGTGLTIITTPEDLPYVILLWRSITQWTGELGIVVVSGALLPFLHRFLRTVYMAERGSRLAPTIISTIRRLFIVYII YTSIGVILLSISGMNILDSIAHSMTAIATGGMSTNSQSIGYWFQGKNYLILATSGIVMVLGAFNFNDLYNLIRFKLRNFFSSPEVRGFIAIS LIFTLVIGIVGYIMNISNKTIIWIYHMLSGFTTTGFQIDNIYNDPDIIKLILILAMVIGGATFSTAGGIKIKRFIIALKSISWELLRPFIPEETIVVK RLGREVLDESEVSMVLSFIFLYFITAIILSSTLYITLIINNIYMYSYIDCLFETISAQSAVGLSIGITNISAPIASKMVLIIAMYLGRLEFLPIYLLI GSYYRKRYVFE
2.2E-41	151	15.7	8.1E-41	149.4	7.4	2.8	2	A0A0F8BUK5_CERFI	Potassium transport protein 1	trk1 CFO_g1391	Ceratocystis fimbriata f. sp. platani	624	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Microascales, Ceratocystidaceae, Ceratocystis, Ceratocystis fimbriata f. sp. platani	88771	>tr|A0A0F8BUK5|A0A0F8BUK5_CERFI Potassium transport protein 1 OS=Ceratocystis fimbriata f. sp. platani GN=trk1 PE=4 SV=1MEESPPGFWPRLKTNLKTFLPTSKPHFSFITIHYIAIVGFSLFGSVLVYTIGNNNLAYIDALFFSTGSSTQAGLNPVDVNLLNTGQQ VVLYLIPMMANPIIMHSMVVYLRLYWFEKHFNQLVKEARLRRTTISKSRTKDQQQADPESQINRQNASSSSVQSSDGSKTANSSGGV RGRRITVMHSSGRPQRMAHDGAMLSPLPDVKSPTPHSIDTAANPLPSDSSQSSSTESETGSKSYKPPASADGNDSEDDGDISPTQT SPSRQPNRIVFGETVKRSDGVDAQTNFKPVSYGAGQLLSQGSTAGSEHVLERPNLSRVISVDGDEVLRIPNPREVEQGIVPTRVPRE SAALYRPESRDDVISEPSRETRDHRQAQNTRNTRMEIAEEAEALKNTFSIFKMPRWLKRCFGREVDNEMPSAYRTRTFSQIRDIISGG EAIQDMPYLSYTPTTGRNSQFIGLSLEQREELGGIEYRSLRTLAVILGCYFWGFHIFGLCFLLPFIKHSNRYGQILDNMAINRTWWGFF TSGSAFMDLGFTLTPNSMYSFNSSTLVMLVMSFLIVIGNTGFPIMLRFIIWLLSLIVPEKSGLWEELSPTWWLFGVLILFNGVDVILFIILD TCLSTLAF
2.4E-41	151	25.6	1.1E-38	142.4	17.7	2.2	1	R5G2Q2_9FIRM	Cation transport protein	BN756_00526	Coprobacillus sp. CAG:698	499	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:698	1262856	>tr|R5G2Q2|R5G2Q2_9FIRM Cation transport protein OS=Coprobacillus sp. CAG:698 GN=BN756_00526 PE=4 SV=1MNKRMILYIIGKLLIAVALLMVLPLIASIIYHFTNGENLNLLAFVIPMALLVGLGFFLSFKKPKDNNIFAREGFVLVGLSWIIISIFGALP FVISGEIKSFFDAFFETVSGFTTTGASILNGDEIETLSHGMLFWRSFTHWIGGMGILVFLIFIPSDGKNIFIMRAESPGPQFGKLVSKIN FSARILYIIYLGLTLLQIIILVCGGMDLFDAIVNSFATAGTGGFAIKADGIAGYNNFCQVVIAVFMMLFGINFNFFFLLLMGKFKQAFKMEE VFTYIGIVVFSTVAIAINLFIVTGNSLAIILKDSFFQVSSIITTTGFSNTDFNLWPEFSRMILIILMFVGACAGSTCGGIKVSRFIILIKSIKRNIK KMLHPKSISNISFESGILDEETISGTSNYFALMIILFAFCVLLLSLDPFNVPANMIPIEGINKFTTNFTAAASCINNIGPGLNLVGPSGSYGF YSDFSKIILSIAMLIGRLEIYPLLLLFSPKVWKNK
2.5E-41	151	20.8	6.5E-40	146.5	14.4	2.1	1	R5SXZ5_9GAMM	Trk system potassium uptake protein	BN527_01968	Acinetobacter sp. CAG:196	486	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, environmental samples, Acinetobacter sp. CAG:196	1262690	>tr|R5SXZ5|R5SXZ5_9GAMM Trk system potassium uptake protein OS=Acinetobacter sp. CAG:196 GN=BN527_01968 PE=3 SV=1MRLNYLAYSFSLTIMYFSFMLMLPVLVALYYHETGAVLPFLLTGAAALMISITIKKVISGIAQIKSINDIKKSEGLCVVSFSWIFAIILA SIPYLFFGISPVDALFEATSGITATGSTILTHFNYPNTVFFWRSFTQWLGGMGIIVLFIAILPQFAIAGRQMFFAEAPGPTEDKFTPRIKNT AAALWKVYAGLTIIEIAFLKINGMSGFEAVCNSLSSISGGGLSPNSQSMIGCSYPLLWITAFFMFFAGVSFNLQYKAWIKLNPLVLFRNE EFRTYFSAIFLIGILLSISLFFNMHYDLAGSITHSFFNVSTLVSSTGFCSVDYTKWDYTSKLLLFAIMLFGSCASSAGGGLKVMRWLLVF KIIKTEMTKILHPKAVCNIKTGSYSVPKEILDQTLMFVAFYFVILGVSAFLIAVLEQNTTIGLTGAVSAVGNIGPGFGAIGPLGSFAPLNALT KLILIFDMLIGRLELIPILVLFQKDFWVLKR

2.5E-41	151	27.5	4.2E-41	150.4	19.1	1.3	1	D9SBJ7_FIBSS	Putative TRK system potassium uptake protein TrkB	FSU_1970	Fibrobacter succinogenes (strain ATCC 19169 / S85)	460	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Fibrobacteres, Fibrobacteria, Fibrobacterales, Fibrobacteraceae, Fibrobacter, Fibrobacter succinogenes (Bacteroides succinogenes), Fibrobacter succinogenes subsp. succinogenes, Fibrobacter succinogenes (strain ATCC 19169 / S85)	59374	>tr|D9SBJ7|D9SBJ7_FIBSS Putative TRK system potassium uptake protein TrkB OS=Fibrobacter succinogenes (strain ATCC 19169 / S85) GN=FSU_1970 PE=4 SV=1MLADSLSENIFKTRTQANPIMLVVLAYLLLIAIGTALLSLPQASTRPVSLIEAFFTSMSAVCVTGLSVVDISSTFTDIGHWFIVVLMQLGGLGIMTASTTLILLAGMHPGFSHQSVFFSEFTQEGNIDAGRILRAVIPFTFVLELIGGIVYFTQFESMEMYDRILCSVFQAVSSFCGVGFTLFPNSLEGFQYNPVMNITTCILVLAGGFGFLAVAELRYIFDFKHKEIRRVSLHTRIATYGTIIVIVASILVFTFTEWNNLFSGHTIGENAQSVLFMAFTSRTAGLNSLSIPDLTQASLFFFIIMFIGANPGSCGGGIKITTAAVIGLLGVNRLLGREKTQVLGRTIPNNTVDKAIRIFVVAMVVIASATLILLCTEIPSGTAYSANSSPFLKILFEVVSAYATCGLSMGLTEELSTVGKIVICGVMFIGRMGPLFLISAVAGKLQDTAWYAEEDIMVG
2.6E-41	151	19.8	1E-19	79.8	1.9	2	2	V4JEF7_9DELT	Trk system potassium uptake protein	N839_11500	uncultured Desulfofustis sp. PB SRB1	491	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfofustis, environmental samples, uncultured Desulfofustis sp. PB-SRB1	1385624	>tr|V4JEF7|V4JEF7_9DELT Trk system potassium uptake protein OS=uncultured Desulfofustis sp. PB-SRB1 GN=N839_11500 PE=3 SV=1MNLRAIIAVLGTLLLVTGCSMVLPVVCALLFGEDDWRALTLSATIIIFGGLLVRRFFRFHGAIQVKDGVLVAVAGWVVISAVSTLPFLVSGYIPSFTDAFFEMMSGYTTTGATILEDIEALPHGLLFWRSQTHLLGGMGFLTLTLIFLPHGVGGVRVFRAESSPGQVITREKFMARNRDTMIWLWIIYLGLNALQTLLLCGGGMAVFDALCTAFGTISTSGYSPRNLSIGAYDSGYVDWVTTCFMWCGGVSFVLYYLLLKGDIATVLRNTELRWYVLLTLLFCLFVSCGLWFGGAYSGFWTALRYGSFQVVSLLTTTGFTTADYELWPAAAQMGLFVVCFVGACAGSTTSGIKIVHYVVLAHYFYGAVVRMFVQPLAVFSVRLNGKPVEQAVIDLSVCYFVINIFMVAVGAMILCVSDHLDMLTSMSAVISALMNIGPGFGGVGPAENFAFLSIFGKWFLAFNMLVGRLEMFTALIVLLPIFWRGVSVRKS
2.9E-41	151	40.1	4.5E-41	150.3	27.8	1.2	1	V6DFE6_9DELT	Trk-type K+ transport system membrane component	ktrB BABL1_gene_968	Candidatus Babela massiliensis	443	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, unclassified Deltaproteobacteria, Candidatus Babela, Candidatus Babela massiliensis	673862	>tr|V6DFE6|V6DFE6_9DELT Trk-type K+ transport system membrane component OS=Candidatus Babela massiliensis GN=ktrB PE=4 SV=1MFVYRQRTFSKIVIFSIILAIIIGTALLKLPISQNIPVPLLDCLFTATSSISVTGILTVPFDSFTLFGKIIIALLIQIGGIGLVTLYLFLFTLFSSKLAITTKIMVGQIFELESLKNIKQVLSFIILFTLTLESIGALIIYFIISSNYSTKEAIFHSIFHSISSFCSAGLSSFENNMINFQQNIPMLLITGILILSGTLGFIMWYELFLYIKNRINHKRLSLSLTTKVILSTTTALILVATLLLIMLESYNFFDFKSFGITLLNMLFNAISYRSTGFTTINLEHAQIATIFLILIYGFIGSSPGSTGGGIKVTTFAIFIATIRSVIKSRTSIELKMRKIPQDEIFKALAILSLSFSWIIFCTFILLLTEKDKNFSQLFFETLSTFATLGVATDTTPQLSIYGKLIVIANMIVGRIGTLTILLAFEKGNEKPELKYPEERITIN
3.4E-41	151	22.9	6.9E-41	149.7	15.9	1.4	1	A7I824_METB6	Cation transporter	Mboo_1367	Methanoregula boonei (strain 6A8)	508	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula boonei, Methanoregula boonei (strain 6A8)	456442	>tr|A7I824|A7I824_METB6 Cation transporter OS=Methanoregula boonei (strain 6A8) GN=Mboo_1367 PE=4 SV=1MKRLDHLAMIIHDVGRICGFLGYLSLLPFVVLVIFQEWDMLIPMASAPIAFLVLGYILTRVEVRDYEPPVSIMLVAVAAAWFLIAIVGALPFMLGMGMSYTDGIFEAMSGWTSTGFTMIQALDQAPMTLLFWRTYMQWIGGIGIIVFGISMRRRSRFSLFQIFRSEGKPEDLMPNLMSTGWRMWKIYIFLTVIFTGLVMLAGIPLWDAVNLVMVAIATGGFTLHSAGLAYYHNPLLEALLIPVMLAGAIPFKIYFLMYRGKMGALFRDRIVRLLLLLALVGSIIVSLELYLFNSMAPYDAIREGSFTAVAAICTCGLQIADLHVWTAVPLAVIALLIFIGGAMGSTAGGIKINRLVLAYEGIKWWFRRFFVSSRVIVPFRYEGKMLSKEISEMEISKNMLVIALYAITACVATILCLHLYITSFRLDEVLFECVSALASSGLTVGFITAQSPVAIKWIFIMLMWLGRLEIVPVIIMVMGIVKGLREELASESPAESEDMHAPAYEENN
3.6E-41	151	16	9.6E-23	89.8	1.6	2.1	2	U7FP80_9RHOB	Trk system potassium uptake protein	Q669_11455	Labrenzia sp. C1B10	467	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Labrenzia, Labrenzia sp. C1B10	1397530	>tr|U7FP80|U7FP80_9RHOB Trk system potassium uptake protein OS=Labrenzia sp. C1B10 GN=Q669_11455 PE=3 SV=1MLILISVLMIVPGIADVFARNSDWQVFLVSALVLGTAGLLMTMAFQGEQPPSHFREAILFVNAAWFTFSFAGAVPFYFSGLGISFTDAFFETASGLTTTGSTILTGLDTLPPGILLWRALLQWVGGIGVVAIGIWLLPGLRVGGSQLFALESSENTSKPYGHVGPFVYRLLALYAGLSIACATLYLLCGMTFFEAVIHSMTTVSTGGFSTSDQSFGQFDGLAVYWVASVFMLGSAVPFLYLIRSIERRHWVKDVQIMLLLAIVAAASISVFLFERFIGHDTPFQMFTFAVFNVVSVITTTGYAANDYLQFGPPVIAIFFVLTFFGGCSGSTSGGFKMFRIAILGSYIQGLFRRMIRPHRVVEPKYQGRAVSNPVLEGVLVFAVLYAGAFAAFSLVYMMLGLDLETALSASITALANVGPGVGDTIGPSGTFQSLPDLAKWFLAVQMILGRLEILAGILLLTPDFWLD
4.1E-41	150	25.1	1.1E-40	149	17.4	1.5	1	B2GH75_KOCRD	Putative Ktr system potassium uptake protein KtrB	ktrB KRH_04800	Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)	481	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Kocuria, Kocuria rhizophila, Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201)	378753	>tr|B2GH75|B2GH75_KOCRD Putative Ktr system potassium uptake protein KtrB OS=Kocuria rhizophila (strain ATCC 9341 / DSM 348 / NBRC 103217 / DC2201) GN=ktrB PE=4 SV=1MSELEQCSAVEESETEAPTTEPLTSRAARGVRDFVDRVADSSPARLAVIVFVIVDLGFALLLWLPVSAQPGRHTHFVDAVFTATSAVTVTGLTTVSTAAQWSVLGQVVILVAIQVGGLGTLTMTSILALAIGRKLGLKSKLITQEALNIGRLGEVGSLLQIIVITSISIEAALAVVLSVGFLAEGEPLGTALWHGVFYAVSSFNNAGFTPHTDGLVPYDHAGPTVWLILLPVSVGVIVGSLGFPVILVLRQVGFRFNRWNLNAKLTVVTTAILLVLAWVLFLAVEWSNPATLGGKSVSERIFQGFFASVMMRSGGFNLVDMPDTSQVTLLLTDAMMFAGGGSASTAGGIKVTTLAVVFLAILAEARGDQSVIAFFRTIPDSVLRIAISVIMMGASVILLGCAVMISLTHLPLDHVLFEVISAYATCGLSTGVSAASPDAGKYALSVIMLVGRIGTNTVATALALRSRRRLYSYPEERPIIG
4.5E-41	150	17.4	3.8E-40	147.2	12.1	1.9	1	E2SB60_9ACTN	Potassium uptake protein, TrkH family	HMPREF0063_11269	Aeromicrobium marinum DSM 15272	448	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Aeromicrobium, Aeromicrobium marinum, Aeromicrobium marinum DSM 15272	585531	>tr|E2SB60|E2SB60_9ACTN Potassium uptake protein, TrkH family OS=Aeromicrobium marinum DSM 15272 GN=HMPREF0063_11269 PE=4 SV=1MRRPAIPAAIAHPVRLLPLSFLALITLGTLLLLMPFARSGGGGPEFMPALFTSTSAVTITGLASVDTSTYWSPAGQGIILFLVQVGGLGIVAMATVLGLFIGGRLGLRTQMVAQVDMHVVSLGEVRPLFRRVAITMLLFQTAVTIMLTARYRATYFDDFGTSLWHGVFHGVMAFNNAGFSLNSDSLVGYAGDGLIILPICVGVFFGAMGFPVLAELFRGWRRPSRWTIHARLTVWGSLFLLGSSAVAFLLLEWGNPDTLGPLSWGQKLVSGLEGGIMPRSGGLNSFDWGGVRGETLTLGTILMFIGGGSASMAGGIKITTFLLLAYVILAELRGDPDVTVGVRRISAPVIRTALTIALLAVMLVTSATMAVMLLSGGTFEDVLFECTSAFATAGLSTGLTPDLPASAQMVLVVLMFVGRVGTIAAASAFVLRRRVPRYHLPEEQPIIG
4.6E-41	150	19	9.7E-39	142.6	13.2	2	1	R5SG61_9CLOT	Uncharacterized protein	BN771_00810	Clostridium sp. CAG:75	282	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:75	1262836	>tr|R5SG61|R5SG61_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:75 GN=BN771_00810 PE=4 SV=1MFHSISAFCNAGFDILGTADNPFPSLTGYSGNVHVNVGIMLLIIVGGIGFLTWDDIYTNKLNIKRYRMQSKIILMTTAGLILIPTVFFFVCDLKNLSAGKRLLAAAFQSVTTRTAGFNTINISKMSEASKAVMILLMLVGGSPGSTAGGMKTTTFTVLILNAIATFRSRENVEAFGRRLDHYVIKNAATIAMLYFTMFFCGGIAISVYEGLPLLDCLYEAASAVGTVGLTLGITPGLHVFSQTVLIILMYLGRVGGLTLIYAVFSGRSKGNAKLPMEKITVG
5.4E-41	150	29.7	1.3E-20	82.8	11	3.1	2	R6XRH6_9BACT	Uncharacterized protein	BN655_01473	Alistipes sp. CAG:435	497	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes sp. CAG:435	1262695	>tr|R6XRH6|R6XRH6_9BACT Uncharacterized protein OS=Alistipes sp. CAG:435 GN=BN655_01473 PE=4 SV=1MNIKVISRNVGYALLVSALFMFLSILVSVANGNDSALAALMISFTITFTVGIFPFIFVRKSADITLKDGYMIIALSWLLSFIFGMLPYALWGGPFTIINAWFESVSGFTTTGSTILDNVEALPNSLLFWRSSTHFIGGLGVVVFLLLIIPSSSQMRLRLTTLELSSLSKREYRSGANKTVYIFTYVYFGLTAASFLMYMLAGMSPFDAINHAMSVVATGGFITHAMGVVATGGFSTRNASIGAYDSITIDLITMLFMVLSSVHFGMIFVAVVTRSLKPFKNEIFKFYLSMMVVAGVIVSISIKAHGFEEAWGRSFLSGFFHVMSFASTTGFSIADNSSWPVLSDTILVLMGVCCGMAGSTTGGIKSDRMMFLCKEVKYQLRMVLHPASVKDIRVNGRVIRQNDIAPHILYIALYGLVVIISLAACLTLDPDNNQSFTAILSSLGNVGLSVDQLGSIYSYSGEPSSLKFIYTLDMFLGRVEIYPILAVVMMIFSRRNK

6.7E-41	150	10.4	2.8E-32	121.3	4.3	3	3	U4L9M7_PYROM	Similar to Potassium transport protein 1 acc. no. P47946	PCON_06476	Pyronema omphalodes (strain CBS 100304) (Pyronema confluens)	585	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, Pezizomycetes, Pezizales, Pyronemataceae, Pyronema, Pyronema omphalodes, Pyronema omphalodes (strain CBS 100304) (Pyronema confluens)	1076935	>tr|U4L9M7|U4L9M7_PYROM Similar to Potassium transport protein 1 acc. no. P47946 OS=Pyronema omphalodes (strain CBS 100304) GN=PCON_06476 PE=4 SV=1MVEPLSRIRSPSERLRLPFHRRVQRTLNALGPFGWHAVYFASICLVASWILYGVGARAGAKRGENLGYLDAVFLGVTSATGAGLGNVALSDLDKIQQIVAFLLILFGGHLWVSACVVNVQRAFLARKIHKRCLEEMKKKKQRLEDERRQLQLQDQQGKVEGDEELEKQGITASSSEAADVSSLSPKLVSPGHHDASSQCTAFDLVGMETPFDKLSLGDTPTDHDTLSALTTLCWLLPAYMTFFQLLGMICIGSYITRHGMDIVAVNNLNPWWYALFNSVSAFNNSGMSLLDANMSPYATRGALVVWTQCVLIIAGNAGFPIFLRTILLFLPKNAGTKLLLDETHGRRLFPYLFGFREFNWLLSMLLVLNLTSWTVFEALAPYTPSLANLNLGQRFLSGLFQGLSVRSGGFGIVAIRELHVGVLLTYVVMLYISAFPIDVTRSPPGSAWNFIKQQLRGLMRAGDLRYLASAVWLICVIDGIGEDEVFGVVFEVASAFGCVGVSFGALGDTRLALVGDWRGGSKLVLAGIMLWGRVREARRGILTEWGRETRERTWYGGIKEGTHDMGIGGKEIDEEENVVVRVEIV
7.9E-41	150	19.8	3.6E-40	147.3	13.7	1.7	1	H8GS87_DEIGI	K+ transporter Trk	trkG DGo_CA1233	Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	430	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus gobiensis, Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	745776	>tr|H8GS87|H8GS87_DEIGI K+ transporter Trk OS=Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0) GN=trkG PE=4 SV=1MLGIALGTALLSLPGMLTPGTQLSLVERLFTATSAICITGLVVVDTGEGFTRLGQVVIILLAQVGGLGIITFGTLFALLAGRRVNFSERQLLVQQISALNVGGAVSLLWTIMLYTLVAEVAGAALLALRFVPQFGWGEGLYQAVFHSVSAYNNAGFVVVLGGMAQYVQDPLVSGVIAVQIVLGGLGFLVQLNVLSHWREPRRNRLLVYSKLTLAMTGALLLGGTLLILALEWGSAATLGPLSAPGKVLAAFFQSVTPRSGGFATINVEALSSASLFLTIALMFIGANSGSTGGGIKTSTFAILVGSAWNLIRGRTELIAFGRRVVPENVVRAGTITTIYTLLVFSAFFGLLVTNPRLDFTHLLFETVSAAATVGLSMNTTPKINDAGLLILTVLMYLGRIGPVTFAVALNSRQTQASPLKYPPERDILVG
1E-40	149	31.2	3.3E-39	144.1	21.6	2.2	1	E4RP86_HALHG	Cation transporter	Halsa_0437	Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	498	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	656519	>tr|E4RP86|E4RP86_HALHG Cation transporter OS=Halanaerobium hydrogeniformans GN=Halsa_0437 PE=4 SV=1MIKSSRVNAIFYYLSYLLFILAIILLFPLALAFIYREGNNLYQAYYYTIILSAFTAIILKVLSDKDNKNINLTTAMQLCAISWIVISFFGAFPFIFALEKSLIDAVFESTAGFTSAGLTVFIGLDFMPKSIIFWRSLMQFLGGLGILTFFLLISTRAGGESWHFFSAEGHKYNLSRPVPNIYRTVKILWSIYIVFVIAQTIILNLLGLSFFDALNISFTTISTGGFTHYDQSIAHFAASGYQYFRLIEYVIIFFMFLGGVNFLLHFRFFTKDFAEIKNNSEFQTLLKIIFYGTLFLFVTIVLLNTAVDSSIEEIFRKSLFQITAIVTTTGFSTESINSSFFPVAARQLFLLLMLIGGSVGSTSGGIKIMRLNILRSLFKRDIKKIYYPRHAVLPVTVDKQILSKDEIYKLTGLVTFWLILIVIGGIITALFSDLNGLEAYSTMFSALGNIGPSFISTERMLSLSPVIKFTYIIGMLAGRLEILPLIILFSRKAWKSQA
1E-40	149	17.7	9.5E-39	142.6	12.3	2.2	1	G0A0F5_METMM	Cation transporter	Metme_4108	Methylomonas methanica (strain MC09)	490	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomonas, Methylomonas methanica, Methylomonas methanica (strain MC09)	857087	>tr|G0A0F5|G0A0F5_METMM Cation transporter OS=Methylomonas methanica (strain MC09) GN=Metme_4108 PE=4 SV=1MSSSDVSRALAQPVRYRVLARYLASIGLVVAVLRLPPILLSWACGDWHFMVGQVLVSAGLLLICLPVTRIWVPEGIRDNEVMVITSLSFAFTALLEALPFIGEGLTGIDALFETVSGVTTTGLSTLTGLQHYSPALLFSRAWMQWYGGLGVVAFSIALLFLDRGMAAHRLAMGDITDSRDILGNARSHALKLLIIYSALSVIAILALWVAGLDPLSAVTHALSGISTGGFSIYDNSLAAIDSAWLQVLVTVIGVLGAVALPLYYHVFKRGFKELATESEALALPVISLGVVGVLFLCINADVGNVWSSLKQAVVMGISAQTTTGFANADIGPMNAGAKLTLITSMIIGGSMGSTAGGIKILRFLIVLRIQLFIVRTALPAHAVLERRLCGDKLEADEIERVLMLIMIFLGTVLLSWFAFLVMGYDPLNALLEVVSACSTTGLSSGITRTALEPSLKAVLIIDMLLGRVEFLAMLVFLYPRTWIKIGSKT
1.1E-40	149	28.6	5.9E-39	143.3	19.8	2	1	Q0VSX8_ALCBS	Potassium uptake protein, TrkH family	ABO_0272	Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2)	453	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Alcanivorax, Alcanivorax borkumensis, Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2)	393595	>tr|Q0VSX8|Q0VSX8_ALCBS Potassium uptake protein, TrkH family OS=Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2) GN=ABO_0272 PE=4 SV=1MRPWFARRLGAPRSHTHKPLVSPPAALAGSFLLLIVLGSLLLKLPMATHSPISWLQAMFTATSAVTVTGLSVVEVGGQFTLFGKWVLLLLIEAGGIGIMTFAAATLLAIGHRLGIGEQQLIRDCMNYSRVSDIAWLIRRILVVVVVVQAVGMALLMCIWVPALGWGEGTFHSLFYTVSAFNNAGFGLSADSLTSWGGHWGIVLVITAMIIVGGLGFTVLADFGKGWRWRGLSLHSKLMLVGTAVLLSVTLVFFMLAEWNNPGTLGGMSLSDKLAASWFHAVTPRTAGFNVVDVRALLLPTSLLYLLLMFIGAGTNSTGSGIKVTTFMVLLLATRAFLRGRPLPVIFGRQISSTLVYKSLAITFIGCGVLFAALMALSVTDAQLGFENLVFEVVSAFGTVGLSRGITDELSSAGQWVIMLVMFVGRIGPLTLSFLLTRPRQPVVRYPEGEVYIG
1.5E-40	149	17.1	4.2E-21	84.4	4.6	2.3	2	A2BK65_HYPBU	Trk-type K+ transport system, membrane component	Hbut_0514	Hyperthermus butylicus (strain DSM 5456 / JCM 9403 / PLM1-5)	508	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Pyrodictiaceae, Hyperthermus, Hyperthermus butylicus, Hyperthermus butylicus (strain DSM 5456 / JCM 9403 / PLM1-5)	415426	>tr|A2BK65|A2BK65_HYPBU Trk-type K+ transport system, membrane component OS=Hyperthermus butylicus (strain DSM 5456 / JCM 9403 / PLM1-5) GN=Hbut_0514 PE=4 SV=1MAGREETSARLEAVARRQRHLPLRVNPLLRYTSLPFIVAGLSHVLAGIFGLFEGDHNYSLQLLAWGSIFIAVGYAWINFMEPSRSITREEAIVLVAYSWVTTPIISALPVYVSLGIPFIDAWFESVSGFTATGLTIFTGQVNPDYGVYIPSIEELPASILWWRAVTEWFGGFGIVVMFFTMVRLGGLPAHLVGFAEGRFERLEPSIARSLRALMELYLMLTIMGAIGLYLAGMTPSDAVYHSMTGIATGGFSTHTTSIGFYDSLLIESVTVVIMLTGAMNFADLYAILKGIPRRFSGEIQSLLAVAFLASTAAAVMLYTAGWSPKGFLRDAIFHVVSALTGTGFGIDDLSSAPPDFKALLIPIMLIGGSIFSTSSGLKQYRLMVIVKSILWSVSEVIYGGRRVIARSVGGRPVTISELQNVISVAALLTLTEFAGALALSALLPTRSFVDAAFETASALANVGLSVGITSAAASIPVKLVLIVIMTLGRLEVAGFLFALASLAKMLRR
1.7E-40	148	23.5	2.5E-40	147.8	16.3	1.2	1	A0K0A1_ARTS2	Cation transporter	Arth_3346	Arthrobacter sp. (strain FB24)	477	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. (strain FB24)	290399	>tr|A0K0A1|A0K0A1_ARTS2 Cation transporter OS=Arthrobacter sp. (strain FB24) GN=Arth_3346 PE=4 SV=1MTQSQPRSKSPANWHPGMPEREGLWIFTGIRDFIDNIANTSPARLALTAFGVVIILFTALLSMPAASATGNFTPLHQALFTAVSAVCVTGLTVVSTAVHWSFFGQLVILIGIFVGGLGTLTLASLLALMVSKKLGVRGKLIAQEAMNNAGRLGEVGTLLRIVITTSVVIEGSLALALIPRFLALGESFGQSVWHGVFYAISAFNNAGFTPHSDGIVPYQTDVLTWILVLPLMLGVFLGSLGFPVVMVLQQNGLNWKKWNLHTKLTIQVSFILLAAGTVLWGLMEWENVRTIGSMDVGDKITHSLFASVMTRSGGFNLVDQNHMESTTMLLTDALMFAGGGSASTAGGIKVTTIAVMFLAIVAEARGDADVKVYGRTIPQGTMRVAISVIVAGATLVSVSAFTLLHISGAPLDRVLFETISAFATVGLSTNLSAELPPSGVYVLTALMFAGRVGTVTLAAALALRQRSQLYHYPEERPIIG
2E-40	148	25.8	7.3E-20	80.3	8.6	2.2	2	R5SG58_9FIRM	Potassium uptake protein KtrB	BN540_00094	Dialister invisus CAG:218	432	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Dialister, environmental samples, Dialister invisus CAG:218	1263072	>tr|R5SG58|R5SG58_9FIRM Potassium uptake protein KtrB OS=Dialister invisus CAG:218 GN=BN540_00094 PE=4 SV=1MRRHMFRWSPARIIAGAFGSISFIGSILLYLPWGHMPGQSITYVDALYTAVSALCVTGLSIVDTAAVFNPFGQAILAVLIQVGGLGVSTMGAGVLLMLGRKVGIRQRNLIHDTMNLDSYSGVVRFLRTLFATTVFIEIIGAFLGYFVFRRDYEMMESIGLSIFHSISSFNNAGLTILTKERSMEMYAEDPFMLILTTALVFVGGLGFIVIRECWVNRFRWRKLSMHSRVSIFMAVFLLIGGAVLLKLTNPISWLVAFFSSQSARSVGYMVYPFESWSPAGLLVMLVLMFIGTSTGSTGGGVKTSTVFALVLGVRRVTTNARAEAFHYSLPPLAFRKAAVVVVLAIADIVISTFILLLVCPELSLAEAFTEMMSAFTTVGLSLGTTASLNEWGKLISILVMLTGRMGPMTIATAWYFYEETRARYPEGNVTVG

2.6E-40	148	26.8	8.3E-38	139.5	18.6	3	1	F4BTN5_METCG	Cation transport protein	MCON_3116	Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) (Methanothrix concilii)	535	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosaetaceae, Methanosaeta, Methanosaeta concilii (Methanothrix soehngenii), Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) (Methanothrix concilii)	990316	>tr|F4BTN5|F4BTN5_METCG Cation transport protein OS=Methanosaeta concilii (strain ATCC 5969 / DSM 3671 / JCM 10134 / NBRC 103675 / OCM 69 / GP-6) GN=MCON_3116 PE=4 SV=1MKIRIILRILGMLAMLLGTLMLIPGIVSAIYKEPLGVVAFGISSLLAIIVGLILKHFGEKSDMGRKDAFAAVSFGWLMAGLIGALPYLLLGLGLVDAFFESMSGFTTTGATILSEYDSQHYWTLSKEAVHSSLAYALVERTTHQLIHWSPIGIIELDFGLTLNFIDLLTIKETYFGLLFWRSFSQFLGGMGIILLFIAILPNLGVAGRELYSVEGLGLMKEALTPRVKSTAKAFWGIYLGLTGMEALLLVAAGLPVYDSLCTSFSSSISTAGFSPRAYSIAEYNSILVEAIICIFLLLGGTNFIIYHQIILKKNLNYLIRDAEFRFYIIIVFISIIILMIFGQIPGGFFDALRSSVFQVITTMTTTGFVNNFNYDSWSLAAKLVLMLLMIIGGCTGSTGGGMKVGRVLIVLKYVHAELIRSLHPKAVITIRMADKVVKENTVKSVILFIQLYVMIFILAAVAFSITEASNPQFGSLSAISAAACCLGVVGPGFGVVAMDFNAISESGKVLATFCMYIGRLEILPVVLMFLPETWSD
3.8E-40	147	19.3	6.6E-38	139.8	13.4	2	1	D6ZJH0_MOBCV	Cation transport protein	HMPREF0573_10550	Mobiluncus curtisii (strain ATCC 43063 / DSM 2711 / V125) (Falcivibrio vaginalis)	456	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Actinomycetales, Actinomycetaceae, Mobiluncus, Mobiluncus curtisii, Mobiluncus curtisii (strain ATCC 43063 / DSM 2711 / V125) (Falcivibrio vaginalis)	548479	>tr|D6ZJH0|D6ZJH0_MOBCV Cation transport protein OS=Mobiluncus curtisii (strain ATCC 43063 / DSM 2711 / V125) GN=HMPREF0573_10550 PE=4 SV=1MKFFANLREKSGKWFDELARRAPARLTLAVFLSIIVVQTVLLSLPIATRDPGHARFIDALFTSTSAVCVTGLTVVPTDTYWSPFGLVVIMLGVEIGGLGVMTLASMLSLAVSRHIGLTARILAAGEKKSSLGEVGSLGKMALLVSVSVESVIALMLFPEFIRQDYGIGLSAWYALFMAVSVFNNAGFVIVPGGVEQFVADFGIIGPMCLGVFIGAIGFPVSLDLARNWRRPKHLSLHSKLTITTYLALSVVGGGINGIIEWDNPRTLGALDLPGKLLAALLGAFNARSLGVSTIDVGSMHEASWFVSSIMMFIGGGSASTAGGIKVTTFAVMVLAIVAEVRGNRDIEAFGRRIGPSTVRLAVAVVAMSALVIGLSTATLLLLTNLPLSEALFEVNSAFGTVGLSTGVTGSLPDSGKILLSLLMFTGRVGTMTFGAALAMRNRRRVIRFPEEAPSIG
3.8E-40	147	24.5	6.4E-40	146.5	17	1.2	1	A0A0F0LC72_9MICO	Ktr system potassium uptake protein B	ktrB RS83_01792	Microbacterium oxydans	476	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium oxydans	82380	>tr|A0A0F0LC72|A0A0F0LC72_9MICO Ktr system potassium uptake protein B OS=Microbacterium oxydans GN=ktrB PE=4 SV=1MSGIVSASSPQRVLRDLGSRGKHIITSSPSRFAIVIFALLILIFTALLSLPIASASRTVTPLSDALFTAVSTICVTGLATVDMANHWSPFGHVLIFIGVNIGGLGVLTLASLMGMVISKRLGLRAKLMAAGDTNPMRAHGGVVNESQTVRLGEVGQLLRTVALSSLIIEAALAVFLYPSLVMAKVDPIAALWEAPYFAAMAFTNTGFAPNDGGVAVFADDYLVLSLLMVGVFLGSIGFPVIYSLAKHVWHVKRWSLHTKLTLVTTVLLFVLGAVVFLILEYSNPKTFGSMDAADTTFQAFFLSAMTRSGGFNVIDMSDLNGSSLVAASMLMFVGGGSASTAGGIKVTTLAVLAIAVWSEAKGRQSVEVFGRRIPSDVQRVALSVVAWGATIVALSTIVIAQITKADISHVLFDVISAFATVGLSTGLTAQLPDAGSYVLAVTIFMGRIGTVTLAAAAVAATSRSQYYSLPVERPIVG
4E-40	147	34.5	4.6E-20	81	6.9	2.4	2	D5VT52_METIM	Cation transporter	Metin_1100	Methanocaldococcus infernus (strain DSM 11812 / JCM 15783 / ME)	461	cellular organisms, Archaea, Euryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus, Methanocaldococcus infernus, Methanocaldococcus infernus (strain DSM 11812 / JCM 15783 / ME)	573063	>tr|D5VT52|D5VT52_METIM Cation transporter OS=Methanocaldococcus infernus (strain DSM 11812 / JCM 15783 / ME) GN=Metin_1100 PE=4 SV=1MITYKDISTILNILGRISLIISLISLIPIFVAFYFKENPFPFIISSLLSFLISLILLKTTKIYKVKLYHCMCVSSLSWILASLIGAIPFYLSIPYFSYLDGVYESASAWTTTGMSLIIDLNVVDKSILFWRSLEQWIGGVGILVFSSLVLSNLASHLYLSEARQEKILPKFLSTIKTIIWIYIFYTIVGILLLYLSGLSPWESLNLTMTGICTGGMSLSNESFPYNSLAKLFMILIMLAGGVVSFSTHYKILSGKLKLDCQIKYSLLVILLSSLFICFKDKINFLDSLFLVTSALTSTGFSTFDLSKLSEPSLILLIFIMFIGGGTGTTTGGVKILRFLIILKIVYYEIKKIVYPRNTVFPKYLSNLKLDDKIVKEAFTIFILYLFSSFTLFFIFSFYTSPLKALFDSVSFVSNIGLSLEVVNINSPAILKIAGIFGMILGRLEIIPILILILTFSKIKRI
4.2E-40	147	14.3	1.6E-20	82.5	0.6	2	2	Q3J5D1_RHOS4	Trk system potassium uptake protein	trkH3 RSP_1854	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides), Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	272943	>tr|Q3J5D1|Q3J5D1_RHOS4 Trk system potassium uptake protein OS=Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158) GN=trkH3 PE=3 SV=1MIDPRPVGYILGLLVATLGALMLVPMALDLAAGDRHWLSFAETATITTVAGSMLALACANGRGQGTGLSLQQSFLLTTGAWVLLPVFGALPFMMGRPDASFTDAVFEAMSGFTTTGTTVFVGLDALPLGTNLWRGMVLQWLGGLGIVIVAMIFLPVMKVGGMQFFRSEGFDTLGKILPRALDISTALIQIYLVLTMACVMTFLALGIPLFEAVVHALTTVSTGGFSSSDRSFGLFQGPAEYACAFFMVLASLPFVRFVQLAQGTFLPLWRDPQVRAYLRWNGYAIGLIVAYEVVTRNAPVLPTLRETTFNVISTFSGTGFSSVDLGLWGTFPFVLLIVVGLIGGCTSSTGGSVKVFRYLILLEAIKVQIRRLQSPSAVIFVDYEGRRVGEDVINSVILFFTMFILSFGVLAVLLSLTGLQTKTAITAAWTAIANVGPAFGPEVSATGAVDRFPAVAKWLMIGGMLVGRLELLSVFVLLTPRFWRS
5.1E-40	147	19.4	1.4E-39	145.3	13.5	1.5	1	A0A0F7JPE9_9DEIO	Potassium transporter KtrB	SY84_11635	'Deinococcus soli' Cha et al. 2014	447	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, 'Deinococcus soli' Cha et al. 2014	1309411	>tr|A0A0F7JPE9|A0A0F7JPE9_9DEIO Potassium transporter KtrB OS='Deinococcus soli' Cha et al. 2014 GN=SY84_11635 PE=4 SV=1MSRRRRRRLNPPQLIALVYLLGIALGAAALHLPGMTRPGADLNAVDLIFTATSAICITGLVVADTGETFTRLGQVTILLLAQVGGLGIITFGTLFALLTGRRVNFSERQQLAQQVNALNVGGVLGLLRIIVLYTVAAQGVGTLLLSLRFVPQFGLGEGLYQSVFHAVSAYNNAGFVVVPGGMLPYAQDPLVSGVIALLIVLGGLGFLVQLNVLTHLASPRRNRLMVYSRLTLVTTGALLVLGTAVLLALEWTGALKGLGTGGKLLTAFFQSVTPRSGGFATVDMTALAPGSVFVMIALMFIGANSGSTGGGIKTSTFAILLVSAWNLIRGRTELIAFGRQIVPENVVRAGTITTIYTLLVFTGFFLMLVTNPTLGFTPLLFETVSAAATVGLSLDVTHRLNDAGLTVLCALMYLGRIGPVTFALALNLRETSRGVIKYPPERDILVG
5.6E-40	147	8.7	8.1E-39	142.8	6	2.2	1	L0GWG9_9GAMM	Trk-type K+ transport system, membrane component	Thimo_1550	Thioflavicoccus mobilis 8321	485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thioflavicoccus, Thioflavicoccus mobilis, Thioflavicoccus mobilis 8321	765912	>tr|L0GWG9|L0GWG9_9GAMM Trk-type K+ transport system, membrane component OS=Thioflavicoccus mobilis 8321 GN=Thimo_1550 PE=4 SV=1MSHAAATLMRAARPMVVAGTLGLLLLVLAALSAVPAIVSLVLGDTGLEWRLFGVAALELLLGTLLVRLPRPDDIQWNEALAVTGLAFLLAAGAMVWPLMGNEIGALDAWFEAVSGVTTTGLTTLRDMAERPAGFLFLRAWMQWYGGLGIAVLTVALIMRHHASGRRLLETTGESLTHASARDHARRVLLVYLGLTGLAVFGVWMSGLAPFQALLHGLAAVATGGFAASDRNIAPLPPVSVAVLSAICLAAAVSLPLYAQLWRKGPRALLGEPDVRALIASAVVTAALLALIGVTLDGVAWPRALADGLVQSISAQTDTGFSTVDIAALPAASQLVLIVSMTIGGCTGSTGGAGGIKLIRLLIILRVQLALRRTAVSERAVLGANVGTARIEPDAVAAALQLLGLWALVLILSWFVFLLHGVAPLASLFEVASATANAGLSAGLTGPDLAPLLKVVLSVDMLLGRVEILALLVLLYYPTWFGRRRAS
6.5E-40	147	6.3	3.2E-39	144.2	1.6	2.1	2	I1BMR5_RHIO9	Uncharacterized protein	RO3G_02199	Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) (Mucormycosis agent) (Rhizopus arrhizus var. delemar)	475	cellular organisms, Eukaryota, Opisthokonta, Fungi, Fungi incertae sedis, Mucoromycotina, Mucorales (pin moulds), Mucorineae, Rhizopodaceae, Rhizopus, Rhizopus delemar, Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) (Mucormycosis agent) (Rhizopus arrhizus var. delemar)	246409	>tr|I1BMR5|I1BMR5_RHIO9 Uncharacterized protein OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_02199 PE=4 SV=1MATTGITNTGLNTITISDMSTYQMLVLFFSTFMGHHALISFFVVMVRRYYFSKRFEDVLVENQKRKEEYKLKKLQKQQENFKMLGPIRRRMSLISIRSTPVQNSAQFSIFSKDRRSSFGTQATKNSEEKPKEYSSIQMDANSNQNEDEQAHSSRRTSGISPFDRDTAADDSTNKNGNSSHISSSNKSTNSSISLDKDKQNNASTTPNAQQITFREDTNILRERERKKFQQQVHQGENNSIPIYRTNSESEIMDRPVAKSQLTRHERYRMGGTEYCALDMLAWLIPIYYLGFVIVFGFMFRIYVACSTYAQAVLETSNPNGPVEPWFFSFFLSLSAFTNLGLNNLDASMVPFQNAPCPLILCIIILILVGNTAFAIMLRFIIWACYRLAPKSKELTKETFRYLLDHPRRCYTTLFPSTQTWWLLIVLIIITLIELVSFLALNYWLPVLSDISWGSRFLDGLFQSVATRNGIDNSNYF

6.9E-40	146	25.8	1.1E-38	142.4	17.9	2.3	1	M9SCK2_9EURY	Potassium uptake protein TrkH	MMALV_07460	Candidatus Methanomethylophilus alvus Mx1201	526	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Methanomassiliicoccales, Methanomassiliicoccaceae, Candidatus Methanomethylophilus, Candidatus Methanomethylophilus alvus, Candidatus Methanomethylophilus alvus Mx1201	1236689	>tr|M9SCK2|M9SCK2_9EURY Potassium uptake protein TrkH OS=Candidatus Methanomethylophilus alvus Mx1201 GN=MMALV_07460 PE=4 SV=1MLFPTLRRRIEHLERWESGTIKVLGMVEVLLAVMLIVVALYAALVGDDASVFARPAPFVLALGLFQYLFFSNRKPMAPSLGILLIVETWLIAFFILAIPFYLSGFSFANSLFESVSAFTTTGATILTDVDAIDGSLLIWRAVMQWAGGITVVIIFTVLLPMLGMGGAGFGSNEFSGVDSSGYAVKISNAAFNFMRIYILMTTVEIILILMILGVTPFESVCIAFSNIPTGGLLPANDSMASYSFAVQFVTLVFMFLGATNYYLLFRTFFTKDHKALGKSSEFKWMVKWFVACSLVITAVIVVSDETAYSIDNLGAVGDSLWHATYCIVSAGTSSGFAITDYTTWPALGLMILLVVEFVGGMSGSTAGGIKIHRMMALRSYIVAGMDKIMHPSMVTSMRIDNKTLESNEVSSAVSTIFLFMVGIVVALCALMFLEPQLDVQTDFGVVFAAIANVGVGSGQIGPFDNYDSLKDATKYLMCLLMWLGRMELVLAIMIFTRGFWEDVRLNAGFRVRAMELRHMYKVNKKYR
8.4E-40	146	32.9	1.9E-39	144.9	22.8	1.5	1	F3ZUD2_9BACE	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Bcop_2217	Bacteroides coprosuis DSM 18011	606	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides coprosuis, Bacteroides coprosuis DSM 18011	679937	>tr|F3ZUD2|F3ZUD2_9BACE H(+)-transporting two-sector ATPase OS=Bacteroides coprosuis DSM 18011 GN=Bcop_2217 PE=4 SV=1MKIYHKFLLYQNKLLRPYVDVSLKIVEALTYVASLIFILTIVYRYGYDVTSEQLHTISLIYKSVWILFLIDFFLHVFLSYSDTKREYKKTTWVLSILLMLSLIPVIFKRPEESGGILQFWEFMSSKTYRSGLLLVFSLFNLSNGLIRLLGRKTNPALMLAGSFIVIIIIGSGLLMLPNCTVDGINWVDSVFVSTSAVCVTGLSPVDIATTFTPIGLTIIIILIQIGGLGVMTFTSFFAMFFMGNTSVYNQLVVRDMMSTNSLGSLFSTLMYILFFTLVIEGVGAFAIWSSIHDTLGMSLNEEIAFSVFHSISAFCNAGFSTLPGGMGDPLVFNQNSIFIYVSLLIVLGGIGFPILVNFKNALKIRFQRLVAFVRHQNPPHIYRLYSLNTKIVLYTSAILILGGTLLIGFLEWNGALAGMGFFEKITKALFMAVSPRSAGFSFIDPDTLRVQTFFIFLLFMWIGGAAQSTAGGVKVNTIAVVFLNVMAMLKRSDRIEVFGRKISSQSVRRAHATVFISLIVLVLSLFILTLLEPNISPSLLGYECVAAMSTCGAGLGITPLFGTPAKFLIVALMLVGRVGIITILLGFIKQKNKRNYNYPSGDIIIN
1.3E-39	146	14.7	7.2E-38	139.7	10.2	2	1	A4X1V8_SALTO	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Strop_0373	Salinispora tropica (strain ATCC BAA-916 / DSM 44818 / CNB-440)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Salinispora, Salinispora tropica, Salinispora tropica (strain ATCC BAA-916 / DSM 44818 / CNB-440)	369723	>tr|A4X1V8|A4X1V8_SALTO H(+)-transporting two-sector ATPase OS=Salinispora tropica (strain ATCC BAA-916 / DSM 44818 / CNB-440) GN=Strop_0373 PE=4 SV=1MQWLLRRPVRLVPIGFGATILIGTLALMLPWATGQQRHTPFVTALFTSASAVSVTGLAVVDTPNYWNDFGLAVITILTQVGGLGIVTGATLVILAVSHQLGLRNRLLVQAETAEFGLGDVRRLLFRIAAIALTTEAIITVILTLRLWVKYDYAFGEALWTGVFHAVQAFNNGGFALYSDGLIGLSSDAWLILPMAFGALLGGLGFPALFEAVRSGRRPRCWSVSTKLTIWGSVTLVTVGFLALLATEWSNPYTLGIRPWPEKILAAFAQNAFFRTGGFNVINIEALGEESIPAIIALMFIGGGSASTAGGIKVSTFFLLAFVIWAELRGEPDVTIRHRRIATASQRQAVTVALLGVAIVVVGTVTLILLTQGVPHHVALFEVTSAFSTAGLSLGVAPDLPDGGQYVLIVLMYIGRVGSLTLGSALALNTRRRLYRYPEEQPLVG
1.3E-39	146	18.2	1.9E-39	144.9	12.6	1.1	1	A0A0F0LSK3_9MICO	Ktr system potassium uptake protein B	ktrB RR49_01804	Microbacterium ginsengisoli	480	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium ginsengisoli	400772	>tr|A0A0F0LSK3|A0A0F0LSK3_9MICO Ktr system potassium uptake protein B OS=Microbacterium ginsengisoli GN=ktrB PE=4 SV=1MAGEVSTPGPARALGTWIARFARDIRDLSTASPARFAVLVFTALILVFTGLLSLPAAAADGRATPFVDALFTAVSTVCVTGLATVDMAAHWSAFGHVIIYVGVNVGGMGVLTLASIMGLVISKRLGLRAKLIAASDTNPLRAHAGPVNEGQTVRLGEVGQLLRTVALSTLVIEAVISVLLYPSILLAGIDPLTALWQAPYYAAMSFTNTGFTPNPGGLAPFAHDYVFLTTLMVSVFLGSIGFPVIYTLARHRWHVRRWSLHAKLTLITTVVLFLAGAVVFLTLEYANPKTFGSMDAFDTTFQSFFLSAMTRSGGFSVVNIGDLNGSSLVVGSMLMFVGGGSASTAGGIKVTTLAVLALAVWSEARGRPSVNAFGRRIPSDVQRVALSVVAWGATIVAASTITIAQITQAPIADVLFDVISAFGTVGLSTGLTAELPDPAAYVMAVTIFMGRIGTVTLAAAVAASSRSQLYTFPTERPIVG
1.4E-39	145	20.9	2.7E-39	144.4	14.5	1.4	1	Q6AHA6_LEIXX	Potassium uptake protein	trkH Lxx01740	Leifsonia xyli subsp. xyli (strain CTCB07)	464	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Leifsonia, Leifsonia xyli, Leifsonia xyli subsp. xyli, Leifsonia xyli subsp. xyli (strain CTCB07)	281090	>tr|Q6AHA6|Q6AHA6_LEIXX Potassium uptake protein OS=Leifsonia xyli subsp. xyli (strain CTCB07) GN=trkH PE=4 SV=1MGRVRAAVNGFAQRSPSRFAILVFAALILVFTLLFSLPISSASGHVTGLADSLFTAISVICVTGLSTVDMATHWSVFGHLLVYLGVQIGAVGVLTMASILGLVISRRLGLRAKLIAASDSNPLRMHSGPVAEGQAVLLGDVGKLLRTVAISMIVIEGLVAVLLFPRMLIAGVNVGTALWESVYYSAMAFTNTGFAPNAEGLTPFVNDFWFLGALMIGVFLGAIGFPVILAIASNLRRRRRRWSIHVKLTLLMSVILLVVGAVLYIVLEHDNAKTFGGLDAGHTVFQSFFLSTMARSGGFSTIDIDDDLHGSSLLVTDMLMFIGGGSASTAGGIKVTTLAVLFLAAVAEARGVEPMDAFRRRIPVDVLRLAVAVALWGATIVAVSAVLILQITKAPLDHVLFDVISAFATCGLSTGLTEKLPDAGVYVMAATMFCGRVGTVTLAAALAQSQRKQLYQNPEERTLVG
1.7E-39	145	38	2.9E-38	141	26.3	2.1	1	E6UGX0_RUMA7	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Rumal_0608	Ruminococcus albus (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7)	465	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus albus, Ruminococcus albus (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7)	697329	>tr|E6UGX0|E6UGX0_RUMA7 H(+)-transporting two-sector ATPase OS=Ruminococcus albus (strain ATCC 27210 / DSM 20455 / JCM 14654 / NCDO 2250 / 7) GN=Rumal_0608 PE=4 SV=1MKIFRKNENDDTPFPHLFGHSILRKLSFSQFLMFGYSLVILIGAALLCLPVSSTERVYTPLHHCIFTTTSALSGTGLTLHDTYTYWSLFGQIVILIIIQIGGVGFMSIGLFALSFMGKKIGLKQRATMRESIGSVSSGGVVKMSRFILKGTVLFESLGTAALCFWFVPRLGWAKGIYFSLFHSISAFCTAGLDLMGYFEPGSSLVTANDSVLLNLPIIILLVVGGIGFFTWSDIVDHKHHIKKYSAQTKIILVVTIVFYVFGMLDMALLEWKNSGTMGELGTGGKIIASSMLVTSGRDAGFASVTVANLRQTSIMLLICFMFVGGSPGSTACGIKVTTFAVMMMTISTVFRKKKSVEFFGRRVDDTTVRNACCITTLYLVLVIVSAMIITGVDGLALTPVVFELVSAISSTGLSMGITTSLSDISIIIVIMIMFFGRIGGISFIVSLHNNYASNRSQLPEEKIML
1.8E-39	145	33.6	2.8E-39	144.4	23.2	1.3	1	G2TL83_BACCO	Cation transporter	Bcoa_3221	Bacillus coagulans 36D1	432	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus coagulans, Bacillus coagulans 36D1	345219	>tr|G2TL83|G2TL83_BACCO Cation transporter OS=Bacillus coagulans 36D1 GN=Bcoa_3221 PE=4 SV=1MSRFQFRPATFKMVFFMYLLGTVIFAILYLLPVSHKQPLLPVDAFFLSASAISATGLSTVTVAQELTTAGKIILLIQMEIGGIGVMALVGALLIALRTNAPVPSQTLMIFDQNQNSSRSISKLMAFIVKYTLIVETAGFLLILPSALQHGSHAFAAFFLSVSTFTNAGFEISGNGLDNFKGEPFVLAVLSCMIILGVLGFAVVMEFLQSRRKKKSLYFKVNVLMHGILLLVGFLFFFVDFIHMPGLSFTEKIIQSLFFSAAPRSGGLASLDLHVFSFPSLLFMIMLMFIGGSPSSCAGGIRTTTFAVILAKLWSVIRGSNETHMFRKTLFAEDVNKAFLVFFAFLFLFFSFFVLSFTEKAAPFPLAFEIMSALSTCGFSLGITAGLTVFGKIWLAFLMLIGRLGVIILIYTFMNQKKSTIKYAKESILIG
1.8E-39	145	20.3	7E-19	77.1	4.5	2.3	2	E7GNZ4_CLOSY	Trk-type K/transport system protein	HMPREF9474_02639	[Clostridium] symbiosum WAL-14163	497	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	742740	>tr|E7GNZ4|E7GNZ4_CLOSY Trk-type K/transport system protein OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_02639 PE=4 SV=1MDENRNEVGGGQLIAGYLGIILMLIGGIILLPIMLLAVYPEESVYTSCFTIPGVTAILAGYVMSLFIRGRDKRRLIGHQDALIVVFSWLLAILFCSVPFMLTGKYNFTQSVFECTSGWSTTGLSVVNVEDCPKIFLLFRSVMLFFGGVGLVLVMISVLSDRHGMRLYCAEGHTDRLVPNLVKSARMIIVIYTGYIISGTLLYIYFGMNWFDALNHSIAALSTGGFSTKAESIGYYGSFGIEAVTIVLMLLGSTNFLAHLYLIRGGGKNFFRYCEVKFQLILCALAAPVLSAFLIYGGLEGHVGQGFRDGLFQVVTALTTTGFQTVPSFAVWSSPLILVMTLLMLIGGGTGSTAGGIKQIRVCIMLKSLCWSIRSKISQKRLIHADGIYRISGYEYLKAEERLEASDFILLYLGVFAAGTFILCAYGFGIGDSMFEFASALGTVGLSVGITGYDASPVVLWTETVGMLAGRLEIYVIFVAAVQFGREIKDGYKKTEGR

3.7E-39	144	25.4	6E-39	143.3	17.6	1.2	1	F7UXU4_EEGSY	Trk type K+ transport system, membrane component	TrkGEGYY_28840	Eggerthella sp. (strain YY7918)	506	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, Eggerthella sp. (strain YY7918)	502558	>tr|F7UXU4|F7UXU4_EEGSY Trk-type K+ transport system, membrane component OS=Eggerthella sp. (strain YY7918) GN=TrkG PE=4 SV=1MWQRFTWYDVRVIGHYLGVLVLFSSMALLAPLITALACGEWEPATRYLLTIGISLIVGSALRFLRIEPGRLNRQQALVVTGFAWIV LAFIATVPLHLSGHYASYLDALFDGVSGLTTTGASLILDLDHLSYADNMWRFMMHFLGGLGLIVVALSFGLFGKRAGASLYMSEGRSE HVVPNIVQTTRLIAKISVILIFIATCILTVMCVFLGMEPLRAFLQALWLSISGFMTAGFTPMSQSVMYYHSLPVEVVLMLLMLLGSINFMLH SEVWKGRVEVFFRDLEIRTLVLWLGIMACVLAASLTASAEFSDLPAMLRRGLFMMISAMTTTGFQNVTSNQLTTVFSSGAFLVIAVLM AVGGSGGSTAGGIKFNRIGIILKSLVAAIKEALAPDSARVVVAYNHVGRRILSPEIVKEAMMVFILYVVTYAVGALVGIAHGYDATQAIFE SVAMASNGGLSSGLASPDMPATLEIFYIIEMWAGRLEFVTLIALIVEIIVSLDPRRLVTRS
4.6E-39	144	37.2	3.1E-37	137.6	25.8	2.2	1	R6D6U8_9FIRM	H(+)-transporting two-sector ATPase	BN718_01822	Ruminococcus sp. CAG:579	451	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:579	1262963	>tr|R6D6U8|R6D6U8_9FIRM H(+)-transporting two-sector ATPase OS=Ruminococcus sp. CAG:579 GN=BN718_01822 PE=4 SV=1MSRIRSFLSNMSFTQILVFGYTMVILVSAVLLMLPISSRERAFTALNDCIFTTTSALSGTGLTLFDTYTYWSLFGQIVILIVIQIGGIG FMSMAIFALSYTGRKIGLKQRFTMRESVAGFSGGGVVKMTRFILKGTIYCETAGAIALSVFFIPKIGVGKGIFFAIFHSISAFCTAGIDIMG YFEPGSSIITAADSWLLNVTLIILLTIGGIGYITWGDVVEHKWHFKKYRLQSKIVIMVTILFYILGIAEMILVEWNAPSLSSADGAGQKLLM SSMLVTSGRDAGFAPLNVALLKESTLLMIICFMFIGGAPGSTACGIKTTTFAVMVLTIASVFRRKKSVECFGRRFENTIIKDASCVTTLYL LVVIISSIVISAIEDVKILPVMFEVVSAISSCGLSMGITAKLSDISCALITIIMFFGRIGGLSFIMSLSNNVKPSKVQLPEEKIIVG
4.9E-39	144	26.4	9.2E-39	142.7	18.3	1.3	1	R5GUA5_9FIRM	Potassium uptake protein TrkH family	BN782_02178	Eubacterium sp. CAG:786	450	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:786	1262893	>tr|R5GUA5|R5GUA5_9FIRM Potassium uptake protein TrkH family OS=Eubacterium sp. CAG:786 GN=BN782_02178 PE=4 SV=1MPVIKKTQKPMQPARTLCIGFMTIILVGALLLWLPFSSKSGGTPFFDCLFTAVSATCVTGLIVTDTFTNWTIFGQAVIMLLIQVGGL GFVTIITFFNVAAGRKLGFRTLANASDGLTESTFQGGRRIFISIIKYSLIFEGAGAVLLSIAFAREHGAFGVWMGVFTSVTAFCNAGFDL CGIEGAYSSLTNHSGDPLVIMTVALLIILGGLGFIVWENFLNIRKMHRLSLHTKAVLIGSGALIVVSTLFYMIAEWDNPATLGGMNFGEKL MNSFFSGVTARTAGYNSISVEGMSDFSKLGTCIFMFIGASPASTGGGIKTTTVLVLIMTVVSYLRSKNDVELLGHKIDKLAVYRTLTVTL LSLMAVILCFSVLYFTLPEDVSGVDCLFEAVSAFSTTGLSAGPTAIAGTPGRILLMITMYIGRVGPVSLVLSMLMNAKHKNIVLPEGQIIV G
1.3E-38	142	12.9	8.9E-28	106.4	4.2	2.1	2	R7EKH5_9FIRM	Trk system potassium uptake protein TrkH	BN640_00557	Anaerotruncus sp. CAG:390	366	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Anaerotruncus, environmental samples, Anaerotruncus sp. CAG:390	1262703	>tr|R7EKH5|R7EKH5_9FIRM Trk system potassium uptake protein TrkH OS=Anaerotruncus sp. CAG:390 GN=BN640_00557 PE=4 SV=1MNRRMIGRTVGKITLLEAVLLVLPMLVCAIYREWLQLFAFFAAAASAAIIGVLLTVISKPRTTEIFVREGFITVALAWIVLSLIGALPF FISREIPSYIDALFETVSGFTTTGASVVTDVEAMSHGILFWRSFTHWIGGMGVLVLMMAIIPTESGSSIHVMRAEMPGPIVGKLVPRIRD TAKILYFIYIAMTVLQTILLVCGGMPLFDSLLHTFGTAGTGGFGIKSDGVAGYSPYCQWVITVFMLLFGVNFNLYYLILIRRFRTAAKSGE MHAYFGIVIAATAAITANILRICSGFGEALRLAAFQVASIITTTGYSTADFNLWPGFSKAVLFILMFIGGCASSTAGGLKXPPADSRSRAL CCFSR
1.3E-38	142	10.2	6.4E-38	139.9	7	1.8	1	Q2VZR2_MAGSA	Trk system potassium uptake protein	amb4109	Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum magneticum, Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	342108	>tr|Q2VZR2|Q2VZR2_MAGSA Trk system potassium uptake protein OS=Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) GN=amb4109 PE=3 SV=1MIDLRPVLSIVGALVCILAAAMWLPAAIDFRDGHEEWRVFATSSGLTLFFGLALLLGTRLPQQRRSVRQTYLAATFGLAVPALFA ALPLVYGPLQLSFVDAAFEATAGLTTSSATVIRGLDVLPRGLLLWRALLGWLGGIGVIALAIAVLPDLAVGGMQMFRVEVPGPAERATS RGRRIAASILAGYCGATGLLALALWLAGMSGFEALVHAMGTISTSGASTSDASIGHFDSGAITVLITFGMVLGGMPFLLFFHFLRGNRK VVLRDHQLRWYFALLTLGTLGVSAWLVSSRGLAPLDALRHGALTVVSVMTGTGHFTLEYGNWGGMPAAILFFLAFVGGCAGSTSGG IKVFRFQFLFADALMQIRRLLRPHAVLIATFNRRPIPEGVLGSVMGFLFVYALSFAMLSMSLAFLGLDFVTAVSGAASALANLGPGLGPE IGPGGSYAGLPDLAKGLLCLGMLVGRLELFTVLVLFVPAFWRQ
1.5E-38	142	26.1	1.9E-36	135	18.1	2.1	1	R5BRL0_9BACE	Trk system potassium uptake protein	BN459_00741	Bacteroides sp. CAG:1060	484	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:1060	1262734	>tr|R5BRL0|R5BRL0_9BACE Trk system potassium uptake protein OS=Bacteroides sp. CAG:1060 GN=BN459_00741 PE=4 SV=1MNWKVISRNIGYALLVSALFMFLSVIVSVSEGNDSALAALAISFTITFIVGVFPFIFVRKSEAISLKEGYVIITLSWLMSFIFGMLPYA LWGGPFSLVNAWFESVSGFTTCGSTILDNVEVLPKSLLFWRSSTHFIGGLGVVVFLLLIIPESSPMRMRLTNMELTSLSRSGYSSRTN KVVYIFAYVYIAIAVAAFLAYLLAGMSLFDAVCHAMSVVSTGGFSTRTTSIAAFDSRWIEGITMIFMYLASLHFGVLYMTVATRSFRPMK NPVFKFYTISILVVSLVLAFGLRAHGDCSAWGEALWKGMFSTLAISSTTGFAIVDNACWPVWMSMMLVMVGIVCGCSGSTSSGLKVD RLLILFKSIGRYVNNILHPYSVNEVRLGKHILKDEDVSPHLLYAALYALVLVVSVFLVICAGIDVENSVAGTVMTLGNVGPATGAMGTMG SFNHMTIAAKVIFSMDMFLGRIEIYPVLAVIGMMMGRNRK
1.5E-38	142	17.3	1.5E-37	138.7	12	1.9	1	D9SYD0_MICAI	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Micau_5605	Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Micromonospora, Micromonospora aurantiaca, Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	644283	>tr|D9SYD0|D9SYD0_MICAI H(+)-transporting two-sector ATPase OS=Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442) GN=Micau_5605 PE=4 SV=1MRRLLRKPVRLVPLGFLAVILVGTGLLMLPWATNEQRYTPFVTALFTSTSAVSVTGLAVTDTPNYWNGFGLVMITVLTQLGGLGI LTGASLVILAVSRQLGLRNRLLVQAETAEFSLGDVRRLLLRIAATVFCETVMTAVIATRLFLAYDYRPGRALWSAVFHSVQAFNNGGF ALYSDGLIAFSRDGWVALPLSIGAIIGGLGFPALFEAVREWRQPARWAVATKLTVWGSVVLTVFGVAYLLMAEWTNPFTIGTFDVPGK LLASFTQIALSRTGGFDVINVGHLTDESYPMLIGLMFIGGGSASTAGGIKVSTFFLLGFAIWAELRGEPDTTVGRRRVAAASQRQALTV ALLSVALVAGGTVGLIALTSHVSFSAALFEVTSAFSTTGLTVGVSGQLSPPGQYVLTALMYIGRVGPLTLGSAIALNTRRRLYRYPEEQ PIVG
1.6E-38	142	16.3	3.5E-37	137.4	11.3	2	1	F4FDH7_VERMA	H(+)-transporting two-sector atpase	VAB18032_01520	Verrucosispora maris (strain AB-18-032)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Verrucosispora, Verrucosispora maris, Verrucosispora maris (strain AB-18-032)	263358	>tr|F4FDH7|F4FDH7_VERMA H(+)-transporting two-sector atpase OS=Verrucosispora maris (strain AB-18-032) GN=VAB18032_01520 PE=4 SV=1MRRFLRHPVRLVPLAFLLAIGIGTGLLMLPSMTVRHEAAPTLTALFTATSAISVTGLAVVDTPGFWSTPGLIVITVLTQIGGLGILTG AALVILTVSRRLGLHNRMLVQAETLEYGIGNLRRLLLHIGGTVLVCETVMTAIVTARLWLGYDYPLGRALWSGGFHAIQAFNNSGFSLY PHGLLSFSRDPWVSLPLALGSIIGGLGFPALFEAAREWRRPTRWAVATKLTIWGSAALVGLGFLTFLLIEWGNARTIGQYAVTDKLLA AFTQIALSRTGGIEVVSTTGLREESYPLLTGLMFIGGGSASTAGGIKVTTFFLLAFVIWAEIRGEPDVTVGHRRVATASQRQAVTVSLLS VAIVAVGTSLLIAVTNKVPFHSALFEITSAFSTTGLSAGVTSALPDSGLLLLTVLMYIGRVGPLTLGSAIALNTRHRLYRYPEEQPIVG
1.8E-38	142	14.3	7.3E-38	139.7	9.9	1.7	1	Q0BYN0_HYPNA	Trk system potassium uptake protein	HNE_2733	Hyphomonas neptunium (strain ATCC 15444)	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hyphomonas, Hyphomonas neptunium, Hyphomonas neptunium (strain ATCC 15444)	228405	>tr|Q0BYN0|Q0BYN0_HYPNA Trk system potassium uptake protein OS=Hyphomonas neptunium (strain ATCC 15444) GN=HNE_2733 PE=3 SV=1MQLRPVLLALGIMTVLLAGAMLPCALLDLADGSDEAHVFWFSSFSSGLVGCLLWVLARGGDPKIGQRETFLLTVAVWVLVPAVA AVPFVVSGISVTDAVFESVSGLTTTGATSLSGLDNMPRGLLLWRGILQWIGGIGIVVTAVAILPQLRVGGMQLFQLESSDITGKFLPRIK DIAAYMGLTYLIISSACAFSYSLAGMNWFDAIVHAMSTVSAGGFANYDASFGHENLQPAMAPAIFFMALAGLPFALLTMVLQGRISPM LRDPQPRLYFALLLFFSATIVIWHEAVVEPPIFDHIFHGITETVFNIVSVMTGTGYASTAYDTWGQPAIIIFLLATFMGGCAGSASCGMK MFRLEITAKALIAWSQRMVQPHRRTPVRYAGKPVDEETLQSVMVFMFLYLTTFMVVAALLSFTGLDALGAISASATMVSNVGPGLGP DVGPSTNFASVTDFAKWVCSAAMLLGRLEFVAVFVVLTGRFWRG

2E-38	142	19.6	1.6E-37	138.6	13.6	2	1	A0A022LRQ2_9MICO	Potassium transporter Trk	H489_0108150	Curtobacterium flaccumfaciens UCD-AKU	477	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Curtobacterium, Curtobacterium flaccumfaciens, Curtobacterium flaccumfaciens UCD-AKU	1292022	>tr|A0A022LRQ2|A0A022LRQ2_9MICO Potassium transporter Trk OS=Curtobacterium flaccumfaciens UCD-AKU GN=H489_0108150 PE=4 SV=1MLDRTEPIPHHVGVGRRRASRIATVLRSSPSRLAIVVFIALIFLFTVLFMTPWATADRSSTHFADALFTAASVVCVTGLSTVDMATHWSVFGKVLVVIGTQIGAVGVLTFASILGLFVTRKLGLRAKLMAAGDSNPLRTHHGAVPEGQAVRLGEVGTLLATVAVSTLSIEIVLGLLLLPSVLIAGIPFWTAVGDSFYYAAMAFTNTGFSPNADGLDPFAHDYWFLSLLMVGVVAGSIGFPVIRALTKQLRTPRRWPIHVKLTLATSAVLLLGGAAVYIALEASNPTTFGEEGAGRTAFQALFLSTMTRSGGFSLVDFDQLNGSSLLVTDMLMFIGGGSASTAGGIKVTTLAVLFLAAVAEARGRQSMEAFGRRIPSDVLRVAVAIVLWGATIVAVATVVLLQITDDSLDRVLFEVISAFSTSGLSSGVSADLPEPGKYVLAATMFLGRVGTVTIAAALAASQSRQLFRRPEERPIVG
3E-38	141	28.2	1.3E-37	138.9	19.6	1.7	1	R7EZ71_9BACT	TrkH family potassium uptake protein	BN677_01828	Prevotella sp. CAG:485	493	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:485	1262927	>tr|R7EZ71|R7EZ71_9BACT TrkH family potassium uptake protein OS=Prevotella sp. CAG:485 GN=BN677_01828 PE=4 SV=1MITAGARKRKFVNLPMLMRIIGLLLLIEAALMIFPLAAEFIYRDGSLWGFIISMGITLGMGIFLVRLKPQSHEMGRREAILLTSLTWIILSAFGMIPFLISRSPMSVTDAFFEAINDFTTTGGSYFPPIEETGHSLLLWRSVMRWLGGMGIILFTLAVAPMLNNSGGIFLFNAEITGITHDKLRPRISSTARGLWIVYTLLTFALIGLLALSDMDIFSAIYESMSVISTSGFTTLNVQGDMFNGYYLKIVLIIFMFLGGVNFSLIYKAFTGHFRNVRVNTVLRWYVIFIFAAYILLTVNVVINGLAKHVDDVTIDPLFQVVGTISSTGISEPDFAQWGALSTIVLVILMFTGACSGSTSGGAKIDRIIVLLKFLKNEFFKMMHPNNVTAVTINGRSVKLSLVQKILAFLCLYMIVIFISGTLLVILGVSLRESFFYTLSAISNTGIGTDTIGIGQQGFASLPDTAKWILSIVMLTGRLELYTVLLVLTPYFWQK
3.1E-38	141	31.8	8E-20	80.2	9.7	2.4	2	A0A0F3NRA4_9RICK	Cation transport family protein	NLO413_0837	Candidatus Neoehrlichia lotoris str. RAC413	486	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Anaplasmataceae, Candidatus Neoehrlichia, Candidatus Neoehrlichia lotoris, Candidatus Neoehrlichia lotoris str. RAC413	1359163	>tr|A0A0F3NRA4|A0A0F3NRA4_9RICK Cation transport family protein OS=Candidatus Neoehrlichia lotoris str. RAC413 GN=NLO413_0837 PE=4 SV=1MKSLRAIIFIVGVFSLLFANIMLVPAMVNFYAEYAWEGFVISSLIVFSFGIICIFIGKLCALKKVLVFSITSNVWIILSILSSIPFVLSDTKLSYIDAFFEATSGITTTGATVLSNLHEKSPGILLWRSILNSIGGLGIIVTGIFLFPCLKVISLHSLYHCESSDTSVRFKFGLFKTLMYTFGVYITLIILCTVFYRIAGMSIFDAICHALSTTSTGGFSNYDDSLQHFNSVYVENVAIVFILLSSCPFNMYLRAMSEKRFFDIQIICLIFIIIGCSILSMIWIYHNNLYIKGEFIRCLRCVVFSFVSLSTSTGFTNCDYSNWGLVSILGCLVMFIGGCSGSTNSGVKMYRILILLKSVQKYIKNIVLGDYKEVYFCFYNRAINSNILLEVSIFFFLYIAILIVSCVLISLSGESIVTSITAVIATLANTGPGIGEIVGPKGNYNSLLPLVKLLLSCLMLIGRLEIIPVFAFAYLIFYKCKKLYIS
3.2E-38	141	27.8	4.4E-37	137.1	19.3	2	1	Q2NG34_METST	Trk-type potassium transport system, membrane protein	Msp_0830	Methanosphaera stadtmanae (strain ATCC 43021 / DSM 3091 / JCM 11832 / MCB-3)	500	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanosphaera, Methanosphaera stadtmanae, Methanosphaera stadtmanae (strain ATCC 43021 / DSM 3091 / JCM 11832 / MCB-3)	339860	>tr|Q2NG34|Q2NG34_METST Trk-type potassium transport system, membrane protein OS=Methanosphaera stadtmanae (strain ATCC 43021 / DSM 3091 / JCM 11832 / MCB-3) GN=Msp_0830 PE=4 SV=1MNSFTINKIKTNELKTIGHYTGYVCIVIGLFMIIPIICAIIFHDEVKYLNSFVSSSIICVAIGFLLWVGFSKKNLTHLSLKGSLIFVLSIWGLTALAAGLPYVISGDLNILDAFFEGMSGITTTGFSLLPPCEHPFSVAIWASLTQWLGGLGIIVLLLVVVPSSVSLKRLYFAEGRTEQMTPNIKHTTIIFIKLYLLLTSIGIILYLLAGLNLFDAICYCFCGIATGGFSVHPASVQYFQTPIIQLITCMCIMILGGLNFVVIYRVIKGAWRNLYKDIEIKAFAFLVISSTLLIGLSLYFQGFYNHDILIILRHSLFQVVSVITSTGFSSTSIDNWSPLCYTVLILLMFTGSSICSTSGGIKLYNIVILFKAIWWEVKSMILPKNTIIIKKVFHDNKYRDVSDKTIKTILIYVISYILIFIASFIVIAIFCNDFQIAFTITASSLGNTGLAPTYLSVSTPLIVKIVMIIDFWAGRIGVWPLLLSIVYTTNIIQGKIEEHRE
5.4E-38	140	15.1	1.1E-35	132.5	10.5	2.9	2	D2V2E7_NAEGR	Cation transporter	NAEGRDRAFT_78284	Naegleria gruberi (Amoeba)	838	cellular organisms, Eukaryota, Heterolobosea, Schizopyrenida, Vahlkampfiidae, Naegleria, Naegleria gruberi (Amoeba)	5762	>tr|D2V2E7|D2V2E7_NAEGR Cation transporter OS=Naegleria gruberi GN=NAEGRDRAFT_78284 PE=4 SV=1MTTTTGNNIEKTSLEPSTTSIELEENTNNNNTDNISIRELAAEQYLSTPTDLHNNIRFEDQFQDSVSYQGSAFSNQPNSMMENVDNESEEEKELNEIEEDMGHEKVDRDDNFGFKIDQFLRVTLGTFYFCKRSKNNLENGGEQATTQKKPKWLYRYYAPIHIAYIIFCGFLFGTLIYVFELNNPKANIPYIDALLMSFANVCLAGFVTQPIVDITVPSQVSLFLAIVSGGPHFTLIPILLIKIFRARKRMFKLREEEAKYQPTMVQLPPTIPQNEAVSFPAQSRIVSFFSALKQKFTSNKQKERFPHSDIEYSALLWLHSITFILVVVINSVGFLILGGVFAGMYNEEKYMHGKSPFWLGLYIAVSAFNNCGSTLLDENLGNFVDDWVICMTVGILIILGNVLFPLVLRYVLVIIYKMSSKRKVVFKYILEKHHHLSPYLFPGIQTTIYGIITILLLVFGIVITLACDWGSPRMADKSVATRILIALFHPISARTGGFNSIDLFTLSFPTLAVYIIMMYTKPQMACSLRENAYKIVDMVRHINDEKKTIKFAHKNERRVKTKPSSPPTISVETPATENNDNLESETSNAKNEDVVFVKLQKRTTREQEAIVELEEEEEKRVYGYTLSRNASVTSLHPMLPPPVDESNHASIPRMQKFKKFAKKSGKLLVKYLSDFWFYFATILSTSNMWMIIMVFIISIAENNSNMKEDPKSFSIFFILFEVISAYANSGLTVGKDGSSLAYCGFWTTFSKVILCIVLVMGRHRGFYGTLIDLEPTSYDQDFKQHSNFLERRSMLRKYKKEIKKLKRVESRRDYGLLKTETNIETSSTAGGPISGNYFDP
7.8E-38	140	31.3	1.5E-37	138.6	21.7	1.4	1	R5FYX0_9ACTN	Trk-type K+ transport system membrane component	BN494_00376	Eggerthella sp. CAG:1427	508	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, environmental samples, Eggerthella sp. CAG:1427	1262874	>tr|R5FYX0|R5FYX0_9ACTN Trk-type K+ transport system membrane component OS=Eggerthella sp. CAG:1427 GN=BN494_00376 PE=4 SV=1MWQRFTWYDVRVIGHYLGVLISFFSIALVIPLIVAVVCQEWEPACRYLLGFGISLILGSALRFLRIQPGRLTHQQALAVTGMSWIVLAFVAAIPLALSGHYGSYLDALFEATSGLTTTGASLVIDLEHLSYADNMWRFTMHLIGGLGLIVIALSLGIFGKSTSGLYSSEGRSEHVLPNIVNTVRLISQIALAVIGVATAVLFLLCIIGGFEPLRALLNALWMAISGFTTAGFSPTSLSAMYYHSFAFEIVCMVLMLLGAVNFALFVKISQGETASFFKDYEIRTGVVWMLIATVVLMFSLCASGGFSDIMALLRRGVFMVVSASTTTGFQTVTNNQMTTVFSSGAFLVVAILMAVGGSSGSTAGGMKFSRLGLIAKSMVSTIKETLAPGTARVSVRYYYHLGKKVLTTEVAKAALTVSALFVFTYLLGSLVGIAHGYDALDAIFESVSMASNGGLSSGIIAHGMPPVLEAVYILEMWAGRLEFITLIALIVKVVVSVGSLAKKKLKEQA
7.8E-38	140	14.4	6.6E-36	133.2	9.9	2.1	1	R5DVQ6_9FIRM	Trk-type K+ transport systems membrane components	BN462_01487	Ruminococcus sp. CAG:108	364	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:108	1262950	>tr|R5DVQ6|R5DVQ6_9FIRM Trk-type K+ transport systems membrane components OS=Ruminococcus sp. CAG:108 GN=BN462_01487 PE=4 SV=1MPKITHRKKRLSSFKLIVLGFAGVIVLGALILMLPFSSTAGVVTPFHEALFTSTSAVCVTGLVVQDTGSYWSAFGQTVILLLIQIGGLGVVTVAALFAMLSGRKISLMQRSTMQDAISAPKVGGIVRLTRFIVRGTFLIELIGMIVMLPTFCGNYGIKGIWMAAFHSVSAFCNAGFDILGTAENKYPSLTGYIGNPAINITIMLLIIVGGIGFLTWDDIYTNKWHFKKYRMQSKVILVTTAILIIVPAVFFFCDFTGLPLAERILASLFQSVTPRTAGFNTADLPAMTGSSKAIMTMLMLVGGSPGSTAGGMKTTTLAVLILSAFSVCRKKDDAQRDTTIFQTGQPPFPYKVIISNILFMFKC
1.4E-37	139	23.3	2.5E-37	137.9	16.1	1.3	1	A0A0F2C921_9MICO	Ktr system potassium uptake protein B	ktrB RS85_02337	Microbacterium sp. SA39	476	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium sp. SA39	1263625	>tr|A0A0F2C921|A0A0F2C921_9MICO Ktr system potassium uptake protein B OS=Microbacterium sp. SA39 GN=ktrB PE=4 SV=1MSGIASASSPRERLEGAVDWVKHIVTSSPSRFAIVIFALLILVFTVLLSLPIASASGTVTPLSDALFTAVSTICVTGLATVDMANYWSPFGHVLIFVGVNIGALGVLTLASLMGMLISRRLGLRAKLMAAGDTNPLRAHGGVVNESQTVRLGEVGQLLTTVAVSALIIEASLAVLLYPALVMAEVDPIAALWEAPYFAAMAFTNTGFAPNDGGVAVFADDYLVLTLLMIGVFLGSIGFPVIYTLAKHVWHVKKWSLHTKLTLVTTVLLFVLGAAVFLILEYNNPKTFGSMDAADTTFQAFFLSAMTRSGGFNVIEMDDLNGSSLLAASMLMFVGGGSASTAGGIKVTTLAVLAIAVWSEAKGRSSVEVFGRRIPSDVQRVALSVVAWGATIVALSTIIIAQITKDDISHVLFDVISAFGTVGLSTGLTAELPDSASYVMAATIFMGRVGTVTLAAAVAATSRSQYYSLPVERPIVG

1.6E-37	139	40	4.8E-37	137	27.7	1.7	1	U4KN25_9MOLU	K+-transporting ATPase	ktrD BN8535900	Acholeplasma brassicae	460	cellular organisms, Bacteria, Tenericutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Acholeplasma, Acholeplasma brassicae	61635	>tr|U4KN25|U4KN25_9MOLU K+-transporting ATPase OS=Acholeplasma brassicae GN=ktrD PE=4 SV=1MNLYLSIKKILFKTPARTIFTIYFMFALVAGFILWLPISQKDGVSISYIDALFISISALASAGLSPIPLYDTFNLFGGIVTLLIIQIGGLGIVLLVASYWVISGKKIGLRERSIIAAEQNQFTVKGIIRLISNALIAILVIQIIYLVVMTFYLYVKQPFDLTFGGAFFHAAFLAASSFANAGFEMFPTLSSFVVFQEKGMYFPQYASMVLIFFGGVGFWPLAEITLYFKSIFKKKRYKISYISKLLMFLHLLILVITIMIYTGLEFNNTLRFMSMPEAITDVLFMSTSVRSAGFTNTSNLAWSESTKLFMSVLMFIGAAPNSSGGGVRMTTIILLFSTLLSYGRHKKQVKVFKKAIKEAAVKRALIVFSMGILLVFVSTFLVSIAEPSKKIMDVAFEVSSAFGTVGLTLNFTSTISNFTKVILMINMFVGRIGILTLLEVLDNKKTANVVTYAEIDMMVG
1.9E-37	138	17.5	5.9E-36	133.4	12.1	2	1	R5CUY2_9FIRM	Trk system potassium uptake protein TrkH	BN705_00819	Firmicutes bacterium CAG:555	357	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:555	1263030	>tr|R5CUY2|R5CUY2_9FIRM Trk system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:555 GN=BN705_00819 PE=4 SV=1MIRSLLFWRSFTHWLGGMGILVLVTAIAAGSGDGSTNILKAEMPGHSLDKFTPKAKNNAKLLYGIYIVLTLLETVLLLAGGMPVFDSVVHALGTAGTGGFGIKADSIASYSAYLQWVITVFMLLFGVSFNIYCLMLVRRWREALRSNELRCYLGIFAAATVIVCINIYPMYGSVSDVIRLSSFQTASIITTTGYATADFNTWPQLSKAVLFILMFCGGCMGSTAGGLKISRVTVLAQVCANEMRRSINPRSVNSVKLNGSVLTSEQEQGVLSYLALYIAVIAVTFILISVNGLGFEEDISAVVSCVNNIGPGFGLIGPSGSYAAYSGFAKIVLSIAMLIGRLEIYPLLALTMIGSRR
2E-37	138	16.2	3.2E-37	137.6	11.2	1.2	1	E8NG16_MICTS	Trk-type K+ transport systems, membrane components	trkH MTES_2315	Microbacterium testaceum (strain StLB037)	480	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium testaceum (Aureobacterium testaceum) (Brevibacterium testaceum), Microbacterium testaceum (strain StLB037)	979556	>tr|E8NG16|E8NG16_MICTS Trk-type K+ transport systems, membrane components OS=Microbacterium testaceum (strain StLB037) GN=trkH PE=4 SV=1MAATPSEVRLSVRARRMAAEAWDRLRNLTTASPARFAVLVFVTLILLFTALFSLPQASATGQRTPFADALFTAVSTICVTGLSTVNMYTHWSPLGHVITYVGVNVGALGVLTLASILGLVISKRLGLRAKLIAAGDSNPLRAHGGPVNEGQTVRLGEVGQLLRTVALSTLVIEAGLTVLIYPSLVIGGIDPLVALWEAPYYAAMAFTNTGFVPNADGLTPFAQDYFLLTVLMMGVFLGSIGFPVIFTLWRHYWRFRQWGSLHAKLTIITTVILFFAGAGVILLLEYDNPLTFGSMDAWDTTFQAFFLSAMTRSGGFSVIDIGDLNGATLIVGSMLMFVGGGSASTAGGIKVTTLAVLALAVFSEAKGRPSVQAFGRRIPSDVQRVALSVVAWGATIVAISTVTISRITDAPIEHVLFDVISGFATVGLSTGLTAELPDPAVYVLAATMFMGRIGTVTLAAAVAASSRSQLYALPVERPIVG
2.1E-37	138	20.8	7.1E-26	100.1	4.6	3.6	3	K3YRH6_SETIT	Uncharacterized protein	Si016870m.g	Setaria italica (Foxtail millet) (Panicum italicum)	532	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3YRH6|K3YRH6_SETIT Uncharacterized protein OS=Setaria italica GN=Si016870m.g PE=4 SV=1MVRSLLVSLKRLRIYSAFLASKLLSFPKLAQQTMKYSYQFIRRSNPLFVQIIYFTSISFGGYAALKILKPQENPHALKYLDLLFTSISASTVSSMATVEMEDFSNSQLWMLTILMLIGGEVFTSMLGLYFMKAKFDAKGSVNKTGYSFYADVESASSENPGPNSTQGTKVMVPISELRLEDKDRVDHETMKSLGYALMVYLLVTNLGGSLAIYLYLILVPDAQEVLKRKDIGYVIFSIFTAISSIGNCGFTPVNENMVIFQKNTILLLLIPKILLGNTLFAPCLRFMMWSLEKITTKKEYHFILQHPKAVGYKHLMNGRECVYLMVTVIVFIIMQTILFCSLEWNSNALQEMNSYQKIVGALFQSVNARHAGENIVDLSSLSSSILVLYTIMMYLPSYTSFLPKDNDQDSNEGMKYKRRSRCENWILSQLSYLAIFVLLICITEKEAMATDPLNFNIFSITFEVISAYGNVGFSLGYSCQRLLNHNIHCKDASYGFVGRWSDKGKMILIIVMVFGRIKSLNMHGGRAWKLR
2.1E-37	138	26.7	1.8E-36	135.1	18.5	1.9	1	B0SNI9_LEPBP	Putative cation transporter putative membrane protein putative signal peptide	LEPBI_I1154	Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris)	508	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira biflexa, Leptospira biflexa serovar Patoc, Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris)	456481	>tr|B0SNI9|B0SNI9_LEPBP Putative cation transporter putative membrane protein putative signal peptide OS=Leptospira biflexa serovar Patoc (strain Patoc 1 / ATCC 23582 / Paris) GN=LEPBI_I1154 PE=4 SV=1MPLVRFKRFFRTLSFARLVCLGFFAAIFLGSFALYISERGELSYVDSLYLSASSICVTGLSPIPLSGLNPSTHWIMLFLIQLGGLGIISFTVIVGFLITKGISRNARFNAFVGAAIDTQTETESLATNEVNRILLSVINISFSIEILGAIGLYLHMPEGAEGNNTRWFFSLFTAISSFNNAGFSITDDLSALRLDPFSLYIVSGLVIFGGIGFPVIILLEKVLLTIFVRIVYRIEVVAETLMMEKALKTGNVPRFLLLPAQFSAILENRIEEYNKHLRGETTRIQSKLLVYGSSALLLFGFIGIYFLERSNPHTFHGMDLVDKISNAFFMSVCSRTAGFSTMDLGHLNDATVIIITVLMFIGGGPQGTAGGIKITTFVLLLAYLKNVIQPSKPVMLFGETVSKYSVAVAIRVYFLATVSLAFVFILLGILDQNQHSLHVIFFELISSFSTVGYSLNLTSQLGDIEKLFYAAVMYVGRVGIFTVLIAATGHSGVPKMGTVDDGVKIQVG
2.7E-37	138	32.7	2.6E-34	128	17.4	2.4	2	B0ELB9_ENTDS	Putative uncharacterized protein	EDI_227750	Entamoeba dispar (strain ATCC PRA-260 / SAW760)	510	cellular organisms, Eukaryota, Amoebozoa, Archamoebae, Entamoebidae, Entamoeba, Entamoeba dispar, Entamoeba dispar (strain ATCC PRA-260 / SAW760)	370354	>tr|B0ELB9|B0ELB9_ENTDS Putative uncharacterized protein OS=Entamoeba dispar (strain ATCC PRA-260 / SAW760) GN=EDI_227750 PE=4 SV=1MRIKLLGYNRIVQLLQSFYAYHTYFTIAMALLIGFLCYVNEMDHSRLTVMEAFFLGVSTSTDTGLLTFDFSITKISTQIIVMIGAELCGVFFASTLIPSVCRWYRLRQIIKQQELLNNDSPNTLVDFSSSSESSEITDETNDETNLQVFTSEIEPMQYDYKLEIKSLEYFIYILLFYTISFKLIGFIVILITCYTSNETVNFLSQQQINPIWFSLFQTISSWNNLGMTVNQNSLNPLINVRCIVITSVFLNMTGNIMIPIITRMLAFIVHRLFEQKSKHCSKPQPLLYILKAPTRMSLSFFSSTQTKLLFVQLFLILLQTIFFSLFYNKNDLSPLYVGFVNSSFTRTAGFSIINVRDLSPPVILTYILSMYIAAYPTVILRQYRDIEVNAKAGLIHIQSNITTILKYVKSLFFSHIIWFYTATLIVMGFYCSAHTTGANQLIDVMFEISSAFGTVGMSLGSSKDPCSFSGDVPIPAQLIICLLMILGRHRGFPTHSYPLDYYSFWKKVNS
2.9E-37	138	24.5	1.1E-35	132.4	17	2.1	1	M4YNN6_9EURY	Trk-type K+ transport systems, membrane component	TALC_01020	Thermoplasmatales archaeon BRNA1	522	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Thermoplasmatales, unclassified Thermoplasmatales, Thermoplasmatales archaeon BRNA1	1054217	>tr|M4YNN6|M4YNN6_9EURY Trk-type K+ transport systems, membrane component OS=Thermoplasmatales archaeon BRNA1 GN=TALC_01020 PE=4 SV=1MITMFAVMKERIRRLQRFQSGTVKTLGVVETLLGVMLLLTAAYALFCGENYEPFLFPAPVFLIMGMIQYMFFYRGSMSPSLGILLMLETWIVSFAAAIVPFVIYGFAPVDAVYEGVSGYTTTGSTIMTDIEGAESCILLWRALIQWAGGITVVIIFTLLLPMIGMGGKNLGSNEFGGSDNGEYSTSLSSVALNFFRIYVLLTAAEFVILIALGMTPFESICTSMSCVPTGGLLPFNNSMADFGFAIQATTLVFMILGASNFLFLFRLFHRDRTLLKSREWRVMLLWFLGVALFMTAVVWFDGNYRTDYIGETFWDSLYAVTCAGTSSGFAVSDYTIWPILAVLMLMVVEFVGGTSGSTAGGIKIYRLMTMKAYIAAGMEKIMHPNAVTTMSVDGSHVDTDNAASVLSTVFLFVVGCLVGIGLILFFQNESGHPIEFLDSIGLVISSICNAGASIGNFGPMSSMAPLQPATKIVMTSLMFLGRMEMVFVLMVFTRRFWNDVRQSSTRIREKAVYTIRRSGKY

3.5E-37	137	32.5	2.3E-34	128.2	17.4	2.3	2	C4LTJ1_ENTHI	High-affinity potassium uptake transporter, putative	EHI_011970	Entamoeba histolytica	482	cellular organisms, Eukaryota, Amoebozoa, Archamoebae, Entamoebidae, Entamoeba, Entamoeba histolytica	5759	>tr|C4LTJ1|C4LTJ1_ENTHI High-affinity potassium uptake transporter, putative OS=Entamoeba histolytica GN=EHI_011970 PE=4 SV=1MALLIGFLCYVNEMDHARLTVMEAFFLGVSTSTDTGLLTFDFSITKISTQIIVMIGAELCGVFFASTLVPSVCRWYRLKQIIKQQQEL LNSDSTNTLVDFSSSESSETTDETNDETNLQVFTSEIEPMRYDYKLEIKSLEYFIYILLFYTISFKLIGFIVILITCYTSNETINFLNQQQINPI WFSLFQTISSWNNLGMTVNQNSLNPLINVHCIVITSVFLNMTGNIMIPIITRMLTFIVHRLFEQKSKHCSKPQPLLYILKAPTRMSLSFFSS TQTKLLFLVQLFLILLQTIFFSLFYNKNDLSPLYVGFVNSSFTRTAGFSIINVRDLSPPVILTYILSMYIAAYPTVILRQYRDIEVNAKAGLIHI QSNITTILKYVKSLFFSHIIWFYTATLIVMAFYCSAHTTGANQLIDVMFEISSAFGTVGMSLGSSKDPCSFSGDVPIPAQLIICLVMILGRH RGFPTHSYPLDYYSFWKKVNS
5.1E-37	137	21.2	2.6E-33	124.7	14.7	2.2	1	Q2GIT2_ANAPZ	Potassium uptake protein, TrkH family	APH_1182	Anaplasma phagocytophilum (strain HZ)	486	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Anaplasmataceae, Anaplasma, phagocytophilum group, Anaplasma phagocytophilum (Ehrlichia phagocytophila), Anaplasma phagocytophilum (strain HZ)	212042	>tr|Q2GIT2|Q2GIT2_ANAPZ Potassium uptake protein, TrkH family OS=Anaplasma phagocytophilum (strain HZ) GN=APH_1182 PE=4 SV=1MGSVAFITGMFTALMAAFLLIPMTVSFLTGSTDWVGFAGAFAIASSAGVLCILNGKRPRSIRGTEAIYLACSVWIALTLVAAVPFV LADTTKLSYVGAVFEAMSGLTTTGATVMSNLSQKSHGVLLWRAMLNAMGGLGVITIGIFLLPNLKMAGLREIYNTEALGRECKSGVVR TVLYVTAIYILLMILCYASYNIVGMSMFDAICHAMTTVSTGGFSNYDDSLKHFDNVKIEIVAIVFMLLSSCPFVAYIHIVFERRFKNSQFLL YMGILTASVLLSTVQFQNYANTDGYWSAFRFTVFTVVSLSTSTGYSIGDFSDCSFMVILVTMLTLCGGCAGSTNSGLKVLRLQILAISA YDNIRNILLRGCSETKNIHIPDNVRNEAGYILFLYLFVFILACLCTSWLGYDLTTAITAVSSTLSNTGIGVGAVVGPEGDFSLLTEGTKLLL TALMLLGRLEIVPVIVLLSTMLRIGIHRVKSMQAACEKT
7.7E-37	136	23.1	3.3E-36	134.2	16	1.7	1	R6Q230_9CLOT	Uncharacterized protein	BN618_00214	Clostridium nexile CAG:348	271	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	1263069	>tr|R6Q230|R6Q230_9CLOT Uncharacterized protein OS=Clostridium nexile CAG:348 GN=BN618_00214 PE=4 SV=1MGSVQPFSSLTGEVGNWYVNLIIMALIIIGGLGFFVWRDILATKLHFHKMQLHTKLVLSVSLFLIAAGTLLLFVCERGTGAYQDLTL SEQVAASAFQSVSARTAGFNSVNLSALTQTGRFLIISLMLIGGSPGSTAGGIKTTTFAVLVLSVITTFRSRKSTEVFGRRLEDFITRKATC IFFLYITFSFSAAMIISRIENIDFLDSLFESVSAIATVGLSTGITPELMPLSHALLAFLMIFGRVGSLTMLLAFSFTRKQLPSALPLEKIQLG
1E-36	136	0	1.5E-19	79.3	0	2	2	E2LXC1_MONPE	Uncharacterized protein	MPER_11924	Moniliophthora perniciosa (strain FA553 / isolate CP02) (Witches'-broom disease fungus) (Marasmius perniciosus)	290	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Marasmiaceae, mitosporic Marasmiaceae, Moniliophthora, Moniliophthora perniciosa (Witches'-broom disease fungus) (Marasmius perniciosus), Moniliophthora perniciosa (strain FA553 / isolate CP02) (Witches'-broom disease fungus) (Marasmius perniciosus)	554373	>tr|E2LXC1|E2LXC1_MONPE Uncharacterized protein OS=Moniliophthora perniciosa (strain FA553 / isolate CP02) GN=MPER_11924 PE=4 SV=1MGAFTGGGLSLVDQGMVPFQKAYLMIISMMFVILAGNHALPIFLRWVGSRVAREGTEAEQAFSFLLDHPRRCFYYLHQTWFLVI CLVMFSATLAEAYESLSIWSTDNLRSIPMISRPSFWVFNSTTCVSRTCTTVSIRRHDVYCLFTRYEEQSLGVFEQPPEDEDEEPQSQD LKGLAVGQRVHRYLGWHLKKQTTVDIWWLVWGVFIITIIERNNLIDPDKKWFDLFRVLFELVSAFGGIGLSLGVPYDNFSFVGAMRPL SKLVVIVIMWGPGQTPRFTGSSRPGCYATS
1.1E-36	136	18.9	4.2E-22	87.7	4.1	2.2	2	B9KGX1_ANAMF	Potassium uptake protein trkH (TrkH) (EC 3.6.3.14)	trkH AMF_845	Anaplasma marginale (strain Florida)	523	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales, Anaplasmataceae, Anaplasma, Anaplasma marginale, Anaplasma marginale (strain Florida)	320483	>tr|B9KGX1|B9KGX1_ANAMF Potassium uptake protein trkH (TrkH) OS=Anaplasma marginale (strain Florida) GN=trkH PE=4 SV=1MSAASALGCRECWFLVAAVRNEACDTSLTHWRALVFVQGAFSLLFALFLLVPMAVDFFMGGEDWEGFATAFSVSAVVGSVCL HFGKSGPIGRHETVYLICAVWTVLSILAAIPFLVSETAKLSYADALFEAVSGLTTTGATVLYNLQAKSPGILLWRVMLNFIGGLGVIAIGV LLLPCLKVVGLKDIYGVESATARQRFKLSVFRTVLYISCMYAMLLVLCTGAYKIAGMSAFDAICHAMSTVSTGGFANYDSSLGHFNSAA IEIVAIVFMLLSSCPFVVYLRLALEGRFRSKQFVVFVCVLVVFSLLGAVNLYSRNMLPEAEFPEVLRRSAFILVSLVTSTGFSNCDYSSW GFLAVSGTILTLCGGCSGSTNSGLKMHRIVILVRGGYRYVKHMLMRTPFTVSEQSAREEALPEAGAFFFLYVFVFCIACIIVAWSEDDL ATIVTSVSSTFTNTGPGIGDVVGPHGTYAPVSATVKFVLTVLMLIGRLELVPVFVLILSLLRGGAGRLLGIGRGAKMLDMFR
1.4E-36	136	26.3	1.5E-18	76	8.4	2	2	F4A0C9_MAHA5	Cation transporter	Mahau_2866	Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	502	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family IV. Incertae Sedis, Mahella, Mahella australiensis, Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	697281	>tr|F4A0C9|F4A0C9_MAHA5 Cation transporter OS=Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON) GN=Mahau_2866 PE=4 SV=1MIEKHVSWWLPICYYIGIIIIGLGLIQYIPAVTSVIYAEWDIFFDFLISSSITLLVGGSMVLLGRRYHEQRMNWGDGMVVTAGSWFL GMLISALPYYLSGNYNSYLDCTFDVMSGLTTTGLTLIRDLDHVSNGINMWRHLLTFVGGQGMVVLALTFLVKGTSGAYKMYVGEGKD EHLMPNAISTARYIWLISLIYLCLGTVTLWIAGIIAGLSVDRAFLHGLWIFMSAWSTGGFAPMSQSILYYHSSIYEIATMIFLTIGSFNFALH YAVLTGKREELRRDIEIISFTVTLTTLTIITTLGLKQSGSYADAMSLFRKGFYQLISAHTTTGFMTIYAKQFYCEWGDIALFAITVAMLFGG NACSTAGGFKGLRIGIIFNAFKNDIKQMVLPESTVSVQKIHHIKDVILEDKMVRSAFLIVLSVLTSTGFSNCDYSSW GNVGLSIGLTSASMPAVLKVTYIIILWVGRLEFMSVLALGLYVARRVKKDV
1.7E-36	135	24.3	8.7E-36	132.8	16.8	1.8	1	I0XUM8_9LEPT	Cation transport protein	LEP1GSC185_1787	Leptospira licerasiae serovar Varillal str. VAR 010	549	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira licerasiae, Leptospira licerasiae serovar Varillal, Leptospira licerasiae serovar Varillal str. VAR 010	1049972	>tr|I0XUM8|I0XUM8_9LEPT Cation transport protein OS=Leptospira licerasiae serovar Varillal str. VAR 010 GN=LEP1GSC185_1787 PE=4 SV=1MFPGLGNSLPGFAGVKIVSGRAVFPFCMSPYKFLKRNVNRIARAFLLLSVARILCLAFAGAILVGSFMIFASEEGRISYADSFYVA ASAICVTGLTTVSISELAFSTQVIIMFLFQIGGLGIITFTVLVGILVVRGLSRSTRIAAFVFEAIDSHESADGKSKNAPYVRRILLSILNISVSI ELLGAFLLYWAMPEDLSGLPGDPNRVFLSLFTAVSAFNNAGFSIVDDLTFLSREPLSLLVVESLVVMGGIGFPVILFFEKTLLEAFRNVM HRVEVVVMETYLMSRALEEGKEPSWIYLILIRMSFWAEERLALYRMALKGEANRIQMKLLLYGTLILVHVGGIGFLLSEWDNPETIGKFD FVDKLFNSFFLSVSSRTAGFNTFDISEMRSPTYVLLCSLMFVGGGPQGAAGGIKITTFVILLMYLRNVINPQARVTIMGEEVSKNSIAIST RIYFLATISIVFFMLVITIANGHRHGIEEIFFEVMSAFGTVGLTKGLTPYITGVEKFLYPCIMYVGRVGVFTLLIAFTGHSGLGTLGAQDDG VKIQVG
2.2E-36	135	22.3	2.4E-35	131.4	12	3	2	M0TBP1_MUSAM	Uncharacterized protein		Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	498	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Zingiberales, Musaceae, Musa, Musa acuminata (Banana) (Musa cavendishii), Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	214687	>tr|M0TBP1|M0TBP1_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1MALSFRRTTNRAREFILTRTYSFDRLNRYLRQLVLFVYRFSALRLSSFCIHLIYFVFLALLGSLIMVLLKPSDPSFSPSYVDMLFMS TSALTVSGLGTVETERLSSAQIAVLTLLMFVGGEVFVTLLGLLLRRTSEHDKREASADLRLSCVRWLRYIVSSYIFTFHLFGTSLLLIYIY RVSNARDILRKKGINVFLFSLSTTVSSFANGGLIATNENMAAFNRNPTMLLLMIAQVLAGNLLFPLFLRLVIWTLKKITKREEFRHMLKST SETRFSPLLPEKQTCFLSLTVVGLMTALLVLFCSMDWDGAVFDGLTSFEKIVSAFFIAANSRHAGENSIDPSLISPAVLVFIIVMMYLPPS ATFWPAEEDDTSSDGIKKQNKKKKSWVQNLLISQLSCIIVYIILICIIERRKMRRDPLNFSSLNMIFEVTSAYGNVGLSTGYSCSRLMKLH PEASCQDKPYSLAGWWSDESKIILSSVMLYGRLKKFSAQDGKAWRLY

2.4E-36	135	24.2	3.9E-22	87.8	7.7	3.4	3	A0A0D9VCT3_9ORYZ	Uncharacterized protein		Leersia perrieri	527	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Leersia (cutgrass), Leersia perrieri	77586	>tr|A0A0D9VCT3|A0A0D9VCT3_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1MIHCLAVSQTFCAFAASKFSSFTKSAQKSIKNSFQFICQNNPLFVHVTYFAVISFTGYSALKVLKPRDKSNTLKDLDVLFTSVSASTVSSMATVEMEDFSSAQLWVLTILMLIGGEVFTSMLGIHFMKAKFGTKESVNIRDHSPCIDIESITSTKFDPRTQGTKVTVSFAELHMENGAHVEPKTIDFLRLVVMGYLLVTNLGGSILIYLYLNLVTGAQQVLKRKGIGIVIFSVFTAISSVGNCGFTPVNENMVIFQKNSVLLLLIIPQILAGNTLFAPCLKLMVWSLKKITGKKYCRYILEHPKAIGYKHLMSTRESVYLILTVVSLIIVQTILFLSLEWSSVALQEMSNYQRIVCAIFQSVNARHAGESVTDLSTLSSAILVLYTIMMYLPGYTSFLPGHDHEDSKTEMKNKRKRLLENWIFSQMCYLAIFVMLICITERKSMATDPLNFNVFSILFEVVSAYGNVGFSFGYSCKRSLIYDAHCKDASYGFAGKWSDKGKAILIIVMLFGRLKSFNMKGGRAWKLR
2.6E-36	135	10.5	4.9E-35	130.4	7.3	2	1	Q3J5D2_RHOS4	Trk system potassium uptake protein	TrkH2 RSP_1853	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides), Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	272943	>tr|Q3J5D2|Q3J5D2_RHOS4 Trk system potassium uptake protein OS=Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158) GN=TrkH2 PE=3 SV=1MLDLRPVGFIIGLLVVALGAAMLLPASVDLLLGDGNGPAILQAAMLTMFTGGAVALACANAPTKQLGIRQAFVLTAAIWFALPAFGSLPLILGEPDLTFTDAMFEAVSGITTTGSTVIVGLDHLPAGTNLWRGMLNWLGGLGIAFIAMIFLPVMRVGGMQFFRTEGFDTLGKVLPRATDIARALLGVYTGLTALCIATYLLIGMEPLDAVVNGVATIATGGFSPSDASFGKYPGAGEYAGTVFMILGAMPYIRFVQLVSGAPQAFFGDSQIRAMLRWMVYGVGIVTLWRVLTSDQGLEPAFREASFNLVSVFTGTGFFSGSFANWGGFGMVVAFCVGMIGGCSSSSSGALSVFRVQVVLTAIRVQIERIGMPDRMASVRYEGRRVEDDVMNALILYVTGYILAIGTLSVALTLTGVDPTSALFGVWTSIGNIGYGYGPLVARTGTFIDFPPELAKWVLILAMLMGRLALLALVVLVLPRFWRQ
3.1E-36	134	18.9	2.9E-35	131.1	13.1	1.9	1	D4LNC7_9FIRM	Trk-type K+ transport systems, membrane components	CK1_36060	Ruminococcus sp. SR1/5	342	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus sp. SR1/5	657323	>tr|D4LNC7|D4LNC7_9FIRM Trk-type K+ transport systems, membrane components OS=Ruminococcus sp. SR1/5 GN=CK1_36060 PE=4 SV=1MGVLVFILTLLPLAGGYHMNLMKAESPGPSVGKLLPKVQSTAKILYKIYIALTVALIILLLLGGMPLYDSLCAAFGTAGTGGFGIKSDSMGSYSLYIQIVITIFMILFGVNFNVYFLLLTRKFSQALKSEEVRCYFFVIIASALMITFNVRHLFDNVWEALQQAFFQVGSIITTTGYATTDFNQWPAVSRTILVLLTFCGACAGSTGGGIKISRLLLLAKSVRKELHLYLHPNAVKKIKMDGKAVSHEVMRATNIYMIVYLMIVATSIFIISFDEFDLVTNFTAVVTTLNNVGPGLSLIGPTGNFGIFSPLSKLVLSFDMLAGRLELFPILILFLRETWKKF
3.4E-36	134	0.5	3.8E-36	134	0.3	1	1	C9SNX3_VERA1	High-affinity potassium uptake transporter	VDBG_06598	Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) (Verticillium wilt of alfalfa) (Verticillium albo-atrum)	135	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, mitosporic Plectosphaerellaceae, Verticillium, Verticillium alfalfae, Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) (Verticillium wilt of alfalfa) (Verticillium albo-atrum)	526221	>tr|C9SNX3|C9SNX3_VERA1 High-affinity potassium uptake transporter OS=Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) GN=VDBG_06598 PE=4 SV=1MVHVRNQLTFDLWYIFLGTFLICIAESTLIMDVAEPTFSIFAVLFEVTSAYANVGLSLGGPSGLVSMSGHYTIFSKVVICAMMIRGRHRGLPYALDRAITLPSEHTLSDESSSAEQIPKSLSLGRTQSSGARSAP
3.5E-36	134	33.6	6.7E-36	133.2	23.3	1.4	1	W8VPQ1_9FLAO	Potassium uptake protein, integral membrane component, KtrB	NMS_0611	Nonlabens marinus S1-08	385	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Nonlabens, Nonlabens marinus, Nonlabens marinus S1-08	1454201	>tr|W8VPQ1|W8VPQ1_9FLAO Potassium uptake protein, integral membrane component, KtrB OS=Nonlabens marinus S1-08 GN=NMS_0611 PE=4 SV=1MTISLSDNFTFFGQFVVMLLFQIGGIGYMTFTTYILLNTSHHTSKWRERILNAAFAIPKSIELRPFLKSVIIFTVLFEIVGTVFFYIGFEGQGYDFWEQLWMSLFHSVSAFCTAGFSLLNSGFVDYVSDGWINFTISFLSIAGSLGFIVFSDFWLKLARKKHEVSYTSKLIFSGFFILLTAGTIAMYFTEPSIVALDGATRFYASFFQTMTAMTTVGFNTIDNGALVVPVAIVTILLMYIGASPSGTSGGLKITTIVATIAYLRSKLKNSSDFLFFNTRIPDERVDAAVSTFIFYFILSFFGILFLTFSETESLEKISFEVLSALGTVGLTKGITGDLSFFGKAVITCLMFIGRLGVLTFGLAMSRAYVVKNENEEEQEQEKDVAV
3.9E-36	134	0.8	2.1E-19	78.8	0	3.3	3	I0IBH1_PHYMF	Cation transporter	PSMK_04500	Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	463	cellular organisms, Bacteria, Planctomycetes, Phycisphaerae, Phycisphaerales, Phycisphaeraceae, Phycisphaera, Phycisphaera mikurensis, Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01)	1142394	>tr|I0IBH1|I0IBH1_PHYMF Cation transporter OS=Phycisphaera mikurensis (strain NBRC 102666 / KCTC 22515 / FYK2301M01) GN=PSMK_04500 PE=4 SV=1MCTRTLGLALGPLTLVATPTLAIAWAEGALPVAAGLLVPMAGGALGWAYGRRGERSPHHASGPTLAAAWAVASLLCAAPFLAAGGAFGPLNALFESASGLTSTGLSVAGDPRELPLSLQWWRSTLQWIGGVGILYFALTLACVERAGPEDGDDEAADGELGSGEAEKRGPSLRRLLERTWIVYGGLTLLSFAGLYLAGMSAWDAANHAQTAAATGGFSTSADSLAAFGTAAQAVACVTMLAGAVGFGTLRLMTFGRRPAALAIDPQARWFAAALLPLFLLVWASGVPAWPAFFEAASGLATAGFTVREGGGGLLPIAALPLALAMLVGASAGSTGGGLKLARLRRLVRAAAGKPDAGHRLAEPVAATRRLAGLYAAAFALGTLALGFASPAGVTWVDAAFEAASALGTVGLSSGFTDAEAPAACRVVLVALMWVGRLEVVGVLALLAAPLRGGAKDRAVAQSG
5.5E-36	134	23.7	5.4E-24	94	11	3.4	2	I1HXT4_BRADI	Uncharacterized protein	BRADI3G05570	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	519	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Brachypodieae, Brachypodium (false bromes), Brachypodium distachyon (Purple false brome) (Trachynia distachya)	15368	>tr|I1HXT4|I1HXT4_BRADI Uncharacterized protein OS=Brachypodium distachyon GN=BRADI3G05570 PE=4 SV=1MKHSRVATKLSSFAKSGQQSMKYSCQFICQTNPLFIQLTYFTLISFAGYEALKVLKSQDKSNTMKDLDLLFTSVSASTVSSMATVEMEDFSSTQLWILAILMLIGSEVFTSILGLHFMRVKFNTEKPANKSDRSSHVDIESINAANFDPSPSQGTEVTVPSSQLCLANKEHVDPKTIKFLGTVVMAYLLITNLGSLLLIYIYLKLVPDAQEVLKRKGIGNFLFSVFTAISSVANCGFTPVNENMVIFQKNSILLLLIIPQILAGNTLFAPCLRYMVWTFKKITGKEECHFILQHPKAIGCRHLMSTRKCVYLVVTVVSFIILQTILFCSLEWSSEALQEMSSYEKIVGALFQSTNARHAGESVVDLSSVSSAITVLYTVMMYLPGYTSFLHNYEDPYSKARERDNSRRLLKDWVFSQLSYLAIFLMLICITEREAMTTDPLNFNVFSILFEIVSAYGNVGFSVGYSCKRLLKHDVYCKDASYGFVGKWSDKGKLILIVVMVFGRLKTFNLKGGSAWKLR

7.3E-36	133	20.1	1E-35	132.6	13.9	1.1	1	D2QAR1_BIFDB	Trk-type K+ transport systems, membrane protein (EC 3.6.3.14)	BDP_1278	Bifidobacterium dentium (strain ATCC 27534 / DSM 20436 / JCM 1195 / Bd1)	444	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium dentium, Bifidobacterium dentium (strain ATCC 27534 / DSM 20436 / JCM 1195 / Bd1)	401473	>tr|D2QAR1|D2QAR1_BIFDB Trk-type K+ transport systems, membrane protein OS=Bifidobacterium dentium (strain ATCC 27534 / DSM 20436 / JCM 1195 / Bd1) GN=BDP_1278 PE=4 SV=1MHRLTALPGRLTIIYFLLLVAISTSLLLTPISTPRGDTTDFTTAFFTAVSAISTCGISIVNSTTHWTTFGQAVLIFSVQMGGLGVMTF ASLIALAVNHHLKATQRLLTANELGTTKLGEIKGVLTVVITTAFVIEGITFIALFPGLYKINHGNVRHTLWESLFFAVMAYNNAGFTPDGA GLHVNNWAVGLPILASAFCGTLGFPVLLNLMRSWRMHRPPKRWSLHTKLTLITTFCIVTASLTWFLIVEWNNKSLFPGNSVEPRLWH AMVAAVMPRSSGFDLSWMPQVSDATKVFLSIVMFIGGGSTSTAGGIRVTTLAVILLVCRAAFTGRREINAFHRRIHTQAVMTAVSVST ACLTLVTVVSMTLMIITDCSLCDALFDTCSAFGLGGYSVGVADAGNPAALYVLAATMFIGRLGPMTIAYAVSRPRNLEAVRYPTEQIVV G
7.8E-36	133	18.8	1.7E-35	131.9	9	2.3	1	A0A0F2S1P2_9RHOB	Trk system potassium uptake protein	VR71_04185	Roseovarius sp. BRH_c41	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseovarius, Roseovarius sp. BRH_c41	1629709	>tr|A0A0F2S1P2|A0A0F2S1P2_9RHOB Trk system potassium uptake protein OS=Roseovarius sp. BRH_c41 GN=VR71_04185 PE=3 SV=1MFDMRPVGYLVGLMVMAMGLTMALPLLVDIAEGREHWPVFAESMIVTCLMGGLVALACKNSVGQGLTIQQAFLLTTLVWVALP LFGALPFILGETRLGFIDAFFEAMSGVTTTGATVIAGLDDLPKGLLLWRGILQWLGGLGIVIVALVFLPEMRVGGMQFFRAEGFDTFGK ALPRTIDISKGVLNVYLGLTAVCTLSYLTLGMGAFDATVHALTTVSTGGFSSYDVSFGAFPGPPQYACVVFMILASLPFVRMMQGVHG NLEPIYRDTQVRTYLRWLFYAFALVAVYDFLMNGRITEESLRERLFNVVSIFTGTGYGDGDVTAWGNFPFVVLIAVGAIGGCTGSTGC SIKIFRYQLMLRALGQQARRIFNPSSVMVLRHEGRKVEDEVLQSVMLLFTVYILSLGFFSVALELTGLTLMESVTGAWTSIFNVGPAFG QSVGATGSLSAFPDAAKVLMILAMLMGRLEILAVIVLILPSFWRP
8.3E-36	133	34.2	1.3E-35	132.3	23.7	1.2	1	R7BQ78_9ACTN	Trk-type K+ transport system membrane component	BN629_01289	Eggerthella sp. CAG:368	506	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, environmental samples, Eggerthella sp. CAG:368	1262877	>tr|R7BQ78|R7BQ78_9ACTN Trk-type K+ transport system membrane component OS=Eggerthella sp. CAG:368 GN=BN629_01289 PE=4 SV=1MWQKFSFYDVRVIGHYLGVLISFFSLLLVVPLVTALVLQEWEPATRYLLAIGLSLIVGSGMRMMRIQPGRLNRQQAMAVTGLAW FFLALIAAVPLALSDHYASYIDALFECMSGLTTTGASIVVDLDHLSNADNMFRFLMHFLGGLGLIVVALSLGILGKGTSGLYTSEGRSEH VLPNIVNTTRLISRIAIILVGVSAVMVTIICLIAGMEPIRAVLHAFWISISGFMTAGFTPTSQSIMYYHSLPLEIICMVLMILGTINFALFVEIW RGNTTAFFKDIEIRTAFIWLLVITVVFMSSLAATLTFSGLPEMLRRGVFMVVSSFSTTGFQVVTSNQITTVFSSGAMLMLALLMAVGGS SGSTAGGMKLSRIGMIAKSVVATIKETLAPDSARVSVVYTHIEKKVLSSDVVKSAMTVSALFIMTFVIGSLAGVAHGYDATSAIFESVSM ASNGGLSSGIVSRGMPISLEFLYIIEMWAGRLEFIALLALLVKLVVSVLPNKPIRRDR
8.9E-36	133	22.7	9.8E-21	83.2	4.7	3.8	3	I1GWP7_BRADI	Uncharacterized protein	BRADI1G34220	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	532	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Brachypodieae, Brachypodium (false bromes), Brachypodium distachyon (Purple false brome) (Trachynia distachya)	15368	>tr|I1GWP7|I1GWP7_BRADI Uncharacterized protein OS=Brachypodium distachyon GN=BRADI1G34220 PE=4 SV=1MGGIKRYYHDFIHIKLHSFSRISRYVADSILFLYRFFTLNVHPFWIQLSYLLAISILSSVLLMSLKPSNPEFSPRYIDMLFLSTSALTV SGLSTVKMEDLSSPQIVVLTLLMFVGGEIFVSLLGLMLRVNHQDMPDISTVKISSVPVELEAIDSASSVTFCDESKLEEATQAIPPKNSD LKRRSLKCLGYVVFGYLAVIHVLGFLLVLLYITHVPTARIPLNKKGINAVLFSVSVTVASFANAGLVPTNENMTIFSKNSGLLLLLTGQSLA GNTLFPLFLRLLVWFLSKLTKVKELGFMIKNPEEVHFGHFLPRLPTVFLSSTVIGLVAATVTLLCAVDWNSSVFDGLSSYQKIVHAFFM AVNTRHSGENSIDCSLVSPAILVIFIIMMYLPSSATFAPPNGDTKTTDDNMEHRRGSLVQNLAFSPLMCNIVFVIVVCITERRRLRNDPLN FSTLNMIFEVVSAYGNVGLSTGYSCSRLQLLHPKSICQDRPYSFSGWWSDGGKLVLVLVMFYGRLKVFSMGTGKSWKVGHS
1.2E-35	132	24.8	1.9E-35	131.7	17.2	1.2	1	A0A0F0KE23_9MICO	Ktr system potassium uptake protein B	ktrB RN50_02392	Microbacterium foliorum	476	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium foliorum	104336	>tr|A0A0F0KE23|A0A0F0KE23_9MICO Ktr system potassium uptake protein B OS=Microbacterium foliorum GN=ktrB PE=4 SV=1MSGIVSASSPRQRLQNAASWSKHIITSSPSRFAIVIFAMLILVFTVLLSLPIASATRTVTPLADALFTAVSTICVTGLATVDMATHWS PFGHVLIFIGVNIGALGVLTLASLMGMLISKRLGLRAKLMAAGDTNPMRAHGGVVNESQTVRLGEVGQLLTTVALSALIIEGALAILLYPA LVMAGVEPIAALWEAPYFAAMAFTNTGFAPNAGGVAVFADDYLVLSLLMVGVFLGSIGFPVIYTLAKHVWHVKKWSLHTKLTLVTTVL LFVLGAVVFLVLEYANPKTFGSMDAADTTFQAFFLSAMTRSGGFNVIEMDDLNGSSLLAASMLMFVGGGSASTAGGIKVTTLAVLAIA VWSEAKGRQSVEAFGRRIPSDVQRVALSVVAWGATIVALSTIIISQITKADISHVLFDVISAFGTVGLSTGLTAELPDSASYVLATTIFMG RVGTVTLAAAVAATSRTQYYSLPVERPIVG
1.2E-35	132	22	3.5E-34	127.6	15.2	2	1	B0RI62_CLAMS	Putative cation transport protein	CMS2552	Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	474	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Clavibacter, Clavibacter michiganensis, Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	31964	>tr|B0RI62|B0RI62_CLAMS Putative cation transport protein OS=Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) GN=CMS2552 PE=4 SV=1MRVRPDHGRPLLGRIRDFLDYFAHSTPARFAILIFAALVLTLTTILMLPGMTSTGDTAPFADALFTAVSAICVTGLATVDMATYWT PLGHAFIALGVQIGGIGVLTLASIMGLIVSRRLGLKARLMAASDSNPLRIHHGPVAEGQAVKLGEIGTLLLTVAISALVIELSIAALLFPRILL EGIPVGQAALDSFYYSLMAFTNTGFVFSEAGFELYHQDYWFLSLLMIGVFLGSIGFPVIYAVYRGWRKPRRFSVHVKLTLWTSLILIVL GTLAYVVLEWDNTKTFALMDPVQHGFQALFLSVMTRSGGFSTLDMADFGNASLLVTDMLMFIGGGSASTAGGIKVTTLAILFLAAFAE ARGSESMEVFERRIPSDVLRLAVSIVLWGATTVALSSIVLLQISGERLDYVLFDAISAFATSGLSTGFTAEASDPAKYVLAATMFLGRVG TVTLAAALAASTRRQLFQRSEERPIVG
1.6E-35	132	24.9	1.1E-33	125.9	17.2	2.1	1	W8TPN2_EUBAC	Trk system potassium uptake protein TrkH	trkH EAL2_808p05740	Eubacterium acidaminophilum DSM 3953	494	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium acidaminophilum, Eubacterium acidaminophilum DSM 3953	1286171	>tr|W8TPN2|W8TPN2_EUBAC Trk system potassium uptake protein TrkH OS=Eubacterium acidaminophilum DSM 3953 GN=trkH PE=4 SV=1MAKSLKFMEVTKIISLLVITMGIILLLPLAASFYYGEMGSEVAFGLPSLVSFAAGGAGYAITRRSHVKLDIASSMLLCFFGWLAASV VGAAPYMLALDKGFIDALFESASGFTTTGATVLTGLESMPKGILVWRCLTQWVGGIGILMFFLLITYKSESDLWRLFDAESHKTRYSRP VPNVYSTVRILWTIYVGLTVALAMILPLFGVSVFDSILHSLTTIATGGFSPYDQSVNQFSMIEGVDFKAVEYIITFFMFISGINFLLHYKLFA SGEGEYAKNHEFNLYAVMIALFTLVIFIESAFVVRPAGAGFEEIFRKALFQVVSLITSTGFSTEYIGSSYFGYGAKQLFLVLMLVGGCVG STSGGLKVVRLSILGKLFTREIKKIAMPRGAVLPVTIDKLPVGADEIFRVSAILFGWIGMIFAGSLLTSFFSDLNMVESISGMLSAVSNMG PMYFGVEKMASLSPVIKLTYILGMISGRLEILPIFILVSMKYRF
2E-35	132	0	4.3E-22	87.7	0	2	2	Q2UTW5_ASPOR	Na+/K+ transporter	AO090009000564	Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	248	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus oryzae (Yellow koji mold), Aspergillus oryzae (strain ATCC 42149 / RIB 40) (Yellow koji mold)	510516	>tr|Q2UTW5|Q2UTW5_ASPOR Na+/K+ transporter OS=Aspergillus oryzae (strain ATCC 42149 / RIB 40) GN=AO090009000564 PE=4 SV=1MLPENDYFAHHRHTLRFLLDYSRRCYTNLFPSRHTWWLLCAVIVLNGLDWAAFGVLNIDNPSVNRIPPGPRALDGCFRRYVSN VYEERSLGIYAGETTPKSNHQQEKPPKTVPSSRLYFVKQQLHVQLAYDIWWLALAVIIISIVKAGSFTRDPVVYSVFNIIFETISAYGYVG ITTGLPDQAYSFSGGWYSLSKVVLRAAMLRGRHRSLPVAIDKAIVLPGDYLERVEEEDAYIRMERSSEQGHGNV

3.1E-35	131	26.1	8.1E-19	76.9	5.1	2.1	2	R7FNE4_9CLOT	TRK system potassium uptake protein TrkH	BN588_01090	Clostridium sp. CAG:288	512	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:288	1262791	>tr|R7FNE4|R7FNE4_9CLOT TRK system potassium uptake protein TrkH OS=Clostridium sp. CAG:288 GN=BN588_01090 PE=4 SV=1MENFIDSLEVDGNDKPVVKGWRLTLGYAGFFMIVVGIMLLVPLITLIFYPSEAKYFIHFLIVGLLNIIIGCIPFFRYIYKRKHAQLATH QDACIVVLCWILAIVMCAIPFATSGLLTFSQAIFESASGITTCGLSIVSDFDNFPHIFFILRSLTHLVGGIGLVLVMISALSDRYGMKLYASE GHYDRFMPNLLKSSRAILLIYLGFIISGVIAYVICGMPVFDAIVHSIAAVATGGFSNKADSIGFYNSRSIEIVSMVLMLCGSTNFLAHVFLF KGKFKNFFMYCENKFMYAFYAVVIPLAAIGLFCAYDKYSIGDSFLISAFHVISALSTTGFQTVKISPSTASSFLFILTLCMLIGGQTNSTAG GLKIYRLNLMIKSIYIKMKDSLMKTKTVHYYRVYQLDEETYITNETLQENNLFLVTWIAIYFISVLVYCFAGIPFVESIFEVASILGTVGMSM GGITANSPAFIFYFSALIMLIGRLEVFVVFYGIIYSIRTPISKILTFKSRRKE
3.2E-35	131	22.3	5.6E-35	130.2	15.4	1.2	1	A0A0A7I7E0_9BIFI	Potassium transporter Trk	AH67_04005	Bifidobacterium pseudolongum PV8-2	487	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium pseudolongum, Bifidobacterium pseudolongum PV8-2	1447715	>tr|A0A0A7I7E0|A0A0A7I7E0_9BIFI Potassium transporter Trk OS=Bifidobacterium pseudolongum PV8-2 GN=AH67_04005 PE=4 SV=1MANLLFDESASNSDASQGYAWWFSGDTFEKAAAEERKPIRRSLSYRINSHPGRLTIIYFVVLVCLSTSLLLLPISTQEGQSTSFST AFFTAVSALSTCGISIVNTTSHWSMFGQAVLIISVQMGGLGVMTFASLIALAVNHHLKAMQRLLTASELGTNKLSEIRGVLTVVLTTTFVI ESITFIALFPGLLHVNKGSVGHSLWESLFFAVMAYNNAGFTPDGAGLYVNNWAVGMPIMLSAFCGTLGFPVILNIFRCTRRHQPPKR WNLHTKVTLITTFAIVLVSLIWFLAVEWDNPALFKHADVETRMRRAMVAAVMPRSSGFDLSWVPQVSEATKVFMSFVMFIGGGSTST AGGIRVTTFAVILLVCKAAFTGHSDVNAFHRRIHTHVIMTAVSITTACFALVLVASMALMLITDASFSHALFDACSSFGLGGYSVGVAQE GSDAALYVLAATMVVGRLGPMTLAYAVSRPKQLDVVRYPTDQIVVG
3.6E-35	131	22.6	1.3E-22	89.4	11.6	3.2	2	A0A0E0JW76_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	531	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0JW76|A0A0E0JW76_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MIHCLVVSHKKLQTFCVFAVSKLFSFTKSAQQSIKNSFQFIYQNNPLFVHVAYFALISFAGYGSLKVLKPRDKSNTLKDLDVLFTS VSASTVSSMATVEMEDFSSAQLWVLTILMLLGGEIFTSMLGIHFMKAKFGTKGSVSTRYHSPCIDIESITSTKFDPSTQGTKVTVSFSEI HMENGGHVEPKSIEYLGFVVMGYLLVTNLGGSLLICLYLNLVPGAHQVLQRKGIGIIIFSVFTAISSVGNCGFTPVNENMIVFQKNSILLL LIIPQILAGNTLFAPCLRLMVWSVEKITGKKECRYILEHPKVIGYKHLMSTRETINLILTVVSLIVLQTVLFLSLEWSSVALHGMSNYQKIV SALFQSVNARHAGESVTDLSSLSSAILVLYTIMMYLPGCTSFLPGHDDEDSKTKKRNKRKGLLENWIFSQMSYLAIFAMLICITERESM ATDPLNFNVFSILFEVVSAYGNVGFSVGYSCKRLLNHDARCKDASYGFAGKWSNNGKAILIIVMLFGRLKTFNMKGGRAWKLR
4.3E-35	131	11.9	1.3E-32	122.3	8.2	2	1	R5I9C6_9FIRM	Trk-type K+ transport systems membrane components	BN729_02486	Ruminococcus sp. CAG:60	308	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:60	1262964	>tr|R5I9C6|R5I9C6_9FIRM Trk-type K+ transport systems membrane components OS=Ruminococcus sp. CAG:60 GN=BN729_02486 PE=4 SV=1MPKKSYKKKHLTSFQLIILGFAGVILLGSFLLMLPFSSVDRTLTPFHEALFTATSAVCVTGLVVKDTGSYWSVAGQTIILMLIQIGG LGVVTVAASVSLLSGKKISLMQRSTMQDAISAPKVGGIVRLTRFILKGTFLIEAAGALFLLPVFLPDYGGRGIWLSVFHSISAFCNAGFDI LGTAANPFPSLTGYSANALVNVVIMLLIIGGIGFLTWDDIYTNKLNFKRYRMQSKIILMTTACLILFPVIFFFTCDLKNLSTGNRLLAAAFQ SVTTRTAGFNTIDISKMSEASKAVMILLMLIGGVPGG
1E-34	129	21.1	2.3E-34	128.1	14.6	1.5	1	B2UR73_AKKM8	H(+)-transporting two-sector ATPase (EC 3.6.3.14)	Amuc_1132	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	584	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales, Akkermansiaceae, Akkermansia, Akkermansia muciniphila, Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	349741	>tr|B2UR73|B2UR73_AKKM8 H(+)-transporting two-sector ATPase OS=Akkermansia muciniphila (strain ATCC BAA-835 / Muc) GN=Amuc_1132 PE=4 SV=1MEMGFGLCTLAALMWLLWWNGFGEIHEDQLSLRYFREILSFLVLGQLTGVIGILREKWLARAIRNPRWVELGLGLVILVMLAGD FFHSTFISKIELQNIFRALCLCYGAAPLLNLKEYFFRIARRNRGFHLPRIRPALLFLLTLIAFIALGGTLLMSPGATKDGIVLSATDAYFISTS AVCVTGLVPLNVHEHFTNYGQTILLVLFQVGAFGIMTFTYFVSLMVGQGLSLRSKVTISNLLDEEGIAQVDRFIKNIIAVTFGVEALGAIG LYFSWRHVPGLEGDTLWWYAVFHSVSGFCNAGFSLFADNLATPGVAYNMGGQITIMVMVLCGSLGFAMYLEIVRRARVALGWDAR NTVSRHWSTYSWLVVRMTAALVLGGGLILFLIKIIDGSLFTSADPWYWILWESLFNATARTAGFNISNMALNSAPYALFLGALMFIGGN PGSTTGGVHTTAFAVSCGEVARILQGKKDVVVMHKRRIARNVVERAVITVILAGAWVGMMTTVMCFAEPRLSLERLFFEVVSSFATVG FSWNVTPELSDAGKWIIVFNMIVGRVGMVAFVLAFMKQPTKSPLRYPETRLPLS
2.7E-34	128	24.5	3E-22	88.2	11.3	2.5	2	M0YEW7_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	532	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0YEW7|M0YEW7_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MNNSPVVHLKSLRTFCAFVATKLSYFAKSAQQSMKYSCQFICHTNPLFIQVTYFALISFAGYEALKVLNSQDKSNTLKDLDVLFTS VSASTVSSMATVEMEEFSSKQLWILAILMLIGSEVFTSILGLHFVRAKFNSENSFNRRDQISHVDIESINVTNFDPTASHGTKDGASFSE FHLANKQHVDPKTTALLGTAVTVYLLITNLGSSLLIYLYLKLVPDAQEVLKRKGIGLFLFSVFTAISSVANCGFTPVNENMIIFQKNSGLLL LIIPQILVGNTLFAPCLRFMVWSLQKITGKQEWSFILEHPKAIGYRHLMSTRKCAYLILTVVGFIILQTILFCSFEWSSEALQEMSSYQKIV GALFQSTNARHAGESIVDLSSISSAIIVLYTVMMYLPGYTSFLPNYDDRYSKDEKRYNRKGLLEDWILSQLSYLAIFVMLICITEREALTT DPLNFNVLSILFEVVSAYGNVGLSMGYSCKRLLKQDLRCKDASYGFAGRWSNEGKMILIIVMVFGRLKASNLKGGKAWKLR
3E-34	128	11.5	4.4E-32	120.6	7.9	2.1	1	S6C1C9_9ACTN	Cation transporter protein	AEQU_1739	Adlercreutzia equolifaciens DSM 19450	514	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Adlercreutzia, Adlercreutzia equolifaciens, Adlercreutzia equolifaciens DSM 19450	1384484	>tr|S6C1C9|S6C1C9_9ACTN Cation transporter protein OS=Adlercreutzia equolifaciens DSM 19450 GN=AEQU_1739 PE=4 SV=1MTVMGKTRGDNLAPAIALGEPGGERSGPGPLLARYVGVAVMFVGLAGLAPLAVLPAYPDEVALAPCFIFPGIGAAMAGYLVYFA SPDPAPGARLTRGQAAACTVLVWVLAIAVYALPYVAAGLLSPVQAVFESTSGLTTTGLSVVDVDACPAIFLFHRSLTCYLGGVGLVLIL TCVVTQTGGLGVYNAEGHTDHLLPSAAKTARVILLIYNGLIIAGAVAYWAAGMTPFDAINISMCAVPTGGFATHGESIAYWNSPVIEAITI VLMVAGGTNFLLLFLLLRGKLKAFLTHIETPLYFGTIAVMALVVAGFFLGQGVSGDGAEALRQGTFQVVSILTSTGFQTIPSFADLGPAL LFLFGLLMLVGAEARSTSGGIKLYRVAVASLGLGHDLHERYGNKRHVTSIKINRFGKRSVLTEVDVAEAQTYVVLYLLLCAAGAFALILC GATLQEAVFDFISCLGSTGVGTGFLGAESGPAPLLIGSAGMLLGRLEIIPLFMGVGTLASLIRKGVRHGR
3.1E-34	128	15.2	4.1E-23	91	5.9	2.4	2	M1P241_DESSD	Trk-type K+ transport system, membrane component	UWK_00969	Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	487	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfocapsa, Desulfocapsa sulfexigens, Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	1167006	>tr|M1P241|M1P241_DESSD Trk-type K+ transport system, membrane component OS=Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1) GN=UWK_00969 PE=4 SV=1MVQQATELRYAVRFRVVCKYFGQMSLVLATLSLAPFVVSVICGDIDISLRYGVVICGLAVLGASLSRLRTPARVQANEGMMLVAL IFFFTPLVMSYPMMGSGLGFFDAFFEAVSGVTTTGLSTKATLVGAPPTFLFARAWMQWYGGLGIVVLSLALVIQPGLDAKGLAVTEAE SDDLVGGTRAHARRVLKVYIILTVLGIIGSLAVGMRCFDGVLYTFAAVSTGGFAPNDTSLAILGWPAQVWISLLCLAGAIPLAFWYGMF KEKWRVGVEFLQMRAIIIVILIVSLTIGAAMRLSTDMAWTQILHHAPLLAFSAQTTAGFSSISCDQLDAGSKLVLISSMLVGGGFGSTSG GFKLLRLLIAVSVLRLILVRTCLPRHAVIEHRLVGRRLRDQDIHAALLLIVLFVAVVLFSWLPFVVMGFSPLDSLFEVVSATGTVGLSVGL TNANLPALLKGVLCVDMLMGRLEIIAWLMMIYPGTWFGRRMEET

7.8E-34	126	35.7	5.8E-33	123.5	24.7	1.9	1	R7AAZ9_9ACTN	Trk-type K+ transport system membrane component	BN592_00247	Eggerthella sp. CAG:298	506	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, environmental samples, Eggerthella sp. CAG:298	1262876	>tr|R7AAZ9|R7AAZ9_9ACTN Trk-type K+ transport system membrane component OS=Eggerthella sp. CAG:298 GN=BN592_00247 PE=4 SV=1MWTRFTFEDIRIIAHYLGTLTSLFTVALLIPLITALVFQEWEPATRYFLAAGISLTIGSLLRMAKVDPGRLTRQQAMALTGFAWMFL AFIASVPLAMSGHFASYLDALFDSVSGLTTTGAALIMDLEHLSYADNMWRFIMHFLGGMGLIVIALSLGLLSSSTSGLYSSEGRSEHVV PNVITTTRLISKISLAVIGIATVLLMLFCFVAGMEPVRAFFHGLWISISGFMTAGFTPTSQSIMYYHSYFLEIACMLLMLLGMINFGLFVAV LRGKTDLFFKDFEIRTGFFWLVFMCIIFIATLSTTPLFSDLLTMIRRGVFMLISASSTTGFSVVTTNQVLTVFSSGAILILAILMAVGGSSG STAGGMKLSRIGLTVKSIVSSIKEATSPDSARVSVVYHHIGKQVLNNEIARAAMTVSTLFVVTYVVGALVGIAHGYDATASIAESVAMAS NGGLSFGITTQGMPKTLELIYILEMWAGRLEFITLIALVVKIVASLLPVRKPKRDR
8.1E-34	126	22	8.7E-25	96.5	8.9	2	2	R5VSS1_9FIRM	Potassium uptake protein KtrB	BN566_01345	Ruminococcus sp. CAG:254	351	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:254	1262953	>tr|R5VSS1|R5VSS1_9FIRM Potassium uptake protein KtrB OS=Ruminococcus sp. CAG:254 GN=BN566_01345 PE=4 SV=1MQIGGLGITSIGAGLIAFTGRKLRMRDQVLVQEALNYPTMKDVQVLIRSVLITTIIVESSAAFVGWFLFRRQFDVLPALGIAIFHSVS TFNHAGFDILGGLLSYRNDVGLQLLTIAENILGGFGFFVILDILRNQRFHKFSLHTKVVLITSGFLDLTSSLLLKAIEGDSLSWVNAFFMGI TSRTSGLTIANVGDFSNASQLLICVLMYIGASPGSTGGGVKVTTIFVLFRTIVAYPRGEQPGAFRKRFSAGTVQQAMVICSLAISIVFAIS FILCLLNPTLPFLSLLFETASAFSTVGLSTGITSSVATFGKWLLMAAMFGGRLGTLTVVSLWFRKHRQTILLPVESISVG
9.9E-34	126	22.5	4E-21	84.5	5.5	3.4	3	I1NXR3_ORYGL	Uncharacterized protein		Oryza glaberrima (African rice)	531	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza glaberrima (African rice)	4538	>tr|I1NXR3|I1NXR3_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1MNHCLVVSHKKLQTFRTFAASKFSSFTKSAQKSIKYSFQFIYQNNPLFVHVAYFALISFAGYGSLKVLEPRDKSNTLKDLDVLFTS VSASTVSSMATVEMEDFSSAQLWVLTILMLIGGEVFTSMLGIHFMRAEFGTKESVSTRDHSPCIDIESITSTKFGPSTQGTKVTVSFSE LRMENGGHVEPKTIKFLGFVVMGYLLITNLGGSLLIYLYLNLVPSAHKILKRKGIGIIVFSVFTAISSVGNCGFTPVNENMIIFQKNSILLLLI LPQILAGNTLFAPCLRLMVWSLEKITGKKDCRYILEYPKAIGYKHLMSTRESVYLTLTVVSLIILQTVLFLSLEWSSVALDGMSNYQKIVS ALFQSVNARHAGESVTDLSNLSSAILVLYTIMMYLPGYTSFLPRHDGEDSKTEKINKRKGLLENWIFSHMSYLAIFVMLICITERDSMAT DPLNFNVFSILFEVVSAYGNVGFSVGYSCKRLLNHDARCKDASYGFAGKWSDNGKAILIIVMLFGRLKTFNMKGGRAWKLR
1E-33	126	22.6	4E-21	84.5	5.5	3.4	3	Q0E3H2_ORYSJ	Os02g0175000 protein	Os02g0175000	Oryza sativa subsp. japonica (Rice)	531	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>tr|Q0E3H2|Q0E3H2_ORYSJ Os02g0175000 protein OS=Oryza sativa subsp. japonica GN=Os02g0175000 PE=4 SV=1MNHCLVVSHKKLQTFRTFAASKFSSFTKSAQKSIKYSFQFIYQNNPLFVHVAYFALISFAGYGSLKVLKPRDKSNTLKDLDVLFTS VSASTVSSMATVEMEDFSSAQLWVLTILMLIGGEVFTSMLGIHFMRAEFGTKESVSTRDHSPCIDIESITSTKFGPSTQGTKVTVSFSE LRMENGGHVEPKTIKFLGFVVMGYLLITNLGGSLLIYLYLNLVPSAHKILKRKGIGIIVFSVFTAISSVGNCGFTPVNENMIIFQKNSILLLLI LPQILAGNTLFAPCLRLMVWSLEKITGKKDCRYILEYPKAIGYKHLMSTRESVYLTLTVVSLIILQTVLFLSLEWSSVALDGMSNYQKIVS ALFQSVNARHAGESVTDLSNLSSAILVLYTIMMYLPGYTSFLPRHDGEDSKTEKINKRKGLLENWIFSHMSYLAIFVMLICITERDSMAT DPLNFNVFSILFEVVSAYGNVGFSVGYSCKRLLNHDARCKDASYGFAGKWSDNGKAILIIVMLFGRLKTFNMKGGRAWKLR
1E-33	126	20.1	1.4E-33	125.6	14	1.1	1	A1A1V7_BIFAA	Uncharacterized protein	BAD_0909	Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a)	487	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium adolescentis, Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a)	367928	>tr|A1A1V7|A1A1V7_BIFAA Uncharacterized protein OS=Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) GN=BAD_0909 PE=4 SV=1MSNLVFDESSSNREASHGYAWWFSGDTFEKAMAEERKPRKRSLMHRLTTHPGRLTILYFMMLGALSTLLLLTPTATPKGEKTT FTTAFFTAISAISTCGISIVNSTTHWSAFGQAVLIFSVQMGGLGVMTFASLIALAVNHHLKATQKLLTANELGTTKLGEIKGVLTVVIATAF TIEGITFVALFPGLYKVNHGNVRHTLWESLFFAVMAYNNAGFTPDGAGLHVNNWAVGLPILVSAFCGTLGFPVLLNLMRSWRNHRPP KRWSLHTKLTLTTTFCIVIASFTWFLLMEWNNKLLFATEGVEPRLWHAMVAAVMPRSSGFDLSWMPGVSDATKVFLSIVMFIGGGST STAGGIRVTTFAVILLTCRAAFTGRHDVNAFHRRIHSQAVMTAVAVTTSCLMLVTVVSMALMAITGCSLSNALFDTCSAFGLGGYSVG VASASSPAVLYILAATMFIGRLGPLTIAYAISRPRNVEPVRYPTEQIVVG
1.3E-33	126	19.6	2.2E-20	82.1	6.7	3.8	3	W5HPT0_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	544	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5HPT0|W5HPT0_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MHLFLTLIHSTMGRVKRFYQDFIHIKLHSFCRISRYVVDSIAFVYRFVALHVHPFWIQLSYFLAIAILGSVLLMSLKPSNPDFSPPYI DMLFLSTSALTVSGLSTITMEDLSSSQIVVLTLLMLIGGEIFVSLLGLMLRVNHQDMQDLPSVKISSVPVELEELDLPNSMALCDESQLE EAAHAIPPKKCTELKRSRSVKCLGYVVFGYFAMIHVLGFLLVFLYITHVPTASAPLNKKGINIVLFSLSVTVASCANAGLVPTNENMVIFS KNSGLLLLLSGQMLAGNTLFPLFLRLLVWFLGRITKVKELRLMINNPEEVRFANLLARLPTVFLSSTVVGLVAAGVTMFCAVDWNSSVF DGLSSYQKTVNAFFMVVNARHSGENSIDCSLMSPAIIVLFIVMMYLPSSATFAPPSGDTKTTNENTKGKVKRGSLVQNLAFSPLGCNII FVMVACITERRRLRNDPLNFSTLNMIFEVISAYGNAGLSTGYSCSRLHQLHPEIICQDKPYSFSGWWSDGGKFVLILVMLYGRLKAFTL ATGKSWKV
1.6E-33	125	6.5	8E-30	113.2	4.5	2.4	1	A8LTS5_DINSH	Potassium uptake system protein TrkH	trkH Dshi_3914	Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12)	491	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Dinoroseobacter, Dinoroseobacter shibae, Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12)	398580	>tr|A8LTS5|A8LTS5_DINSH Potassium uptake system protein TrkH OS=Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12) GN=trkH PE=4 SV=1MSVKRAAAFRGGTSPLMQVARAPVVALMLAKHAPVFVILCAPPAIWAVAEGQAILALALAIPATFAALVFLAVARRPLPDDLRGV EAIVTIALVFGMSAVFVTPAFMALGMPVVDALFEAVSGATTTGLSVAFNPDAWPFAGHFLRAWVQWCGGLVMATAVLAMLLPSGLP ARKLGQAGIDQGDRIASTRKQARQLLTAYAALTGIMTLATMATIPDWREALAVTLSAVSTAGFAPRSDSLASYAPLAQGMVMLSCVLG AVSLLSFVLLSQGKWRQAWRLGSLRRVGLTVILFVAALIAFLVAAGERDAGAIYSSALNLISGLTTAGFSTGPISDLGPVLLLIVVAMVLG GDVGSTAGGLKLARVAVIVGAILHAGQRLRLPRNAVAPLRQNGEPVAPETLVSILGLLGIYLGALMLLWLHILAHGHDALGALFEATSTL STVGLSTGITGPSMSVDLKLSMTFAMWLGRVEFFAVLLLLAPRTWRGTTGG
2.1E-33	125	24.3	3.6E-33	124.2	16.8	1.3	1	A0A0A7I7A0_9BIFI	Potassium transporter Trk	AH68_06240	Bifidobacterium kashiwanohense PV20-2	487	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium kashiwanohense, Bifidobacterium kashiwanohense PV20-2	1447716	>tr|A0A0A7I7A0|A0A0A7I7A0_9BIFI Potassium transporter Trk OS=Bifidobacterium kashiwanohense PV20-2 GN=AH68_06240 PE=4 SV=1MSNLVFDESSSNREASHGYAWWFSGDTFEKAMAEDRKPRKRGLMHRLVNHPGCLTIFYFLTLATLSTTLLMTPIATPKDETTTF TTAFFTAVSAISTCGISIVNSTTHWTTFGQGVLIFAVQMGGLGVMTFASLIALAVNHHLKATQRMLTANELGTTKLGEIKGVLTVVITTAF VIEGITFVALFPGLYKVNHGNVRHTLWESLFFAVMAYNNAGFTPDGAGLHVNNWAVGLPILASAFCGTLGFPVLLNLMRSWRMRRPP KRWSLHTKLTLTTTFCIVIASFTWFLLMEWNNKLLFAGDGIEPRLWHAMVAAVMPRSSGFDLSWMPGVSDATKVFLSIVMFIGGGST STAGGIRVTTFAVILLTCRAAFTGRHDINAFHRRIHTQAVMTAVAVSTACLMLVTVVSMALMIITDCSLCDALFDTCSAFGLGGYSVGVA SESSPTALYILAATMFIGRLGPLTIAYAISRPHNLEAVRYPTEQIVVG

2.1E-33	125	24.6	1.3E-32	122.4	17	1.8	1	C7N1C1_SLAHD	Trk-type K+ transport system, membrane component	Shel_01400	Slackia heliotrinireducens (strain ATCC 29202 / DSM 20476 / NCTC 11029 / RHS 1) (Peptococcus heliotrinreducens)	508	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Slackia, Slackia heliotrinireducens, Slackia heliotrinireducens (strain ATCC 29202 / DSM 20476 / NCTC 11029 / RHS 1) (Peptococcus heliotrinreducens)	471855	>tr|C7N1C1|C7N1C1_SLAHD Trk-type K+ transport system, membrane component OS=Slackia heliotrinireducens (strain ATCC 29202 / DSM 20476 / NCTC 11029 / RHS 1) GN=Shel_01400 PE=4 SV=1MWQKFTFRDLRVIVKFLGVLVTFSAGAMCVPLVVALAMREWSSATHYIVGIGVALCMGSLMRLAYVKKAKLTTQQALAVTGFA WLLLAVTGSVPLALSGHFGSYLDAFFESMSSWTTTGASLAQDVDHMSFADNTWRFTMQCIGGQGVVVIALSLGLFGRAVDSSLYES EGRSEHVIPNIMQTTRFIVKLSAVVGVAGLIVFTILCLAIGMEPVRAFFNGLWLSVASFNTGGMTSMSPGINYYHSLAIELVVILLAMYGS INFTLHGEIWKGHIVPFFQDIEVKTSVVWLTVATAAFVAALCAAGAYADYPTLVRRGIFTILAAFTSSGFQTISPNQLTTVVSSGALIIVF VMIIGGSAGSTSGGIKILRVGVLGKEVVAYIKDLLAPPSARQVVTYYHVGRRPLAYSLVRANLAVFVLYVGAFLITTIATVAYGYDAMPSI FESVSMVSNIGMTAGIIEPDMPVVLKFVYMFDMWAGRLEWVTLIALAVSVIMSFKPRKKVKGRVY
6.5E-33	123	33.8	5.6E-25	97.2	8.4	2.7	2	A3DNV3_STAMF	Cation transporter	Smar_1219	Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1)	462	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Staphylothermus, Staphylothermus marinus, Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1)	399550	>tr|A3DNV3|A3DNV3_STAMF Cation transporter OS=Staphylothermus marinus (strain ATCC 43588 / DSM 3639 / JCM 9404 / F1) GN=Smar_1219 PE=4 SV=1MIRWRLIAYYLSNMLYLLGFSQIVPIIFSIIVGESIGFILLLIFDLLIMVSLAYILRRISFLGEINIVEAYTVMVLAFIIPSFTFALPVMVYN VDFINALFEGASAITTTGLSALPPHTLTTGVHFLRSYYQWLGGIGIALLTLSFFLSPGTAAYNIYVAHLGKYKLKPLSISTIKIIVKIYIAFTLL YIFLYLVSGTPLLDAVLNSLTTISTGGFSRISSFKNGSMYMALFLMFMSAQPIAIYYFLFRGKLREILKDPQLSCFILISIIGFIAVSISVGNIS SEILFQVISALSTTGYSAFDNKLLSEPAKFILSILMIIGAGFGSTGGGLKQLRIIIIFKSITANIKRLYMPKDAVIPVKIRNKVVSSSEILFSYTL LGMYLIVLIVSTYIISLYGYSIADSFFEASSALATTGLSVGISSPSLSFIPKITLIIDMWLGRVEIIPFIIVLTNLYYSTKKR
7E-33	123	24.7	1.3E-21	86	11.3	2.8	2	W5H5R1_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	532	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5H5R1|W5H5R1_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MNNSLVVYLKSLQTFCAFASTKFSSFAKSAWQSMKYSCRFICQTNPLFIQVTYFTLISFAGYEALKVLNSQDKSNTLKNLDVLFT SVSASTVSSMATVEMEEFSSKQLWVLAILMLIGSEVFTSVLGLHFMRAKFNKENSLNTRDHISHIDIESINVANFDPNTSHGTKDAVSF SEIRLANKQHVDPKTTVLLGTAVTVYLLITNLGSSLLIYLYLKLVPDAQEVLKRKGVGLFLFSVFTAISSVANCGFTPVNENMVIFQKNSG LLLLIIPQMLVGNTLFAPCLRFMVWSLQKITGKQEWCYILEHANAIGYRHLMSTRKCACLILTVVGFIILQTILFCALEWSSEALQEMSSY QKIVGALFQSTNARHAGETIVDLSSISSAIIFLYIVMMYLPGYTSFFTNYDDRYSKDEKRYNRKGLLEDWILSQLSYLAIFVMLICITEREA LTTDPLNFNVFSLLFEIVSAYGNVGFSMGYSCKRLLKQDLHCKDASYGFVGKWSDEGKMILIIVMVFGRLKGYNLKGGKAWKLR
7.1E-33	123	24.3	6.9E-26	100.2	2.9	3.3	2	A0A022RIN8_ERYGU	Uncharacterized protein	MIMGU_mgv1a004645mg	Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	517	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Lamiales, Phrymaceae, Erythranthe, Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	4155	>tr|A0A022RIN8|A0A022RIN8_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a004645mg PE=4 SV=1MEKLSDFIEKAKHGYRYFRTLLHHSFRGLMSMIFVVFPMNQFWSELCYFTTLSFIGFLALKFSKPSVLLPSHHLPKNIDLFFTSLS AATASSMSTLEMEVFSNIQLFVLTVITFVTGEVFTSILELHFSKSAKSDSSTFKYYSNNSNRRTDQLGIVISGEAEEEEGLLKFKSIQTLA VLVGCYLLLVHVAGATLISVYLNLVPSARNVLKKKGLNQQIFTIFTAVSTFANCGFLPTNENMMAFRTNSGLQLILILLLILMGNTLYPLCLR FTILALEKITGKEEFRYMLKNSRELGYRHLIPGNTMDSVYLGITALGFLSVQLILFCTLEWNSEAVVDGMSGYEKAVGSLFQVVSSRHA GESVFDLSAVSPAVLVLFLLMMYLPAYTSFVPIIYVENGIQKKKRRGDFWEQILFTQLGYITIFVILVCITEAESMKTDPLNFSVFAIVFEVI SAYGNVGFSIGYSCERRINSDGKCRDAWYGLAGKWSNGGKFVLMVVMLFGRLKKFNVRGGRAWKLF
7.1E-33	123	20.3	6.1E-30	113.5	9.7	3.6	2	C5XW71_SORBI	Putative uncharacterized protein Sb04g005010	Sb04g005010 SORBIDRAFT_04g005010	Sorghum bicolor (Sorghum) (Sorghum vulgare)	532	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Andropogonodae, Andropogoneae, Sorghinae, Sorghum, Sorghum bicolor (Sorghum) (Sorghum vulgare)	4558	>tr|C5XW71|C5XW71_SORBI Putative uncharacterized protein Sb04g005010 OS=Sorghum bicolor GN=Sb04g005010 PE=4 SV=1MVHSPVAFLRKLQTSSSSLATELISFSKYAQKSMKYSWQFICQNNPLFIQVTYFTLISFAGYAALKIIKPRDEQDTLKDIDLLFTSV SASTVSSMATVEMEDFSSAQLCILTILMLIGGDIFTSMLGIHFMRAKFGRKEPVNTRDHSSYIDIEPITSTKFNPSTQDMKVTVSFSEP LHLEEKKQVEPKIIESLGHALLVYLLVSNLGSSLVIYLYLISVPDAQGVLKRKGIGFVIFSVFTAVSSVANCGFTPVNENMIIFQKRSILLLLI IPQILAGNTLFAPCLRFLVWSLKKVTGQEDYRFILQHPETIGYKHLMSSKECVYLMSTVFSFIITQTILFCLSLEWSSEALRAMNSYEKIIG ALFQSTNARHAGEYIVDLSSLSSAILVLYTVMMYLPGETSLLPRDGEQHSRAEIKHHKRKRLLENWIFSQLSYLAIFVMLICITEREALITDP LNFNVFNILFEVVSAYGNVGFSVGYSCKRLLNHDVYCKDASYGFVGKWSGKGKVILIIVMVFGRLKAFNMKGGRAWRLR
9E-33	123	22.1	4E-20	81.2	6.4	3.5	3	J3LA24_ORYBR	Uncharacterized protein	OB02G14910	Oryza brachyantha	531	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza brachyantha	4533	>tr|J3LA24|J3LA24_ORYBR Uncharacterized protein OS=Oryza brachyantha GN=OB02G14910 PE=4 SV=1MIHCLLVSQQKLRTFFAFATTKLSYFTKSARWTRKNFIQYICQNNPLFVHVTYFALISFAGYAALKVIKPRDKLNTLRDLDVLFTSI SASTVSSMATVEMEDFSSAQLWVLTILMLIGGDIFTSMLGIHFMRAKFGRKEPVNTRDHSSYIDIEPITSTKFNPSTQDMKVTVSFSEP HMENEGHVEPSTIEFFGFVVMGYLLMTNLGGSLLIYLYLNLVPSAQQILKRKGIGMVIFSVFTAISSVGNCGFTPVNENMIIFQKNSVLLL IIIPQILAGNTLFAPCLRLMVWSVEKITGKKDCRYILERSKAIGYKHLMSSREGVYLILTVVSFIIMQTVLFLSLEWNSAALHEMNSYQKIV CALFQSVNSRHAGESITDLSNLSSAILVLYTIMMYLPGYTSFLPRNDDGDSKTKMIKERKRLLENWIFSQISYLAIFVILICITERESMATD PLNFNVFSILFEVVSAYGNVGFSVGYSCKRLLNHDAHCKDASYGFAGKWSDSGKAILIIVMLFGRLKAFNMKGGRAWKLR
1E-32	123	19.6	1.6E-32	122.1	13.6	1.1	1	B8DU68_BIFA0	Cation transporter	BLA_1259	Bifidobacterium animalis subsp. lactis (strain AD011)	487	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium animalis, Bifidobacterium animalis subsp. lactis (Bifidobacterium lactis), Bifidobacterium animalis subsp. lactis (strain AD011)	442563	>tr|B8DU68|B8DU68_BIFA0 Cation transporter OS=Bifidobacterium animalis subsp. lactis (strain AD011) GN=BLA_1259 PE=4 SV=1MANLLFDESASNSETSKGFGWWFSGDTFERNAYEERNPHSRSLSYRLNSHPGRLTIIYFLALITVSTSLLCLPIATQPGKKTSFS TAFFTAVSALSTCGISVVNTTDHWTIFGQVVLIFSVQMGGLGVMTFASLIALAVNHHLKAMQRLLAANELGTNKLSEIRGVLQVVLMTT LVIEVVTFFALFPGLLSVNKGNVGRTLWESLFFAVMSYNNAGFTPDGAGLYVNNWAVGLPIMMSAFCGTLGFPVLLNIFRTARMHKS PKHWSLHTKITMIMTFAIVFMSLIWFLAVEWDNPVLFKDGDVDTRMRRAMVAAVMPRSSGFDLSWVPGVKECTKVFMSIVMFIGGG STSTAGGIRVTTLAVILLVCKAAFTGHTDVNAFHKRVPQHVIMTAISITASCVALVFIASVALMLITDSSLSHAMFDTCSAFGLGGYTVGV AQENNPASLYVLAAAMVVGRLGPMTLAYAVSRPKELDVVRYPEGQIVVG
1.2E-32	122	17.6	1.2E-32	122.4	12.2	1.9	1	R6QYQ8_9FIRM	Uncharacterized protein	BN661_00937	Firmicutes bacterium CAG:449	238	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:449	1263023	>tr|R6QYQ8|R6QYQ8_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:449 GN=BN661_00937 PE=4 SV=1MIFLGGLGFIVIFDVTDKKSFRKLTLHSKVIITTTIILLIVSSILYKLFSPNISLTKCIFMAFSTRTAGFAIFNMNELSTASYILTLFLMFIG AGPSSTAGGIKVSTLFALIICFKSFATGKNECIAFKRKISQEQITKAFVLTTFAFTFICILTICISLNESYSFQEILFEVISGFGTVGLSYGITP SLKTISKLILCLAMYVGRLGPITFISLFQKESKILTKDKVGYVEENIIIG
1.4E-32	122	22.1	3.6E-27	104.4	9.9	3.8	2	M0UQP5_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	542	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0UQP5|M0UQP5_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MHLFLALIYSTMGWVKRFYQDFIHIKLHSFCRISRYVVDSIAFVYRFVALHVHPFWIQLSYFLAIAILGSVLLMSLKPSNPDFSPPYI DMLFLSTSALTVSGLSTITMEDLSSAQIVVLTLLMLVGGEIFVSLLGLMLRVNHQDMPDLPRVKISSVPVELEEIDLANSMALSDESQLE EATHAITPKKCTGLKRSRSVKCLGYVVFGYFAVIHILGFLLVFLYITRVPTASAPLNKKGINIVLFSLSVTVASIANGGLVPTNENMVIFSK NSGLLLLLSGQILAGNLLFPLFLRLLVWFLGRLTKVKELRLMIKNPEEVHFGNLLPRLPTVFLSSTAIGLVAAGVTMFSAVDWNSSVFDG LSSYQKAVNAFFMVVNARHSGENSIDCSLMSPAIIVLFIVMMYLPPSATFAPPDGDIKTTNENTKAKRGSLVQKLAFSPLGFNIIFVIVAC ITERRRLRNDPLNFSTLNMIFEVISAYGNVGLSTGYGCSRLHQLHPEIICQDKPYSFSGWWSDGGKFVLILAMLYGRLKAFTMTMGKS WKV

2.1E-32	122	20.9	5E-19	77.5	5.9	2.2	2	A4XFW6_CALS8	Cation transporter	Csac_0149	Caldicellulosiruptor saccharolyticus (strain ATCC 43494 / DSM 8903 / Tp8T 6331)	503	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family III. Incertae Sedis, Caldicellulosiruptor, Caldicellulosiruptor saccharolyticus (Caldocellum saccharolyticum), Caldicellulosiruptor saccharolyticus (strain ATCC 43494 / DSM 8903 / Tp8T 6331)	351627	>tr|A4XFW6|A4XFW6_CALS8 Cation transporter OS=Caldicellulosiruptor saccharolyticus (strain ATCC 43494 / DSM 8903 / Tp8T 6331) GN=Csac_0149 PE=4 SV=1MDKSVFKSDHIELRHVLYMTGKTLSAIGLVEIVAVITSLLYKEWNMAFNLMIGTGLFFVLSFIFIFIGRDTKDQRFSWGAGMSMVG LTWALGGLISAIPPYLSGHFASYLDAFFEVMSGYTTTGLVLIQDLDHAPMGLNMWRHLITYIGGQGMVLMTLSFLASGMRGLLKVYMG EARDEQIFPNVIHTARIIWFVSLLYLALGTAALTITGVLIGLPLDMAFFRGLWMFLGGWDTAGFAPQSQNAMYFHSTSYEIISMMIMLLG TINFALHYFILSGNYKEGIRNAEIKSLFVTITSLSVLGIIALKAVYSTPIIAFRKVFYHFVSAHTGTGFATLYSQQFFYEWSDAAIILIVIAMLA GGSVCSTAGGIKALRIAILANALVNDIKKMIRPDSAVVVEKFHHLKEVALQDRHVRNASIIVLLYIVTFTIGTLAGTFYGYPLKQAMFESAS ALGNVGLSSGITQPSMPDGLKVIYIFMMWVGRLEFMSVIALFAFLFKEAREG
2.3E-32	122	17.8	6.2E-30	113.5	12.3	2.1	1	A2SPU2_METLZ	Cation transporter	Mlab_0172	Methanocorpusculum labreanum (strain ATCC 43576 / DSM 4855 / Z)	493	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanocorpusculaceae, Methanocorpusculum, Methanocorpusculum labreanum, Methanocorpusculum labreanum (strain ATCC 43576 / DSM 4855 / Z)	410358	>tr|A2SPU2|A2SPU2_METLZ Cation transporter OS=Methanocorpusculum labreanum (strain ATCC 43576 / DSM 4855 / Z) GN=Mlab_0172 PE=4 SV=1MGYLRELPAIGRDIGSVLLLIGTATLVPIIVGCFFQEWYALPWMASSTFAMLGLGGLLHLLPKNTKPPRASLSISATAVIWALVGFL GCFPFIFAGMPLIDAAFESMSAWTGTGFSIATNIESWPKTILLWRSLMQWIGGLGIVAFTLTVASRSGLVTQNLYRSEGGSESFMPSVI ATAFQMWKIYLILTLIAIIAILLTGLSLWDAVNVAFCAIATGGMTIYAAGITHFNNFALEMVLIPIMLAGALPFRLYYVVYVSRSFREILHDRI LHLMVGVYLFVAAVLIVELFTAGMPLMETLRESLFMAGSVVSSTGFQNTTFAGWGLAPIIFLSIFLMIEGAQGSTSGGIKLNRLQVMLE ALGWWFRKTLQSPKAVVPMRHDGKPIYGKEGETLIAKSLLMILLFVLLMLGTLIVFLHDPYFSENLAHTIYDLCSCIGNNGSSTGVVGP MMPDYAKVVVMFFIMWIARLEIIPVLILIWGILRGFDTQKKSDRRD
2.3E-32	122	26.3	2.3E-32	121.5	18.2	1.7	1	I6ZQV7_MELRP	H(+)-transporting two-sector ATPase	MROS_1197	Melioribacter roseus (strain JCM 17771 / P3M-2)	486	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Ignavibacteriae, Ignavibacteria, Ignavibacteriales, Melioribacteraceae, Melioribacter, Melioribacter roseus, Melioribacter roseus (strain JCM 17771 / P3M-2)	1191523	>tr|I6ZQV7|I6ZQV7_MELRP H(+)-transporting two-sector ATPase OS=Melioribacter roseus (strain JCM 17771 / P3M-2) GN=MROS_1197 PE=4 SV=1MKKELRENIARFSKIIVIISSLLGIASIIVEYGFRIKSSDAGTLHFITIGVIIVFILYHILQLYIAEDKVAHIKSHKFEMIIISFIFIEGLLSFFN LSLVERIGAALKLKDITYLYIVFAQIFIVVGIISGTLRYNIKLLQSQIHPSRLFIFSFLFTIIVGTFALMLPAATVEGKISFVDALFTSTSAVCVT GLITVDTATYFTTFGKMTIMALFQIGGLGLMTFTTFFAIFLSGGLGIKERILLHDLLEEENIGAITKVLTYLLAITFIIEAVGAAILFYSSRNSF DSIENAAFISIFHSVSAFCNAGFSLFTMNLMDPAVRYNHVFTTTISILIILGGLGFPTIISFLKFKNITSKMGKLSIKLPLQTRIVVVSTILLIVF GAASFYFLEQHNTLKNLNLFEKLNASYFQSVTARTAGFNTIDFGILITTPTAVLFFLLMFIGASPGGTGGGVKTTTFALLFYGSIAILKNKK KSTYTTERFQTK
2.8E-32	121	13.5	2.5E-31	118.1	7	3.2	1	K3Y679_SETIT	Uncharacterized protein	Si009720m.g	Setaria italica (Foxtail millet) (Panicum italicum)	564	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3Y679|K3Y679_SETIT Uncharacterized protein OS=Setaria italica GN=Si009720m.g PE=4 SV=1MAGAHKLGELLHHLRQCSAAALDRAMSLVCSLSQAYAEHQVTERVARSRRTLGGQVWRAAVDVAARLNSLLIHVVYFVALSCA GWGLLSALKVRAPHGSPRGIDMFFTAVSAATVSSMSAVEMEVFSNGQLLIITALMFAGGEVFISLVGLSSKWSKLRKRIINRSQRVES HDDGVELETPAAIAAEAEAAADADDERSSMTITTVTEDHTGPVVDSKMLRLNAVRSMFYIVLAILLVVHVVGAVAVAVYMHAAPGARQ TLRRKALNVWTFAVFTTVSTFSSCGFMPTNENMMVFSRDVPLQLLLVPQALVGNTLFPPLLAACVWAAAAATRRQDLAEMARKGSG EDLLPARRCWMLAGTVAWFLAVQVALVCAMEWGGALQGLSSGEKVANALFLAVNSRHTGESTLDLSTLAPAILVLFVLMMYLPPYTT WFPFEENSTTRDHSTESQGIRFLKSTVLSQLSYLTIFVIAICITERRKLKEDPLNFNVLSIIVEVVSAYGNVGFSMGYSCSRQINPDQLCT DRWTGFAGRWSDSGKLILIIVMFFGRLKKFSMKGGKAWKLS
2.8E-32	121	17.3	5.9E-20	80.6	4.8	3.6	3	W5H677_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	544	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5H677|W5H677_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MHLFLTLVHSTMDRVKRFYQDFIHIKLHSFSRISRYVVDSIVFIYRFVALHVHPFWIQLSYFLAIAILGSVLLISLKPSNPEFSPPYID MLYLSTSALTVSGLSTVKMEDLSSSQIVVLTLLMLVGGEIFVSLLGLMLRVNHQDMQDLPSVKISSVPVELEVLDLANSMALCDESQLE DASHAIPPKKCTELKRSRSVKCLGYVVFGYFAVIHVLGFVLVFLYITHVPTASAPLNKKGINIVLFSLSVTVASCANAGLVPTNENMVIFS KNSGLLLLLSGQMLAGNTLFPLFLRLLVWFLGKLTKVKELRLMTKNPEEVHFANLLPRLPTVFLSSTVIGIVAAGVTLFCSVDWNSSVF DGLGSYQKTVNAFFMVVNARHSGENSIDCSLMSPAIVVLFIGMMYLPSSATFAPPSGDTKTTNENTKGKGKRGSLVQNLAFSPLGCNI IFVIVACITERRRLRSDPLNFSTLNMIFEVISAYGNVGLSTGYSCSRLHQLHPEIICQDMPYSFSGWWSDGGKFLLVLVMLYGRLKVFA VSTGKSWKV
2.9E-32	121	16.8	4E-32	120.8	11.7	1.2	1	A0A0F2SJ42_9FIRM	ATP synthase subunit J (Fragment)	VR66_04105	Peptococcaceae bacterium BRH_c23	282	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c23	1629714	>tr|A0A0F2SJ42|A0A0F2SJ42_9FIRM ATP synthase subunit J (Fragment) OS=Peptococcaceae bacterium BRH_c23 GN=VR66_04105 PE=4 SV=1MSPSRVLVLGFAVLIVFGALLLTLPQATQDGLGLTTLNAVFTATSAVCVTGLVVVDTATTFTLFGQWVILFLIQVGGLGFMTFATL FAMILGKKITLKERLLLQEALNQVSVEGVVRLMKSVLLISFAFEAMGTLILTLHWYSDFGFSKALYYGLFHSISAFNNAGFDLMGNFTSL TAFVGDPVVNITIMLLFICGGLGFIVMADLLAHRKKFRLHTKIVLLVSGVLILLGTVIILIMEFANPDTLGPFPLGTKIMAALFQSATSRTAG FNTINIAGMYDTT
3.8E-32	121	13.2	8.3E-22	86.7	5.3	2.6	2	F6I5R0_VITVI	Putative uncharacterized protein (Fragment)	VIT_11s0103g00010	Vitis vinifera (Grape)	371	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, rosids incertae sedis, Vitales, Vitaceae, Vitis, Vitis vinifera (Grape)	29760	>tr|F6I5R0|F6I5R0_VITVI Putative uncharacterized protein (Fragment) OS=Vitis vinifera GN=VIT_11s0103g00010 PE=4 SV=1AQNEQPCSNLEKGIEASCDEDLKYHSIKCLGYVVLFYLLVVHVVGSALIVLYLNLVPSAREVLKNKGLRILTFSVFTVVSTFSNCG FIPTNENMVVFKKNSGLLLILPQILLGNTLFAPCLRFVIWVLVKITRRVEFNYMLKNSREISYDHLLPGLYSCLLAITVFGFILVQFLLLCF MEWNSEDLAGLNAYQKIVGMLFQTANSRHSGESIFDLSVISPAVLVFLVMMYLPPHTSFLPIDGGEKALQKEERRTEKRKYVEHLLLS QLSYLVIFVILVCIIEREKMKKDPLNFSVLNITIEIVSAYGNVGFSAGYQCNLQLKHEPHCKDLCYGFVGRWSNSGKFVLMFVMFFGRLK KFSMHGGRAWKLD
3.9E-32	121	26.3	3.9E-31	117.5	15.9	3.1	1	D7LY37_ARALL	Potassium transporter	ARALYDRAFT_489874	Arabidopsis lyrata subsp. lyrata (Lyre-leaved rock-cress)	500	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Camelineae, Arabidopsis, Arabidopsis lyrata (Lyre-leaved rock-cress) (Arabis lyrata), Arabidopsis lyrata subsp. lyrata (Lyre-leaved rock-cress)	81972	>tr|D7LY37|D7LY37_ARALL Potassium transporter OS=Arabidopsis lyrata subsp. lyrata GN=ARALYDRAFT_489874 PE=4 SV=1MDRVAAKIAKIRSQLMKSSSLFLLYFIYFLLFSFLGFLALKITKPRTTSRPHDLDLFFTSVSAITVSSMSTVDMEVFSNTQLIFLTILM FLAGEIFTSFLNLYFQHFTNFVFPHNKIRHLVGSFNSDRCDLETVTDHREGLSKIEERASKCLYSVVLSYHLVSNLVGSVLLLVYVNFVK TARDVLSSKDISPLTFSVFTTVSTFANCGFVPTNENMIIFRKNSGLIWLLIPQVLMGNTLFPCFLALLIWGLYKITKRDEFGYILKNQKKM GYSHLLSVRLCVLLGVTVLGFLIIQLLFFCAFEWTSESLEGMSSYEKLVGSLFQVVNSRHTGETIVDLSTLSPAILVLFILMMYLPSYTLF MPLTEQKTIEKEGDDDSGNGKKVTKSGLFVSQLSFLTICIFLISITERQKLRRDPLNFNVLNITLEVISAYGNVGFTTGYSCERRLDISDG SCKDAGYGFAGRWSPVGKFVLIIVMFYGRFKQFTAKSGRAWILYPSSS
4.2E-32	121	3	5.1E-32	120.4	2.1	1	1	R6UHB4_9FIRM	Cation transport protein	BN580_00677	Firmicutes bacterium CAG:272	198	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:272	1263015	>tr|R6UHB4|R6UHB4_9FIRM Cation transport protein OS=Firmicutes bacterium CAG:272 GN=BN580_00677 PE=4 SV=1MIGFNIYPIYKNISDCARLSVFQVASIMTTTGYSTCDFNKWPEFSKAVLLLLMFIGGCAGSTAGGLKVSRVILLFRMMKRDIRRML HPRSVGVIKFEGSRIDDATLNSVSVYFSVYCLAFAVIFLLISLEPFDFETAFSATSACFNNIGPGLGAAGPMSSYNVFSAPSKVLLSVAM LLGRLEIFPIFLALSPSTWLKN

4.7E-32	121	24.6	2.4E-28	108.3	14.6	3.9	3	J3MHB2_ORYBR	Uncharacterized protein	OB06G34060	Oryza brachyantha	509	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza brachyantha	4533	>tr|J3MHB2|J3MHB2_ORYBR Uncharacterized protein OS=Oryza brachyantha GN=OB06G34060 PE=4 SV=1MPIRLHIFVSSARHAISSSVFICRFIAFHLRPLLIHLAYFLIIDVLGFVALVVLRPSNHRYNPRYVDMFFLSTSAVTVTGLATTQMEDLSSSQILVLTLLMFLGSEMFLSFLGLVHESGKQNRHDHENRRVGSATSCEESQLEEATAQTPPTNSDDIKKRCLRYLVFVMLAYMIIILVTGSLLVFMYIAHVSSARDVVTRKSINKALFSVSVTVSSFTNGGLLPTNESMAVFSSNNGLLLLLISQILAGSTLFPVFLRLVIWALRGLRLARAEEPGFIMSNTRAVGFNHLLPSMKTALLAAMEVALVAIAVMLFCCLNWGSAVFAGLTSLQKIINALFMAVNARQAGENSIDCSLVAPAVLVLFMAMMYTPSLTTFFSACQDHKQSNPEQDNKARKGNPFLKRMTLSPLAFNAALTMLVCITERRSLSTDPLNFSTFNIVFEVISAYGNIGLSTGYSCSRLLLMQPEKKGIACHDKPYSFSGWWSDSGKLVLVFVMLYGRLRGFHKHTS
7E-32	120	22.6	2E-31	118.4	13.8	2.5	1	A0A022QAM9_ERYGU	Uncharacterized protein	MIMGU_mgv1a005209mg	Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	493	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Lamiales, Phrymaceae, Erythranthe, Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	4155	>tr|A0A022QAM9|A0A022QAM9_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a005209mg PE=4 SV=1MCTMKWKHTPSYFLHILLFRLNPFLFELGYFVTLSSVGFLALKSTSSNPARKIDLFFTSASAVTVSSMSTLEMEVFSTTHLVILTVLMLLGGEVFTSMLGLRLTKAKINNNQIRSRQMIAEFDRSNSDVNMKRKCIEILASLVTWYLLAVHAVGSASIVVYLSLVPSARRVLERKGIGMGIFSVFTAVSTFANCGFVPTNENMIVFKKNSGLLLILIQLVFMGNTLYPVCLRLLIWFTEKVTKRAELRYVLENSRELGYGHLMPGLESVYLGITVLGFVVVQMVVFCSLEWNNNFLGVSNYYERIVGCLFQVVNSRHAGESVFDLGVVSPAVLVLFVIMMYLPPYTSYLPINEHQVADENITKHIINTTLTSRNKVYYKWENIVFSQLTYLSIFVILICITERQNMKTDPINFNVLNIVVEVISAYGNVGFSVGYSCEKQMHYSGGGAAVCKDAWYGFAGRWSDEGKFVLIVVMFIGRLKKFNMRGGRAWILA
1E-31	119	19.9	4.5E-31	117.3	13.8	1.7	1	A0A0E3S635_9EURY	Potassium uptake protein TrkH	MSLAZ_1436	Methanosarcina lacustris Z-7289	283	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanosarcinales, Methanosarcinaceae, Methanosarcina, Methanosarcina lacustris, Methanosarcina lacustris Z-7289	1434111	>tr|A0A0E3S635|A0A0E3S635_9EURY Potassium uptake protein TrkH OS=Methanosarcina lacustris Z-7289 GN=MSLAZ_1436 PE=4 SV=1MLAGMSLYDALTHTFAGMACGGFSPYNAGIEAFHSPLIEFILTFFIFVAGANFALYYRAIKIDKDLLFKDEEFRVYTSILLGFTGLLTLILYKDMEYSLFNSFRYAVFQITSVMTATGFASIDFNLWTDSAKILVLAVMFIGGCAGSTGGGMKIVRFLLLLKYARRELFKFIHPRLVRPIRFNNKSVPADVLQSILAFVVIYISVFIFSAMLLTLLGVDIISSVTASITTLGNIGPGLSLFGPMGNFESLLSLGKIILISNMWIGRLEVYTVLVLFTSDFWRS
1.1E-31	119	10.7	1.3E-31	119.1	7.4	1	1	T0VK65_9ENTE	Potassium uptake protein, integral membranecomponent, KtrB	HSIEG1_3800	Enterococcus sp. HSIEG1	214	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	1316414	>tr|T0VK65|T0VK65_9ENTE Potassium uptake protein, integralmembranecomponent, KtrB OS=Enterococcus sp. HSIEG1 GN=HSIEG1_3800 PE=4 SV=1MLAFVILFIGGTIAIYFLEKDHLFKDYGFSSTWINSMFYSMTTRNAGLQIHDLGNFQTTTLIVFSLLMFIGCSPSSVGGGIRTTTIAIIGLYLYAFLKSEDNINIFGRRIDEDDVRKSVVVFMLSLGMCFFCVLFLTATEDIPLIAIIVEVASAFGTTGLSLGITDDLSSVGKLVIALLMFIGRVGMLYTLLLFVPKETRDLGYEYPTEKIIIG
1.2E-31	119	28.3	1.2E-31	119.2	19.6	2.5	1	R6I524_9ACTN	Trk-type K+ transport system membrane component	BN534_00932	Eggerthella sp. CAG:209	505	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, environmental samples, Eggerthella sp. CAG:209	1262875	>tr|R6I524|R6I524_9ACTN Trk-type K+ transport system membrane component OS=Eggerthella sp. CAG:209 GN=BN534_00932 PE=4 SV=1MWLRFTLFDVRVVAHYLGVLVSFFTIALAVPLVVAIAMQEWEPASRYLLAVGISLIVGSGLRLLCVQPGKLTHQQALAVTGLSWIVLAFVASVPLALSGHYGSYLDSLMEAVSGLTTTGVTLVIDLEHLSTADNMWRFVMHLIGGLGLIVVALSLGLLGKATSGLYSSEGRSEHVLPNIVNTVRLISRISLTAIAVAAVILFVMCVLSGMEPVRAFFHSLWISISGFITGGFAPTSQSIGYYHSFALEIVCMVLMLLGAINFSLYVKTQRGETDSFFRDLEIRTGAIWLIVATITLMASTCASGGFSGLMALLRRGVFMVVAAATTTGFQNVTNNQLTTVFSSGAFLIIAMCMAIGGSSGSTAGGIKLSRIGLIAKSMVSTIKETLSPSTARVSVRYYHLGRKVLTTDAAKSAMTVSALFVVTYLIGSLAGIAHGYDAISSIFESVAMASNGGLSSGIVSRGMPPTLEAVYILEMWAGRLEFVTLLALVVKVVVSIAPRRKAVRS
1.5E-31	119	25.3	4.7E-24	94.1	6.3	3.7	3	A0A087GQ40_ARAAL	Uncharacterized protein	AALP_AA6G186200	Arabis alpina (Alpine rock-cress)	505	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Arabideae, Arabis (rockcress), Arabis alpina (Alpine rock-cress)	50452	>tr|A0A087GQ40|A0A087GQ40_ARAAL Uncharacterized protein OS=Arabis alpina GN=AALP_AA6G186200 PE=4 SV=1MERVTSKLAEFRSQLAKSRFSFFLYFIYFMSFSVLGFLALKISKPRTTSRPHDLDLFFTSVSAITVSSMSTVDMEVFSNSQLIFLTILMFLGGEIFTSFLNLYFTHFSNFVFPHNKIRHLIGSFKLDHPMEDPRSDLETVTDHREAPIQIHERASKCLYLVVLGYHLVTNLVGSVLLLVYVTFVKTARNILSSKEISPLTFSVFTTISTFANCGFVPTNENMIIFRKNSGLLWLLITQLLMGNTLFPCFLRLLIWGLDKFTKREEFGYILKNRKKMGYSHLLSVRLCVLLGLTVFGFLMMQLLLFGVFEWSSESLEGMSRYEKFVGSLFQVANSRHAGETILDLSTLSPAILILFILMMYLPSYTLFMPLTEEKNKKEGDDDSENGKTREKSGLFVSQLSFLAICVFLISITERQKLRQDPLNFNVLNITLEVVSAYGNVGFTTGYSCKRRLDVSDVSCKDAGYGFAGRWNPIGKFILIIVMFYGRFKQFSARSGRAWILYPSSS
1.5E-31	119	24.3	3.1E-31	117.8	16.8	1.4	1	C8WPQ7_EGGLE	Cation transporter	Elen_3058	Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (Eubacterium lentum)	506	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Eggerthella, Eggerthella lenta, Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) (Eubacterium lentum)	479437	>tr|C8WPQ7|C8WPQ7_EGGLE Cation transporter OS=Eggerthella lenta (strain ATCC 25559 / DSM 2243 / JCM 9979 / NCTC 11813 / VPI 0255) GN=Elen_3058 PE=4 SV=1MWQRFTLYDVRVIGHYLGVLVLFSSLALLVPFVTALACAEWTPATHYLLTIGIALIVGSALRFLRIDPGRLNRQQALAVTGFAWIVLAFVAAVPLYLSGHYLSYLDALFDGVSGLTTTGASVIVDLDHLSNADNMWRFMMHLLGGFGLIVVALSFGLFGKRAGASLYMSEGRSEHVVPNVVQTTQFIAKIGMGMIFVATVILTAMCLFLGMEPLRAFLQSLWLAISGFTTGGFAPMSQSVMYYHWFPLEIVLMLLMLLGSINFVLHSEMWKGHVEVFFRDLEIRTMVLWLAVMTCVLAASLSASPEFSSLPAMLRRGLFMVISAFSTTGFQNITTNELTTALSSGAFFVLAILMAVGGSGGSTSGGLKFSRMGIIMKSIVATIKEALAPDSARVVVSYNHVGRRILSPEVVKEAMTVFVLYVATYAVGTLVGIAHGYEAPQAIFESVAMASNGGVSSGLAAPGMSPSLELFYIAQMWAGRLEFVTLLALVAEIIVSLNPKRRVLKS

1.7E-31	119	2.4	2.6E-15	65.3	0	3.8	3	B8P9V5_POSPM	Predicted protein	POSPLDRAFT_104193	Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	3220	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Postia, Postia placenta, Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	561896	>tr|B8P9V5|B8P9V5_POSPM Predicted protein OS=Postia placenta (strain ATCC 44394 / Madison 698-R) GN=POSPLDRAFT_104193 PE=4 SV=1MLSRFPFDNIYFTFAKTVFRWLWTDFTTFVVRIAWHPKVFGGELLQATVSTTHEKWPTIAETNARHVAPPYPGSRAWSSADHD SFATVRDPSTHLRTRTRPVPVQSMFAGSMAAQGREAVVCRHWRTVALNTPQLWTTVPVTSKATMSMMSEYLGRSGGRPIDVNIVIL HPDSLYETDDHYPVLRYLLLEHAARWRSVSIINDKSEVMHFLLALLNQEPFPMLEVLEIDFPSSFHYTFSMFEGNWPKRLLAKGAPRL REVSILQGRLTNITMEPLASLEKLVLMTPNWTLPLLKKISVESSRLTHLTLYCNIARTTIHPSEVFSDLFFPCLTHLRLRYTVSGIPLLRIME APELTVLQLEDLHFKRNEIVVALLNALRIGGDPDAPCKFPCISSLRFEIPQTKTEGLPEVFGGHLLEFLRLFPAVEQLAIQGFRIDEIVRS MTSTAPPDIVLPRLKRFVMLGYPHAEHLHSAETLVRWRAAAGASISNVFLIGIPASNFPLYTKHYGLGMLLEWQLSPKRVLLSLLTSRA APSYYGGLHAGADWMQDEQTRRGRLGFYGPYPPYTSPLERANDVTKERSLTDNTISARNCWNPYDYGCYPVRNLSFPIELSTSGPY LQKRSFLAIFETVYRRLYSNCASAVSIAQRLRPQLDLILETVRKKLLKYTPVLALNTPRLWTLVPINSRATTYTVFDYLGRSGVLPIEIDIR VPGPDMPFSEDELLGICTLLAWNSERWRCFSLVCRNPMLLYSVLHFLGQRDVPILEVLDLDVPLPGPEIPLLLQQWPEVLLQKGAPRL REIHIMQGRLTEITLKPLTVLDTLVLMTTHWNLPRLKHLADTSSLITHLSLYCLTMSNAPQEDAVETMVGISLLSMLTAPLLEVLQLEELS FGTKVEARMLLDSLKTEDAPDALCKFPRILSVRFEIMQMKNEGLPEVFGGHLLEFLHLFPLAEHLAVQGCRIEDIMVCITPPNITLPRLE RITLLAPLSEEYLSAVDALRQQRQKIGMPVPSVHIIGMCASNMPQHARNYESAPMVWGFVKFISMGTQKGLRFSPMSDSTDEDEWM QDRQLSRNRLRLKQPDMLTLMLSMCGLRGTDDDNVREVYWALQGSSVSLGGFETSCGGEKGVGENGGGESESHSFPSQRDGRR KTPAISGSAGGEDIGGRRKTEVEAKFRRELLASKAPFALVAFGEMTFRRSCRESQSAERHVCRRILPVQTWDNLIIVIAKLGDVCVPVL DVLVRGTIAICGNQLRMTLAEGALQNKATAYTRHPYQWNCGLNAAGRETFQDACKVSQKHLERSRKPPWLDADIPLNHWPGLGCIV ELRLLQRKWTRRPPYLSTSDDLNALMRREAQIITWRPLNLGRPQLAKRRVLPVARLTNATRGTRDQRVAPSALGESSKGCCCNASFI SLATCKADRNMETDSVSLVVPITFRSSITGDALELNTNTVARSWASASASCLIAWGCSDASEQRDLEEKLPSHGLAFGCDDGTVFLFG SQLAFPRKHDITGSPTNTPPEPAEQVEAPKNYVDFDDEPEKLKGMLRGKATRSELLSPDVDRTAKLDRLSVSTSTRSIKAFSPAASLR SLSPPSSPCSPTANSPAQRETGLFLKSHILPSSLGSTHAVAALEVYDDGITSGVKAASDASILWIWKSIQVGSVGESIDVAEGDAETQT RILVCELREGPQLDGSDMTLIKKGDWVLDGPAESVGFYQELDGTLAVHYMSSDHRLVIRILSFNEELSPPDIRDMKSNSTTMLPLPNPF KAFKNLSRERLSGETGNDDASELSLSAPMDLGDVLLAVPVIGTSLVVHGDGVRIAYWSEYGLCIFDLNRQTMSSVCTYELADITKWQ WISVDSFVVTRPYAFIKHEPDYEVHSSLFSNKNAPKLTWRWVTAPFFLVSFDEGVVGDIPSLQSTTASDRGGDPLVIGGSDDGSIGIW SAGARTLELRAHWTIFVTPLVNVVSLREDQIGRLRGCVLCISQDGTIAILAVDDLQFVVLVPASVAPLKMVHMREDDILLVYTDNRARL WDCKTMEFRRSMNKSKADELLGQGAWAGWPAEPVKPSVPVEIVSLPVFAGLDSACSLLLDMGSFLHSNTGHMPGRTSASKHDRG KTRSILATLLTPGISKEIDDICTERLRVYPSCASVGYHGSLNARDNTVLYAFQSSQAVWSISPEISAFRAVILVTLLQVLIDNDDASTMMT FYVASLPGVIGPSYQSPSLTFLAKYYLRSSVQEVRSAARLLFDAGVARLSNDDTILIVEKWKQYLPSVQQERDTESFRSAMALHMCGF VAAEKYNLLSTNVLTEISKSIGLYLHREGSPYRALAIELCSRGFTLWQQYVDAVEMLRAVCTLATTSRKEAISIQNVGSQARSAVLHIAA ANTPLFMTTLTIDILQPRSVQHRKAVMQLVIFLIRKNPLVLYSNLPRLVEAVVKSLDPNSTFNRDAVLDSATDILGHIVQTFPNVDFHMST QRLAMGTAEGAVVMYDLKTATRLYVLEGHKKRTTACSFSPDGRRLVTVSLEESVVLVWKVGSSLTSFFNPGAPPRQGHGGSDPYKT LSFNIGSEAHMTLAATLEAVRFEWPADRSNTYKTLYCLDGLNQPTFPTSLFLEAGRTSMIVPLFMAAIFSASNGRFKIPFIDALFMCISA GTGTGLTTIDLSSMSVWQQAIIVVLEFIGNQVFVTWAYFTKHLKHIVTAKLERRSPQEDPFLSEHSVVFPRILPENDLKRRRAEMDELV SATVTHRGLQVKGSPPKFCPNVIRRVDIVPHLADPMRRRSESRDHDTATNTHLLEGGHGPATGHEFTHMSSASTRRVVYFGGFPGPY ELFARVIGRIFPQFYRSVQRRLTIPRTKMLVPHTTGGSPPRSAHRVPYISFNAIVDRNSVFKNLTEENIQELGGVEYRALSALLWIIPSDS LLTEYYLGLLVISFIVIIPYMSRPGWHSMMHPPEQHRMINMIGFSTFQVVGAWANTGMSLVDQNMAPYSTAYPMITVLILCVLAGNAAY SAIFYTWLLLAIQLATGREADQRRATKCGRTKRRLPVRPSQLCPTFFPALKTLSVRSTNVYEARSLGIYKADNDTEDADSPNDAASGF RVAIWGPYLCHHVRKQLSFDMWWLALSLFVLCIIERAPLMAAEDATRFTIFALIFELVSAYGTVGLSLGAPYHWAPANNNRAVLLPHEF QTAKSAEMKSEEMRTPSVEAKRNASEIPLDAGKRSKALNIPI
2.9E-31	118	15.4	7.3E-28	106.7	5.6	2	2	R5IVB2_9CLOT	Uncharacterized protein	BN757_00643	Clostridium sp. CAG:7	298	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:7	1262832	>tr|R5IVB2|R5IVB2_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:7 GN=BN757_00643 PE=4 SV=1MYIIYFCITVATAVFLLIGKMPVFDTICMSLGAAGTGGFACRNSGQAGYTVYQQAVLSIAMILFGINFNVYYLLLIRKPKEAFKCEE MRGYLAIILIAVVLITVNIRSMFPSLFLAAHHALFQVASIITTTGYSTVDFDKWPEFSKCIIVLLMFIGACAGSTGGGMKVSRIMIAFKEAKR EISTMIHPRSVKVLKYEGKVIGNDTLRVLNCYIIVYFMLFVASVLIVSLDNYDFTTSFTAVAANFNNIGPGLSVVGPASNFSMMSYLSKSV LIFDMLAGRLELFPVLVLLSPGTWKRG
3.5E-31	118	23.9	1.3E-18	76.2	8.6	3.5	3	M1CXU4_SOLTU	Uncharacterized protein	PGSC0003DMG400029966	Solanum tuberosum (Potato)	501	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Solanales, Solanaceae, Solanoideae, Solaneae, Solanum, Solanum tuberosum (Potato)	4113	>tr|M1CXU4|M1CXU4_SOLTU Uncharacterized protein OS=Solanum tuberosum GN=PGSC0003DMG400029966 PE=4 SV=1MKPLSFSFFKIMSLRVKPFWIELGYFTTLSFLGFLALNYFSKPRTLPSFRPQNLDVFFTSVSSTTVSSMSTIEMEVFSNVQLVFMT ILMFLGGEAFTSFLRLKLIKKENKDESFSCKDYELGNVINVDDKLEDVIITNPIEDHSHHDHHDEIIKIKSIRLLSNVVFGYILVIILLGSSLVS LYIIIIPSAKQILNKKGLNLHTFSLFTTVSTFANCGFVPTNENMMIFKQNSGLLLILIPQILLGNTLFAPCLRLVIMFLWKITKRHEFEYILKNS KRIGFSHIFPCYETISIAITVVGLIVFQFVVFCSLEWNSKGTSGLSTYEKIVGSLFEVVNTRHTGQSVFDLSTFTPAILVLFASMMYLSSYT TFLPVYNYEEKSEKMKKRKGRSLMDYISLSQPSCLVIFTILICVVEKDKMKNDPLNFNVLNILFEVISAYGTVGMSIGYSCARQINPDGH CKDATYGFAGKWSNTGKFILIIVMFFGRLKKYNQRGGKAWKVL
3.7E-31	118	25.9	8E-31	116.5	18	1.5	1	D6E8G5_9ACTN	Trk-type K+ transport systems, membrane components	GPA_13910	Gordonibacter pamelaeae 7-10-1-b	512	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Gordonibacter, Gordonibacter pamelaeae, Gordonibacter pamelaeae 7-10-1-b	657308	>tr|D6E8G5|D6E8G5_9ACTN Trk-type K+ transport systems, membrane components OS=Gordonibacter pamelaeae 7-10-1-b GN=GPA_13910 PE=4 SV=1MWQRFSLYDIRVIGHYLGVLVLFSTIALLVPLATAIACGEWEPASHYLLTIGITLILGSGLRFLRIEPGRLGRQQALAVTGFAWIVLA CVASIPLYLSGHFASYLDALFDGVSGITTTGASIILDLDHLSYADNMWRFMMHLLGGFGLIVVALSFGLFGKRSGASLYSSEGRSEHVV PNVVQTTQFIAKIGMGFIILATGILSLVCLFIGMEPLRAVLQSFWLAVSGFMTGGFAPMSQSIMYYHSFPIEVVLMLLMLLGSVNFVLHS EIWKGHVAVFFRDLEIRTMVLWLAVMTCVFAASLSASLNFSDLPAMLRRGGFMVISAFSTTGFQNITTNQLTGALSSGAFLVVALLMA VGGSGGSTSGGVKFSRVGIIAKSIVATIKEALAPDSARVVVSYNHVGRRMVTPEVVKEAMTVFTLYVLTYVIGALVGIAHGYEATQAIFE SVSMASNGGVSSGLAAPGMPATLEAFYIVQMWAGRLEFVTLLALIVEIFVSFKPRRRAPQIRTGEVL

4.8E-31	117	38	1.7E-18	75.8	5.2	7.5	5	A0A0D3FZY3_9ORYZ	Uncharacterized protein		Oryza barthii	1029	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza barthii	65489	>tr|A0A0D3FZY3|A0A0D3FZY3_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1MMHPFSSILVTSQHLPLAMKIPQPKFQVVRDITEKVKHLHVFISMRLRSLSKCAVCFFRRCFWFFMFQSNPLIVQLVYFISISFVGFLALKILKPRHKPTPRDLDLMFTSVSTATVSSMATVEMEDFSNQQLWVLILLMILGGEVSISMLALHFNNAETNTNEVLPKRSPSTRRNIESFDAVNDSNQNSSQGFQSEATISLKWVQGSRTMKQKCRNMLAHIVTGYFIAAVVCSSLVIIIFAQIDSDTRQLLKSKDIKIWTFSIFTAVSSFANCGFTPVLAGNTILSPLLRLSIWILRKVSRREEYAYILQHPEDTGYRYLQLQKNSVNMVLTVGGLVLLQVMFLSYFEWNSKCETVNTRHAGEAVIDISTLSPPILVLFALVMYYPSDNSALPINADNKPLTERGRNSNDQAIWKNFIISKSACLAIFTIIACITERKSISTDPLNFNIFSIAFEIISAYANVGYSLGYSCKRLLKPDATCKATSYGFVGKWTDEDTLKRIKLYIAMKLLLPNSEVLRIYWEKAQHLCGFLSMKLISRARCVASSVKQSYSFLVCKSNPLVVQLVYFVIISFAGFLALKNLKPQGKPGPKDLDLLFTSVSTLTVSSMATVEMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLPSISLDIESNSPANNGDHKITECGQSEETMSQNQVQQNKSITYNPCAVLVRIVTDARNVLKSKEINMYTFCIFTAVSSFANCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLCVWVLGKVSGKAEYAYILQHPGETGYKHLHVRRNSVYIVLSVTGLILLQVMFICSFEWNSESLEGMNWLQKLVGLLFQSVNTRQAGESILDISTLSPSTLLLFAVVMYLPSDASFLTANADNQPLTDKKTNLISRALWRNFTVNKLSCLAMFTFLACITERKSISSDPLNFNIFSIVFEIIRQQTEITPFYFHSAFGNVGYSLGYSCQKLLKPDATCKDASYGFVGRWTEEGKLIVILVMFLGRLKEFILK	
5.2E-31	117	11	6.2E-31	116.8	7.7	1.1	1	C4XEZ8_MYCFP	Putative uncharacterized protein	MBIO_0455	Mycoplasma fermentans (strain ATCC 19989 / NBRC 14854 / NCTC 10117 / PG18)	233	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma fermentans, Mycoplasma fermentans (strain ATCC 19989 / NBRC 14854 / NCTC 10117 / PG18)	496833	>tr|C4XEZ8|C4XEZ8_MYCFP Putative uncharacterized protein OS=Mycoplasma fermentans (strain ATCC 19989 / NBRC 14854 / NCTC 10117 / PG18) GN=MBIO_0455 PE=4 SV=1MTYFVTTLVAFILIISFEGTFKNDNYFWRSDDKNLGNKWEKAWALLFTTFSTRSAGFSTINFSKLTSTSLIICSILMFIGAAPASTGGGIRTTTMAILFLSLFSKIMGRPSVRAFRRRIDDETVRMSSIVFSISIFLIIFISFITMSSLNNYSGQIDSNKYNFIHIFFEVNSAFGTTGLTCGITDKLNNASKVFLSILMFIGQFGISSTILVWGKKKNYSNKYEYISEPVAIG
5.3E-31	117	16.6	5.3E-31	117	11.5	3.5	1	M4F9Z8_BRARP	Uncharacterized protein	Bra037912	Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	496	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica campestris (Field mustard), Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	51351	>tr|M4F9Z8|M4F9Z8_BRARP Uncharacterized protein OS=Brassica rapa subsp. pekinensis GN=Bra037912 PE=4 SV=1MERVMAKLAKSRSLFFIYFFYFLSFSFLGFLALRISKPRTTSRPHDLDLFFTSVSAITVSSMSTVDMEVFSNTQLIIITILILLGGEIFTSFLHLYFSHCANFGFPYNKLRHLVCSLSSDTPIEDRCRDLENVTNHLKRPSQINERASKCLYSVVLGYHLVTNLVGSMLLLAYVSFSVKDVLSSKDISPLTFSVFTTVSTFSNCGFVPTNENMVIFRKNSGLLWLLIPQVFMGNTLFPCFLVFILWGLGKITKREEFGYILKNHKKMGYSPLLSVRLCVLLCLTALGLVLTQFLLFCTSEWNSKSLGGMNSYQKLVASLFQVVNSRHTGETIVDLSTLSPAILVLFIFMMYLPPYTLFMPFARENDKKDGEYDSKNEKKVKKNGVYVSQLAFLVICVLLISITESKKIRRDPLNFSILNITLEVISAYGNVGFSTGYSCKRRLDVRDGSCKDAGYGFAGRWSPVVKMIIVTVLHQYCLECLVNLTVNFFLIELKLGRGVVDLFILDLYSGISLRLPESL	
6.5E-31	117	26.5	2.7E-28	108.1	18.3	2.9	1	A0A022Q381_ERYGU	Uncharacterized protein	MIMGU_mgv1a005068mg	Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	498	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Lamiales, Phrymaceae, Erythranthe, Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	4155	>tr|A0A022Q381|A0A022Q381_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a005068mg PE=4 SV=1MKNYACSLQRTRFLICCSYHDFLAKLKPFLLYTFYFSSISFVGFGILTGLKPRTSFKPRNLDLLFTSVSSATVSSMSTVEMEVFSTSQLIVITILMFMGGEVFTSMVELLLKRSKIIGTCNFDGRKIESIESEPTRFEYSTNPFLKYDSIKFLGHVVLGYLVVIHILGISSVLLYLGLVSSAEDVLRNKGLKKFMFAVFTVVSTFANCGFVPTNENMVVFIKNSGLLWILIPQILLGNTLFPSCLRFVIWVLGKKIKKAEANYLLENDTTSKSSVYLHLFPSQHSVLLAATVFGFTILGFVIFSSLEWNSAALSGLNTYQKIVGILFQCVNARHSGETIVDLSIISPAVTVFFVVMMYLPPYTSFLPITKDEETPLESVIRKKRRKTAAENLVLSQLSYLVIFIIIICLTERKSLKEDPVNFSVLNITVEVISAYGNVGFTTGYSCERQIRPDPNCVNKWYGFSGKWSDKGKIVLIIVMFFGRLKKFNMNGGQAWKLL	
8.8E-31	116	14.9	1.4E-30	115.7	10.3	1.2	1	I3WIE4_BIFBI	Putative cation transporter	BBB_1065	Bifidobacterium bifidum BGN4	487	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium bifidum, Bifidobacterium bifidum BGN4	484020	>tr|I3WIE4|I3WIE4_BIFBI Putative cation transporter OS=Bifidobacterium bifidum BGN4 GN=BBB_1065 PE=4 SV=1MSNLVFDESSANREASHGYAWWFSGDTFEKAAAEERTRRKRSFIHHLTSHPGRLTIIYFLLLVALSTSLLLLPVSSHEEEPTSFSTAFFTAVSALSTCGISIVNATTHWTAFGQVVLLVSVQMGGLGVMTFASLIALAANHHMKATQRLLTANELGNTKLNEIRGVLTVVITTTFIIESVTFLALFPGLYGINRGNVRHTAREALFFAVMSYNNAGFTPDGAGLHVNNWAVGMPIMASAFCGTLGFPVLLNLMRCARHRTPPRRWSLHTKITLVTTFSLVLLSLAWFLLVEWDNPFLFKGADVETRLRYGVVAAVMPRSSGFDLSWVPQVSEPTKVFMSVIMFIGGGSTSTAGGIRVTTFAVILLICRAAFTGHTDINAFRRRIPTRVAMTAVSITAACLFLVLSASLALMLASGCSLTDALFDACSSFGLGGYSVGVAREDNPAALFILATAMVVGRLGPMTIAYAINRPRALESIRYPNEPIVVG	
1.5E-30	116	24.6	1.8E-28	108.7	10.4	3.4	2	A0A072UBQ8_MEDTR	High-affinity potassium transporter (Uncharacterized protein)	MTR_6g092840	Medicago truncatula (Barrel medic) (Medicago tribuloides)	550	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago (medics), Medicago truncatula (Barrel medic) (Medicago tribuloides)	3880	>tr|A0A072UBQ8|A0A072UBQ8_MEDTR High-affinity potassium transporter OS=Medicago truncatula GN=MTR_6g092840 PE=4 SV=1MHILNSFLKKLQHLCSTSLQRIACQTKSIFFLAACFCRFILLRANPLWVQIVYFTSLSTLGFGFLKVLKPLGETPKNLDLFFTSISATTVSSMSTVEMQNFSNPQLIIITILMFIGGEVFTSMVGLFFIRSRLKTELDKIASSHARLASINTFNIEQIHLEVEMVTNEVHNKSHESLHNKSHQSLHNMSHESLSTTNENLRYLSMKYLGYVVFAYFLIHIIGVIGVSIYLAIIPSAKQILKNKGLKMFTFSVFTIVSTFASCGFVPTNENMVVFRKNSGLLLMLIPQVLLGNTLYPPCLRFCIWVLGKFYKKKECRYLLKHSEEVGYKHLLKGKHSICLVATVFGLIMVQVTLFCAMDWDSEGLKGLNFYQKMIGVLFQIVNSRHTGETVVDISNLSQAILVLFVLMMYLPPYTSFLPLKSDGKNSERSKRMKKIRGKVTENLIFSQLSYLVIFIILVCITERKKLKEDPLNFNVLNIVVEVVSAYGNVGFTMGYSCERQLHLEINCENKWIGFVGKWSDEGKIILILIMLFGRLKKFNMDGGKPWKLL	
1.9E-30	115	15.1	1.9E-30	115.3	10.5	3	1	A0A0D3E8X3_BRAOL	Uncharacterized protein		Brassica oleracea var. oleracea	533	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica oleracea (Wild cabbage), Brassica oleracea var. oleracea	109376	>tr|A0A0D3E8X3|A0A0D3E8X3_BRAOL Uncharacterized protein OS=Brassica oleracea var. oleracea PE=4 SV=1MASFNSYTEPGNKMERVVAKLAKSRSLFFIYFFYFLSLSFLGFLALRISKPRTTSRPHDLDLFFISVSAITVSSMSTVDMEVFSNTQLIIITIFILLGGEIFTSFLHLYFSHCANFGFPYNKLRHLVCSLSSDTPIEDRRRDLENVTNHLKRPSQINERASKCLYSVVLGYHLVTNLVGSMLLLAYVSFSVKDVLSSKDISPLTFSVFTTVSTFSNCGFVPTNENMVIFRKNSGLLLLLIPQVFMGNTLFPCFLVFIIWGLGKITKREEFGYILKNHKKMGYSPLLSVRLCVLLCLTALGLVLIQFLLFCTFEWNSKSLGGMNSYQKLVASLFQVVNSRHTGETIVDLSTLSPAILVLFIFMMYLPPYTLFMPFARENDKKDGEYDSKNEKKVKKNGVYVSQLAFLVICVLLISITESKKIRRDPLNFSILNITLEVISAYGNVGFSTGYSCKRRLDVRDGSCKDAGYGFAGRWSPVVVKMIIVTVLHQYCLECLVNLTVNFFLIELKLGRGVVDLFILDLYSGISLRLPESL	

2.1E-30	115	22.4	4E-21	84.5	5.5	3.4	3	HKT6_ORYSJ	Probable cation transporter HKT6 (OsHKT6)	HKT6 Os02g0175000 LOC_Os02g07830 OSJNBa0073A21.31	Oryza sativa subsp. japonica (Rice)	530	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>sp|Q6H501|HKT6_ORYSJ Probable cation transporter HKT6 OS=Oryza sativa subsp. japonica GN=HKT6 PE=2 SV=1MNHCLVVSHKKLQTFRTFAASKFSSFTKSAQKSIKYSFQFIYQNNPLFVHVAYFALISFAGYGSLKVLKPRDKSNTLKDLDVLFTS VSASTVSSMATVEMEDFSSAQLWVLTILMLIGGEVFTSMLGIHFMRAEFGTKESVSTRDHSPCIDIESITSTKFGPSTQGTKVTVSFSE LRMENGGHVEPKTIKFLGFVVMGYLLITNLGGSLLIYLYLNLVPSAHKILKRKGIGIIVFSVFTAISSVGNCGFTPVNENMIIFQKNSILLLLI LPQILAGNTLFAPCLRLMVWSLEKITGKKDCRYILEYPKAIGYKHLMSTRESVYLTLTVVSLIILQTVLFLSLEWSSVALDGMSNYQKIVS ALFQSVNARHAGESVTDLSNLSSAILVLYTIMMYLPGYTSFLPRHDGEDSKTEKINKRKGLLENWIFSHMSYLAIFVMLICITERDSMAT DPLNFNVFSILFEVVAYGNVGFSVGYSCKRLLNHDARCKDASYGFAGKWSDNGKAILIIVMLFGRLKTFNMKGGRAWKLR
2.9E-30	115	29	3E-29	111.3	20.1	2	1	S6C7C8_9ACTN	Cation transporter protein	AEQU_2002	Adlercreutzia equolifaciens DSM 19450	506	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Adlercreutzia, Adlercreutzia equolifaciens, Adlercreutzia equolifaciens DSM 19450	1384484	>tr|S6C7C8|S6C7C8_9ACTN Cation transporter protein OS=Adlercreutzia equolifaciens DSM 19450 GN=AEQU_2002 PE=4 SV=1MWQRFTLYDLRVIGHYLGTLLLFFAALMALPLATALVFQEWEPAARYLAAIGITMVAGCSLRFLRIEPGRLDRRQALAVTGFAWV VLALFASFPLYFSGHYMTYLDAIFDGVSGLTTTGASLIVDLDHLSYADNMFRFAMHALGGLGLIVVALSFGLFGRGGGASLFSSEGRSE HVVPNVVQTTQFIARITLVIVSVATVIITALCLFMGMEPTRAFLNALWVSTSGFVTGGFTPMQLSIMYYHSFPLEAILMVLMILGSISFVIH AEVWKGRPLPFFRDIETKTMVLWIGVMAFVFTATLALSPFDDMLALLRRGLFMIISAFTTTGFQVVTTNQITTAFSNGAFLTLAFIMAVG GASGSTAGGIKFSRMGIIFKSIVSNVKETLAPDSARVVVSYNHVGRRTLTPEIVKEAMTVFILYVITYVIGALVGIAHGFEAIPAISESVAM TSNGGIITSVAGPGMAGTLELFYIFQMWAGRLEFMTLFALIVEVVASLVPRPRPKERS
3.2E-30	115	30.1	3.2E-30	114.5	10.2	3.1	2	HKT1_ARATH	Sodium transporter HKT1 (AtHKT1)	HKT1 At4g10310 T9A4.5	Arabidopsis thaliana (Mouse-ear cress)	506	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Camelineae, Arabidopsis, Arabidopsis thaliana (Mouse-ear cress)	3702	>sp|Q84TH7|HKT1_ARATH Sodium transporter HKT1 OS=Arabidopsis thaliana GN=HKT1 PE=1 SV=1MDRVVAKIAKIRSQLTKLRSLFFLYFIYFLFFSFLGFLALKITKPRTTSRPHDFDLFFTSVSAITVSSMSTVDMEVFSNTQLIFLTILM FLGGEIFTSFLNLYVSYFTKFVFPHNKIRHILGSYNSDSSIEDRCDVETVTDYREGLIKIDERASKCLYSVVLSYHLVTNLVGSVLLLVYV NFVKTARDVLSSKEISPLTFSVFTTVSTFANCGFVPTNENMIIFRKNSGLIWLLIPQVLMGNTLFPCFLVLLIWGLYKITKRDEYGYILKNH NKMGYSHLLSVRLCVLLGVTVLGFLIIQLLFFCAFEWTSESLEGMSSYEKLVGSLFQVVNSRHTGETIVDLSTLSPAILVLFILMMYLPPY TLFMPLTEQKTIEKEGGDDDSENGKKVKKSGLIVSQLSFLTICIFLISITERQNLQRDPINFNVLNITLEVISAYGNVGFTTGYSCERRVDI SDGGCKDASYGFAGRWSPMGKFVLIIVMFYGRFKQFTAKSGRAWILYPSSS
3.3E-30	115	13.9	2.3E-18	75.4	6	4.5	3	A0A0E0PDU2_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	664	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0PDU2|A0A0E0PDU2_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MLVKLSLSPILVLFALVMYYPSDNSALPINADNKPLTERGRNSNDQAIWKNFIISKSACLAIFTIIACITERKSISTDPLNFNIFSIAFKII SAYANVGYSLGYSCERLLKPDATCKATSYGFVGKWTDEDTLKRIKLYIAMKLLLPNSEVPRIYWEKAQHLCGFLSMKLISRARCVASS VKQSYSFLVCKSNPLVVQLVYFVIISFAGFLALKNLKPQGKPGPKDLDLLFTSVSTLTVSSMATVEMEDLSDRQLWVLILLMLMGGEVF TSMLGLYFNNANANRNENSQRSLPSISLDIEFNSPGNNGDHKITECGQSEETMSQNQVQQNKSITYNPCAVLVRIVTDARNVLKSKEI NMYTFCIFTAVSSFANCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLCVWVLGKVSGKAEYAYILQHPGETGYKHLHVR RNSVYIVLSVTGLILLQVMFICSFEWNSESLEGMNWLQKLVGLLFQSVNTRQAGESILDISTLSPSTLLLFAVVMYLPSDASFLTANADN QPLTDKKTNSISRALWRNFTVNKLSCLAMFTFLACITERKSISSDPLNFNIFSIVFEIIRQQTEITPFYFHSAFGNVGYSLGYSCQKLLKP DATCKDASYGFVGRWTEEGKLIVILVMFLGRLKEFILK
3.7E-30	114	32.9	2.8E-29	111.4	20.7	2.3	1	H6LIZ1_ACEWD	K+ uptake protein, membrane subunit TrkH1	trkH1 Awo_c05550	Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	509	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Acetobacterium, Acetobacterium woodii, Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	931626	>tr|H6LIZ1|H6LIZ1_ACEWD K+ uptake protein, membrane subunit TrkH1 OS=Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655) GN=trkH1 PE=4 SV=1MNTFNGRFYSILIISYYTGYVVLGIALLMILPILTAVGLQEWNPFWDFIITMAISIILGFSLIIIGKETRLNKNFVQWKHGFVVASLSWII LMFLCAIPYLLSGHVNSILDACFDVMSGFTTTGMVLTQDLDHISLSLNMWRHMITFIGGQGMIVLALTFLLKETGGAYIFYVGEAKDIEL VPNVKGTARIIWKISLVYLVIGTAALWIDGMVIGLSPLSAFFNGLFIFASSWSTGGFAPYSQNIMYYHSFSYEIITMIFFILGSLNFGLHHA VFSGNKKELLKNIETQSFFITSFLASALAVLWLARTDVYADAVSIFRRVVYNVLSAHTTTGFGSIYARQFALEWGDFGILVMIIVMLIGGS ACSTAGGFKGLRIGIVFKSIFTDVKRLLSSERNVKVFRFHHIKDQILTDGLVKASALIIICYLITFASGTLIGTFCGYPLASAAFEAASITGN VGLSIGITTPDMPAILKIYDIIAMYLGRLEFLSVFALIGFIIGGLKKCLTKQ
3.9E-30	114	22.2	1.4E-27	105.8	15.4	2	1	R5WZH0_9FIRM	Uncharacterized protein	BN568_01857	Blautia sp. CAG:257	291	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	1262756	>tr|R5WZH0|R5WZH0_9FIRM Uncharacterized protein OS=Blautia sp. CAG:257 GN=BN568_01857 PE=4 SV=1MGFASVILIGTILLLMPVSVKEGAEVSFIDALFTSTSAVCVTGLIVVDTADHFTALGQGIIAVLIQIGGLGVTSVGVGLVLAAGKRVSI KSRLMVKEALNVGDLKGMVKLVKAILIMTLCFESIGAALSFVVFVQNYSPLHALGISIFHSIAFNNAGFDILGGLRNLIPYQNNVLLNLTTC FLIIAGGIGFLVILDIKKNKRFKKLSFNSKIVLSTSVILLAVGTLLLKMTEDISWMGAFFNSVSARTAGFSTYSVGSFSNAGLFVLCFLMFI GASPGSTGGGIKTSTFFA
4.3E-30	114	11.8	3.3E-18	74.8	0.6	3.6	3	B8ATV6_ORYSI	Sodium transporter HKT14	OsI_17315	Oryza sativa subsp. indica (Rice)	500	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>tr|B8ATV6|B8ATV6_ORYSI Sodium transporter HKT14 OS=Oryza sativa subsp. indica GN=OsI_17315 PE=2 SV=1MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLG GEVFVSLVGLASKWSKLRSDAMDRSQRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHV VGAVAVAAYVLASPGARRTLGDKSLNTWTFAVFTTVSTFSNCGFMPTNENMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVWAAA AATRREELVEMAREGGRAAAAGYAHLMPARRCWMLAATVAAFVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGES TVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVS AYGNVGFSMGYSCSRQINPDHLCTDKWTGFVGRWSDSGKLILIFVMFFGRLKKFSMKGGKAWKLS
4.9E-30	114	12	3.3E-18	74.8	0.6	3.6	3	HKT7_ORYSJ	Probable cation transporter HKT7 (OsHKT7)	HKT7 Os04g0607600 LOC_Os04g51830 OSJNBa0060N03.4	Oryza sativa subsp. japonica (Rice)	500	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>sp|Q7XPF7|HKT7_ORYSJ Probable cation transporter HKT7 OS=Oryza sativa subsp. japonica GN=HKT7 PE=2 SV=2MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLG GEVFVSLVGLASKWSKLRSDAMDRSRRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHV VGAVAVAAYVLASPGARRTLGDKSLNTWTFAVFTTVSTFSNCGFMPTNENMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVWAAA AATRREELVEMAREGGRAAAAGYAHLMPARRCWMLAATVAAFVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGES TVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVS AYGNVGFSMGYSCSRQINPDHLCTDKWTGFVGRWSDSGKLILIFVMFFGRLKKFSMKGGKAWKLS

4.9E-30	114	12	3.3E-18	74.8	0.6	3.6	3	Q0JAB3_ORYSJ	Os04g0607600 protein (cDNA clone:002-148-F09, full insert sequence) (cDNA clone:J023029F13, full insert sequence)	Os04g0607600	Oryza sativa subsp. japonica (Rice)	500	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>tr|Q0JAB3|Q0JAB3_ORYSJ Os04g0607600 protein OS=Oryza sativa subsp. japonica GN=Os04g0607600 PE=2 SV=1MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLG GEVFVSLVGLASKWSKLRSDAMDRSRRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHV VGAVAVAAYVLASPGARRTLGDKSLNTWTFAVFTTVSTFSNCGFMPTNENMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVWAAA AATRREELVEMAREGGRAAAAGYAHLMPARRCWMLAATVAAFVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGES TVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVS AYGNVGFSMGYSCSRQINPDHLCTDKWTGFVGRWSDSGKLILIFVMFFGRLKKFSMKGGKAWKLS
7.1E-30	113	42.4	8.3E-28	106.5	29.4	2.1	1	A0A0A7LE57_9EURY	Candidatus Methanoplasma termitum strain MpT1, complete genome	Mpt1_c06870	Candidatus Methanoplasma termitum	503	cellular organisms, Archaea, Euryarchaeota, Thermoplasmata, Methanomassiliicoccales, Methanomassiliicoccaceae, Candidatus Methanoplasma, Candidatus Methanoplasma termitum	1577791	>tr|A0A0A7LE57|A0A0A7LE57_9EURY Candidatus Methanoplasma termitum strain MpT1, complete genome OS=Candidatus Methanoplasma termitum GN=Mpt1_c06870 PE=4 SV=1MFHTLKLRIKNIAIWESSTVKVLGLVELMLGMALLMPAVIAFMYDEDPMVFIVPAPILLILGAFQYLFFKRGQTLRPASGLMMIFLV WWIAFFVSAVPLYLYGMSFVDSLFQGISGFTATGASIMNGISSHSLVFWVAFTQWAGGLAIIVLFLYLIPMMGLGGKAFLNNELAGSE SYNFSMKISGAVSNFVAIYVLLSAVEAILLVISGVSVFESVTTMFSTISTGGFMANGSMADYSFVVQFIVLAFMFLGGTNFYLHYRAIYK RELSAYRTSQEFIWTVISVIASTVIIMAIIFAIGNGQISDIGGTFWDTLFTVVSFGTTTGYAVVDQPFWPIATYVVFWLVMLAGFMSGSTS GGIKIYRFLIIKSYITNGVYKMFHPLAVKDVKMDNQSVNNDAVVSAVLVISMFIGTVVVSLLITILEPSLSISESTGLAVAAISNSGVNMGT ATFMELKDATKIFMAFMMWVGRLEVIIALLLFTKTFWSDLAMDIKGNRAKRGKA
7.9E-30	113	11.7	3.3E-18	74.8	0.6	3.6	3	I1PPJ4_ORYGL	Uncharacterized protein		Oryza glaberrima (African rice)	500	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza glaberrima (African rice)	4538	>tr|I1PPJ4|I1PPJ4_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLG GEVFVSLVGLASKWSKLRSDAMDRSRRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHV VGAVAVAAYVLASPGARRTLGDKSLNTWTFAVFTTVSTFSNCGFMPTNENMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVWAAA AATRREELVEMAREGGRAAAAGYAHLMPARRCWMLAATVAAFVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGES TVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVS AYGNVGFSMGYSCSRQINPDHLCTDKWTGFVGRWSDSGKLLLIFVMFFGRLKKFSMKGGKAWKLS
9E-30	113	36.5	1.7E-13	59.3	11.4	2	2	U4KLK6_9MOLU	Trk system potassium uptake protein TrkG	trkG BN8542670	Acholeplasma palmae	434	cellular organisms, Bacteria, Tenericutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Acholeplasma, Acholeplasma palmae	38986	>tr|U4KLK6|U4KLK6_9MOLU Trk system potassium uptake protein TrkG OS=Acholeplasma palmae GN=trkG PE=4 SV=1MRKIKMTPYMIIALSFFTVIILGTILLKLPITLKEHGSLSWIDAFFTSTSLITITGLTPVLDLGSSFTIFGKVVIACMIQIGGLSVLTLTVYI MTLIGSKIGFNNRAILKESLNQNSLQGLVKLVKRIIMISFIIEFIGFIINLFIFIPTMDNTYHAIGVSAFHAISAFNNAGLEILGFNNHFLNYHN NLLFNINTGVLSILGGLGVIVIYEVMKKRSWKKLSIQTKITLKMTLGLLIMGTVLFKLIEQNQMTFLEVSFLSINTRTAGFLTVDLTKVKSLS IAIIIPLMFIGAGPMSTGGGIKVTTLYVMLKSLFSFGRGSQTLTHKRLITDETKIKAFVLIQSAMILIGISTFLLLAFEETNIQTALFESVSAFS NTGMTLNFTHKIGLGSKTILILMMYIGRIGPLTILHLIYSKKASNSNLVYIDEKIVIG
1.1E-29	113	20.5	3.1E-29	111.2	14.2	1.7	1	R5ZT29_9CLOT	TRK system potassium uptake protein TrkH	BN713_00979	Clostridium sp. CAG:568	528	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:568	1262821	>tr|R5ZT29|R5ZT29_9CLOT TRK system potassium uptake protein TrkH OS=Clostridium sp. CAG:568 GN=BN713_00979 PE=4 SV=1MRKQAKGYRLIFGYLGIFLILIGIITMLPLILLAFYPGESNCWLSFFIPGMSSIGLGFLLFLLIYKRERTQLEKFQDSALLVMIWLSAILI GSVPFMLRGYTTPDFAKYRMNFSDAVFESTSGYTSTGLTVFNFDMSYPGYHIFTFYRSILLLFGGIGLVLIVTSAISDKYGLKLYTAEGH NDKLMPNLAKSARLILLIYIGYIILGFLSYWLIGGMEPFDAINHAIAAIATGGFSTREGGIPEIINEGGYNSITGWPVNGLAINITSIILMLLGG TNFVLHLFLFKGKLKKILKDSEIKFFLILSIIMIPLFYTSIFTSLSQQLSVLDSWREGTYLYFSALTTTGFSTTTDIKQLGEAALILSIIAMTIG GGMGSTAGGVKQYRFVVAYKALYWSLRDRLSSKRKFYPHTIYRLGESKEINKLDFLESYGYLILYVTIMMVGGTIITILGKNTDGYSAIE CIFEFASALSGTGLSVGVTTGVGLPIANAVAIRWVLVFGMFAGRLELICIYLAFYRFVRDILRRPTY
1.2E-29	113	30	7E-19	77.1	16.2	3.7	2	I1GWP6_BRADI	Uncharacterized protein	BRADI1G34210	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	508	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Brachypodieae, Brachypodium (false bromes), Brachypodium distachyon (Purple false brome) (Trachynia distachya)	15368	>tr|I1GWP6|I1GWP6_BRADI Uncharacterized protein OS=Brachypodium distachyon GN=BRADI1G34210 PE=4 SV=1MPSRLHIFVSSARHVTNSSVFISRFIASHLSPLLIHLSYFVIFDILGFVALMALKPSNPNYTPRYIDMLFLSTSALTVTGLATIKMEDL SSSQILVLTLLMLLGSEMFVSLLGLVHELSKQNKHDPEDSRVRSVTVLNESQVEEAIPATPSTNSNGLKKSCLKYLGFVLVAYMVTILLV GSLLVFMYVTHVSTARDVLARKSINTVLFSISVTTSSFTNGGLLPTNESMAVFASNQGLLLLLTGQILAGSMLLPVILRLVIWALKGLRM TKVKPEEFEFMMHNTKAMGLNHLLPNLQTVFLAVTVTALTAVAVTLFCCLNWYSAVFTGLTSSQKITNALFMAVNARQAGENSIDCSL VAPAALLLFMAMMYIPASTTVFSVQDDDARGDTEHKDGPKKRSLSLNNMLFSPLACNAAMIMIVCITERRLLFTDPLNFSTFNMIFEVIS AYGNVGLSIGYSCSRLLHPEKESICHEKPYSFSGWWSDQGKVVLVLVMLYGRLKCFHKHKN

1.7E-29	112	20.7	3.8E-19	78	6.1	3.5	3	I1PPJ3_ORYGL	Uncharacterized protein		Oryza glaberrima (African rice)	552	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza glaberrima (African rice)	4538	>tr|I1PPJ3|I1PPJ3_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1MHPPSLVLDTLKRIKLYIAMKLLLPNSEVLRIYWEKAQHLCGFLSMKLISRARCVASSVKQSYSFLVCKSNPLVVQLVYFVIISFAG FLALKNLKPQGKPGPKDLDLLFTSVSTLTVSSMATVEMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLPSISL DIESNSPANNGDHKITECGQSEETMSQNQVQQNKSITYNPCAVLVRIVTGYFVATVISSSVIIIIYFWIDSDARNVLKSKEINMYTFCIFTA VSSFANCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLCVWVLGKVSGKAEYAYILQHPGETGYKHLHVRRNSVYIVLSVT GLILLQVMFICSFEWNSESLEGMNWLQKLVGLLFQSVNTRQAGESILDISTLSPSTLLLFAVVMYLPSDASFLTANADNQPLTDKKTNLI SRALWRNFTVNKLSCLAMFTFLACITERKSISSDPLNFNIFSIVFEIISAFGNVGYSLGYSCQKLLKPDATCKDASYGFVGRWTEEGKLI VILVMFLGRLKEFILK
2E-29	112	8.1	2.3E-17	72.1	1	2.2	2	Q166R2_ROSDO	Trk potassium uptake system protein, transmembrane component	trkH RD1_2465	Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)	476	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseobacter, Roseobacter denitrificans, Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)	375451	>tr|Q166R2|Q166R2_ROSDO Trk potassium uptake system protein, transmembrane component OS=Roseobacter denitrificans (strain ATCC 33942 / OCh 114) GN=trkH PE=4 SV=1MVLQSARLSRVSLALAKHGVLLPLVFLPPTVWAASELAWGLVLALLAPAALGGGLSLAVARTALPKDLRQVEAIVVLALLFVLTPV LSIPAFMTLGMPPVDALFEGMSALTTTGLSVATNADTWPFAGHLLRSWMQWCGGLAMATAVLAMLIGPGVTARKLGKVNMDDGDLI SSTRTHARQLLGAYAGITLVFGAAISASIGSVPEGLLLTLSAVSTGGFAYLPDSVASYAPMTQGLTISASLCGAVSLLAVALLCKRDWS NAWLTGSLQRMALWSMGCVLTLCICVWVLGGSGYYVHAWNLLSAISTAGYSIGAMPTEPVLLVFFIAVMAIGGDVGSTAGGIKLARF LTLMRTGQHAARGPRLPVNAVAPMREHGQVLKQSQLIALLALLLFYSVFVLSLWTLFLAHGHPPLPALFDAVSAFSTVGLSTGVIGAD NPALLKIATTFAMLLGRLEFVAVLLLVLPRTWHIPHHRRK
2.3E-29	112	23.4	8.1E-29	109.8	12	3.3	1	I1GZU0_BRADI	Uncharacterized protein	BRADI1G45940	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	507	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Brachypodieae, Brachypodium (false bromes), Brachypodium distachyon (Purple false brome) (Trachynia distachya)	15368	>tr|I1GZU0|I1GZU0_BRADI Uncharacterized protein OS=Brachypodium distachyon GN=BRADI1G45940 PE=4 SV=1MVSCTPQYSKIQRVYHLFVFCVHPFWLQLMYFVSTSLLGFLILKALPMKTSLVPRPRDLDLIFTSVSATTVSSMVALEMESFSNS QLLLLTLLMLLGGEVFTSILGLHFTYTKSKKEQPSSQELISSTTPMDDDTHSQTEHGFKNLQRYDQFGGSLARILLFIVLGYHIMVHLAG YTLILVYLSVASGARAVLVGKGISTHTFSIFTVISTFANCGFVPTNEGMISFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIWALHKVTKRS ELSELLRIERSSYGYEYDHLLPSRNTWFLALTVAAFVLLQLVLFCAMEWSSDGLRGLTAPQKLVAALFMSVNTRHAGEMVVDLSALSS AVVVLYVVMMYLPPYTMFLPIAEDNHPQTGEHSSSRSSQKKSSIWHKLLMSPLSCLAVFVVVICITERQRIADDPINFNVLNIVVEVISAY GNVGFSTGYSCGRQVRPDGSCRDAWVGFSGKWSSEGKLVLMAVMFYGRLKKFSMQGGQAWKIA
2.7E-29	111	22.5	5.2E-16	67.6	3.5	7.4	5	A0A0D9W965_9ORYZ	Uncharacterized protein		Leersia perrieri	1034	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Leersia (cutgrass), Leersia perrieri	77586	>tr|A0A0D9W965|A0A0D9W965_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1MAGSVHHKLVELLHRLRRSTAAGLHHAMSLVCSLSRAYAHHQVNDRVSRSRRALAAGRRAVTAPLAIHVVYFLALSCLGYGLLG AIETRGDAPRGIDRFFTAVSAATVSSMSAVEMEVFSNAQLLVITALMLAGGEVFVSLFGLASNVIPYSSLLYTLRRQAVHKSRRVEIHA CDVETPTATTTTENADTTPRHVDAARFLFYVVLAILVASHALGAASVAAYVLRLSPSARDTLRAKSLNPWTFAAFVTVSTFSSCGFTPN NENMAAFARDAPLQLLLLPQALLGNTLFPPLLAACVWAATRRRKDLAEKLGGYGYEYYYHLMPARRCWMLCGTVAALVAAQAAMVC GMEWGGGGALRGMSAWEKLVNAVFLAVNSRHTGESTVDLSTLAPAIIVLFVLMMYLPPYTTWFPFEDDSNAKEHTAESQGIRLLKST VLSQLSNLTIFVIAICITERRKLKEDPLNFNVLSIIVEVVRQWHMLDNNTHQNRHFFFVESDRFIYVCSAYGNVGFSMGYSCSRQINPDH LCIDRWTGFVGRWSDSGKIILIFVMFFGRLKKFSMKGGKSWKLISSQHLPLSMKLPQLNSEVVRNIAEKVKHIHVFISMRALQLVYFVSI SFVGFLALKILKPRHKPTPRDLDLMFTSVSTATVSSMATVEMEDFSDQQLWVLILLMLLGGEVFISMLALHFNNAGINTNDILPKRFPST NRNIESFDAVNNRNQNNSEDCQLSPNWVQESKAMKQKCRNILAHIVLVTGYFIAAVVFSSLIDSDTRHLLKSKDIKIWTFSIFIAVSSFA NCGFTPVNDNMVLAGNTMLSPLLRLSIWALGKVSRRQEYFDILQHPEDTGYKYLQPQKNSVRMILTTGGLILLQSMNTRHAGEAVIDIS TLSPSILVLFALVMYHPCDNSDLPINADYQHLTKRRRKSNDQAIWKNFIISKSGFLGIFTILACITERKSISADPLNFNIFSIAFEIIRAYANL GYSLGYSCEKLLKLDATCKASSYGFVGKWTDEDTLQHIKSYIAMKLLLLNFEVPQI
2.9E-29	111	21	2.6E-26	101.6	11.2	3.5	2	HKT4_ORYSJ	Cation transporter HKT4 (OsHKT4)	HKT4 Os04g0607500 LOC_Os04g51820 OSJNBa0060N03.3	Oryza sativa subsp. japonica (Rice)	552	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>sp|Q7XPF8|HKT4_ORYSJ Cation transporter HKT4 OS=Oryza sativa subsp. japonica GN=HKT4 PE=1 SV=2MHPPSLVLDTLKRIKLYIAMKLLLPNSEVPRIYWEKAQHLCGFLSMKLISRARCVASSVKQSYSFLVCKSNPLVVQLVYFVIISFAG FLALKNLKPQGKPGPKDLDLLFTSVSTLTVSSMATVEMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLPSISL DIEFNSPANNGDHKITECGQSEETMSQNQVQQNKSITYNPCAVLVRIVTGYFVATVISSSVIIIIYFWIDSDARNVLKSKEINMYTFCIFTA VSSFANCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLCVWVLGKVSGKAEYAYILQHPGETGYKHLHVRRNSVYIVLSVT GLILLQVMFICSFEWNSESLEGMNWLQKLVGLLFQSVNTRQAGESILDISTLSPSTLLLFAVVMYLPSDASFLTANADNQPLTDKKTNSI SRALWRNFTVNKLSCLAMFTFLACITERKSISSDPLNFNIFSIVFEIISAFGNVGYSLGYSCQKLLKPDATCKDASYGFVGRWTEEGKLI VILVMFLGRLKEFILK
2.9E-29	111	21	2.6E-26	101.6	11.2	3.5	2	C7J0U7_ORYSJ	Os04g0607500 protein	Os04g0607500	Oryza sativa subsp. japonica (Rice)	552	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>tr|C7J0U7|C7J0U7_ORYSJ Os04g0607500 protein OS=Oryza sativa subsp. japonica GN=Os04g0607500 PE=4 SV=1MHPPSLVLDTLKRIKLYIAMKLLLPNSEVPRIYWEKAQHLCGFLSMKLISRARCVASSVKQSYSFLVCKSNPLVVQLVYFVIISFAG FLALKNLKPQGKPGPKDLDLLFTSVSTLTVSSMATVEMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLPSISL DIEFNSPANNGDHKITECGQSEETMSQNQVQQNKSITYNPCAVLVRIVTGYFVATVISSSVIIIIYFWIDSDARNVLKSKEINMYTFCIFTA VSSFANCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLCVWVLGKVSGKAEYAYILQHPGETGYKHLHVRRNSVYIVLSVT GLILLQVMFICSFEWNSESLEGMNWLQKLVGLLFQSVNTRQAGESILDISTLSPSTLLLFAVVMYLPSDASFLTANADNQPLTDKKTNSI SRALWRNFTVNKLSCLAMFTFLACITERKSISSDPLNFNIFSIVFEIISAFGNVGYSLGYSCQKLLKPDATCKDASYGFVGRWTEEGKLI VILVMFLGRLKEFILK
3E-29	111	1.6	6.2E-27	103.6	1.1	2.5	1	W8RV26_9ROHOB	Potassium uptake protein TrkH	roselon_02815	Roseibacterium elongatum DSM 19469	489	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseibacterium, Roseibacterium elongatum, Roseibacterium elongatum DSM 19469	1294273	>tr|W8RV26|W8RV26_9RHOB Potassium uptake protein TrkH OS=Roseibacterium elongatum DSM 19469 GN=roselon_02815 PE=4 SV=1MGVKRAAAFRGGSGPLVQAARLRVVSLTLAKHAPIFIFLLAPPALWAVIEGQMALSLSLALPAVLCLGLFGIVWRLPLPDDLRGIE ALVSIALVFGLSALLAVPAFMSLGMPPLDALFEAVSAATTTGLSVAAAPDAWPFAGHFLRAWVQWCGGLVMATAVLALLLPSGLPAR KLGQAGIDQGDRIASTRRQAQQLLGVYVGLTALMAGLAALAIPDTREAVVLTLSAISTAGFAPRSDSLASYSALGQGIVMLTCVFGAISL LTFILILQRKPKEAWAIGSARRVLLAILGFGAVYATMLYLGGMRSWASVYPEMLNLISGLTTAGFSTGAMPPPGAALLVIVIAMLAGGDV GSTAGGLKLARLGIVARAVLHAAQRPRPLPANALALPLRHHGEPVEDRTLVSILALIGIYLAVLVVLWMHMLGHGHPAMPALFEVVSTLST VGLSTGIVGPDLSDDLKLSLTFGMWLGRLEFFAVLLLLAPRTWMKGR

4.1E-29	111	6.4	1.6E-26	102.3	4.4	3	1	D6ZYH1_STAND	Cation transporter	Snov_1779	Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	482	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Starkeya, Starkeya novella (Thiobacillus novellus), Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	639283	>tr|D6ZYH1|D6ZYH1_STAND Cation transporter OS=Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113) GN=Snov_1779 PE=4 SV=1MIAVARHSALTAGVMAGFLLIAALVALFRNEDGADVFLMTALLTVFGAGAVYLSVRNRGNRLDRLGAYGLLVVLWFGVPVIAAIPIAATTSLGPVDAWLEAVSAFTTTGAVQVHDIADVPRATLGWLLTLQWAGGLLTLVGFVAVLGPAGIGGLPDRSARASLLGVTEQTALDDALRLVLPIYLGATILCTLMLFAVGVRMFDALGLAGSALSTGGLLPDSDGIPAYGHFAVKLVLIVFMLVGGTSVLWHRMLLTRRIRLALGQYENLVLIALCFVIGIAVAAMSYRVPLGEIALPMALEDGMFTAVSLVTTTGIEPHAGSFASLPLTLVIAIVFVGGASFSTAGGIKIYRAGIMMLQSYLELERLVHPNAIHPRRLGQQNVTLQMMKAIWIMFGIACMTIAALSAAIAPAMPSFEAAFVSIVAAMSNMGPVYAAGWSTEVAWPEWGALPAYAQTILAIAMILGRLEILVVLGLANFALWRR	1262777	>tr|R5WEZ7|R5WEZ7_9CLOT Cation transport protein OS=Clostridium sp. CAG:167 GN=BN512_01784 PE=4 SV=1MGGYSAYIQWVVTIFMILFGVNFNAYYFILYKKVKKALKLEEVRYYFLIILVATGIIFMNLLQTSMGIWDSLRHAAFQVATIITTTGYSTVDFNAWCQTSKTVLVLLMFVGACAGSTGGGIKVSRFVILIKTVGKELQSYIHPKSIKKINIDKKPVEHDVVRATNVYFITFVILFVASVFLISFEDKDLVTNFTAVAATINNIGPGLDLVGPTQNFDCFSAPSKYVLIFDMLAGRLELFPLLILFHPVMLRQFFIRKKKTNKK
4.2E-29	111	13.5	4.1E-28	107.5	9.3	1.9	1	R5WEZ7_9CLOT	Cation transport protein	BN512_01784	Clostridium sp. CAG:167	263	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:167	1262777	>tr|R5WEZ7|R5WEZ7_9CLOT Cation transport protein OS=Clostridium sp. CAG:167 GN=BN512_01784 PE=4 SV=1MGGYSAYIQWVVTIFMILFGVNFNAYYFILYKKVKKALKLEEVRYYFLIILVATGIIFMNLLQTSMGIWDSLRHAAFQVATIITTTGY STVDFNAWCQTSKTVLVLLMFVGACAGSTGGGIKVSRFVILIKTVGKELQSYIHPKSIKKINIDKKPVEHDVVRATNVYFITFVILFVASV FLISFEDKDLVTNFTAVAATINNIGPGLDLVGPTQNFDCFSAPSKYVLIFDMLAGRLELFPLLILFHPVMLRQFFIRKKKTNKK
5.7E-29	110	17.8	4E-19	77.9	3.4	3.5	3	K3YET3_SETIT	Uncharacterized protein (Fragment)	Si012750m.g	Setaria italica (Foxtail millet) (Panicum italicum)	516	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3YET3|K3YET3_SETIT Uncharacterized protein (Fragment) OS=Setaria italica GN=Si012750m.g PE=4 SV=1SRLGSISKCANYFFRRSYMVLQRNPLNPLLVHLIYFMSISFTGFLALKSLTPQHKPIPRSLDLAFTSVSTLTVSSMATVEMEDFSD QQLWVLILLMLLGGEVFTSMLGLHLKNARANTYDILQKRLPSTCRDIEFVDSVNRSCWNNMEDINPEATTSHKQVQESKSMNQNYCN ILAHVVAGYFVVCIICSCLVITIYIWTDSEAKYLLKSKNIKIWTFSIFTAVSSFVNCGFTPVNDNMAIFRKNRGILLLVIPQIPAGNTLFTPLL RLSIWALGRISRREEYTYILQYPVETGYMHMQQKKNVINLVLAAVGIILLQVMFLCYFGWDSKPMEGLKWFQKLVCTLFQSVNRRHAG ETVIDISNLPPAILVLFALFMYLPSDGSSLPNSVDDQTLTEKGEDKNSRTLWKNFIISKPTCLATFIILACITERKSMSLDPLNFNIFSIVFE VVSAYGNVGYSLGYSCERLLKPDATCKAVSYGLVGKWTDEGKLIIILVMFLGRFKRFGLRARKPRVSM
6E-29	110	25	9.5E-28	106.3	11.6	3.4	2	B9IN02_POPTR	Sodium transporter family protein	POPTR_0018s13210g	Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa)	506	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Malpighiales, Salicaceae, Saliceae, Populus (poplars), Populus trichocarpa (Western balsam poplar) (Populus balsamifera subsp. trichocarpa)	3694	>tr|B9IN02|B9IN02_POPTR Sodium transporter family protein OS=Populus trichocarpa GN=POPTR_0018s13210g PE=4 SV=1MCSIRSFLRVLVFQIHPFWVQLAYFVILSLVGHMALKVSKPRPGSLRPASLDIFFTSVSSATVSSMSTVEMEVFSNTQLIIMTILML LGGEVFTSILGLYLSRFKFSKHETKESRVSSVYHNPPKRTNFPGLEIEKPTNVDLECNLNSLDNDHSLKLNSLKSLACVALGYFSVVHIT GSSLVAMYTSLVPSARQVLGSKGIKIQTFSVFTTVSTFSNCGFVPTNENMVAFKKNSGLLLILPIQILLGNTLYPSCLRFLIWILEKITRKV EFRYILMNTREMGYGHLLSFSHSCLLAITVSGFILVQFILFCSMEWNSGAKDGLNPYQKLMGALFQVVNSRHTGESIVDLSIISPAILVLF VVMMYLPPYTSFMPKKQQEEVDSETGQKCKNQRKSLVQCLLFSPLSTLAIFVILICVSEREKLKKDPLNFNVLNITIEVVSAYGNVGFST GYSCKRQLEPDSSCKDAWFGFVGRWSNMGKFILILVMFFGRLKKFSINGGKAWKLS
6.8E-29	110	11.8	4.9E-27	104	6	3.4	1	C5YFK1_SORBI	Putative uncharacterized protein Sb06g027900	Sb06g027900 SORBIDRAFT_06g027900	Sorghum bicolor (Sorghum) (Sorghum vulgare)	563	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Andropogonodae, Andropogoneae, Sorghinae, Sorghum, Sorghum bicolor (Sorghum) (Sorghum vulgare)	4558	>tr|C5YFK1|C5YFK1_SORBI Putative uncharacterized protein Sb06g027900 OS=Sorghum bicolor GN=Sb06g027900 PE=4 SV=1MAGAHKFAGFLQHLRRCSAAVLDSAMSLVCSVSKAYAHHQVMERVARSRRTLRCSAGQAWRRAADVAARLNSLLVHVVYFV AISCVGWGLLDALKVRAPSGRRPRGIDTFFTAVSAATVSSMSAVEMEVFSHGQLLVLTALMFGGGEVFLSLVGLASKWSKMRKQIMN RSRRVESHDDDDIELETTTAAEADSRSITTAVTEENDDDIPVDAKVLRRNAVRSLFFIVLGILLVVHVVGAVAVAAYVYAAPGARQTLRR KALNVWTFSVFTTVSTFSSCGFMPTNENMMVFSRDVPLQLLLVPQALVGNTLFPPLLAACVWAAAAATRREEMVEIARKGREATGYY HLLPARRCWMLAGTVGGLIAVQVALVCGMEWGGALRGMSAGEKLSNALFLAVNSRHTGESTLDLSTLATAILVLFVLMMYLPPYTTW FPFEENSKRGHHSTESQGIRLLKSTVLSQLSYLTIFVIAICITERRKLKEDPLNFNVLSIVVEVVSAYGNVGFSMGYSCSRQINPDGLCT DRWTGFAGRWSDSGKLILIAVMFFGRLKKFSMKGGKAWKLS
8.4E-29	110	26.5	4.4E-19	77.7	5.4	2.2	2	K0IIC4_NITGG	K+ transporter family protein	Ngar_c27540	Nitrososphaera gargensis (strain Ga9.2)	617	cellular organisms, Archaea, Thaumarchaeota, Nitrososphaeria, Nitrososphaerales, Nitrososphaeraceae, Nitrososphaera, Candidatus Nitrososphaera gargensis, Nitrososphaera gargensis (strain Ga9.2)	1237085	>tr|K0IIC4|K0IIC4_NITGG K+ transporter family protein OS=Nitrososphaera gargensis (strain Ga9.2) GN=Ngar_c27540 PE=4 SV=1MASYATNRFLLIDGRTNVAVAVRQMQVNKMEAIVVTHGGSPVGIVTDSDILEKVVIKGEDSDEVLLKDVMTSPIITLPKGSTGKEA LESMKSNKIKRILITDRENGGNDRIIGMVTQKTLANAVRTSVIERTFRKYRASIRERYKPVLGNLGFVMQFAGILMVVPAFLGTAHEEFA PTTGMYLAVVGMFSTGFVLNAYGERGPLSLKEASILVISSFILLSFFGSFPYMYLNPFWPEIDGLSLFVNSFFESISGFTTTGMTMITQP ENLPQSFVFFRSYTQWIGGLSFIYLIMAIFYPEKKLKAIRGVLGGDALEYRQLIVTIVLIFSAYTAVLFLILLFLNVSNPVYDISLVFSAIVGG GFTPDSTIVSVGNIVHLLVASVAMIISALPFAFHYSIFYKSMRIRKIGIEVLAYIVLLVTSAAILAAIAGIEWLPAAFHSVSASTNTGFQFVDI QVLPTEAKIVMIVLMLIGGTAFSTAGGIKIGRFLLLFQKLVKRTDMIETPSSISRLAVVPDQAIDFKAKKESDKLLRETLLVIALFPAVAVLS GLALGYLNNANTLDAVFSSTSSLTNTGLQVGLVSMDSDLITKSILAANMIAGRFEIIAILYIFFASLRRV	1237085	
8.6E-29	110	29.9	1E-26	102.9	13.7	3.6	2	A0A0D3AT80_BRAOL	Uncharacterized protein		Brassica oleracea var. oleracea	507	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica oleracea (Wild cabbage), Brassica oleracea var. oleracea	109376	>tr|A0A0D3AT80|A0A0D3AT80_BRAOL Uncharacterized protein OS=Brassica oleracea var. oleracea PE=4 SV=1MERVGARILAKIRSQVFAKHLSPLCLYFIYFLTFSILGFLALKISKPRITSRPHDLDLFFTSVSALTISSMSTIDMEVFSNTQLIFLTIL MFLGGEVFTSFLNLYFSHFTKFVYPHNKVRHLTDSFDLDRRMEEPRIDIENVIDHQEGSIQMIERASKCLYSVVLGYHVITHLVGSLLVL VYVNFIKTARDVLSSKDISPLTFSVFLTVSTFANGGFVPTNENMIIFRRNSGLLWLLIPQGLMGNTLFPCFLVLIIWGLYKITKRNEFGYIL KNHKKMGYYHLLSVRVCILLGLTVLGIFLLQFLLFCTFEWSSESLEGMSWYEKLVGSLFQVVNSRHTGETIVDISTLSPATLIFFITMMFL PAYTLFIPLTKENNNKDEEEDSGNGNKRKRSGFFVSQLSFLVICIFLVSIVEEEQLRRDPLNFNVFNITLEVISAYGNVGFTTGYSCKRR LDASDGVCKDASYGFVGRWSPTGKIILILVMLYGRFKHFTSKSGRAWILYPSSF
9.5E-29	110	27.6	1.9E-28	108.6	19.2	1.4	1	C4FFV5_9BIFI	Cation transport protein	BIFANG_03220	Bifidobacterium angulatum DSM 20098 = JCM 7096	486	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium angulatum, Bifidobacterium angulatum DSM 20098 = JCM 7096	518635	>tr|C4FFV5|C4FFV5_9BIFI Cation transport protein OS=Bifidobacterium angulatum DSM 20098 = JCM 7096 GN=BIFANG_03220 PE=4 SV=1MARDLDEPVEAEHRFKITLSRLRTGKSKSSSPARRIRRVSLTDHLFSHPGRLSIMYFMALIVIATALLLLPFATQTGEITSFPVAFFT AVSALSTCGIQVVNTNTYWSFFGQIVILFSIQLGGLGVMTFASIVALGISRRLRVSQRMLTANELGTNKLSEIKSVITVVLTITAITEALTFT LLLPELLRVNNENDAGRTLWQAIFYAVSAYNNTGFTPDTSGLYVSNWGVGLPILISAFIGTLGFPVVLNVVQCARKRQSPRHWSLHTK LTLVTTAILVAASLVWFLIVEWHNVNLFPDDDLSLKFRRAMVAAVMPRSAGFDISWVPGVSSESKLFMSIIMFIGAGSSSTGGGIRVTT FAVIMLICGAAFTGHRDVTVFRRRIPRRIQMTAISVTTSCLSLVAIASMALMFVTDCSLGDAVFETCSAFSLGGYSVGVVSAGNPASQFI LAATMIIGRLGPMTIAYSISRPLAPEPIRYPQENVIVG
1.1E-28	110	23.5	1.6E-28	108.9	16.3	1.2	1	Q8G5G7_BIFLO	Uncharacterized protein	BL1045	Bifidobacterium longum (strain NCC 2705)	488	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium longum, Bifidobacterium longum (strain NCC 2705)	206672	>tr|Q8G5G7|Q8G5G7_BIFLO Uncharacterized protein OS=Bifidobacterium longum (strain NCC 2705) GN=BL1045 PE=4 SV=1MANDFDESSANEEASKGLSWWYSADVLSRDKSDKTAKRIRRISITDRLLRHPGRLSMVYFGALIIVTGLLLLPISTSDIIFTNFPIA FFTAVSALSTCGIPVVNTGEYWSMFGQVVVLFSIQFGGLGVMTFASMVALGVSRRLKVSQRMLTANELGTTKLSEVKGVLTVVLGTSI IAEVLTFVLLLPDLFRVNHGNMGRTLWQALFYAVSAYNNTGFTPDATGLHVNRWGVGLPILISAFIGTLGFPVVLNLVQCARRRLSPKR WTLHTKLTLVTTAVLVATSLAWFLLVEWSNTGLFPADDPGMKMRRAMSAAVMPRSAGFDISWVPEVTNETKVFMSILMFIGAGSSST AGGIRVTTFAVILLICRAAFTGHRDVTVFRRRIPRRIQMTAVSVTTACFALVMVGAMMLMFTTGCAFVDAVFEACSAFSLGGYSVGVA SAGNPASLFILSAEMIVGRLGPLTIAYSISRPMAPEPIRYPQENIIVG

1.2E-28	109	18.4	1.8E-27	105.4	12.7	1.9	1	R7MDX8_9CLOT	Trk system potassium uptake protein trkG	BN790_01104	Clostridium sp. CAG:813	283	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:813	1262843	>tr|R7MDX8|R7MDX8_9CLOT Trk system potassium uptake protein trkG OS=Clostridium sp. CAG:813 GN=BN790_01104 PE=4 SV=1MPVYDSICNSMSTMSAGGFSPHPQSIGGYNSNVINWIIIIFMFIAGTSYTLQSRVLTRRRLSLFWKSEEFRTYATIVLFVSLALSGI LYFEHHYSLIHSLTAGFYQMLSISSSTGSASEDFQLWNFDAHVILFFCLFISSCSGSAGGGLKLTRWILIFKFIKNEIYKILHPNAVVPVKI DGKVVSTDVVRQTIFFIFAFFGLWAISATFLTVTEQNLEIGLTSAITSIGDIGPGLGNVIGPMGNYSSLHSFSKIIFIFNMLVGRLEIIPFLVL FHKDFWTIKR
1.2E-28	109	27.7	2.9E-28	108	19.2	1.5	1	C7MLJ9_CRYCD	Trk-type K+ transport system, membrane component	Ccur_00720	Cryptobacterium curtum (strain ATCC 700683 / DSM 15641 / 12-3)	510	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Cryptobacterium, Cryptobacterium curtum, Cryptobacterium curtum (strain ATCC 700683 / DSM 15641 / 12-3)	469378	>tr|C7MLJ9|C7MLJ9_CRYCD Trk-type K+ transport system, membrane component OS=Cryptobacterium curtum (strain ATCC 700683 / DSM 15641 / 12-3) GN=Ccur_00720 PE=4 SV=1MWQRYTFYDLRVIAHYLGVLLVYTGAAMAVPLVTAAASSEWEPAARYLFSMGIALTVGSAMRMLRIEPGRLNRQQAIAVTSFA WIVVAAIAAIPLALSPHYQSYLNALFDSVSSFTTTGVTIISNPDHISNADNMWRFISVYAGGAGLVVVAMSFGLFGRVADSSLYESEGR SEHVLPNVVQTARFILRFSLAVIVVASIVLAAICLLHGMQVPRALLHGFWLAVSGYMTGGLTPMSTSITYYHSVMVEGVLMVLMLLGSV SFLLQSEVLRGRVQGYFRDIEVRTAVVWIGIMLALFIVTLSSSTLMRSLPELARTGLFTFISAATTTGFSTLTSNQLTSIMPSGALLILALV MSVGGASGSTAGGIKLKNIAIIGKSAFETLKGVASPDSARVVTTYYHIGRRRCLGAEEVKRAMTVFTMFVIMYIVGALVGVAHGYDAVSA ITESVAMASNGGISTGITQASMPALLKIMYIAEMWAGRLEFITLLAVGVKICASLRARGLLGARKGRS
1.4E-28	109	32.4	1.5E-22	89.2	8.4	3.8	3	A0A0D3B7Z4_BRAOL	Uncharacterized protein		Brassica oleracea var. oleracea	514	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica oleracea (Wild cabbage), Brassica oleracea var. oleracea	109376	>tr|A0A0D3B7Z4|A0A0D3B7Z4_BRAOL Uncharacterized protein OS=Brassica oleracea var. oleracea PE=4 SV=1MDRVAGRKFCKIRSKLYKSRSCFLNFVYFLSFSFLGFLAVKVSNPRTTSRPHDLDIFFTSVSAITVSSMSTVDMEVFSNTQLIIITIL MFIGGPIFTSFLNIYLSHFTKFVFPHSKIKHFIGSFKADHTIEDLRLDQENITDRHEIPSQTNEKASKCLYLVVIGYHLVTNIAGSMLLLVYV SFVKTARDVLRSKEISALTFSIFTTVSTFATCGFVPTNENMIIFRKNSGLLWLLIPLVLMGNTLFPCFLRLLIWGLSKTTKREEFGYILKNR KKMGYSHLLSVRLCVFLGLTVLGFILIQLFLFCTFSWSSESLAGMNWYEKLVGSLFQVVNSRHTGETIVDLSTLSPAILILFILMMYLPPY TLFMPFTMKKKNKKEEENDSGYKKGGKKSGLLVSQLSFLVICIFLISITERQKLRRDPLNFNVLNITLEVVSAYGNVGFTTGYSCERRLN VSDGGCEDAGYGFAGRWSSSGKFILIIVMFYGRLKQFTAKTGRAWILYPSRLPDTRYIQV
1.4E-28	109	11.1	2.8E-26	101.5	4.3	3.5	2	I1J1J8_BRADI	Uncharacterized protein	BRADI5G21030	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	539	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Brachypodieae, Brachypodium (false bromes), Brachypodium distachyon (Purple false brome) (Trachynia distachya)	15368	>tr|I1J1J8|I1J1J8_BRADI Uncharacterized protein OS=Brachypodium distachyon GN=BRADI5G21030 PE=4 SV=1MAEAHPRRVLSTSSSALELHKAMLSAMSSLVTDRVARLRRALRTPLRLGSLLLHAAYFLAVSFLGYLILRTLSFRVSRRPRGIDVF FTAVSAATVSSMSTVEMEAFSNSQLIVITFLMFLGGEVFVSLAGLASQWHSLRKDATHKSQRVESHAELEMPISATTVDLEDDNNDNR NTSSPTMDAKKRRLGAVRALFWVVLSVLLSAHVLGAVTVAAYVARGAAATRRTLREKALNVWTFAAFATASTFSSCGYLPTNENMIP FKRDVGLQLLLIPQALLGNTLFPPLLWACVRALAAALMPMPMLADMARHGSRELTGYCHLLPAKRCAMLAATVAALVAVQVALVCGM EWGGALAGMGPWEKMVNAAFLAVNSRHTGESTIDLSTLAPAVLVLFVLMMYLPPYTTWFPFEETSSTKDHHPKQSQLGIKLIKSTVL SQLSYLTIFVIAICITEARKLKEDPLNFNVLSIVVEVVSAYGNVGFSMGYSCSRQINPDQLCTDRWTGLAGRCSDSGKLILILVMFFGRL KKFSMKGGKAWKLS
1.7E-28	109	22.4	2E-27	105.2	8.6	3.4	2	G7KJW5_MEDTR	High-affinity potassium transporter (Uncharacterized protein)	MTR_6g092820	Medicago truncatula (Barrel medic) (Medicago tribuloides)	522	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago (medics), Medicago truncatula (Barrel medic) (Medicago tribuloides)	3880	>tr|G7KJW5|G7KJW5_MEDTR High-affinity potassium transporter OS=Medicago truncatula GN=MTR_6g092820 PE=4 SV=2MNILSTSCQKLVCLSKSIYISAACLYRFILLRSNPLCVQIVYFISISTLGFGFLKALKPLGQTQKNLDLFFTSVSSTTVSSMVTVEMGI FSNTQLIIITILMFIGGEVFTSLVGLFFIRSRLKIDLDKIASSHARLASRNPFIIVDRFHLEDEMVTNEVHKHESLSTTNENLRYLSMKYLGY VVIGYILFLHVIGVIGVSLYLTIIPSTKQLLKNKGLKMLTFSVFTIVSSFSSCGFVPTNENMIDFRKNSGLLLMLIPQLLLGNTFYPPCLRLCI CGLGKFYKKRECRYLLKHSEKVGYKHLLQRKHTIFLVATNCGLIVVQVTLFCVMDWNSKGLKGLNFYQKLIGVLFQSVNSRHAGTSIV DISILSQAILVLFVVMMYLPPYTSFLPLKYDGKISENSKKMKKRRGKVTENLIFSQLSYLVIFIILVCITERKKLKEDPLNFNVLNIVVEVISA YGNVGFSTGYSCELQLHPETNCENKWIGFVGKWSDEGKIILIFVMLFGRLKKFNMDGGKAWKLH
1.9E-28	109	27.7	1.6E-22	89.1	6.8	3.6	3	M4EWK5_BRARP	Uncharacterized protein	Bra033189	Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	507	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica campestris (Field mustard), Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	51351	>tr|M4EWK5|M4EWK5_BRARP Uncharacterized protein OS=Brassica rapa subsp. pekinensis GN=Bra033189 PE=4 SV=1MERVGARILAKIRSQVFAKHLSPLCLYFIYFLTFSILGFLALKISKPRITSRPHDFDLFFTSVSALTISSMSTIDMEVFSNTQLIFLTIL MFLGGEVFTSFLNLYFSHFTKFVYPHNKVRHLTDSFDLDRRMEEPRIDIENVIDHQEGSIQMIERASKCLYSVVLGYHLITHLVGSLLVL VYVSFIKTARDVLSSKDISPLTFSVFMTVSTFANGGFVPTNENMIIFRKNSGLLWLLIPQGLMGNTLFPCFLVLIWGLYKITKRNEFGYIL KNHKKMGYYHLLSVRVCILLGLTVLGFFLFQFLLFCTFEWSSEPLEGMSWYEKLVGSLFQVVNSRHTGETIVDISTLSPATLIFFITMMF LPPYTLFMPLTEENNNKDEEDDSGNGNKRKRSGFFVSQLSFLVICIFLVSIVEEEQLRRDPLNFNVLNITLEVISAYGNVGFTTGYSCKR RLDASDGVCKDASYGFVGRWSPTGKIILILVMLYGRFKHFTSKSGRAWILYPSSF
2.3E-28	108	28.5	3.3E-18	74.9	9.5	3.8	3	HKT3_ORYSJ	Probable cation transporter HKT3 (OsHKT3)	HKT3 Os01g0532600 LOC_Os01g34850 OJ1619_F12.15	Oryza sativa subsp. japonica (Rice)	509	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>sp|Q8L481|HKT3_ORYSJ Probable cation transporter HKT3 OS=Oryza sativa subsp. japonica GN=HKT3 PE=2 SV=1MPIRLHIFVNSARHAINSSAFICRFIAYHLSPLLIHLSYFLIIDILGFVSLVVLRPSNHKYNPRYVDMFFLSTSAVTVIGLATIQMEDLS SSQIAILTLLMFLDSKMFLSFLGLVLESSKQNKHDPENRRVSSVTVCKQSQLEEATPQTPSMNSIDIKKRCLKYLVFVVLAYMIIILVTGS LLVFMYIAHVSSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMVVFSSNNGLLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKAE EPDFMMNNSSAVGFSHLLPNLQTIFLAVVEVAFVAMTVILFCCLNWDSVVFAGLSSLQKITNALFMAVNARQAGENSIDCSLVAPAALV LFMVMMYTPSLTKLFSACQDHKRIGPESDDRTSKGKPFLKMMAFSPLGFNTTVIMLVCITERRSLSTDPLNLSTFNIIFEVISAYGNIGLS TGYSCSRQLQHQEGIACHEKAYNFSGWWSEPGKLILVLAMLCGRLNSKDSTSARTR
2.3E-28	108	28.5	3.3E-18	74.9	9.5	3.8	3	Q0JM66_ORYSJ	Os01g0532600 protein	Os01g0532600	Oryza sativa subsp. japonica (Rice)	509	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>tr|Q0JM66|Q0JM66_ORYSJ Os01g0532600 protein OS=Oryza sativa subsp. japonica GN=Os01g0532600 PE=4 SV=1MPIRLHIFVNSARHAINSSAFICRFIAYHLSPLLIHLSYFLIIDILGFVSLVVLRPSNHKYNPRYVDMFFLSTSAVTVIGLATIQMEDLS SSQIAILTLLMFLDSKMFLSFLGLVLESSKQNKHDPENRRVSSVTVCKQSQLEEATPQTPSMNSIDIKKRCLKYLVFVVLAYMIIILVTGS LLVFMYIAHVSSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMVVFSSNNGLLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKAE EPDFMMNNSSAVGFSHLLPNLQTIFLAVVEVAFVAMTVILFCCLNWDSVVFAGLSSLQKITNALFMAVNARQAGENSIDCSLVAPAALV LFMVMMYTPSLTKLFSACQDHKRIGPESDDRTSKGKPFLKMMAFSPLGFNTTVIMLVCITERRSLSTDPLNLSTFNIIFEVISAYGNIGLS TGYSCSRQLQHQEGIACHEKAYNFSGWWSEPGKLILVLAMLCGRLNSKDSTSARTR

2.4E-28	108	17.6	1.5E-19	79.2	0.9	3.5	3	I1J1J7_BRADI	Uncharacterized protein	BRADI5G21017	Brachypodium distachyon (Purple false brome) (Trachynia distachya)	537	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Brachypodieae, Brachypodium (false bromes), Brachypodium distachyon (Purple false brome) (Trachynia distachya)	15368	>tr|I1J1J7|I1J1J7_BRADI Uncharacterized protein OS=Brachypodium distachyon GN=BRADI5G21017 PE=4 SV=1MKLPISSFEVLRIIMVKVNHFQELVSTRLGSLSKCTADLFRRSYLLLLFQSNPLIVQIIYFMLLPLAGFLALKNLKPLNKPTTRNLDL MFTSVSTVTVSSMATVEMEDFSGQQLWILILMLFGGDMFTKMLGLHLKNARGNTGDTLPKRSSFISRDIETCDVFNNNSQNNMEAIQ SEATIPHNKVQESKGLNLNSCNILAHVVTGYFIAAIVCGSVVITIYLLIDSDARQLLKSKDIKICTFSVFTAVSSFANCGFTPVNDNMAIFR NNPTLLLLVTPQILIGNTLFPPLLRLSIWALGKVSRREEYAYILQHPKEIGYRHLRPYKNSVHLVLTGVLIILLQAIFLCYFEWDSKALEGM KWFQKLVGSLFQSANSRHAGETVINISTLSPPILVIFAVVMYLPSDTSFFPTYGDRHILTNKKENPNSRAMWKKFIITKPACLAILTILACI TERKSMSADPLNFSIFSVVFEVISAYGNVGYSLGYSCDKLLKPDPRCKDFSYGFVGRWTDKGKVIIIVVMFLGRFKTFTLNGRKP
2.8E-28	108	8.5	3.2E-28	107.9	5.9	1	1	R5QEK8_9FIRM	Uncharacterized protein	BN734_00994	Ruminococcus torques CAG:61	210	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus torques CAG:61	1263108	>tr|R5QEK8|R5QEK8_9FIRM Uncharacterized protein OS=Ruminococcus torques CAG:61 GN=BN734_00994 PE=4 SV=1MYLGVVAAAIVTITINILSMYETVAHAFRYASFQVGAIITTTGFYTADFEQWPELSKTILMMLMVIGACGGSTGGGIKVSRFMILCK SIRQEIHKMLHPNAVTMVRMNGKKVGADTMRSINIYFSAYVFIIIVSVLLVSLDNFDFATSFSGVLTTINNVGPGISQVGPTDNFHAFSAL SKIVFSFDMLFGRLEIFPYLLILSPDLWRKRF
3E-28	108	0.4	6.5E-28	106.9	0.1	1.6	1	C9SNX4_VERA1	Putative uncharacterized protein	VDBG_06599	Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) (Verticillium wilt of alfalfa) (Verticillium albo-atrum)	440	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Plectosphaerellaceae, mitosporic Plectosphaerellaceae, Verticillium, Verticillium alfalfae, Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) (Verticillium wilt of alfalfa) (Verticillium albo-atrum)	526221	>tr|C9SNX4|C9SNX4_VERA1 Putative uncharacterized protein OS=Verticillium alfalfae (strain VaMs.102 / ATCC MYA-4576 / FGSC 10136) GN=VDBG_06599 PE=4 SV=1MTFREGDCVPSPLSSRRRIYGILLPVGREETGCAEEDSLSWYELIRHADAWILLCSLSAFPVLYTYGNLTAEDALLFGCSASTES GLNPVDVKDLKTYQQVYLYVVPIITNMMFLNAIVVPVRLFWFRQRLRQAGIAREVTRNDEEEARPATRRESQETAFIDEPAPALAPAPS PPFSAPQRTTTITFDDKAIASGYSRSEKQVLRIPNPRESDRGAPITEIEPGLRRSYTEEDPDAIKPLPEFRSGRSRRSSFHAEGTILSAA TSIEKAATSAFILGKVRPAPRRRTTSKSRVSANNKLDLPNLSRHATVGRNSNFHNLTEADRETLGGIEYRALKLLLKFVFGYFFGLHFF GAICLLPWIHNAPSKYLDVLAESGVGATWWAFYSAQTMSNNLGFALTPDSMASFKDATWPLLVMTFLAFAGNTCYPVSYAVSSGLH H
3.4E-28	108	25.3	3.4E-27	104.5	9.6	3.4	2	A0A072UBR1_MEDTR	High-affinity potassium transporter (Uncharacterized protein)	MTR_6g092940	Medicago truncatula (Barrel medic) (Medicago tribuloides)	545	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago (medics), Medicago truncatula (Barrel medic) (Medicago tribuloides)	3880	>tr|A0A072UBR1|A0A072UBR1_MEDTR High-affinity potassium transporter OS=Medicago truncatula GN=MTR_6g092940 PE=4 SV=1MEILGCYMKKFQLLCNTSFQKFACLTKSFFFLGICFYRFILLRANPLCVQILYFISISFFGFGFLKALNPLYQTSPKNLDLFFTSVSS TTVSSMSTVEMEFFSNPQLIIITILMFIGGEIFTSMLGLYFIRLKLKTDLGKIDSSHARFAFANPIIVDQIQIEVEMVTNSNPHITSLSNPNIK SHEPLSTTSENLRYLSMKYLGYIVLGYIIILHIIGVFGVSLYLAMIPSAKQVLENKGLKMFTFSLFTIVSTFSSCGFIPTNENMVVFRKNSG LLLILIPQLLLGNTLYPPCLRFCIWVLGKFYKKKECRYLLNNVEEVGYKHLLHWKHTLYLMATVFGFIIIQVTLFCLMDWNSEGLKELNYY QKLIGVLFQSINSRHAGETIVDLSIISQAILVLFVLMMYLPPYTSFLPWEDNGKMSESSERKQNKRREKVTENKILSRISYLVIFIILVCITE RKQLKDDPLNFNVFNIAVEVVSAYQNVGFTMGYSCERQLHREANCENKWIGFVGKWSDEGKIILILVMLLGRLKKFNTDAGNPWKLL
3.5E-28	108	27.7	4.1E-26	100.9	13.9	3.5	2	F6I5Q6_VITVI	Putative uncharacterized protein	VIT_11s0103g00130	Vitis vinifera (Grape)	556	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, rosids incertae sedis, Vitales, Vitaceae, Vitis, Vitis vinifera (Grape)	29760	>tr|F6I5Q6|F6I5Q6_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_11s0103g00130 PE=4 SV=1MMISASFVGKRLHRLCTCLSFKLECLGRSIWFLVSSFYSLVVLRVNPFWIQLCYFPCLSFQGFLVLKALKPRTYSFRPRNLDLFF TSVSAATVSSMSTVEMEVFSNNQLLILTLLMFVGGEVFTSMVELHLRRSKLEKPWIAENKIDSVTSINGSAPLSPGKPFGQVELRVVTV PSTDKYSKLETEQVHRQIEGQTESLSTSESLKYRSIKFLGFVVMGYLVVVHVVGVALVSAYVALSSARDVLKQKGLKLFTFSLFTTVS TFASCGFVPTNENMIVFSSNSGLLLIIPQVLLGNTLFPSCLRFSIWTLGKFFNKAESNYLLMNAREIGFLYLLPSLHSTLLVPTVLGFILIQ FTLLCSMDWNSEGLNGLNSYQKIIGALFQSVNSRHTGETIVDISILSPAILVLFVVMMYLPPYTSFLPIEDYEQSSPTCSGRRRRKRGKI VENLIFSQLSYLVIFIILICITERKNMKDDPLNFTVLNIVIEVISAYGNVGFTAGYSCERLMKPDSSCQSKWFGFSGKWSDEGKIILILAMF FGRLKKFNMDGGRAWKLL
3.5E-28	108	18.5	4.7E-19	77.7	7.2	2.7	2	M0S2H4_MUSAM	Uncharacterized protein		Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	461	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Zingiberales, Musaceae, Musa, Musa acuminata (Banana) (Musa cavendishii), Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	214687	>tr|M0S2H4|M0S2H4_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1MPPPSTVMDITFHRNSLIHLLSQVNPFWIQFFYFLSSSITGFLLLKLLPTRDATSRPTNVDLLFMSVSANTVSSMDTMEMEVFSN YQLAMRDSALDAAGTELATLSDQRRSSDLKFSSRKHLFFVVLGYLLVGHVVGFLLILVYLRLVPEAGAVLERKGINASLFSIFITVSTFAN CGFVPTNENMVVFRTYSGLLLILTVQVLVGNTLYASCLWAVIWLLKKLTKRREYDYLLTNYGEMECNHLLPGSHSLYLALTVAGLVLVQ FGLFCCMEWTSEILSGLSTYQKVVGVVFQCVNSRYAGETIVDLAAVAPAILVLFVVMMYIPPYTCFLPRKGDKQLLKGRERSRKKQGL SLIFSPLSYIAIFTIIACITERRQISEDPINFSVLNIVVEVVSAYGTVGFTTGYSCKRQVKADVHCKDVSAGFSAKWSSKGKLVLIVVMLFG RLKRFSMRGGKHWKFI
4.3E-28	108	29	2.5E-27	104.9	12.8	3.7	2	M4C929_BRARP	Uncharacterized protein	Bra000707	Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	585	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica campestris (Field mustard), Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	51351	>tr|M4C929|M4C929_BRARP Uncharacterized protein OS=Brassica rapa subsp. pekinensis GN=Bra000707 PE=4 SV=1MTHGAVGSSSAASSAANRLHQENRGRFATCSDKRKQATPPSKEAQWSFVQHGKNTTGGSGQARSMFQMREMISGGTISLK RIYSRNSTRLVISIVGYQYHKKPKENSQDRNNGLGFLALKVFKPRATSRLHDLDIFFTSVSAITVSSMSPVDMEVFSNTQLIIITILMFIGG PIFTSFFNIYLSHFTKFVFPQSKIKHLIGSFKADHTIEDRHLDQENINDRHEIPSQINEKASKCLYLVVIGYNLVTNIAGSMLLLVYVSFVKT ARDVLRSKEISTLTFSIFTTVSTFATCGFVPTNENMIIFRKNSGLLWLLIPLVLMGNTLFPCFLRLLIWGLSKTTKREEFGYILKNRKKMG YSHLLSVRLCVFLGLTVLGFILIQLFLFCTFAWSSESLAGMNWYEKLVGSLFQVVNSRHTGETIVDLSTLSPAILVFILMMYLPPYTLFM PFTIKKKNKKEEENDSGYEKGGKKSGLLVSQLSFLVICIFLISITERQKLRRDPLNFNVLNITLEVVSAYGNVGFTTGYSCERRLNVSDG GCEDAGYGFAGRWSSSGKFILIIVMFYGRLKQFTAKSGRAWILYPSSS
4.5E-28	107	23.1	2.1E-17	72.2	11.5	2.9	2	I1NNS1_ORYGL	Uncharacterized protein		Oryza glaberrima (African rice)	492	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza glaberrima (African rice)	4538	>tr|I1NNS1|I1NNS1_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1CLFGCISLSILQGMPSTHRHSFVGSSHTILARFXFTYPIFLSLMYLVLFPWWCSGQATTSTILAMLICFSYQHLQLQSQDXPPYK WRIFPALRXLSXLSXCSXAVRCSFPFLALSLSQASKTNMILKTVESVQLLCASNHSXRCLKYLVFVVLAYMIIILVTGSLLVFMYIAHVSSA RDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMVVFSSNNGLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKAEEPDFMMNNSSA LGFSHLLPNLQTIFLAAVEVAFVAMTVILFCFLNWDSVVFAGLSSLQKITNALFMAVNARQAGENSIDCSLVAPAALVLFMVMMYTPSL TKXFSACQDHKRIGPESDDRTSKGKPFLKMMAFSPLGFNTTVIMLVCITERRSLSTDPLNFSTFNIIFEVISAYGNIGLSTGYSCSRQLQ HQEGIACHEKAYSFSGWWSEPGKLILVLAMLCGRLNSKDSTSARTR
5.2E-28	107	27.6	8.2E-26	99.9	13.4	3.6	2	F6I5Q5_VITVI	Putative uncharacterized protein	VIT_11s0103g00150	Vitis vinifera (Grape)	551	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, rosids incertae sedis, Vitales, Vitaceae, Vitis, Vitis vinifera (Grape)	29760	>tr|F6I5Q5|F6I5Q5_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_11s0103g00150 PE=4 SV=1MMNSASFTGNKLHRLCTCSSFKLECLGRSICFLVSSFYRFVILRFNTFSVQLCYFLCLSFQGFWVLKALKPRTPLRPRNLDLFFT SVSAATVSSMSTVEMEVFSNNQLLILTLLMFVGGEIFTSMVELQLWRSKLKKPLIAENQVNSVSNNSSAPPDPRNPFGQFELRVVTVP STSNSTLETDEVQSQIEGRTKSLSSESLKYHSIKFLGFVVMGYLVVVHVLGVTLVSAYIALVSSARDVLKQKGLKLFTFSLFTTVSTLAS CGFVPTNENMIVFSKNSGLLLIIIPQVLLGNTLFPSCLRFSIWTLGKFKKVESNYLLTNTREIGFLHLLPSLHSTLLVPTVLGFILIQFTLFC SMEWNSEGLNGLNSYQKIIGALFQSVNSRHTGETIVDISILSPAILVLFVVMMYLPPYTSFLPTKGDEQSSEICNGGRKRRRGKIVENLI FSQLSYLAIFIILICITERRKMKDDPLNFTVLNIVIEVISAYGNVGFTAGYSCERLLKPDSSCQSKWFGFSGKWSDEGKIILIFVMFFGRLK KFNMDGGRAWKLL

5.5E-28	107	22.7	1.4E-18	76	11.5	3.5	3	W5HB56_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	508	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5HB56|W5HB56_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MPVRLHTFLSSARHISNSSVFIFQFIAFHLSPLLIHLSYFVVIDVLGFAALMALKPSNPNYSPRYVDIFFLSTSAVTVTGLATIKMEDL STSQVVILTLLMLLGSEMFVSLLGHIHELSKQNKHDPEDSRVTSVTVQDESQIEEAIPATPSINTTSLKKSCRKYIGFVLLAYMVLILLVG SLLVFLYVAHVSTARDVLTRKSINTMLFSISVTVSSFTNGGLIPTNESMAVFSSNQGLLLLLTGQILAGNTLLPVFLRLMIWALRGLRITR AKPEELEFMMNNTKALGSNHLLPNKQTVFLAASVAALIAVATVFFCCLNWESAVFAGLTPNQKITNALFMAVNTRQAGENSIDCSLVA PAVLILFIAMMCIPASTSFLSLHEGAERGITEHKDGANKRRMSLNKMLFSPLACTAVLIMLACITERRSLSADPLNFSTFNMIFEVISAYR NVGLSTGYSCARLPHAEKQSVCQDMPYSFSGWWSDQGKVVLVLVMLYGRLKCFHRQRS
7.2E-28	107	34.2	5.2E-24	94	8.1	3.7	3	V4L883_EUTSA	Uncharacterized protein	EUTSA_v10028594mg	Eutrema salsugineum (Saltwater cress) (Sisymbrium salsugineum)	505	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Eutremeae, Eutrema, Eutrema salsugineum (Saltwater cress) (Sisymbrium salsugineum)	72664	>tr|V4L883|V4L883_EUTSA Uncharacterized protein OS=Eutrema salsugineum GN=EUTSA_v10028594mg PE=4 SV=1MERIDAKFAKLGSQLAKFRSPFFLYLFYFFSFSVLGFLALKISKPRTTSRPHDLDIFFTSVSAITVSSMSTVDMEVFSNTQLIIITILM FLGGEIFTSFLQLYFSHFTKFVFPHYKIGHHMGSFNLECPITDPGSDLENVTDHVKISSQINERASKCLYSVVVSYLLVTTIAGSTLLLVY VNFVKTARDVLSSKEISPLTFSVFTAVSTFVNCGFVPTNENMVIFRKNSGLLWLLIPQALMGNTLFPCFLFFLVSGLDKITKRDEFGYILK NHKKMGYSHLLSVRLCVLLGLTVLGFVMIQFLLFCTFEWNSVSLEGMNSYEKIVVSLFQVVNSRQTGETVVDFATLSPAILVLFILMMY LPPYTLFMPLTEEKTKREGEDHCGNEKKGKKSGFFVSQLSFLAICVFFISITESQNLRRDPLNFNVLNITLEVISAFGNVGFTTGYSCER RLDISNGGCKNEGYGFAGRWSPTGKFVLIIVMFYGRFKQFTAKSGRAWILYPSSS
8.3E-28	107	14.1	8.3E-28	106.5	9.8	3.6	1	HKT8_ORYSI	Cation transporter HKT8 (OsHKT8) (HKT1;5)	HKT8 HKT1.5 SKC1 OsI_001542	Oryza sativa subsp. indica (Rice)	554	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>sp|Q2QWE2|HKT8_ORYSI Cation transporter HKT8 OS=Oryza sativa subsp. indica GN=HKT8 PE=2 SV=2MSSLDATTPRYDEFKRIYHLFLFHAHPFWLQLLYFLFISLLGFLMLKALPMKTSMVPRPMDLDLIFTSVSATTVSSMVAVEMESFS NSQLLLITLLMLLGGEVFTSILGLYFTNAKYSSKMIATLPDDDDHGGSGKPPPATTSPSSTLVELELAPPMDVVVVNPTTTATTHDEVEL GLGRRNKRGCTCTTTHTSSSSSASKTTTTRLLMFVVMGYHAVVHVAGYTAIVVYLSAVGGAGAVVAGKGISAHTFAIFTVVSTFANCG FVPTNEGMVSFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIAALERVTGWPELGELLIRRRRGGGEGYHHLLPSSRTRFLALTVAVLVVA QLALFCAMEWGSDGLRGLTAGQKLVGALFMAVNSRHSGEMVLDLSTVSSAVVVLYVVMMYLPPYTTFVPVQDKHQQTGAQSGQE GSSSSSIWQKLLMSPLSCLAIFIVVICITERRQIADDPINYSVLNIVVEVISAYGNVGFSTGYSCARQVRPDGSCRDLWVGFSGKWSKQ GKLTLMAVMFYGRLKKFSLHGGQAWKIE
8.3E-28	107	14.1	8.3E-28	106.5	9.8	3.6	1	HKT8_ORYSJ	Cation transporter HKT8 (OsHKT8) (HKT1;5)	HKT8 HKT1.5 SKC1 Os01g0307500 LOC_Os01g20160 OSJNBb0022N24.25 OSJNOa173H09.1	Oryza sativa subsp. japonica (Rice)	554	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>sp|Q0JNB6|HKT8_ORYSJ Cation transporter HKT8 OS=Oryza sativa subsp. japonica GN=HKT8 PE=3 SV=1MSSLDATTPRYDEFKRIYHLFLFHAHPFWLQLLYFLFISLLGFLMLKALPMKTSMVPRPMDLDLIFTSVSATTVSSMVAVEMESFS NSQLLLITLLMLLGGEVFTSILGLYFTNAKYSSKMIATLPDDDDHGGSGKPPPPTTSPSSTLVELELAPPMDVVVVNPTTTATTHDEVEL GLGRRNKRGCTCTTTHTSSSSSASKTTTTRLLMFVVMGYHAVVHVAGYTAIVVYLSAVGGAGAVVAGKGISAHTFAIFTVVSTFANCG FVPTNEGMVSFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIAALERVTGWPELGELLIRRRRGGGEGYHHLLPSSRTRFLALTVAVLVVA QLALFCAMEWGSDGLRGLTAGQKLVGALFMAVNSRHSGEMVLDLSTVSSAVVVLYVVMMYLPPYTTFVPVQDKHQQTGAQSGQE GSSSSSIWQKLLMSPLSCLAIFIVVICITERRQIADDPINYSVLNIVVEVISAYGNVGFSTGYSCARQVRPDGSCRDLWVGFSGKWSKQ GKLTLMAVMFYGRLKKFSLHGGQAWKIE
8.3E-28	107	14.1	8.3E-28	106.5	9.8	3.6	1	A0A0E0MVA4_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	554	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0MVA4|A0A0E0MVA4_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MSSLDATTPRYDEFKRIYHLFLFHAHPFWLQLLYFLFISLLGFLMLKALPMKTSMVPRPMDLDLIFTSVSATTVSSMVAVEMESFS NSQLLLITLLMLLGGEVFTSILGLYFTNAKYSSKMIATLPDDDDHGGSGKPPPPTTSPSSTLVELELAPPMDVVVVNPTTTATTHDEVEL GLGRRNKRGCTCTTTHTSSSSSASKTTTTRLLMFVVMGYHAVVHVAGYTAIVVYLSAVGGAGAVVAGKGISAHTFAIFTVVSTFANCG FVPTNEGMVSFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIAALERVTGWPELGELLIRRRRGGGEGYHHLLPSSRTRFLALTVAVLVVA QLALFCAMEWGSDGLRGLTAGQKLVGALFMAVNSRHSGEMVLDLSTVSSAVVVLYVVMMYLPPYTTFVPVQDKHQQTGAQSGQE GSSSSSIWQKLLMSPLSCLAIFIVVICITERRQIADDPINYSVLNIVVEVISAYGNVGFSTGYSCARQVRPDGSCRDLWVGFSGKWSKQ GKLTLMAVMFYGRLKKFSLHGGQAWKIE
8.3E-28	107	14.1	8.3E-28	106.5	9.8	3.6	1	B8A6S2_ORYSI	Sodium transporter HKT1;5	OsI_01579	Oryza sativa subsp. indica (Rice)	554	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>tr|B8A6S2|B8A6S2_ORYSI Sodium transporter HKT1;5 OS=Oryza sativa subsp. indica GN=OsI_01579 PE=2 SV=1MSSLDATTPRYDEFKRIYHLFLFHAHPFWLQLLYFLFISLLGFLMLKALPMKTSMVPRPMDLDLIFTSVSATTVSSMVAVEMESFS NSQLLLITLLMLLGGEVFTSILGLYFTNAKYSSKMIATLPDNDDHGGSGKPPPATTSPSSTLVELELAPPMDVVVVNPTTTATTHDEVEL GLGRRNKRGCTCTTTHTSSSSSASKTTTTRLLMFVVMGYHAVVHVAGYTAIVVYLSAVGGAGAVVAGKGISAHTFAIFTVVSTFANCG FVPTNEGMVSFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIAALERVTGWPELGELLIRRRRGGGEGYHHLLPSSRTRFLALTVAVLVVA QLALFCAMEWGSDGLRGLTAGQKLVGALFMAVNSRHSGEMVLDLSTVSSAVVVLYVVMMYLPPYTTFVPVQDKHQQTGAQSGQE GSSSSSIWQKLLMSPLSCLAIFIVVICITERRQIADDPINYSVLNIVVEVISAYGNVGFSTGYSCARQVRPDGSCRDLWVGFSGKWSKQ GKLTLMAVMFYGRLKKFSLHGGQAWKIE
1E-27	106	22.2	7.8E-26	100	15.4	2	1	R6I1X3_9FIRM	Cation transport protein	BN556_01612	Firmicutes bacterium CAG:240	342	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:240	1263013	>tr|R6I1X3|R6I1X3_9FIRM Cation transport protein OS=Firmicutes bacterium CAG:240 GN=BN556_01612 PE=4 SV=1MGVLVFLLAIAPVAREGGSMFLLRAEFPGPMASKLVPRMQKSAKLLYEIYIAMTVLQIVLLLLGGIPLFDSVNISLSTVSTGGFCVR NDSMASYGAYAQNVTLVFMTLCSMSFSLFYCVLALEFLRIRRSRELRAFVIVVLGVALLMGIDTASKFASVADGVHHTLFQVVSIISTTC YVSIDASFWSPFVWAMLTVLMITGPMSGSTGGGMKLSRVMILCKSTYRAIARTVTPNSVHLIHLDGEIVEEDTVSAVESFAVAYFMAVI FTAVVLSINGLSIGDGMLAAISSLSNVGYGIDSNTFTMGVSGLNIISKAVLCFDMFLGRLEIFPMLVLFAPETWRK
1E-27	106	0	1.2E-27	106	0	1	1	R1EAT0_BOTPV	Putative potassium protein	UCRNP2_8763	Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	183	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, dothideomyceta, Dothideomycetes, Dothideomycetes incertae sedis, Botryosphaeriales, Botryosphaeriaceae, Neofusicoccum, Neofusicoccum parvum, Botryosphaeria parva (strain UCR-NP2) (Grapevine canker fungus) (Neofusicoccum parvum)	1287680	>tr|R1EAT0|R1EAT0_BOTPV Putative potassium protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_8763 PE=4 SV=1MRNSNVYEERSLGIYDDDPYLDHANGGEEKKSSVFGFIRDRLTGTSSGEQTKGYFVQQQLRAQLAHDLWWLVLAVFVIMIIEG GQFERDPANFSVFNVIFETVSGYGCVGVSVGVTYDAFSFCGSWHKLSKLVLCAVMLRGRHRGLPVAIDKAVLLPSEAQYQAEEEDA QLRMERTVSRHGMA

1.6E-27	106	24.2	3.3E-17	71.6	12.8	3.6	3	W5I253_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	508	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5I253|W5I253_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MPIRLHTFLSSARHVSNSSVFIFQFIAFHLSPLLIHLSYFVIVDVLGFAALMALKPSNPNYSPRYVDIFFLSTSAVTVTGLATIKMEDL STSQVVILTLLMLLGSEMFVSLLGHIHELSKQNKHDPEDSRVRSVTVQDESQIEEAIPVTPSTNTTSLKKGCRKYIGFVLLAYMVLILLVG SLLVFLYVAHVSTARDVLTRKSINTMLFSISITVSSFTNGGLIPTNESMAVFSSNQGLLLLLTGQILAGNTLLPVFLRLVIWALRGLSITRA KPEELEFMMNNTKALGSNHLLPNKQTVFLAASVAALIAVAVTFFCCLNWESAVFAGLTPNQKITNALFMAVNTRQAGENSIDCSLVAP AVLILFIAMMCIPASTSFLSLHEHAERGITEHKDGANKRRLSLNKMLFSPLACTAVLIMLVCITERRSLSADPLNFSTFNMIFEVISAYRNVV GLSTGYSCARLPHPEKQSVCQDMPYSFSGWWSDQGKVVLVLVMLCGRLKCFHRQRS
1.7E-27	106	16.8	2.8E-27	104.8	11.6	1.3	1	M4RU80_9BIFI	Putative cation transporter	D805_1745	Bifidobacterium thermophilum RBL67	487	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium thermophilum, Bifidobacterium thermophilum RBL67	1254439	>tr|M4RU80|M4RU80_9BIFI Putative cation transporter OS=Bifidobacterium thermophilum RBL67 GN=D805_1745 PE=4 SV=1MSNLVLDESSMNREASRGYSWWFSGDAFERQAAQDRRPPRRNLSAKLWSHPGRLTILYFFALIALATVLLELPISAHNRMVTD PVVAFFTAVSAASTCGIQVVNTTTHWSLFGQAVILLAVQFGGLGVMTFASLIALAVNKHIKASQRMLTARELGATKLSETKGVLNAVLV TTLLIEVITFLALFPGLLHVNHGNVRHALWEALFFAVISYNNAGFTPDGAGLHVNSWGVGLPVLLSAFCGTLGFPVLLNLMRAARKHTP PKRWTLHTKITLIGTFCMVAVSLLWFRCVEWNNHILFSHADLQTRLRYALTAAVMPRTSGFDPSWVPDVSDPTKVFMSAFMFIGGGS TSTAGGIRVTTFTVVLLVCRAAFRGKRDVTVFHKRINERTTMTAVSIMTTCLILVFSVSLALMAVSGCSLSNALFDTCSAFGLGGYTVG VADQSDPAALLLLAMTMVIGRIGPMTIAYAINRPSEAQAVRFPEEPIIVG
2E-27	105	18.5	4.7E-19	77.6	2.7	3.5	3	W5BDF1_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	576	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5BDF1|W5BDF1_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MHRFSSALVFLQNLPSHTAMKLPLFSLEALRITKEMVKHFHEFVSTRLGSLSKCTADLFRRSYLFLVFKSNPLVVQLIYLMSISFA GFLALKNLAPLNKPSPRNLDLIFTSVSTVTVSSMATIEMEDFSGQQLWVFIILMILGGEVFTSMVGLHFKNARANTEGALQTRLAFISRD IESSDDFNNSSQNYMEGIQPEETMPHNQVQESKGMNHKSRNILAHVVAGYFIAAIVCSSVVITIFLWIDSDARHLLKSKHIKMWTFSIFT AVSSFANCGFTPLNDSMAIFKNNPTFLLLVTPQILVGNTLFAPLLRLSIWTLGKLSSREEYAYILQHPKEIGYRHLQPHKNSVQLVLTGV MLILLQAMLICYFEWDSKSLEGMGWFQKLIGSLFQSANSRHAGETVIDISTLSPPIMVIFALVMYLPSGTSILATCGDNRSLADKKENPN GRATWKKFAMTKRTCLVIITILACITERKSMTADPLNFSIFSVIFEVMSAYGNVGYSLGYSCDKLLRPDSACRDASYGFVGRWSDKGR LIIILVMFLGRFKAYTLRGKKTLNVHPCRRTAPHQRPEVAGN
2.4E-27	105	23.5	7.4E-25	96.8	16.3	2	1	D4J122_BUTFI	Trk-type K+ transport systems, membrane components	CIY_09510	Butyrivibrio fibrisolvens 16/4	319	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, Butyrivibrio fibrisolvens, Butyrivibrio fibrisolvens 16/4	657324	>tr|D4J122|D4J122_BUTFI Trk-type K+ transport systems, membrane components OS=Butyrivibrio fibrisolvens 16/4 GN=CIY_09510 PE=4 SV=1MLYLIYLGLCALEIILLLLAGMTPFEAINTGIATAGTGGFGIYSSSIGGFNVACQWIVAIFMFIFGVNFNFYYYVLFHHARDAFRMEE VRMYSLLTLISIGIITVNTLSCSAGLFDALTKAAFQVTSIQSSTGFSTADFAAWPQTSRCVLVLLMFIGACAGSTGGGIKVSRFILMGKAV HKELISYIHPRSVRKTLMDGKPVTHDTVRSNNVFFGTFMLVFFVSAFILSFENLDFSTIFTAVIACMSNIGPGLSMVGPTKNFLFFTDLSK IILIIDMLAGRLELFPILMLFHPNIWQDLFAKRRLKELKHAGKVLNEDF
3.2E-27	105	11.7	8.9E-16	66.8	0.9	3.1	3	F0YFL8_AURAN	Putative uncharacterized protein	AURANDRAFT_65827	Aureococcus anophagefferens (Harmful bloom alga)	1206	cellular organisms, Eukaryota, Stramenopiles, Pelagophyceae, Pelagomonadales, Aureococcus, Aureococcus anophagefferens (Harmful bloom alga)	44056	>tr|F0YFL8|F0YFL8_AURAN Putative uncharacterized protein OS=Aureococcus anophagefferens GN=AURANDRAFT_65827 PE=4 SV=1MAEDAGEARVRDSSDVELPELPGSKRVSFAAGPEEPCRRSSLSVGGEFLTSSAGGVSEVQQMPYASVVVAWILVVAVVGGSA IHLVERGGRTGASWLDCCFVALNCVTATGLATVDVTALRSASLVLMGAFMQLGAATILSLLPIVLRLRALRAALPHLKLDRGDTSPTAS LRGRKRRWCQHEAVTFDLRNYKRVPEWLVEYKALLILQRVILAYHAACYLVYGGLIAAYVARVPSARRAATADVAAAPLPWAAFHTLS ASAFNNVGFSLQRDGFMGFARHPALLYLVMGLVLHGNVLYPPCVRWIIVGLSAAAPRTSNRKVYFRYLLLHGRRLTPCLFSSQQNWL LVAAQVAMFLVQVAVLLSICYRDDGFRGESWWTRYNIAAFQAVNTRHAGMTAVALSGLRASALMLQLLMMYLAPVPFVVALRQSVR VARARPSDEAPRRASLAGAPDAPPRPSAEARRRYAAGRRLSLGPSGASPLHAGDARAPGRAASKASSLDDAMIDTRELLMVRYPDA APPWRARVALRAAALRFHVRAFARAVATSTGFVRDAAFLFLAWFLIAAIMRYEGDGGRTAASGEAAMGGSGLRSGALFYIVFELTSA FGNVGLSLGSIADPSRPTSYSGDLTAAALLIVCAVQIFGRTRDMPAAVDSALSLPTVDAADVLRQSLSLDAPENLSEAGRPSDLAATTA ASAGTAAVSAMMVATSVAISLTTEGDVADLLYLDCLATQNLGHAAFLVGFATSYWRGGHVLGKCFVVTAPWLLAAHGAASLAAAGP RPLVVAFVAVAPALYAAALPEPALYAEGYTLAFHVAFVSAVGLACADALERGAAADAVIYGVGFVSASATTAATLAVDALAAPAPLFYA AGAGVWAAAAAGAAAALSGGRPEPAAPAAPAPARGPVVDLAALAAAAVPGAAAAWPLAVAHGATFVGQALLVAVAADPPGSRFDR GVNFAIHGAGIFVFNAYLMFSDARAFPRLRAISVFACFAGGAGAARTAAGLAAGAAAPLRRAAAALFAARAAVGAALGVALARLPRDA HDRVAPPEKAPDREAPRTGDPGPFRLDRAVRHQRSHFAPYWCACFLAFAAFAFLRRSSPDAHAPRRVLETPHAYLLGFHFVFILSGF AAHGLRTRVVASLRVASAFLAAAGVVAAAQLVLAPPALVAALAACVAAGARLRALVEDALGDAGAAGAPGDAANFWQ
4.4E-27	104	14.4	2.5E-14	62.1	2.8	3.7	2	K3XH43_SETIT	Uncharacterized protein	Si001214m.g	Setaria italica (Foxtail millet) (Panicum italicum)	488	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3XH43|K3XH43_SETIT Uncharacterized protein OS=Setaria italica GN=Si001214m.g PE=4 SV=1MKTSAVPTPSGLDLIFTSVSATTVSSMVAVEMESFSNSQLLLVTLLMLLGGEVFTSMLGLHFTYTKLKKRETQIPHDLDGNNGSP PPSPSLELRTMGGGAPAAVAALEQMETRFKNNLDFTSIARTRMLMFVVLGYHVVVHLAGYTLMLIYLSAVTGAREVLIGKKINPSTFSIF TVVSTFANCGFVPTNEGMVSFKSYPGMLLLAMPHVLLGNTLFPVFLRLSIGALERVTRRRDLGELLVSGGGGGGPGRAAATSTIGYD HLLPAARTWHLAFTVAALVAAQLVLFCAMEWGSDGLRGLTASQKLVAALFMSVNSRHSGEMAVDLAAVSSAVVVLYVVMMYLPPYT TFLPVPVEDDHQHREAQSDEKSKTTTSKNIWQKLLMSPLSCLAIFIIVICITEQRQIADDPINFSVRNIVVEIISAYGNVGFSTGYSCGRQ VKPDGSCRDAWVGFSGKWSREGKLTLMAVMFYGRLKKFSMHGGQAWRLG
4.5E-27	104	29.5	2.6E-16	68.6	15.6	3.7	2	HKT9_ORYSJ	Probable cation transporter HKT9 (OsHKT9)	HKT9Os06g0701600 LOC_Os06g48800 P0596H10.8	Oryza sativa subsp. japonica (Rice)	509	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>sp|Q8L4K5|HKT9_ORYSJ Probable cation transporter HKT9 OS=Oryza sativa subsp. japonica GN=HKT9 PE=2 SV=1MPIRLHIFVSSARHAINSSALICRFIAFHLSPLLIHLSYFLIIDVLGFVALVVLRPSNHKYNPRYIDMFFLSTSAVTVTGLATTQMEDL SSSQIAVLTLLMFLGSEMFLSFLGLVLESSKQNKHDPENRRVSSVTVCEQSHLEEAIPQTPSMNSTDIKRSCHKYLVFVVLAYMIIILVT GSLLVFMYIAHVSSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMAVFSSNNGLLLLIGQILAGSTLLPMFLRLVIWALRGLRLA KAEEPDFMMNNSSSVGFSHLLPNLQTIFLAAVEVAFVGMTVILFCCLNWDSAVFAGLTSLQKITNALFMAVSARQAGENSIDCSLVAP AALVLFMVMMYTPSLTKLFSACQDHKQIGPESDDRTSKGKPFLKTMAFSPLAFNTTVIMLVCITERRSISTDPLNFSTFNIIFEVISAYGN IGLSTGYSCSRQLQHQDGIACHEKPYSFSGWWSEPGKLILVLAMLYGRLNSKDSTSARTR

4.5E-27	104	29.5	2.6E-16	68.6	15.6	3.7	2	A0A0E0Q292_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	509	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0Q292|A0A0E0Q292_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MPIRLHIFVSSARHAINSSALICRFIAFHLSPLLIHLSYFLIIDVLGFVALVVLRPSNHKYNPRYIDMFFLSTSAVTVTGLATTQMEDL SSSQIAVLTLLMFLGSEMFLSFLGLVLESSKQNKHDPENRRVSSVTVCEQSHLEEAIPQTPSMNSTDIKRSCHKYLVFVVLAYMIIILVT GSLLVFMYIAHVSSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMAVFSSNNGLLLLLIGQILAGSTLLPMFLRLVIWALRGLRLA KAEEPDFMMNNSSSVGFSHLLPNLQTIFLAAVEVAFVGMTVILFCCLNWDSAVFAGLTSLQKITNALFMAVSARQAGENSIDCSLVAP AALVLFMVMMYTPSLTKLFSACQDHKQIGPESDDRTSKGKPFLKTMAFSPLAFNTTVIMLVCITERRSISTDPLNFSTFNIIFEVISAYGN IGLSTGYSCSRQLQHQDGIACHEKPYSFSGWWSEPGKLILVLAMLYGRLNSKDSTSARTR
4.5E-27	104	29.5	2.6E-16	68.6	15.6	3.7	2	Q0D9S4_ORYSJ	Os06g0701600 protein	Os06g0701600 OsJ_22537	Oryza sativa subsp. japonica (Rice)	509	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>tr|Q0D9S4|Q0D9S4_ORYSJ Os06g0701600 protein OS=Oryza sativa subsp. japonica GN=Os06g0701600 PE=4 SV=1MPIRLHIFVSSARHAINSSALICRFIAFHLSPLLIHLSYFLIIDVLGFVALVVLRPSNHKYNPRYIDMFFLSTSAVTVTGLATTQMEDL SSSQIAVLTLLMFLGSEMFLSFLGLVLESSKQNKHDPENRRVSSVTVCEQSHLEEAIPQTPSMNSTDIKRSCHKYLVFVVLAYMIIILVT GSLLVFMYIAHVSSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMAVFSSNNGLLLLLIGQILAGSTLLPMFLRLVIWALRGLRLA KAEEPDFMMNNSSSVGFSHLLPNLQTIFLAAVEVAFVGMTVILFCCLNWDSAVFAGLTSLQKITNALFMAVSARQAGENSIDCSLVAP AALVLFMVMMYTPSLTKLFSACQDHKQIGPESDDRTSKGKPFLKTMAFSPLAFNTTVIMLVCITERRSISTDPLNFSTFNIIFEVISAYGN IGLSTGYSCSRQLQHQDGIACHEKPYSFSGWWSEPGKLILVLAMLYGRLNSKDSTSARTR
8E-27	103	25.7	2.2E-25	98.5	9.8	3.6	2	I1ZHS7_EUTSA	Potassium transporter (Uncharacterized protein)	HKT1.1 EUTSA_v10028595mg	Eutrema salsugineum (Saltwater cress) (Sisymbrium salsugineum)	505	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Eutremeae, Eutrema, Eutrema salsugineum (Saltwater cress) (Sisymbrium salsugineum)	72664	>tr|I1ZHS7|I1ZHS7_EUTSA Potassium transporter OS=Eutrema salsugineum GN=HKT1.1 PE=2 SV=1MERVGAKLAKFRLQLAKNPSVLCLYFVYFLSFSFLGFLALKISKPRTTSRPHDLDLFFTSVSAITVSSMSTIDMEVFSNTHLIFLTIL MLLGGEVFTSFLTLYFSHFTKFVLPHNKNIRHLMGSFDLDSPIEDRRIDLENVTDHRVDPSQINERASKCLYSVVLGYHLVTNIAGSVLV LVYVNFVKTAGDVLSSKEISPLTFSVFTAVSTFGNCGFVPTNENMIIFRKNSGLLWLLIPQALMGNTLFPCFLLFLVSGLDKITKYDEFG YILNNYKKMGYYHLLSVRRCVLLGLTVLGFLTIQLIFFCVYEWSSESLEGMNWYEKFVGSLFQVVNSRHTGETILDVSTLSPTILILFILM MYLPPYTLFMPFTEETNEKGEDDSENGKKRKKSGLFVSQLSFLVVCIVLISISEREKLRRDPLNFNVLNITLEVISAYGNVGFTTGYSCK RRLNVSDGGCEDASYGFVGRWSPAGKVILILVMFYGRFKHFTPKSGRAWILYPSSF
8.8E-27	103	26.7	8.3E-14	60.3	9.6	4	3	A0A0D3EPS7_9ORYZ	Uncharacterized protein		Oryza barthii	434	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza barthii	65489	>tr|A0A0D3EPS7|A0A0D3EPS7_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1MPIRLHIFVNSARHAINSSAFICRFIAYHLSPLLIHLSYFLIIDVLGFVSLVVLRPSNHKYNPRYVDMFFLSTSAVTVTGLATIQMEDL SSSQIAILTLLMFLGMFVVLAYMTIILVTGSLLVFMYIAHVSSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMVVFSSNNGLLLLLI GQILAGSTLFPVFLRLVIWALRGLRLAKAEEPDFMMNNSSALGFSHLLPNLQTIFLAAVEVAFVAMTVILFCFLNWDSVVLSSLQKITNA LFMVVNARQAGENSIDCSLVAPAALVLFMFSACQDHKRIGPESDDRTSKGKPFLKMMAFSPLGFNTTVIMLVCITERRSLSTDPLNFST FNIIFEVISAYGNIGLSTGYSCSRQLQHQEGIACHEKAYSFSGWWSEPGKLILVLAMLCGRLNSKDSTSARTR
9.2E-27	103	20.7	3.7E-25	97.8	10.2	3.8	1	HKT1_ORYSI	Cation transporter HKT1 (OsHKT1) (Ni-OsHKT1) (Po-OsHKT1)	HKT1 OsI_023492	Oryza sativa subsp. indica (Rice)	530	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>sp|A2YGP9|HKT1_ORYSI Cation transporter HKT1 OS=Oryza sativa subsp. indica GN=HKT1 PE=1 SV=2MTSIYHDFIHNKLQSFGRIGRYFVNFVVLAHRFIALHIHPFWIQLSYFLLISILGSVLLMFLKPSNPEFRPGYIDMLFLSTSALTLSSLI TIEMEVLSSSQIVVITLLMLLGGEVFVSFLGLMLRLNHKHNPEFSGDKVSSVPIELDTINSASTVISCEELQLEAAIPEVPSSTIKDLKRSK RLRWFLGFVVFSYFVVIHVAGFLLVLWYISRVSSAKAPLKKKGINIALFSFSVTVSSFANVGLVPTNENMAIFSKNPGLLLLFIGQILAGN TLYPLFLRLLIWFLGKVTKLRELKLMIKNPEELQYDYLLPKLPTAFLASTVIGLMASLVTLFGAVDWNSSVFDGLSSYQKIINALFMAVNA RHSGENSIDCSLIAPAVLVLFIILMYLPPSTTFALSNGDEKTANKKAKRKLGLVVQNLAFSQLACISVFVIVAFITERSRLRNDPLNFSALN MIFEIISAYGNVGLSTGYSCSRLQKLHPGSICQDKPYSLSGWWSDEGKLLLVFVMLYGRLKAFTKGTGEYWRLW
9.2E-27	103	20.7	3.7E-25	97.8	10.2	3.8	1	HKT1_ORYSJ	Cation transporter HKT1 (OsHKT1) (Ni-OsHKT1) (Po-OsHKT1)	HKT1 Os06g0701700 LOC_Os06g48810 P0596H10.9	Oryza sativa subsp. japonica (Rice)	530	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. japonica (Rice)	39947	>sp|Q0D9S3|HKT1_ORYSJ Cation transporter HKT1 OS=Oryza sativa subsp. japonica GN=HKT1 PE=1 SV=1MTSIYHDFIHNKLQSFGRIGRYFVNFVVLAHRFIALHIHPFWIQLSYFLLISILGSVLLMFLKPSNPEFRPGYIDMLFLSTSALTLSSLI TIEMEVLSSSQIVVITLLMLLGGEVFVSFLGLMLRLNHKHNPEFSGDKVSSVPIELDTINSASTVISCEELQLEAAIPEVPSSTIKDLKRSK RLRWFLGFVVFSYFVVIHVAGFLLVLWYISRVSSAKAPLKKKGINIALFSFSVTVSSFANVGLVPTNENMAIFSKNPGLLLLFIGQILAGN TLYPLFLRLLIWFLGKVTKLRELKLMIKNPEELQYDYLLPKLPTAFLASTVIGLMASLVTLFGAVDWNSSVFDGLSSYQKIINALFMAVNA RHSGENSIDCSLIAPAVLVLFIILMYLPPSTTFALSNGDEKTANKKAKRKLGLVVQNLAFSQLACISVFVIVAFITERSRLRNDPLNFSALN MIFEIISAYGNVGLSTGYSCSRLQKLHPGSICQDKPYSLSGWWSDEGKLLLVFVMLYGRLKAFTKGTGEYWRLW
9.2E-27	103	20.7	3.7E-25	97.8	10.2	3.8	1	A0A0E0Q293_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	530	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0Q293|A0A0E0Q293_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MTSIYHDFIHNKLQSFGRIGRYFVNFVVLAHRFIALHIHPFWIQLSYFLLISILGSVLLMFLKPSNPEFRPGYIDMLFLSTSALTLSSLI TIEMEVLSSSQIVVITLLMLLGGEVFVSFLGLMLRLNHKHNPEFSGDKVSSVPIELDTINSASTVISCEELQLEAAIPEVPSSTIKDLKRSK RLRWFLGFVVFSYFVVIHVAGFLLVLWYISRVSSAKAPLKKKGINIALFSFSVTVSSFANVGLVPTNENMAIFSKNPGLLLLFIGQILAGN TLYPLFLRLLIWFLGKVTKLRELKLMIKNPEELQYDYLLPKLPTAFLASTVIGLMASLVTLFGAVDWNSSVFDGLSSYQKIINALFMAVNA RHSGENSIDCSLIAPAVLVLFIILMYLPPSTTFALSNGDEKTANKKAKRKLGLVVQNLAFSQLACISVFVIVAFITERSRLRNDPLNFSALN MIFEIISAYGNVGLSTGYSCSRLQKLHPGSICQDKPYSLSGWWSDEGKLLLVFVMLYGRLKAFTKGTGEYWRLW
9.4E-27	103	30.3	7E-17	70.5	14.8	3.8	3	A0A0E0MXI4_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	509	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0MXI4|A0A0E0MXI4_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MPIRLHIFVNSARHAINSSAFICRFIAYHLSPLLIHLSYFLIIDILGFVSLVVLRPSNHKYNPRYVDMFFLSTSAVIVIGLATIQMEDLSS SQIAILTLLMFLGSKMFLSFLGLVLESSKQNKHDPENRTVSSVTVCKQSQLEEAIPQTPSMNSIDIKKRCLKYLVFVVLAYMIIILVTGSLL VFMYIAHVSSARDVLTRKSINKALFSISVTVSSFTNGGLLPTNESMAVFSSNNGLLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKAEE PDFMMNNSSAVGFSHLLPNLQTIFLAAVEVAFVAMTVILFCCLNWDSVVFAGLSSLQKITNALFMAVNARQAGENSIDCSLVAPAALVL FMVMMYTPSLTKLFSACQDHKRIGPESDDRTSKGKPFLKMMAFSPLGFNTTVIMLVCITERRSLSTDPLNFSTFNIILEVISAYGNIGLS TGYSCSRQLQHQEGIACHEKAYNFSGWWSEPGKLILVLAMLCGRLNSKDSTSARTR
1E-26	103	19.9	1E-26	102.9	13.8	3.5	1	A0A0D3E8W9_BRAOL	Uncharacterized protein		Brassica oleracea var. oleracea	499	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica oleracea (Wild cabbage), Brassica oleracea var. oleracea	109376	>tr|A0A0D3E8W9|A0A0D3E8W9_BRAOL Uncharacterized protein OS=Brassica oleracea var. oleracea PE=4 SV=1MERVLAKLAKIRLQLANFRSPFFIYFFYFFSFSLLGFLALKVSKPRTTSRPHDLDLFFTSVSAITVSSMSTIDMEVFSNTQLIITVLM FLGGEVFTSFLDLYFSHFSNFVFPHNKIRHLMGSLNIKPPTEDRRRDLENITDHLKRPSQINERASKYLYSVVLGYHLVTNLAGSVLVLV YVTFVKTAKVVLSSKEISPVTFSIFTTVSTFGNCGFVPTKENMVIFRKNSGLLWLLIPQVFMGNTLFPCFLFLLIWGLDKITKREEFGYIL KNHKTMGYSHLLSLRLCALLGLTVLGFAMIQFFVFCTFEWNSVSLEGMNPYEKLVGSLFQVVNSRHTGENIVDLSTLSPAILVLFIVMM YLPPYTLFMPLTTIEKYKEEVESHTGNEGKRKKTGFFVSQLSFLAICVFFISITESQNLRRDPLNFNILNITLEVISAFGNVGFTTGYSCER RLDINNGSCKDTSYGFVGRWSPNGKFILIILMFYGRFKQFTAKSGRPW

1.2E-26	103	0	1.4E-26	102.5	0	1	1	B8NRM8_ASPFN	Uncharacterized protein	AFLA_049330	Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	181	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Eurotiales (green and blue molds), Aspergillaceae, Aspergillus, Aspergillus flavus, Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)	332952	>tr|B8NRM8|B8NRM8_ASPFN Uncharacterized protein OS=Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167) GN=AFLA_049330 PE=4 SV=1MHIFVYPVVITMRSSNVYEERSLGIYAGETTPKSNHQQEKPPKTVPSSRLYFVKQQLHVQLAYDIWWLALAVIIISIVEAGSFTRDPVVYSVFNIIFETISAYGYVGITTGLPDQAYSFSGGWYSLSKVVLRAAMLRGRHRSLPMAIDKAIVLPGDYLERVEEEDAYIRMERSLEQGHGNV
1.4E-26	103	13.2	6.6E-19	77.2	2	3	2	W5BQT8_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	457	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5BQT8|W5BQT8_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MATIEMEDFSGQQLWVFIILMILGGEVFTSMVGLHFKNARANTEDALQTRLAFISRDIESSDDFNNSSQNYMEGIQSEETMPHNQVQESKGMNHKSRNILAHVVAGYFIAAIVCSSLVITIFLWIDSYARHLLKSKHIKMWTFSIFTAVSSFANCGFTPLNDSMAIFKHNPTFLLLVTPQILVGNTLFAPLLRLSIWTLGKVSSREEYAYILQHPKEIGYRHLQPYKNSVKLVLTGVMLILLQAMLICYFEWDSKSLEGMGWFQKLIGSLFQSADSRHAGETVINISTLSPPIMVIFALAMYLPSGTSILATYGDIRSLADKKENPNGRATWKKFAMTKRTCLVIFTVLACITERKSMTADPLNFSIFSVVFEVISAYGNVGYSLGYICDKLLKPDSACRDASYGFVGRWSDKGRLIVILVMFLGRFKAYTLKGKKTLNVHPCRSGTPHQRPEVAGN
1.5E-26	102	15.1	1.2E-23	92.9	9.1	3.6	1	M8A985_TRIUA	Cation transporter HKT1 (Uncharacterized protein)	TRIUR3_27777	Triticum urartu (Red wild einkorn) (Crithodium urartu)	458	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum urartu (Red wild einkorn) (Crithodium urartu)	4572	>tr|M8A985|M8A985_TRIUA Cation transporter HKT1 OS=Triticum urartu GN=TRIUR3_27777 PE=4 SV=1MEDLSSSQIVVLTLFMLVGGEIFVSLLGLMLRVNHQDMQDLPNVKISSVPVELEEIDSANSAAQSDESQLEEAARAIPPKKCTELKRSRTVKCLGYVVFGYFAVIHVLGFLLVFLYITHVPSASAPLNKKGINIVLFSLSVTVASCANAGLVPTNENMVIFSKNSGLLLLLSGQILAGNTLFPLFLRLLVWFLERLTEMKELRHMIKNPEEVHFANLLPRLPTAFLSSTVIGLVAARVTMFCAVDCNSSVFDGLSSYQKTVNAFFMVVNARHSGENSIDCSLMSPAIVVLIFIVMMYLPSTTTLAPPNGDIKTTDENTKGKRGKRGSLVQKLAFSPLGFNAIFVVIACITERRRLRNDPLNFSTLNMIFEVISAYGNAGSTGYSCSRLHQLHPEIICQDKPYSFSGWWSDRGKFVLILVMLYGRLKAFAMATGQASVPLIKSSLHLAVIIKVSMQLKN
1.5E-26	102	13.4	9E-24	93.2	0.8	3.8	3	K3Y2S5_SETIT	Uncharacterized protein (Fragment)	Si008505m.g	Setaria italica (Foxtail millet) (Panicum italicum)	491	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3Y2S5|K3Y2S5_SETIT Uncharacterized protein (Fragment) OS=Setaria italica GN=Si008505m.g PE=4 SV=1SARHVVSSSVFLCRLVVFHLSPLLLHLSYFLAIDLLGFLALVLLKPSSPGYRPRYVDVFFMSTSAATVTGLATVKMEDLSSSQVVVLTILMLLGSEMFVSLLGLVLESRKRRRRGRDPDHGGRVRSVVTVSDESNLEAANPSASSGDHKESCLGSLALVMLVYMAMVLVLGSVLVFVYVAGVPSARDVLARKGISAALFSAVVTVSSFTNGGLLPTNESMAVFSANRGLLLLLAGQILAGNTLLPVILRPAIWATRRLERVFAGRHGSEEEGLESMTKDAVAAGFGHLLLPGLQTVFLAVTVVAVAAATATLLCCLNWDSAVFAGITAGEKVTNALFMAVNVRQAGENSIDCSLLAPAVLVLFLAMMSVTSPRVLVFGQMSTETRTGRDKSGKHFSGAFRPRRHSSLYTTAAQWGNQAAENQNARMGRAYGNVGLSTGYSCSRLLRPEESSACHDKPYSFSGWWSDQGKLVLVLLMLYGRLKGFHRKQRRS
1.7E-26	102	25.1	5.4E-18	74.1	8.2	3.3	2	I1KEI5_SOYBN	Uncharacterized protein		Glycine max (Soybean) (Glycine hispida)	574	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine, Soja, Glycine max (Soybean) (Glycine hispida)	3847	>tr|I1KEI5|I1KEI5_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=2MKNFAYLSQKQHRFCSFFPHSLGFFVHFLAFHVHPFFVQLCYFVILSLLGYLGLKVSKPRTPVRPNDLDLFYTSVSASTVSSMVAVEMEVFSNSQLILLTLMFVGGEVFTSVLDLIFARYKFTQSVQNKVPTHHSYQTQSEFSPVEHICGLDKNNDTNPFSPTKKPPINANQIELGLVSIDHSESENHKPSDSKLPDTYLQFLQIKKTKSNINVPKGTVESFNDSDRLKYNCLSFLTFVVLGYLVVVQFVGFSFVSLYITLVPSARQVKLKNKGIKIATFSLFTIVSTFASCGFIPTNENMMVFKKNSGLLLLVLPHILLGNTLYPPCLRLVIMALKRVTRREEYSHLLKNFKDVGYDHMLSALHCCLLVATVLGFNLVQFVMFCSVEWNTKIMEGLNVYEKVVASLFQVTNARHSGESVFDLSSISSAILVLFVVMMYLPPYTTFLPVREHENDVKRNEKSVVECLVFSQLSYLVIFIILICITESNSLKEDPLNFNVLNITLEVISAYGNVGLSMGYSCARQLKPDATCKDSWVGFSGRWSSKGKFILILVMFFGRLKKFNMKGGKAWNLS
1.9E-26	102	33.7	1.2E-25	99.4	15.4	3.5	2	K4CC88_SOLLC	Uncharacterized protein	Solyc07g014690.2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	555	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Solanales, Solanaceae, Solanoideae, Solaneae, Solanum, Lycopersicon, Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	4081	>tr|K4CC88|K4CC88_SOLLC Uncharacterized protein OS=Solanum lycopersicum GN=Solyc07g014690.2 PE=4 SV=1MSSLSYLGEKLQHLFSSIFLYVSCLCGSTCFLISSLYRSILFKVNKFFIQLFYFIFISIFGFLILRNLNPRHSEDFTSTNLDLFFTSVSSATISSMSTLEMEVFSNSQLIVITFLMFIGGEVFISMIELYLIRPKFKPWRKNSKIESILSSNNSTTSSPRNSNFNNDDDYNIELDIVVLPDSPKSIKSDKDKDDFTSSDNNLKYQSIKFLGVVTLVYLLVINIVGMSLVLMYLAFVSSAKDVLINKGLNTYIFTIFTTISSFVSCGFVPTNENMMVFSKNSGLLWILIPLLLVGNALYPMCLRFSIRLMGKLFVSKKREAKYLLKNSREIGHLHLFSRQHSRLLVVTMFGFILVQFILFCALEWNSNGLNGLNSYQRFVGSLFQVVNARHTGETIVDISTLSPPILVMFIVMMYLPPYTSFIPVKGVEENTEEYLFGEKQKRGKVVENFIFSQLCYLSLFIVLICITERKKMKDDPLNFNVLNITLEVISAYGNVGFTTGYSCDRMINGDQSCKNKWYGFVGKWSDEGKIIIIIIMFFGRLKKFNMQGGKAWKLL
2.5E-26	102	15.9	2.5E-26	101.7	11.1	3.8	1	A0A0D3EMY9_9ORYZ	Uncharacterized protein		Oryza barthii	555	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza barthii	65489	>tr|A0A0D3EMY9|A0A0D3EMY9_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1MSSLDATTPRYDEFKRIYHLFLFHAHPFWLQLLYFLFISLLGFLMLKALPMKTSMVPRPMDLDLIFTSVSATTVSSMVAVEMESFSNSQLLLVTLLMLLGGEVFTSILGLYFTNAKYSSKMIATLPDDDDHGGSGKPPPPTTSRSSTLVELELAPPMDVVVVNPTTTATTHDEVELGLGRRNKRGCTCTTTHTSSSSSASKTTTTTRLLMFVVMGYHAVVHVAGYTAIVVYLSAVGGAGAVVAGKGISAHTFAIFTVVSTFANCGFVPTNEGMVSFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIAALERVTGWPELGELLIRRRRGGGEGYDHLLPSPRTRFLALTVAVLVVAQLALFCAMEWSSDGLRGLTAGQKLVGALFMAVNSRHSGEMVVDLSTVSSAVVVLYVVMMYLPPYTTFVPVQDKHQQTGAQSGQEGSSSSSIWQKLLMSPLSCLAIFIVVICITERRQIADDPINYSVLNIVVEVISAYGNVGFSTGYSCARQVRSDGSCRDLWVGFSGKWSKQGKLTLMAVMFYGRLKKFSLHGGQAWKIE
5.2E-26	101	22.4	1.1E-17	73.2	4.9	3.4	3	M0WVT1_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	586	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0WVT1|M0WVT1_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MPELESPQTSMHRFSSALVILQNLPSHTAMKLPLSNLEVLRITKEKVKRFHEFVCTRLSSLSKCTADLFRRSYLFLVFKSNPLIVQLIYLLSISFAGFLALKNLRPLNKPSPRNLDLMFTSVSTVTVSSMATVEMEEFSGQQLWVFIILMILGGEVFASMIGLHFKNIRANTEEAFQTRLDFISRDIESSDVFTNSGHNNMEGTQSEETMPHNQVQESKAMNQKSRNVLAHVVAVYFIAAIVCSSVVITIFLWVDSDARHLLKSKHIKIWTFSIFTAVSSFANCGFTPLNDSMAIFKNNPTFLLLLTPQILVGNTLFAPLLRLSIWTLGKVSSREEYAYILQHPKEIGYRHLQPHKNSVKLVLTGVMLILLQAMLICYFEWDSKSLEGMGWFQKLTGSLFQSANSRHAGETVINISTLSPPIMVIFALAMYLPSGTSILASRGDNRSLADKKENPNGRATWKKFAMTKRTCLVIFTILACITERKSMTADPLNFSIFSVIFEVISAYGNVGYSLGYSCDKLLKPDATCRDASYGFVGRWSDQGRLIIILVMFLGRFKAYNLKGKKPLNVHPCTGATPHERPEVAAN
7.4E-26	100	25.3	2.4E-25	98.4	17.5	1.6	1	A0A0A8B1W6_9ACTN	Cation transporter	JI75_00970	Coriobacteriaceae bacterium 68-1-3	512	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Coriobacteriales, Coriobacteriaceae, unclassified Coriobacteriaceae, Coriobacteriaceae bacterium 68-1-3	1531429	>tr|A0A0A8B1W6|A0A0A8B1W6_9ACTN Cation transporter OS=Coriobacteriaceae bacterium 68-1-3 GN=JI75_00970 PE=4 SV=1MWRRLSLNDVRVIAHYLGVLVSFLTVGLALPLVVALAFQEWVPASHYLLTAGITLVVGSALRFVRIQPGRLTYQQALIITGLSWVVLAFFAAIPLHLSGHYGRFLDALFDAVSGVTTTGVSIILDLDHLSMADNMWRFTMHATGGLGFIVVGTTFGLFRRGGASLFSSEGRGEHIVPNVVQTARFISRIALIFISFSTLVLAIGLMLRGFEAPRAFFHSLWLSISAFATGGFTPMDLSVLYYHSFPVELMLMVVMLAGSVSFVLHSSIVRGRAIEFFRDMETVATFLWLLAITVVLAATISGSEVFSDLPTMLRTNLFTVVSAFSTTGFLNITPSQLTGTLTSGALMTIAVLMGVGGGTESTSGGIKIKRVGIIFKSIVATIKQTLAPESARVGTSYYHLGRRPLDPDLVRGAMTVMSLYAITYIVGTLAGIASGYDATQAIFEGVSMASNAGLTAGVVGSGMPVPLELFYIFAMWAGRLEFVTFLALIVKVAVSLYPRETVDDVVEAWRGR

9.4E-26	99.7	33.3	1.9E-25	98.7	23.1	1.4	1	A0A0G1GS00_9BACT	Ktr system potassium uptake protein B	UV79_C0011G0005	candidate division TM6 bacterium GW2011_GWF2_43_17	460	cellular organisms, Bacteria, unclassified Bacteria, candidate division TM6, unclassified candidate division TM6, candidate division TM6 bacterium GW2011_GWF2_43_17	1619085	>tr|A0A0G1GS00|A0A0G1GS00_9BACT Ktr system potassium uptake protein B OS=candidate division TM6 bacterium GW2011_GWF2_43_17 GN=UV79_C0011G0005 PE=4 SV=1MEPRLSKKTTRITPARIIIATFLALILLGTLLLRAPFAHQEFELSWWDAFFVSSSAVSTTGLMSVPLSTFSFWGKLIIICLAQLGGLGFLTLFVPILGLFKNVRMRTHLITGQQFDLQQWSSNWVYSKKIVQFVAVFSFIAEVIGFLIVYYALDGVPLTEPRWFSAIFHTVSSFCNLGVSVFPQPFATLAMHRLFILATTTLIALGSFGFIPIYEIFLHIRQRILRPANGIPRARFSLQTKILFLYMPLLTGVLAIFLLVAEWEALRQFAWIDKINIAVFNGFSFRSCGFSTFNFLQVSQVVLFVSMVFCLLGSSPGSVGGGSGLKVTTLALSLSSIKAIVLGKEHVEIFKRRIPKEQMLVTLAFLSIYLLWIFSTLFLVLITENQTGEGMVNFMFESISAVANRGITIQSFIAMTRAGQLVLTFGMIVGRLNSLSLLIAIKHKRDRVSFKYPEETLSMG
1.3E-25	99.2	24.4	2.4E-17	72	7.6	3.2	2	K7K118_SOYBN	Uncharacterized protein		Glycine max (Soybean) (Glycine hispida)	512	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine, Soja, Glycine max (Soybean) (Glycine hispida)	3847	>tr|K7K118|K7K118_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1MMKSTLSYFSRSLRFLAGLIAFHFHSFFIQLCYLMILSLVGYLGLKVSKPRNPVRLNDLDLFYTSVSASTASSMVAVEMEVFSNSQLILFTLLMFLGGEVFTSMLDLLFAGYKLQNKVSINPFPPTNHANQIELGLVLSIPHSDSENNNPCDSNIINVASCDRLKYNCLSYLTYAVLGYLVMVQFVGFSFVSLYMTLVPSARQVLKNKGIKIVTFSLFTVVSTFASCGFVPTNENMLVFKKNSGLLLLILPHVFLGNALYPPCLRLLIMVLKKVTKKEEFSYLLKNSIDVGYEHLLSDLRCCFLVATVLGFNLIQFVMLCSLEWKTKIMEGLNVYEKVVASLFQVTNARHAGESVFDLSSISSAILVLFVVMMYLPPYTTFLPVREHEKDVNKRNEKSVVDCLVLSQLSYLVIFIILICITESKSLKEDPLNFNVLYITLEVISAYGNVGFSTGYSCARQLKTDATCKDSWVGFSGRWSSKGKFILILVMFFGRLKKFNMKGGKAWKLSWPV
1.3E-25	99.2	18	1.3E-25	99.2	12.5	3.7	1	A0A0E0JHM5_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	523	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0JHM5|A0A0E0JHM5_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MSSLDVSTTPRYDKFQRIYHLFLFHAHPFWLQVLYFLFISLLGFLMLKALPMKTSMVPRPMDLDLIFTSVSATTVSSMAAVEMESFSNSQLLLITLLMLLGGEVFTSILGLYFTNTKSKMIGGKPPPTSTLVELAPMDVVVVNPTTVTQDEIELGLGQNKRSYTTTHTSSSTTTTRLLMFVLMGYHAVVHVAGYTLILVYLSVVGGAGAVLAGKGISARTFSIFTVVSTFANCGFVPTNEGMVSFRSFPGLLLLVMPHVLLGSTLFPVFLRLAIAALERVTGWPELGELRRRRGGGSEYDHLLPSARTWFLALTVAVLVVAQLVLFCAMEWASDGLRGLTAGQKLVGALFMAVNSRHSGEMVVDLSTVSSAVVVLYVVMMYLPPYTTFVPVQDKHHQTGAQSAQEESSSSNSIWQKLLMSPLSCLAIFVVVICITERRQIADDPINFSVLNIVVEVISAYGNVGFSTGYSCGRQVRADGSCRDLWIGFSGKWSKEGKLTLMAVMLYGRLKKFSLHGGQTWKIH
1.4E-25	99.2	20.3	1.2E-23	92.8	10.2	3.8	1	I1Q4Z7_ORYGL	Uncharacterized protein		Oryza glaberrima (African rice)	530	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza glaberrima (African rice)	4538	>tr|I1Q4Z7|I1Q4Z7_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1MTSIYHDFIHNKLQSFGRIGRYLVNFVVLAYRFIALHIHPFWIQLSYFLLISILGSVLLMFLKPSNPEFRPGYIDMLFLSTSALTLSSLVTIEMEVLSSSQIVVITLLMLLGGEVFVSFLGLMLRLNHQHNPDFSGDKVSSVPIELDTIDSAGTVISCEELQLEAAIPEVPSSTIKDLKRSKRLRWFLGFVVFSYFVVIHVAGFLLVLWYISRVSSAKAPLKKKGINIALFSFSVTVSSFANVGLVPTNENMAIFSKNPGLLLLFIGQILAGNTLYPLFLRILIWFLGKVTKLRELKLMIKNPEELQYDYLLPKLPTAFLASTVIGLMASLVTLFGAVDWNSSVFDGLSSYQKIINALFMAVNARHSGENSIDCSLIAPAVLVLFIILMYLPPSTTFALSNGDEKAANKKAKRKLGLVVQNLAFPQLACISVFVIVAFITERSRLRNDPLNFSALNMIFEIISAYGNVGLTTGYSCSRLQKLHPGSICQDKPYSLSGWWSDEGKLLLIFVMLYGRLKAFTKGTGEYWRLW
1.7E-25	98.9	23.2	3.3E-25	98	10.5	3.4	1	A0A022Q4G4_ERYGU	Uncharacterized protein	MIMGU_mgv1a018321mg	Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	525	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Lamiales, Phrymaceae, Erythranthe, Erythranthe guttata (Yellow monkey flower) (Mimulus guttatus)	4155	>tr|A0A022Q4G4|A0A022Q4G4_ERYGU Uncharacterized protein OS=Erythranthe guttata GN=MIMGU_mgv1a018321mg PE=4 SV=1MDNLGSNYVKKVKNLCSDSWQLTRLFLRCSYSYLLFTLNPFLIHIFHFFNPFSTRILYFSSLSFAGFGILNALKPRTAALFAPKTLDLFFTSVSVATVSSMSTVEMEVFSNSQLLVITVLMFLGGEVFTSMVGLHFTHTYSKNITRWKSEGRVESVESGPTSPIPAEYSFDQIDLSIAEFLGYVVLGYLLVIQFLGLASVLLYLSVVESAGNVIRKKGIKTATFAVFTVVSTFASCGFLPTNENMIVFRENSGLMWILIPQILLGNTLFPSCLRFTIWVLGRKVKKAEAEFLMKNAAEVGYLHLLPGLHSVLVAATVVGFVLVGFLMFCSLEWDSAALGGLSGYRKVVGVLFQCVNARHTGETIVDLSTVAPAVLVFFVVMMYLPPYTSFLPIIKRDDDQQQNPEIIRNQKRKTSAENLVFSQLSYIVIFIILICITERKSLKDDPINFSVLNIIVEVVSAYGNVGFTTGYSCGRKVSPDPNCVDKWYGFSGKWSDEGKVILIIVMFFGRLKKFNMNGGQAWKLL
1.9E-25	98.8	18.5	8.5E-25	96.6	9.6	3.6	1	K3XH63_SETIT	Uncharacterized protein	Si001234m.g	Setaria italica (Foxtail millet) (Panicum italicum)	485	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3XH63|K3XH63_SETIT Uncharacterized protein OS=Setaria italica GN=Si001234m.g PE=4 SV=1MKTSAVPTPSGLDLIFTSVSATTVSSMVAVEMESFSNSQLLVTLLMLLGGEVFTSMLGLHFTYTKLKKRETQIPHDLDGNNGLPPPSSSLELRTMGGGAPAAVAALEQMETGFKNNLDFTSIARTRMLMFVVLGYLVVVHLAGYTLMLIYLSAVAGAREVLIGKKINPSTFSIFTVVSTFANCGFVPTNEGMVSFKSYPGMLLLAMPHVLLGNTLFPVFLRLSIGALERVTRRRDLGELLVRGGGPGPAAATSTIGYDHLLPAARTWHLAFTVAALVAAQLVLFCAMEWGSDGLRGLTASQKLVAALFMSVNSRHSGEMAVDLAAVSSAVVVLYVVMMYLPPYTTFLPVPVEDHHQYREAQSDEKSKITSSKNIWQKLLMSPLSCLAIFIIVICITERRQIAHDPINFSVRNIVVEIISAYGNVGFSTGYSCGRQVKPDGSCRDAWVGFSGKWSREGKLTLMAVMFYGRLKKFSMHGGQAWKLG
2.2E-25	98.5	9.6	8.2E-25	96.6	6.6	1.8	1	W2CUG0_9PORP	Uncharacterized protein (Fragment)	T230_03245	Tannerella sp. oral taxon BU063 isolate Cell 1/3	341	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, Tannerella sp. oral taxon BU063, Tannerella sp. oral taxon BU063 isolate Cell 1/3	1411022	>tr|W2CUG0|W2CUG0_9PORP Uncharacterized protein (Fragment) OS=Tannerella sp. oral taxon BU063 isolate Cell 1/3 GN=T230_03245 PE=4 SV=1MFHQLNVRFIIKFLGTMHMLESLFMLSAVAVSFWYNDSDLIPLAISCAIMFAAGLAMYITGRHADDYRSGRREGMISVTLTWILLSLFGMLPYLISGYIPNVTDAFFETISGFTTTGATILDDIERLPHGLLFWRSLTQWQGGIGMIVFTVALLPMFGGAASQLFDAETPGITHDRFRPRITQVAQRIFGLYVLITLAFLLLLWIGPMNLFDALNHALTTVATGGYSTKNNGLAYWHSAYTEYIVILGMFIGATNFTLLYFALRGHSQKLFHDHEFRWFCIVIATTTIVTTAWILLRHNETNPELAFRHALFHITALVSNTGLLTVNYSSWGSFFAVIALF
2.4E-25	98.4	23	2.3E-21	85.2	5.4	3.4	3	A0A0D3F1E4_9ORYZ	Uncharacterized protein		Oryza barthii	525	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza barthii	65489	>tr|A0A0D3F1E4|A0A0D3F1E4_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1MNHCLVVSHKKLQTFCAFAASKFSSFTKSSQKSIKNSFQFICQTNPLFVHVTYFALISFAGYAALKVLKPRDKSKNMKDLDVLFSSVSASTVSSMATVEMEDFSSAQLWVLTILMLIGGEIFTSMLGIHFMRAKFGTKESVSTSDHSPCIDIESITSTKFDPSTQGTKVTVSFSELHKENGGHVEPKTIKFLGFVVMGYLLVTNLGGSLLIYLYNLLPSAHQILKRKGIGIIVFSVFTAISSVGNCGFTPVNENMIIFQKNSILLLLIIPQILAGNTLFAPCLRLMMWSLEKITGKKDCRYILEYPKAIGYKHLMSTRESVYLTLTVVSLIILQTVLFLSLEWSSVALDGMSNYQKIVSALFQSVNARHAGESVTDLSSLSSAILVLYTIMMYLPGYTSFLPGHDEDSKTEMRNKRQRLFENWVFSQISYLAIFVMLICITERDSMATDPLNFNVFSIFAYGNVGFSVGYSCKRLLNHDARCKDALYGFAGKWSDNGKAILIIVMLFGRLKTFNMKGGRAWKLR
2.5E-25	98.3	17.4	5.5E-15	64.2	1.5	3.5	3	M0XC46_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	582	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0XC46|M0XC46_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MHIHPPSPNPQHVHTYIVTSNMAGAHRKVCELLYHTRRRSTAALNNVVSLMRSLSGSYAQHHVKERVARWRRALAGRLSPRLGSLLVHVAYFLAVSWLGYLVLAQLRFRAGGEGTRRPGAIDLFFTAVSAATVSSMSTVEMEAFSNGQLLVLTVLMFVGGEVFLSLLGLASKWSRLRKQAVSKSRRVEIHHVAELEMPPVAAAGEFDNPTSMTSTAEEEVSKPLDRFDDTRLRRDAVLSLFFVVLAILLTVHVLGAAAIVAYIFHASSSARRTLRKKALNEWTFAVFTTVSTFSSCGYMPTNENMAVFKRDTGLQLLLVPQALVGNTLFPPLLAACVRAAAAATRRVELKETAKEGEVLTGYYHLLPARRCAMLAATVAGLVAVQVAMLCGMEWGGALRGMSAWEKVSNAVFLAVNSRHTGETTLDISTLAPAILVLFVLMMYLPPYTTWFPFGESSGVKDHPTEETKGLRLLKGTLLSQLSYLAIFVIAICITEREKLKEDPLNFNLLSIVVEVVSAYGNVGFSMGYSCSRQISPDRLCTDRWTGFAGRWSDSGKVILILVMLFGRLKKFSMSAGKAWKLS

2.6E-25	98.3	5.4	2.9E-25	98.1	3.8	1	1	R5VD07_9BACE	Uncharacterized protein	BN536_00543	Bacteroides plebeius CAG:211	188	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides plebeius CAG:211	1263052	>tr|R5VD07|R5VD07_9BACE Uncharacterized protein OS=Bacteroides plebeius CAG:211 GN=BN536_00543 PE=4 SV=1MPVADKWVHAFFNSSCPRTAGFASVGLTSLSTQTLLLMVVLMMIGGGTQSTSGGVKVNVFAVVLINLWAVVRGADRVAILRRELSHDSIRRSNAALILYLFMVFLAIFLLSVLEPEAGLLAITFECVSALSTVGSSLDLTPTLGNSSKLLVILLMYIGRVGAFTLLTGLVRQEKKRNYRYPSDNIIIN
2.8E-25	98.2	3.2	1.3E-22	89.3	0.5	2.1	2	H1UZL8_COLHI	Na+/K+ transporter	CH063_05617	Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)	357	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Sordariomycetes, Hypocreomycetidae, Glomerellales, Glomerellaceae, Colletotrichum, Colletotrichum higginsianum, Colletotrichum higginsianum (strain IMI 349063) (Crucifer anthracnose fungus)	759273	>tr|H1UZL8|H1UZL8_COLHI Na+/K+ transporter OS=Colletotrichum higginsianum (strain IMI 349063) GN=CH063_05617 PE=4 SV=1MSSQARETLHHRGRHQDDSHQPEEDDGGHDVSSSRPSTNSGLRSFLPPLNFITLHYAYFIGTTLLASAVFYASSNPHGSIGYVDSLFLVISAMTEAGLNTVNLSEMTVWQQVMLWLLIIVGSSIWVSIWTVLARKHVFEKSLREAVKGEKERRDQHDQLPIFHDGGAALRGKAEVRVTGVRGTGCSTQARTMGNHITVDTSENPTRRSTSSSSSSIQSARPWLSFFSSAKEGRNSQFHSLTASERSRLGGYEYRALRLLSVVVPLYSVLWQVLGSLALGAWIANNMPSVATSNGANPWWAGIFFAVSAFNNSGMSLLDANMVPFQQAYFVLITMGLLILAGXTAYPVSQTPIFPGLP
2.8E-25	98.2	22	3.6E-22	87.9	15.2	3.5	1	M0YPN0_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	508	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0YPN0|M0YPN0_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MPIRLRTFLSSARHVSNSSVFIFQFIPFHLSPLLVHLSYFVIIDVLGFVALMALKPSNPNYSPRYVDIFFLSTSAVTVTGLATIKMEDLSSSQVVILTLLMLLGSEMFVSLIGHIHELRKQNKHDPEDSRVRSVTVQDESQIEEAIPATQSISTTSLKKSCLKYIGFVLLAYMVLILLVGSLSVFLYVAHVSTARDVLTRKSINTMLFSISVTVSSFTNGGLIPTNESMAVFSSNQGLLLLLTGQILAGNTLLPVFLRLVIWALRGLRIGRAKPEEFKFMMNNTKAVGFNHLLPNQQTVFLAASVAALIAVTVTFFCCLNWDSPVFAGLTANQKITNALFMAVNTRQAGENSIDCSLVAPAALVLFITMWCIPASTSFISLHEGDERGITEHKDRANKRRLSLNKMLFSPLACSAALIMLVCITERRSLSADPLNFSTFNMIFEAISAHRNVGLSMGYSCARLPHAEKESGCQDMPYSFSGWWSDQGKVVLVLMMLCGRLKCFHRHRS
3.9E-25	97.7	22.4	3.9E-21	84.5	5.5	3.4	3	A0A0E0PHW8_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	526	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0PHW8|A0A0E0PHW8_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MNHCLVVSHKKLQTFRTFAASKFSSFTKSAQKSIKYSFQFIYQNNPLFVHVAYFALISFAGYGSLKVLKPRDKSNTLKDLDVLFTSVSASTVSSMATVEMEDFSSAQLWVLTILMLIGGEVFTSMLGIHFMRAEFGTKESVSTRDHSPCIDIESITSTKFGPSTQGTKVTVSFSELRMENGGHVEPKTIKFLGFVVMGYLLITNLGGSLLIYLYLNLVPSAHKILKRKGIGIIVFSVFTAISSVGNCGFTPVNENMIIFQKNSILLLLILPQILAGNTLFAPCLRLMVWSLEKITGKKDCRYILEYPKAIGYKHLMSTRESVYLTLTVVSLIILQTVLFLSLEWSSVALDGMSNYQKIVSALFQSVNARHAGESVTDLSNLSSAILVLYTIMMYLPGYTSFLPRHDGEDSKTEKINKRKGLLENWIFSHMSYLAIFVMLICITERDSMATDPLNFNVFSIFAYGNVGFSVGYSCKRLLNHDARCKDASYGFAGKWSDNGKAILIIVMLFGRLKTFNMKGGRAWKLR
4.8E-25	97.4	14.1	2.2E-21	85.4	6.6	4.2	2	C5Z968_SORBI	Putative uncharacterized protein Sb10g029000	Sb10g029000 SORBIDRAFT_10g029000	Sorghum bicolor (Sorghum) (Sorghum vulgare)	545	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Andropogonodae, Andropogoneae, Sorghinae, Sorghum, Sorghum bicolor (Sorghum) (Sorghum vulgare)	4558	>tr|C5Z968|C5Z968_SORBI Putative uncharacterized protein Sb10g029000 OS=Sorghum bicolor GN=Sb10g029000 PE=4 SV=1MPIRFHVLASAARHAVSSSVLVCRLIAYHLTPLLLHLTYFLAVDLLGFLALVLLKPSNPGYRPRYIDVFFMSTSAVTVTGLATVEMEDLSSAQLVVLTLLMLLGSEMFVSLLGLVLESSRNRRQQQRDHQDHDSRVMAAAAVRDEPDLEEANGPAAAPSADSSGDGGDRNRKESSRDVRSLALVVSAYMAAILVVGSVLVFAYVATVPTARDVLARKRLSAALFSVFATVSSFTNGGLLPTNESMAVFAPNRGLLLLLAAQILAGSTLLPVFLRLVVSATRGLARALSLFTGRGGSVEELVPMDMEKSAAAAGFGHLLPSGSRAASLAATVVAVATAAAALLCCLNWNSAVFAGLTTGEKLTNAVFMAVNVRQAGENSVDCSLVAPAVLVLFLAMTCIPASATLLSVQDDGGEKTRSGAGEPERKDGAEKKRRRRLSLNSMLLSPLACNAAAVMLACITERRSIAGDPLNFSTFNVIFEVISAYGNVGLSTGYSCSRLPPPPATTACHDKPYSFSGWWSDQGKLLLVLLMLYGRLKGFHGQRRRR
6.1E-25	97.1	10.7	7.1E-25	96.9	7.4	1	1	D4KDH4_9FIRM	Trk-type K+ transport systems, membrane components	MHY_16060	Megamonas hypermegale ART12/1	164	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	657316	>tr|D4KDH4|D4KDH4_9FIRM Trk-type K+ transport systems, membrane components OS=Megamonas hypermegale ART12/1 GN=MHY_16060 PE=4 SV=1MDTGALHEASLFFIIILMFLGASPGSTGGGIKTTTFAIIFATVTSIIRGNEEVTLFKRRIEHDLIVKSLAIFYIAAALVVLGTMFLCLTEDFPFIKILFEVTSALATVGLSTGITSSLTVYGKSILVLIMFIGRLGVLTFLMAIAMRNRKTAKIGYPSERIGVG
7.3E-25	96.8	9	2.2E-24	95.2	5.6	2.2	1	B9L3I2_THERP	Potassium uptake protein KtrB, putative	trd_A0346	Thermomicrobium roseum (strain ATCC 27502 / DSM 5159 / P-2)	468	cellular organisms, Bacteria, Chloroflexi, Thermomicrobia, Thermomicrobiales, Thermomicrobiaceae, Thermomicrobium, Thermomicrobium roseum, Thermomicrobium roseum (strain ATCC 27502 / DSM 5159 / P-2)	309801	>tr|B9L3I2|B9L3I2_THERP Potassium uptake protein KtrB, putative OS=Thermomicrobium roseum (strain ATCC 27502 / DSM 5159 / P-2) GN=trd_A0346 PE=4 SV=1MRRPGDRIVRREPLPSEVIRLRLVPRRRITLPLLVVLWLILGGAVMIGMLLLRWPATWQHAEGPSWWEAFFTALSATCTAGFAPLDVATTWNRWGQLVILLLVEAGGLAYVAIAVLLLSGIVRRTTVYEAHHVLGMRLGEEQLGELWPLVRRLLVATLLVQFGGMLLLLPASWREHQDGASALWWAMATAVTAFHNAGFDFEPGYRGLAAYQRDWGVVLPVAMLVLIGSIGFPTLSDLVTRRSWRRLYPDTRLVLVTTALLLSIGTLGIWFLERSNAATLAGVPWYQQLLDAFSVAVSRTGGPRVIDTRMLGEETSFLLGGLTFIGGASGSVAGGVKVQTFSLLLLAILATIRGSQRVVAFSREVPDRQVFRALSIAVFALSVTFAGTVWLAFLVPYTLPVIWLLVVQAFSLAGAESELLAALGTPGQLVLAFLIVLGRFGPLGLALIFATQVPRETVHYARETVRLG
7.4E-25	96.8	22.2	4.2E-17	71.2	7.4	3.2	2	I1LSK8_SOYBN	Uncharacterized protein		Glycine max (Soybean) (Glycine hispida)	562	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine, Soja, Glycine max (Soybean) (Glycine hispida)	3847	>tr|I1LSK8|I1LSK8_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=2MMKNFAYYFSQKQQHQRFCRFFPHSLGFLVRFLAFHVHPFFIQLCYFVILSLLGYLGLKASKPRTPLRPNDLDLFYTSVSASTVSSMVAVEMEVFSNSQLILLTLLMFVGGEVFTSMLDLVFARYKFTRSVQNKVSTNHSYLTRTRLPPVDDTSGLDQIFFSSNPFLSTKKPSINANQIELGLVSIHHSESENHKPSDSNNTNVPKGTVVSFNDSDRLKYNCLSYLTYLVLGYLVVVQFVGFSSVSLYITLVPSARQVLKNKGIKIATFSLFTIVSTFASCGFIPTNENMMVFKKNSGLLLLVLPHILLGNTLYPPCLRLVIMVLERITKREEYSHLLKNFKDVGYDHMLSALHCCLLVATVLGFNLIQFVMLCSMEWNTKIMEGLNVYEKVVASLFQVTNARHAGESVFDLSSISSVILVLFVVMMYLPPYTTFLPVREHENDAKRSEKSVLECLVFSQLSYLVIFIILICITESKSLREDPLNFNVLNITLEVISAYGNVGFSTGYSCARQLKPDATCKDSWVGFSGRWSSKGKFILILVMFFGRLKKFNMKGGKAWDLS
1.3E-24	96	15.4	3.6E-23	91.2	4.9	3.6	2	W5BBV2_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	578	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5BBV2|W5BBV2_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MHPNTSTHTYSDSSTSNMAGAHRKVRELLEHTRRRSTAALNNVMSLMRSLSGSYAQHHVKERVARWRRALAGRLSPRLGSLLVHVAYFLAVSWLGYLVLAQLRFRAGGEGTRRPGAIDLFFTAVSAATVSSMSTVEMEAFSNGQLLVLTVLMFVGGEVFLSLLGLASKWSKLRKQAVRKSRRVEIHDVAELEMPPVAAAGEFDNPTSITSTADDEMSKPLDRFDDTRLRRDAVLSLFFVVLAILLTVHVVGAVAVAAYILHASPAARRTLREKALNEWTFAVFTTVSTFSSCGYMPTNENMAVFKRDTGLQLLLVPQALVGNTLFPPLLAACVRAAAAATRRVELKETAKEGGELTGYYHLLPARRCAMLAATVAGFVAVQAAMLCGMEWGGALSGMSAWEKVSNAVFLAVNSRHTGETTLDLSTLAPAILVLFVLMMYLPPYTTWFPFGESSSVKDHPTEETQGVRLLKSTLLSQLSYLAIFVIAICVTEREKLKEDPLNFNLLSIVVEVVSAYGNVGFSMGYSCSRQISPDGMCTDRWTGFAGRWSDSGKLILILVMLFGRLKKFSMNAGKAWKLS

1.4E-24	95.9	17.3	7.8E-15	63.7	2.6	3.6	2	C5XIQ7_SORBI	Putative uncharacterized protein Sb03g012590	Sb03g012590 SORBI DRAFT_03g012590	Sorghum bicolor (Sorghum) (Sorghum vulgare)	498	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Andropogonodae, Andropogoneae, Sorghinae, Sorghum, Sorghum bicolor (Sorghum) (Sorghum vulgare)	4558	>tr|C5XIQ7|C5XIQ7_SORBI Putative uncharacterized protein Sb03g012590 OS=Sorghum bicolor GN=Sb03g012590 PE=4 SV=1MKSISVPRPSALDLVFTSVSATTVSSMVAVEMESFSNSQLLLMTLLMLLGGEVFTSMLGLHFTFTKFIKKREIPHSNNNSLHGNIN GPAPAAPSSLEHGHRRRPMEMEAQAAAVQMELAGFNNDDQRDFASIARLLMFIVLGYLSVVHLAGYTLILIYLSVVGSAREVLVGKRIS LSTFSVFTVVSTFANCGFVPTNEGMASFKSFPGMLLLVMPHILLGNTLFPVFLRLSITALERVTRRGDLRELLRDGGPGGGGGGGGG PAAAAIGYDHLLPGGRTWCLALTVAVFLAGQLLLYCAMEWGSDGLRGLTAFQKLVAALFMSVNSRHSGEMVVDLATVSSAIVVLYVL MMYLPPYTTFLPIAMEDHQQQQNEAQSDDKSKSSSSISIWQKLLMSPLSCLTIFIVVICITERRQIADDPINFSVLNIVVEVISAYGNVGF STGYSCSRQVTPDGSCRDAWVGFSGKWSREGKLTLMAVMFYGRLKKFSMHGGQAWKLG
1.8E-24	95.5	13.2	3.5E-21	84.7	5.2	3.5	2	A0A0E0KUX2_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	516	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0KUX2|A0A0E0KUX2_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MKLLLPDSEVLRIYREKAQHLCGFLSMKLISLSKCVIHSVKQSCSFLVCKSNPLVVQLVYFVTISFAGFLALKNLKPQGKSGPKDL DLLFTSVSTLTVSSMATVDMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLLSISMDIESNSPANNGVHKITEC GQSEETMSQNQVQKNKSITYNPCAVLARIVTDARDLLKSKEINMYTFCIFTAVSSFANCGFTPLNSSMQPFRKNWVLLLLVIPQILAGN TLFSPLLRLSVWVLGKVSGKAEYAYILQHPGETGYKHLHVRRNSVYIVLSVTGLILLQVMFICSFEWNSESLEGMNLLQKLVGLLFQSV NTRQAGESVLDISKLSPPTLLLFAVVMYLPSDASFLTANADNQPLTHKKINSISRELWRNFTANKLSCLAMFTFLACITERKSISADPRN FNIFSIVFEIIRQTAITAFGNVGYSLGYSCQKLLKPDGTCKDVSYGFVGRWTDKGKLIVILVMFLGRLKEFILK
2.1E-24	95.3	20.9	2E-13	59.1	5.4	3.9	2	A0A096QKF8_MAIZE	Uncharacterized protein		Zea mays (Maize)	493	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Andropogonodae, Andropogoneae, Tripsacinae, Zea, Zea mays (Maize)	4577	>tr|A0A096QKF8|A0A096QKF8_MAIZE Uncharacterized protein OS=Zea mays PE=4 SV=1MLRVLPMKSSSVPRPSALDLLFTSVSATTVSSMIAVEMESFSNAQLLLMTLLMLLGGEVFTSMLGLHFTCTKLRNKRETPHNNL HGNSLEQSRRRHRPMEMEAQAAAVQMELAGFNKDGHGDFASMARLLMFIVLGYILVVHIAGYALILIYLSVVGSARAVLVRKRISLSTF SVFTVVSSFANCGFVPTNEGMVSFKSFPGMLLLVMPHILLGNTLFPIFLRLSITALERVTRWRDLCELLRDRGPGGGPAAAAAAAIGY DHLLPGPRTWFLALTVAVFLAVQLVLYCAMEWGSGGLGGLNAFQKLVAAVFMSVNSRHSGEMVVDLATVSSAVVVLYVLMMYLPPY TTFLPVAVEDDQQQQNEAQPHDNSTSKSSTSISIWHNLLMSPLSCLTIFIVVICITERRQIARDPINFSVLNIVVEVISAYGNVGFSTGYS CSRQVTPGGGCCKDAWVSLSGKWSVEGKLTLMAIMFYGRLKKFSMLGGQAWRLN
2.1E-24	95.3	2.3	4.2E-11	51.4	0.2	3.3	3	B8P9V4_POSPM	Predicted protein	POSPLDRAFT_104192	Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	611	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Postia, Postia placenta, Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	561896	>tr|B8P9V4|B8P9V4_POSPM Predicted protein OS=Postia placenta (strain ATCC 44394 / Madison 698-R) GN=POSPLDRAFT_104192 PE=4 SV=1MPQMEDILSNSWTLYLFALTAWQQAIIVILELTGNQAFTSWVVVYFRRRYFLKHLEHIVIAESERGAAQHDRVGEAPSLRTIRDVL LQRSQSANEEGHARRKGLFFSAKDDRTPIRPEMVRRVDVEPHRIDPTGRQASPYTSAVDEHIHGGADEALRRTASRSDSLRTDRSPP PSPRNTTEDDLGGFPDPPQVLSGVLRALFPGLHNRLRRRMMMPRTETLVPQASIVDGRAPSSGRWKAVSYLPFSATVGRNSAFRGL SAEQIDQLGGIEYRALTALLWIVPLYYFGLLAISFVVIAPYMTLPRWQYLFAPPEQHRKINSIWFSAFQVIGAWANTGMSLVDQNMVPF REAYPMIIFLVICVLAGNSALIIGHATDVIQLAIDLIAFVFDILNLGNPVTDSIPAGVRVINAVLAAAGVRSSGFQSISVSTLTPANHVRSTN VYEERALGIYTGDHDDVEDNINEKEWRSGQESRVAIWGRHILRHARKQLSIDMWWLSLSLFFICIIERSPLMNTDNASWFNIWAITLDR AIMLPREFQRHEDDGARVPGRISEASSVQKEHEPSTLKSTSKAESTGRVSFAEDDKRPSRVGTHTLNQISEVERGDESRY
2.3E-24	95.2	35.4	9.3E-24	93.2	24.5	1.9	1	A0A0G1DBU4_9BACT	TrkH family potassium uptake protein	UV38_C0002G0140	candidate division TM6 bacterium GW2011_GWE2_42_60	454	cellular organisms, Bacteria, unclassified Bacteria, candidate division TM6, unclassified candidate division TM6, candidate division TM6 bacterium GW2011_GWE2_42_60	1619076	>tr|A0A0G1DBU4|A0A0G1DBU4_9BACT TrkH family potassium uptake protein OS=candidate division TM6 bacterium GW2011_GWE2_42_60 GN=UV38_C0002G0140 PE=4 SV=1MTFHRPFTISPWRVIIFSIIFITIMGSLLALPAAQKTPHSFVDLFFTSSSAVCVTGILTVPLDSFSFLGKIIILFLIQVGGLGLLTLIIPLV SLFFNVRMRTHLITGHQFELENWSHNWIYSRHVITFIVCFSLMIEAIGSVTTYFLIGNEPLSDPRWFAALFHGISSFCNSGIAIFPGDMAS VQSNGPLIALTSVLMVIGGFGFVPLYEISIRLWNKFRGIPNHSRHLTLQSKIIIYFTPALTLIFAPLIWISEHIQFAGMTFWQTINMTLFNAIS LRSCGFCTLDLSTMTDITLLLILVFAFIGSSPGSVGGGTGIKVTSFVLALASIRTAILGKEQVELFGRRIPVEQIFRAFAIIVVSLSWCIFSTL ILMITESGSPHPFMHFLFEAVSAFANHGVTLGLAPSMTGIGKYFFSVGMIFGRISSLTLILALKKHKEKSDIRYPEERILLV
2.3E-24	95.1	13.7	4.8E-14	61.1	4.5	2.9	2	B8B251_ORYSI	Putative uncharacterized protein	OsI_24358	Oryza sativa subsp. indica (Rice)	467	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>tr|B8B251|B8B251_ORYSI Putative uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI_24358 PE=4 SV=1MEDLSSSQIAILTLLMFLGSKMFLSFLGLVLESSKQNKHDPENRRVSSVTVCKQSQLEEAIPQTPSMNSIDIKKRCLKYLGARDVL TRKSINKALFSISVTVSSFTNGGLLPTNESMAVFSSNNGLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKAEEPDFMMNNSSAVGFS HLLPNLQTIFLAAVEVAFVAMTVILFCCLNWDSVVFAGLSSLQKITNALFMAVNARQAGENSIDCSLVAPAALVLFMVHSILDKVVLSMS RSQTNRPESDDRTSKGKPFLKMMAFSPLGFNTTVIMLVCITERRSLSTDPLNFSTFNIIFEVISAYGNIGLSTGYSCSRQLQHQEGIACH EKAYNFSGWWSEPGKLILVLAMLCGRLNSKDSTSARTRWIWFLVRSQKISVGFDTKLTLVIIGAVGGGAAIGGGAAAGAASGGAAAE APKAEEKEEEKEESEDDLGFSLFD
2.9E-24	94.8	15.9	7.8E-22	86.8	11	2.1	1	R5WH07_9DELT	Cation transport protein	BN495_00323	Corallococcus sp. CAG:1435	363	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, environmental samples, Corallococcus sp. CAG:1435	1262867	>tr|R5WH07|R5WH07_9DELT Cation transport protein OS=Corallococcus sp. CAG:1435 GN=BN495_00323 PE=4 SV=1MNFRVIFQIFGRVSVLVGVLMCLPMILSACLGESCWWAFAIAIAIAVAVGVPVVVLCKPKSKAFFSKEGLVLVSLSWIWVSLVGA LPFVISGAIPSYIDAFFETVSGFTTTGATILQGSYIEQMAKGLLFWRSFTHWIGGMGVIVFVMMIASNLENHSIHVLRAEMPGPTVDKLV PRARTTAKILYLLYIGLTLLEITLLIFGGMPIFDSVVHSFGTAGTGGFGIKADSIAGYNAFCQWVIAIFMLLFGVNFNLYYLMILCKFRQAF SSRELWLYAGVIVFSATVVTFNVISQLPYTKTTADAVRFAVFHVASFLTTTGYTAIPASSSINAWPLLSKSLLFCLMFIGGCAXXXWLRR QYCRWS
3.8E-24	94.4	34.4	9.3E-23	89.9	23.8	2.1	1	R6Y3V9_9FIRM	TRK system potassium uptake protein TrkH	BN617_01086	Firmicutes bacterium CAG:345	513	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:345	1263020	>tr|R6Y3V9|R6Y3V9_9FIRM TRK system potassium uptake protein TrkH OS=Firmicutes bacterium CAG:345 GN=BN617_01086 PE=4 SV=1MNREIKKEMVISGGKLALGYIGLLTGIIGIVLLIPLFVSISLPLERKYWWNFFAPAIIMIICGFSTFLGLLYKKEHGQLSNRQSSFIVLT SWIISILGTAVPFWSSGLLNFHQSIFEVSSGWTTTGMSVLDVEQGNIYSFLTLRALCMLFGGIGIILVMISVFSDRYGLRLYSAEGHGDS FLPNLLRSARLMFAIYIGLITVGIISYMIFGMSFFDAFVHSITAVATGGFSNYNDSIAHFSIENGYNIIQVCGIQVTSIILMFSGSISFISFAFL LRGDFKTFFKNFENHAELVILVIVIPLILILSITSNTVTSNNALMYSVFFTISAMSTTGFQIMSIDINTLNPAICFIFILIMLIGCQSSSTCGGIK VGRISLLYHSLVIKLRNSANNLNIKRADYVNVYGKDMFLDEALLHDNNIFILTYLGIYLAGAFLFTLGGSSLNQSLFESASMISTIGFSTGM VNLSSPTYYYYVGASLMIFGRFELFMVIYGIIYIFSIPFNKIKLLLSRRK
4E-24	94.4	19.2	1.6E-23	92.4	13.3	1.7	1	R6S508_9FIRM	Trk-type K+ transport systems membrane components	BN661_00936	Firmicutes bacterium CAG:449	282	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:449	1263023	>tr|R6S508|R6S508_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:449 GN=BN661_00936 PE=4 SV=1MDAFSSLCITLGTAGTGGFSITNAGISSYGMYSQYVIAIFMFLFGINFTNFYLIAIKKYKDVFKNEELRLYIILVFLSTMIIFINLLINCA SIYSPEEAFRAAFFQVSSIISTTGYGTTDYEVHWPSLSKSILVFLMLTGPCAGSTGGGVKLQRINILFKNIIRKIKIMISPHRIEIIKQDEQIL DEETSNDALVFFSLYIFLLMGSTLIISIDGHDFATNFTASLSCISNIGPGLGKVGPYGNFKMFSNFSKLVLSFLMITGRLELFPMICLFNPR TWRKR

4.7E-24	94.1	22.8	8.1E-24	93.4	14.1	1.8	1	V4N0M2_EUTSA	Uncharacterized protein	EUTSA_v10028767mg	Eutrema salsugineum (Saltwater cress) (Sisymbrium salsugineum)	354	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Eutremeae, Eutrema, Eutrema salsugineum (Saltwater cress) (Sisymbrium salsugineum)	72664	>tr|V4N0M2|V4N0M2_EUTSA Uncharacterized protein OS=Eutrema salsugineum GN=EUTSA_v10028767mg PE=4 SV=1MERVVDKLAKIFSQHAKSLPLFFLYFFYFLFFSFLGFLALKISKPRTTSRPHDLDLFFTSVSAITVSSMSTIDMEVFSNTQLIIITILMF LGGEIFTSFVNLYFSHFINFKIKHLVGSFNFDRPINDPGSDLENVTNHVKLSSQINERASKCLYSVVLGYLFVTNIAGSTLLLLYVNFVKT ARDVLSSKKISPLTFSVFTAVSTLSDCGFVPTNENMIIFRKNSGLLWLLIPQVFMGDTLFPCFLVLAIWGLHKITNREELGYILKNHKKM GYSHLLSVRLCVLLALTVLGLVMIQFLLFCTFEWNSESLEGMNSYEKLVGSLFQVVNSRHTGETVVDLSTLSPAILVLFILMM
5.1E-24	94	24.1	2E-21	85.5	15.8	3	2	W5HMW0_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	462	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5HMW0|W5HMW0_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MPIRLPIFLSSARHVSNSSVFIFRFIAFHLSPLLIHLSYFVIIDVLGFVALMALKPSNPNYSPRYVDIFFLSTSAVTVTGLATIKMEDLS SSQVVVLTLLMLLGSEMFVSLLGHIHELSKQNKHDPEDSRVRSVTVQDESQIEEAIPATPSINTISLKKSCLRYIGFVLLAYMVSILLVGS LLVFLYVAHVSTARDVLTRKSINTMLFSISVTVSSFTNGGLIPTNESMAVFSSNQGLLLLLTGQILAGNTLLPVFLRLVIWALRGLRITRAK PEEFEFMMNNTKGVGFNHLLPTQQTVFLTASVAALIAVAITLLCCLNWNSAVFAGLTPNQKITNALFMAVNTRQAGENSIDCSLVAPAA LVLFIAMWCIPASTSFLSLHERDKRGITEHKDGANKRRLSLNKMLFSPLACTAVLIMLVCITERRSLSADPLNFSTFNMIFEVISAYRNVG LSIGYSCAR
6.6E-24	93.7	7.3	3.8E-10	48.3	0.7	4.1	4	R1DQW6_EMIHU	Uncharacterized protein	EMIHUDRAFT_210516	Emiliania huxleyi CCMP1516	925	cellular organisms, Eukaryota, Haptophyceae, Isochrysidales, Noelaerhabdaceae, Emiliania, Emiliania huxleyi (Pontosphaera huxleyi), Emiliania huxleyi CCMP1516	2903	>tr|R1DQW6|R1DQW6_EMIHU Uncharacterized protein OS=Emiliania huxleyi (strain CCMP1516) GN=EMIHUDRAFT_210516 PE=4 SV=1MPQPFERDLLGEQLDAARDGIPASVSQRLLLNLPEASLDVALAATIEAKASTKVNIWQGLFARSAANAASQPTAGAPAPTPEVV ATAAAATRLQAIERGHLLRRHQAEQANAAAKIEAAARERIGRRGRNQAAPPPRTTAAVDLPDPDVAPQSLDSAAPDVVPMKASLLHH RRVPFKGMVVAWYLLLGGLGGLLLYAIESKQSGLGLADAIFLAVSASTCTGLATFNITAFGDAAKALLGLLMVAGSSILISAVPLHLRHA ALRRNVPEGLRHVALKDLRRCPEWLVELNSMRLLLYAIYIYQAALLGGFCFIYVSVLATPVEERGVCDYPSYSTASTAGQPPSNVTGL PCRPGRFAAFVSVAAFANAGMTSEPGSLEAFNEEIGLLSVVTVLALAGNVLYPVLLRLSLQAYLQCIPIDDARRLWARHLLLSGRKMY GYLFSTEQTTTLFLTQLAVWAAQTFTTWSFFVREAHRGMIRVYGSRLGGVSKILSDLAACDADVQCFRTMEERLALPDDMFMSVETR HAGFAIYSLANENTPVLAMYMLAMMMAPVPLMIAVHASSRHGAALESPLHDGPHTAAPTALGVGGRKSVSIAEHWARRHSIVRTTGT GAARAALSRSRIRMAEQIDELSLALARIPSVDPRVSAESRTSEASVADLGVLQLQAMLWHGELTWGQTLRHHLTAFSHAVGGFVGGP TLQRDLLFAWLAWFLVLAFDPDLPHGSNGAAFDALFEVCSAFGNVGLSMGYSRDTELENVRPGTPQTFVDSLPRGETGLSYCACWP NLSKAVLVAVMIYGRTRALPQQVDYALTLAIEIPSSDMSPVELLLSPGGERDSDERDSTRARGSWLFSQADLRGLARRLTGSTPAHHP GAVPQRDGVSSGNESTDEAGTLGDLLDARAPDDEGASGSHARPEQRANKVLV
8E-24	93.4	11.7	9.4E-24	93.1	8.1	1	1	D4KDH5_9FIRM	Trk-type K+ transport systems, membrane components	MHY_16070	Megamonas hypermegale ART12/1	215	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	657316	>tr|D4KDH5|D4KDH5_9FIRM Trk-type K+ transport systems, membrane components OS=Megamonas hypermegale ART12/1 GN=MHY_16070 PE=4 SV=1MLPIASNDGSSLSFIDALFTATSAVCVTGLIVVDTGQYFSIFGQLVIIMLIQIGGFGVMTMTTVFALILGKRIQLRSRLIAQESLNRLT VGGVVKLIKLLVKTTLCIEFIGGVLLSFRLYPDYGLHGIYMAFWHSISAFCNAGFDIFGGTNIFKYNTDPLFCLVIAFLIILGGIGYGVTVEL YQKHNWKMFSLHAKVALLTTLILLVIGTIVLFF
8.9E-24	93.2	17.8	8.9E-24	93.2	12.3	3.2	2	M4F9Z6_BRARP	Uncharacterized protein	Bra037910	Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	513	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, malvids, Brassicales, Brassicaceae, Brassiceae, Brassica, Brassica campestris (Field mustard), Brassica rapa subsp. pekinensis (Chinese cabbage) (Brassica pekinensis)	51351	>tr|M4F9Z6|M4F9Z6_BRARP Uncharacterized protein OS=Brassica rapa subsp. pekinensis GN=Bra037910 PE=4 SV=1MERVLAQLAKIRLQLAKFRSPFFIYFFYFFSFSLLGFLALKVSKPRTTSRPHDLDLLFTSVSAITVSSMSTIDMEVFSNTQLIIITILM FLGGEVFTSFLDLYFSHFSNFVFPHNKIRHLMGSLNIKPPTEDRRRDLENITDHLKRPSQINERASKYLYSVVLGYHLVTNLAGSVLVLV YVTFVKTAKVVLSSKEISPVTFSIFTTVSTFGNCGFVPTKENMVIFRKNSGLLWLLIPQIFMGNTLFPCFLFLLIWGLDKITKREEFGYILK NHKTMGYSHLLSLRLCVLLGLTVLGFVMIQFFVFCTFEWNSVSLEGMNPYEKLVGSLFQVVNSRHTGENIVDLSTLSPAILWNKLFLA MNFNTFSLKRYLPPYTLFMPLTTIKKYKEEVEDHTGNEEKRKKTGFFVSQLSFLAISVFFISITESQNLRRDPLNFNILNITLEVISAFGNV GFTTGYSCKRRLDINNGSCKDTSYGFVGRWSPNGKFILIIVMLYGRFKQFTAKSGRPWILYP
9.5E-24	93.1	0.1	4.4E-23	90.9	0	1.9	1	A5E1G8_LODEL	Putative uncharacterized protein (Fragment)	LELG_03455	Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) (Yeast) (Saccharomyces elongisporus)	741	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Lodderomyces, Lodderomyces elongisporus, Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) (Yeast) (Saccharomyces elongisporus)	379508	>tr|A5E1G8|A5E1G8_LODEL Putative uncharacterized protein (Fragment) OS=Lodderomyces elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) GN=LELG_03455 PE=4 SV=1MNSFSRLRKRFKERRFHFEFGLHFRNFIHRVVSAVYPYAKKVLPNFRAVHYFYILSCAIIGSILVYPVKTARYIDILFLTSGASTQA GLNTVNLVDLSLYQQIVLFLLASLTTPIFIHGSLLFVRLYYFERHFDNIKEKSKLDFKMRRSATLARTRSGTSMDSTRVNTNNNKGLGIY DHEKEADTSGSPQSSTLTNKHAGSADTNNDVEHMTEPSDDEKDVNERLNHRRDADEEEEVETYSAGQYNSHNNNNKSNNNKNDKN DTINNINSSSSKTQGIKFGALPHPPKRKKSIDPEDMLRSINMLQEKQKQKQKQNPHSIQFVNVSSPSRERREQADHSNYNNDHHHHH HHHQMHNRLMDHEISSKHGEFSHDDVNNDDSNNNNNNNNDNDSRIHHDDDDDDDDVLIIKPPNEVEHFGSHNSIFTKKHNHSTLH FKEPIMKKKWLQGGVNARKHYRPWTSKLRKTFSNRRFSTASSDIEDDDASIDSEHDMSHRSEDDGDGDQDEDEEEDEAEDADDEN DDDDDGLSDAHYEDENAITEDDDDEEEEEDDDDEDRRRTGSSRHKVRSTSRTIHPTQSIGLNDVELGNIKYLNAKPARKSGKTKTPA RRRRKRRFDVKKIKTPSLYPSLSNHSGAIRPTNTSESTHSNGLSRTMSGNYLSWTPTVGRNSTFIKLTEEQKDELGGIEYRAVKLLIKII VIYYLGFHIVPGIMFIIWVYCMPNYKKMLDGLSIVPAWWAFFT
1.1E-23	92.9	20.9	2.4E-20	81.9	6	2.4	2	A8A8X4_IGNH4	Cation transporter	Igni_0192	Ignicoccus hospitalis (strain KIN4/I / DSM 18386 / JCM 14125)	462	cellular organisms, Archaea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Ignicoccus, Ignicoccus hospitalis, Ignicoccus hospitalis (strain KIN4/I / DSM 18386 / JCM 14125)	453591	>tr|A8A8X4|A8A8X4_IGNH4 Cation transporter OS=Ignicoccus hospitalis (strain KIN4/I / DSM 18386 / JCM 14125) GN=Igni_0192 PE=4 SV=1MSLVVSSLAFFLASLTSLTYPYFDDYVALSFVIAAAYAYAASRLVKYAIAVTNPAIMIKALVLFWFLTPFLVALPFSYITGLGLIDSYF EMVSGFTGTGLTVLNPSAETPFVNALRASSQWAGEVGALFLTLILAIVFHVSPTGIVSALGKGERVRPSMYNTLIDLILIYLVLTIIPIVYM KLVGMSLYDAIVYTFAALATGGFAPTAGGTADLPFVQQLAVILTCVLGAVNFSVYLNLRYNKVRNALKHPELRLLIASILFYALLLFVWK RFDAEHLWSALFHSASAVTTSGFQIQDVSKFGESSKYIITVAMIVGASAFSTGGGVKLYRAYVLGKSIMKQIKSLGTPRGYVSTVTVM GKEITSEELTTMLTVVATYLFTMFALALVLTEQLSAHKVKVPSIDVIFEVASAMSGTGLSSGLTAIAPPDVKITLSIAMILGKLELVLPFLFFL YDSLRSLKK

1.2E-23	92.8	21.9	1.4E-22	89.3	10.4	3.4	2	A4ZGN6_WHEAT	HKT8 (Uncharacterized protein)	HKT8	Triticum aestivum (Wheat)	516	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|A4ZGN6|A4ZGN6_WHEAT HKT8 OS=Triticum aestivum GN=HKT8 PE=2 SV=1MGSLHVSSSATQHSKLERAYQLLVFHVHPFWLQLLYFVSISFFGLVILKALPMKTSTVPRPMDLDLIFTSVSATTVSSMVAVEMESFSNPQLLLLTLLMLLGGEVFTSMLGLHFTYVKSKKKEAQAPHDHDDGDKGKPAPSSSLELAVTTGMDDVDRVEQGFKDQPRYDRAFLTRLLLFIVLGYHVVVHLAGYSLMLVYLSVVSGARAVLTGKGISLHTFSVFTVVSTFANCGFVPNNEGMIAFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIWALRRVTRRPELGELRSIGYDHLLTSRHTWFLAFTVAAFVLAQLSLFCAMEWGSNGLRGLTAVQKLVAGLFMSVNSRHTGEMVVDLSTVSSALVVLYVVMMYLPPYTTFLPVEDDSDQQVGADQRDQKRITSMWRKLLMSPLSCLAIFIAVVCITERRQISDDPLNFNVLNITVEVISAYGNVGFSTGYSCGRQVTPDGGCRDTWVGFSGKWSWQGKLALIAVMFYGRLKKFSMHGGEAWRIV
1.5E-23	92.5	15.6	1.6E-19	79.2	7.5	4.4	2	A0A096S8Y3_MAIZE	Uncharacterized protein		Zea mays (Maize)	555	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Andropogonodae, Andropogoneae, Tripsacinae, Zea, Zea mays (Maize)	4577	>tr|A0A096S8Y3|A0A096S8Y3_MAIZE Uncharacterized protein OS=Zea mays PE=4 SV=1MPVRLHVLASTARHAASSSALVFRLVAFRLTPLLLHLSYFLAIDLLGFLALVLLRRSSPAAGAYRPRYVDVLFMSTSAVTVTGLATVEMEDLSASQLVVLTLLMLLGSEVFVSVLGLVLESSRQQRQQRGQSRRQDHAGRVIRPSSVTAAVRDEPDLEEAGNNINSQAPPSSSEDSSGDGDNHKERCRAVRSLALVLSAYMAAVLVAGSVLVFAYVATVPAARDVLARKRLGAALFSVSATVSSFTNGGLLPTNESMAVFAANRGLLLLLAGQILAGCTLLPVFLRLAVGATRWVARAVSAGRGGHDEELEPVSVDRSAAAAGFGHLLPSVPRAASLAATVVAVAAAAAAALLCCMNWNSAVFAGLTPGEKVTNAVFMAVNVRQAGENSVDCSLVAPAVLVLFLAMMCIPASATLLSVHDSGSDRKRSGAGEAERKDGTEKKRRLSLNSMLLSPLACNAAAVMLACVTERRSIAGDPLNFSTFNVIFEVVSAYGNVGLSTGYACSRLLPAAAEATTACHDKPYSFSGWWSDQGKLLLVLLMLYGRLKCFHGQRRRG
2.1E-23	92	7.8	2.5E-23	91.8	5.4	1.1	1	C4XEZ7_MYCFP	Putative uncharacterized protein	MBIO_0454	Mycoplasma fermentans (strain ATCC 19989 / NBRC 14854 / NCTC 10117 / PG18)	280	cellular organisms, Bacteria, Tenericutes, Mollicutes, Mycoplasmatales, Mycoplasmataceae, Mycoplasma, Mycoplasma fermentans, Mycoplasma fermentans (strain ATCC 19989 / NBRC 14854 / NCTC 10117 / PG18)	496833	>tr|C4XEZ7|C4XEZ7_MYCFP Putative uncharacterized protein OS=Mycoplasma fermentans (strain ATCC 19989 / NBRC 14854 / NCTC 10117 / PG18) GN=MBIO_0454 PE=4 SV=1MKNSKIAAWWRKSKIRQFFANYRVWRLNITKVKYIFLAYLLTVIIATLFLLSPWTHKDSSVKVSFWDALFTTSSAFSDTGLVTKTTYNTWNMFGQAIIAILIFLGGLGIFALRIFLINLIFFKRRNSLSELEVVSHERGSGDSGQTKKLIMDSIGTLLIIWIIFSFGLTFYFYYNEPKAYSDFDKYGDYISPYKNWGLSFRYGFFHCISALNNAGFDIIGKNSLMPYYHNIGLQIIFLTLLIIGGLGYPVIHDILNFFRFLIKYKGKRRYQWRLFTKISL
2.9E-23	91.5	14.1	5.9E-23	90.5	9.8	1.4	1	T0U8J1_9ENTE	Potassium uptake protein, integral membranecomponent, KtrB	HSIEG1_3799	Enterococcus sp. HSIEG1	258	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	1316414	>tr|T0U8J1|T0U8J1_9ENTE Potassium uptake protein, integralmembranecomponent, KtrB OS=Enterococcus sp. HSIEG1 GN=HSIEG1_3799 PE=4 SV=1MNFTRFARLTQRKSKYFIAQNVSSIQVIVFYYILMTIISLGLFYLPFFREPRSHASFIDMFFMAVSTVSVTGLTTFPIDDVFNDRGVVLLEVLFQVGGLGIMMISTFFAIVSRRKISLKQRQLIMTDMNQPKLSGIVRMIRITFTIILLCQAISGAIFSIYFYFNGYYDNWRDALFYGFYQAISAVTNSGFDVTGNSILPFAHDYFFLICIMFLIFTGGIGFPVIMDFREWALFKLKKIADNCLFAFHCLQKSRCWLL
3.9E-23	91.1	0.8	5E-23	90.8	0.5	1	1	H0EQ13_GLAL7	Putative Potassium transport protein 1	M7I_4756	Glarea lozoyensis (strain ATCC 74030 / MF5533)	163	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Helotiaceae, Glarea, Glarea lozoyensis, Glarea lozoyensis (strain ATCC 74030 / MF5533)	1104152	>tr|H0EQ13|H0EQ13_GLAL7 Putative Potassium transport protein 1 OS=Glarea lozoyensis (strain ATCC 74030 / MF5533) GN=M7I_4756 PE=4 SV=1MVRHLALNHSNPTFNALSPAHRNLDGLVQTIFIRSAGFTVISISSLRIGLQALYVPMMFISAFPVAITMRSSNVYEERSLGIYASQLRAQAPNTTESASLLSRSSRTRLYFLRQQLAHQLSHDFWFVVICAIAVIWIETASYERDPLTFSVFNILFEVINVAK
4.1E-23	91	13	4.1E-23	91	9	3.7	1	A0A0D9V057_9ORYZ	Uncharacterized protein		Leersia perrieri	522	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Leersia (cutgrass), Leersia perrieri	77586	>tr|A0A0D9V057|A0A0D9V057_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1MNSLDASTPSYDKLQRIYHLFLFHAHPFWLQVLYFLFISLFGFLMLKVLPMKTSMVPRPTDLDLIFTSVSATTVSSMVAVEMESFSNSQLLLITLLMLLGGEVFTSILGLYFTHLKSNKIATLPANHGSNNKPPQTSTIVELTPMDDQNQIELGYLDQNKDSNNTHTSSSTSTTRLLMLIVMGYHVVVHLAGYTLILVYLGVVDGARAVLAGKRISPHTFSIFTVVSTFANCGFVPTNEGMISFKSFPGLLLLVMPHVLLGNTLFPVFLRLAIAALEMVTRRPELGELRRRQKGDGGVDYDHLLPGSRTRFMAATVVVFLLVQTVLFCAMEWGSDGLQGLTAGQKLVGALFMSVNSRHSGEMILDLSTVSSAVVVVYVVMMYLPPYTTFIPVQRKHKQTGDKSGQEPSSSSIWQKLLMSPLSCLAIFIVVICITERRQIADDPINYSVLNIVVEVISAYGNVGFSTGYSCARQVRPDGSCRDVWVGFSGKWSREGKLTLMAVMLYGRLKKFSLHGGQAWKIE
5.8E-23	90.5	7.4	5.8E-23	90.5	5.1	1.8	1	W1PR48_AMBTC	Uncharacterized protein	AMTR_s00025p00189380	Amborella trichopoda	322	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, basal Magnoliophyta, Amborellales, Amborellaceae, Amborella, Amborella trichopoda	13333	>tr|W1PR48|W1PR48_AMBTC Uncharacterized protein OS=Amborella trichopoda GN=AMTR_s00025p00189380 PE=4 SV=1MFYMSASATTSSSLGSVEMEDFSNAQLVVLTVLMLLGGEIFTSMLGLQIRKFMSNDKSQKTNLRVITRENHHSNPFKIEKEIDLESITNENNDPDLRVSNGVGSLETKIEGDLKLNSLRLLRNVVLCYYSVIHIFGTALIAMYLSLASHAKHLLRSRGIQMLTFSAFLTVSSFANCGFVPTNENMIAFKKDTLLLLLIIPQFLLGNTLFPSCLRLVISFLRRLTRREEFGYLLENYKQIGFDHLFSFEESVYLFLTVSGFIVVQFVVFFWLQWNSEAFSGFGNGEKVVAGLFLSVNTRYSGESVVDLSLLKPALLVLYCLMM
7.7E-23	90.1	16.4	7.4E-14	60.5	5.3	2.9	2	M9RE68_9RHOB	Trk potassium transport system integral membrane component TrkH	trkH OAN307_c25000	Octadecabacter antarcticus 307	484	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Octadecabacter, Octadecabacter antarcticus, Octadecabacter antarcticus 307	391626	>tr|M9RE68|M9RE68_9RHOB Trk potassium transport system integral membrane component TrkH OS=Octadecabacter antarcticus 307 GN=trkH PE=4 SV=1MVAPAIHALSIEDHEVARAFFYAALLFMVLTLFIGLATANYKNTLARGYLVSLLAAFLVLPLMLAVPMYESVPSMSFLEAWFESVSSITTTGATLYDSPRELPPSVHLWRALMGWLGGLLIWVSAIAILAPLNIGGFEVRATRGGSASEKTFAQIGRVTDPSERLVRYGSKLIPFYAALTALLWFSLTMSGEVSFVALCHAMSVMATSGISPVGGIIFSPAGFLGEFIIVLFFVFALSRVAFSRGVSGQEVSPLYKDNEFRLALSLIGVLVAILFLRHGVVAFEDGSNNGLGNAARALWGALFTITSFLTTTGFESADWTATRNWSGLGTPGLMLVGLSLIGGGVATTAGGIKLLRVYALWKHGQREIERLVLPSSVGGAGAGARQIRRQGAQIAWIFFMLFTISIAAVMVLLALTGVQFETAMVLSVAALSTTGPLAAIAAETPISYAGIPDGAKIILAFAMVLGRLEALAIIALLNPEFWRR
8.6E-23	90	19	2.1E-22	88.7	13.2	1.5	1	R6F0N5_9FIRM	Uncharacterized protein	BN497_01959	Firmicutes bacterium CAG:145	251	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:145	1263005	>tr|R6F0N5|R6F0N5_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:145 GN=BN497_01959 PE=4 SV=1MEIVVAVFMFLAAINFNLFYMVKKRGVLQIFKDEETKFYTTVTISAGLLIAVYNFISDSFSQFGEKLLNSFFQVISILTTTGYATDDYDVWPTFSKMVLFTLFFIGGCSSSTAGGIKGVRVLIGLKIIRRSISLKVHPSRITPITLNESELSSGTAIKISNFIFTYLFVFFAGTVLLSLNGFDLMTNVSAAASCLGNIGPGFNLVGPTMNFSMFSWFSKFVCSILMIIGRLELYTVLVLFSKYYWNPNRTR

9.2E-23	89.9	14.5	1.5E-09	46.3	1.8	3.4	2	J3KZ66_ORYBR	Uncharacterized protein	OB01G22720	Oryza brachyantha	364	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza brachyantha	4533	>tr|J3KZ66|J3KZ66_ORYBR Uncharacterized protein OS=Oryza brachyantha GN=OB01G22720 PE=4 SV=1MAATAEYSDKPPPISTPVELAAMDVVVINPATAQNQMELGLDQKKRSCTHTSSSSPSSMTRLLMFVVMGYHVVVHLAGYTLIVVYLSVVSGARAVLAGKRISPHTFSIFTVVSTFANCGFVPTNEGMISFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIAALERLVLFCAMEWGNEGLQGLTAGQKLVGALFMSVNSRHSGEMVVDLSTVSSAVVVLFVVMMYLPPYTTFLPVQEKHQQTGDQSGQERRSSSSIWQKLLMSPLSCLAIFTVVICITERRQLADDPINYSVLNIVVEVISAYGNVGFSTGYSCARQVRPDGSCRDLWVGFSGKWSWEGKLTLMAVMLYGRLKKFTMHGGQAWKID
1.5E-22	89.2	23.7	2.6E-22	88.4	16.4	1.4	1	R6CDF7_9BACE	Uncharacterized protein	BN697_01363	Bacteroides sp. CAG:530	494	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:530	1262741	>tr|R6CDF7|R6CDF7_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:530 GN=BN697_01363 PE=4 SV=1MDKWERLLLYRKKLILPQVHRVLSILSLLTYASSLIFMLTMVYEYGFMVSDSELNIIHIIYKCVWAEMLLQAIATILFRSSSDDDSRYGPWMWLLYSLLFLTLLPIIFHEPEVQTPGVYYIWHFFNSPYYFKAILILMSVFALSGSLVRLMGRRTNPSLILASSFLFILMVGTGLLMLPRATIDGISWIDALFTATSATCVTGLSTVDVPSVFTLEGQIIILLLIQIGGLGMMTITSFFALFFMGNTSIYNQLLVGDMISSNSLNSLLLSTLLYILGFTLAIEGVGMGVIWYSVHGTMGMSVHQELYFAIFHSVSAFCNAGFSTLPGNLGNPLVMTGHNLLFMTVSALVILGGIGFPILVNIRETIVYHARYCWAWLWRLITGRHASIKGQRVHLYSLNTKIVLVMTALLLVVGTVVIAVLEWNVSLAGMPVADKLVHAFFNAVCPRTAGFCSVSFNSMTVQTLLVMLLLMVIGGGTQSXXXRRWYTVNRRWYQD
2.1E-22	88.7	40.3	2.5E-21	85.1	18	2.5	2	A0A0G1HVI9_9BACT	TrkH family potassium uptake protein	UW09_C0003G0154	candidate division TM6 bacterium GW2011_GWF2_43_87	454	cellular organisms, Bacteria, unclassified Bacteria, candidate division TM6, unclassified candidate division TM6, candidate division TM6 bacterium GW2011_GWF2_43_87	1619086	>tr|A0A0G1HVI9|A0A0G1HVI9_9BACT TrkH family potassium uptake protein OS=candidate division TM6 bacterium GW2011_GWF2_43_87 GN=UW09_C0003G0154 PE=4 SV=1MQVRRPFTISPWRVIIFSIVFIAIVGALLLSLPAAQRVPLSFIDVLFTSASAVCVTGILTVPLDAFTFLGKCIILLLIQIGGLGLLTLVIPLVALFFNVRMRTHLITGHQFELENWSHNWIYSRQVIIFIVCLSLFCETIGAFAIYGVIGSEVLTEPRWFIAMFHGISSFCNSGIAPFPGDMPSVQHNGALIVITSILMVIGGFGFVPLYELSTRAWNRIKGIPSHSLHLTLHSKIIIYFTPALTLIFTPLLWLSEHRQFAGMSFLETLNLSLFNAISLRSCGFCTLDLSLMTDITLLLILIFAFIGSSPGSVGGGTGIKITSFVLALATIRTAILGKAQVELFGRRIPFEQIFRAFAIIVVSLSFCILSTMLLMITESGSPHPFMHFLFEAISAFANHGVTLGLAPSMTVLGKFIFSLGMIFGRISSLTLILAIKKKNKEKTEFQYPEERILLV
2.4E-22	88.5	14.1	4.1E-15	64.6	2.9	3.5	3	J3M177_ORYBR	Uncharacterized protein	OB04G31520	Oryza brachyantha	552	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza brachyantha	4533	>tr|J3M177|J3M177_ORYBR Uncharacterized protein OS=Oryza brachyantha GN=OB04G31520 PE=4 SV=1MLHPFTSILVTSQHLPLMKLPKSNFEVVRKITGKVKHLHVFISVRLCSISKCAMCFFRRCFWYFMFQSKPLIVQLLYFMTLSFVGFLDLKIHKPRHKPTPRTLDLMFTSVSTVTVSRMATVEMEDFSDQQLWVLILLTLLGGEVFISMLALHFSNAGINTNEILPKRLSSTSRDIESFDAVNNSTQNNSEDCQSEATTSPNWVQESKTMKQKCRNILAHIVTGYFIAAVFCSFLVTIIFVQIDSYTRLPLKSKDIKIWTFSIFPAVSSFANCGFTPVNDNMAIFRKNTSLLLLVIPQVLAGNTMLSPLLRLSIWALGKVSRRQEYAYMLQHPKDTGYRYLQPQKNSVDTVFTVGGLILLQVMFLSFFEWNTSAFDGLNWLQKLVCSLFQSANTRHAGEAIVDISTLSPPILLLFALVMYHPSDDAVCPINFYNQPLTERERNSNDQAIWMNYILSKSCLAMFTILACITERKSISADPLNFIFRIAFEIISAYANVGYSLGYSCEKLLKPDATCKATSYGFVGKWTDEGKLIIILVMFLGRFKKFTLTGRNF
5E-22	87.4	0.5	6.3E-22	87.1	0.4	1.1	1	V4JFM2_9GAMM	Uncharacterized protein	N838_34025	uncultured Thiohalocapsa sp. PB-PSB1	159	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiohalocapsa, environmental samples, uncultured Thiohalocapsa sp. PB-PSB1	1385625	>tr|V4JFM2|V4JFM2_9GAMM Uncharacterized protein OS=uncultured Thiohalocapsa sp. PB-PSB1 GN=N838_34025 PE=4 SV=1MAVAIARFQEKWEEKWVSFFVAILFRSQVSFFVAKKSGCPFSWHAFSWHGVREAAFTVVSLVTSTGFATVDHVHWPDFLPVLLLLAFVGGCGGSTAGGMKVMRAMLLAKQGFYEVRRLIHPRAMTKLRIGRRVVDAQLMQSVWGYFALYMITFVICGL
9.5E-22	86.5	24.2	3.6E-21	84.6	16.8	1.7	1	I0GLZ4_SELRL	Putative Trk system potassium uptake protein TrkG	trkG SELR_00730	Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421)	492	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Selenomonas, Selenomonas ruminantium, Selenomonas ruminantium subsp. lactilytica, Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421)	927704	>tr|I0GLZ4|I0GLZ4_SELRL Putative Trk system potassium uptake protein TrkG OS=Selenomonas ruminantium subsp. lactilytica (strain NBRC 103574 / TAM6421) GN=trkG PE=4 SV=1MRMQKETGLELFWLLMGQMSILMAGALCVPLIVALLWQESEAWLFVLPAAFAYGLGRKMLELGHSEERGRQLTIREGVFFMSFVWLFMGFIGLMPYAISGLFPSFAAAFFETVSSLTTTGLSCLPFDRIGLPRTLLLWHGVMSWLGGLTFVVIMVTVLPQVSGCFGLTLSARQSIFFSPVWNKMAQSARQGTAVYVALTVMSTAVYYLAGLGPFESLLRAMVTISSSGGTSAYAFIYYDNPALELAAFAAMLLSSMSLLLLWRSWKMKSLRLLWQDTEIRHFLLVVFLAGGVLAAHLYYQGVYDFTGSLRYGYFQAMAFISTNGFVAAPFWLWPSFDIYVLFLLVFVGGCIGSATGGLKIMRLLVLLRLSWAELRRTLHPRMVVMLKVDGLPVPVKIVGRILSFFFLYTVVFVAFALVLSLSGISIVQSLGLAAGCLTSTGASAELFGIGSLDILPDWAKLVCSLLMIMGRVEIFSFLVLLDMARRSLQKRW
2E-21	85.5	0.1	2.2E-21	85.4	0.1	1	1	C6HRS5_AJECH	Potassium uptake transporter	HCDG_08660	Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	88	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Ajellomycetaceae, Histoplasma, Ajellomyces capsulatus (Darling's disease fungus) (Histoplasma capsulatum), Ajellomyces capsulatus (strain H143) (Darling's disease fungus) (Histoplasma capsulatum)	544712	>tr|C6HRS5|C6HRS5_AJECH Potassium uptake transporter OS=Ajellomyces capsulatus (strain H143) GN=HCDG_08660 PE=4 SV=1MLFEVTSGYGNVGLSLGYPGINTSLSGKFSVFGKLIMCAMMLRGRHRGLPSQLDRAVMLPSDRLVDGDERENTTEIRNSTKIKRHHTH
2.5E-21	85.1	13.8	1.1E-05	33.6	0.1	4.8	4	K3Y1N4_SETIT	Uncharacterized protein	Si008100m.g	Setaria italica (Foxtail millet) (Panicum italicum)	471	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3Y1N4|K3Y1N4_SETIT Uncharacterized protein OS=Setaria italica GN=Si008100m.g PE=4 SV=1MESLFHHEFIHSKMRSFIRLGRYVLDSFVFVYRFVASHVHPVFIQLGYFLTIAMLGSVLLISLKPSNPEFSPQYLDMLFLSTSALTVSGLSTVTMEDLSSSQIVVLTLLMFAGGEVFVSFLGLMLRPPNHQANPTDPTGNKVVAIELDMVEPASVVANIGEELQLEEATHGAPTLSSRSSSSSDLKNNSSLYITHVPSARAILTKKGINVALFSASITVSSFANGGLITNENMAIFSKNAGLLLLLTGQILAGNLLFPLFLRLFVWFLGRVTKLERLKLMIRDSKELQYSYLLPKLPTAFLSSRSYQKIVSALFTAVNARHSGENSIDCSLISPAVLVLLIAMMYLPPWTTFAPPNGDDKTKDEKMLGCNVIFVIVACITERRRLRNDPLNFSTLNMIFEVISAYGNVGMSTGYSCSRLQQLHPESICQDKPYSFSGWWSDEGKLLIVLIMLYGRLKAFSTGTGKAWKLD
3.2E-21	84.8	20.2	1E-10	50.2	6.1	3.2	2	A0A072UN44_MEDTR	Sodium transporter HKT1 (Uncharacterized protein)	MTR_6g092970	Medicago truncatula (Barrel medic) (Medicago tribuloides)	413	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago (medics), Medicago truncatula (Barrel medic) (Medicago tribuloides)	3880	>tr|A0A072UN44|A0A072UN44_MEDTR Sodium transporter HKT1 OS=Medicago truncatula GN=MTR_6g092970 PE=4 SV=1MEVFSNSQLILLTFLMLVGGEVFTSMLQLFLDRFNFTQKDCVKNECSSCVSSTSLSHKIHQMELGSVSMPQSENHDQIEKNNINDKDKLKYNSLSLVTLYITYIPSAKNILQNKGINIETFSLFTIVSTFASCGYIPTNENMMVFKKNSGLLLLVLPHVLLGNALYAPCLRLIITFLKSITKREEFSYLLNNSKEMGYDHLLSTLHCWHLVGTVFGFNVIQFILFCCMEWSSKIMEGLNIYQKLVASLFQVTNVRHSGESVFDTYSISSAILVLFIVMMYLPPYTTFLPVRDQNDVKKDQNSLVDRIIFSQLSYLVIFIILICITERQSLKDDPLNFNVLTITLEVISAYGNVGLSTGYSCSRQLKPNLMCRDSWIGFSGRWSTEGKLILILVMFFGRLKKFNMNGGKAWHLS

7.6E-21	83.6	16.1	2.4E-18	75.3	5.6	2.1	2	M0UQP7_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	402	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0UQP7|M0UQP7_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MHLFLALIYSTMGWVKRFYQDFIHIKLHSFCRISRYVVDSIAFVYRFVALHVHPFWIQLSYFLAIAILGSVLLMSLKPSNPDFSPPYIDMLFLSTSALTVSGLSTITMEDLSSAQIVVLTLLMLVGGEIFVSLLGLMLRVNHQDMPDLPRVKISSVPVELEEIDLANSMALSDESQLEEATHAITPKKCTGLKRSRSVKCLGYVVFGYFAVIHILGFLLVFLYITRVPTASAPLNKKGINIVLFSLSVTVASIANGGLVPTNENMVIFSKNSGLLLLLSGQILAGNLLFPLFLRLLVWFLGRLTKVKELRLMIKNPEEVHFGNLLPRLPTVFLSSTAIGLVAAGVTMFSAVDWNSSVFDGLSSYQKAVNAFFMVVNARHSGENSIDCSLMSPAIIVLFIVMM
1.1E-20	83.1	15.6	1.4E-20	82.7	10.8	1.1	1	M0YEW8_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	394	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0YEW8|M0YEW8_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MNNSPVVHLKSLRTFCAFVATKLSYFAKSAQQSMKYSCQFICHTNPLFIQVTYFALISFAGYEALKVLNSQDKSNTLKDLDVLFTSVSASTVSSMATVEMEEFSSKQLWILAILMLIGSEVFTSILGLHFVRAKFNSENSFNRRDQISHVDIESINVTNFDPTASHGTKDGASFSEFHLANKQHVDPKTTALLGTAVTVYLLITNLGSSLLIYLYLKLVPDAQEVLKRKGIGLFLFSVFTAISSVANCGFTPVNENMIIFQKNSGLLLLIIPQILVGNTLFAPCLRFMVWSLQKITGKQEWSFILEHPKAIGYRHLMSTRKCAYLILTVVGFIILQTILFCSFEWSSEALQEMSSYQKIVGALFQSTNARHAGESIVDLSSISSAIIVLYTVMM
1.4E-20	82.7	9.9	1.3E-13	59.7	1.9	3.1	2	Q0APP9_MARMM	Cation transporter	Mmar10_1446	Maricaulis maris (strain MCS10)	467	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Maricaulis, Maricaulis maris, Maricaulis maris (strain MCS10)	394221	>tr|Q0APP9|Q0APP9_MARMM Cation transporter OS=Maricaulis maris (strain MCS10) GN=Mmar10_1446 PE=4 SV=1MTPVAFLRPLGALWVLLAGVALIAAFVAAAIGETHLAPLFGTTALIAFIPGIFILSATRGLRSKASALDALGLALLSWITAPAMAALPFWLTGYFDPIDAVFEAYSAVTTTGATLLPADELPRSLIFWRAILAWLGGYATLLLAIGIFAALDRDVPAIRKSALLTLRSDDVFSHLPLAAKRVGIVYATLTSLVWLGLLFGGNGLFDSTVLSMSAISTSGYTVEDGGLLATIGPISTFWVVIGCLVGSLNIALFWDVLRDRSVLRDPDIAGIAALIIGLAAFFILARPGAPFSDVIDAAFIVSTSGFSAGGGVIPALAASIFVVLIGGSAASTTGGIKVSRILLLWKRMGAELAILSDPRSVVPVSFRGRRVRETALVGVWSYVLAFVAAIGFGTMALTATGLDFETAFIAMAASLANIGPMLDQSQPLASWTQIPDQSKPILISAMILGRLEVLAAVAAVWAIFIRK
1.5E-20	82.5	18	7E-20	80.4	12.4	1.8	1	G0VQR5_MEGEL	Putative TRK potassium uptake system protein	MELS_1545	Megasphaera elsdenii DSM 20460	484	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megasphaera, Megasphaera elsdenii, Megasphaera elsdenii DSM 20460	1064535	>tr|G0VQR5|G0VQR5_MEGEL Putative TRK potassium uptake system protein OS=Megasphaera elsdenii DSM 20460 GN=MELS_1545 PE=4 SV=1MNRSIVFYLVSRLALINGLALVIPMLAAWWWGEAGLRYFAPALAAALMVAAFCQYRGRHHKRHLGPGEGAWYMVSAWVLLGLGMIPYVMAGIFASPVDAFFESVSAFTTTGTSCLADGGAALPQSLLLWHSLMEWLGGLNFILMLVSVMPQVSGCFGLTLSVHQSVAFSPMVARMQEAARQAGRIYLAITAFSMLLYWLAGLPLGMAINQGFMTMSTSGGDALFDFSRYDSLALEAVGAVSMLLASGNFLLYWKGWERRDFKGLFKDAELQVFLAVLVAAGLVVSFHLWRFGVYDGWDNLRYGFFQVLSFSSTSGFASASYQDWPEFDKYVLFALAFVGGCIGSATGGLRVMRFMVLFKMAAQEMRRTLHPHMVISLKVDGVPVDMKIISRVLSYFFLFMATFFVSMLIISLSGVTPMQAMGMAVGCLSSVGSTMDLFGVADVSVLPAWTKIYCSFLMILGRVEIFSFLVVIQTAFGYLRRRW
2E-20	82.2	12.4	1.5E-19	79.3	8.6	1.9	1	R6VT16_9BACT	Trk system potassium uptake protein TrkH	BN673_01736	Prevotella sp. CAG:474	257	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:474	1262926	>tr|R6VT16|R6VT16_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:474 GN=BN673_01736 PE=4 SV=1MENFHSPALEYTCTTFCFLAGINFTLLYFTVARRRIGMLFKSDEFKFYLFMTAACTAFVMFQLMAYRGYDAEHAFRCGAFQVVNFLTTTGLFNDNAALWPHVTWVVLAVCMFVGACSGSTSGAFKSIRSMMVLKVIRNELRQILHPNAVLPLRVDGVNVPIQKRVTLLAFLATYVIMLLVVAFIMIACGIDHTNAITICLSSLGNVGPSLGLEIGPTMSWSQLPDLAKWTCSFMMLVGRLEIFTVLVIFTPTFWKDN
2.5E-20	81.8	2.3	2.8E-20	81.7	1.6	1	1	D4MRN3_9FIRM	Trk-type K+ transport systems, membrane components	CL3_20780	butyrate-producing bacterium SM4/1	145	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, unclassified Clostridiales, unclassified Clostridiales (miscellaneous), butyrate-producing bacterium SM4/1	245012	>tr|D4MRN3|D4MRN3_9FIRM Trk-type K+ transport systems, membrane components OS=butyrate-producing bacterium SM4/1 GN=CL3_20780 PE=4 SV=1MIIGGSPGSTAGGIKTTTFALAVLCILSVFQNQEDIHCYKRRVPYDILRNAIAILVLYLFLFLSASFLITRADGVSMMESSFEAASAIATVGLSLGITEDLGIFSKIILILLMYLGRVGGLTMLYALTNHRKFPVHLPQERITVG
2.8E-20	81.7	8.1	2.6E-18	75.2	0.6	3.1	3	A0A0E0PDU5_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	453	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0PDU5|A0A0E0PDU5_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLGGEVFVSLVGLASKWSKLRSDAMDRSRRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHVVGAVAVAAYVLASPGARRTLGDKSLNTWTFAVFTTVSTFSNCGFMPTNENMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVWAAAAATRREELVEMAREGGRAAAAGYAHLMPARRCWMLAATVAAFVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGESTVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVRQVRLNGFLPEKKNADQVN
2.9E-20	81.7	7.3	1.2E-14	63.2	2.6	2.3	2	A8LKU6_DINSH	Potassium uptake protein	trkH Dshi_1568	Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12)	502	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Dinoroseobacter, Dinoroseobacter shibae, Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12)	398580	>tr|A8LKU6|A8LKU6_DINSH Potassium uptake protein OS=Dinoroseobacter shibae (strain DSM 16493 / NCIMB 14021 / DFL 12) GN=trkH PE=4 SV=1METLRKFPLIVILIGIGALAMFIPALHAGALGDNATARPFLYGGILFLVLAGFLGIATMNSPAANSERRQLVALLLAFAALPLMLALPLSEAVPATRFFNAYVEMVSALTTTGATLFEPDRLPISVHLWRATVAWLGGFLIWVTAFAVMAPLTLGGFEVTSIQEAGQGGSTGRNEGHAEPATRLLRFASRLAPIYITLTGVLWLIMILCGIPGAHGLIYAMSTLSTSGITAGELPGNAPRGGLAELAIFTFLIFAITRRSFINGWSPNWHELRRDRELRIAAVFVTVIPAFLFLRHWLGAFEVDAGGFDGNALAALWGSVFMVLSFLTTTGFESASWTQAQNWSGLGTPGLLLAGIALFGGGVATTAGGVKLLRVYVLYKHGLREMERLIHPSSINSAGYTGRRLRREGSTIAWIFFMLFALSIALVMSALALTGMSFEEATLLTFAALTTTGPIASIATEAPISYAALPDAAKAILCAAMVLGRLETLAILALLNPDFWRN
4.8E-20	80.9	6	7.5E-18	73.7	0.3	2.2	2	A0A0D9W964_9ORYZ	Uncharacterized protein		Leersia perrieri	327	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Leersia (cutgrass), Leersia perrieri	77586	>tr|A0A0D9W964|A0A0D9W964_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1MKLTSLSICVAHSVKQSYSFLVYQSNPLVVQLIYFVIISFVGFLALKNLKPQGKPGTNDLDLMFTSVSALTVSSMATIEMEDLSDRQLWVLILLMLLGGEVFISMLGLYFNNADVNRNENRQRSLRSISMDIESNSPANNGDHNARGVLKSKEINMYTFCIFEEVSSFVNCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLSVWILGKISTKEEYAYILQHPEKTGYKHLHVQRKSVYMVLSVTGLALLQVMFICSFEWNSKTVEGMHWLQKLVGSLFQSVNTRQAGESVVDISTLSPPTLLLFAVIMLVPPSTPVSE

6.1E-20	80.6	20.3	3.1E-18	74.9	6.8	3.2	3	B8AIK1_ORYSI	Putative uncharacterized protein	Osl_06054	Oryza sativa subsp. indica (Rice)	458	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>tr|B8AIK1|B8AIK1_ORYSI Putative uncharacterized protein OS=Oryza sativa subsp. indica GN=Osl_06054 PE=4 SV=1MNHCLVVSHKKLQTFRTFAASKFSSFTKSAQKSIKYSFQFIYQNNPLFVHVAYFALISFAGYGSLKVLKPRDKSNTLKDLDVLFTSVSASTVSSMATVEMEDFSSAQLWVLTILMLIGGEVFTSMLGIHFMRAEFGTKESVSTRDHSPCIDIESITSTKFGPSTQGTKVTVSFSELRMENGGHVEPKTIKFLGFVVMGYLLITNLGGSLLIYLYLNLVPSAHKILKRKGIGIIVFSVFTAISSVGNCGFTPVNENMIIFQKNSILLLLLPQILAGNTLFAPCLRLMVWSLEKITGKKDCRYILEYPKAIGYKHLMSTRESVYLTLTVVSLIILQTVLFLSLEWSSVALDGMSNYQKIVSALFQSVNARHAGESVTDLSNLSSAILVLYTIMIAYGNVGFSVGYSCKRLLNHDARCKDASYGFAGKWSDNGKAILIIVMLFGRLKTFNMKGGRAWKLR
6.4E-20	80.5	29	8.1E-07	37.3	4.8	4.4	3	M0S2H3_MUSAM	Uncharacterized protein		Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	453	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Zingiberales, Musaceae, Musa, Musa acuminata (Banana) (Musa cavendishii), Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	214687	>tr|M0S2H3|M0S2H3_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1MCAGRWQTKFAPLPCVYMYTSPPTLIAASKLLPSGTAMAVTAITSHTKSFIHKLSRSIESIPTLVASLYRFLLFQANPFWIQSCYFFSLSMAGFLLLKILPLRDVTSKPTNVDLLFMSASANTVSSMDAMEMEVFSNYQLGVLTLLMVTGGEVFVSLLGLHFAKINSRKHLFFVVLGYLIVAHVVGFLLILVYLRLVPDAGTVLDRKGINASMFSIFTTVSTFANCGFVLTNENMVVFRTCSGLLLIVIVQALVGNTMYASSLRAWTSDSITGLSTYQKIVGAVFMSVNSRYAGESIVDLSAISPAILVLFVVMMYLPPYTCFLPREDDRRLLEDGETSRRTTGLGLILSPLSSIAIFTIIICITERRQMSRDPLNFSVLNVVVEVVSAYGTVGYTTGYSCKRQVKADVHCKDVSAGFSAKWSNKGKLVLIAVMFFGRLKKFSMGGGKYWQFI
6.7E-20	80.4	35.3	1.6E-19	79.2	9.4	4.3	3	D7UBL8_VITVI	Putative uncharacterized protein	VIT_11s0103g00140	Vitis vinifera (Grape)	540	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, rosids incertae sedis, Vitales, Vitaceae, Vitis, Vitis vinifera (Grape)	29760	>tr|D7UBL8|D7UBL8_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_11s0103g00140 PE=4 SV=1MMNSASFTGNKLHRLCTCSSFKLECLGRSICFLASSFYRFVILRFNTFLVQLCYFLCLSFQGFWVLKALKPRTPLRPRNLDLFFTSVSAATVSSMSTVEMEVFSNNQLLILTLLMFVGGEIFTSMVELQLWRSKLKKPLIAENQVNSVSNNSSAPPDPRNPFGQFELRVGRTKSLSSESLKYHSIKFLGFVVMGYLVVVHVLGVTLVSAYIALVSSARDVLKQKGLKLFTFSLFTTVSTLASCGFVPTNENMIVFSKNSGLLLIIPQVLLGNTLFPSCLRFSIWTLGKFKKVESNYLLISTREIGFLHLLPSLHSTLLVPTVLGFILIQFTLFCSMEWNSEGLNGLNSYQKIIGALFQSVNSRHTGETIVDISTLSPAILVLVVVMMYLPPYTSFLPIKEICNGGRKRRRGKIVENLIFSQLSYLAIFIILICITERKKMKDDPLNFTVLNIVIEVISLQDQYLSSLKRIQFLVAYGNVGFTAGYSCERLLKPDSSCQSKWFGFSGKWSDEGKIILIFVMFFGRLKKFNMDGGRAWKLL
1.1E-19	79.7	14.6	3.9E-18	74.6	1.3	3.8	3	A0A0E0KUX3_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	520	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0KUX3|A0A0E0KUX3_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MKLLLPDSEVLRIYREKAQHLCGFLSMKLISLSKCVIHSVKQSCSFLVCKSNPLVVQLVYFVTISFAGFLALKNLKPQGKSGPKDLDLLFTSVSTLTVSSMATVDMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLLSISMDIESNSPANNGVHKITECGQSEETMSQNQVQKNKSITYNPCAVLARIVTDARDLLKSKEINMYTFCIFTAVSSFANCGFTPLNSSMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLSVWVLGKVSGKAEYAYILQHPGETGYKHLHVRRNSVYIVLSVTGLILLQVMFICSFEWNSESLEGMNLLQKLVGLLFQSVNTRQAGESVLDISKLSPPTLLLFAVVMYLPSDASFLTANADNQPLTHKKINSISRELWRNFTANKLSCLAMFTFLACITERKSISADPRNFNIFSIVFEIIRQVHILTKFLCAETERYSLGYSCQKLLKPDGTCKDVSYGFVGRWTDKGKLIVILVMFLGRLKEFILK
1.2E-19	79.6	3.2	1.3E-09	46.5	1.3	2.1	2	A0A0B5DVB7_9RHOB	Trk system potassium uptake protein TrkH	P73_2249	Celeribacter indicus	515	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Celeribacter, Celeribacter indicus	1208324	>tr|A0A0B5DVB7|A0A0B5DVB7_9RHOB Trk system potassium uptake protein TrkH OS=Celeribacter indicus GN=P73_2249 PE=4 SV=1MNRFSRMPFFVQLMLVSGGAMLVPAFYALILREWDDARAFLYPSVLVCSLAGFIAIALFRPEATEARDGRRDRDREGRNQLLTLLGTYTALPLVLAVPFVEATQDTTFLNGYFEMVSALTTTGATLFDDPARLSRPEHLWTALVAWLGGLFAWVTAVAVLAPLNLGGFEVISSRQPGQSDARASQITRIAAAPERMARFTTKLFPIYIGLTLALWFALAMVGSPAFVALIHAMSVMSTSGISPVGGLTNTRTGFVGELLIFAFLFLALSRKTFTADNPRPDAPPLWRDPEMKIGLALMVAVPLLLFLRHWVAVLEVSGDWTFGRALSSLWGSMFMVLSFLSTAGFESMGWEEARLWSGLQAPGVLLMGLAIFGGGVATTAGGVKLLRLYALVRHGEREIEKLVSPHSVGGAGANARRIRREGAYVAWVYFMVFAFTIAGVMMLLALLGLDFERAAIFTISALTTTGPLVRVAGTDPMSYAALTDPMKLVLAGTMVLGRLEMLAIIALLNPEFWRR
1.2E-19	79.3	30.9	1E-17	73.2	0.6	6.2	4	A0A0E0PDU3_ORYRU	Uncharacterized protein		Oryza rufipogon (Brownbeard rice) (Asian wild rice)	874	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza rufipogon (Brownbeard rice) (Asian wild rice)	4529	>tr|A0A0E0PDU3|A0A0E0PDU3_ORYRU Uncharacterized protein OS=Oryza rufipogon PE=4 SV=1MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLGGEVFVSLVGLASKWSKLRSDAMDRSRRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHVVGAVAVAAYVLASPGARRTLGDKSLNTWTFAVFTTVSTFSNCGFMPTNENMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVWAAAAATRREELVEMAREGGRAAAAGYAHLMPARRCWMLAATVAAFVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGESTVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVRQVRLNGFLPEKKNADQINPDHLCTDKWTGFVGRWSDSGKLILIFVMFFGRLKKFSMKGGKAWKLRTFHCHPCTKLTLHSKCWQFQISSILVTSQHLPLAMKIPQPKFQVVRDITEKVKHLHVFISMRLRSLSKCAVCFFRRCFWFFMFQSNPLIVQLVYFISISFVGFLALKILKPRHKPTPRDLDLMFTSVSTATVSSMATVEMEDFSNQQLWVLILLMILGGEVSISMLALHFNNAETNTNEVLPKRSPSTRRNIESFDAVNDSNQNSSQGFQSEATISLNWVQGSRTMKQKCRNMLAHIVTGYFIAAVVCSSLVIIIFAQIDSDTRQLLKSKDIKIWTFSIFTAVSSFANCGFTPVLAGNTILSPLLRLSIWILRKVSRREEYAYILQHPEDTGYRYLQLQKNSVNMVLTVGGLVLLQVMFLSYFEWNSSALNGMN
1.5E-19	79.3	0.3	1.6E-19	79.1	0.2	1	1	R5QVF8_9FIRM	Trk-type K+ transport systems membrane components	BN747_01685	Firmicutes bacterium CAG:646	148	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	1262995	>tr|R5QVF8|R5QVF8_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:646 GN=BN747_01685 PE=4 SV=1MLMFVGACAGSTGGGIKVSRFVILLKSMGKEIKQYLHPRQVRKIQLDGKPVEHEVVRNVNVFMVVYTMIFGFSMLILAFDGNDLISNFTAVAATFNNIGPGLELVGPSANFDLFSHPAKLVLIFDMLAGRLEIFPLLLLFVKDTWKKF
1.5E-19	79.3	16.5	7.4E-19	77	11.5	1.9	1	K7L1F4_SOYBN	Uncharacterized protein		Glycine max (Soybean) (Glycine hispida)	410	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine, Soja, Glycine max (Soybean) (Glycine hispida)	3847	>tr|K7L1F4|K7L1F4_SOYBN Uncharacterized protein OS=Glycine max PE=4 SV=1MMKIRKQDRFFRFLVLFLPFQHFHPFFIQLGYFVILSLVGYLGLKVSKPRTPVIPNDLNLFYTSVSASTVSSMVALEMELFSNSQLILLTLLMFLGGEVFTSMLDLLFATYKFQNRSVISTNQIELGLVSIPDSKSENYHKPSDDSNINDDSDRLKYNCLSYLTFVVLGYLVVVQFVGFSFVSLYITLVPSARQVLKNKGIKIVTFSLFTIVSTFASCGFVPTNENMMVFKKNSGLLLLVLPHILLGNTLYPPCLRLLIMVLKKVTKKEEFSYLLKNFKDVGYDHMLSALHCCLLVATVLGFNLIQFVMLCSLEWNTKIMEGLNVYEKVVASLFQVTNARHAGESVFDLSSISSAILVLFVVMMYLPPYTTFIPVREHENDVEKQKKRSGVSCIISTLLLGHFHYSDLHH

1.6E-19	79.2	10.9	5E-18	74.2	7.5	2.2	1	I7EZ38_PHAIB	Putative trk system potassium uptake protein TrkH	trkH PGA1_c14840	Phaeobacter inhibens (strain ATCC 700781 / DSM 17395 / CIP 105210 / NBRC 16654 / BS107)	515	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Phaeobacter, Phaeobacter inhibens, Phaeobacter inhibens (strain ATCC 700781 / DSM 17395 / CIP 105210 / NBRC 16654 / BS107)	391619	>tr|I7EZ38|I7EZ38_PHAIB Putative trk system potassium uptake protein TrkH OS=Phaeobacter inhibens (strain ATCC 700781 / DSM 17395 / CIP 105210 / NBRC 16654 / BS107) GN=trkH PE=4 SV=1MSRHRKPSQERTRGLFRLPLFLLILVAALAMWVPAIHALILDDHQTSRSFFYSGVVGLMVVVLVGLSMGNRVPRYSMPGQLTS LLASFAVLPAFLAVPVQDALGNTSYLNAYFDMVSAITTTGADVFSDPNRLPPSVHLWRAMVGWLGGLLMWVAASAILAPLSLGGFEV TARGEPGRGTETPLHMQRADPRRKLVVVTKTLAPLYAGLTLVLWILLIITGETALVALGHAMSVLATSGISAVGGVENGASGIAGEMV MFLFMFFALSRLTFSTDTVTSGHSRLDRDPEFRIGLLIVFGVPLLLFLRHWIASFDVATTSDLMQGLHSWWGATFTVLSFLSTTGFESA DWETARQWSGLNTPGMILLGLAVIGGGVATTAGGVKLLRVYALYLNGLREMERLVHPSSVSNEGKGNRRLQSNGAFVAWVFFMLF ALSLAVISISLAAVGSDFEQALILTIATLSTTGPLTEIAGSEPIALIHLTATAKLILCFAMVLGRLETLAIIALMTPNLWRS
2E-19	78.9	0.9	4E-10	48.2	1.5	2.1	2	Q3J2L6_RHOS4	TrkH1 protein	trkH1 RSP_2842	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	503	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides), Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	272943	>tr|Q3J2L6|Q3J2L6_RHOS4 TrkH1 protein OS=Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158) GN=trkH1 PE=4 SV=1MRRVRSVPLIVVLMAGGAAAMYVPAAHAVALRQHEVARAFFYAGTFLLILIAMIAIATQNRPPPRAARAHLSTLVGAYLILPPMLA LPFQMAVPDTSFTNAWFEMLSSFTTTGATLYDTPGRLPPSVHLWRALVGWLGGFFVLTAAMAVLAPLSLGGMEVISGHVPGREQAS QITRIADPTERLVRQSLALFPAYGGLTLALWGLLLLAGETGLVGLCHAMGTLSTSGISPLETMTAGEAGFRGEFLIFLFLFLAVTRRLMP GTSMVYRDTPIQRDPEVMMAFFFLIGVPVVLFLRHWIGAIETEETQNIAAAARAMWGGLFTTLSFLTTTGYESRDWVASRSWSGLGT PGLILLGLAIVGGGVATTAGGVKLLRVYALYRHAERELERIVHPSSIGGQGVVARRLRREGAYMAWIFFMLFAFSIAVVTAALSLAGLG FERAMVLGIAALTTTGPLADLAVETPIRWSELGPAAKVIAGAAMIVGRMETLAILALLAPASWRR
3.2E-19	78.2	14.7	3.3E-10	48.5	0.1	4.4	4	B8PDR0_POSPM	Predicted protein	POSPLDRAFT_97544	Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	2742	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Polyporales, Coriolaceae, Postia, Postia placenta, Postia placenta (strain ATCC 44394 / Madison 698-R) (Brown rot fungus) (Poria monticola)	561896	GN=POSPLDRAFT_97544 PE=4 SV=1MLSRFPFDNIYFTFAKTVFRWLWIDFTTFVVRIVWHPKAFGGELLQATRPLVRALGLGRPPTTIHSLPYETLAHIFALGRDPSPCK TCSQAPWRLREGKPLALNTPQLWTTVPVTSKATMSMMSEYLGRSGGRPIDVNILEDLHFKRNEVVVALLNALRIGGNPDAPCKFPCI SSLRFEIPQTKTEGLPEVFGGHLLEFLRLFPAVEQLAIQGFRTDEIVRSMTSTAPPDVVLPGLKRFVMLGHPHAEHLDSAETLVRWRA AAGASISNVFLIGVPASNLPLYTNHYGLRLLLGWQLSPKRVLLSLVTSRAAPSYYGGLHAGADWMQDEQTRRGRLGFYGPYPPYTSP LERANDVTKELSLTIIQLSTWALSFPIELSSPARTYENPTAGALASIFKTVFRRLYSNCVSAVSIAQRFRCQLVLILETVRKKLLKYTPVLA LNTPRLWTVVPINSRATTYTVLDYLGRSGVLPIEIDIRVPGPDMPFSEDELLGICTLLAWNSERWRQRDVPILEVLDVDVPLPGPEIPLL LQQWPEVFLLQKGAPRLREIHIMQGRLTEITLEPLAVLDTLVLMTTHWNLPRLKHLADTSPLITHLSLYCLTMSNAPQEDAVETMVGIPLL SMLTAPLLEVLQLEELSFGTEVEARMLLNSLKTEDAPDALCKFPRILSVRFEIMQMKNEGLPEVFGGHLLEFLHLFPLAEHLAVQGCRIE DIMVCITPPNITLPRLERITLLAPLSEEYLSAVDALRQQRQKIGMPVPSVHIIGMCASNMPQHARNYETAPMVWGFVHFLSMGTQKGL RFSPMSDSIDEDEWMQDRQLSRNRLRLKQPDMLAIMQPDMLTLMLSMCGLRGTDDDNVREVYWALQGSSVSLGGFETSCGGEKG VGENGGGESESHSFPSQRDGRRKTPAISGSAGGEDIGGRRKTEVEAKFRRELLASKAPFALVAFGEMTFRRSCRESQSAERHVCRR LLPVQTWDNLIIVIAKLGDVCVPVLDVLVRGTIAICGNQLRMTLAEGALQNKATAYTRHPYQWNCGLNAAGRETFQDACKVSQKHLER SRTPPWLDADLSYGCCSANGHVGRRTQGYFCTEESATLLASGRMDNLHSTRIVPMTEGSERQVTRVTRDRRVAPPSQRSALGEVE QRFESCCNASLISLATCKANRNMETDSVSLVVPITFRSSITGDAPETNTNNVARSWASASASCLTAWGCSDASEQPDLEEKLPSHGL AFGCDDGTVFLFGSQLAFPRKHDIPGSPTNTPPEPAEQVEAPKNYVDFDDEPEKLKGMLRGKATRSELLSPDVDRTAKIDRLSVSTST RSIKAFSPAASLRSLSPPSSPCSPTANSPAQRETGLFLKSHILPSSLGSTHAVAALEAYDDGSITSGVKAASDASILWIWQTIQVGSVG EARLVVASASGDTSYMSQSIDVAEGDAETQTRILVCELREGPQLDGSDMALVKKGDWVLDGPAESVGFYQEMDGTLAVHYMSSDH RLVIRILSFNEELSPPDIGDMKSNSTTMLPLPNPFKAFKNLSRERLSGETGNDDASELSLSAVISLHLVQSDRGGDPLVIGGSDDGSIGI WSAGSLTASEVTSQLMFVCISVVLVPASVAPLKMVHMREDDILLVYTDNRARLWDCKTMEFRRSMNKSKADELLGQGAWAGWPAE PVKPSVPVEIVSLPVFAGLDSACSLLLDMGSIIHSNTGHMPGRTSASKHDRGKTRSILATLLTPGISKEIDDICTERLRVYPSCASVGYH EFSSQAVWSISPEISAFRAVILVTLLQVLIDNDDASTMMTFYVASLPEAIGPSYQSPSLTFLAKYYLRSSVQEVRSAARLLFDAGVARLS NDDTILIVEKWKEYLPSVQKERDTESVRSAMALHMCGFVAAEKYNLLSTNVLTETSKSIGLYLHREGSPYRALAIELCSRGFTLWQQY VDAVEMLRAVCTLATVSRKEAISIHNVGSQARSAVLHIAAANTPLFMTTLTIDILQPRSVEHRKAVMQLVIFLIRKNPLVLYSNLPRLVEA VVKSLDPNSTSNRDAVLDSATDILGHIVQTFPNVDFHMSTQRLAMGTAEGAVVMYDLKTATRLYVLEGHKKRTTACSFSPDGRRLVT VSLEESVVLVWKVGSSLTSFFNPGAPPRQGHGGSDPYKTLSFNIGSEAHMTLAATLEAVRFEWPADRSNTYKTLYCLDGLNQPTFPT SLFLEAGRTSMIVPLITAAIFSASNGRFKIPFIDALFMCISAGTGTGLTTIDLSSMSVWQQAIIVVLGFIGNQVFVTWAYFTKHLKHIVTAK LERRSPQEDPFLSEHSVVFPRILPENDLKRRRAEMDELVSATVTHRPCELFARVIGRIFPQFYRSVQRRLTIPRTKMLVPHTPGGSPPR SAHHVPYISFNAIVDRNSVFKNLTEENIQELGGLLSVLPGFFAEDSLLTEYYLGLLVISFIVIIPYMSLPGWHSVMHPPEQHRMINTVWF STFQVVGAWANTGMSLVNQNMVPYRTTYPMITVFTLCVLAGNAAYTWLLLAIQLVIGLIALSFNLLLNPAMDHIPIGVRLINAVLQSSAV RSVVFQSAPVLSFVPAVQEDDNAEGVDSPNDAASGPRVAIWGQYLCHHVRKQLSFDMWWLALSLFVLCIIERAPLMAAEDATRFPIF ALIFELVSAYGTVGLSLGVPYVRMIRTTYGTGHPLIVVGELLAPGGFAPSFEDRRTAKSAEMKGEEMRTPSVDAKRNASEIPLDADKR SKALNIPI
3.6E-19	78	10.6	1.2E-11	53.2	2.3	2.3	2	Q165Q5_ROSDO	Trk system potassium uptake protein	trkH-2 RD1_2756	Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)	517	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseobacter, Roseobacter denitrificans, Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)	375451	>tr|Q165Q5|Q165Q5_ROSDO Trk system potassium uptake protein OS=Roseobacter denitrificans (strain ATCC 33942 / OCh 114) GN=trkH-2 PE=4 SV=1MSRAAHKTPRKPLSAYLLDQQLFVLIFGLAAFSMIIPALHSGATRSLETSRAFFYTGLFGIVIFAMIVIAQTGRTPRHGVLGNLMSIF ATFVFLPAFLALPLYESLQTTRFLNAYVEMVSAITTTGATVFDDPSRLNNTLHLWRAQVAWMGGVMMWIAASAILAPLNLGGFEVTAQ AEPGQRESRFGELDKTNPREKLMRIVVALVPIYVSLTLLLWVLLLISGDPSLVALTHAMSIMSTSGISAIGGLEGSGSGLTGEVLMLLFM LFALSRLTFSSDTVTATQGGIQTDPEFRLGMLIVIGVPLVLFLRHWIGAFDVAAEDDFWLAIRALWGSVFTVMSFLTTTGFASADWAQ AQAWSGLETPGLILMGLALMGGGVATTAGGVKLLRVFALYLNGKRELERLVHPSSVSRAGKESRRLQRNGAFIAWIFFMLFAMTMAA LTLLFALFGVAFEDALVLSIAGLSTTGPLLNLATETPISLAELGPYAKSVFCAAMVLGRLETLAIIALLTPDLWRS
5.2E-19	77.5	13.3	5.3E-17	70.9	3.3	3.1	3	A0A0E0KUY1_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	442	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0KUY1|A0A0E0KUY1_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MSPSRRAVGGALSVHVAYFVAVSCLGYGLLGMLKVREPGSAPRGIDRFFTAVSAATVSSMSTVEMEVFSNAQLVVLTVLMLLG GEVFISLVGLASKWSKLRRHAIDRSRRVESHGDVALQPATDVENPTSTAEEASRRRPMDADTLRRNAVRALFYVVLAIFLVVHVVGAV AVAAYVLASPGARQTLMAKSLNPWTFAVFTTVSTFSNCGFMPTNENMVVFKRDTPLQLLLVPQVLVGNTLFAPLLAACVWAAAAATR REELVEMARKGGQAAATGYSHLMPARRCWMLVATVAAFVAVQVALVCGMEWGGALQGMSPWEKVVNALFLAVNSRHTGESTVDL SILAPAILVLFVLMMYLPPYTTWFPFEENSNTKDNNAENQGIRLLESTVLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIIVEVVRQVRL TGFLPEK

7.5E-19	77	1.2	4.5E-07	38.1	0.9	2.8	2	W5B972_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	285	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5B972|W5B972_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MPNNENMAAFRRDTGLQLLLMPLALAGNTLFPTLLAVCVRAAAAATRRPELVEMTARNGRELTGYYHLLPARRCAMLAATVAG LVAVQVCMVCGMEWGGALRGMGPWEKVSNAVFVAVNSRHTGESTLDLSTLAPAILVLLVLMMYLPPYTTWFPFEESSGVKDHPTE ETPGVRLLKSTALSQLSYLAIFIIAICVTERENLEENPLNFSLLSIVVEVVSAYGNVGFSMGYSCSRQISPDALCTDRWTGFVGRWSDS GKLILILVMLFGRLKKFSIKGGKAWKLG
8E-19	76.9	6.6	9.5E-19	76.6	4.6	1	1	R5N356_9FIRM	Trk-type K+ transport systems membrane components	BN514_00300	Ruminococcus sp. CAG:17	150	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:17	1262951	>tr|R5N356|R5N356_9FIRM Trk-type K+ transport systems membrane components OS=Ruminococcus sp. CAG:17 GN=BN514_00300 PE=4 SV=1MILLMLIGGSPGSTAGGMKTTTFSVLILNAIATFRSQENAGAFGRRLEYHVIKNAATIAMLYFALFFGGGIAISVYEGLPLLNCLYE AASAVGTVGLTLGITPELHVFSQVVLIILMYLGRVGGLTLIYAVFSGRNKGNAKLPLEKITVG
1E-18	76.5	30.4	5.1E-18	74.2	16.3	3.1	2	I1Q4Z6_ORYGL	Uncharacterized protein		Oryza glaberrima (African rice)	445	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza glaberrima (African rice)	4538	>tr|I1Q4Z6|I1Q4Z6_ORYGL Uncharacterized protein OS=Oryza glaberrima PE=4 SV=1MPIRLHIFVSSARHAINSSAFICRFIAYHLSPLLIHLSYFLIIDVLGFVALVVLRPSNHKYNPRYVDMFFLSTSAVTVTGLATIQMEDL SSSQIAVLTILMFLGSEMFISFLGLVLESSKQNKHDPENRRISSVTVCEQSQLEEAIPQTPSMNSTDIKMRCLKYLVFVVLAYMIIILVTGS LLVFMYIAHVSSARDVLTRKSINKALFSVSVTVSSFTNGGLLPTNESMAVFSSNNGLLLLLIGQILAGSTLFPVFLRLVIWALRGLRLAKA EEPDFMMNNSSSVGFSHLLPNLQTTFLAAVEVAFVAMTVILFCCLNWDSAVFAGLTSLQKITNALFMAVNATQAGENSIDCSLVAPAA LVLFMVMMYTPSLTKLFSACQDHKRIGPERDDRTSRGKPFLKTMAFSPLAFNTTVIMLVCITERRSISTDPLNFSTFNIIFEVIR
1.1E-18	76.4	8.1	5.8E-12	54.3	3.9	2.3	2	Q5LRP3_RUEPO	Trk system potassium uptake protein TrkH	trkH-2 SPO2082	Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) (Silicibacter pomeroyi)	511	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Ruegeria, Ruegeria pomeroyi, Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) (Silicibacter pomeroyi)	246200	>tr|Q5LRP3|Q5LRP3_RUEPO Trk system potassium uptake protein TrkH OS=Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) GN=trkH-2 PE=4 SV=1MVRRRQTSETGLLRQLPLALLIWGLFSLMMWVPAVYALTLNDHPTSRSFFYAGILGLVVVTTISLARAGRPSRHGLLGQLAVLLS TFAVLPLFLAVPFHDALKTTSFLNAYFEMVSAITTTGAEMFPDPGRLSAPLHLWRAQVGWLGGLVMWIAASAILAPLSLGGFEVTAQG QPGRVLVGQGESVDPRGRLLRVAATLAPVYAGLTLVVAILLLAAGDSGLVAICHAMSVMATSGISPVGGLSGGASGLTGEAILFLFMF FALSRLTFSSDTAMRGHARLDQDPEFRIGLLILLGVPALLFLRHWSGAIDIASGENLTLALRALWGSLFTVMSFLSTTGFESTDWAEAR QWSGLGTPGMILLGLSVIGGGVATTAGGVKLLRVYALYLNGTRELQRLVHPSSVSSATGRNRRIQRGGAFIAWVFFMLFAISLAAIALA LAAAGSDFETAMVLSIATLSTTGPLIEIGAQEPIRLIEMPAAAKLILSGAMIIGRLETLAFIALITPALWRN
2.2E-18	75.5	6.3	2.5E-07	39	0.7	3	3	A0A0E0KUX9_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	305	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0KUX9|A0A0E0KUX9_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MKQKCRNILAHIVTGYFIAAVVCSSLVIIIFVEIDSDTRQLLKSKDIKIWTFSIFTVVSSFANCGFTPVNDNMAIFRKNSSLLLPVTPQ VLAGNTMLSPLLSLSIWILSKVSRREEYVYILQHPEDTGYRYLQSQKNSVNMVLTVGGLVLLQSVNTRHAGEAVIDISTLSSPILVLFALV MYHPSDNSALPINADNKPLTERGRNSNDQAIWKNFIISKSACLAIFTIIACITERKSICTDPLNFNIFGIAFKIISAYANVGYSLGYSCERLL KPDATCKATSYGFVGKWTDEDLVEECIHQVQC
2.3E-18	75.4	19.4	2.7E-08	42.2	0.2	4.6	4	M1CXU5_SOLTU	Uncharacterized protein	PGSC0003DMG400029966	Solanum tuberosum (Potato)	417	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Solanales, Solanaceae, Solanoideae, Solaneae, Solanum, Solanum tuberosum (Potato)	4113	>tr|M1CXU5|M1CXU5_SOLTU Uncharacterized protein OS=Solanum tuberosum GN=PGSC0003DMG400029966 PE=4 SV=1MKPLSFSFFKIMSLRVKPFWIELGYFTTLSFLGFLALNYFSKPRTLPSFRPQNLDVFFTSVSSTTVSSMSTIEMEVFSNVQLVFMT ILMFLGGEAFTSFLRLKLIKKENKDESFSCKDYELGNVINVDDKLEDVIITNPIEDHSHHDHHDEIIKIKSIRLLSNVVFGYILVIIILLGSSLVS LYIIIIPSAKQILNKKGLNLHTFSLFTTVSTFANCGFVPTNENMMIFKQNSGTSGLSTYEKIVGSLFEVVNTRHTGQSVFDLSTFTPAILVL FASMMYLSSYTTFLPVYNYEEKSEKMKKRKGRSLMDYISLSQPSCLVIFTILICVVEKDKMKNDPLNFNVLNILFEVISAYGTVGMSIGY SCARQINPDGHCKDATYGFAGKWSNTGKFILIIVMFFGRLKKYNQRGGKAWKVL
2.9E-18	75	9.2	2.9E-18	75	6.4	2.4	1	B8B252_ORYSI	Putative uncharacterized protein	OsI_24359	Oryza sativa subsp. indica (Rice)	422	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>tr|B8B252|B8B252_ORYSI Putative uncharacterized protein OS=Oryza sativa subsp. indica GN=OsI_24359 PE=4 SV=1MFLKPSNPEFRPGYIDMLFLSTSALTLSSLITIEMEVLSSSQIVVITLLMLLGGEVFVSFLGLMLRLNHKHNPEFSGDKVSSVPIELD TINSASTVISCEELQLEAAIPEVPSSTIKDLKRSKRLRWFLGFVVFSYFVVIHVAGFLLVLWYISRVSSAKAPLKKKGINIALFSFSVTVSS FANVGLVPTNENMAIFSKNPGLLLLFIGQILAGNTLYPLFLRLLIWFLGKVTKLRELKLMIKNPEELQYDYLLPKLPTAFLASTVIGLMASL VTLFGAVDWNSSVFDGLSSYQKIINALFMAVNARHSGENSIDCSLIAPAVLVLFIILMYLPPSTTFALSNGEEKTANKKAKRKLGLVVQN LAFSQLACISVFVIVAFITEYPSLIDDDDDDDGEMTMISSDVELMKLEIDWHDFDELKDVQ
3.4E-18	74.8	11.7	1.1E-16	69.8	8.1	2.4	1	A0A085BUV4_9RHOB	Potassium transporter TrkH	IV89_13480	Sulfitobacter sp. CB2047	511	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Sulfitobacter, Sulfitobacter sp. CB2047	1525218	>tr|A0A085BUV4|A0A085BUV4_9RHOB Potassium transporter TrkH OS=Sulfitobacter sp. CB2047 GN=IV89_13480 PE=4 SV=1MRRKSYIRREILELPLFLLIFGVFSASTIFPAIFALTTQDHLASRAFFYSGLLGVIIFTLIAVAHAGRRARHGALGPLMSLFSSFVFLP ALLAIPFLEALPTTRFLHAYFDMVSAITTTGATLFDDPGRISDTLHLWRAQVAWMGGLLMWIAASAILAPLHLGGFEVTSQAEPGNPDE RRSNMGQIDPRQRLLRSAAALTPTYLALTLMLWLLLLANGDRSLVALCHAMSVLATSGISPLGGTHDTGVGFGAEAMMMLFMLFALS RLTFSKDTVTATQGGLFTDPEFRMGLALILGVPVVLFVRHFLGAFDVDASAEALETGSAFWGAMFTVTSFLTTTGFVSASWAEAQSW SGLETPGLILMGLALIGGGVATTAGGVKLLRVFALYRNGVREMERLVHPHSVSGAGQAGRRLQSNGAFIAWIFFMLFALSLAGVTLLL TFVGAPFADALVMSVATLATTGPLMEFAADAPIALIQLGDGAKMILCAAMVLGRLETLAIIALLTPDLWRA
5.7E-18	74.1	14.4	3.4E-15	64.9	10	3.1	1	X5MN87_9PROT	Potassium uptake protein TrkH	BN1012_Phect2863	Candidatus Phaeomarinobacter ectocarpi	489	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, unclassified Alphaproteobacteria, Candidatus Phaeomarinobacter, Candidatus Phaeomarinobacter ectocarpi	1458461	>tr|X5MN87|X5MN87_9PROT Potassium uptake protein TrkH OS=Candidatus Phaeomarinobacter ectocarpi GN=BN1012_Phect2863 PE=4 SV=1MFAIIGIVLAASLSVIALAHLLPVLVAVSTGNNEQAIVFAMTGLLTAFIAGALGFATGGQKHRPVVAERLTALSIVWLIVPGFAAIAF VGVDPKALYVDAYFDAVSALTTTGSVSLINEMSSAPAVMIWRATLQWIGGYATLLMSMLVLAQLGLAGLSLRRAPIPPGDTSGPFGRY WPAMLALGLVYGSVTLAGVIGLLVGGMALVPAIGLAFSAAATGGLMPNGGTLVASVSVFSGIVVATLLLLGATNYLRHAGLVRRSPRT YWGDPEFRYMVLGITVGGIVLAGLVAITSGASLPLINAIMWVLSLLSTSAFAVDEAGFGSIPLLVALTVVFVGGSTMSTAGGLKLMRIAIL MKQGSREIARLSHPHGIVHTDFGGRSFTMPLMRGVWTMFVLMLVFALLAALALTVLGVPFEHAITASIGALTNAGPVLGFATGGDGLP IGIGTSEVYASMPATAKLVLSLAMVAGRVELLAFVGVVTAFTTQDS

5.9E-18	74	10.7	4.4E-17	71.2	1	2.1	2	S3D8X0_GLAL2	Uncharacterized protein	GLAREA_06602	Glarea lozoyensis (strain ATCC 20868 / MF5171)	343	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, sordariomyceta, Leotiomycetes, Helotiales, Helotiaceae, Glarea, Glarea lozoyensis, Glarea lozoyensis (strain ATCC 20868 / MF5171)	1116229	>tr|S3D8X0|S3D8X0_GLAL2 Uncharacterized protein OS=Glarea lozoyensis (strain ATCC 20868 / MF5171) GN=GLAREA_06602 PE=4 SV=1MKFPSPTKLWRVLVHQISSHMSAPSFLLLHHLYFLSIIFVCSIAFWLFSRPHDSVPFIDCLFVVISSLTSTGLTTRNLSTFNTAQQALIWLLIVFGSPTFISVSVVWIRRRAFESKFATVIHGKQHREDPVQYNPAPAPSPATTSIQEFISIPYSDPIVKEEAKESSTTIGHDSSAELKSQHAPNVVSNPLPGNFVLEYSDFNSGSPTLKSKASTGSFLGVVKVFGNAMVGRNSQFYGLTREEREQLGCIEYKALKLLSYLVPAYLLTFQVVGSIVLGSFISVHQSSLAYDNGSTPWWLGVFLGVSAFNNTGMSLLDLSMIPFGTSYYVLLTVAFLTLAGNTA
6.6E-18	73.9	20.5	1.4E-17	72.8	14.2	1.5	1	A0A0F4RKI5_9RHOB	Potassium transporter TrkH	TW80_04645	Loktanella sp. S4079	506	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Loktanella, Loktanella sp. S4079	579483	>tr|A0A0F4RKI5|A0A0F4RKI5_9RHOB Potassium transporter TrkH OS=Loktanella sp. S4079 GN=TW80_04645 PE=4 SV=1MGWIVKLPFFVVLMGIGALAMLVPAVHGVILEDFTTMRVFFYGFLLFSMLTLVVGLATAGYAPTNVARSQLIGLLSAFTLLPLMFAVPFYEAIGNTTYINAWFEMVSSFTTTGATVYDTSGRLTPSLHLWRALVGWLGGLLVWVTAVSIFAPMNLGGFEVRATSNIGKGAGSALTQISRIADPSERLVRYTLTLTPIYVGLTFVLWIGLVVAGEFPYVALCHAMSTLSTSGISPIDGLYYAVSGFWGELLILGFLIFALSRLTFSRGMMGEANKGLWHDPEFRTAMVLIGLVTAALFFRHFIGAADQQSMVTIQQIFAALWGSLFTVTSFLTTTGFESHFWDGAASWSGLNTPGLFLTGMALIGGGVATTAGGVKLLRIYALFRHGEREQERLLHPSSIGGGGKEARRIRKQGAYISWIFFMLFALSIAAVMTLMSLTGVQFETSMVLSVSALSTTGPLAAVAAEVPIAYSGIPDSAKVILAAAMVLGRLETLAIIALFNPEIWRG
1.5E-17	72.7	0.1	6.2E-14	60.7	0	2.1	2	A0A080WSM2_TRIRC	Uncharacterized protein	TERG_11997	Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) (Athlete's foot fungus)	383	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Pezizomycotina, leotiomyceta, Eurotiomycetes, Eurotiomycetidae, Onygenales, Arthrodermataceae (dermatophytes), Trichophyton, Trichophyton rubrum (Athlete's foot fungus) (Epidermophyton rubrum), Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) (Athlete's foot fungus)	559305	>tr|A0A080WSM2|A0A080WSM2_TRIRC Uncharacterized protein OS=Trichophyton rubrum (strain ATCC MYA-4607 / CBS 118892) GN=TERG_11997 PE=4 SV=1MFRMFYSIVWPRVSRPSFIVVHYAYIVFLCLLGMVMIYPLKNMTAIDALFQGVGAATMTGLNSIDFKELTTYQQVVLYISPILGNICFVNFIVVLVRLYWFESKFKEIVRFSRLPSTERSHHIEHGPRSHRATASATATEIPAISSEPAEAGEPEGLKHRNAHPPDEKVQDDPKRATVEKQLPNAGPGHVSFSTDTFRPREKALRIPGPREFEAGHRVHEVDEETDGDELTKATSVDPSIAGASSVRERGKLGKILSHATSVEQAASSAFVLGSASRPRSRSRSVSRSLQPLSRTGSRGSQAPYLSYTPTIGRNSQFLNLTEEQRIELGGIEYRSLKLLARIVGGYFFGFLLLGSICLVIWIYSADSSHRQYLATNGINPVWW
2.6E-17	71.9	16.3	8.3E-15	63.6	5.4	3.6	2	A0A0D9W962_9ORYZ	Uncharacterized protein		Leersia perrieri	480	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Leersia (cutgrass), Leersia perrieri	77586	>tr|A0A0D9W962|A0A0D9W962_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1MKLTSLSICVAHSVKQSYSFLVYQSNPLVVQLIYFVIISFVGFLALKNLKPQGKPGTNDLDLMFTSVSALTVSSMATIEMEDLSDRQLWVLILLMLLGGEVFISMLGLYFNNADVNRNENRQRSLRSISMDIESNSPANNGDHSNMECGQLEETISQNQVQQTKSITHNPCTVLARVVTDARGVLKSKEINMYTFCIFEEVSSFVNCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLSVWILGKISTKEEYAYILQHPEKTGYKHLHVQRKSVYMVLSVTGLALLQVMFICSFEWNSKTVEGMHWLQKLVGSLFQSVNTRQAGESVVDISTLSPPTLLLFAVIIYLPSDASFLTVNAENKPLTDNKRNSISRAMWRNFTVTKLACLAMFTFLACITERKSISADPLNFNIAFGNVGYSLGYICQKLFNPDVTCKAASYGFVGRWTREGKLIVILVMFLGRLKEFILKGGEA
3.1E-17	71.6	16.2	1.5E-14	62.8	5.5	3.6	2	A0A0D9W961_9ORYZ	Uncharacterized protein		Leersia perrieri	444	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Leersia (cutgrass), Leersia perrieri	77586	>tr|A0A0D9W961|A0A0D9W961_9ORYZ Uncharacterized protein OS=Leersia perrieri PE=4 SV=1MKLTSLSICVAHSVKQSYSFLVYQSNPLVVQLIYFVIISFVGFLALKNLKPQGKPGTNDLDLMFTSVSALTVSSMATIEMEDLSDRQLWVLILLMLLGGEVFISMLGLYFNNADVNRNENRQRSLRSISMDIESNSPANNGDHNARGVLKSKEINMYTFCIFEEVSSFVNCGFTPLNSNMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLSVWILGKISTKEEYAYILQHPEKTGYKHLHVQRKSVYMVLSVTGLALLQVMFICSFEWNSKTVEGMHWLQKLVGSLFQSVNTRQAGESVVDISTLSPPTLLLFAVIIYLPSDASFLTVNAENKPLTDNKRNSISRAMWRNFTVTKLACLAMFTFLACITERKSISADPLNFNIAFGNVGYSLGYICQKLFNPDVTCKAASYGFVGRWTREGKLIVILVMFLGRLKEFILKGGEA
4E-17	71.3	23.5	3.9E-09	44.9	0.4	4.4	4	K4CC87_SOLLC	Uncharacterized protein	Solyc07g014680.2	Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	391	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, asterids, lamiids, Solanales, Solanaceae, Solanoideae, Solaneae, Solanum, Lycopersicon, Solanum lycopersicum (Tomato) (Lycopersicon esculentum)	4081	>tr|K4CC87|K4CC87_SOLLC Uncharacterized protein OS=Solanum lycopersicum GN=Solyc07g014680.2 PE=4 SV=1MSLRVKPFWIELGYFTTLSLLGFLALNYVSKPRTLPSFRPQNLDVLFTSVSSTTVSSMSTIEMEVFSNVQLVFMTILMFLGGEAFTSFLSLKLIKNKESKDKSFSNKDYELGNVINVDNKLEDVIIINPIEDHIHDHHDEIIKIKSIKLLSNVVFGYILVVILLGSSLVSLYIIIIPSAKQILDQKGLNLHTFSLFTTVSTFWNSEGTSGLSTYEKIVGSLFEVVNTRHAGLSVFDLSTFTPSILVLFALMMYLSSYTTFLPVDNYEEKSEKMKKRKGRSLMEYISLSQPCCLVIFTILICVVEKDKMKNDPLNFNVLNILFEVISAYGTVGLSIGYSCARQINPDGHCKDVTYGFAGKWSNTGKFILIIVMFFGRLKKYNQRGGKAWKVL
4E-17	71.3	6	1.2E-15	66.4	4.1	2.2	1	V9VTC1_9RHOB	Potassium transporter TrkH	METH_09875	Leisingera methylohalidivorans DSM 14336	511	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Leisingera, Leisingera methylohalidivorans, Leisingera methylohalidivorans DSM 14336	999552	>tr|V9VTC1|V9VTC1_9RHOB Potassium transporter TrkH OS=Leisingera methylohalidivorans DSM 14336 GN=METH_09875 PE=4 SV=1MRRPVKAPIGVLRLPLFLLIWGIASLAMWLPAVHALVLDDHHTSRSFFYAGVAGLVLVVLIGLSMGNRVPRYGMPGQLLSLLATFTVLPLFLAVPVQDALVSTRFLNAYFDMVSAITTTGADIWGDPGRLPPSVHLWRALVGWLGGLLMWVAASAVLAPMSLGGFEVTAKGEPGGGMAGPLHMERADPRRQLVLVTRTLAPVYAGLTLVLWLLLMITGEQALAGLSHAMSVMATSGISATGGVENAASGLAGEMVMFLFMFFALSRLTFSSDTVTAGEGRLDKDPEFRTGLLIVFGVPLLLFLRHWVAAYEVDAGQDLLQALRALWGTVFTVLSFLSTTGFESAHWEAAQAWSGLETPGMILLGLAVFGGGVATTAGGVKLLRVYALYLNGLREMERLVHPSSVSGEGNRTKRLQKNGAFVAWVFFMLFALSLAVVSTALAAVGSDFEQSLVLAVAALSTTGPLAEAAGSTPIVLNLLTAPAKLILCIAMVLGRLETLAFIALLSPNLWRS
4.6E-17	71.1	17.5	1.6E-16	69.3	12	1.9	1	F2E1K5_HORVD	Predicted protein (Uncharacterized protein)		Hordeum vulgare var. distichum (Domesticated barley)	370	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|F2E1K5|F2E1K5_HORVD Predicted protein OS=Hordeum vulgare var. distichum PE=2 SV=1MPIRLRTFLSSARHVSNSSVFIFQFIPFHLSPLLVHLSYFVIIDVLGFVALMALKPSNPNYSPRYVDIFFLSTSAVTVTGLATIKMEDLSSSQVVILTLLMLLGSEMFVSLIGHIHELRKQNKHDPEDSRVRSVTVQDESQIEEAIPATQSISTTSLKKSCLKYIGFVLLAYMVLILLVGSLSVFLYVAHVSTARDVLTRKSINTMLFSISVTVSSFTNGGLIPTNESMAVFSSNQGLLLLLTGQILAGNTLLPVFLRLVIWALRGLRIGRAKPEEFKFMMNNTKAVGFNHLLPNQQTVFLAASVAALIAVTVTFFCCLNWDSPVFAGLTANQKITNALFMAVNTRQAGENSIDCSLVAPAALVLFITMW
6.1E-17	70.7	0.1	7E-17	70.5	0.1	1	1	R5WRF4_9DELT	Trk system potassium uptake protein TrkH	BN495_00324	Corallococcus sp. CAG:1435	150	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, environmental samples, Corallococcus sp. CAG:1435	1262867	>tr|R5WRF4|R5WRF4_9DELT Trk system potassium uptake protein TrkH OS=Corallococcus sp. CAG:1435 GN=BN495_00324 PE=4 SV=1MAAPXXXGCAGSTAGGLKVSRVAILGCSVRKELRKILHPRNANSVKFEGKVLSKEVLQSATNYFGIYMLVLISTFLILSFDGCPDLTIEANITAAASCLNNIGPAYGTVASGYYMYSPLSKIVLSVAMLLGRLEIYPLLLTLSPKTWIRR
9.9E-17	70	1.4	1.2E-16	69.7	1	1	1	Q8YLG2_NOSS1	All5336 protein	all5336	Nostoc sp. (strain PCC 7120 / UTEX 2576)	160	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	103690	>tr|Q8YLG2|Q8YLG2_NOSS1 All5336 protein OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=all5336 PE=4 SV=1MSLGMIFGAGSTCGGLKLSRIVTLYKAVVWHLQQIFLKPDEQIKYKLDGQEVTEIEAHRQIRTATVLATLWLGFLGVGVLLLLQVVEAQYTVPDVILESASAMGTSGLSVGITNPNLHWIGKLILILFMWMGRVEIIPVMVLFAFVFRPLQQIIRIKKSR

1E-16	70	13.9	2.9E-16	68.5	7.7	2.5	2	M7YI81_TRIUA	Putative cation transporter HKT6 (Uncharacterized protein)	TRIUR3_19223	Triticum urartu (Red wild einkorn) (Crithodium urartu)	365	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum urartu (Red wild einkorn) (Crithodium urartu)	4572	>tr|M7YI81|M7YI81_TRIUA Putative cation transporter HKT6 OS=Triticum urartu GN=TRIUR3_19223 PE=4 SV=1MATVEMEEFSSKQLWVLAILMLIGSEVFTSILGLHFMRAKFNTENSLNTRDHISHIDIESINVANFDPNTSHGTKDAVAFSELRQA NKQHVDPKTTVLLGTAVTVCLLITNLGSSLLIYLYLKLVPDAQEILKRKRTGLILFSVFTAISSVANCGFTPVNENMVIFQKNSGLLLLIIPQ MLVGNTLFAPCLRFMVWSLQKITGKQEWCYILEHANAIGYRHLMSTRKCAYLILTVVGFIILQTILFCSLEWSSEALQEMSSYQKIVGAL FQSTNARHAGETIVDLSRISSAIVVLYTVMIAYGNVGFSMGYSCKRLLKQDLHCKDASYGFVGKWSHEGKIILIIVMVFGRLKGYNLKG GKAWKLR
1.4E-16	69.5	6.8	1.4E-16	69.5	4.7	2.2	2	M0WVT3_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	430	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0WVT3|M0WVT3_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MPELESPQTSMHRFSSALVILQNLPSHTAMKLPLSNLEVLRITKEKVKRFHEFVCTRLSSLSKCTADLFRRSYLFLVFKSNPLIVQ LIYLLSISFAGFLALKNLRLPLNKPSPRNLDLMFTSVSTVTVSSMATVEMEEFSGQQLWVFIILMILGGEVFASMIGLHFKNIRANTEEAFQ TRLDFISRDIESSDVFTNSGHNNMEGTQSEETMPHNQVQESKAMNQKSRNVLAHVVAVYFIAAIVCSSVVITIFLWVDSDARHLLKSK HIKIWTFSIFTAVSSFANCGFTPLNDSMAIFKNNPTFLLLLTPQILVGNTLFAPLLRLSIWTLGKVSSREEYAYILQHPKEIGYRHLQPHKN SVKLVLTGVMLILLQAMLICYFEWDSKSLEGMGWFQKLTGSLFQSANSRHAGETVINISTLSPPIMVIFALAM
2.2E-16	68.9	9	7.5E-07	37.4	1.8	3	3	A0A0E0KUX4_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	298	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0KUX4|A0A0E0KUX4_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MKQKCRNILAHIVTGYFIAAVVCSSLVIIIFVEIDSDTRQLLKSKDIKIWTFSIFTVVSSFANCGFTPVNDNMAIFRKNSSLLLPVTPQ VLAGNTMLSPLLSLSIWILSKVSRREEYVYILQHPEDTGYRYLQSQKNSVNMSVNTRHAGEAVIDISTLSSPILVLFALVMYHPSDNSAL PINADNKPLTERGRNSNDQAIWKNFIISKSACLAIFTIIACITERKSICTDPLNFNIFGIAFKIISAYANVGYSLGYSCERLLKPDATCKATSY GFVGKWTDEVHPHRRKILNVHEKLP
2.2E-16	68.8	5.6	7.2E-14	60.5	3.9	2.6	1	M7ZUG2_TRIUA	Putative cation transporter HKT7 (Uncharacterized protein)	TRIUR3_30865	Triticum urartu (Red wild einkorn) (Crithodium urartu)	217	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum urartu (Red wild einkorn) (Crithodium urartu)	4572	>tr|M7ZUG2|M7ZUG2_TRIUA Putative cation transporter HKT7 OS=Triticum urartu GN=TRIUR3_30865 PE=4 SV=1MEVFSNGQLLVLTVLMLVGGEVAMLCGMEWSGALRGMSAWEKVSNAVFLAVNSRHAGESTLDISTLAPAILVLFVLMMYLPSY TTWFPFAGSSGTTDHAEETQGIRLIKSTALSQLSYLTIFVIAICVTEREKLKEDPLNFNLLSIVVEVVSAYGNVGFSMGYSCSRQISPDQ LCTDRWTGFVGRWSDSGKLVLILVMLFGRLKKFSMKGGRAWKLS
3.2E-16	68.3	26.6	5.4E-13	57.7	5.6	2.5	2	A9A4H1_NITMS	CBS domain containing protein	Nmar_0764	Nitrosopumilus maritimus (strain SCM1)	605	cellular organisms, Archaea, Thaumarchaeota, Nitrosopumilales, Nitrosopumilaceae, Nitrosopumilus, Nitrosopumilus maritimus, Nitrosopumilus maritimus (strain SCM1)	436308	>tr|A9A4H1|A9A4H1_NITMS CBS domain containing protein OS=Nitrosopumilus maritimus (strain SCM1) GN=Nmar_0764 PE=4 SV=1MSTNPERAVSYVLNKSVTEYMDKDVLILSQNTLTREATRMLQHYETDDIIVTNEDRVPVGIVTDEDILSKVSDVTVYAEATKLKDI MTTPLVTINEKATLQDALHKMRDNSIRKLPVLSKKNQVIGMIFQTTIANVIRDATASEPRLLSPPVKAVLGNLGFVLQFAGVLLLVPAIIST ILENTLTATGIYLTTVLLLVTGFFLNSYGEKSSLNLQQASILVFSSLFLLSLFGTVPYLYVFPSEETNVEVFGNAFFSSAAGFTTGGISLFD TPEEQLTQSFTFYRSYTQLVGGMSFIYLVITAFYPESKLQSMRGFISGRTLHMKELFSTITVIFAVYIVIVAILLYFFGQENLLDDFSLAMS TLATGGFVPSSTIIENLGWQEEVILMGAMILGALPFTFHYAFVRKKFLAPKLGKEVLTYFAILGGATILFISISGLDPLDSAFYSVSASTTA GLQLQSLAGLGGFAHAILITLMFIGGCGFSTAGGLKIFRLFHLRNCRSFFSSVRRKELSTQTKKEITSTLIIIALFPVISAITGLHLAETEDV SYQDAFFEAAGVITTGGLSAGVIDSDTDPATKIVLGFLMIFGRLEIIAIIYIFVPRLS
5.4E-16	67.6	9.1	1.1E-06	36.8	1.8	3	3	A0A0E0KUX5_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	356	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0KUX5|A0A0E0KUX5_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MKQKCRNILAHIVTGYFIAAVVCSSLVIIIFVEIDSDTRQLLKSKDIKIWTFSIFTVVSSFANCGFTPVNDNMAIFRKNSSLLLPVTPQ VLAGNTMLSPLLSLSIWILSKVSRREEYVYILQHPEDTGYRYLQSQKNSVNMSVNTRHAGEAVIDISTLSSPILVLFALVMYHPSDNSAL PINADNKPLTERGRNSNDQAIWKNFIISKSACLAIFTIIACITERKSICTDPLNFNIFGIAFKIISAYANVGYSLGYSCERLLKPDATCKATSY GFVGKWTDEDQTLGTLKSPHHQGYFLGIVSSYILSSEHPHIGQRYTLETYEICHSNTLWVANSNAILYKPTDLVEECIHQVQC
7E-16	67.2	2.8	3E-08	42	0.4	2.6	2	M0XC45_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	243	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0XC45|M0XC45_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MHIHPPSPNPQHVHTYIVTSNMAGAHRKVCELLYHTRRRSTAALNNVAMLCGMEWGGALRGMSAWEKVSNAVFLAVNSRHT GETTLDISTLAPAILVLFVLMMYLPPYTTWFPFGESSGVKDHPTEETKGLRLLKGTLLSQLSYLAIFVIAICITEREKLKEDPLNFNLLSIVV EVVSAYGNVGFSMGYSCSRQISPDRLCTDRWTGFAGRWSDSGKVILILVMLFGRLKKFSMSAGKAWKLS
1.1E-15	66.5	16	1.7E-14	62.6	11.1	2.5	1	C9LX16_SELS3	Cation transport protein (Cation transporter)	Selsp_2204 SELSPUOL_02022	Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	482	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Selenomonas, Selenomonas sputigena, Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	546271	>tr|C9LX16|C9LX16_SELS3 Cation transport protein OS=Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28) GN=Selsp_2204 PE=4 SV=1MDARIVSFLLGRMAFLEGAALFLAFGLAIFWADEHPLAFGVPAALSFVLWRVFSHLSKGHRHTIGVTDGAVFLFAAWLLNSLLGA LPFFLTGELSAADSFFASVAAFTTTALLFTPTGLESSLGFWQIFQGWIGGMYFLCLLVTIMPQVGGCFGLTLSVQQGTNFSPLLRRMN AAAQKMALLYACLTLVALGLFLLAGESFLSSAVLALTSISTTGLDPRGLVLKGSGFTTELAAEAAMLLAGVNFLLWQRAAARRDVRALF ADAELRIFLLVVFLGGAALACYLAVVGVHDVEHSLRMGFFHAISFATTTGFAAAPLASWPTFPHAVLLLLATLGSSVGAVGGGFKVMR LLVLVKMAKREILRTIHPRMIVNIKIDGKSVPHKLYGRILSFFFLYVVVLILATLGLALAHIDTLPAMGFAVGCLSGTGTVVTLLYGGKDFLL LPGWVKVFAGFLMILGRLEIFSFLILLRAGIDRLHRRQW

1.2E-15	66.4	4.5	1E-13	60	3.1	2.6	1	W5BR00_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	210	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5BR00|W5BR00_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MLAATVVGFLAVQVAMLCGMEWGGALRGMSPWEKVSNAVFLAVNSRHTGESTLDLSTLAPAILVLFVLMMYLPPYTTWLPFG ESSSVKDHPREETQGVRLLKSTLLSQLSYLAIFVIAICVTEREKLKEDPLNFNLLSIVVEVVSAYGNVGFSMGYSCSRQISPDGMCTDR WTGFAGRWSDSGKLILILVMLFGRMKKFSMKAGKSWKLS
1.8E-15	65.8	4.7	9E-14	60.2	3.3	2.5	1	W5B8F1_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	211	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5B8F1|W5B8F1_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MLAATVVGFLTVQVAMLCGMEWSGALRGMSPWEKVSNAVFLAVNSRHTGESTLDISTVAPAILVLFVLMMYLPPYTTWFPFEG NSSTKDHPKHEEARGIKLIKSTILSQLSYLTIFVIAICVTEREKLKEDPLNFNLLSIVVEVVSAYGNVGFSMGYSCSRQISPDQLCTDRWT GFVGRWSDSGKLILILVMLFGRLKKFSMKGGKAWKLS
3.7E-15	64.8	10.9	4E-15	64.7	7.6	1	1	M0YPM9_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	198	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0YPM9|M0YPM9_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MVLILLVGSLSVFLYVAHVSTARDVLTRKSINTMLFSISVTVSSFTNGGLIPTNESMAVFSSNQGLLLLLTGQILAGNTLLPVFLRLV IWALRGLRIGRAKPEEFKFMMNNTKAVGFNHLLPNQQTVFLAASVAALIAVTVTFFCCLNWDSPVFAGLTANQKITNALFMAVNTRQA GENSIDCSLVAPAALVLFITMW
4E-15	64.7	16.4	6.9E-15	63.9	11.4	1.4	1	A0A072UCC7_MEDTR	High-affinity potassium transporter (Uncharacterized protein)	MTR_6g092890	Medicago truncatula (Barrel medic) (Medicago tribuloides)	346	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Trifolieae, Medicago (medics), Medicago truncatula (Barrel medic) (Medicago tribuloides)	3880	>tr|A0A072UCC7|A0A072UCC7_MEDTR High-affinity potassium transporter OS=Medicago truncatula GN=MTR_6g092890 PE=4 SV=1MKNNFGKNSKNLCTYFPNKFNFNFNGFLPRSLSFQFNHFFIHLFYYIILSLFGYLGLKFSKPRSSVRQKDFDLFYTSVSASTVSS MTSIEMEVFSNSQLILLTFLMLVGGEVFTSMLQLFLNMFNFNKNQCLNGECSRSNYPPIKINQIELGLVSIPHLVTLYITNVPWPSAKNV LKNKGIKIETFSLFTIVSTFATCGYVPTNENMIVFKKNSGLLLLILPHVLLGNTLYPPCLRLFIKVLKSVNKREEFSYLLKNSKEMGYDHLL SSLHCWLLLVTVFGFNVIQFVLFCSMEWSSNIMEDLNLYEKVVATLFQVSNARHSGESVFDLSTISSAILVMFMFVVMM
4.6E-15	64.5	0	6.7E-15	63.9	0	1.3	1	D4J123_BUTFI	Uncharacterized protein	CIY_09520	Butyrivibrio fibrisolvens 16/4	184	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, Butyrivibrio fibrisolvens, Butyrivibrio fibrisolvens 16/4	657324	>tr|D4J123|D4J123_BUTFI Uncharacterized protein OS=Butyrivibrio fibrisolvens 16/4 GN=CIY_09520 PE=4 SV=1MNTSIIRFILLYVVGFIGLFLLLPVIVALIYHENVWSNYLVVAIPCIIAGIINSYLKPKESSFYLKEGFFCTGAAWVILSALGAIPLWLSN EIPHYIDALFETVSGFTTTGASILENVEALSHASLFWRSFTHLVGGMGVLVFLLSVIPLAGGDGSFNLMKAESPGPSVGKLVPKLKIQLR CFI
7.3E-15	63.8	0.1	7.8E-15	63.7	0.1	1	1	E2LVU0_MONPE	Uncharacterized protein	MPER_11329	Moniliophthora perniciosa (strain FA553 / isolate CP02) (Witches'-broom disease fungus) (Marasmius perniciosus)	79	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetidae, Agaricales, Marasmiaceae, mitosporic Marasmiaceae, Moniliophthora, Moniliophthora perniciosa (Witches'-broom disease fungus) (Marasmius perniciosus), Moniliophthora perniciosa (strain FA553 / isolate CP02) (Witches'-broom disease fungus) (Marasmius perniciosus)	554373	>tr|E2LVU0|E2LVU0_MONPE Uncharacterized protein OS=Moniliophthora perniciosa (strain FA553 / isolate CP02) GN=MPER_11329 PE=4 SV=1MSAYTGGGLSLVDQGMLPFQQAYLMIISMMFVILAGNNALPIFLRFVIWVGSRVAREGTEAEQAFSFLLDHPRRCFYYL
1.2E-14	63.1	1.8	2E-09	45.9	1.3	2.4	2	Q1GGX6_RUEST	Cation transporter	TM1040_1357	Ruegeria sp. (strain TM1040) (Silicibacter sp.)	512	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Ruegeria, Ruegeria sp. (strain TM1040) (Silicibacter sp.)	292414	>tr|Q1GGX6|Q1GGX6_RUEST Cation transporter OS=Ruegeria sp. (strain TM1040) GN=TM1040_1357 PE=4 SV=1MIRRPLKQVRGVLRLPLLLLIWGVFAIAMWIPAVHAVIVDDHQTSQSFFYSGIVGLTLVAFVGLSVSNRVPRYGMPGQLMTLLAT FVLLPLYLAIPLQDALKNTSYLNAYFDMVSALTTTGADIFDRPGRVPDSVHLWRVLVAWLGGMFMWIAASAVLAPLSLGGFEVTTRAE PGRSDAILRESQRPDPRRKLIIVTRALAPVYAGLTFALALLLMLCGESGLVAVSHAMSIMATSGLSPIGGIQDAQAGLAGEMIMFLFLLF ALSRLTFSSDTVAVGHGRLDKDPEFRSGILILGVPMLLFLRHWLASLEVNASDDWGMALTSLWGAIFTVASFLTTNGFESAYWFSAQ EWSGLETPGMILLGLAVMGGGVATTAGGVKLLRVYALYLNGLREMERLVLPSSVSGEGRGNRRLQSNGAFVAWIFFMLFALSLTLIS VALSAFGIPFEQAMILAVAGLSTTGPLVEAAGQVPIELNLLDAPAKLILCFAMVLGRLETLAIIALLSPNLWRN
2.9E-14	61.8	0.1	3.7E-14	61.5	0.1	1.1	1	I3YDK1_THIV6	K+ transport system, NAD-binding component	Thivi_3192	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	438	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiocystis, Thiocystis violascens, Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	765911	>tr|I3YDK1|I3YDK1_THIV6 K+ transport system, NAD-binding component OS=Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) GN=Thivi_3192 PE=4 SV=1MKIIILGAGQVGTSVAANLVSEANDITVVDHNPELLRELQERFDLRTVLGHGAHPDVLARAGADDADMIIAVTNSDETNMVACQV AYTLFHTPTKIARVRAQSFLDQPRLFGTDALPIDVAISPEALVTSYILRLIENPGTLQVLDFAGGRIRLVAVKAYYGGPLVGHELRALQEH MPQVDARVAAIYRQDRAIQPEGDTVIEADDEVFFLAAPIHIRAVMGELRRLDKSYKRLIVAGGGNIGTRLARALEANYRVKLIERNLNHC KRIAEDLEKTIVLHGDAADQELLLEENIENTDVFCAVTNDDEAKILSAMLAKRLGAHEIGRLIHPNAQLPVRIGGKSVNHRVVDAVWGFF SLYVASFVLMYLLLAATGLDLLTAFSAVAACINNLGPGLAQVGAHYADLHDLAKWILCFAMLLGRLEIFTLLVLLSPAFWQR
6.7E-14	60.6	7.3	4.2E-11	51.4	2	2.1	2	W5HXA3_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	335	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5HXA3|W5HXA3_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MGRVKRFYQDFIHIKLHSFSRISRYVVDSMVFIYRFVALHVHPFWIQLSYFLAMAILGSVLLMSLKPSNPEFCPPYIDMLYLSTSAL TVSGLSTVKMEDLSSSQIVVLTLLMLVGGEIFVSLLGLMLRVNHQDMQDLPSVKISSVPVELEVLDLANSMALCDESQLEEAAHAIPPK KCTELKRTESVKCFGHVIFGYFAVIHVLGFLLVFLYITHVPTASAPLNKKGINIVLFSLSVTVSSFANAGLVPTNENMVIFSKNSGLLLLLS GQMLAGNTLFPLFLRLLVWFLGKLTKVKELRLMIKNPEEVHFANLLPGLRTVFLSSTVVGLAAAGVT

6.8E-14	60.6	10.8	6.6E-06	34.3	0.3	3.5	3	M0WVT2_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	491	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0WVT2|M0WVT2_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1MPELESPQTSMHRFSSALVILQNLPSHTAMKLPLSNLEVLRITKEKVKRFHEFVCTRLSSLSKCTADLFRRSYLFLVFKSNPLIVQ LIYLLSISFAGFLALKNLRPLNKPSPRNLDLMFTSVSTVTVSSMATVEMEEFSGQQLWVFIILMILGGEVFASMIGLHFKNIRANTEEAFQ TRLDFISRDIESSDVFTNSGHNNMEGTQSEETMPHNQILVGNTLFAPLLRLSIWTLGKVSSREEYAYILQHPKEIGYRHLQPHKNSVKL VLTGVMLILLQAMLICYFEWDSKSLEGMGWFQKLTGSLFQSANSRHAGETVINISTLSPPIMVIFALAMYLPSGTSILASRGDNRSLAD KKENPNGRATWKKFAMTKRTCLVIFTILACITERKSMTADPLNFSIFSVIFEVISAYGNVGYSLGYSCDKLLKPDATCRDASYGFVGRW SDQGRLIIILVMFLGRFKAYNLKGKKPLNVHPCTGATPHERPEVAAN
7.9E-14	60.4	9	2.3E-05	32.5	0.2	2.7	2	D7UBM5_VITVI	Putative uncharacterized protein	VIT_11s0103g00050	Vitis vinifera (Grape)	222	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, rosids incertae sedis, Vitales, Vitaceae, Vitis, Vitis vinifera (Grape)	29760	>tr|D7UBM5|D7UBM5_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_11s0103g00050 PE=4 SV=1MLNNSREIGYNYLLPSVHSFVMAIVVLVLIVFEFLFFCSMEWNSEALYGLDGNEKFVASLFQVVNLRHTGESVFDLSIVTPAVLVV FIVMMYLPARTSFFAIEGHETDVKNGEGKTKQKRLMGHDTFSPLTFLVPFVIFICMTERDKLKEDPLNFNVLSIALEVISAYANVGLSTG YHCARQLKPDPFCKPVWYGFVGRWSAGGKLLLVIVMFLGKLRKFGK
1E-13	60	12.7	6.2E-06	34.4	5.1	2.8	3	A0A099TD29_9RHOB	Potassium transporter TrkH	PM04_01265	Thalassobacter sp. 16PALIMAR09	493	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Thalassobacter, Thalassobacter sp. 16PALIMAR09	1225651	>tr|A0A099TD29|A0A099TD29_9RHOB Potassium transporter TrkH OS=Thalassobacter sp. 16PALIMAR09 GN=PM04_01265 PE=4 SV=1MGIMCAAAMYIPALHALAFDDHRPARIFFYYGTFLLFIAGAVGVATANHRSAKPARAQLLSIAGVFTVLPLFLALPFREVVGNTTY LNAVLEMVSALTTTGATLFDDPDRLPLSLHVWRALVAWLGGLFMWVAAVAILAPLRLGGFEVSTPRRQQAETRPTTGLDQVISPEVR MWRAARTMGPIYLFLTLNLALILMLAGDGPTTAAIHAMSTLSTSGISAVGGLQDAVSGRVGEVAVFFFLIFAVSRQTFAAEWRKGHLG LLRDDRELRIAAFFVAAIPLALFARHWTGALEVRLEDDMWQGLEALWGAMFTVLSFLTTTGFESSGWTAAQYWSGLSTPGLLLMGL SVLGGGVATTAGGVKLLRVYALYRHGRQEMALLVEPHAVAGVKSESRRVHPEGAQAAWIFFMLFAMSIAGLSALFALSGVSFEAAMV MTVAGLSTTGPLLSVAMEGGVQLSDQNTATKIIFAGAMVLGRLETLAIIALLNPEFWRR
1.4E-13	59.6	12	1.8E-13	59.2	8.3	1	1	D3LVT4_9FIRM	Uncharacterized protein	HMPREF0889_1091	Megasphaera genomosp. type_1 str. 28L	188	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megasphaera, Megasphaera genomosp. type_1, Megasphaera genomosp. type_1 str. 28L	699218	>tr|D3LVT4|D3LVT4_9FIRM Uncharacterized protein OS=Megasphaera genomosp. type_1 str. 28L GN=HMPREF0889_1091 PE=4 SV=1MRLALRYSFFQVVSFLSTAGFFVTNIQQWPDFSKFILFLSSLVGGCIGSVAGGLRIMRGIILFKLAAQEMKRTLHPQMVTCLKVN SVPVDRKIVSRITGYFFLFIGVFFISAVVIAGSGVQPLTAMGLAAGALSGSGTTAHLFGNITIRALPAWTKVYCALVMIVGKMEIFSFLIIL QSGIGYIRRRW
1.7E-13	59.3	2.6	2E-13	59.1	1.8	1	1	R7KC00_9FIRM	KtrB	BN810_00178	Acidaminococcus sp. CAG:917	126	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Acidaminococcaceae, Acidaminococcus, environmental samples, Acidaminococcus sp. CAG:917	1262688	>tr|R7KC00|R7KC00_9FIRM KtrB OS=Acidaminococcus sp. CAG:917 GN=BN810_00178 PE=4 SV=1MIFSIIANVRRKKDITVGNRRIDSANVHQAYGLLSMYLALAIIGCGIICIVAPEYSLADVVFEVVSALSTVGYSVGLSVHVAVVGKVV LILLMYIGRVGMLSFAMIFAGKNKVVPLERPTEKIIIG
2.2E-13	59	10.8	8.5E-10	47.1	2.3	2.7	2	A0A0F2RYY1_9RHOB	Potassium transporter TrkH	VR71_09330	Roseovarius sp. BRH_c41	506	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseovarius, Roseovarius sp. BRH_c41	1629709	>tr|A0A0F2RYY1|A0A0F2RYY1_9RHOB Potassium transporter TrkH OS=Roseovarius sp. BRH_c41 GN=VR71_09330 PE=4 SV=1MIARLLTFPLILILAGVAAFLMFLPAIDAAMRGYSGVGRAFAFSGILGLALVMSVGLALSGRTNQKMNDTQNLISLLLAYLLLPVFLA LPFYEGVRNTTFLNAYFEMVSSFTTTGASLFDAPGRLKDSLHLWRALVGWSGGLLIWISASAVLAPLSLGGFEVTARGEPGQDETVL GRFERAAPAKRLAQSTAVLAPVYIGLTAALWIILMIGGERAFVAAVHAMSTMATSGISSIGGLQNGAAGFAGEFAIFLFLFFSLSRLTFS SDTITAARPGVINDPEFRLGVMLVIGVPLILIVRHWLATLGIEETGDWRVALRALWGALFTVLSFLSTTGFESADWQEARDWSGLGTP GLILLGLSLIGGGVATTAGGVKLLRVYALYLHARRETERLVHPSSVGRATGLGRRIRRQGAYIAWVFFMLFAMSLTFVTALLTLFGQGGF ESALILTISGLSTTGPLILTASEAPIRLLELSAGAKMVYAMAMVLGRLETLALIALLNPSIWRD
6E-13	57.5	13.2	5.8E-06	34.5	1.5	2.2	2	G4R904_PELHB	Potassium uptake protein TrkH	KKY_1399	Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	479	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Pelagibacterium, Pelagibacterium halotolerans, Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	1082931	>tr|G4R904|G4R904_PELHB Potassium uptake protein TrkH OS=Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2) GN=KKY_1399 PE=4 SV=1MGLPTIGILSAGVFGVFALSLVLPLFVALVEGNWRALEAIFLVGIGYGFLSAVTILSLSRRARTLNRAGVFTAAIVVWLSLIAAAVPL FVLIEGQPLIPAIFEATSAAVTLGSTLRPPADMSPSMIFYRATVAWVGGLTTLTLAVYVLGPYRVGGIPNANLRQVQHARTENDPRILVT LQSIAVPYLTLTIACAMLLIIVRVPADDAIVVAMSMLSTNGFVPPGSTTSVLDNRLAEFIMMIFMLVGATSIIWHRLLVGRSGEGSREHDE GMLYLTAIALLVGVAVLASILAPPEGLQGFESAFNYVFDMISIATTTGVTHDQQLGIAIPFEAILIIVFIGGCSYSTSGGIKAFRLLTMLKHV GNELDRLVYPSAILRDDVQYDTQQRIIAKSVWSTFFLGVLAVTIALLIFAAQGHSLPSAMALAAGAFSQVGNLVDSAVPGLSQGVASDS TLLTMSALAAVARMEILVVLAAITGNRW
8.9E-13	56.9	1.4	8.9E-13	56.9	0.9	2.1	2	W5BDA3_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	424	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5BDA3|W5BDA3_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MAGARHKVGELLRHARRRSTAALDKALSLLSSPSWSYVQHHVVKERVARWRRALAGRFWRRLGSLLVHVAYFLAVSWLGYLL LAQLRFRAGSDGTRRPRGMDLFFTAVSAATVSSMSTVEMEVFSNGQLVVLTTLMFVGGEVFLSLLGLASKWSKLRKQTVHKSSRRV DNHDVPELEMPPVDAATELDNPTSMTSTVDDEMSKPLDHFDDTRLRRDAVLSLFFVVLAILLAVHVLGAGAIVAYIVHASPAARRTLRD KALNVWTFAVFTTVSTFSSCGYMPTNENMIVFKRDTGLQLLLVTQALVGNTLFPPLLAACVRVAAAATRRVELKETAKKGRELTGYYH LLPARRCAMLAATVVGFLAVQVAMLCGMEWGGALRGMSPWEKVSNAVFLAVNSRHTGESTLDLCTLAPAVLVLFVLMMK
1.4E-12	56.3	11.9	1.6E-05	33	1.3	2.4	2	C6XJQ1_HIRBI	Cation transporter	Hbal_1658	Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418)	470	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hirschia, Hirschia baltica, Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418)	582402	>tr|C6XJQ1|C6XJQ1_HIRBI Cation transporter OS=Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418) GN=Hbal_1658 PE=4 SV=1MNLSSVLKHLGLTAIVIGACALLCGLFASISGDASSARGFLFSGVLGTFLGGSFLILLWDVPAKTGAREGLLFVLGFWFLMPLIAA PPFWASGVSNSWIEASFEAVSNLTTTGTTAGEAVQPDSIRYWRAILQFIGGVLGVVMAVIVLAALNLSGPGVHRSHLLTLTRDDLFGRI GRITATVALVYGIAAIIGTFAIVLAGAEFIDAFTRSLAAISTSATLSGAAGAYAYSPAAAAVITLLLFIGATNIALHADILRQSSWRVYLRDTE TQILILGVLAFVLLMAISKQKFDFRLISEALSFVSTSGMNVTGSEKVLDILPQPIPDVFVFVGAAALSTAGGLKMTRVLVLFSRALTEFKR LSFEHSTAKLKFQGRTRADAIVVGVWVYLIAYLGAAIILGMLLALTGLNVENAFRGAIGAIANAGPLMDAAVVDQSPSSTSLFVLAIGCIL GRIEVLALAPLFSSDFWRK

1.9E-12	55.9	13.7	3.2E-07	38.6	0.1	3.9	3	Q38BH0_TRYB2	Transporter, putative	Tb10.70.2940	Trypanosoma brucei brucei (strain 927/4 GUTat10.1)	599	cellular organisms, Eukaryota, Euglenozoa, Kinetoplastida (kinetoplasts), Trypanosomatidae, Trypanosoma, Trypanozoon, Trypanosoma brucei, Trypanosoma brucei brucei, Trypanosoma brucei brucei (strain 927/4 GUTat10.1)	185431	>tr|Q38BH0|Q38BH0_TRYB2 Transporter, putative OS=Trypanosoma brucei brucei (strain 927/4 GUTat10.1) GN=Tb10.70.2940 PE=4 SV=1MASQGETVSSPICVSNRIASTGLVGLEVGATSPVRDRAHQGGARVRLDRGLRECEDAGEVPCFNTRIGAKTTLSAISELLELKT DAGLSLTEAQECLVRRINFIRRHYIYLHAAYIMLIALTGATALCYTEDNLAFVDALFAAMSAVCCCGLSTVEVAEWKAETHAFLHVMMLA GGAILTSAYQPLLRLWAVSKLCPMLEGDTKDSDGGNALGGNYLSKSMRLWYASALCVVTTLMYVILVHISLAFFLGMFNRSNLRVPDV VLLAVASFHGAIFTPMEPYVDDPAVVAVASVGCALGFTMFPVLLRCFLRMEWFFFSGVKRLFSSFRQTSTVRQRSLFPADNGEEAAL LGCVDVPLKKGAKEGEFEGGVKGYSTWDRAFCDILKSKQPASMHTFLFDLRETVYLGVAWVVITVIAAAPFWFQQWSGDGLLAPYS APYKVFLALCQAAIVRFGGASFLSCLDYSDSHIAITIMAMYVPPIPVPTYRVYKKWKSVPLAYAIRPFTSRKFWLFVAVFCILIFEEEWPD GPDAPYYDMITRTMFEVVSAFSGCGLSLPPRWSALSFSGTLGVFSKLVIVAVMFAGRHYTVDFSIDIGFNSLP
2.9E-12	55.2	4	7E-11	50.7	0.4	2.1	2	M5C1P8_THACB	High-affinity potassium transport protein	TRK1 BN14_06974	Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)	749	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Cantharellales, Ceratobasidiaceae, mitosporic Ceratobasidiaceae, Rhizoctonia, Rhizoctonia solani, Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)	1108050	>tr|M5C1P8|M5C1P8_THACB High-affinity potassium transport protein OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=TRK1 PE=4 SV=1MTTSGLNTVNLSTTTVWQQVILAFLMFIGNSTSISLVVLFVRRSYFKAKCEAAVRMALQQRHERALIRQVIAGSQGAGPSMLARV RARAQTIFGHQAAPEPKPEAREDGLAEKSMLPTEPEQQQRMRGRVRGETIVGSIHTIGSDETHIEADAGNHLGSSEKFGDEYGKAPT DDNDASSGASTDGKINGHHLENAVRGSGPENSHEHFNDQHHVNSFTPPTFTQTAPTPSPTMALLPEVSESPADESNGLAPETASNS APAHVRPKLRPRSLALGHESDRDIRKTRAMGGTTRPGDVEIVQSDAPEYDHESNRLPNDHDRHSLSRSPRDRKLGLESVGEESAQD VQTTSPTEMSRHSGSPNGTTHFHFTNSISPKEETFATSPNEMSEFAHSPPSSPPAHRIPGSPGLNGHGILMHSNYTSPNGGHQTLPH VKEPLTRPRQATISSPSTRKATLSPVVRPVFLHAPHLTTGGRRTTFAEQVHPLHPYGPMRERAPSINPEMRTARRAALRARNGTITSP LPPFANLPEGDQHHGSPLRAHSKLADEYGQGYNQHPLRRPRAQTGTGGFANPIGLVAQWGIDYISGVKHFVDAHERVVNETEGRD RRGSVHQRTDSVGSHGTDPTPPGDDVSLDEDDLERMGGDEYNALVVLSWIVAGHYFFNHMIAFIILAPYSAKVPLVRDVIEAQNQSS GRKLNPTWFALFSVISAYANAGLTVVDTSLTQMSTAYVMIFVIIWLILVGATAFPLR
6.4E-12	54.1	2.6	6.8E-12	54	1.8	1	1	R6FHV5_9FIRM	Uncharacterized protein	BN538_00480	Lachnospiraceae bacterium CAG:215	91	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	1262985	>tr|R6FHV5|R6FHV5_9FIRM Uncharacterized protein OS=Lachnospiraceae bacterium CAG:215 GN=BN538_00480 PE=4 SV=1MLYLSLSLSVSMIIARIENIEFLDALFESVSAIATVGLSTGITPELLPLSHFLLAFLMIFGRVGSLTMLLAFASKRKQNLSALPLEKIQI G
9E-12	53.6	20.2	4.1E-09	44.8	3.2	2.5	2	A0RW24_CENSY	TRK type K transport system, membrane component	CENSYa_0909	Cenarchaeum symbiosum (strain A)	609	cellular organisms, Archaea, Thaumarchaeota, Cenarchaeales, Cenarchaeaceae, Cenarchaeum, Cenarchaeum symbiosum, Cenarchaeum symbiosum (strain A)	414004	>tr|A0RW24|A0RW24_CENSY TRK type K transport system, membrane component OS=Cenarchaeum symbiosum (strain A) GN=CENSYa_0909 PE=4 SV=1MSTEPQRAVKYVMGRPVSVYMKNDVLVLPRGMLTRRAASMMQSSEHDDVVVTEGGVPVGIVTDEDILGKVGDYKVTAEETTL GDIMSEPLHTIDEHASLREAINKMNKHGIRKLPVLSKKNTVIGIITHGAVAVAVRNAAATKPRLLSPPVKAILGNLGFVLQFAGALLLVPAI VATVLNDTVTATGIYLTTVLLLVTGFFLNSYGEKASLNMQQASILVFVSLFILTLFGTIPYLYVAPPGEGSAAEVFANSFFSSAAGFTTGG ISIYDPDELPQSFTFFRSFTQLVGGMSFIYLVITAFYPESKLRSMRGFISGRTLHMRELFGTITFIFGLYIVIVATLLYLFGEQDILDNISLA MSTLATGGFVPSSTILEDMVWQEHLILMAAMILGALPFTFHYGFVRKKFLSPRLGKEVLAYFALLGGAALLFTWVSGLGPVFGTFYTV SASTTAGLQISSLESLSGPAHAILILLMFVGGCGFSTAGGIKIYRFMQVRGAWRLLRGGLRGGEDATKDEKDERKETATAVLIIMLFPLI AGVTTIHLMGITDATLDNAFLEAAGLITTGGLSADVITAELDPATMITFGFLMIFGRLEIIAILYIFVPRLAP
1E-11	53.5	0.1	1.2E-11	53.2	0.1	1.1	1	Q59X75_CANAL	Uncharacterized protein	CaO19.602 CaO19.8235 orf19.602	Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)	131	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Debaryomycetaceae, Candida/Lodderomyces clade, Candida, Candida albicans (Yeast), Candida albicans (strain SC5314 / ATCC MYA-2876) (Yeast)	237561	>tr|Q59X75|Q59X75_CANAL Uncharacterized protein OS=Candida albicans (strain SC5314 / ATCC MYA-2876) GN=CaO19.602 PE=4 SV=1MSMGYPGVDCSLSGEFNVISKLVIIAMMIRGRHRGLPYTIDRAIMLPNAAMKRHDRLQEEHAINRHNTMERTTTLGRVATFGNG PIDGGNNLLTRAITNIEHRLRNRRDGRSESSTVSEDPRYVVRTVSEV
1.2E-11	53.2	8.1	2.4E-09	45.6	3	2.6	2	Q28Q52_JANSC	Cation transporter	Jann_2243	Jannaschia sp. (strain CCS1)	505	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Jannaschia, Jannaschia sp. (strain CCS1)	290400	>tr|Q28Q52|Q28Q52_JANSC Cation transporter OS=Jannaschia sp. (strain CCS1) GN=Jann_2243 PE=4 SV=1MAAYFRNLPFFVILIFVAGGAMLAPSAVALAWKDYGTARVFLYTGLMVLMAAVLLGFASQTPRRPPSERSHLASLFLAYLWLPL VLGMPMDQAVGNTRFINVYLDMVSALTTTGAEVFDPGRLSPAVHLWRGLVGWFGGLLIWITAFAVLAPLNLGGYEVTSEAVVQGKV VNARGQMRAADASNRLRKHAARLTPIYAGLTIALTAALAAAGEEPLVAVIHAMSTLATSGISPAGGLEGRPIGLFGEVLIFIFFLFALSRR TYSSGIGREFRERLTKDREIRLALFAGIVLPTLLFARHWVGALEVDDLADGRAAFSALWGSVFTVFSFLTTTGFVSDAWGDARAWSG LQTPGLLLVGLVLMGGGVATTAGGVKLLRVYALYKHGTREMGKLIYPNSVAGAGRLGRRIRREGAYIAWIVFMLLVLSIATVMTALAAT GLDFESATILAISSLTTTGPLASVAGAQPIDYFTLSDMAKLICAAAMIVGRIETLVMIALLNPGFWRD
1.6E-11	52.8	0	1.8E-11	52.7	0	1	1	R7EMR7_9FIRM	Cation transport protein	BN640_00556	Anaerotruncus sp. CAG:390	122	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Anaerotruncus, environmental samples, Anaerotruncus sp. CAG:390	1262703	>tr|R7EMR7|R7EMR7_9FIRM Cation transport protein OS=Anaerotruncus sp. CAG:390 GN=BN640_00556 PE=4 SV=1MIKNNLRRMLHPRAVSRVRHEGETVDNATLSEVNAYFALYMLILAAVFLLLSLEPFDIETNLSAAVSCLNNVGPGFGTVGPASSY AAYSDPATLLLTITMLIGRLEIYPVIFILSPKTWTKR
2.8E-11	52	2.5	3.3E-09	45.2	1.7	2.1	1	W5ATI6_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	323	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5ATI6|W5ATI6_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1HEAAARRGAVAVLRRPRHLPCGARPRRRGHRGVHPARVAGGEADAAGQGPERVDLRRVHDGVHVLELRVHADEREHGSVP AGHRAAAAARVAGAGREHAVRAAAAATRRVELKETLKQGRELTGYSHLLPARRCGMLAATVAGFLAVQVAMLCGMEWSGALRGMS AWEKVSNAVFLAVNSRHAGESTLDISTLAPAILVLFVLMMYLPSYTTWFPFAGSSGTTDHAEETQGIRLIKSTALSQLSYLTIFVIAICVT EREKLKEDPLNFNLLSIVVEVVSAYGNVGSPWATVAAGRSARTSCAPTGGPASSGGGAILASSSSFS
2.8E-11	52	0.2	4.6E-11	51.3	0.1	1.2	1	A0A099NRT3_PICKU	Uncharacterized protein	JL09_g5575	Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)	301	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Ascomycota, saccharomyceta, Saccharomycotina (true yeasts), Saccharomycetes, Saccharomycetales (budding yeasts), Pichiaceae, Pichia, Pichia kudriavzevii (Yeast) (Issatchenkia orientalis)	4909	>tr|A0A099NRT3|A0A099NRT3_PICKU Uncharacterized protein OS=Pichia kudriavzevii GN=JL09_g5575 PE=4 SV=1MRQKLSNEKGNVVNLCGDNTVSIGPQFPNIKFGDLPKPVKNDLQQSNYESMTSSVQQDMRRSKGNTTHKRKPMHYKMHKKLI KNKKRNQEKMALPHLNTSTNDFEMVELKQFLNESTMNQGTANFERSFSSPIQIRSGVPNDYFLYSTGSLKPFLRLKKIPKSNTLDYQL PSTTETKKDHFSENYGFKFLKRDLSKVFCKTETGANLEGLSDEEFIINYTFDVPSNYLSWTPTIGRNSNFIALTRKQKIELGGVEYQAT MLLSKIIFVYYFGLNVLGSIMMVAYVTSKKEYANLGGDYLHP

1.5E-10	49.6	3.1	1.6E-05	33	2.6	2.9	2	A0A0D6TBM8_9RHOB	Cation transporter	SY26_14725	Paracoccus sp. 361	543	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 361	1603292	>tr|A0A0D6TBM8|A0A0D6TBM8_9RHOB Cation transporter OS=Paracoccus sp. 361 GN=SY26_14725 PE=4 SV=1MTGFLLRMPLLVLLVGLAAVLMLAPAGFASVTGYAAIARNFFYAALLTLTFCGLIGLAAQANPRGQTAREMLLLMLGVYGLLPLLLAVPFAESQPDTGFFNAWWEMVSSLTTTGASLYSADLLPLPLHLWRSMVGWMGGFFVLVAAVAILAPLRVGGFEIMSNPYGREEYREHLPPSDQPRRPVLHLSDPSFDTQLADPASRLGRAALQVGPLYLGFTLVLWVGLLMLGDPSFVALTRAMGTLSTSGISPVIGPSGEASGIPGEMLVFIFLIPALSRRFWPGGAELRATERLIEDPELRMALGLVLGVGVMLFLRHFLGAIEVDRAAPPDPTGMAEVRRALSAMWGSMFSALSYLTTTGWTSVAWAGARSWSGLDAPGLVLAGLALAMGGGIATTAGGVKLLRVYALATHGQREMERIIHPHSVSGGGRIARRLRREGAYLAFIFFMLFAISIALVVSLVSIHAIEFETATILSIAALTNAGPLASAIPLTPAFEGTAGIASAPWEGWSGLPDFTKAVLACAMVLGRIETLAVLALFSPEFWRR
1.6E-10	49.5	8.6	9E-09	43.7	0.1	3.5	3	A0A0E0KUX8_ORYPU	Uncharacterized protein		Oryza punctata (Red rice)	342	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza punctata (Red rice)	4537	>tr|A0A0E0KUX8|A0A0E0KUX8_ORYPU Uncharacterized protein OS=Oryza punctata PE=4 SV=1MKLLLPDSEVLRIYREKAQHLCGFLSMKLISLSKCVIHSVKQSCSFLVCKSNPLVVQLVYFVTISFAGFLALKNLKPQGKSGPKDLDLLFTSVSTLTVSSMATVDMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLLSISMDIESNSPANNGVHKITECGQSEETMSQNQVQKNKSITYNPCAVLARIVTDARDLLKSKEINMYTFCIFTAVSSFANCGFTPLNSSMQPFRKNWVLLLLVIPQILAGNTLFSPLLRLSVWVLGKVSGKADAFGNVGYSLGYSCQKLLKPDGTCKDVSYGFVGRWTDKGKLIVILVMFLGRLKEFILK
2.2E-10	49	12.7	4.1E-10	48.1	0.4	3.6	2	B9SDN6_RICCO	Putative uncharacterized protein	RCOM_0422820	Ricinus communis (Castor bean)	348	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Malpighiales, Euphorbiaceae, Acalyphoideae, Acalypheae, Ricinus, Ricinus communis (Castor bean)	3988	>tr|B9SDN6|B9SDN6_RICCO Putative uncharacterized protein OS=Ricinus communis GN=RCOM_0422820 PE=4 SV=1MEVFSNSQLVILTVLMFVGGEVFTSLVGLLFRKSQLRRKWISNVGLVSSVRSDTDGTYKMQTKQGILLVLVYLASVKSARNVLETKGLNIFTFSLFTIVSTFASCGFVPTNENMMVFSKNSGLLLILIPQFVLFCSLEWNSEALNGLNSFQKIIGVLFQTVNSRHTGETIVDLSAISPAILYTKQWCMREKLSRNARKVTFPVRTCKSSKYLPPYTAFLPIKDDTEIDGRSKRWRGKLLENIIFSQLSYLVIFVILICITERHKMKQDPLNFNVLNIVLEVISAYGNVGFTAGYSCKRQIHPDSICQDKWYGFSGRWSDEGRVILIMVMFFGRLKKFNMNGGRAWILL
2.5E-10	48.9	0.6	2.7E-10	48.8	0.4	1	1	R6YNN7_9BACT	Trk system potassium uptake protein TrkH	BN769_02282	Prevotella sp. CAG:732	127	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:732	1262934	>tr|R6YNN7|R6YNN7_9BACT Trk system potassium uptake protein TrkH OS=Prevotella sp. CAG:732 GN=BN769_02282 PE=4 SV=1MLVKMVKNEFRQILHPNAVLPLKIDGVNVPMQKRVTLLAFLTTYLIICLGISFTMIAMGIDNTNAITITLSCVGNVGPTLGTEIGPTMSWSELPDVAKWFCSLMMLIGRLEIFSVLVIFTPAFWKEN
2.8E-10	48.7	6.7	0.0017	26.3	0	3	3	M0THZ0_MUSAM	Uncharacterized protein		Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	262	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Zingiberales, Musaceae, Musa, Musa acuminata (Banana) (Musa cavendishii), Musa acuminata subsp. malaccensis (Wild banana) (Musa malaccensis)	214687	>tr|M0THZ0|M0THZ0_MUSAM Uncharacterized protein OS=Musa acuminata subsp. malaccensis PE=4 SV=1MLFMPTSALTVSGLAAVEMENLSSAQIVVLSLLMFHGGKVFVTLGLLFGRGKQDEPGSSAGRVDSACIELESVDPSQNTIDRIESGISPPAAGADESSVRSLGYVVSGYVAIFHLIGTSLLLGARGILKTKGIDVFLFCLSATVSSFANGGLIASNENMAIMNKDPVVLLLMIAQVLGGNTVFPLQEEVSQLSYIAIFIIAICITERRKMTRDPHNFSTLKLIFEVISGYRNVGLPTGHSCWRLLRLHPQAYPGSSSSMEG
3.7E-10	48.3	1.3	4.4E-10	48.1	0.9	1	1	Q8EQN1_OCEIH	Na(+)-transporting ATP synthase (Divided with OB1663 and OB1664)	OB1663	Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)	170	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Oceanobacillus, Oceanobacillus iheyensis, Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831)	221109	>tr|Q8EQN1|Q8EQN1_OCEIH Na(+)-transporting ATP synthase (Divided with OB1663 and OB1664) OS=Oceanobacillus iheyensis (strain DSM 14371 / JCM 11309 / KCTC 3954 / HTE831) GN=OB1663 PE=4 SV=1MSRFPIFWKLSLNPPQILTLGFIAVIIVGTFLLTLPISTSEPISVIDALFTATSATTVTGLVVLDTGTEFTLFGQIVIMILIQLGGLGLMTFAIMIVLILGKKIGLRERILVQESFNQSTLGGLVRLVKSLLIFTFSMEIIATVLLSIRWVPEYGFGGHIYKFVSCSFCL
8.8E-10	47.1	0.5	9.1E-10	47	0.3	1	1	A0A0D1UYZ2_ANEMI	Strain NCTC 7096 contig_238, whole genome shotgun sequence	TS65_23085	Aneurinibacillus migulanus (Bacillus migulanus)	80	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Aneurinibacillus group, Aneurinibacillus, Aneurinibacillus migulanus (Bacillus migulanus)	47500	>tr|A0A0D1UYZ2|A0A0D1UYZ2_ANEMI Strain NCTC 7096 contig_238, whole genome shotgun sequence OS=Aneurinibacillus migulanus GN=TS65_23085 PE=4 SV=1MILCITENDDFLTILFETTSAFGTIGMSMGLTSHLTTFGKILLSLVMFAGRVGPLIVAFALSWDRKKKHFRSSEGKIIIG
1.1E-09	46.8	16.8	1.5E-06	36.4	0.8	3.5	3	K4ECD9_TRYCR	Trk system potassium uptake protein	TCSYLVIO_000967	Trypanosoma cruzi	592	cellular organisms, Eukaryota, Euglenozoa, Kinetoplastida (kinetoplasts), Trypanosomatidae, Trypanosoma, Schizotrypanum, Trypanosoma cruzi	5693	>tr|K4ECD9|K4ECD9_TRYCR Trk system potassium uptake protein OS=Trypanosoma cruzi GN=TCSYLVIO_000967 PE=4 SV=1MQRVPSADRVASALRSRFAVNDTNSPDEPYVTLDNNAEGATRSSQLLEYEGPVVLPLSTTQDSIARRINFFKKWYLLMHITYIFSIACVGSLLFYVMEDELAYIDAFFIAISSVCCCGLQTVDVATWKKSTNILRHFLMIGGGMVFTSAHQPLLRIWMLNKMWPLLEPHRDDLFLEGRLRASRRKYAQRLWHTSVICLLTPLLYFGIVNVTLIFLLAVFNQSNLSFLEIVEMAIASFHGSVFLPMEQYVRDPAVVLTVTIGCGLGFTLFPVFLRGFLYAEWFTFRLVRRVCRRLLPSPHTDLESPLAAPLSEDFPLLFSLQEREGDILPHQFDAVDDMLHVNAWDKGFRDILKNKHPVSFHAFLFVRSETFYLGVAWCVITLAQSIPFWVQQWSGDGLLAPFPTAYKIFLSVCQAAVVRFAAASFISCLDYSNAHIAITIFCMFLPALPIPTDRTYRKWKQVFSASMVRLFTSRLFCLFLAILCLLFGEEGWLTQELKDSRFDVMTRSFFEVISAFAGCGLSLSLPGTRVSFVGSLGMFSKLVVAAVMLGGRHRTVDLGIDLGFSVLQADQKIPYTVARRLSQSSPTQISGI

1.4E-09	46.4	2.6	0.00014	29.9	0	2.4	2	E0TDY2_PARBH	K+ transporter Trk	PB2503_11939	Parvularcula bermudensis (strain ATCC BAA-594 / HTCC2503 / KCTC 12087)	470	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Parvularculales, Parvularculaceae, Parvularcula, Parvularcula bermudensis, Parvularcula bermudensis (strain ATCC BAA-594 / HTCC2503 / KCTC 12087)	314260	>tr|E0TDY2|E0TDY2_PARBH K+ transporter Trk OS=Parvularcula bermudensis (strain ATCC BAA-594 / HTCC2503 / KCTC 12087) GN=PB2503_11939 PE=4 SV=1MRIGPVLRFTAYAHFGIATAMLPAALLSALAADGSLGGYVIGLFASVTVAVLCLSADRGYDPRPMVRNGLRELLLALVIAWTFLPLAASIPLMVDGETLGDAWFEAVSALTTTGGWLSDPIARSTAYDVIYRASLQWLGGLISLATAAAVFVRPEFIGVSTIVPPFARGESGSFLRAFDHAFRAFLPVYVGLTLGGGVAFVLVGVPVIDSFAMAMSLIATGGFIPAANGIGAYPDGAVYVAATMMLLGAVNFLLISGMLLGRARRLGAAGDKETLAFLAVLPFVALLFWVATGAGDLDRLGAQAFNAISLLSTNGPTLGEVPPLTPLLVSAVIGGAAVSTAGGIKILRWMVAIRRTGDELWRITHPGAVLGRPSEPNELGIWIHTMAFALLLAAVVLTVAFYGHSLEVSAATAVAVLANVGPIVEYAPLMTADYRIFDPSLRVLLVFAMISGRLELVVFLMMLSRRFWMG
1.4E-09	46.4	1	5.2E-09	44.5	0.7	1.7	1	W5AY48_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	161	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5AY48|W5AY48_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1CTLCSYTLSSLTFCFFLLACRYLPPYTTWFPFEESSGVKDQPREETQGVRLLKSTLLSQLSYLAIFVIAICITEREKLKEDPLNFNLLSIVVEVVSAYGNVGFSMGYSCSRQISPDGMCTDRWTGFAGRWSDSGKLILILVMLFGRMKKFSMKAGKAWKLS
1.4E-09	46.4	17.2	1.6E-06	36.4	0.9	3.5	3	Q4DCI6_TRYCC	Transporter, putative	Tc00.1047053511469.60	Trypanosoma cruzi (strain CL Brener)	592	cellular organisms, Eukaryota, Euglenozoa, Kinetoplastida (kinetoplasts), Trypanosomatidae, Trypanosoma, Schizotrypanum, Trypanosoma cruzi, Trypanosoma cruzi (strain CL Brener)	353153	>tr|Q4DCI6|Q4DCI6_TRYCC Transporter, putative OS=Trypanosoma cruzi (strain CL Brener) GN=Tc00.1047053511469.60 PE=4 SV=1MQRVPSADRVASALRSRFAVNDTNSPDEPYVTLDNNAEGATRSSQLLEYAGPVVLPLSTTQDSIARRINFFKKWYLLMHVTYIFSIACIGSLLFYVMEDELAYIDAFFIAISSVCCCGLQTVDVATWKKSTNILRHFLMIGGGMVFTSAHQPLLRIWMLNKMWPLLEPHRDDLFLEGRLRASRRKYAQRLWHTSVICLLTPLLYFGIVNVTLIFLLAVFNQSNLSFLEIVEMAIASFHGSVFLPMEQYVRDPAVVLTVTIGCGLGFTLFPVVLRGFLYAEWFTFRLVRRVRRRLLPSPHTDLESPLAAPLSEDFPLLFSLQEREGDVLPHEFDAVDDMLHVNAWDKGFRDILKNKHPVSFHAFLFVRSETFYLGVAWCVITLAQSIPFWVQQWSGDGLLAPFPTAYKIFLSVCQAAVVRFAAASFISCLDYSNAHIAITIFCMFLPALPIPTDRTYRKWKQVFSASMVRLFTSRLFCLFLAILCLLFGEEGWLTQELKDSRFDVMTRSFFEVISAFAGCGLSLSIPGTRVSFVGSLGMFSKLVVAAVMLGGRHRTVDLGIDLGFSVLQADQKMPCSVARRVSQSSPTQINGI
1.5E-09	46.3	0.3	7.1E-09	44.1	0.1	1.8	1	W5E7W9_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	232	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5E7W9|W5E7W9_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1MPMDLDLIFTSVSATTVSSMVAVEMESFSNPQLLLLTLLMLLGGEVFTSMLGLHFTYLKSKTKEAQAPHEHDHADKGKPAPSSSLQLTANTCMDDDVDRVEQGFKDQPRYDRAFLTRLLLFIVLGYHVVVHLAGYSLMLVYLSVVSGARAVLAGKGISLHTLSVFTVVSTFANGGFMPNNEGMVAFRSFPGLLLLVMPHVLLGNTLFPVFLRLAIWALRRVTRRPELGELQSI
1.9E-09	45.9	5.7	0.008	24.1	0	4.9	4	A0A0D3FZY4_9ORYZ	Uncharacterized protein		Oryza barthii	444	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza barthii	65489	>tr|A0A0D3FZY4|A0A0D3FZY4_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLGGEVFVSLVGLASKWSKLRSDAMDRSRRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHVVGAVAVAAYNMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGESTVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVRQVRLNGFLPEKKNADQINPDHLCTDKWTGFVGRWSDSGKLLLIFVMFFGRLKKFSMKGGKAWKLRTFHCHPCTKLTLHSKCWQFQIRAGLRVKTNS
3.5E-09	45.1	3.1	0.0061	24.5	0	4	3	A0A0D3FZY6_9ORYZ	Uncharacterized protein		Oryza barthii	366	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza barthii	65489	>tr|A0A0D3FZY6|A0A0D3FZY6_9ORYZ Uncharacterized protein OS=Oryza barthii PE=4 SV=1MPTSRRALAGGALSMHVAYFLAISCLGYGLLGVLKVREPGAAPRRIDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMLLGGEVFVSLVGLASKWSKLRSDAMDRSRRVESHGDVALADIDGGDVENPTSSGEEAASRRRPMDADTLRHNAVRALFYIVLAIFAVVHVVGAVAVAAYNMVVFKRDAPLQLLLVPQVLAGNTLFAPLLAACVAVLMALVCGMEWGGALQGMSPWEKVVNALFLAVNARHTGESTVDLSILAPAILVLFVLMMYLPPYTTWFPFEENSTTKDSNAENQGIRLLESTLLSQLSYLTIFVIAICITERRKLKEDPLNFSVLSIVVEVVRQVRLNGFLPEKKNADQVN
3.8E-09	45	0.8	1.1E-08	43.4	0.6	1.8	1	M0XC47_HORVD	Uncharacterized protein		Hordeum vulgare var. distichum (Domesticated barley)	179	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Hordeinae, Hordeum, Hordeum vulgare (Barley), Hordeum vulgare var. distichum (Domesticated barley)	112509	>tr|M0XC47|M0XC47_HORVD Uncharacterized protein OS=Hordeum vulgare var. distichum PE=4 SV=1GKSVPFLGFSPQLRSYNIITIVASLVVLVVSPAFCFASRYLPPYTTWFPFGESSGVKDHPTEETKGLRLLKGTLLSQLSYLAIFVIAICITEREKLKEDPLNFNLLSIVVEVVSAYGNVGFSMGYSCSRQISPDRLCTDRWTGFAGRWSDSGKVILILVMLFGRLKKFSMSAGKAWKLS
6.5E-09	44.2	0.9	7.4E-09	44	0.6	1.1	1	R5H5K3_9FIRM	Trk-type K+ transport systems membrane components	BN555_00578	Firmicutes bacterium CAG:24	125	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:24	1263012	>tr|R5H5K3|R5H5K3_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:24 GN=BN555_00578 PE=4 SV=1MLANTAATFRQRENAQFFGRRIDFSAVKTAATILTMYLTLFFGGAVFISVYEDLTLSACLYETASAVGTVGLTLGITPQLHIPSQIVLIVLMYLGRVGGLTLIYAAFSGKKINGAKLPQEKIMIG
7E-09	44.1	1	7.6E-09	44	0.7	1	1	R6CP83_9BACE	Uncharacterized protein	BN697_01364	Bacteroides sp. CAG:530	125	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:530	1262741	>tr|R6CP83|R6CP83_9BACE Uncharacterized protein OS=Bacteroides sp. CAG:530 GN=BN697_01364 PE=4 SV=1MLNLKSVLRGSDRVRILHRELSADSVRRSNAVVTLYMLMLFVGVFLLSLLEPKVGILPLVFECVSALSTVGSSLDLTPTLGTYGKMLIVILMFIGRVGAFTLVIGLIKQEKKRNYRYPTDHIIIN

8.8E-09	43.8	0	0.00046	28.2	0	2.1	2	R1BJS1_EMIHU	Uncharacterized protein	EMIHUDRAFT_1207000	Emiliania huxleyi CCMP1516	257	cellular organisms, Eukaryota, Haptophyceae, Isochrysidales, Noelaerhabdaceae, Emiliania, Emiliania huxleyi (Pontosphaera huxleyi), Emiliania huxleyi CCMP1516	2903	>tr|R1BJS1|R1BJS1_EMIHU Uncharacterized protein OS=Emiliania huxleyi CCMP1516 GN=EMIHUDRAFT_120700 PE=4 SV=1MLWHGELTWGQTLRHHLTAFSHAVGGFVGGPTLQRDLLFAWLAWFLILAFDPDLPHGSNGAAFDALFEVCSAFGNVGLSMGY SRDTELENVRPGTPQTFVDSLPRGETGLSYCACWPNLSKAVLVAVMIYGRTRALPQQVDYALTLAIEIPSSDMSPVELLLSPGGERDS DERDSTRARGSWLFSQADLRGLARRLTGSTPAHHPGEVPQRSGVSSGNESTDEAGTLGDLLDARAPDDEGASGSHARPEQRANKE LV
9E-09	43.7	2.6	9.9E-09	43.6	1.8	1	1	R6JYF6_9CLOT	Uncharacterized protein	BN486_03706	Clostridium clostridioforme CAG:132	93	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium clostridioforme CAG:132	1263065	>tr|R6JYF6|R6JYF6_9CLOT Uncharacterized protein OS=Clostridium clostridioforme CAG:132 GN=BN486_03706 PE=4 SV=1MTALSALVVCLGTFFMCILEPAVPFEDILFEITSAFGIVGLSTGITPGLSSLSKLLEVLVMYIGRLGPLTIVTIWVFKPTKSVSYAEGS ISIG
2.9E-08	42	21	1.5E-06	36.4	0.8	3.6	3	Q4DEQ4_TRYCC	Transporter, putative	Tc00.1047053506295.120	Trypanosoma cruzi (strain CL Brener)	592	cellular organisms, Eukaryota, Euglenozoa, Kinetoplastida (kinetoplasts), Trypanosomatidae, Trypanosoma, Schizotrypanum, Trypanosoma cruzi, Trypanosoma cruzi (strain CL Brener)	353153	>tr|Q4DEQ4|Q4DEQ4_TRYCC Transporter, putative OS=Trypanosoma cruzi (strain CL Brener) GN=Tc00.1047053506295.120 PE=4 SV=1MQRIPSADRVASALRSRFAVNDTNYPDEPYVTLDNNAEGATRSSQLLEYAGPVVLPLSTTQDSIARRINFFKKWYLLMHVTYIFS IACVGSILFYVMEDELAYIDAFFIAISSVCCCGLQTVDVATWKKSTNILRHFLMIGGGMVFTSAHQPLLRIWMLNKMWPLLEPNRDDLFL EGRLRASRRKYAQRLWHTSVICLLTPLLYFGIVNVTLIFLLAVFNQSNLSFLEIVEMAIASFHGSVFLPMEQYVRDPAVVLTVTIGCGLG FTLFPVILRGFLYAEWFTFRLVRRVRRRLLPSPHTDLESPLAAPLSEDFPLLFSLQEREGDVLPHEFDAVDDMLHLNAWDKGFRDILKN KHPVSFHAFLFVRSETFYLGVAWCVITLAQSIPFWVQQWSGDGLLAPFPTAYKIFLSVCQAAVVRFAAASFISCLDYSNAHIAITIFCMF LPALPIPTDRTYRKWKQVFSASMVRLFTSRLFCLFLAILCLLFGEEGWLTQELKDSRFDVMTRSFFEVISAFAGCGLSLSLPGTRVSFV GSLGMFSKLVVAAVMLGGRHRTVDLGIDLGFSVLQADQKIPYTVARRLSQSSPTQISGI
4.7E-08	41.4	5.2	0.00007	30.9	2.9	2.4	2	Q0C0N7_HYPNA	Putative potassium uptake protein TrkH	HNE_2007	Hyphomonas neptunium (strain ATCC 15444)	468	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hyphomonas, Hyphomonas neptunium, Hyphomonas neptunium (strain ATCC 15444)	228405	>tr|Q0C0N7|Q0C0N7_HYPNA Putative potassium uptake protein TrkH OS=Hyphomonas neptunium (strain ATCC 15444) GN=HNE_2007 PE=4 SV=1MNYASVIRVLALLMLILAGCAASAALLAWALGETPQIISFGATALGISVFASSVLLLAPKPRRRARPSDALAVTLMWWFLSPAAAA MPFVFGVANNSVSVALFEAASCLTTTGHSILDFPDGAWPVSLLYWRGLLHLLGTYAAVIMAAGVFAAINLGGPGVHRTVLFTVPDASY FDAMPRIYTGVGIMLGITISFILILLLMAGVPPVRALADAVSVISTGLVLPDAETFLPVNPVAGMIMAFGLAIGALGLAVWLPLRIGAVKTAI TDPETVVFILLMVIFAAAVIPVGISLQDALGWSLSSLSTSGIPLSAAAREQQIPLTIAVLPALIGGSALSAAGGIKIARFIVLGQRAGQEFR QLGYRRSILSFRFRDRELDERSVIGVWVYFIVYAGAVFSVITAFAFFEVPFEDSIRLSIGALTSSGGLIGQATDNLGPAGQILLSIAMVLG RVEILTVLPALSLSFWRG
5.4E-08	41.1	3.8	0.00034	28.6	3.8	2.9	2	A1B9J5_PARDP	Cation transporter	Pden_4125	Paracoccus denitrificans (strain Pd 1222)	540	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus denitrificans, Paracoccus denitrificans (strain Pd 1222)	318586	>tr|A1B9J5|A1B9J5_PARDP Cation transporter OS=Paracoccus denitrificans (strain Pd 1222) GN=Pden_4125 PE=4 SV=1MGLLLRLPLIVILGAIGALAMVLPGLYAHALDSHKIGSIFLGTAGLFVILAAILGLATADRPEGLRARGVLLTMLGTMVLLPAMLAVP FALALPDTGFFNAWWEMISCLTTTGASLYSADLLPAPLHLWRAIVGWLGGLFMLVAAIALLAPLRVGGFEIMSSPYGRSERFERLPRS ADGPDALAPLTHPAFQTELADPVHRVMRAGRVVLPVYAGLTLSMWMLLLMLGETGLVALTRAMGTLSTSGISPVTGPAGQQSGIAGE VVIFLFLIPALSRRFWPGGGELKASESWVGDPELRMAAGVVLLISAVLFARHFVGAIGVSPTGAKGVLDTLDSAASAAWGGIFNGLSY LTTTGWNSVEWQGARNWSGLSSPGLMLAGLAMMGGGVATTAGGVKLLRVYALARHSERELERIVHPASVGGGGLMARRLRREGA YLAFIFFMLFASSIAVTVMLISLQRIEFDSATILSIAALTNTGQLAGAIPLTPTFQGSAGMAGAPWAGWAGLPGLTKAVLAGAMIVGRVE TLAILALVSPEYWRR
8.5E-08	40.5	0.4	1E-07	40.3	0.3	1	1	Q8YEG1_NOSS1	All5337 protein	all5337	Nostoc sp. (strain PCC 7120 / UTEX 2576)	100	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	103690	>tr|Q8YEG1|Q8YEG1_NOSS1 All5337 protein OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=all5337 PE=4 SV=1MLLLGLLGMPWWEALNYAMTTISTGGFAITSEGLTVYAPIVQLAAIAIMITGATSFSVHAKLLSQHRLSILWRDPQHRMLWLLLVL EYYCYWNITRLQAH
1E-07	40.3	0	1E-07	40.2	0	1	1	F7PQH3_9EURY	Potassium transport system protein TrkH3 (TRK potassium uptake system protein)	trkH3 HLRTI_001864 HTIA_1131	Halorhabdus tiamatea SARL4B	70	cellular organisms, Archaea, Euryarchaeota, Halobacteria, Halobacteriales, Halobacteriaceae, Halorhabdus, Halorhabdus tiamatea, Halorhabdus tiamatea SARL4B	1033806	>tr|F7PQH3|F7PQH3_9EURY Potassium transport system protein TrkH3 OS=Halorhabdus tiamatea SARL4B GN=trkH3 PE=4 SV=1MLSPDHPLEYVIFDVMSAQSNVGLDSGTTGPTMPATANRMLIVNMWVGRLEIIPIAVLLGAIFQRLDLFR
1.2E-07	40	2.7	2.5E-05	32.4	0.2	2.1	2	J3M179_ORYBR	Uncharacterized protein	OB04G31540	Oryza brachyantha	431	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza brachyantha	4533	>tr|J3M179|J3M179_ORYBR Uncharacterized protein OS=Oryza brachyantha GN=OB04G31540 PE=4 SV=1MAAAHEKLGVVELLHRLRRSTAAMLHGAMSLLCSLSRAYAHHQVRERVARSRRALRCGAGQAWRSAVTALPLDEPPPALRCG AGQAWRSAVTALPLAGPLAVHVAYFLAISCLGYGLLGKLKVRDPGRAPRGVDRFFTAVSAATVSSMSTVEMEVFSNGQLVVLTVLMF IGGEVFISLVELASKWSKMRRQRIYKSRRVESHGEIALQAPAIADVENPASMITSTTTTEDATGTTDANTLRHNAVRALFYIVLAILVVVH VLGAVAVAAYVYASPGARRTLRGKSLNLWTFAVFTTVSTFSNCGFMPTNENMAVFKRDAPLQLLLVPQAXXXXXXXXXXXLPGAAGA PVLDAGGDGDRVPRRAGGAGVRHGVGRHASGDEPVGEGGERAVPRRELPAHRRVHRRSLHPRAGHPRALRAHDVSTSIHDVVSV
1.4E-07	39.8	0.5	3.2E-06	35.3	0.3	2	1	B9S7S6_RICCO	Putative uncharacterized protein	RCOM_1381500	Ricinus communis (Castor bean)	163	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Malpighiales, Euphorbiaceae, Acalyphoideae, Acalypheae, Ricinus, Ricinus communis (Castor bean)	3988	>tr|B9S7S6|B9S7S6_RICCO Putative uncharacterized protein OS=Ricinus communis GN=RCOM_1381500 PE=4 SV=1MLSSSLAFNVQLASLLLYLPPYTSFLPVKQQEEELVPRNGRERKNEKKTLFQDLLFSQLSYLVIFIVLICVVEREKLKTDPLNFNVL NITLEVISAHGNVGYSTGYGCARARQVNPNITSCKDAWFGLVGKWSNFGKFIIIIVMFFGRLKKFSINAGKAWKLS

1.5E-07	39.7	13.2	0.035	22	1.8	2.7	2	A0A0F2REN0_9RHOB	Uncharacterized protein	VR74_12925	Hyphomonas sp. BRH_c22	468	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, Hyphomonas, Hyphomonas sp. BRH_c22	1629710	>tr|A0A0F2REN0|A0A0F2REN0_9RHOB Uncharacterized protein OS=Hyphomonas sp. BRH_c22 GN=VR74_12925 PE=4 SV=1MNYASIVRVLALLMLVVAGSALLPIAVAIVAGETDQVIALLVTTIGIAVLASSVLLLTPRPSRKARPSDALAVVIIWWFIAPVASALPFVLGVANGSLLNAIHEAAACLTTSGQSVIRTESNVWPVSLVFWRGVLHIIGGMATIITAASVLAAINLGGPGIHRTVLFTVPESSFFDAVPRVARSVSIMMLVFLIVLLGLLIMSGVPFFPRALSDAVSAMTTGAVDPNTVSRVSLQPFPSIILGMGLIVGALGLAVWLPLKDRKPRAALMDPETVTFLFLITMFAAVVLLLGIGVGDALAWATSALSTSGLILSSAPTRDLVPLPILVLPALIGGSALSAAGGVKIARLIVLARRAGQEFRQLGYRRSVLGFRFRDRELDERSVIGVWVYLVAYIVAVFIVMIGFSFQNLPFEETIRLSIGGLTNSGALLMGHTSDLGGGATTLLIISMILGRLEILAIIPALSPSFWRG
1.7E-07	39.5	6.9	1.7E-07	39.5	4.8	1	1	R6MMI9_9FIRM	Putative ATP synthase F0 A subunit	BN515_01177	Firmicutes bacterium CAG:170	96	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:170	1263006	>tr|R6MMI9|R6MMI9_9FIRM Putative ATP synthase F0 A subunit OS=Firmicutes bacterium CAG:170 GN=BN515_01177 PE=4 SV=1MTLFMLMLTLAFVGAALICACSGCSLSAALYETVSALATVGLTAGLTATLTTLPKLLLIVFMFFGRVGIMTISIGFLTASRAEDRFEYAPARMLIG
2E-07	39.3	12.2	7.7E-05	30.8	3.3	3.8	2	B8ATV4_ORYSI	Putative uncharacterized protein	Osl_17311	Oryza sativa subsp. indica (Rice)	440	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Oryzoideae, Oryzeae, Oryzinae, Oryza, Oryza sativa (Rice), Oryza sativa subsp. indica (Rice)	39946	>tr|B8ATV4|B8ATV4_ORYSI Putative uncharacterized protein OS=Oryza sativa subsp. indica GN=Osl_17311 PE=4 SV=1MKLLLPNSEVLRIYWEKAQHLCGFLSMKLISRARCVASSVKQSYSFLVCKSNPLVVQLVYFVIISFAGFLALKNLKPQGKPGPKDLDLLFTSVSTLTVSSMATVEMEDLSDRQLWVLILLMLMGGEVFTSMLGLYFNNANANRNENSQRSLPSISLDIESNSPANNGDHKITECGQSEETMSQNQILAGNTLFSPLLRLCVWVLGKVSGKAEYAYILQHPGETGYKHLHVRRNSVYIVLSVTGLILLQVMFICSFEWNSESLEGMNWLQKLVGLLFQSVNTRQAGESILDISTLSPSTLLLFAVVMYLPSDASFLTANADNQPLTDKKTNSISRALWRNFTVNKLSCLAMFTFLACITERKSISSDPLNFNIFSIVFEIIRQVHILFFCYSLGYSCQKLLKPDATCKDASYGFVGRWTEEGKLIVILVMFLGRLKEFILK
3.1E-07	38.7	14.8	4.9E-06	34.7	0.6	3.3	3	E9AEI5_LEIMA	Trk system potassium uptake protein	HKT1 LMJF_35_0080	Leishmania major	579	cellular organisms, Eukaryota, Euglenozoa, Kinetoplastida (kinetoplasts), Trypanosomatidae, Leishmaniinae, Leishmania, Leishmania, Leishmania major species complex, Leishmania major	5664	>tr|E9AEI5|E9AEI5_LEIMA Trk system potassium uptake protein OS=Leishmania major GN=HKT1 PE=4 SV=1MPSGVNVPATLHRQVLPFEGGEQPPLTPLPTAPRDDYSRTSQLLFEVPVLLPLTADQRHLIKQLDFFKKWYLFCHFVYICTWILIGFLGLLAMVPHLATVDAFFVAVSSVCNCGLQSVDVGEWSAGATLFRHFLLLPGGVVITSSFQPLLRLFMLHRVRHVFYPEEKDTPQEALLRTKKRAEARRLHYAALVSAITPFVYFVVVNGALMTLLWDLNVSHLSAFDVFCMTLASFHSSIFLPMEAYARDAAVTGLVTAACALGFTAFPVLLRFFMLCEWCLLWAVRRLTGLLCRCVELCRSPLDDTSDGEERSASETEDISAALLHAPSHHSYSLLRCLDNMDAAFREAMSSKEPGTFHPFLFRPSETVFLGFAWCALTLMQAAPFWYEQWDGVLHGHTWQYKIYLSLCQAAVVRFAAASFVPLLEYSNAHVAVTILAMYLPALPISTDRTYRKWRQMFRTSVVRLLTSRLFWLFTGMVLILFAEEAEMRAQLLKSRFDIMTRTLFEVISAYAGCGLSLSLPDSNVSFVGCTDSFCKLIIAAVILGGRHRFVDLGIDLGFSSLQSDVDATSSSERISSSQM
4.7E-07	38	0.3	5E-07	38	0.2	1	1	I6ZZN9_MELRP	Potassium transporter ATPase	MROS_1196	Melioribacter roseus (strain JCM 17771 / P3M-2)	78	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Ignavibacteriae, Ignavibacteria, Ignavibacteriales, Melioribacteraceae, Melioribacter, Melioribacter roseus, Melioribacter roseus (strain JCM 17771 / P3M-2)	1191523	>tr|I6ZZN9|I6ZZN9_MELRP Potassium transporter ATPase OS=Melioribacter roseus (strain JCM 17771 / P3M-2) GN=MROS_1196 PE=4 SV=1MTITERADLTKVAFEAFSAFGTVGLSMGLTQELTWGGKIIVVLLMFIGRVGPLAFLYTFMSGAKEDYYELPHENISIL
5.1E-07	38	0.9	5.4E-07	37.9	0.6	1	1	M5C0B7_THACB	Uncharacterized protein	BN14_06975	Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)	81	cellular organisms, Eukaryota, Opisthokonta, Fungi, Dikarya, Basidiomycota, Agaricomycotina, Agaricomycetes, Agaricomycetes incertae sedis, Cantharellales, Ceratobasidiaceae, mitosporic Ceratobasidiaceae, Rhizoctonia, Rhizoctonia solani, Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) (Lettuce bottom rot fungus) (Rhizoctonia solani)	1108050	>tr|M5C0B7|M5C0B7_THACB Uncharacterized protein OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=BN14_06975 PE=4 SV=1MYLFPSHQSWYLLFTLVVIFVLDWAAYLTFNIGMPGIEAVPIGPRIVGGFLQAVGQRAGGFTTINLQAIAPALQVVYIATM
6.3E-07	37.6	0.5	8.1E-07	37.3	0.4	1.1	1	R7C2J3_9FIRM	Trk-type K+ transport systems membrane components	BN579_00366	Firmicutes bacterium CAG:270	103	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:270	1263014	>tr|R7C2J3|R7C2J3_9FIRM Trk-type K+ transport systems membrane components OS=Firmicutes bacterium CAG:270 GN=BN579_00366 PE=4 SV=1MSFFGAMLFVINGDIPSVVDAMFETDSGFTTTGYASTDFNKWPEFSKIILVMLMFSGACAGSTGGGMKVSRLVIMLKFPMPLLINPYTWKEMKLKKNKKKGRS
8.3E-07	37.3	4.3	8.3E-07	37.3	3	1.1	1	K0IJP9_NITGG	K+ transporter family protein	Ngar_c33750	Nitrososphaera gargensis (strain Ga9.2)	99	cellular organisms, Archaea, Thaumarchaeota, Nitrososphaeria, Nitrososphaerales, Nitrososphaeraceae, Nitrososphaera, Candidatus Nitrososphaera gargensis, Nitrososphaera gargensis (strain Ga9.2)	1237085	>tr|K0IJP9|K0IJP9_NITGG K+ transporter family protein OS=Nitrososphaera gargensis (strain Ga9.2) GN=Ngar_c33750 PE=4 SV=1MQVIREVLGIKLVREILIVIGLYIGISTLTRSALSYTMGRSLDDGMFEAVSALSTTGMSTGITSLALDSSSKLMLIANMILGRFEIISVLYIFFSSLRR
9.8E-07	37	1.4	1E-06	37	1	1	1	W8KJI8_HALHR	Uncharacterized protein	M911_09480	Halorhodospira halochloris str. A	79	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Halorhodospira, Halorhodospira halochloris (Ectothiorhodospira halochloris), Halorhodospira halochloris str. A	1354791	>tr|W8KJI8|W8KJI8_HALHR Uncharacterized protein OS=Halorhodospira halochloris str. A GN=M911_09480 PE=4 SV=1MALFALMMLTLMATGLDQVTAFSAVAATITNLGPGLGAVAENYAAISDLAKWVLMFAMLLGRLEVFTLLVLLTPAFWRH
1E-06	37	1.8	3.2E-06	35.3	1.3	1.7	1	K7MMY2_SOYBN	Uncharacterized protein (Fragment)		Glycine max (Soybean) (Glycine hispida)	124	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, fabids, Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine, Soja, Glycine max (Soybean) (Glycine hispida)	3847	>tr|K7MMY2|K7MMY2_SOYBN Uncharacterized protein (Fragment) OS=Glycine max PE=4 SV=1KDVNKRNEKSVVECLVLSQLSYLVIFIILICITESKSLKEDPLNFNVLYITLEVISGYGNVGFSTGYSCARQLKIDATCKDSWVGFSGRWSSKGKFILILVMFFGRLKKFNMKGGKAWKLSWPV

1.2E-06	36.7	5.3	1.3E-06	36.6	3.7	1	1	R6UXE6_9FIRM	TrkH family potassium uptake protein	BN746_03169	Erysipelotrichaceae bacterium CAG:64	99	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, environmental samples, Erysipelotrichaceae bacterium CAG:64	1262981	>tr|R6UXE6|R6UXE6_9FIRM TrkH family potassium uptake protein OS=Erysipelotrichaceae bacterium CAG:64 GN=BN746_03169 PE=4 SV=1MGIFFINLVVLFTGIFLLNIVEQKPFLSLSFEAVSAMATVGSSLGITTSLGVGGKLIIIFLMYVGRIGISTLILSLTRNKPNRNSANKVSFPNGNIIVG
1.3E-06	36.7	0.7	1.4E-06	36.5	0.5	1	1	D9RZR0_THEOJ	Cation transporter	Toce_1965	Thermosediminibacter oceani (strain ATCC BAA-1034 / DSM 16646 / JW/IW-1228P)	115	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family III. Incertae Sedis, Thermosediminibacter, Thermosediminibacter oceani, Thermosediminibacter oceani (strain ATCC BAA-1034 / DSM 16646 / JW/IW-1228P)	555079	>tr|D9RZR0|D9RZR0_THEOJ Cation transporter OS=Thermosediminibacter oceani (strain ATCC BAA-1034 / DSM 16646 / JW/IW-1228P) GN=Toce_1965 PE=4 SV=1MYNGSVWGSTAGGIKNIRILLIFKIIRNAVLNIVHPRAVYSVRDGGMGVKKETKMEVLIYFVMYMIIFFSAVVIVALDGKDIVTTFTSVVANLCNVGPGLERVGPAGIFRIFLFE
1.4E-06	36.5	7.8	0.036	21.9	5.9	2.7	2	A0A099GB97_9RHOB	Cation transporter	IX56_15230	Paracoccus sp. 5503	543	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 5503	1545044	>tr|A0A099GB97|A0A099GB97_9RHOB Cation transporter OS=Paracoccus sp. 5503 GN=IX56_15230 PE=4 SV=1MDRLGRLPVLVIAALVLALAMLIPAAHAAATGAPDIAAIFASSAAGLLVLGVIAGLATASAPATAPAPQVLATLLGVFAGLPLLAAVPFAAVIPDTGLFNAWWEMLSCLTTTGASLYVAEKLPPTLHLWRATLGWLGGMFILVAAIAMMAPLRLGGFEVMDRSAGADDRFGRIEGPTRSQLRPGRDYAAHLADPALRMIRWGQSIVPMYAGATGLLWLLLMMTGAGSLDSLIRAMGTLSTSGVGLTGQPVGASGGVAAEALIAAFMLTALTRRGWPGGGELKASRRLRNDPELRMAAGLVLLVTLVLFLRPFIGAFDDGVQPVSTPEPAADSLAGGLARAAAAAWGAGFTALSFLTTTGWTSVHWDGARAWAGLSAPGLMLAGLAIMGGGVATTAGGVKLLRVFALGLHARRELDKIVHPASVAGGGPITRRLRGSGAYLAFVFFMVFALSIVVTIALVSLRPVAFETATILSVAALTNTGQLAEAIPLIPVFEGSAGIAGSPWAGWAGLSTVNKAILAAAMVAGRLEMLAILALLSPGAWRR
1.6E-06	36.3	15.4	5.5E-05	31.2	10.7	2.1	1	K3YCU7_SETIT	Uncharacterized protein	Si012047m.g	Setaria italica (Foxtail millet) (Panicum italicum)	354	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, PACMAD clade, Panicoideae, Panicodae, Paniceae, Cenchrinae, Setaria, Setaria italica (Foxtail millet) (Panicum italicum)	4555	>tr|K3YCU7|K3YCU7_SETIT Uncharacterized protein OS=Setaria italica GN=Si012047m.g PE=4 SV=1MHPSSSILHTLQRVKLYLATNLSSSNLEAARIIEDKFQKLLGFLSMKLATLSRCLTQFITHSFWRLVFQSNPFVVQLIYFMAISFAVIFDLMFTSVSTATVSSMSTIQMEDLSDQQLWVLILLMLLGGEVFTSMLGLHFNNAKANKEELSRRSLSSNSREIEVSIPANSIKQIDMESGQPEPVISHNQVQQTKSTRHSSRAILAHIVTGYFLASVMSSSVVIISYFWLNSDARQVLQSKEIKVCTFAIFIAVSSFANCGFTPLNSNMQAFTKNYILLLLVIPQILAGNTLFSPLLRLSVWALGKISGKQECAHILRYPEETGYKHLPTQRNSVYIFLTVIGLILLQVICVCSLE
1.7E-06	36.2	1.9	2.5E-06	35.6	1.3	1.3	1	K0IFX2_NITGG	K+ transporter family protein	Ngar_c33760	Nitrososphaera gargensis (strain Ga9.2)	212	cellular organisms, Archaea, Thaumarchaeota, Nitrososphaeria, Nitrososphaerales, Nitrososphaeraceae, Nitrososphaera, Candidatus Nitrososphaera gargensis, Nitrososphaera gargensis (strain Ga9.2)	1237085	>tr|K0IFX2|K0IFX2_NITGG K+ transporter family protein OS=Nitrososphaera gargensis (strain Ga9.2) GN=Ngar_c33760 PE=4 SV=1MAGLSFTGFFLMAYGEKGQMNLRQASIFIVTSFVVMSLFGSLPYIYLTRLGRTLMAICSVNSLFESASGFTTTGLSMITQPENLPQSFNFYRAYTQWVDGLSFIYLVMIFFPEEKLSAWKSVLGGGMLQFKEFLVTLVCIFSVYTVVLVFLLLLTGQIADIYAVSAVFATITGGGFFAYLRFYFAGQHWFPRSHQRRHDTLRAPLRLPLLHL
1.8E-06	36.2	2.5	1.8E-06	36.2	1.7	1.1	1	D4W3V9_9FIRM	Conserved domain protein	CUW_2655	Turicibacter sanguinis PC909	90	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Turicibacter, Turicibacter sanguinis, Turicibacter sanguinis PC909	702450	>tr|D4W3V9|D4W3V9_9FIRM Conserved domain protein OS=Turicibacter sanguinis PC909 GN=CUW_2655 PE=4 SV=1MFILIGISTPIMIFSLLTTVYPTLNETFRNSLFQIISAISTTSYATVSFNDWTPFALFLMIILMIMSGGAGSTSGDIKLYRILLLCKQCI
4.3E-06	34.9	7.2	4.3E-06	34.9	5	3.6	3	A0A076JYU0_9RHOB	Putative Trk system potassium uptake protein trkH	RCA23_c15790	Planktomarina temperata RCA23	494	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Planktomarina, Planktomarina temperata, Planktomarina temperata RCA23	666509	>tr|A0A076JYU0|A0A076JYU0_9RHOB Putative Trk system potassium uptake protein trkH OS=Planktomarina temperata RCA23 GN=RCA23_c15790 PE=4 SV=1MWVRFQKLPLAISIPTLLIVMMTIPSVHGFISGDSHEGRSFFYAVLMGLFGLSFLGFSLQGTVFPMHRHARLWSLISFFLGFPILLAIPLYEVSGAGGFIDAYLDIVSTVTTTGLPVFAPGSLSETLVIWRVSLGWASGFLIWVFAWSIFAPLNLGGFEHLGARGEAMTRSQSARQTAGRLPAEKFWREAHRLGPVYLWITLVAALALLIVSGDPTYAILRAMATIATFGIEIPGHAGVGGVSGEVILAFVMLFALSRSTFSTVFARARKWRMTEDPELRVAAGLVLVAALVLIGQGARYVEGLGAGLELIWGAFFTSLSFLTTTGLASEFLPSGLVTLDPVEIILVALAMIGGGVATTAGGIKLLRVFILAGHSQAEVNRLTAPSQVISGQIESRSHDHHSAMLACVFLVLFILVLGVTTLALTLTGSPVKEALYLTLATVTNTGPLLPTGDGTQTLVMALPTQAKMILAAAMVLGRLEVLALLALLNPDIYR
5.8E-06	34.5	8.9	6.4E-05	31	3	3	2	S5XWB4_PARAH	Trk system potassium uptake protein TrkH	JCM7686_0581	Paracoccus aminophilus JCM 7686	541	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus aminophilus, Paracoccus aminophilus JCM 7686	1367847	>tr|S5XWB4|S5XWB4_PARAH Trk system potassium uptake protein TrkH OS=Paracoccus aminophilus JCM 7686 GN=JCM7686_0581 PE=4 SV=1MTILNRLPLLVILAGIGTALMLIPASYAAVLGQEKLADIFRMSALVLMVLIVVTGIASAAAPRGDTTRTLLLTVIGVMTILPALFAVPVMVALPDTGFFNAWWEMVSCLTTTGASLYSPDRVAEPLHLWRGIVGWMGGLFILASATAILAPLRIGGFELMSDAYGEDSRRQRAAARAGGRASGQSFSSSPAFNTELIDPVSRVLRIGKTVLPIYAVLTLALWIILLMLGDPGLVALMRAMGTISTSGITPLGAGTGQYSGLGGEVVVVLFMLPALSRRFWPGGGELRASELWRDDPELRLAALVVLGVAFVLFARHFIGAVEISRNQPEDLRSSFDSALVAGWGGLFNALSYLTTTGWNSGSWQGARSWSGLTSPGLILAGLAMMGGGVATAAGGVKLLRIYALLAHAEREMEKLIHPNSVAGGGRMARRLRTEGAFLAFIFFMLFAISIAVVVALISLQRIEFESATILAVSALTNTGPLAGAIPLTPTFEGSAGAAGAPWAGWAGLPDFTKAVLAGAMIVGRIETLAILALFNPEIWRR
6.3E-06	34.3	0.2	6.6E-06	34.3	0.1	1.2	1	C1D3M4_DEIDV	Uncharacterized protein	Deide_3p01600	Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	116	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus deserti, Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923)	546414	>tr|C1D3M4|C1D3M4_DEIDV Uncharacterized protein OS=Deinococcus deserti (strain VCD115 / DSM 17065 / LMG 22923) GN=Deide_3p01600 PE=4 SV=1MFHSVSAFNNAGFGLYPDNMIRFAEDPLVLLTTSTLVILGGLGYLAVLGVALYLRDPHRNRLSLNTIIILVTSASLVVLRTVVAGEQQHRGGGDSALRYKGAPTGRAGCGLRIVHQ
7E-06	34.2	0	7.7E-06	34	0	1	1	W5E7J8_WHEAT	Uncharacterized protein		Triticum aestivum (Wheat)	93	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, Liliopsida, Petrosaviidae, commelinids, Poales, Poaceae, BOP clade, Pooideae, Triticodae, Triticeae, Triticinae, Triticum, Triticum aestivum (Wheat)	4565	>tr|W5E7J8|W5E7J8_WHEAT Uncharacterized protein OS=Triticum aestivum PE=4 SV=1QQVGADQHHQKRVTSIWRKLLMSPLSFLAIFIAVVCITERRQISDDPLNFNVLNITVEVISAYGNVGFSTGYSCARQVTADGGCRDTWVGFSG

7.2E-06	34.2	7.9	1.2E-05	33.4	5.5	1.3	1	D3LVT3_9FIRM	Uncharacterized protein	HMPREF0889_1090	Megasphaera genomosp. type_1 str. 28L	296	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megasphaera, Megasphaera genomosp. type_1, Megasphaera genomosp. type_1 str. 28L	699218	>tr|D3LVT3|D3LVT3_9FIRM Uncharacterized protein OS=Megasphaera genomosp. type_1 str. 28L GN=HMPREF0889_1090 PE=4 SV=1MNGRMFSFLLGRMLWVDGGVFGITWLAAQGFRQAHAVYLCIPALVALGSAGILQYVSRRHRRSIHVRESAFYMAFLWLIMSILG AVPFYLTGAYSISDAFFESVSACTTTGLSLYPDLWQQMPCLFTWQCMLKWLGGLHFIILLVTVVPQVSGCFGLFLSARQGMSFSPVIH QMEERARRLAFVYAFFSLVLVWLYSQAGLSWQQALYQSLLTVSTGGGDTGADFRYYHRFSVEIVGIAGMLAGAEIFCFTVKADFSIAL KRYIWMWKVGFLSVFWRFFHYLLLPICVVIKAIPCD
0.00001	33.6	0	1.2E-05	33.5	0	1	1	D7UBM2_VITVI	Putative uncharacterized protein	VIT_11s0103g00090	Vitis vinifera (Grape)	93	cellular organisms, Eukaryota, Viridiplantae, Streptophyta, Streptophytina, Embryophyta, Tracheophyta, Euphyllophyta, Spermatophyta, Magnoliophyta, Mesangiospermae, eudicotyledons, Gunneridae, Pentapetalae, rosids, rosids incertae sedis, Vitales, Vitaceae, Vitis, Vitis vinifera (Grape)	29760	>tr|D7UBM2|D7UBM2_VITVI Putative uncharacterized protein OS=Vitis vinifera GN=VIT_11s0103g00090 PE=4 SV=1MIFELASFDKLNIYLSHNSYLVLFIILICITERDKMREDPLNFNVLNVTIEVVSAYGNVGFSTGYSCARKLKPDPSCKDAWYGFVGR WSDKES
1.1E-05	33.5	2.9	1.1E-05	33.5	2	3.4	3	A4HM47_LEIBR	HKT1 protein	HKT1 LBRM_34_0120	Leishmania braziliensis	580	cellular organisms, Eukaryota, Euglenozoa, Kinetoplastida (kinetoplasts), Trypanosomatidae, Leishmaniinae, Leishmania, Viannia, Leishmania braziliensis species complex, Leishmania braziliensis	5660	>tr|A4HM47|A4HM47_LEIBR HKT1 protein OS=Leishmania braziliensis GN=HKT1 PE=4 SV=1MPSSFRVRAALSRQALPFEGSVQPALSQRPTDPRHDHSRTSQLLFEAPVLLPLTEDQRKLIEQLNFFKKWYLFCHFVYICALVMI GFLGLLVMVPHIAAIDAFFIAVSSVCNCGLQSVNVGQWSTGATLFRHLLLLPGGVVITSSFQPLLRLFMLYRVRRVFYPKEKDTPQEAL LRAKKRAEARRLYYAALVSAVTPFVYFVVVNVILMTLLWYLNVSHLSAFDVFCMTLASFHSSIFLPMEGYAGDAAVTGLVTATCALGFT AFPVLLRPFMLCEWCLVRAIRRLAGPSCGCVAFCRSPPDVIGEDQERNTAETDDISAALLHAPPRHPSSLLGCVDEADAAFQEIMTSK EPGTFHPFLFRPSETFFLGCAWCALTLIQAVPFWYEQWDGVLHGYTWPYKLYLSLCQAAAVRFAAASFVPLLEYSNAHVAVTILAMY LPALPISTDRTHRKWKQMFRTSVVRLLTSRLFWLFTGMVLVLFAEEARMRAQLLNTRFDIMTRTFFEVISAYAGCGLSLSLPGSSVSF VGFTSTFGKLIIAAVILGGRHRFVDLGIDLGFGSLQSALNPTSPSNEQASSAPT
1.2E-05	33.4	10	0.037	21.9	0	2.9	2	A9D8V5_HOEPD	Trk-type K+ transport system, membrane component	HPDFL43_07614	Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43)	478	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Hoeflea, Hoeflea phototrophica, Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43)	411684	>tr|A9D8V5|A9D8V5_HOEPD Trk-type K+ transport system, membrane component OS=Hoeflea phototrophica (strain DSM 17068 / NCIMB 14078 / DFL-43) GN=HPDFL43_07614 PE=4 SV=2MGVMFALIVPSVLFAIADGARDLALSMLLIGALGVFAALMVLGSIAGFERRLGRASGYLALVAAWILLPIAAAISFKTLGGLSWVDS WFEAVAALTTSGITLLPRETAPRAILFWRASLEWYGGFLTIVSIIHVLAPAGFGGLPGGDRRVLTGNSSEMTVDLSSFRDVLTQYVLITV VIFIALMLAGVNGPFAAMMSMIAIATGGFLPFEGALEDHAGPAAQFVLAIGLALGTVSVFWRQRLLRAPRNLIRDNPEVFVVVVAIIVIAV FYAARLSAVSGGSDLPPIFVESLLAATSLVATSGIESRPGVIALWPEILVLVVVLVGGGIYSTTGGFKIYRISAMAVHSARELNRLIYPSS VSSLRFGRYLIDEVSMRAIWTYFALSLVVIASAALMFTLTATDFEAGVTMAISLFSNTGPVYDALIPPVYTTDPANDIWPHFEAIPASAKL AGILLMTLGRLEVMVVFTVLNLRYWLTR
1.2E-05	33.4	1.4	0.033	22.1	0.3	2.2	2	A8IBJ7_AZOC5	Putative Trk-type K+ transport systems membrane component	AZC_3081	Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	468	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Azorhizobium, Azorhizobium caulinodans, Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	438753	>tr|A8IBJ7|A8IBJ7_AZOC5 Putative Trk-type K+ transport systems membrane component OS=Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571) GN=AZC_3081 PE=4 SV=1MAPILRLFALVLALLAAAALVPALVGLGARDGSAPVFIATAVASLFLAGAVHLAVRGRPGRLRRLHLFAALGVLWLLVPIMAAPAV AVLAPMAFGGAVLEALSAFTTTGLSSVGEAPASLHVWLALLQWAGGLLTLVAGIAVLAPAGVAGLPDRAVHPGETVEAIDLLDALGTV APIYGLATLVAFIAMLGAGASLLSAATLATAVISTGAHVPPEVHEFLAASVPGRWVTIPFLLWSATSVRWHKALVSRRIHAAPEQGESLI LFGYWAVFGLVMGAYFFRGAAGLHTHEAVLDGLFGAASLISTTGLAPHRGAFDELPPALVLAVAFVGGGALSVSGGLKILRVRAMLLR ARGDLMRLVYPNLVQPSRTGEGGVGSAMRGVWVGMVALCLTFAAALILIAGSMPSFEAAVSTAVSALSNTGPLLDGTPGPEDFDLLA AVGAGFAMIAGRLETVGAFVIIHLAFWRT
1.6E-05	33	0.1	1.9E-05	32.8	0.1	1.1	1	D4JCB8_9FIRM	Uncharacterized protein	EC1_00280	Faecalitalea cylindroides T2-87	155	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Faecalitalea, Faecalitalea cylindroides, Faecalitalea cylindroides T2-87	717960	>tr|D4JCB8|D4JCB8_9FIRM Uncharacterized protein OS=Faecalitalea cylindroides T2-87 GN=EC1_00280 PE=4 SV=1MENSQKKIRRALDYFSAPQLLMVGFASVILTGAVILMLPISVREGATVSFIDALFTSTSAVCVTGLIAIDTADHFTVFGRAVVAALIQ IGGLGVTCVGVSLILAAGRKIDFHTRKLIKESWNIDSYQGLVKLVKQVLKLTFAFVSCWRSFEFPCI
8.8E-05	30.6	22.5	0.00011	30.2	1.7	3.5	3	A4IAQ9_LEIIN	Trk system potassium uptake protein	HKT1 LINJ_35_0080	Leishmania infantum	579	cellular organisms, Eukaryota, Euglenozoa, Kinetoplastida (kinetoplasts), Trypanosomatidae, Leishmaniinae, Leishmania, Leishmania, Leishmania donovani species complex, Leishmania infantum	5671	>tr|A4IAQ9|A4IAQ9_LEIIN Trk system potassium uptake protein OS=Leishmania infantum GN=HKT1 PE=4 SV=1MPSGVGVPATPHRQALPFEVGEQPPLTPLPTAPRDDYSRTSQLLFEAPVLLPLTADQRHLIEQLDFFKKWYLFCHFVYICTWVLI GFLGLLVMVPHLATVDAFFVAVSSVCNCGLQSVDVGKWSAGATLFRHFLLLPGGVVITSSFQPLLRLFMLHRVRHVFYPEEKDTPRE ALLRAKKRAEARRLHYAALVSAITPFVYFVVVNSALMTLLWSLNVSHLSAFDVFCMTLASFHSSIFLPMEAYARDAAVTGLVTAACALG FTAFPVFLRFFMLCEWCSLWVVRRFTGLLCRCIELCRSPLDDTSDGEERSASETDDISAALLHALPRHSYSLLRCLDNMDAAFREAMS SKEPGTFHPFLFRPSETAFLGFAWCALTLMQAAPFWYEQWDGVLHGYTWPYKIYLSLCQAAAVRFAAASFVPLLEYSNAHVAVTILS MYLPALPISTDRTYRKWRQMFRTSVVRLLTSRLFWLFTGMVLMLFSEEAEMRVQLLKSRFDIMTRTLFEVISAYAGCGLSLSLPDSNV SFVGFTGTFCKLIIAAVILGGRHRFVDLGIDLGFSSLQSDVDATSSSERISSSQT
0.00012	30.1	16.6	0.91	17.3	2.9	3.4	3	A0A0F2QH04_9RHOB	Uncharacterized protein	VR75_12625	Hyphomonadaceae bacterium BRH_c29	468	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Hyphomonadaceae, unclassified Hyphomonadaceae, Hyphomonadaceae bacterium BRH_c29	1629720	>tr|A0A0F2QH04|A0A0F2QH04_9RHOB Uncharacterized protein OS=Hyphomonadaceae bacterium BRH_c29 GN=VR75_12625 PE=4 SV=1MNYASVVRILALVMLILAGASLPAVLTAAAYGEYDQVFAFLAMVLGISVIAASILFLTPRPTQKSRPSDALGLVILWWFLAPVAACL PFVVGVQNQSLLQAIHEAAACLTTTGQSVIAVEGDRWPSSLIVWRGTLHFVGGAASIITAASVLAALNLGGPGIHRSALFVMPETSFFD AVPKVARSVVLIMTVSITVTVLALELAGMSAGRAMSDAVSVWTTGLVDPAPYGRANAGPVADIILAFGLMGGALGLAVALPLRERRLV KAATDPETTMFVFLVILFTVMAVASGVKVFESLGWAISALATSGLPLGSADTWNLVPLPVFVLPALIGGSALSAAGGVKIARLIVLARRA GVEFRQLGYRRSVLGFQFRDREMDERSVIGVWVYLVAYILTVFLVMVGFAFTGLPFESSIRLAIGCLTNSGGLVAGHVAQLDNAASILA IFSMVLGRLEILAIIPAISVSFWRG
0.00013	30	0.2	0.00013	30	0.2	1	1	V4L8F3_9GAMM	Uncharacterized protein	N838_34020	uncultured Thiohalocapsa sp. PB-PSB1	69	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiohalocapsa, environmental samples, uncultured Thiohalocapsa sp. PB-PSB1	1385625	>tr|V4L8F3|V4L8F3_9GAMM Uncharacterized protein OS=uncultured Thiohalocapsa sp. PB-PSB1 GN=N838_34020 PE=4 SV=1MIHAGLEPVSAFSAVATSINNLGPGLGEVAYSFQGVSDQGKLVAVAAMLLGRLEIFTILVLLMPEFWRG
0.00026	29	0	0.0003	28.8	0	1.2	1	R7MCN0_9CLOT	Sodium transport protein	BN790_01103	Clostridium sp. CAG:813	174	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:813	1262843	>tr|R7MCN0|R7MCN0_9CLOT Sodium transport protein OS=Clostridium sp. CAG:813 GN=BN790_01103 PE=4 SV=1MDIGLVTFIPIAVAIYYCEWGSILPFFTAGIFSLFVGDILCRSFNRGSDALNDIKRSEALMTVSLSWLAFGVVCAIPYLFYGLSPVDS LFESVSGITTTGATILENFDYPRTIMFWRSFTQWLGGILYYLLQFYLNLLLQGVKCFLLKLQGQLRINLLQELKILPLLCGLFMRV

0.00027	28.9	0.1	0.00048	28.1	0.1	1.3	1	E9PYY6_MOUSE	Protein BC021785	BC021785	Mus musculus (Mouse)	479	cellular organisms, Eukaryota, Opisthokonta, Metazoa, Eumetazoa, Bilateria, Deuterostomia, Chordata, Craniata, Vertebrata, Gnathostomata (jawed vertebrates), Teleostomi, Euteleostomi, Sarcopterygii, Dipnotetrapodomorpha, Tetrapoda, Amniota, Mammalia, Theria, Eutheria, Boreoeutheria, Euarchontoglires, Glires (Rodents and rabbits), Rodentia, Sciurognathi, Muroidea, Muridae, Murinae, Mus, Mus, Mus musculus (Mouse)	10090	>tr|E9PYY6|E9PYY6_MOUSE Protein BC021785 OS=Mus musculus GN=BC021785 PE=4 SV=1MGSRGSGPTSVEQHLLQVETQGKNGLQAVGRTLRWFTTVVLNAAFLGMGVSAAVLGPTFPDLARNVNRNVSSLSEIFVGRAL GYLCGSVVGGVLFDCMNHFLLLGLSNLLTIAGLYLTPFCKTAALLTTMMSVTGVSFGVLDTGGNVLILDLWGDKGAPHMQALHFSFAL GAFLAPLLAKLAWGTTTSAQNYTEPQSDRSALNQSFEATLDSVFAVPDDKNLLWTYASIGTYVLVVSVFLFAPFFKKNSKQKKSEASA QGARRAKYHRALLCLLFLFFFYVGAEVTYGSFVFSFAITHVGMEESEAAGLNSIFWGTFAACRGLAIFFATFLQPGTMIVLCNIGSLV SCFFLVLFDKSPLCLWIATSVYGASMAATFPSSISWIEQYTSINGKSAAFILIGAALGLMATPALSGILQGHYPDLPVVLYTCLGSAVLTT VLFPVMYKVATLPLDQKQEKSINSEGQKTLLSSFRLIKEAK
0.00054	28	0.4	0.00059	27.8	0.3	1	1	R6QXU7_9CLOT	Trk system potassium uptake protein TrkH	BN621_01497	Clostridium sp. CAG:352	88	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:352	1262798	>tr|R6QXU7|R6QXU7_9CLOT Trk system potassium uptake protein TrkH OS=Clostridium sp. CAG:352 GN=BN621_01497 PE=4 SV=1MGKSAFISVALCLEEFIVTSFTAVTATINNIGPGLELVGPTQNFSVFGSFSKYVLMFDMLAGRLELFPLLILFHPSALKDMVKKSNN Y
0.0048	24.8	0	0.0052	24.7	0	1.1	1	R6JRF7_9CLOT	Uncharacterized protein	BN486_03707	Clostridium clostridioforme CAG:132	114	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium clostridioforme CAG:132	1263065	>tr|R6JRF7|R6JRF7_9CLOT Uncharacterized protein OS=Clostridium clostridioforme CAG:132 GN=BN486_03707 PE=4 SV=1MKYLERQSPARIIAIGFLAVILTGFSLLMLPVCVKPGVRLHYVDALFTSTSAVCVTGLIAVDTADTYTALGQTVVALLIQIGGLGVPS KELPAMRSPTPSITGFPRRHFTRQPL
0.0062	24.5	48.9	0.0065	24.4	10	2.7	2	Q4FM27_PELUB	TrkH-like cation transport protein	SAR11_0950	Pelagibacter ubique (strain HTCC1062)	469	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Pelagibacterales, Pelagibacteraceae, Candidatus Pelagibacter, Pelagibacter ubique, Pelagibacter ubique (strain HTCC1062)	335992	>tr|Q4FM27|Q4FM27_PELUB TrkH-like cation transport protein OS=Pelagibacter ubique (strain HTCC1062) GN=SAR11_0950 PE=4 SV=1MKYFKLIYLSVFFGIVSILAFFNITYSYYLNLYLNLNTYIFTFIVSILLTILFYYSKNNDEKKITIYDKILTILLGYFLLPLVISIPFYFSIYNL TFVNAFFESISGFTSTGFTIFNNINHIDQSLILWRSASQWIGGLYFLFSIILLIDIFDHSFKKSLTNFLSFNKSETFKQAFKIFLFYSLITLSIFI ILSLFDIRLFNSLNLAMTIISSGGFLPSNNLSNILVNNSQVIIISTLLLSSFFSIFLIYNLIFTKNHNLNFFNEDIHLLFYFLFLLIIFFVFLNFENN FSELFLSLTSSISNVGFSLNNSSNNLSFVFLILVIIGGSFFSTSSGIRFLKIYSLFKYSINEILSYSRPKNIYINKHLFSKDTFKLDEIYKYFLS VIVFIISLLILTFLLTLSEIDFESSFKLSILTIMNTVNSSMFGLADFSFYDLHFITKYYLIFFMIIGRLELLTLLIICKKFLFKN

Sheet 6

All DUF4118 proteins retrieved from the RFP (For classfication of these proteins, see sheet 7 in this data set)																		
Annotation on prediction	**HMMER search output**									**Protein names**	**Gene names**	**Organism**						
	Whole protein prediction			**DUF4118 domain prediction**														
	E-value	**score**	**bias**	**E-value**	**score**	**bias**	**exp**	**DUF4118 domain number per protein**	**Uniprot entry name**	**Protein names**	**Gene names**	**Organism**	**Protein length**	**Organism ID**	**Taxonomic lineage (ALL)**	**Protein sequence**	**Whole protein domain architecture predicted by CDD: (domain start~~domain name~~domain end) (unpredicted domain labled is not shown)**	
	3E-32	120	9.1	5.8E-32	119	6	1.7	1	B2JMX2_BURP8	Uncharacterized protein	Bphy_5287	Burkholderia phymatum (strain DSM 17167 / STM815)	492	391038	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia phymatum, Burkholderia phymatum (strain DSM 17167 / STM815)	>tr|B2JMX2|B2JMX2_BURP8 Uncharacterized protein OS=Burkholderia phymatum (strain DSM 17167 / STM815) GN=Bphy_5287 PE=4 SV=1MNTQANEHSAPRARHRRRQAQSVGAGSWWARVIAPPRGTAHRRAIAALETIVATVFAVALCWAFDHDDPLLIKTGFGWIWIVPLMIALRYGTIAGVFSGLILLASWYALYPEYGTASAPASFAHALVAPPTMRRFPVSFFLGGFVITMLCGQFGDIWITRLRQGRIANDYLAERLSILTRNQFMLRISHERLEQDLLARPATLRDSLARLRTLILDQEPTDAQHGIVDLRGAQPFLEAAAQACQLESASVHAWRGGKPAATVAASIGAPAAFEPDDPLVREALDTRTLVHVESKTNLDASISRYVAVVPLIDVRNNPVGVLAVERMPFLALTRDNLQFLLVLCNFYADGVQHAVVTRETLAAFPACPHTFALDYARLVHLKRDTQVQSSIVALVFHNDEHGTTLFQHVLRTRRALDVQWPLRDEHRLVVLTLMPLSGDSAVDGYLLRIEENLHAQYGVDFEAARVAVHSMAVPADEPIAELRRLLERCDVRF	48~~DUF4118 (0.000000000000014279)~~160;X;235~~GAF (0.000000000042772)~~352	non-KdpD DUF4118 protein
	1E-23	92.5	12.4	2.4E-23	91.7	8.6	1.4	1	C5AI27_BURGB	Polysaccharide transport system component transmembrane protein ragD	bglu_2g11670	Burkholderia glumae (strain BGR1)	491	626418	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia glumae (Pseudomonas glumae), Burkholderia glumae (strain BGR1)	>tr|C5AI27|C5AI27_BURGB Polysaccharide transport system component transmembrane protein ragD OS=Burkholderia glumae (strain BGR1) GN=bglu_2g11670 PE=4 SV=1MNTQATGPGEPGKRGAPARTVRATGAAAWWSALIAPPDRSPRRRAIALAETLVFTLVVIALCRVFAADDPLLIHAGFGWIWLAPVLIALRAGSAAGLVSGFMVLAAWYLLYPAVPVPAAAAGFAGETTLVRPFPTGFFFGGFLLTLLTGQFGDIWIARLRQNRIANDYLSERLSILTRNQFMLRLSHERLEQDLLSRPATLRDSLARLRAVVFDATPSAAEQGEVALRGAQAFLDAAAQAVQLEVASVHAWRHGAPAAEAAAAIGGAAPLDAGDPLVREALDTRKLVHVEARGDAAASIGSRYLACVPLLDVKGAPVGVMAIERMPFLALTRDNLQFLLVLCNFYADGVRHAEVTREMLAAFPDCPHRFALDYARLVHLRRDSGVLSAVVTLVFDSDERGAALCEHVVRTRRALDSQWEIVGARRRAVLTLMPLSGTSGVDGYLMRIEDSLRAQFGIDFEGAHVAVYSMHVPAEEPMRPLVKLMEHCGVAG	47~~DUF4118 (0.00000000063769)~~111;X(120);231~~GAF (0.000000579601)~~351	non-KdpD DUF4118 protein

	3E-23	91.5	5.6	5.5E-23	90.6	3.9	1.5	1	Q9HZE7_PSEAE	PelD	pelD PA3061	Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	455	208964	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	>tr|Q9HZE7|Q9HZE7_PSEAE PelD OS=Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228) GN=pelD PE=1 SV=1MSAHKDFTLAPRASGSVSWVETLVISALALGLGWWFSPDDPLQVNATFPWVILAPLLLGMRYGFVRGLASAALLVAALFAFRARGVEAYAQVPAAFIVGVLLCAMLVGEFRDIWERRLERLELANEYRQLRLDEFTRAHHILRISHDRLEQRVAGNDQSLRSSLLGLRQLLRELPGDEAPLDALAETVLALLAQYGSLRIAGLYRVRYDRTPEPQPLATLGEMPALDADDLLVRTCLERGELVSVRQELLERGEQRAHSALQVCVPLVDTDGRILALLAVEQMPFFVFNERTFSLLAILAGHIADLLQSDRRALQLADIDAQRFSQYLKRSLLDARDHGLPACLYAFELTDARYGEEVQRLLEGSQRGLDVQLRLRNDEGRRVLLVLLPLTSAEGSQGYLQRLRILFAERFGQARELESLGVRIRQYELDAGNDRQALGHFLFNECGLNDQQVAI	19~~DUF4118 (8.53786E-15)~~117;X;181~~GAF (0.00000000152722)~~304	non-KdpD DUF4118 protein
	4E-22	87.8	7	3.9E-22	87.8	4.9	1.6	1	A6V314_PSEA7	Uncharacterized protein	PSPA7_2076	Pseudomonas aeruginosa (strain PA7)	455	381754	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	>tr|A6V314|A6V314_PSEA7 Uncharacterized protein OS=Pseudomonas aeruginosa (strain PA7) GN=PSPA7_2076 PE=4 SV=1MSAHKDFTLAPRASGSVSWIETVLITALALGLGWWFEPSDPLLVQASFPWVILAPLLLGMRYGFVRGLASAALLVAALFAFRAQGLEAYAQVPAAFIVGVLLCAMLVGEFRDIWERRLERLELANEYRQLRLDEFTRAHHILRISHDRLEQRVAGNDQSLRSSLLGLRQSLRELPDDEEPLAALAETVLALLAQYGSLRIAGLYRVRQDRAADPRPLATLGEMPALDGDDLLVRTCLERGELVSVRQDLLERGEQRAHSALQACVPLIDTEGRVLALLAVAQMPFFVFNDRTFSLLAILAGHVADLLQSDPRALRLADVDAQRFSQYLKRSLLDARDHSLPACLYAFELTDERCGEEVQRLLESSQRGLDVQLRLRNAEGRRVLLVLLPLTSTEGSQGYLQRLRILFAERFGQASELESLGVRIHGYELDAGNEHQALGHFLYNECGLNDQQVAI	19~~DUF4118 (5.56316E-15)~~117;X;181~~GAF (0.0000000348944)~~304	non-KdpD DUF4118 protein
	2E-21	85.8	12.8	4.3E-21	84.5	8.9	1.7	1	F2LN48_BURGS	Putative transmembrane protein	bgla_2g14860	Burkholderia gladioli (strain BSR3)	507	999541	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia gladioli (Pseudomonas marginata) (Phytomonas marginata), Burkholderia gladioli (strain BSR3)	>tr|F2LN48|F2LN48_BURGS Putative transmembrane protein OS=Burkholderia gladioli (strain BSR3) GN=bgla_2g14860 PE=4 SV=1MNTQATGPDPGESRAAPRSRTVRATGAAAWWSTLIAPPEGSARRRTVALLETLGFTLIAIGLCRAFSADDPLLIHSGFGWIWLVPVVVSLRYGSVAGLVSGFVLLAAWYLLYPAVPVPVVTAVAAGAGPAGASASAVFAGDTVLSRPFPVGFFFGGFFLTLLTGQFGDIWMSRLRQNRIANDYLSERLSILTRNQFMLRLSHERLEQDLLSRPATLRDSLARLRAVVFEQLPSPAEQGDLALRGAQAFLDAAAQAVQLEVASVHAWRQGAPAAEAAASVGGAGPLDVHDPLVREAIETRRLVHVDAQAHAGAAAIGSRYLACVPLLDVKGEPVGVVAIERMPFLALTRDNLQFLLVLCSFYADGVRHAEVSHEMLSAFPACPQRFALDYARLVHLRRDSQVLSSVVTLVFDNDEQGAALSEHIVRTRRALDSQWEVIGSKRRAVLTLMPLSGASGVDGYLLRIEDNLRAQFGVDFEAAHVAVYSMNVPASEPIRPLVKLMEHCGVAG	48~~DUF4118 (0.000000000949168)~~111;X(135);246~~GAF (0.0000000151869)~~367	non-KdpD DUF4118 protein
	4E-21	84.6	3.9	8.1E-21	83.6	2.7	1.5	1	Q39U78_GEOMG	Membrane protein, putative	Gmet_1967	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	459	269799	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter metallireducens, Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	>tr|Q39U78|Q39U78_GEOMG Membrane protein, putative OS=Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) GN=Gmet_1967 PE=4 SV=1MAFNKDSTMILDRWLETFAITAIAVTGGFLLNSSDPLFVHARFPWVWFGPLLIALRYGIAPGLVSTGGICLALLVMPRFGLPIGEFPTNYVLGGLLMVLITGQFSDIWSKRLRHANQLSNHTSERFEQLSRAYFMVRLSHDRLEQNLISRPVTLRDAMINLRNLLAKHDGRMDSETSAALLSILMHYCSLESAAIYPANDDGELLDVPIAKCGKGAPLNRDDLLLRSAIESGYSAYQAINRHIVEGRPSAPSALSSAVWSVDVSRDESKEQTSYLVVAPMRTSSGKLLGLLLVTEMPFLNLHRETLQIMGVLLAYSSDQAESVERARDILGLFPDCPPNFAAELIKTVRLKRDLHVSSALVMVQVMADSRLDEICKTMERQQRGLDHSWLRTTDWGAQFVTLMPFSGPASIEGYKSRIHEILQRQVGRSTGQEGITMHSTSVTTDDPLVQLVALLEEKQ	13~~DUF4118 (1.4592E-21)~~111	non-KdpD DUF4118 protein
	2E-19	79.5	3.1	2.8E-19	78.7	2.2	1.5	1	Q4KCF2_PSEF5	Putative polysaccharide auxiliary transport protein PelD	pelD PFL_2975	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	456	220664	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	>tr|Q4KCF2|Q4KCF2_PSEF5 Putative polysaccharide auxiliary transport protein PelD OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=pelD PE=4 SV=1MNSPHMDYALAPRASGPASWLETFLVTALVIGVGLWLAPEDPLQVQGEFPWSVLAPLLLGVRYGFVRGLISASLLVAAFFALRHSGLASYAQVAPSYIVGVLVCGMLVGEVRDLWERRLLRLQMANEYRQYRLDDFTRAHQILRVSHDRLEQRLAGSDQSLRSSLLGLRDRLRAAPNGGDPLSLLAEPVLTLLGQYGSLRVAGLYRVEQGASAAPQLSLLASIGTMGPLDSQDLLVRMCLEREELVSVREELLDSGAQASVSSLQACVPLVDTQGQVLAILAVRQMPFFAFQERTLSLLALLAGHIADLLHPDPQVLQLQSADAQHFTRQLKRSLVDVERHGLSGCLYAFELTQPNDELARLFERSQRGLDLHLSLANARGHELLLVLLPLTSAEGAQGYLARLGKLVHEHFGMSVELAGLGVKVLPYDLESARQRDGLRNYLYNECGLNDQQVAV	20~~DUF4118 (1.10032E-17)~~118;X;185~~GAF (0.0000000508809)~~311	non-KdpD DUF4118 protein
	3E-19	78.6	4.7	5.9E-19	77.6	3.2	1.5	1	A9BX96_DELAS	Putative transmembrane protein	Daci_5543	Delftia acidovorans (strain DSM 14801 / SPH-1)	459	398578	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Delftia, Delftia acidovorans (Pseudomonas acidovorans) (Comamonas acidovorans), Delftia acidovorans (strain DSM 14801 / SPH-1)	>tr|A9BX96|A9BX96_DELAS Putative transmembrane protein OS=Delftia acidovorans (strain DSM 14801 / SPH-1) GN=Daci_5543 PE=4 SV=1MPDQASTPKAAPHSAAPRRAGIAAEFRGSPLGLLVQTSAKPWVVVGETLLLPVLALLIGMWANPDNPLWVESEFPWAWLAPVVVALRYGPVAGLSAAGVLLLAWLGVNQRDLSLFPEQYFLGGLILVMVVGEISSLWRARIRRARTAQNYMDQRTEQLIRQHYLLRLSHDRLEQELIGRPVSMRDAINVLSGLSGAEGDAQSLLNLLSRFSQISVASLVPVRNEVLDPTPIAQLGGERPIHVHDPLVRQALDSHVLCHVSQSMAEGQQTQYIVVAPMLDLEGEIYGLLLVEEMPFFALQEEALQTINLLLGYYTDSVAANSLAAPLLQAYPDCPPHFAFELQRMEHVNRSARLSSVVVALELSPSAVQAQMAQQIMRLERMLDRSWLQESDGRQLLAIFMPLGTNATAEGYLNRIEGWLAQRGVASLADAGIFPRTILLDRCSASSVLERLHQMGQGHA	58~~DUF4118 (0.000000000018941)~~137	non-KdpD DUF4118 protein

	3E-19	78.5	3.7	5.7E-19	77.7	2.5	1.4	1	A1U1W3_MARHV	Uncharacterized protein	Maqu_1901	Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)	443	351348	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Alteromonadaceae, Marinobacter, Marinobacter hydrocarbonoclasticus (Pseudomonas nautica), Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)	>tr|A1U1W3|A1U1W3_MARHV Uncharacterized protein OS=Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8) GN=Maqu_1901 PE=4 SV=1MQDTRATTTVAQSGHATEVHGWLKWLEVVLVTGLFLAAGFWLRPDDPLHVGNTFAWPVLAPLLIGLRYGF FPALMSSLLVLLVAGWHYDKAAATAYPWGWAAGMLACGLLAGEFRDYWERQLRRANAVNEYSLQRLEEFTRNF YLMKVSHDRLEQQLAGSSGSLREALRRLYGELSQTRSEGLNEESAALMLRVLARYGQLQTAAILAVEGNRNIQPK ALATVGDYEAVSESDPLIRYAMQERTLVSVQTEFRKHLKKLDTDLLVVIPLISSTDDLVALCVVESIPFFSFQNRTLR LMAILAGHMADMLCQRDQTMAGSHEWQSLCSQARRAARDAEAFGLPSVLLKLQVNEQDLATLADRMTGLLRGL DVIAVNRANESPSVVLLMPLTDELGLAGYLHRLELDIRENAGRSLWDFASQQSLVVKTEAQVAEWLAREGGAID	24~~DUF4118 (3.59973E-14)~~121;X;185~~GAF (0.000000681773)~~306	non-KdpD DUF4118 protein
	9E-19	77	3.1	1.4E-18	76.5	1.8	1.6	1	U7DG76_PSEFL	Deleted.								non-KdpD DUF4118 protein
	2E-18	76.2	10.8	2.8E-18	75.4	7.5	1.4	1	C7RUE2_ACCPU	Histidine kinase (EC 2.7.13.3)	CAP2UW1_1684	Accumulibacter phosphatis (strain UW-1)	897	522306	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, unclassified Betaproteobacteria, Candidatus Accumulibacter, Candidatus Accumulibacter phosphatis, Accumulibacter phosphatis (strain UW-1)	>tr|C7RUE2|C7RUE2_ACCPU Histidine kinase OS=Accumulibacter phosphatis (strain UW-1) GN=CAP2UW1_1684 PE=4 SV=1MTERPDPDRLLARVQEEEAKAARGKLKIFFGASAGVGKTYAMLGAARQQKELGTDVVIGVVETHGRKETEA LLAGLERLPLRDIAHRDRMLKEFDLDGALARRPALILMDELAHSNVAGSRHPKRWQDVHELLVAGIDVYSTVNVQH LETLNDVVSGIAGIRVWETVPDRVFDAADEVVLVDLPPDELLQRLKEGKVYLPQQAERAIRNFFRKGNLIALRELAL RRTADRVDDEMLAYRRETSINTVWQTRDALLVCIGPGTGGERLVRTAARLAGRLEAPWHAVHVDTHTAGPEPEL QRQRIVRALDLASSLGAETATLSADDAVATVVDYAREHNLSRVLVGRDHPRRWQPWYRSMVERVGHAAPDLDV VQVARNDDARTAVPSPTAPPTPGEWLAYFKATAICAVATALAAPLAGAIELTNIAMLFLLAVLIVAMRLGRGPAVLS AFLAVAAFDFFFVPPRFSFAVSDAQYLMTFGVMLIVALITGQLTARYKQHAEVATQREARARGLYEMARDLSAALL PVQIAEACDRFLVVEFGARAALLLTDTRDHLQAAILAAKAAAGETPVVDEGVARWAFDHGEAAGLSTDTLPGSPLL YLPLKAPMRTRGVLAIAPRDPLRVQGPEARRQLETFASLVAIAVERMHYVDVAQTTLVQMESESLRNSLLSAISHD LRTPLSVLVGLAESIRLTQPPPTDAQATIAATLKEEALRMSTKVNSLLDMARLQAGKVQLKRQWQPLEEVVGSALM ATDVSLAAHSVHTALPDDLPLLEIDGVLIERVLCNLLDNAAKYTPAGTPVSIGAAARENEVEVWVDDSGPGLPRGR EESIFEKFERGARESTTSGVGLGLAICRAIVEAHGGRIHAENRPRGGARFIFSLPRGVPPTVVEEGGAT	21~~KdpD (8.64417E123)~~231;X;254~~Usp(1.69802E-35)~~375;X;398~~DUF4118 (5.64124E-27)~~498;X;525~~GAF (4.96081E-15)~~646;X;663~~HisKA (0.00000000015512)~~728;X;781~~HATPase_c (3.73258E-30)~~882	KdpD protein
	3E-18	75.5	12.1	5.3E-18	74.5	8.4	1.5	1	Q0JZ41_CUPNH	Uncharacterized protein	H16_B2201	Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	479	381666	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus necator (Alcaligenes eutrophus) (Ralstonia eutropha), Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	>tr|Q0JZ41|Q0JZ41_CUPNH Uncharacterized protein OS=Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) GN=H16_B2201 PE=4 SV=1MSVANTADKTYRARQGQGIGLGGRYARLLAPAVSGRAAVVELVVAMLAAMGLAWLVLPQNPLLLGMGFPW AWLLPVILALRYGTLIGVGSVLMLLGGWYFYQQTGVMAGPFPRLFFLGGLLLVLVAGQFGDIWGTRLARARAVNR YLDERLAALTKNHYLLRISHERLENDLLARPTTLRDTLSQLRSVALDEAARTGQVLAGAQPMLQVVAQACQLEAAA LHACDGEHVDGVPVASIGPEFTLDTTDPLVRHCLDTRQLAHLSADGLQHGAQTRYVAVAPVLAGSDHLIGLLVVER MPFLSLTYENLQMLMVLLGYYADGVEHAGATRTIQAALPACPYPFALDYARLSRLRRETGIESSVVALVFDADPER DALFEQVVRSRRALDVAWPVVNAHHRAMLTLMPLSDAQAVAAYLVRIEDMLRAQFGTDFTSAGIGVYTLAVPGAG SEDALVKLLRRAQVDGAIAPATLPAGEAPHV	38~~DUF4118 (0.00000000829171)~~136;X;207~~GAF (0.00000000185738)~~324	non-KdpD DUF4118 protein
	4E-18	74.8	4.1	6.4E-18	74.3	2.8	1.3	1	B9M091_GEODF	Cyclic diguanylate phosphodiesterase	Geob_2520	Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	320	316067	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter daltonii, Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	>tr|B9M091|B9M091_GEODF Cyclic diguanylate phosphodiesterase OS=Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32) GN=Geob_2520 PE=4 SV=1MPIKGQVQTSAIIKLIILSVIVLVVTLLHFMTPTEPHIYHQLHIIFRKLYFLPPVMAGAWFGLRGALITTLSISILFSL HAFLDWPGNYMEQANQLGELAGFWVVGLVPGYLFDRQKKLLIDVANANEETLIALVSALDLREHNTQMHSRRVR EYALLIARQLGIDERRSVNIGFGALLHDVGKIAVPDHILLKQGRLTEDEWKEMRKHPEAGYGIIKKINFLKEAAEIAYT HHERFDGQGYPRGLRGEEIPYGARIFMVADVFDALSSTRSYHTASTYEECTKMIKEESGKHFDSKVVGAFLLIDRK QIEAIQTEYADG	11~~DUF4118 (0.000000000013032)~~118;X;143~~HDc (4.1752E-22)~~281	non-KdpD DUF4118 protein
	7E-18	74.2	2.5	1.5E-17	73.1	1.7	1.6	1	D0IZJ0_COMT2	Putative transmembrane protein	CtCNB1_0694	Comamonas testosteroni (strain CNB-2)	455	688245	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Comamonas, Comamonas testosteroni (Pseudomonas testosteroni), Comamonas testosteroni CNB-1, Comamonas testosteroni (strain CNB-2)	>tr|D0IZJ0|D0IZJ0_COMT2 Putative transmembrane protein OS=Comamonas testosteroni (strain CNB-2) GN=CtCNB1_0694 PE=4 SV=1MQDHATTPAATPDSARRVGIAAEFRSSPLGLLVQTSERPGVVAAETLLLPLLALLIGYVFSRNDPLWVRAEFP WSWLAPMIVALRYGPIGGLSAAGVLLLGWLGFNREDLSRFPEQYFLGGLMVVMIVGEISSLWRARIRRERTAQHY MDQRTEQLIRQHYLLRLSHDQLEQELIGRPVSMRDALSGLSALGGAPGDAQSLLNQLAQFCQISAACLVAVRDDRI EPQPIAQLGGAHEVRPEDPLLRQALEARMLTHVSQGLRDAQQTRYLVVAPMLDLGGEIYGLLLVEEMPFFALQEE TLQTINLLLGYYTDSVAANRLAQPLLQAYPLCPRPFASELQRMEHVNRSAGLCSVVVALELSPQAVQSQMAQQLM RLERMLDRSWLIEGRNRQWLAILMPLGTGATAEGYLNRIEGWLGQRGMDSLGAAGIFPRTVLLDRCSALSVLEQI DRMAHD	56~~DUF4118 (0.000000000008637)~~138	non-KdpD DUF4118 protein

	7E-18	74.1	8.5	1.6E-17	73	5.9	1.6	1	Q141I2_BURXL	Putative transmembrane protein	Bxe_A2972	Burkholderia xenovorans (strain LB400)	472	266265	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia xenovorans, Burkholderia xenovorans (strain LB400)	>tr|Q141I2|Q141I2_BURXL Putative transmembrane protein OS=Burkholderia xenovorans (strain LB400) GN=Bxe_A2972 PE=4 SV=1MAVNTAAVENNPGASKPRHAHPFGNLGRVRRFLAPAVARPFAIVETVVLVLVVLAVARWLHPEDPLLLRAGFPWLWLVSLLVALRYGSLLGLLSGAFILGAWALFYPHGGPFPTLYFAGGLIQTILAGHFGDTWGSRAQRASSLNDYLNDRLVALTNSHYLMRLSHERLEKDLLSRPTTLRDSITELRRLSVSSETALAVPAVAREGHPLGGASGLLEFVAQACQIEVAALYPVRDNKLDSEAIGRIGDPFELEVHDELVMHALNTLSVAHLKNEDTVVPVSQYLVCAPLVSADGELRALLVVKRMPFLSLNFDNLQLLLVLLGYYADGVEHSAFVQRILDSVPNCPYEFALDLSRLARLQQKAGVASSLVALAFPRDEEGDSLFEHVMRRRRSLDVMWPVQTAKQSVLVNLMPATDTTGIDGYLARIEASLTAQFNTDLERARVGVHTLHLEGDEPGAALMRLLKRSGLDV	42~~DUF4118 (0.000000000152757)~~137	non-KdpD DUF4118 protein
	8E-18	73.9	8.2	1.5E-17	73.1	5.7	1.4	1	Q0VR57_ALCBS	Uncharacterized protein	ABO_0893	Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2)	444	393595	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Alcanivorax, Alcanivorax borkumensis, Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2)	>tr|Q0VR57|Q0VR57_ALCBS Uncharacterized protein OS=Alcanivorax borkumensis (strain ATCC 700651 / DSM 11573 / NCIMB 13689 / SK2) GN=ABO_0893 PE=4 SV=1MLEHLSNGRLAGLFMPQPRVLWSMCEAIILTALAVGLGLWLRYDDPLTLIGTFRWVLLVPILLALRYGSLLGVFGMLCLVSSWFILRFFGFYPSLPFPESTMLGGFVIILICGEFADMWRVKLMRADSASSYALERLQNLTQRYVLLRLSHDRLEENLLVKPYTVRDALARLRELTLDESDSIRLPAADDLVHLLAEYCQLQRCALYRVVNGRIDDEPAALLGENGPLDRDNELLQHALDHRLLAHVQQQGHDSNYHGQYLVAAPIINSGGDLIGMMVIERLPFLSINYENLQLLSVLLNFYADIVHAGDEVDEMLDRWPTMPFRIASELAALVRLREGGRVDTSLTLFVADESEQAGLILDALARGLRSLDLAWWISDRVLMIMMPMTGESSLEGYVLRTEKWLQEEYVFMSLRQAGIQFFYRHLDQRDPEVQIARLLEAAGV	24~~DUF4118 (2.16567E-15)~~120;X;189~~GAF (0.00000000149921)~~298	non-KdpD DUF4118 protein
	1E-17	73.7	4.9	1.8E-17	72.9	3.4	1.4	1	A1TKZ9_ACIAC	Putative transmembrane protein	Aave_1040	Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	467	397945	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax citrulli (Acidovorax avenae subsp. citrulli), Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	>tr|A1TKZ9|A1TKZ9_ACIAC Putative transmembrane protein OS=Acidovorax citrulli (strain AAC00-1) GN=Aave_1040 PE=4 SV=1MPPEKSPPPSPGRRRAVGAAPASGRTGLRPLPQQLLGKLAATDTRPAIMLLETLLLPGLAIALGLLLHPQDPIWSEGDFPWAWLAPVIVALRYGPLAGLGGAVVLLAGWLLTNLGHYDRFPQLFFLGGLILVLIVGEFSSLWQARTRRAENVQLYLDQRLEHLVRQYYLLRLSHDRLEQELIGRPMSMRDALSTLQSVDTGAPEDAAQGAQTLLRLLAQYCQLESAALHAATEDRVEAEPVARIGSGSEPLDTQDPLVLQALETRKLCHISQLLTHKQQTRYLAVAPLLDLGGEIYGLLVIEDMPFFSLQDENLQTINLLLGYYTDGLAMQTLARPIMERLPDCPADFAFEARRLSHMRDTTGVPSIIVALEFLPRAVERGLPAQIERLKRELDESWLITGPERQVLAVLMPLGDTATAEGYINRLENWSRQKGGQPLAESGIFPHVLPLEGEPLAVLEQLHRIAHA	68~~DUF4118 (0.000000000027046 9)~~145;X;211~~GAF (0.0000000196105)~~323	non-KdpD DUF4118 protein
	1E-17	73.5	10.3	1.9E-17	72.7	7.1	1.4	1	Q7NXN0_CHRVO	Histidine kinase (EC 2.7.13.3)	kdpD CV_1596	Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	895	243365	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Chromobacterium group, Chromobacterium, Chromobacterium violaceum, Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	>tr|Q7NXN0|Q7NXN0_CHRVO Histidine kinase OS=Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757) GN=kdpD PE=4 SV=1MTDQRPDPDALLDELKREALEAQRGRLKIFFGACAGVGKTYAMLAAARVKRQEGVRVLVGVVETHGRKETAEQLEGLDILPLSRIEYKGRALSEFDIDAALAAKPQLILIDEFAHSNAPGSRHPKRWQDVEELLAAGIDVYTTLNVQHLESLNDVVGQITGIIVRETLPDHVFDMADEVSLVDLPPDELLSRLAAGKVYLPHQAERAVKNFFRKGNLLALRELALRRTADRVDAQMRAYRADQSIKPVWHARERLLVCVGPGPGTEKLVRSAKRLAANLDADWIAVYVETPRLQRLPEEQRARILKGLKLAQELGAETTVLGGSSLAATLLAYARTRNVSKLVVGKSNRGWAARLWEGSLVGELSRLSGDVDVYVVAHELEEEADQRGKRVPSLLFSDSESGHAARGYLAAAAICFATTELNHLLVPYFALSNVIMVHLLAVVLIATRYGRGPGVLASFLSVAAFDFFFVPPQLSFAVSDTQYLLTFGVMLVVALIISQLTARFRFEATIATYRERRTRALYDLGRELASALTASQIIETAVGRLEPLFRAKVMLFIPNSEDRLRAATETGNDADAGVAQWVFDNQQPAGLGTNTLPSNAALYVPLKAPMRVRGVIALLPEDAVHPFLPEQQRLLETCAAQIALALERVHYVEVAQDAIVAMESERLRNSVLSVVSHDLRTPLTTMLGLANMLNAPTLPPGRQSEIAQSIQDEAIRMTKLVTNLLDMAKLQSGVKLNKEWQLLDEVVGSAVRACEHSLRHHKLELKLSRDLPVLEYDAVLIERVLVNLLENAGKYTPAGSRIELEAARHDGDKVRITVTDDGPGLPASMEHRAFDKFTRGAPESTTPGVGLGLAICRAIIENHGGTIEAGNAQPHGARFSFTLPAGSPPELPPEDA	22~~KdpD (6.65683E-112)~~232;X;254~~Usp(2.71236E-45)~~377;X;414~~DUF4118 (2.0082E-24)~~505;X;536~~GAF (4.12424E-16)~~648;X;665~~HisKA (3.30403E-14)~~729;X;781~~HATPase_c (1.63047E-31)~~882	KdpD protein
	2E-17	73.1	9.1	2.7E-17	72.3	6.3	1.4	1	A0A0D5ELX2_9BURK	GAF domain protein	BW23_2721	Burkholderia ubonensis MSMB22	481	1249668	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	>tr|A0A0D5ELX2|A0A0D5ELX2_9BURK GAF domain protein OS=Burkholderia ubonensis MSMB22 GN=BW23_2721 PE=4 SV=1MAIDSKSTRLGAGMNAQADAPPRRPRPGLRARLLRRASAARFASLLPRDHAAAYVALETLVLFVAVFALCRVLSPADPLLIGKSFPWMWLLPLFVALRYGTVAGLGGGVLLGVAWGVFYARLPLADVFPRDFFVGGFITMLIAGQFSDTWAARLSQARVSNDYLSERLSVLTNNQYLLRLSHDQLEQDLLVRPSTLRDALARLREMMLHDAACAHAALPGAQRFLDTVAQACQIEAAQIHALHDGVPAAAPVAATGAPFDFDAGDPLVVAALDELALAHLQSLDARDRAHTRYYVACAPLIGAGDEVIGVLVVSQLPFLALTAENLQLMFVMGSYYANGVHHAAVTRDVLQAFPDCPYDFALEYARLADLQRTSGIASSVVRLQFGASRQAQAIFDHVERTNLDFHVQWVVRAGGTCALVFLMPLCDEAAVDAQLQRIETDVRNRFGLGFADARIVARWAPLAGAPSDRALRQILADRDDLA	57~~DUF4118 (0.00000000189987)~~153;X;222~~GAF (0.000000649592)~~341	non-KdpD DUF4118 protein
	2E-17	73	11.3	3E-17	72.1	7.8	1.5	1	Q1LFQ1_CUPMC	Uncharacterized protein	pelD Rmet_4158	Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	487	266264	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus metallidurans, Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	>tr|Q1LFQ1|Q1LFQ1_CUPMC Uncharacterized protein OS=Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) GN=pelD PE=4 SV=1MAKTVETRRQGQGIGLGGRYARWLAPAGGGAAAVIEMIVIMAAAMGITWLVLPQNPLLLGMGFPWAWLLPVILALRYGTLVGVGAVLMLLGGWFFFDEIGAHSGAFPRMFFMGGLLLVLVAGQFGDVWNTRLARARAVNRYLDERLAALTKNHYLLRISHARLENDLLARPTTLRDTLSQLRAVALQDAMNGGKSGPLAGAQPMLQVVAQACQVEGAALYACDGERVVPNAVASIGPAFEIDVNDPLVRHCLETRALAHLRSTGLQQDAQTRYVAVAPVLAGSDRLIGVLVVERMPFLSLTYENLQMLMVLMGYYADGVEHARATHGIQEMAPAIPYAFALDYARLSRLRHETGIQSSVVALVFDLDEARDALFEQVVRSRRALDVAWPVRNAHHRAMLTLMPLSDAQAVSAYLVRIEDMLRAQFGTDFSSAHIGVYTLSVPAEGAEEALMRLLHRCQLDGASTITAVQADGTRDASVASAGPARAG	35~~DUF4118 (1.18163E-14)~~131;X;204~~GAF (0.000000000000282873)~~321	non-KdpD DUF4118 protein

	2E-17	72.5	9.8	4.4E-17	71.6	6.8	1.5	1	B3EAM6_GEOLS	Putative transmembrane protein	Glov_3203	Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	437	398767	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter lovleyi, Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	>tr|B3EAM6|B3EAM6_GEOLS Putative transmembrane protein OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) GN=Glov_3203 PE=4 SV=1MSVLNGITSRFPQLSQWLETLVLTLLVPLLGCLLSKDDPFFVQSAFPWLWFGPLLVALRYGIAPALSSVSFLAVLWFALSLAGLLKGAFPLHFMLGGALLSLIAGQFSSVWTTRLRRSDQLSRHASERFQQLSRAYFMVRHSHDRLEQNLVSRPVTLRQAMMELRRLLVERGGEVSNELAGELMVILAHYCSLSSAAIYAVRRGVPDPVPLAQCGQGASYRPDDLLLRSALESGTTAYQAASRLGDGQHSSYLVAAPLRTSSGRMLGVLLVSDMPFMALHRETLQILGVLLAYAADHVEAATIAKRLIAVYPDCPTVFGAELVKMTRLRRDLDIVSTVVVINLQPGPRLDELCQVLERQQRGLDHGWRRDLGWCVQFVTLMPFTGPAALEGYQARLNEVLRKQFGMTLQSVGITIKYAVLSGDEPLIQLANLLTEDV	23~~DUF4118 (0.000000176377)~~114;X;177~~GAF (0.0000000337851)~~299	non-KdpD DUF4118 protein
	3E-17	72.4	7.2	4.3E-17	71.6	5	1.4	1	Q2Y890_NITMU	Uncharacterized protein	Nmul_A1734	Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849)	423	323848	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosospira, Nitrosospira multiformis, Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849)	>tr|Q2Y890|Q2Y890_NITMU Uncharacterized protein OS=Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849) GN=Nmul_A1734 PE=4 SV=1MKKPWLEGIEVVDVNTPVSAWGGWFETFVITAVVIAASFITQQADPFRLSGGFPWAVLAPLLAGLRYGFVFGFVSALLTLAVLGVAIDQQWQAAKSFPLPWAIGVVVVAMVAGEFRDMWGRRLHRLEGAYQYRAERLEEFTRSYQLLRLSHDRLEQTVANSGFSLREGIMHLQSTLDAIDGMTESSLQKLIEFVAEYGALTQACIIGITADRIDTSNVLACVGERFPIDVTDPVLRMALDSGELATLNLLQESEMDQAQLLAVVPLTDSVGEINAVLAVRSMPFFSFHESNLKLIAVLVAHGVDHLRFGTARPSVRRFIASFERAYQDFSRFKLDTVLLRLSGNPEEVRSVHEKLRFSIRAIDFICLAREKDQYVVWAMLPLTDITGARAWAQRVADIPATTAQEWMSINEIDPQRIRSLEQG	24~~DUF4118 (0.000000000573763)~~83	non-KdpD DUF4118 protein
	4E-17	71.9	6	5.9E-17	71.2	4.2	1.4	1	D8IUI2_HERSS	Transmembrane protein	Hsero_4245	Herbaspirillum seropedicae (strain SmR1)	491	757424	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herbaspirillum, Herbaspirillum seropedicae, Herbaspirillum seropedicae (strain SmR1)	>tr|D8IUI2|D8IUI2_HERSS Transmembrane protein OS=Herbaspirillum seropedicae (strain SmR1) GN=Hsero_4245 PE=4 SV=1MSDTPRQGRGAGPQRPWAAGMSTALTAGQKRQKFWSRFFTRFDTDSGSPRKAVLRIIETVALVLAALLFAHHWVAPEDPMGIRAQFPWLWLVPAILAMRYGSTLGVVAVATMMAGWYLLVHGHQASEADAVAAAAQAFPQSYFLGGLVLTLLCGQFAEVWNARSRRLRAINAYLDERLTMLTKNHFLLRLSHERLEQDLLSKPLTLRESLDRMRALTLTQILLDPSRMPAPDAFLQILAQSCQVASAAVYVCDAAGHITPEPAASVGKVSELAADDALVRYCLAQRKLGHIQTESLNQNLRNQSRYLVCAPLLNFDGRLFGLLVVEQLPFVALNEDTLQLMSVLIDYYADGIEVGGTARSILQQLPTCPPELAVDVVRLHRLKRSTDIDSSLVALVFGDDEISRDMFDQIRRLKRAADVVWTYKAGGRNVLMTLLPLAGAAAVDGYLMRVEAASQAQFGAKSLANYAAIHTAAIGGDEPSRLLPNLVERCAA	55~~DUF4118 (0.00000141204)~~162;X;231~~GAF (0.0000000628043)~~352	non-KdpD DUF4118 protein
	4E-17	71.8	6.1	8.7E-17	70.7	4.2	1.6	1	B2JCL5_BURP8	Putative transmembrane protein	Bphy_1835	Burkholderia phymatum (strain DSM 17167 / STM815)	471	391038	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia phymatum, Burkholderia phymatum (strain DSM 17167 / STM815)	>tr|B2JCL5|B2JCL5_BURP8 Putative transmembrane protein OS=Burkholderia phymatum (strain DSM 17167 / STM815) GN=Bphy_1835 PE=4 SV=1MNTVTAQSAVSAAKPRQSNPFGNLGAWRRLVAPAVSRPFSIVETIVFVGVVFAVCYGLDRDDPFLLHAGFPWLWFAPLVVALRYGTLLGLLGCAMLVGSYQVLTQLLHQGGAAAWPTLFFTGGVLQTIVAGHFGDTWGSRAQRANAINDYLNDRLVAITNSHYLMRLSHERLEKDLLTKPTTLRDSITELRRISVAHGLDTATHRSSDIPGARELLEFVAQACQLEMAALYPVHDDKVGRQALARVGDTFDFDPRDDLVQRALETRAVAHLKSEDRPVANTRLLVCAPLISADGRMLAMLAIRRMPFLSLNFDNLQLLLVLLGYYADGVEHSQQVRDILEAVPDCPYEFALDVGRLTRLERSAGITSSLVALVFPHDDAGDSFFEHVMRRRRALDLMWPVKAAGRSVLLNLMPATDATGVDGYLARIESSLRSQFNLDLEGARIGVHTLHLGGDEPGPALKRLLMRSGLDG	41~~DUF4118 (6.93344E-14)~~140;X;213~~GAF (0.00000191193)~~311	non-KdpD DUF4118 protein
	5E-17	71.4	6.4	1.3E-16	70.1	4.4	1.7	1	B1Y565_LEPCP	Putative transmembrane protein	Lcho_0019	Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) (Leptothrix discophora (strain SP-6))	461	395495	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Leptothrix, Leptothrix cholodnii, Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) (Leptothrix discophora (strain SP-6))	>tr|B1Y565|B1Y565_LEPCP Putative transmembrane protein OS=Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) GN=Lcho_0019 PE=4 SV=1MTVASLRTLWQRAVPVMREALLARNAEGERPFWMLGEVPVLTLVVLVGGLLVSPQDPLFTHASVPWSWVAPVLLALRYGVLSGLASMALLLAAWALLMPAAEPLPAQVFIGGLLLTMVCGEFSGSWRGRVDRLAEANSYLEDRIERVTGRLFTVQRSHDLLQQELLQRPTTLRHSLDGLERRALVAEQSVATAAQAFLDHLAASCQLEDAQVIAYDEQAGRPGAVLAQLGEATAVEFDDPLVQYALSREGLAHVQVGLPDGPLSTRYLVVAPLRIGRQQLPALLVVARMPFLALHDETLQMIAVLCSAFSSAAQVSEAVAAVLAQVGHCPLRLAEELGRLDRIAREHAIVSQLVLLRFDDPARSEEQVNMAQRRARAPDVNWAFADEAGRHRLLTLMPLASAAAVEGYLARFTEMVVGRYRAEVAAPSLAGLNIGVRVLTLGGERPLGEALRLLIADEETT	53~~DUF4118 (0.0000898588)~~129;X;189~~GAF (0.0000375181)~~312	non-KdpD DUF4118 protein
	7E-17	71	9.6	1.1E-16	70.3	6.7	1.4	1	Q47H45_DECAR	Histidine kinase (EC 2.7.13.3)	Daro_1080	Dechloromonas aromatica (strain RCB)	902	159087	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Dechloromonas, Dechloromonas aromatica, Dechloromonas aromatica (strain RCB)	>tr|Q47H45|Q47H45_DECAR Histidine kinase OS=Dechloromonas aromatica (strain RCB) GN=Daro_1080 PE=4 SV=1MADQRPDPDQLLNRVNAEEARSKRGKLKIFFGASAGVGKTYAMLGAARQQLLAGVDVVIGIVETHGRMETEVMADGLEYLPLRDIPYRDRLLKEFDLDGALARKPQLILMDELAHSNVAGSRHAKRWQDIEELLAAGIDVYSTVNVQHLESLNDVVSGITGIRVWETVPDKVFDAADEIVLVDLPPDELLQRLQAGKVYLPNQAERAIRNFFRKGNLIALRELALRRTADRVDDQMLQYRRDQLVSPVWQTRDSLLACIGTGAGGEKIVRTTARVANRLEAPWHAIYIETPALQRLSENSRHRILRNLKLAEELGAQTATLSGNDAEGVAVKYARDHNLSKIFVGRDHPRPWRPWYRSFADRLGQRAPDLDVLQVARADIDREPGQAARESIGDSIFDQWPAYAKAAAGCALAGVAAAALFPIVDLPNIVMVFLLAVVLVSVRYGRGPGVLASFLSVAIFDFFYVPPRFSFAVSDVQYLMTFAVMLAVGLITGQLTAGSKYQAKVATRREQRVRSLYEMSRDLSAALMPDQITEIGERFIVAELGAKAAFLLTDDNDRLQPALPSANGLPAVDMGIAQWAFDHAEAAGQGTNTLAASPILYLPLKAPMRQRGVLALEMRDTDRLLIPEQRRLLDTFASLIAIALERVHYVEVAQNTTVQMESERLRNSVLSAISHDLRTPMSVLVGLADSMFLTQPPPTQPQAEIAHSLKEEALRVSSQVNNLLDMAKLQSGRVELNRQWQPLEEVVVSALKTLERAFAEHQISVSLDENLPLVNIDSVLMERVIYNLLENTVKYTPPGSLVEIGANVTERMIEVWVEDNGPGLPEGKEEIIFKKFERGQPESATRGVGLGLAICRAIVEAHGGEIYAVNRPQGGARFMFTLPRGNPPSLDAEEMPADEEAH	22~~KdpD (3.89419E126)~~232;X;255~~Usp(5.81856E-42)~~376;X;428~~DUF4118 (3.68437E-22)~~502;X;529~~GAF (4.1625E-19)~~646;X;663~~HisKA (0.0000000019614)~~728;X;781~~HATPase_c (1.23747E-27)~~882	KdpD protein

	1E-16	70.4	6	1.7E-16	69.7	4.2	1.3	1	D5WZ66_THIK1	Uncharacterized protein	Tint_1010	Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	491	75379	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Thiomonas, Thiomonas intermedia (Thiobacillus intermedius), Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	>tr|D5WZ66|D5WZ66_THIK1 Uncharacterized protein OS=Thiomonas intermedia (strain K12) GN=Tint_1010 PE=4 SV=1MKLDNLSTRVSRRMRSESARMRWQWLRYWRPNTQSGRLMAMFEAVLLPVLVLWLGAKLRPDDPLGAHAGFPWAWFGPWLIAVRYGAGYGLFGVGFYAAFWKFSPTLFHSAPAVEFPAEFFLGGMLMTLILGEFGAAFRNRQVLHREVTKDLTARLERTKRRLFVIKEALSTLEQELTDRPMTLRDALLDLRRTFTFQGNRPALAAPAATPGLPTPAPLPDPRAFLQLLSQSCRLVEAGIFVREIGPLGLQWRLAASLGQTLPPLDPGEVLINRILETHQSVHIAQAHLNETDGSNPWVFAAPLRLDEYDEVDALLAVHTMPFMSFEENNLQRLQVLCASYLDFSQLELSVEDVRSAWVQAPISLQQEWAQLSELGQNFKLRSYCAVWSGQGRVSDDALAEFAGLQPVESSTWTLKGRGGKPALIVLLPLLSSGGLANYRRDMASQLVQILSRSNQRPDQAFDLDFLEVSGAPSFLELRRLLSSAAAETKTS	58~~DUF4118 (0.00000000002445)~~140	non-KdpD DUF4118 protein
	2E-16	69.9	5.9	2.6E-16	69.1	4.1	1.4	1	R5Z8R2_9ACTN	Uncharacterized protein	BN511_01294	Collinsella sp. CAG:166	422	1262850	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Coriobacteriales, Coriobacteriaceae, Collinsella, environmental samples, Collinsella sp. CAG:166	>tr|R5Z8R2|R5Z8R2_9ACTN Uncharacterized protein OS=Collinsella sp. CAG:166 GN=BN511_01294 PE=4 SV=1MRTLSIKCLETGVAWVLFEVLEHLFSQSAQLNVLDYRLLYVVLIGTLYGLDFGLVAALLASVGLAASYFTQYGYTFQGLFYEPSNWLPFIAYFVVGAVCGYVQLRNSEAIRAERDQNELVRNRNTFLTQLYHDAIEDKRAYRRQIVGRHDSFGKIFAVTQELDVLNPRDIYRKCCELLGEILENDSVAIYHVSGGAFARLVAASPAIAEDAARSLTLEQLAPLLGDGGRSNLWVNRELTPGLPMFGYTIERDGAPAVLIFVRSAAENQMTLYYQNLLRILCGLVESALGRAFDYEAVAQDKRCVDGTCVLKQAAFGQELATAQALADSKMGSFLLLRVVPGMEPVGELVGAIGSAIRESDAAGLVDGDVLYLLMRQAKACDLPIIRERLSAKHIAVEPVDGEDIVELLQHISYTGDGEGGAA	7~~DUF4118 (1.03775E-18)~~109;X;166~~GAF (0.000000000012536 1)~~290	non-KdpD DUF4118 protein
	2E-16	69.7	10.8	3.8E-16	68.6	7.5	1.6	1	Q8XX45_RALSO	Probable polysaccharide transport system component transmembrane protein	ragD RSc2273	Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	483	267608	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia solanacearum (Pseudomonas solanacearum), Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	>tr|Q8XX45|Q8XX45_RALSO Probable polysaccharide transport system component transmembrane protein OS=Ralstonia solanacearum (strain GMI1000) GN=ragD PE=4 SV=1MGADTVQADPSTKARPAAAASDARQQDRRRNAQGIGASTWYGRLVAPTLTRRTPILETIGATMVAIGIVWLFEPNNPLLLGYGFPWIWLVPLILALRYGTLLGAVAALVVVGAWWVFYGQGTFPRMYFLGGLMMMLVGGQYGDIWGARLSRARIVNGYLNDRLAALTKNHFLLRLSHERLENDLLAKPTTLRDTLTQLRSLALAAREHASGDDAPDVAQLPGATQFLQWAAQACQLEVAAMVRVTGNRVDPEPVARVGAAFEVVADDPLIRHCIDTHTLGHPQAPELRQEDGSRYVACAPILSGADELIGVVVVQQMPFLSLSYENLQFLLVLLGYYADGVRHLTVSSEILDLVPDAPYEFALDLGRLARLHRDTGIDSSVVALTFGNDEASDALFEHVVRSRRALDVVWQMRGSACRAIVTLMPLSGAGAVSAYLVRIEDSLRAQFGVDFEAAQVNVQTLYVTGEHPGEALARFIGRCHLDG	54~~DUF4118 (0.000000000775442)~~148;X;230~~GAF (0.00000139401)~~343	non-KdpD DUF4118 protein
	2E-16	69.6	12.6	3.2E-16	68.8	8.7	1.4	1	A0A0F3K4W7_9NEIS	Sensor protein KdpD	VI06_17085	Aquitalea magnusonii	898	332411	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Aquitalea, Aquitalea magnusonii	>tr|A0A0F3K4W7|A0A0F3K4W7_9NEIS Sensor protein KdpD OS=Aquitalea magnusonii GN=VI06_17085 PE=4 SV=1MTDTRPDPDALLDAIKQDELAAQRGRLKIFFGACAGVGKTFAMLSAARVRQQEGCKVLVGVVETHGRKETEAQLHGLEVLPLTQIEYKGRSLAEFDLDSALARQPQLILMDEFAHSNVPGSRHSKRWQDVEELLAAGIDVYTTLNVQHLESLNDVVGQITGIVVRETLPDHVFDQAAEVALVDLPPDELLARLAAGKVYLAHQAERAVKNFFRKGNLLALRELALRRTADRVDAQMRAYRADQSIKPVWHARERLLICVGHGPGTEKLVRSGKRLAASLDADWIAVFVETPELQRLSESKRSRIMKGLKLAQELGAETTVLGGSDLAATLLAYARTRNVSKLVVGKSSVRKLQRLWRRPLLEQLSRQANDVDVYVVAHELEDGQPQQNDGFNSLLFGEASRQQQRHGYVAALLSCLLTTGLASLLTPFFELSNVVMVYLLAVVLVAVRFGRGPGVLASFLAVATFDFFFVPPRMSFSVSDTQYLLTFAVMFAVALIISQLAARLRFEANIATYRERRTRALYELGRELAAALTANQIIDIAVSRLQPLFNASIVLLTPNSQEQLRAENDSTAQADLGVAQWVYDKQQAAGLGTQTLPSNAMLYLPLKAPMRNRGVLAVLPEQLDQVFLPEQQRLLETCAAQIALALERVHYVEVAQDAIVAMESERLRNSVLSVISHDLRTPLTTLVGLSSLLAEGQVDARKQASIAQSIQEESLRMNHLVTNLLDMARLQSGVKLNKAWQLLDDVVGSALRACQRNLQGHQLEVALASDLPVLEYDAVLIERVLVNLLENAAKYTPPGSHITLLAQPEGATIRVCVQDDGPGLPSGLEQKLFDKFSRGNSESTTPGVGLGLAICRSIVEAHGGQITASNRQPHGAAFCFTLPVSQMPALPGDEEIQP	22~~KdpD (5.96218E111)~~232;X;254~~Usp(4.79538E-42)~~377;X;408~~DUF4118 (5.47561E-25)~~505;X;535~~GAF (2.80587E-14)~~648;X;665~~HisKA (0.000000000000935642)~~729;X;781~~HATPase_c (2.10795E-30)~~882	KdpD protein
	2E-16	69.5	10.4	4E-16	68.5	7.2	1.5	1	A0A0C4YFY0_9BURK	Extracellular Matrix protein PelD	RR42_s0242	Cupriavidus basilensis	481	68895	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus basilensis	>tr|A0A0C4YFY0|A0A0C4YFY0_9BURK Extracellular Matrix protein PelD OS=Cupriavidus basilensis GN=RR42_s0242 PE=4 SV=1MIVANTADKIREGQGIGAGGRYLRLLAPATSGPVSAVELVVTMALAMGLGYLLLPNNPLLLGLGFPWAWLLPVILALRYGTLIGVGSVLMMLGGWFFFHQIGAQPGAFPRLFFLGGLLMVLVAGQFGDVWGTRLARARAVNRYLEERLAALTKNHYLLRVSHARLENDLLAKPTTLRDTLSQMRAVTLEDAAQGGVLVGARPMLQVVAQACQLEAAALYAVDGETVSATASAQIGPAFEFDPDDVLVRHCLETRQLAHLQADGLSRQSPDHPQTRYVAVAPVLSGADKLVGLLVVERMPFLSLSYENLQLLMVLMGYYADGIEHAASTRAIAAAIPGCPYEFALDYARLSRLRRDTGIDSTIVALVFDLDESRDALFNQVIRSRRALDVAWPLTSAHQRALLTLMPLSGNEAASAYLVRIEDMLRAQFGTDFEAARIGVHTLAVPASAPVEPLIRLLHRCHVDVQPAPVPVPVALGEVGRG	37~~DUF4118 (0.000000000903175)~~133;X;203~~GAF (0.000000000271126)~~324	non-KdpD DUF4118 protein
	3E-16	68.8	11.9	3.2E-16	68.8	8.3	1.6	1	B2U9G9_RALPJ	Putative transmembrane protein	Rpic_2471	Ralstonia pickettii (strain 12J)	491	402626	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia pickettii (Burkholderia pickettii), Ralstonia pickettii (strain 12J)	>tr|B2U9G9|B2U9G9_RALPJ Putative transmembrane protein OS=Ralstonia pickettii (strain 12J) GN=Rpic_2471 PE=4 SV=1MKTESTGSAQSAGRAAADARAQGGRTERRRNAQGIGASTGYGRLIAPAVSSPSAALETLGAVVAAIGIVWLFAPDNPLLLGYGFPWIWLVPLILALRYGTLLGALAALVVLGAWAVFYGQTAAAGSFPRMYFLGGLMLVLIGGQYGDIWGARLSRARTVNGYLNDRLAALTKNHFLLRLSHERLENDLLAKPTTLRDTLTQLRNIALAAREHGTAENAPDVAQLPGAEPFLQWTAQACQLEVAAMVRVTGNRIDTEPVARVGTPFDIVADDPLIRHCIDTHTLGHPQAPELRNVNNPEESSRYVACAPVLSGADELIGLVVVHQMPFLSLSYENLQFLLVLLGYYADGVRHLTVSSEILDLVPDAPYEFALDLGRLARLHRDTGIDSSVVALIFDQEEASDALFESVVRSRRALDVVWQASGKGRRAIITLMPLSGAGAVSAYLVRIEDSLRAQFGVDFEGGHISVQTLHVTGEHPGEALQRFLSRCHLDA	56~~DUF4118 (2.35093E-14)~~152;X;235~~GAF (0.000279664)~~351	non-KdpD DUF4118 protein

	4E-16	68.5	5	4E-16	68.5	3.5	1.6	1	Q3IF82_PSEHT	Uncharacterized protein	PSHAa0706	Pseudoalteromonas haloplanktis (strain TAC 125)	433	326442	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas haloplanktis (Alteromonas haloplanktis), Pseudoalteromonas haloplanktis (strain TAC 125)	>tr|Q3IF82|Q3IF82_PSEHT Uncharacterized protein OS=Pseudoalteromonas haloplanktis (strain TAC 125) GN=PSHAa0706 PE=4 SV=1MKTHFFRPREVPELQIWAEVFIFTALALGLPVLFNTADPFWTQGGFSWPVLGPLLVALRYGFSKGFISILSLLIGQLLLVETDILTPQSDFNINAILGYVIVIMVTGEFRDVWDRTNQRQTIQLEYVTERLEVFTRQYHLISSSHDRLEQVLAGHTLSLRESLQAVRESIGQLEERCLDKAAQSILNLFVEYGTLEKAGIYKVENNIIVDPPLAAIGKMNTVSMSDPLVSAMFAENELVSVKDVKASLGVSQYHIAIPITDISDTVYGVILVEKVQFFALKNTTLTLLAVMAGHIGDLLRHEITNPVMQANEAPYFIKQVKRANKEAKRYKIPSHLLKITATNINPESRQLMKYLSEARRGLDIYLYNNEKQTLLLLMPLADELEKTGFIARLNSWSKGRTGKNLTDLGIVIEQQIALPINNDDLKRLVAFHD	17~~DUF4118 (0.000000000000566105)~~115;X;178~~GAF (0.0000000641776)~~301	non-KdpD DUF4118 protein
	5E-16	68.3	8.3	2.5E-15	66	6.6	1.6	1	A0A0C1Q9F8_9ACTN	Histidine kinase (Fragment)	LK07_36815	Streptomyces pluripotens	606	1355015	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pluripotens	>tr|A0A0C1Q9F8|A0A0C1Q9F8_9ACTN Histidine kinase (Fragment) OS=Streptomyces pluripotens GN=LK07_36815 PE=4 SV=1MPADQRPNPDQLLAELQSGKEQSARGKLRIYFGASAGVGKTYAMLAAAKAARAAGIDAIIGLVETHGRAETAALVADLEHLPTRQIEYKGRTLPEFDLDAALARKPALILVDELAHSNVAGSRHPKRWQDIEDLLAAGIDVWTTVNVQHLDSLNEAVGSITGIRVWETVPDAVFDAANEVILVDLPADELLRRLAEGKVYMPEQAQHAARNFFRKGNLIALRELARRTADRVDDDVQAYRRARRIENVWRTRETVVACLDPQGDGEQVIRSAARLAAQLECDWHAVAVVMPHLRAADARTERLHALLKLAEDAGAKVETLAGTNAVEAITGYIRRHNITKAVIGRPPEKRWRSARAVVVALRLAIGLERRLPSGDFAEALARHCPEVDVIRAAADPAHIQLQPRAAEVGRADVRSEAQRAADAQAGWLKPAYVAACVYVGVATALSSLVRPVFDLANIVMLFLAAVVAVAMRHGRGPAALASVLSVALFDFFFVPPRFSFAVSDVQYLLTFGVMLAVGMLVGQLTAGLREQAEVAVQREAAAHALYEAARELSAALTLDQIVSIGGRFVNATFGGRCAFFFVGLDGRLGAPQVAKPEGSTDAPSG	KdpD protein
	5E-16	68.2	12.5	7.7E-16	67.6	8.7	1.3	1	A0A0C1SU15_9ACTN	Sugar ABC transporter (Fragment)	LK07_47720	Streptomyces pluripotens	204	1355015	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pluripotens	>tr|A0A0C1SU15|A0A0C1SU15_9ACTN Sugar ABC transporter (Fragment) OS=Streptomyces pluripotens GN=LK07_47720 PE=4 SV=1MKTESASSAQSAGRPGADARAQGGRNERRRNAQGIGASTWYGRLIAPAVSSPSAVLETLGAAVAAIGIVWLFVPDNPLLLGYGFPWMWLVPLILALRYGTLLGALAALVVLGAWAVFYGQTAAAASFPRMYFLGGLMLVLIGGQYGDIWGARLSRARTVNGYLNDRLAALTKNHFLLRLSHERLENDLLAKPTTLRDTLTQLRN	54~~DUF4118 (0.000000000000397702)~~152	non-KdpD DUF4118 protein
	5E-16	68.1	5.3	5.4E-16	68.1	3.7	1.6	1	A1W439_ACISJ	Putative transmembrane protein	Ajs_0770	Acidovorax sp. (strain JS42)	464	232721	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax sp. (strain JS42)	>tr|A1W439|A1W439_ACISJ Putative transmembrane protein OS=Acidovorax sp. (strain JS42) GN=Ajs_0770 PE=4 SV=1MPTPSDSPGARRQTAGENARPRALPGTGLPRHLLGRLAIAATHPAVTVGETLLLPLLAVALGLAWAPQDPLQIQATFPWPWLAPVVLALRYGPMAGLGGASVLLACWLGLNAGHWGNFPQLYFLGGLILVMLVGEFSSLWQARTRRAETLQLYLDQRLEHLVRQHYLLRLSHDRLEQELIARPMSMRDALAALRHAGSEDGGDALAPQALLRLLSQYCQLECAAMHAVSDGHAAARPSASIGAYDGLHADDPLVRQALQTGQLCHVSQAVTAQQDTRYLVAAPLLDLAGDMYGLLVVQDMPFFALQEESLQTIQLLLGYYTDGLSMSQLAQPIVQQFPDCPPLFAFELQRLAHIHRSTQVPSIVVALELQQRALEQDLPPQIERLKRELDEVWRIEAPGRQVLAVLMPLGNATTAEGYIHRLEGWMQHKSQQSLAQAGIFPHVVQPDSAQPVRTVQRLHAIAHA	67~~DUF4118 (0.00000000200775)~~~143;X;208~~GAF (0.000000883885)~~319	non-KdpD DUF4118 protein
	5E-16	68.1	5.3	5.4E-16	68.1	3.7	1.6	1	F4G7V1_ALIDK	Putative transmembrane protein	Alide2_0841	Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	464	596154	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Alicycliphilus, Alicycliphilus denitrificans, Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	>tr|F4G7V1|F4G7V1_ALIDK Putative transmembrane protein OS=Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601) GN=Alide2_0841 PE=4 SV=1MPTPSDSPGARRQTAGENARPRALPGTGLPRHLLGRLAIAATHPAVTVGETLLLPLLAVALGLAWAPQDPLQIQATFPWPWLAPVVLALRYGPMAGLGGASVLLACWLGLNAGHWGNFPQLYFLGGLILVMLVGEFSSLWQARTRRAETLQLYLDQRLEHLVRQHYLLRLSHDRLEQELIARPMSMRDALAALRHAGSEDGGDALAPQALLRLLSQYCQLECAAMHAVSDGHAAARPSASIGAYDGLHADDPLVRQALQTGQLCHVSQAVTAQQDTRYLVAAPLLDLAGDMYGLLVVQDMPFFALQEESLQTIQLLLGYYTDGLSMSQLAQPIVQQFPDCPPLFAFELQRLAHIHRSTQVPSIVVALELQQRALEQDLPPQIERLKRELDEVWRIEAPGRQVLAVLMPLGNATTAEGYIHRLEGWMQHKSQQSLAQAGIFPHVVQPDSAQPVRTVQRLHAIAHA	67~~DUF4118 (0.00000000200775)~~~143;X;208~~GAF (0.000000883885)~~319	non-KdpD DUF4118 protein
	6E-16	68	4.9	1.4E-15	66.8	3.4	1.6	1	C5ACV3_BURGB	Putative transmembrane protein	bglu_1g30050	Burkholderia glumae (strain BGR1)	469	626418	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia glumae (Pseudomonas glumae), Burkholderia glumae (strain BGR1)	>tr|C5ACV3|C5ACV3_BURGB Putative transmembrane protein OS=Burkholderia glumae (strain BGR1) GN=bglu_1g30050 PE=4 SV=1MNSVAMQSAADASKTRSSNALGRLGPMRRFIAPAVTRPFAIVEAVAFVMLALAVSRLCSPHDPLLLQAGFPWLWFPPMIVALRYGTLLGLLGGALMVAAWKLGYPPGAPWPVMMFVGGLTQTVIAGHFGDTWGHRARRASTLNDYLNERLVAITNSHYLMRLSHERLEKDLLSKPTTLRDSITELRRLSVGAEPQDGPGAPAPLRALPSAAGMLEFVAQVCQIEIGAVFPVLDGRPATEAVACVGDAFPLCTSDELVVHALRTRSVAHLRGEHADLAQSAYLVCAPLVSADGEVIALLAVPRMPFLALNFDNLQLLLVLLAYYADGVEHASVVRDILADVPGCPYDFALDLGRLARLNRDAGIASSLVALAFPRSEAGDSLFEHVLRRRRALDLMWPLQTASHSVLVNLMPATDTTGVDGYLARIETSLDSQFGLDMERAHIGVHTLHLGPLEPGAALRRLLKRSGVDV	40~~DUF4118 (0.0000503483)~~135;X;213~~GAF (0.0000477991)~~309	non-KdpD DUF4118 protein

	7E-16	67.8	6.3	1.2E-15	67	4.4	1.4	1	D0IYP3_COMT2	Histidine kinase (EC 2.7.13.3)	CtCNB1_0533	Comamonas testosteroni (strain CNB-2)	897	688245	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Comamonas, Comamonas testosteroni (Pseudomonas testosteroni), Comamonas testosteroni CNB-1, Comamonas testosteroni (strain CNB-2)	>tr|D0IYP3|D0IYP3_COMT2 Histidine kinase OS=Comamonas testosteroni (strain CNB-2) GN=CtCNB1_0533 PE=4 SV=1MPSSTPSSAAQRPDPDALVAQLQADRQRAHLGKLRIYFGSNAGVGKTYSMLAAAQRERQAGRKVLVGLVETHGRAETEQQLHDLELLPRRTLVYQGRQLDEFDLDAALARRPEVLLLDELAHSNVSGSRHPKRWQDVQELLEAGIEVWTTLNVQHLESLNDVVGGIVGIQVHETVPDHIFDDADEVIVVDIPPEELLKRLKSGKVYPLEQAERASRNFFRQGNLLALRELALRRTADRVDEDMRDYRRERSIGDVWPTRERLLVGVGGRAGDDALVRQVARLARRLEADWVVVYVDAPERQHRPRAAQEAVLKTLALAARLGAETATIPGAHVAQALVDFARERNASHLVLARVHEPLSRWLRWRASSLSEQIAALDPGLDVLLLSVKQSKNESTLRLPAAREKTIPWKGYAGVTLACLAATAVAELLLRVFDPANVVMLFLLVVVLSAVRWGRGPGAWAALLSVLLFDFYFVPPRNSFSVNDTQYLFTFSLMLGVALVCGQLTARLRHEARVAAERERRAGALARLARDLSGALTQEQVTQIALTTISGVFDAQTGLLVPDADERLQLAPGSEAQIDTSVGRWSMEHGQMAGHGTDTLAAAPALYVPLMAPVRSRGVLVLQLRAPQRLRVPEERRLLEACASQIALALERVHFVEVAQQTQIAMEGERMRNTLLSAVSHDLRTPLTGILGAAQAALPHAPQGPAHHMLVQIRNQAQALQQLVDNLLAMARLQQGGVQLKREWLPVDELVGSALAQMRERLAAHALQTSLPADLPLLQLDAVLMERVLVNLLDNAIKYTPEGTTITVAASVADGDCVLSVQDAGPGLPVHLSAEQLFEPFTRGQAESAVFGMGLGLALAQRIVQAHGGRLRVAQADPGPGTIFSVHLPVPEQPAMDE	29~~KdpD (3.23472E-102)~~239;X;261~~Usp(2.20231E-29)~~386;X;416~~DUF4118 (0.000000000001227 31)~~508;X;536~~GAF (2.38775E-14)~~651;X;668~~HisKA (0.000000000030076 7)~~731;X;784~~HATPase_c (3.13309E-27)~~887	KdpD protein
	9E-16	67.4	5	1.5E-15	66.7	3.5	1.3	1	A9C186_DELAS	Histidine kinase (EC 2.7.13.3)	Daci_5921	Delftia acidovorans (strain DSM 14801 / SPH-1)	904	398578	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Delftia, Delftia acidovorans (Pseudomonas acidovorans) (Comamonas acidovorans), Delftia acidovorans (strain DSM 14801 / SPH-1)	>tr|A9C186|A9C186_DELAS Histidine kinase OS=Delftia acidovorans (strain DSM 14801 / SPH-1) GN=Daci_5921 PE=4 SV=1MPISSSAEPAPPGMPRPDPDALVARLRHERAQEGRGKLRIYFGSNAGVGKTYAMLAAAQRERQGGREVLVGLVETHGRKETAQQLHGLEQLPLRELPHQGRTLREFDLDAALARHPRVLLLDELAHSNAPGSRHPKRWQDVQELLDAGIDVWTTINVQHLESLNDVVGGIVGITVRETVPDQIFDDADEVIVVDISPDELLRRLKDGKVYMLEQAERASRNFFRRGNLLALRELALRRTADRVDEDMRDYRRERSIGTVWPARERLLVAVAGRAGDDALVRQVARMARRLDADWMVVYVDAPQRQHRPRSVQAAVLKTLALAARLGAETATLPGADVAEALVAFARERNASRLVLAQPPRPAWSPWRWWTRSLPDRITHLHPDIDVLVLSGGSSAARTEAAPAATSALPRRAPLPWKGYAGVTLACLAATALAEQLLRVFDPANVVMLFLIVVLSSLRWGRGPGAWAALLSVLCFDYFFVPPRGSFHVNDTQYLFTFVLMLGVALVCGQLMARLRHEARVAAERERRAGALARLARDLSGALTQEQVVEIALRTVSGVFDAQAGLLLPDADERLRPAGGGPCAMDDSIARWAMDHGQQAGQGTDTLPAAPARYVPLAAPVRMRGVLVLQLRAPQRLEVPEEQRLLEACASQVALALERQHFVAVAQQTQIAMEGERMRNTLLSAVSHDLRTPLTTILGAAEAAQRHVPPGGAADMLEQVRIQAQAMQRLVENLLDMARLQQGGVHLQREWLPLDEVVGSALRQMRARLGQHLVSTDVPASLPLLQLDALLMERVLVNLLDNAAKYTPAGTPLAISARVQDGELLLSVRDGGPGLPSHLPVETLFEPFTRGTAESTVSGIGLGLALVRSIVEAHGGRIEAAAARPGPGTIFTLRFPVPEQPALD	33~~KdpD (2.55703E-107)~~243;X;265~~Usp(7.56805E-32)~~390;X;436~~DUF4118 (4.84071E-20)~~516;X;544~~GAF (7.8336E-17)~~659;X;676~~HisKA (0.000000000000198015)~~739;X;792~~HATPase_c (1.21452E-26)~~895	KdpD protein
	1E-15	67.3	6.4	1.6E-15	66.6	4.5	1.4	1	F9ZT99_ACICS	Putative transmembrane protein	Atc_0046	Acidithiobacillus caldus (strain SM-1)	427	990288	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus caldus, Acidithiobacillus caldus (strain SM-1)	>tr|F9ZT99|F9ZT99_ACICS Putative transmembrane protein OS=Acidithiobacillus caldus (strain SM-1) GN=Atc_0046 PE=4 SV=1MRLLTSIPRWREGWLEAILLPALVLVLTHFLAPQDPLLLQQPFPWLILVPLLIALRYEFLPGAVAALILAAACWWHPYPSATLLPDAAGTLLVTLIAAEYAAYWSRREVDRALQEKITATRLRQLADDLYVTRTSLDRLEQSLVYQPVSIRSALEELRQDLRRGKGEMDAPLLEKMLYFLNQLAGVQVASWYRWEAGAAEPRRLASFGPVAEWDGGDPVARAALAEGRSQQLADLQVERIQRYLSVHLNGEPGQDRHMLCIEDMTFFAITFESIQIIEVFFQYLCHYRDGCVHAQELLSRWPDCPVDFAVDFLQLRRLAGIVPQPGVCQSFVFRAGREAREIADKIQKLRRGLDVFWVHEDGEYLRVLTLLPFAGTTAAEGQRARVEAELQRCCAGLWQSAFLGADFMRIDARPAAEQLAHWLGSRP	14~~DUF4118 (0.000000000052976 7)~~107	non-KdpD DUF4118 protein
	1E-15	67	9.3	2E-15	66.3	6.5	1.4	1	C6XCM9_METGS	Histidine kinase (EC 2.7.13.3)	Msip34_1057	Methylovorus glucosetrophus (strain SIP3-4)	906	582744	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylovorus, Methylovorus glucosotrophus, Methylovorus glucosetrophus (strain SIP3-4)	>tr|C6XCM9|C6XCM9_METGS Histidine kinase OS=Methylovorus glucosetrophus (strain SIP3-4) GN=Msip34_1057 PE=4 SV=1MSHTRPDPDALLEKLQQEDARQQRGRLKIFFGSCAGVGKTFAMLTAAHARMQEGEDVLVGVIETHGRRDTESHLQGLPQLPLKSLSYRDKTLHEFDLDAALARRPGLLLVDELAHSNAEGSRHRKRWQDVEELCSAGIDVYTTLNVQHLESLNDVVGQITGIRVSETVPDKVFDLADEVTLVDLPPEELLQRLQEGKVYMSQQAERARRHFFRKGNLIALREMALRRTADRVDAQMREYRTDQSIQHVWQTHERILVGLGPGPEAEQLVRTAARLAISMKAEWLAAYVETPALQKLGHAERQAILDNLRLAQTLGAATTATLSGDEVSTVLLDYARSRNVSRLVVGKPRRPLLMRLFIPSVTDQLAKEATDIDLHVVVRQPKPRHKPAPQHSLQMAANAHLSGLKKRGYLWALAISAATSVIAGMLLQYFELSNVIMLYLLGVMLISIRYGRGPGILSSILSVSAFDFFFVPPKLSFTVSDTQYLLTFGIMLSVALVISNLTSSLRYQAVIANYRERRSLALYEIGKELASTMTTQHIVEVSVHHIASLFQSRAAILLPDADDKLRAPEADAGHGHTLADVDLGIAQWTFDHQEHAGLGTNTLPSSPVLYVPLKAPMRTRGVLAIVPENKAAIFLPEQRQLLDTFAAQIALALERKHYVEVARDALISMESERLRNSLLSAISHDLRTPLTSLLGIADQLRQAPDMPSDRHAQLETLYDQAFRMQQLVVNLLDMARLQAGSVQLNSQWQVLEEVLGSALRAMQPVSQQHRIEVTLPPELPLLQFDAVLLERVFCNLLDNACKYSPPNTTIRISAQQHPGEVWVTVADEGWGLPAGMETQIFQKFTRGKVESPQPGVGLGLSICKAIIQAHGGALWAEAQQPHGTRFIFSLPLGEPPAPPLAEETPA	23~~KdpD (9.47952E-121)~~232;X;254~~Usp(5.54459E-41)~~377;X;409~~DUF4118 (6.14071E-25)~~508;X;534~~GAF (2.91814E-19)~~655;X;672~~HisKA (0.000000000001544 45)~~736;X;789~~HATPase_c (1.21369E-27)~~890	KdpD protein
	1E-15	66.8	9.5	2.7E-15	65.9	6.6	1.5	1	V5UDP4_9BURK	Membrane protein	X636_08300	Pandoraea sp. RB-44	470	1380774	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Pandoraea, Pandoraea sp. RB-44	>tr|V5UDP4|V5UDP4_9BURK Membrane protein OS=Pandoraea sp. RB-44 GN=X636_08300 PE=4 SV=1MNTANQQDASVDAKPRVAGQVRRSEPFGNVSTYGRLLAPAATRPVMVFEVITGMALAVAIAWLLHPQDPLLIELGFPWMWLVALVMALRYGALLGVVAGLVLAAAWYGLYGQHGQPFPTMFFTGGFTMIVVGGHFCDIWGNRATRARGINTYLNDRLLALTSNHYLLRVSHERLERDLLTKPSTMRDAITRLRELTLTEDAPGKDTPLPNAQPMLEFAALTCQIETASLFPVHRNRLDTAAVASVGEAFAPDESDPLVQTCLREGRLAHVREDTTVGEDSAYVVCAPLTDGNGEINGMLIVRSMSFLALNHDNLQLLLVLLSYYADGVAQQAPVASVRDEVPAAPYDFALELGRLARAKRESGIQSSLVALVFPRGASGDSLFEQTVRSRRALDAQWIQSTPRHQIAISLMPITDDSGIDGYLLRIENGLRQQYGLDFQTGHIAVHTASVDERAPGEGLKKLLERCQDHA	48~~DUF4118 (4.29231E-14)~~142;X;214~~GAF (0.0000154449)~~310	non-KdpD DUF4118 protein
	2E-15	66.7	3.1	2.7E-15	65.9	2.2	1.5	1	Q2Y696_NITMU	Uncharacterized protein	Nmul_A2436	Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849)	464	323848	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosospira, Nitrosospira multiformis, Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849)	>tr|Q2Y696|Q2Y696_NITMU Uncharacterized protein OS=Nitrosospira multiformis (strain ATCC 25196 / NCIMB 11849) GN=Nmul_A2436 PE=4 SV=1MEKSMMPGNVLQNKWLESIAVSLSLPIIGYAVDPSDPFFVDYRFPWLILAPLLIGLQYGFACGIASAALLISVISIGFFLRLPQVPFFPKEMVTGLLLLTVITAEFRESWVRKIRLLEHQYNYLKVRMDKFARSYHLIKGSHYQLEQHLASQAKSLRLSLLDLKKKILSLEENRGEPLAGISEDILKILASYANVQTAGIYAVDEQRNINVNPVARLGQPRTLSSSDSVIREALSTGHVASIEVERNDSAPATGALVAIPLVDVYQKIWGMVVVSEMPLFAFQEATMDFLAVLGGKIGDLIKRRAESYSQDNDGRKAFEARLRRILGELKYLKTTAVAIAVTINTEELQREFLVKFQSELRGVDEILIAKDRDDRSLFLILLPSTDVTGANEFLNRIELSRPSADAICEGPDRTAFSFRDDNIRVCMWILHNKTSSEEVLLEIERFCKNEFIYKEFRESECLYS	14~~DUF4118 (9.05078E-17)~~113;X;181~~GAF (0.00000000246537)~~303	non-KdpD DUF4118 protein

	2E-15	66.4	3.8	3E-15	65.7	2.6	1.4	1	A0LBX7_MAGMM	Uncharacterized protein	Mmc1_2979	Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1)	508	156889	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Magnetococcales, Magnetococcaceae, Magnetococcus, Magnetococcus marinus, Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1)	>tr|A0LBX7|A0LBX7_MAGMM Uncharacterized protein OS=Magnetococcus marinus (strain ATCC BAA-1437 / JCM 17883 / MC-1) GN=Mmc1_2979 PE=4 SV=1MTQAQQPHKQSEPNDQASRADAITAIAGGRTLGGVQRSALIEIALFFALVFSIDFGLFDGSRFAQVAPHPYW FIVIVISVQYGTTEGLLAAISATVALRSWNIPQPTFNQEVFDYLLLLMRQPMMWLMAAVLMGELRTRQKRFQLELR DALLETRERERQRITEAYNRVNRTKEMLETRAAGQMRTVVSSIQAAKAVEQQEPALVMNGAADIVAQVLNPKKFSL FALDKGGLKMRISRGWDGDERFKTSLPESSALYQRVVGQHEFLSVVKSDQRDALDGEGMLVGPLLSKETGTVSG VMKLEELGFMDLNVSTVENFKALCEWIGTSLDNANRYQNAKSDSVLNHEHQLFSFGFFPKQVQLFTSLARRLKFE VCLVIIRLENADDLNLEERRKVPPVLSEALRTVMRNTDMAFDYERPGYDFALLLPATPVKNLHFVLKKLDEAIETLIR PTAPRAKFSIQTQILHQEEAPPEHAPSPSMLDGTPPVATAGHVAGPQGLPLATESSPP	39~~DUF4118 (6.47281E-21)~~142;X;200~~GAF (1.094E-21)~~330;X;366~~Nucleotidyl_cyc_III (0.00231224)~~460	non-KdpD DUF4118 protein
	2E-15	66	6.6	4.2E-15	65.2	4.6	1.4	1	A0A0F7KCD0_9PROT	Uncharacterized protein	AAW31_01525	Nitrosomonas communis	457	44574	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas communis	>tr|A0A0F7KCD0|A0A0F7KCD0_9PROT Uncharacterized protein OS=Nitrosomonas communis GN=AAW31_01525 PE=4 SV=1MIPSRKGEITKWIESIIITILLPVIGYVINSSDPFFVNYHFPWLILAPLLIALRHGLAYGIVATTVLVGIVATGFLFD WQEVPFFPKEMIVGLLLVTIISAEFHEIWMRKIKYLESKYNHINARMDKFTREYHLLKGSHRQLELHVASQAKSLRS FLHDLERHILSLEKNEGEPLKGIGASILKLFGDFASVQIAAIYAITDDERKEINPEPVAYLGHAPPLLISDPLVKEALKT GLVASIKLENENAMDTPETLVAIPLIDVYQKIWGLVVVNEMPLFALQESTMDLFAVLGGSIGDLVKRRAEAYSYIDD KGKDVELKLRRVLNEIKLLKTSAMLIGAIIDSEEVQNKYLTRFQANLRGVDKIWIFNEEQNYKTYLILLPYTDENGANE FLNRIGLSELLAKKVCNESNTKGAGYHDSEVSLNIWSLNNKTSLKKLVSEIFQFYKKRTAYFDIQR	11~~DUF4118 (0.00000000212317)~~110;X;178~~GAF (0.0000154298)~~302	non-KdpD DUF4118 protein
	3E-15	65.9	9	5.5E-15	64.9	6.3	1.6	1	B2U711_RALPJ	Histidine kinase (EC 2.7.13.3)	Rpic_3592	Ralstonia pickettii (strain 12J)	938	402626	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia pickettii (Burkholderia pickettii), Ralstonia pickettii (strain 12J)	>tr|B2U711|B2U711_RALPJ Histidine kinase OS=Ralstonia pickettii (strain 12J) GN=Rpic_3592 PE=4 SV=1MPADQRPNPDQLLAELQSGQEQSARGKLRIYFGASAGVGKTYAMLAAAKAARAAGIDAVIGLVETHGRAET AALVADLEHLPTRQIEYKGRTLPFEDLDAALARKPALILVDELAHSNVAGSRHPKRWQDIEDLLAAGIDVWTTVNVQ HLDSLNEAVGSITGIRVWETVPDAVFDAANEVILVDLPADELLRRLAEGKVYMPEQAQHAARNFFRKGNLIALRELA LRRTADRVDDDVQAYRRARRIENVWRTRETVVACLDPQGDGEQVIRSAARLAAQLECDWHAVAVVMPHLRAAD ARTERLHALLKLAQDAGAKVETLAGTNAVEAITGYIRRHNITKAVIGRPPEKRWRSARAIVVALRLAIGLERRLPSGD FAEALARHCPEVDVIRAAADPAHIQLTPRAAEVGRADVRSEAQRAADAQAGWLKPSYVAACVYVGVATALSSLVR PVFDLANIVMLFLAAVVAVAMRHGRGPAALASVLSVALFDFFFVPPRFSFAVSDVQYLLTFGVMLAVGMLVGQLTA GLREQAEVAVQREAAAHALYEAARELSAALTLDQIVSIGGRFVNATFGGRCAFFFVGLDGRLGAPQVAKPEGSTD APSGMPNLDRVLADWTYQHGQPAGTGTHTLPSGSVLYLPLKAPMAIRGVLAVEPETFHVLAQPDNRRQIDACATL VAIAIERVHYVEVARDALVRIESERLRNSLLAAVSHDLRTPLTGLVGMAETLLRAQPPLPPLQAEAAAAIGQQAQRM RTMVTNLLDMARLQNQDVKLRLEWQSVEELVGAALQANPLPDHRVVVDHLAALPLIRCDGPLMERVLSNLLENAG KFAPAGTEVRISGEIVHDEARGNELRLRVRDHGPGVPAGSVQTIFEKFTRGEKESATTGVGLGLAVCEAIVSAHHG RIWVEAPADGGACFVVALPAAEPPPVEDAEPIA	23~~KdpD (2.05216E-116)~~233;X;256~~Usp(1.80811E-29)~~390;X;433~~DUF4118 (2.70967E-23)~~532;X;558~~GAF (0.000000000000099 38)~~684;X;701~~HisKA (0.000000000667415)~~766;X;817~~HATPase_c (1.45984E-25)~~923	KdpD protein
	4E-15	65.4	13.8	6.9E-15	64.5	9.6	1.4	1	A2SIR9_METPP	Histidine kinase (EC 2.7.13.3)	Mpe_A2503	Methylibium petroleiphilum (strain PM1)	906	420662	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Methylibium, Methylibium petroleiphilum, Methylibium petroleiphilum (strain PM1)	>tr|A2SIR9|A2SIR9_METPP Histidine kinase OS=Methylibium petroleiphilum (strain PM1) GN=Mpe_A2503 PE=4 SV=1MTESRPDPDQLLVQLRDDEARAARGRLRIYFGASAGVGKTCAMLTAARKLRDDGVDVLAGVVETHGRAET QALLHGLELLPPAVVRHRDRTLPEFDLDAALARRPALLLVDELAHSNVSGSRHPKRWQDVEELLDAGIDVYTTLNV QHLESLNDVVSGITGIRVHETLPDTFFDRADEVVLVDTPADELIERLKAGKVYLPAQAERAVGHFFRKGNLMALREL ALRRTADRVEDDVQAYRVEQAIAPVWKTEAALLCCIGPRDDSDHVVRSAARLAQQLAVAWHAVYVETPALQRLP AAQRERILQTVKLAGELGAVTAVLSAQDVATALAAHARENLSKLLMGHNRERPWWRRDTFSQRLARLAPDVDLI EVGEGQRHAMPVTRERQGEGRLAPGRPEGYLWAAAACALTTLVALPLQPVFELANIVMLFLLAVVGVALRFGRG PAVLAAFLNVAAFDFFFVAPQLSFAVSDVQYLLTFAVMLVVGLLTGQLTAGLRYQASVATHREARSRALFELARDL SGELLTDQVVHTAEQAIEREFRGRARTFLQDEAGRLQWPRSGADAPGLDLGTAQWVLDHGDAAGLGTDTLPGT AWLYLPLKAPMRSRGVLALQPTQPRLLLVPEQRRQLETFAVLTAIALERVHYVEVAQQATVQIESERLRNSLLSAL SHDLRTPLAALYGLADTLVDGTQGEAQEMARALGAEARRLNAMVGKLLDMARLQSGAVQLDRQWQPIEEVVGS ALRSLGPALARHPVRTELPDGLPLVCFDAALIERVLCNLLENAAKYTPSGSAVTIGARVQGEELVVSVSDLGPGLPA GREEALFEKFVRGERESATAGVGLGLAICRAIVEAHGGHIRAGRGDGPPERPGASFGFSLPLGTPPALPQPEAVT VDAALDGAVP	22~~KdpD (1.73831E-118)~~232;X;255~~Usp(6.89754E-37)~~375;X;402~~DUF4118 (2.23184E-21)~~501;X;575~~GAF (0.000000000045464 5)~~644;X;661~~HisKA (0.000000000207282)~~723;X;776~~HATPase_c (7.4781E-25)~~881	KdpD protein
	6E-15	64.7	11.9	1E-14	64	8.2	1.3	1	A0A097R090_HAFAL	Histidine kinase (EC 2.7.13.3)	AT03_06750	Hafnia alvei FB1	901	1453496	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Hafnia, Hafnia alvei, Hafnia alvei FB1	>tr|A0A097R090|A0A097R090_HAFAL Histidine kinase OS=Hafnia alvei FB1 GN=AT03_06750 PE=4 SV=1MLDDEELRRPDPDTLLAQVCEKPRGKLKVFFGACAGVGKTYAMLQEAQRLRAQGLDVLVGVVETHGRAET AAQLEGLDILPLKRIHHRGRQVREFALDQALARHPALILMDELAHSNAAGSRHPKRWQDVEELLDAGIDVLTTVNV QHLESLNDVVGSVTGIRVRETVPDRIFDDASEIVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIALRELA LRRTADRVDEQMREFRNSQDKERVWHTRDAILLCIGHNVDNDKLVRTASRLAARLGCIWHAVYVETPRLHRLPEN QRRAILRSVKLAQELGAETTTLSDPNEEKAILRYAREHNLGKIIIGRRNKKERRWWWHESFADRLAKLGPDLDLIIV AVEDKPRTTSKESDSRPFSEKWRIQIRGCLVAIALCALITLLARMIFPNFDQANIVMVYLLGVVIVALFYGRWPSVLS AVVSVASFDLFFIQPQWSFAVTDVQYLVTFGVMLTVGIVIGNLTAGVRYQARVARYREQRARHMYELSKALSNAIT NEDIARSGSYFLNSSFNARTSVLIPSDDTPLVQVTPPQEGVSGVDFAIAHWCFDKQQPAGAGTDTLPGVPYQLLP LSTSQQTFGVLAIEPMNMRQLMVPEQQRLLQTYAVMIASALERLHLAQTAASARMDTEREQLRNSLLAALSHDLR TPLTVLFGQAEILTDLAAEKSPHAQQANQIRQQILNTTRLVNNLLDMARIQSGGFNLRKEWQSLEEIVGSAVNTLE PMLNSHPLTIDLPADLPLVNCDGSLIERVIQNLLENAGKYAGLESPLAIRAKASEDWLEVEIEDRGNGIPAEQLQLIF NKFTRGDKESAIPGVGLGLAICRAIIEVHGGKIWAENIAQGGACFHFTLPLEAPPDIEDELEHPSS	24~~KdpD (9.76017E-127)~~232;X;255~~Usp(1.42236E-40)~~377;X;406~~DUF4118 (1.10642E-24)~~504;X;532~~GAF (0.000000000008108 85)~~648;X;665~~HisKA (0.000000000032355)~~730;X;783~~HATPase_c (5.57482E-29)~~884	KdpD protein

	7E-15	64.4	13.6	2.3E-14	62.9	8.7	2.1	1	Q4K7X9_PSEF5	Histidine kinase (EC 2.7.13.3)	kdpD_2 PFL_4570	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	890	220664	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	>tr|Q4K7X9|Q4K7X9_PSEF5 Histidine kinase OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=kdpD_2 PE=4 SV=1MPPRDGRPDPDALLEKLQQEEQAAQRGKLRIYFGSNAGVGKTCAMLTAARNEVAQGRDVVAGVVETHGRRETAELLQGLQVLERHRLMHRDYALPEFDLDAALARHPAVLLVDELAHSNVPGSRHPKRWQDVEELLRAGIDVWTTLNVQHLESLNDIVSGIIGIRVRETVPDHLFDEAHEVLVIDLPPDDLLRRLKDGKVYLGPQAERASRHFFRKGNLLALRELTLRRTADRVDAQMRDYRRERSINALWPARERLLVGIAGDPADERLVREAARLAQKLEADWMVVHVASAQRRGAGAARYAAAMKTLALAAEFGAETATLPGMDVAEALVACAREHNANRLVLGHYPRKVWQFWHQSVSDRISRQHPEIDQIVIANGPLSRRPAPVDKPEAGLPPSRAPAYLWASLACFAATAVAALLLKVFDPANVVMLFLLTVVLVALRYGRGPGVWAAMLAVLCFDFFFVQPVWSFTVNDTQYFFTFALMLGIALITGQLTARLRHEARTAAAGERRATSLAGLARELSAALTEEQICAVALRTFSGVFEARVGLALPDAENRVRALSANTLAIDESIAQWAYDHDQPAGRGTDTLAAAKGCYLPLKAPMRVRGVLVLEAEDAERLKEPEEQRLLEACMSQLAIALERVHYVEVAQSTVLQMEGERMRNTLLAAISHDLRTPLTTIIGAADAALPHAAQGPLKHLLAGIHDQASSMQRLIENLLDMARMQERGVRLNRQWNSLEEIVGSALRQLREPLAGHQLRVAMAPQLPLVEVDALLLERVLVNLLDNAAKYTPAGTLVQISARQVDQQIILQVSDSGPGCPKGSSPASLFEAFSRGQQESAVAGIGLGLALAKRIVEAHGGRIEAQPHADAGLSFVITLPAGQPPSMETL	24~~KdpD (1.03935E-111)~~234;X;256~~Usp(5.62132E-28)~~378;X;429~~DUF4118 (3.92327E-20)~~501;X;529~~GAF (1.58996E-14)~~644;X;661~~HisKA (0.00000000012683)~~724;X;777~~HATPase_c (8.75509E-25)~~879	KdpD protein
	8E-15	64.3	9.9	1.5E-14	63.5	6.9	1.4	1	Q1LSE9_CUPMC	Histidine kinase (EC 2.7.13.3)	kdpD Rmet_0041	Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	967	266264	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus metallidurans, Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)	>tr|Q1LSE9|Q1LSE9_CUPMC Histidine kinase OS=Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) GN=kdpD PE=4 SV=1MYAWQSPAWHNHRHQPPLPMTDPDARPDPDALLQRMQAERARAARGKLRVYFGASAGVGKTFAMLGAARALREQGVDVVVGVVETHGRAETEALLDGLERLPLREVPYRDRVLAEFDLDGALARRPALILVDELAHSNAAGSRHPKRWQDIQELQATGIDVWTTVNVQHLDSLNQAVGGITGVRVWETVPDAVFDGADEVVLVDLPADELLRRLREGKVYLPDQARHAARNFFRKGNLIALRELALRRTADRVDDDVRAYRHAESIDLVWRTREALVACIGAGDDAEQVVRSAQRLAGQLDCDWHVVTIATPQLMPPSNEVRARMRAAMQLAEELGARTETLAGNDMVKAVAGYVRRHNLTKVLLGRAPADWYARGNWIDKGRALLARALSPLLGVGNRLFGRQMFADALAAGCPEIDVIRVAADSTRADLRPRRVQEGLSTEAHDAEAEALARVRRHNYGWAVVWCMAATFLSTLTRPWFDLVNIAMLFLVAVVGVALRHGRGPAALASVISVAAFDFFFVPPRMSFAVSDVQYLLTFFVLLTVGLVIGQLTAGLREQAQVSVRRETDARTLYELARELSAALTAQQIVEIGGRFLRAAFDADGTFFLVAENGRLMPMAGGEKTPEPRTGKGDAIDKVLAQWVFDHGQPAGTGTHTLPGSTVLYLPLKAPMQTRGVLAVEPRAWRALADPALRRQADVFATLIAIAIERIHYVDVAQRALVSIESERLRSSLLAAVSHDLRTPLTGLIGMAETLQRAEMPLPASVAETVEAMRVQAQRMRTMVVNLLDMARLQHHDLALKRGWQSLEELIGAALASMRDVLGRHHVEVMNLVELPLVECDDVLMERVLCNLLENAAKYTPAGTAIRIRGAVVGDEVQLSVEDEGPGVQSGQERYIFEKFTRGERESATSGVGLGLAVCEAIMQAHGGRIWVEAAHPHGSRFTLALPRGNPPAIEPESLDEPIPDHH	43~~KdpD (2.45004E-112)~~253;X;276~~Usp(2.39786E-26)~~375;X;459~~DUF4118 (3.09444E-23)~~559;X;587~~GAF (6.74302E-17)~~710;X;727~~HisKA (8.77552E-14)~~792;X;845~~HATPase_c (6.61734E-27)~~946	KdpD protein
	1E-14	64.1	9.7	1.9E-14	63.2	6.7	1.5	1	Q8XU09_RALSO	Histidine kinase (EC 2.7.13.3)	kdpD RSc3385	Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	937	267608	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Ralstonia, Ralstonia solanacearum (Pseudomonas solanacearum), Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)	>tr|Q8XU09|Q8XU09_RALSO Histidine kinase OS=Ralstonia solanacearum (strain GMI1000) GN=kdpD PE=4 SV=1MDETRPNPDTLLAELQSGEEKAARGKLRIYFGASAGVGKTYAMLSAAKVARAEGIDVVVGLVETHGRAETAALVEGLEHLPPRQVEYRGRTLPEFDLDAALARKPALILVDELAHSNVAGSRHPKRWQDIEDLLAAGIDVWTTVNVQHLDSLNEAVGSITGIRVWETVPDAVFDSAAEVILVDLPADELLRRLAEGKVYLPEQARHAARNFFRKGNLIALRELALRRTADRVDDDVQAYRRARRIENVWRTRETIVACLDPQGDGEQVIRSAARLAAQLECDWHAVAVVMPHLRAADAAERLHALLKMAEDAGARIETLAGTNAVEAITGYVRRHNITKVVVGRPPARRWRSARAIVVALRLAIGLERRLPSGDFAEALARQCPEVDVIRAAADPARVVQLPPRAASIGRVDVRDTAQRAAAEAEGTWLRPAYLAACVYVGAATLLSSLVRPVFDLANIVMLFLAAVVAVAMRHGRGPAALASVLSVALFDFFFVPPRYSFAVSDVQYLLTFAVMLAVGLLVGQLTAGLREQAEAAVQREAAARALYEAARELSAALTLDQIVSIGGRFVNATFGGRCAFFFVGPDGRLGAAQVARPEGTPDAPSGMPNLDRVLADWTCQHGQPAGTGTHTLPSGSVLYLPLKAPMAIRGVLAVEPETFQVLAQPDNRRQIDACATLIAIAIERVHYVEIAQDALLRIESERLRNSLLAAVSHDLRTPLTGLAGMAETLLRTQPPLSPLQAEAAAEAIGEQAQRMRAMVTNLLDMARLQNHDVKLRLEWQSIEELVGAALKGTPLPTHAVVVDDLADLPLLRCDGPLMERVLSNLLENAGKFAPAGTEVRISAGVVHDAAHGDEMCVRVRDHGPGVPAGAERVIFEKFTRGDKESATGGVGLGLAVCEAIVSAHGGRIWVETPADGGACFVVALPASDQPAMEDDIPA	22~~KdpD (7.13463E-126)~~232;X;255~~Usp(3.82539E-30)~~389;X;432~~DUF4118 (3.09553E-23)~~532;X;558~~GAF (6.77085E-15)~~684;X;701~~HisKA (3.84336E-15)~~766;X;817~~HATPase_c (7.31882E-27)~~923	KdpD protein
	1E-14	64	9.5	1.6E-14	63.4	6.6	1.3	1	B3EAQ0_GEOLS	Histidine kinase (EC 2.7.13.3)	Glov_3227	Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	890	398767	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter lovleyi, Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	>tr|B3EAQ0|B3EAQ0_GEOLS Histidine kinase OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) GN=Glov_3227 PE=4 SV=1MTIPDTTIRPTPEAMLKLAQAEEAQSGQGRLKVFLGYAAGVGKTYAMLEAARERKRDGRDVVVGYVESHGRSETDALLDGLELIPRRELSYAGVLLPEMDLDAILTRKPQIVLVDELAHCNVPGSRHEKRWQDVEELLAAGIDVYTTVNIQHFESLNDVVAQITGITVRETVPDRLLDIAFEIKLIDLPPEDLLQRLHEGKVYIPDQAAKAIEKFFRPGNLMALRELSLRRTAARVDDQMRAYMETQSIPGPWPTAERLLVCVSGSPFSEQLIRATRRLAEELKAPWHTVYIETPGSDRQTRENRERIWQDLRFAESLGAQVATLTATSVPDAVVEYAVRHNVTRIVVGKPSRSRWQELLHPPIVDQIIRRSISSDVFVVRISSDGRQGGAQQQVKHPHHAHPFGYPAAALLVAAATLLCGLVSRFLEPTNLVMVYLLAVVVAAVRLGRRPAMLTAFLGVLAFDFFFVPPHITFVVADTQYLITFAGLLVVGLVISSLVARSQERADVIRVREIQTASLYYLSRDLAAAADISKVLKSVIRNVEEALNAKAVMLLPEGERLELQAASDGLILDSKEQAVADWAFRNRQPAGRGTDTLISAELLYLPLQTPASQLGVLGIRMEDELDYRSTESRRLLDAFATQAAMAIERVQFSHQAEQAQILQARENLERALLNSISHDLRTPLVTVTGVLASLRDDGMHLNDQARDELLDTAAGEAERLNRFVGNLLDMTRIEAGAIRLNSELCDIQDLVGCAMAAIKQRVGGRTIRIRLPDDLPMVPMDLVLMTQVLVNLLDNSLKYSPAESSIEISARLERGWLLLEIADQGPGVPEQDLKRVFDKFYRIPVPEGVGGTGLGLSICKGIVEAHNGSIRAINKSGGGLMMVIRLPLSR	26~~KdpD (1.98443E-120)~~236;X;258~~Usp(5.05909E-43)~~380;X;430~~DUF4118 (9.45088E-19)~~505;X;531~~GAF (0.000000000016542)~~649;X;666~~HisKA (0.00000000624432)~~732;X;787~~HATPase_c (2.20769E-30)~~886	KdpD protein

	1E-14	63.7	14.1	2.1E-14	63	9.8	1.4	1	A4G5J6_HERAR	Histidine kinase (EC 2.7.13.3)	kdpD HEAR1623	Herminiimonas arsenicoxydans	921	204773	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herminiimonas, Herminiimonas arsenicoxydans	>tr|A4G5J6|A4G5J6_HERAR Histidine kinase OS=Herminiimonas arsenicoxydans GN=kdpD PE=4 SV=1MPPADYQRPDPDALLAHVQEQERRAERGKLRIYFGASAGVGKTYAMLSAARRMQAEGHDVIVGIVETHGR NETAALLDGLEMLPRKEIAYRDKIISEFDIDAALVRRPALILVDELAHSNAPGSRHPKRWQDVHELLDAGIDVFTTVN VQHLETLNDVVGGITGIRVAETLPDTVFDQADEVVLVDIPADDLLARLSTGKVYQPQQAERASRNFFRKGNLIALRE LALRRTADRIGDDVQAYRIEKSINGVWKTDSDLLVCVGPGTNCEHVIRSAAQLAGQLNAKWHAVYVETPQLQSLP PAHREHILKTLKLAQDLSATTAVLSGNTVANEIVNYARSHNFSRIVLGRDHSKWPWQTSHLKLIAHHLPDIDLIEIGRI EGKGSSSSQNLSARLSSGLDETPGGTKPRFMPYVWTVVACIFTALLATPLLPHLDLANIVMLFLLAEVLIAVRFGRG PAVLAAFLSVAVFDFFFVLPRFSFAVSDVQYLVTFSVLLVVGLIVGQLTSGLRFQARIAAHREGRARALYEFARELS SALQAEQIFEITQSFIQRTFRAKAVLLLPDDAARLRLPAQAADDIGSDAANGKNVAELDIGVAQWAFDRATPAGMG TDTLPASTYFYLPLVAPMRTRGVLAIQPGNRRWILIPEQRKQLDTFAALAAIALERVHYIEVAQDALVRMESERLRN SLLSALSHDLRTPLTSLVGLSESLTMSKPPLTSSQQELAQALHDEARRMSNLVSNLLDMARIQSGEVKFNLQWLQF EEVVGSALRASQSAIAHHEIKTRLAPDLPLVRFDAVLIERVLCNLIENAAKYTPAGSRIVIAAEISGRFLEVSVYDNGP GLPAGQEEAIFDKFTRGERESATPGVGLGLAICRAIVEAHQGTIRAAHSPDGGASINFTLPLGTPPAIDESEITTLDQ RP	25~~KdpD (7.79129E-123)~~235;X;258~~Usp(3.76172E-34)~~377;X;411~~DUF4118 (1.59161E-22)~~511;X;539~~GAF (8.32682E-19)~~665;X;682~~HisKA (0.000000000000358193)~~747;X;800~~HATPase_c (7.91806E-29)~~901	KdpD protein
	1E-14	63.7	11.6	2.6E-14	62.7	8	1.5	1	Q0K8I9_CUPNH	Histidine kinase (EC 2.7.13.3)	kdpD1 H16_A2600	Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	949	381666	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus necator (Alcaligenes eutrophus) (Ralstonia eutropha), Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	>tr|Q0K8I9|Q0K8I9_CUPNH Histidine kinase OS=Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) GN=kdpD1 PE=4 SV=1MPEPRQPDDPRPDPDHLLQRMQAAGERAARGCLRIYFGASAGVGKTFAMLAAARAQREQGGDVVVGVVE THGRAETEALAEGIERVPLRRVDYRGRTLQEFDLDAALARRPALILVDELAHSNAPGSRHPKRWQDIAELLSAGID VWTTVNVQHLDSLNQAVAGITGIRVRETVPDTVFDDAGEVVLVDLPADELLRRLREGRVYVPEQARHAVQHFFRK GNLIALRELALRRTADRVDDDVRAYRQEASIEPVWRTREAVLACVGHGSDAAQVVRSARRLAGQLDCDCHVVTV SVPRLAPVPDAQREQLDQAMRLAEALGARTETLAGSDMVAAVAGYVRRHNLTKVLIGRTPARWADGGASLSGR MHALLARALAPWLGARAWLFGRTSFADALAAACPEIDVIRVADDSVRQETPADAPVLPGTEPPQADARPAQWPG LLWAVAWCAGATALSALARPWFDLVNIAMLFLLAVAGVALRHGRTAGAFAALVAVGAFDFFFVPPQLSFAVTDVQ YLVTFLVMLAVGLVIGQLTAGLREQAQVSVQRETDARTLYELARELSAALTDAQIVGIGSRFLRAAFDARAAFFLVG ADGRLLPAATAPEAGGAAQSDAVDHVLAQWVFNHGQPAGTGTDTLPSGTVLYLPLKAPMQVRGVLAVEPRTWR AFAQPALRRQVDVFATLIAIAIERLHYVEVAQQALLAMESERLRSSLLAAVSHDLRTPLTSLIGMAETLQRGTTPLAP EVAETVGAMRDQARRMHAMVANLLDMARLQSRSVALRKEWQSFEELAGAALASLRDALARHRVVVADLSALPLV ECDGVLMERVLCNLLENAAKYTAPGTEIRVRGELSDDAVHLVVEDDGPGVPAAMARQVFEKFTRGERESATTGV GLGLAVCEAIVQAHGGSIRVEPVHARAQGEGTGARFVVTLPRGNPPVLELEAAGLPA	28~~KdpD (9.05127E-113)~~238;X;261~~Usp(2.78738E-29)~~357;X;442~~DUF4118 (5.44568E-22)~~541;X;595~~GAF (0.000000000000298902)~~690;X;707~~HisKA (7.39726E-14)~~772;X;825~~HATPase_c (3.58596E-28)~~932	KdpD protein
	1E-14	63.6	10.2	2.5E-14	62.8	7	1.4	1	C6WWQ9_METML	Histidine kinase (EC 2.7.13.3)	Mmol_1452	Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540)	914	583345	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylotenera, Methylotenera mobilis, Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540)	>tr|C6WWQ9|C6WWQ9_METML Histidine kinase OS=Methylotenera mobilis (strain JLW8 / ATCC BAA-1282 / DSM 17540) GN=Mmol_1452 PE=4 SV=1MNDDRPNPDLLLEKINKDAEKEKRGRLKIFFGACAGVGKTFAMLSTARTLRQEGLDVVVGIVETHGRIGTQS QLANLEVLPLKKLIYRERELTEFDLDAALARKPDLILVDELAHSNVEGSRHPKRWQDVEELLIAGVDVYTTLNVQHIE SLNDVVGQITGIRVSETIPDKVFDIADEVTLVDLPADELLQRLQDGKVYQPQQAKRAGKSFFRKGNLIALREMALRR TADRVDSQMREYRTNSSISQVWQAKDRLLVCVGPDSESERLVRVAARLAQSLKSDWLAVYVETPKLQRISDKQR NLILKTLKLAETLGAETATLSGTKVAETVLSYARSRNVTKLVVGKSTRTTLERLILPGVVDDLTNHATDIDLHVVSRE RTLAERLATNHDNTDNLERASGDKSYAGYYIAAIVCAITAILSAQLLDYFELANVVMLYLLGVILISSKYGRGPGIFSS FISVATFDFFFVPPKLSFSVSDTQYLLIFAVMLVVALVISNLTANLRYQAMVAMNREKRSRALYDLGKSLASALTAAH IIEISIPHLSGIFKAKVAILLPDSQEKIVNTSLHKISNAKPDLNSNFDVDLAVAQWVYDHQQQAGFGTDTLPSAPALYI PLQAPMRTRGVLVILPDTNLSKGNRTIFLPEQRQLLDTFSSQIAIAIAIERVHYVEVAQEALISMESERLRNSVLSAISHD LNTPLTTIIAAAGWLKQETEINDKRYEYVSMLNEQSIRMKNLVVNLLDMARLQSGKVKLNKQWQLLEEVVGTSLRT MSEVVSKHTIVIDMPHDLPLIEFDAVLIDRVLCNLLDNASKYSPAGNRIFISARTQQNDVWISVADEGSGLPENLEN QLFEKFTRGEKESSKAGVGLGLSICKAIIEAHDGKIWANNKPPHGAIFTFSLPLGTPPSLPPDDDLV	22~~KdpD (7.00768E-121)~~232;X;254~~Usp(2.76401E-44)~~377;X;409~~DUF4118 (4.62241E-22)~~507;X;537~~GAF (3.48397E-19)~~664;X;681~~HisKA (0.000000000011655 1)~~745;X;798~~HATPase_c (6.86056E-29)~~899	KdpD protein
	1E-14	63.6	9.5	2.2E-14	63	6.6	1.3	1	A5GAF9_GEOUR	Histidine kinase (EC 2.7.13.3)	Gura_1224	Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	889	351605	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter uraniireducens, Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	>tr|A5GAF9|A5GAF9_GEOUR Histidine kinase OS=Geobacter uraniireducens (strain Rf4) GN=Gura_1224 PE=4 SV=1MTDNDDKRPSPEALLKLAQAEEKEDGRGKLKIFLGYAAGVGKTYAMLEAGWQRKMEGRDVVAAYVESHG RFETDSLLSMSGVEIIPKAQIEHMGVLLPELDTDAVLARKPQIALVDELAHTNARGSRHEKRWQDVEEILASGIDVY TTVNIQHFESLNDIVAQITGVVVRETVPDRLLDEAAEIRLVDIPPDELLQRLHEGKVYIPKQATLAMEKFFKPGNLIAL RELSLRRAAVRVDEEMRAYMETRSIAGPWPAAERLLVCVSGSPFGEKLIRSTRRLADEMKAHWYTVYIETPGSGK HVQENRERVWKDLRLAESLGGEVATVSATSVADSVIDFAVKHNVTKIVVGKPTKPRWMEFLNPPLVDQIIRRSGTI DVYVVSIEPSEKSEGTALARRKSPSPWSGYMKSLALVAAATLACELVRPFLAPTNMVMAYLLAVVLAALRLGLKPA IVTAFLGILAFDFFFVPPRLTFAVADTEYLITFVALFTVGVVISTLVARSRERAEAIRKREVQTASLYYLSRDLAVSADI GAVLDAVAKNFGESFNGRLAVLIPEGERLEIKAASREMQLDTKELAVADWAFRNRQSAGHGTETLSSARLLYLPL QTSASVLGVLGVELEDEADYANTQSRRLLDAFTTQTTLAIERVQLGKQAAQALILQGRETLERALLNSVVSHDLRTPL VSITGALGTLRDKEHRLSDTRRRELLDAAWEEAGRLNRFVGNLLDMTRLEAGAVTLKEEPCDIQDLVGCALAALEQ RIGAREVKVQLPDGLPLVKLDMALMTQVLVNLLDNALKYSPHASIIDIAARVDDGRLTLEVSDRGPGVPESDLKRIF DKFYRIPVPEGAGGTGLGLSICKGIVEAHHGKIRAENRDGGGLRVIATLPVK	26~~KdpD (1.15235E-114)~~237;X;259~~Usp(5.29755E-42)~~382;X;430~~DUF4118 (8.81965E-19)~~505;X;531~~GAF (0.0000000159054)~~649;X;666~~HisKA (0.0000000115186)~~732;X;787~~HATPase_c (3.49449E-31)~~886	KdpD protein

	2E-14	63.3	11.8	2.8E-14	62.6	8.1	1.4	1	Q39SW3_GEOMG	Histidine kinase (EC 2.7.13.3)	kdpD Gmet_2436	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	888	269799	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter metallireducens, Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	>tr|Q39SW3|Q39SW3_GEOMG Histidine kinase OS=Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) GN=kdpD PE=4 SV=1MTDINDERRPSPEALLRLAQKEEAQAEQGRLKIFLGYAAGVGKTYAMLEAARQRKGEGRDVVAAYVESHGRAETDALLEGVEIIPPARIEYQGVTLREVDVDAVLARKPQLALVDELAHTNAPGSRHEKRWQDVEELLAAGINVYTTVNVQHFESLNDVVVQITGIAVRETVPDSLLDQATEIRLVDIPPEDLLQRLREGKVYVPEQAAFATEKFFRPGNLIALRELSLRRAASRVDEEMRAYMESRAIPGPWPATERLLVSVSGSPYSERLIRTTRRLADELKAPWFTVYVETPGGGRQEQENRKRVWKDLRLAESLGAHVATLTATSAADAIIDYARSHNVTQIVVGKPAKPRWRELLRLPLVDQIIRLSGAIDVHVVSFEPAGAKKGPVIPRQRRPISLTGYMASLALVAATTLVCLLGRPFLAPTNMVMIYLLAVVLAALRLGLKPAILTAFLGVLAFDFFFVPPRLTFAVADTQYLITFVALFTVGVVISTLVSKARERAEAVREREVQTAALYYLSRDLAAAADIETLVQAVVRNIGESLAAGSTVLLPKGDRLEVAAASKGLKPDVKEMAVADWAFRNRQPAGQGTETLVSAGLLYLPLQTSGNILGVLGIRLKNVADYRSTQPRRLLDAFVTQTAMALERVQLSRQAEQTQILQARETLERALLNSISHDLRTPLVSITGALDTLREKVHTLANEARMELLDTAWEEAERLNRFVGNLLDMTRLEAGALKVKKELCDVQDLVGCALAAALERRIGGRQVDVHLPPDLPLVRMDMVLMTQVLANLLDNALKYSPPESGIEISVRVNDGRLEMEVADHGPGIPEQDLKRVFDKFYRIPIPEGSRGTGLGLSICKGIVEAHGGAIRAENRARGGLRVIVTLTIK	26~~KdpD (8.03267E-120)~~236;X;258~~Usp(3.08242E-47)~~381;X;405~~DUF4118 (1.29882E-22)~~504;X;530~~GAF (0.0000000002768)~~648;X;665~~HisKA (0.00000000096013)~~731;X;786~~HATPase_c (9.08781E-33)~~885	KdpD protein
	2E-14	63.3	11.8	3.8E-14	62.2	8.1	1.6	1	W0SHY8_9RHOO	Histidine kinase (EC 2.7.13.3)	SUTH_01761	Sulfuritalea hydrogenivorans sk43H	501	1223802	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Sulfuritalea, Sulfuritalea hydrogenivorans, Sulfuritalea hydrogenivorans sk43H	>tr|W0SHY8|W0SHY8_9RHOO Histidine kinase OS=Sulfuritalea hydrogenivorans sk43H GN=SUTH_01761 PE=4 SV=1MNEAAPSRGIGDYIRAALACVATTLLTLPLAGVVDAANIVMIFLLAVVMVAVWLGSGPAILAAFGGVALFDFFFVEPRFSMAVADAQYLITFAVMLVVALVIGQLAARLREKALLATRREDEMRALYDMAKLLSGAITVEQVADIVRDFLASRLEIEAVLYLPRGDDALVAMPARQGGDRHQAHVSAVYEQGQPMHLAAEESGYAPALALPLVSSVQTRGVLLVYSDHAERFSATERRPLLDAVASLAAIAVERLHYVEVVQEVTLGMESERLRTALLSTVSHDLRTPLTVLVGLADALTLARPSLPAPALESAVAIRDQALRLSGLVHNLLDMARLHTGKIVLNREWQPLEEVVGSSLKAMAGVLAGREVRVELAPDLPPLEFDAVLLERVFCNLLENAAKYAPQGTILITAHVAGELVEIAVVDAGPGLPPDGEDSVFDLFERGRHSGAGGGLGLAICRTIVEVHGGRIRAERRVEGGTRIVFTLPLGTPPVLEEEAGE	(1.98594E-18)~~112;X;138~~GAF (0.000000120994)~~254;X;271~~HisKA (0.000000000066787)~~336;X;389~~HATPase_c (7.78067E-21)~~487	non-KdpD DUF4118 protein
	2E-14	63.1	14	3.2E-14	62.4	9.7	1.4	1	Q74AA7_GEOSL	Histidine kinase (EC 2.7.13.3)	kdpD GSU2483	Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	899	243231	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter sulfurreducens, Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	>tr|Q74AA7|Q74AA7_GEOSL Histidine kinase OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) GN=kdpD PE=4 SV=2MSDMDDERRPSPEAMLKLAQAEEAEAKRGKLKIFLGYAAGVGKTYAMLQAARERRHEGRDVVAAYVESHGRPETDALLEGLEILPAARIEYQGVMLPELDIDGVLARRPQLALVDELAHTNAPGSRHEKRWQDVEELLAAGIDVFTTVNVQHFESLNDVVAQITGIAVRETVPDRLLDLAAEIRLVDIPPEDLLQRLREGKVYVPEQAAFAAEKFFRAGNLIALRELSLRRAAVRVDEEMRAYMEARAIPGPWPAAERLLVSISGSPFSERLIRTTRRLADELKAPWFTVYVETPGNGRHEQENRKRVWKDLRLAESLGAQVATVTATSVAEALIDYARRHNVTRIVVGKPAKPRWREFLRLPLVDRIIRLSGAIDVHVVSYEPAEAGKGPVLPVRRGPISFSGYLASLALVVAASLACLLLRPFLAPTNMVMIYLLAVVLAALRLGLKPAILTAFLGVLAFDFFFIPPHLTFAVADTQYLITFVALFTVGVVISTLVSTVRERAEAVREREEQTASLYYLSRDLAAAADIETLVAAVIRNIGETLFARAAVLLPEGDRLRVAAASKGLKPDVKEMAVADWAFRNRQTAGQGTETLASAGFLYLPLQTSGSVLGVLGVRLKNDADYRSTQVRRMLDAFTSQTAMALERVQLSRQAEQAQILQARENLERALLNSISHDLRTPLVAITGALDTLRDKVHTLADESRLELLDTAWEEAERLNRFVGNLLDMTRLESGAIKLKRELSDVQDLIGCALAALERRIGERGIDVRLAPDLPLVRIDMVLMTQVLVNLLDNALKYSPPDSGVEITARVDGGRLRIEMADRGPGIPEQDLKRVFDKFYRIAVPEGAQGTGLGLSICKGIVEAHGGSIRAENRTGGGLRVIVTLPLAGGAKEGVSHGP	26~~KdpD (3.39061E-119)~~236;X;258~~Usp(9.71227E-45)~~381;X;405~~DUF4118 (1.06472E-22)~~504;X;530~~GAF (0.000000000002536)~~648;X;665~~HisKA (0.00000000040703)~~731;X;786~~HATPase_c (2.56594E-33)~~885	KdpD protein
	2E-14	63	7.5	3E-14	62.5	5.2	1.3	1	B5EHI0_GEOBB	Histidine kinase (EC 2.7.13.3)	Gbem_1171	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	356	404380	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	>tr|B5EHI0|B5EHI0_GEOBB Histidine kinase OS=Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622) GN=Gbem_1171 PE=4 SV=1MVAIRGYLISLLLVAGATAICELVRPHLIPTNMVMVYLLAVVAAAAKLGRRPAIATAFFSVLAFDFFFVPPRLTFSVAEKEYLVTFLGFFVVGVMISSLVAKVREQSLERERLSHEAEKARILQARENLERALLNSISHDLRTPLVSIKGALSALKEQGGRLSPEARRDLLETANEEAERLNRFVGNLLDLSRLEAGALRPRIEPCDLQELIGCAISAMESRLGDRNVSVQLPQGLTLVPLDLVLMTQVLVNLLDNANKYAPAQGSIEVEARVAGAWLSLTVADRGPGAPEAELSHIFDKFHRVQVPEKTGGTGLGLSICKGIVEAHGGRIAARNRPQGGLAVEILLPLQQGAEEP	7~~DUF4118 (0.000000000000011152)~~106;X;127~~HisKA (0.000000000000152792)~~193;X;248~~HATPase_c (4.27653E-30)~~347	non-KdpD DUF4118 protein
	2E-14	63	12.4	3.4E-14	62.3	8.6	1.3	1	Q7CJR5_YERPE	Sensor for high-affinity potassium transport system (Two-component regulatory protein sensor kinase KdpD) (EC 2.7.3.-) (Universal stress family protein)	kdpD kdpD1 y1262 YP_2492 YPO2689 ACX52_679 ACX54_2498	Yersinia pestis	908	632	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia pseudotuberculosis complex, Yersinia pestis	>tr|Q7CJR5|Q7CJR5_YERPE Sensor for high-affinity potassium transport system OS=Yersinia pestis GN=kdpD PE=4 SV=1MVDAEPTRPNPDSLLAVANEKPRGRLKVFFGACAGVGKTYAMLQEAQRLRAQGLDVLVGVVETHGRSETAALLEGLTALPLKRIHHRNRQIREFDLDAALARRPALILMDELAHSNANGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGGVTGIRVRETVPDHMFDEASEVVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAFRDTQGRERVVWHTRDAILLCIGHHAGNEKLVRTAARLAARLGCIWHAVYVETPRLHGLPEAKRRAILRTLKLAQELGAETATLSDPSEEQAVLRYAREHNLGKIIIGRRTEQHWKLRGSFADRLGKLGPDLDLVIIALDADPPTNVAKEPDSRPFTEKWRMQLRGCVAAIALCALITVLSLWLIPRFDQANLVMVYLLGVVIIALFYGRWPSVLAAVINVASFDLFFVQPHWSLAVTDVQYLLTFGVMLIVGIVVGNLTAGVRYQAKIARYREQRARHLYEMSRSLSRALTPEDIAKTSRHFLSSSFQAKTSLLLPQEEGHLQPIMPDDGGILSVDDAIAHWSFNQGAPAGAGTDTLPGVPYQLLPLTAAQQTYGVLAIEPANLRQLMVPEQQRLLQTFTSLIANALERLHLARSAELAKLDAEREQLRNSLLAALSHDLRTPLTVLFGQAEILTLDLAAEGSRHAPQANQIRQQVLSTTRLVNNLLDMARIQSGGFNLRKEWQSLEEIIGSALYMLETTLSQHQIRVELPDEMVLINCDASLLERVFINLLENAHKYAGHAALLGIRAEVQGEWLNVDVWDNGPGVTIGQENLIFDKFSRGNKESAIPGVGLGLAICRAIIDVHGGRIWVEKRQEGGASFRFVLPLEKVPEIDADNIDTNNIDTENNDIS	23~~KdpD (9.32591E-124)~~231;X;254~~Usp(1.98006E-39)~~374;X;404~~DUF4118 (3.16208E-24)~~502;X;528~~GAF (2.81733E-15)~~646;X;663~~HisKA (0.000000000129128)~~728;X;781~~HATPase_c (3.52491E-26)~~882	KdpD protein

	2E-14	62.9	9.8	3.9E-14	62.1	6.8	1.4	1	A7I6Q3_METB6	Osmosensitive K+ channel His kinase sensor	Mboo_0896	Methanoregula boonei (strain 6A8)	658	456442	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula boonei, Methanoregula boonei (strain 6A8)	>tr|A7I6Q3|A7I6Q3_METB6 Osmosensitive K+ channel His kinase sensor OS=Methanoregula boonei (strain 6A8) GN=Mboo_0896 PE=4 SV=1MPNPSDCRQDQRPDPDALLACVQKEELQKVRGKLKIFLGYIAGVGKTYEMLKAAHLRKDEGVDVRIGYIEPHGRKETEALMEGIPVIPNRTIEYHGVKLNEMDLDAILAAHPQLVLVDELAHTNVPGSRHLKRYQDVEELLAAGIDVYSTLNVQHIESLNDVVARITGVIIKEKIPDRVIDEAAEIEVVDLAPPELLQRLREGKVYVPEMAARAIEQFFNEGNLYALRELALRRAAERVDNQMLAYMQTRSIPGPWAVGEYLLVCIGPGPLAERLIRTARRQADRINARWCAIYYVETPTHHRLSLEAKEQVDRSLQLAEKLGATTASVFGLNVANTVLEYARQHNVTRIIIGKTLRPRWQEFVFGSVVDQLIHNSGPIDVYVISSGKDLPEKPAEAEPLLPASPPRDYVDSLTLVVAVTILGWLFHSLISPVNQLMFYLLAVVVIAFKRGLKPAIFTSVVGVLAFDFFFVPPYLTFRVSDTQYLVTFLGMIIVGSVISLLVARARRHADAAQTRERETSTLYALSQDLAGALDADAIMNAVGQHIKEIFQWESAFFLPENGHLAAHAKSPGLVMDGDDLAVATWAFQHGTTAGYDTDTLHGSKLRYIPLRSTRGVLGIMAVQPAEANGVITYEQSRILTAFANQAALALERVNLAKPA	31~~KdpD (4.96405E-125)~~239;X;262~~Usp(1.00358E-45)~~384;X;408~~DUF4118 (1.45741E-18)~~501;X;533~~GAF (0.0000000000176199)~~651	KdpD protein
	2E-14	62.8	7.2	4.2E-14	62	5	1.4	1	A0A0D5EL36_9BURK	Histidine kinase (EC 2.7.13.3)	BW23_2577	Burkholderia ubonensis MSMB22	951	1249668	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	>tr|A0A0D5EL36|A0A0D5EL36_9BURK Histidine kinase OS=Burkholderia ubonensis MSMB22 GN=BW23_2577 PE=4 SV=1MNRPDPDQLLDKLQRDEEKQRRGQLKIFFGASAGVGKTYAMLQAARQRRQEGVDVVVGIVETHGRSETAALLDGLDVLPLAKLDYRGRALAEFDLDAALARKPELILVDELAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWETVPDRVFDAADEVTLVDLPAEELLERMRDGKVYLAQQAERAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPTLVRAAARLAASLKADWIAVYVETPRLQRLPDAQRERTLNALKLAAELGAETATLAGGDAVAALIGYAKVRNVSKVVAGGSRKTGLARWFARPFGEKLAERAGDVDLMLIRASASDEVRAAPLDARARDWRDAFARLGGHRSPPRHYAYAAAICAAITMVATVVSERLDLTNLVMLYLLGVVFSAVRLGRGPGVLQSFLSVAAFDFFFVPPRMSFSVSDTQYLLTFFGMLLTSLVISHLLTSTLTREASIAQRRERRTGAIYAMARELAAALTIEQIVEIGSRHVSEVFRARVAILLPDSADKVQQKIEEPDAAVTLTGPDLDNDVGQWVYDQQKPAGHGTDTLPATAALYLPLKAPMRTRGVLAIVSTDPRELEEPEQQRMLDAFAAQIALAIERVHYVEIARDALVSMESERLRNSLLSAISHDLRTPLTTIVGFSSMLANARAAATRGDATAAPRHGPREDELVEAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGAALAACRRVLARHPARVALPADLPLLQMDAVLMERLFTNLFENAAKYTPADTPLEIGAQCVTEDGQPFVRVHVDDHGPGLPPGMETRIFDKFTRGEKESATPGIGLGLAICRAIVEAHGGRIGALNRIGPDGRVTGARFWFTLPVDTPPAAPAVSDDEADALRALPFAPSSSEPPRDHE	21~~KdpD (6.06801E-122)~~230;X;252~~Usp(2.38127E-33)~~374;X;422~~DUF4118 (6.34598E-19)~~510;X;536~~GAF (2.23256E-18)~~659;X;676~~HisKA (0.0000000000173651)~~752;X;805~~HATPase_c (3.91477E-22)~~915	KdpD protein
	3E-14	62.7	7.8	4.9E-14	61.8	5.4	1.5	1	A0A0C4Y5W5_9BURK	Histidine kinase (EC 2.7.13.3)	RR42_m0094	Cupriavidus basilensis	977	68895	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus basilensis	>tr|A0A0C4Y5W5|A0A0C4Y5W5_9BURK Histidine kinase OS=Cupriavidus basilensis GN=RR42_m0094 PE=4 SV=1MPDTAQRDAPGRPDPDALLQRMQQEGERAARGKLRVYFGASAGVGKTFAMLTAARALREQGSDVVIGVVETHGRAETEALIAGLERLPMKAMPHHKLDDRVLQEFDLDGALARRPALILVDELAHSNASGSRHPKRWQDIEELLSAGIDVWTTVNVQHLDSLNEAVGGITGIRVWETVPDTVFDDADEVILVDLPADELLRRLRDGKVYLPEQARTAATNFFRKGNLIALRELALRRTADRVDDDVRAYRHAESIRPVWRTREAVLACIGTGDDAAQVVKSARRLAGQLDCDWHVVTVATPRLAPLGGHERANIEEAMRLAEELGARTETLAGSDIVQAVAGYVRRHNLTKVVVGRAPGNWRRSGGSLLARGRALLALGLSPFLGARAWLFGRHSFADSLALGCPEIDVIRVAADAMGADTRGRAQPAGGRADVREDPAPNDDSSVVAHRIDYLWAVAWCGGASLLSALTRPWFDLVNIAMLFLAAVVGVALRHGRGPAALASVLSVAAFDFFFVPPRMSFAVSDVQYLVTFAVLLTVGLVIGQLTAGLREQAQVSVERETDARTLYELARELSAALMPEQIIDISSRFLQAALGARSAFFLVSPKGRLLPPVIDPTQRGNDAIDPVLAQWVFDHGQPAGTGTHTLPGSTVLYLPLKAPMQTRGVLAVEPQKWRAFARPERRRQIDVFATLIAIAIAERLHYVEVAQQALVSMESERLRSSLLAAVSHDLRTPLTSLIGMAETMQRTEPPLPASLSETVDAMREQALRMRTMVVNLLDMARLQSRDVRMQKEWQSLEELVGAALAGMRDALSRHRVSVADLSALPLVECDAVLMERVLCNLLENAAKYTPPGTGIRISGEVAETEVRLAVADDGPGVPRGQELSIFQKFTRGERESATAGVGLGLAVCEAIVQAHGGRIWVESVNADHTGARFVVALPRGNPPAIEPEPPEALESALLAAHGNGGVPVAHDAANKESS	29~~KdpD (9.00623E-120)~~242;X;265~~Usp(2.25299E-31)~~371;X;453~~DUF4118 (8.75719E-23)~~552;X;579~~GAF (7.72505E-18)~~698;X;715~~HisKA (0.000000000000182756)~~780;X;833~~HATPase_c (1.36855E-26)~~936	KdpD protein
	4E-14	62.2	12.9	6.2E-14	61.5	9	1.3	1	I4MR07_9BURK	Histidine kinase (EC 2.7.13.3)	Q5W_1528	Hydrogenophaga sp. PBC	907	795665	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Hydrogenophaga, Hydrogenophaga sp. PBC	>tr|I4MR07|I4MR07_9BURK Histidine kinase OS=Hydrogenophaga sp. PBC GN=Q5W_1528 PE=4 SV=1MNDTPQRPDPDILLAQVQADEDRARRGRLKIFFGASAGVGKTYAMLSAARAAQAEGTAVTIGVVETHGRPETQALTQGLPRLPLRSVPHKGHALHEFDLDAALAFGAAHPGALVLLDELAHSNAPGSRHPKRWQDAEELLATGVDVWTTMNVQHLESLNDVVSGITGVRVWETVPDRLFDEADEVVVVDLPPDELLERLHSGKVYLPTREGDDQRAERAAANFFRKGNLLALRELALRRTADRVDDEVRAFRQAGAVRPVWPNRESLLACVGPGASADKVVRSAARMAAQLDVPWHAVHVQALSHEPDAATQKALDLAESLGASVSSFSDRDPAAALVRHAREHNLTRLVLGRSRRAWPWARPMAERIAAQAGELELLHVAEPHGQRERSEPAHAPGEVPRGPRWPGYVAATVACGLTALLATPLIPVLELSNIVMIFLLVVVGIALRFGRGPAVLAAFLGVALFDFFFVPPRFTLAVSDVEYLVTFAVMLVVALAIGQLTAVLRQQADAATRRERRVRALHDMSRDLSAALLPEQVADIGARFVQAEFGMRSTLLAADEHDRLQALPGGQAPVDMAVTQWAFERGEPAGRGTDTLPASATLVVPLKAPMRTRGALVIDPGATVAPGTGQRQALDTEQRRALQACASLLAISLERIHYIEVAQHSTVQIESERLRNSLLAAISHDLRTPLASLVGLGDALRLTPPPLAPAQAELAEAIAQSARRMAALVTNLLDMARLQAGAVPLQRAWQPLEEVVGSALAACGDALHGRAIDVHLPADLPLLQFDAVLMERVLVNLLENAAKYTPAGSAIRLWAAADAESVRLCVDDHGPGLPRGQEARIFEKFERGARESATPGVGLGLAIGRAIVEAHGGRIEGRNRERDGRVEGARIEITLPRGTPPADNSTQ	24~~KdpD (7.2088E-102)~~244;X;267~~Usp(5.32913E-27)~~381;X;408~~DUF4118 (6.57787E-24)~~507;X;534~~GAF (0.000000000000752615)~~655;X;672~~HisKA (0.000000000000653236)~~737;X;790~~HATPase_c (7.85769E-26)~~895	KdpD protein

	4E-14	62.1	8.6	4.1E-14	62.1	6	1.8	1	A0A068NN19_9BACT	Histidine kinase (EC 2.7.13.3)	OP10G_0757	Fimbriimonas ginsengisoli Gsoil 348	879	661478	cellular organisms, Bacteria, Armatimonadetes, Fimbriimonadia, Fimbriimonadales, Fimbriimonadaceae, Fimbriimonas, Fimbriimonas ginsengisoli, Fimbriimonas ginsengisoli Gsoil 348	>tr|A0A068NN19|A0A068NN19_9BACT Histidine kinase OS=Fimbriimonas ginsengisoli Gsoil 348 GN=OP10G_0757 PE=4 SV=1MLRIAQREMTERTRGRLKIFLGMSAGVGKTYAMLSEAHEQIARGIDLVVGYAETHGRKETEALLVGLPSLPLREVEHRGILLKEFDIDEALRRRPRLLVVDELPHTNAPGSRHLKRYQDVEELLAAGIDVHTAINIQHVESLRDVVASMTGVFVQETVPDTFIDAADEIELVDIPPDELRQRVQEGKVYVPAQTERALEGFFCRGNLLALRELALRRAADRVDAEIQSFRRADASPGSMGSRQRILVCVAPNRLGERVIRAAARYGTAMHAQVLAISVISDRQTNRSDEDRDRAERAMRLAEALGMETLSRSGHDIVAEILTVARQRGAGLIIVGKPIRSRWHELVRGSVVDDLVRRSGDIDVHVITGESETPSERPTPIQVADARPEEYAASVLAVAATTALCFLLSPWVHLSNLIMLYLLAVGLVSTRVGRGPSLLSAILSVAAFDFFFVSPRYTFAVSDVEFLPTFVVMFAVSVILSGLNSRFRRQAADAASRERRTSALYEVSRDMAASRTKQEIAEAAARRIGDEFDTDAVLLPDARSMLTVVVPSVTSFEADDSEMAVAQWAFEHGKPAGAGTDTLPGSAAMYLPLRASRGSVGALALSPRSKSEALTLAQRTLLETFATGLAVALERTLLAKESHEARLQAESEKMRNALLSSISHDLRTPLTAIAGAASAMRERGGAEQELAETIYEESMRLNLQVQNLLDMTRLNSGEIRPNVEWQSLEELIAAALDRTRVVLSDRPVEIHIPSDLPLLELDGALMEKVFANLFENAAVHAQGNSPIEVSAWAGDETVYVEVSDRGPGIPVGSEATIFERFQRPKRDGDGGRFGLGLAICRAIVRLHGGRIWAKNRTGGGSTFVIELPKPDRAPEVPVG	14~~KdpD (2.41379E-105)~~206;X;244~~Usp(9.65402E-34)~~367;X;390~~DUF4118 (1.21375E-22)~~489;X;517~~GAF (2.38162E-14)~~635;X;652~~HisKA (0.000000000034671 7)~~713;X;766~~HATPase_c (3.36347E-29)~~867	KdpD protein
	5E-14	61.9	12.8	8.9E-14	61	8.8	1.5	1	K8WI51_9ENTR	Histidine kinase (EC 2.7.13.3)	OO7_12939	Providencia sneebia DSM 19967	638	1141660	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia sneebia, Providencia sneebia DSM 19967	>tr|K8WI51|K8WI51_9ENTR Histidine kinase OS=Providencia sneebia DSM 19967 GN=OO7_12939 PE=4 SV=1MRAAARLAAKLGCVWHAVYVETPTLHQLPEGKRRAILKALRLAQNLSAETATLSDPSKEKAILRYAREHNLGKILIGRRDKRRQWAKIQFRSGFAERLGKLGPDLDLVIVALEEQSDWDKEPERKPFAEKWRSDINGYLVAIVMCAAITLFSRAFLLALDKANLVTLYLLGVVLIALFYGRRPSIFAALINVISFDLFFVQPHFSLAIIDMQYLITFTVMLIVGLVVGNLTAGMRYQARIARYREQRTRHLYEMTKELGQALNTEEIGRTGYHFINNAFQAKTCLLMPNENGELLPLQCQGFSSLQIDKAIAKWCFDKRQPAGAGTDTLPSVPYQLQPITTADKTLAVLAIEPRNIRQLLIPEQQRMLQTFTGLIAGALARLQLAQQAELAKLDIEREQLRNSLLAALSHDLKTPLTVLFGQTEILMLNLSAANSPFTEQVDKMRQQVLSTSRLVNNLLDMARLQSGSIQPNLEWESLQEITSSAVRTLDYTLHSHPLDIDIPADLLLYCDANLIERVLINLLENAVKYSSEDTPIGIKAYIEKPVGIEKSEGTQKIHIEVWDASNAIPDGQEKTIFDKFSRAQKESAIPGVGLGLAICRAIIQLHEGKIWAQNNDKGGASFHFILPLKQLPEIESEI	12~~Usp(1.18704E-25)~~111;X;138~~DUF4118 (6.13095E-22)~~237;X;263~~GAF (1.02572E-15)~~381;X;398~~HisKA (0.000000000115701)~~463;X;515~~HATPase_c (9.813E-23)~~626	non-KdpD DUF4118 protein
	5E-14	61.9	10.4	9.6E-14	60.9	7.2	1.6	1	Q0K2T7_CUPNH	Histidine kinase (EC 2.7.13.3)	kdpD2H16_B0895	Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	948	381666	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Cupriavidus, Cupriavidus necator (Alcaligenes eutrophus) (Ralstonia eutropha), Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) (Ralstonia eutropha)	>tr|Q0K2T7|Q0K2T7_CUPNH Histidine kinase OS=Cupriavidus necator (strain ATCC 17699 / H16 / DSM 428 / Stanier 337) GN=kdpD2 PE=4 SV=1MPDAELREAGSRPDPDALLQMVQEEGARASRGKLRVYFGASAGVGKTFAMLTAARTASARGTDAVIGIVETHGRAETEALIAGIERLPMKDVPYRERVLQEFDLDAALVRRPALVLVDELAHSNAPGSRHPKRWQDIQELQAAGIDVWTTVNVQHLDSLNEAVGGITGIRVWETVPDVVFDSADEVVLVDLPADELLRRLKEGKVYLPEQARHAARNFFRKGNLIALRELALRRTADRVDSDVRAWRQSEAVQGVWRTREAVLACIGSGDDAEQVVRSARRLAGQLDCDWHVVTIATPRLAPPSDFAKTRLQTAMRLAEELGARTETLAGNDMVQAIVGYVRRHNLTKVVIGRAPADWRRGGASVAERARSLLGLALTPFVNAPAWLFGRRSFADALALGCPEIDIIRVAADTTRVDLRPRHGTEAPDAPAPGDGATRKDYLWAAAWCAGATALSALAFPWFDVVNIAMLFLAAVVGVALRHGRGPAALASVLAVAAFDFFFVPPRLSFAVSDVQYLLLTFLVLLSVGLVIGQLTAGLREQAQVAVQRENDARTLYELARELSAALVPNQIVSIASRFLRAAFDANSAFFLVSAEGRLLPPVSDVEQHDTGARTDSIDRVLAEWVFDHGQPAGTGTHTLPGSTVLYLPLKAPMQTRGVLAVEPAVSRAFAQPALRRQVDVFCTLIAIAIERLHYVEVAQLALLSMESERLRSSLLAAVSHDLRTPLTSLIGMAETMQRSDPGLAPSLAETVAAMLEQARRMRTMVVNLLDMAKLQGREVRMSKEWQSVEELVGASLAAMREALEHHRVVVVDLSRVPLVECDAVLIERVLCNLLENAAKYTPAGTEIRLSAAPVDDEIRIAVEDDGPGVPKGKERQIFEKFTRGERESATAGVGLGLAVCEAIVQAHGGRIWVEPAQRPDRPGGQAGARFLVALPRGNPPAVEPEQTDA	29~~KdpD (6.33579E-118)~~239;X;262~~Usp(6.94588E-32)~~360;X;454~~DUF4118 (0.000000000000427 46)~~540;X;567~~GAF (2.50938E-16)~~690;X;707~~HisKA (0.000000000000373 313)~~772;X;825~~HATPase_c (2.09923E-28)~~933	KdpD protein
	5E-14	61.9	8.4	6.9E-14	61.3	5.8	1.3	1	Q188W9_PEPD6	Histidine kinase (EC 2.7.13.3)	CD630_05200	Peptoclostridium difficile (strain 630) (Clostridium difficile)	535	272563	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptoclostridium, Peptoclostridium difficile (Clostridium difficile), Peptoclostridium difficile (strain 630) (Clostridium difficile)	>tr|Q188W9|Q188W9_PEPD6 Histidine kinase OS=Peptoclostridium difficile (strain 630) GN=CD630_05200 PE=4 SV=1MKKERLQHEDLKEYDYDEDGYLSKKIIIKDFIKTILVMTIATGISVVFEKVGFNESNIILVYILGVLFATSITYGYFFGILSSVIGVLSFNFFFTHPLYTFLAYRKDYPMTFCIMLMAAIITSTLTSRIKREVRLSHKREKMIRLLYENNKTLLKAKNKNQIIEFCGSNLVNILNRTVIVTIADENNNLGKPSIYICNNDGSENIFHSVLEKEAIKEAFRTGNPVGIGTKYCKNSSAYYFPIKGQESNVLGVIGVACFKIDIITENEKILLEAVSTQVALAIDRENLFEKNKKANLEAERERLRGNLLRSISHDLRTPLTSILGSSSTILENDDVIDKETRVELLKNIYEDTSWLTHSVENILSMTRIDEGKLDIEKRPEVVDEIIAESILRVKKFANSRDIKTNIPDEIIIVHVDVLLIEQVLVNLIDNAIRHTPKNSKIELTVKKESNQVLFEVADNGKGIPNEDIGNIFNRFYTKNKSRNLERRGIGLGLEICKSIVEAHGGEIVAFNNPSGGATFRFSIPMYDEEGKDKWK	30~~DUF4118 (2.5857E-19)~~132;X;158~~GAF (0.00000048765)~~284;X;301~~HisKA (0.000000000087699)~~367;X;420~~HATPase_c (3.6195E-30)~~523	non-KdpD DUF4118 protein
	5E-14	61.9	7.5	7.6E-14	61.2	5.2	1.3	1	A4JGG6_BURVG	Histidine kinase (EC 2.7.13.3)	Bcep1808_2370	Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))	997	269482	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia vietnamiensis, Burkholderia vietnamiensis (strain G4 / LMG 22486) (Burkholderia cepacia (strain R1808))	>tr|A4JGG6|A4JGG6_BURVG Histidine kinase OS=Burkholderia vietnamiensis (strain G4 / LMG 22486) GN=Bcep1808_2370 PE=4 SV=1MNRPDPDQLLDKLQRDAAKQRRGQLKVFFGASAGVGKTYAMLQAARQRKQDGVDVVVGIVETHGRSETAALLDGLDVLPLAHIEYRGRTLAEFDLDGALARAPQLILVDELAHSNVQGARHLKRWQDVHELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWETVPDRVFDAADEVTLVDLPAEELLERMRDGKVYLAQQAERAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADRSIQRIWQARERLLVCIGPGPEAPTLVRAAARLAASLKADWIAVYVETPRLQRLPDARRQRTLDALKLAAELGAETATLAGDDAVAALIGYAKVRNVSKIVAGGSPKVGVVRRFARPFGEQLAERAGDVDLMLIRASASDEVRAAPLDARARDWRDAFAQFGTRRSPPRHYLYAAAICAAITGLASVVSGRLDLTNLVMLYLLGVVFSAVRLGRGPGVLQSFLSVAAFDFFFVPPRMSFSVSDTQYLLTFFGMLLTSLVISHLTSTLTRQASIAQRRERRTGAIYAMARELGAALTTEQIVEIGSRHVSEVFRARVAFLLPDSADQVRQKIEDPDAAVTLTGAELDSDVGQWVYDQQKPAGRGTDTLPATAALYLPLKAPMRTRGVLAVVSREPHELEVPEQQRMLDAFAAQIALALERVHYVEIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLANGRAAAEGASASLASPASPESSASPVSSAAPAAPAAPTTPTTPTTPAPPSPLDAAAAQRLAQRERELVDAIHDEALRMTGIVTNLLDMARLQAGSLQIKRQWSLLEETVGAALAACKRVLARHPARVSLPADLPLLQMDAVLMERLFTNLFENAAKYTPADAPIEIGAERVSDDGQPFVRVYVDDHGPGLPHGMETRIFDKFTRGKESATPGIGLGLAICRAIVEAHGGKIGALNRTAPDGRVTGARFWFTLPVDTPPAVPAAPDDDIDDDIDAPGASFPSEPLPDHD	21~~KdpD (4.53325E-113)~~230;X;252~~Usp(2.79606E-32)~~374;X;410~~DUF4118 (4.66414E-22)~~510;X;536~~GAF (1.03045E-17)~~659;X;676~~HisKA (0.000013224)~~798;X;851~~HATPase_c (2.62652E-22)~~961	KdpD protein
	6E-14	61.7	8	1E-13	60.8	5.5	1.5	1	O7DEJ3_PSEFL	Deleted.									

	6E-14	61.5	13	1.2E-13	60.6	9	1.5	1	K0I504_9BURK	Histidine kinase (EC 2.7.13.3)	C380_12765	Acidovorax sp. KKS102	910	358220	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax sp. KKS102	>tr|K0I504|K0I504_9BURK Histidine kinase OS=Acidovorax sp. KKS102 GN=C380_12765 PE=4 SV=1MPMQDRPDPDALLQRIQQEQAQQQRGRLKVFFGACAGVGKTFAMLSAARAAQAQGLPVTIGVVETHGRT DTEALTAHLPRLPLRALPYKDRTLPEFDLDAALAWGAANPEGLVLLDELAHSNVAGSRHPKRWQDAEELLAAGID VWSTMNVQHLESLNDIVSGITGIRVWETVPDQFFDAADEVVVVDLPPDELLARLKAGKVYLPQQAERAAANFFRK GNLLALRELALRRTADRVDDEMRAYRRASTTTPEAVWPNREALLACVGTGDNAEKVVRSCARLAAQLDLPWHAV HVETPEQQGQSATLHPQVERTLKIAQQLGAAACAVLPAAQPAQALVRYAREHNLVRVVMGRSTRRWPWQATLA EQIGQSASDLDLLQVGTLPGRDAATDRKAPRTSTAAPRAAFWPGYIAAALACCIAAVIATPLANVLELTNIVMLFLLV VVGVALRFGRGPAIMAAFLGVGFFDFFFVPPRFNFAVSDAQYVVTFAVMLVVALVVGQLTAGLKVQAEAATDREH RVRSLYDMARDLSAALLPEQVAEIGARFITGEFSAGSTLVVADDDNRLQVLPGGTAPVDMAVAQWAFERGEPAG RGTDTLHSSPTLVLPLKAPMRIRGVLVVAMPQGQVPGVEPRRLLQTCASLLAISLERIHYIDVAQKSTVQIESERLR NSLLSAISHDLRTPLASLVGLAESLAMVQPPLPAHQQELTGAIQQSAQRMSALVNNLLDMARLEAGAVQLNKAWQ PLEEVVGSALAASAPAIAAHRVEVTLPDDLPLLQIDAVLMERVLVNLLENAAKYTPADTTIHISAQPQSDAVALTLTD EGPGLPKGREELLFEKFERGTRESATPGVGLGLAICRAIVQAHGGSIRGDTIHNAQGQPAGARFTLLLPRGTPPTD LGTDADTTSEV	>tr|A0A0A1B9F9|A0A0A1B9F9_9ENTR Histidine kinase OS=Pantoea sp. PSNIH2 GN=PSNIH2_18265 PE=4 SV=1MNDDIARPNPDALLQSGRHRGKLKIYFGACAGVGKTYAMLQEARRLRAQGLDVLVGIVETHEREETASLLE GLSVLPRRATGRSRYEEFDLDAALARRPAVILMDELAHSNVPGSRHPKRWQDIDELLEAGIDVMTTVNVQHLESL NDVVGGITGIQVRETVPDPFFDRADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALRELALRRT ADRVDDQMRAWRDAQGREKVWHTRDAILLCIGDNTGSEKLVRTAARLASRLGSVWHAVYVETPRLYRLSEARR RNILRTLRLAQELGAETATLADSDEAQAVLRYAREHNLGKIVIGRRPTRRWRRDSFADRLGQLGPDLDLLVVALEE ATRELTGQLSDTRAFGEKWATQLRGMAAALLLCALITFCGQYWLPDFDPANGVMIYLLGVVIIALRYGRWPSVAAT VMNILAFDLFFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRYQARVARYREQRARYLYELARSLSSALRH EDIAAAGQRSIFATLQARSALLLPDEKGELVITGDSSLTLPPDGAIARWSFSKGQPAGAGTDTLPAMPWQMLAKT QEKRWGLLVVEPDNLRQLMIPEQQRLLETYCVLLANALARSEAASRLAAEREQLRNALLSALSHDLRTPLTVLFGQ AEMLMLDLSAENSTFTSQASQIREQTLSTIRLVSNMLDMARIQSGGLNLHQEWLLLEELVGSALTQLAAILPRDNV QLALPDGMVWLHGDSTLLERVFINLLENSVKYAGAQTPRGIRAVERAGRLEIEVWDSGPGIPAGQEEKIFDKFTRG DKESAVPGVGLGLAICKAIIETHGGQINARARAEGGASFLISLPQATPPALPEAEQEELK	28~~KdpD (3.97277E101)~~237;X;262~~Usp(5.12789E-25)~~382;X(155);537~~GAF (1.53964E-14)~~650;X;667~~HisKA (7.78624E-15)~~732;X;785~~HATPase_c (7.2271E-27)~~891	KdpD protein
	6E-14	61.4	10.9	1E-13	60.7	7.6	1.3	1	D8ML40_ERWBE	Histidine kinase (EC 2.7.13.3)	kdpDEbC_43370	Erwinia billingiae (strain Eb661)	889	634500	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Erwinia, Erwinia billingiae, Erwinia billingiae (strain Eb661)	>tr|D8ML40|D8ML40_ERWBE Histidine kinase OS=Erwinia billingiae (strain Eb661) GN=kdpD PE=4 SV=1MNDELHRPDPDSLLLQATESGRGKLKIYFGACAGVGKTWAMLQEARRLRAQGLEVLVGVVETHGREETAA LLDGLTVLPRKATGQNRHPEFDLDAALARHPAVILMDELAHTNAPGSRHPKRWQDIEELLDAGMDVMTTVNVQHL ESLNDVVGGVTGIRVRETVPDPFFDAADEVVLVDLPADDLRQRLKEGKVYIGDRAERAIENFFRKGNLFALRELAL RRTADRVDDQMRAWRDSQGREKVWHTRDAILLCIGDNTGSEKLVRTAARLAARLDSVWHAVYVETPRLHRLSEA RRRGILRTLQLAQDLGAETATLSDPDDANAVLRYAREHNLGKIILGRRSARRWRRDSFAERLGKLGPDLDMVIVAL DEPVSAPASALADNRPGGDKWRNPLRGCLASLILCSLVTLAGRWLLPGVDSVNLVMVYLLAVVVVALRYGRWPS VVATVLNIVAFDLVFVMPTGTIAVSDVQYLVTFGVMLAVGVIVGNLTAGVRYQARVARYREQRARHLYEMAKTLSR ALSQQDIAQALPRSLDTTLQARSELLLPDEQGELVAVGESRLNNVPDNAIARWSFDKGQPAGAGTDTLPGVPWQI LPLKSGNETLGLLVLEPLNLRQLMIPEQQRLVETFTVLIANALERIALSQREAVSRLAAEREQLRNALLSALSHDLRT PLTVLFGQAEILTLDLATEGSKHAIQASEMREQTLNTIRLVNNLLDMARLQSGGFSLRAEWMALEELIGSTLKMMA PSLGNRKVALALPQEMLLIHVDGPLMERVLTNLLENALKYAGDDAQIGIRAGVQAQRLEIEVWDSGPGIPGGQETQ IFEKFSRGNKESAVPGVGLGLAICQAIVSIHEGKIRAENRAEGGARFIITLPVKEPPVIEEYQ	20~~KdpD (4.4394E-120)~~228;X;251~~Usp(4.52389E-34)~~370;X;400~~DUF4118 (0.000000000070009 5)~~498;X;524~~GAF (5.43205E-14)~~641;X;658~~HisKA (0.000000007752 61)~~723;X;776~~HATPase_c (8.04794E-28)~~877	KdpD protein
	7E-14	61.3	11.1	1.5E-13	60.3	7.7	1.6	1	C5CPD0_VARPS	Histidine kinase (EC 2.7.13.3)	Vapar_4991	Variovorax paradoxus (strain S110)	920	543728	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Variovorax, Variovorax paradoxus, Variovorax paradoxus (strain S110)	>tr|C5CPD0|C5CPD0_VARPS Histidine kinase OS=Variovorax paradoxus (strain S110) GN=Vapar_4991 PE=4 SV=1MSDIPRPDPDALLAQLRSDEARALRGKLRIYFGASAGVGKTWAMLSAAQRERAAGRDVLIGVAETHGRSET AALLAGLELLPLREVDHRGRRLAEFDLDAALARKPAVLLVDELAHTNAPGSRHAKRWQDVQELLAAGIEVWSALN VQHLESLNGTVGAITGVRVHETVPDTVLDEADEVVLVDVTPDELAARLAAGKVYLPQQAERAAQNFFRKGNLIALR EIALRRTAEHVEDDVRGWRVEQSGAAGRNGKDGQGGELQAWNTSGAILACVGPHEGDAQTVRTAARLAGQLN VRWHAAYVETPRLQRLAAEERDRILAVLKLAEELGAATAVLTGSDVAEQLAEQARRLNCATLVLGQPEPATGWRR WWPATPMPLPRALARRAPALDIMEVGRADSSRRLSRAPIAATRADDDDHEKAPVHWPGYAWATAASIALTLLCT PLAHVLELSNIVMLFMLGVVGVAMRFGRGPSALAALLNVAAFDYFFVPPRLSFAVSDVQYVLTFAIMLGVGLLVGQ LMAGLRFAAGVSTSRERRARSLFELTRELSAALESTQVVALGAAAVQGHFGGQALVLVTDAADQLVLPKSPPEGF DAQVADWAFRHGQPAGLATATLAAQPWHYVPLQAPMRVRGVLALSPAQPRWLLIPEQAQQLDTLARQIAIALER VHYVEVAQQAVVEMESERLRNALLGAISHDVRTPLTALIALAESLQTLPPEAHAEAARAIVAQAHELHALVNNLLDM ARLESGIAGGAVNLRRDWQSVEEVVGSAIRAARPALGPAVVQTALEPGLPLVEFDAVLIERVLVNLIENATKYGAP PIVVGARAEPGMLRLTVRDHGPGLPAALLGREQKLFDKFTRGETESATPGVGLGLAICRAVVSAHGGEIAAANAQ GGGAEFTVSLPRREPPETAEEAQP	25~~KdpD (1.12176E109)~~233;X;269~~Usp(2.32151E-28)~~395;X;428~~DUF4118 (2.88072E-15)~~525;X;556~~GAF (0.000000000172446)~~668;X;685~~HisKA (0.000000000299846)~~747;X;804~~HATPase_c (7.01953E-23)~~906	KdpD protein
	7E-14	61.3	9.4	1.2E-13	60.6	6.5	1.4	1	A0A0A1B9F9_9ENTR	Histidine kinase (EC 2.7.13.3)	PSNIH2_18265	Pantoea sp. PSNIH2	887	1484157	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH2	>tr|A0A0A1B9F9|A0A0A1B9F9_9ENTR Histidine kinase OS=Pantoea sp. PSNIH2 GN=PSNIH2_18265 PE=4 SV=1MNDDIARPNPDALLQSGRHRGKLKIYFGACAGVGKTYAMLQEARRLRAQGLDVLVGIVETHEREETASLLE GLSVLPRRATGRSRYEEFDLDAALARRPAVILMDELAHSNVPGSRHPKRWQDIDELLEAGIDVMTTVNVQHLESL NDVVGGITGIQVRETVPDPFFDRADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALRELALRRT ADRVDDQMRAWRDAQGREKVWHTRDAILLCIGDNTGSEKLVRTAARLASRLGSVWHAVYVETPRLYRLSEARR RNILRTLRLAQELGAETATLADSDEAQAVLRYAREHNLGKIVIGRRPTRRWRRDSFADRLGQLGPDLDLLVVALEE ATRELTGQLSDTRAFGEKWATQLRGMAAALLLCALITFCGQYWLPDFDPANGVMIYLLGVVIIALRYGRWPSVAAT VMNILAFDLFFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRYQARVARYREQRARYLYELARSLSSALRH EDIAAAGQRSIFATLQARSALLLPDEKGELVITGDSSLTLPPDGAIARWSFSKGQPAGAGTDTLPAMPWQMLAKT QEKRWGLLVVEPDNLRQLMIPEQQRLLETYCVLLANALARSEAASRLAAEREQLRNALLSALSHDLRTPLTVLFGQ AEMLMLDLSAENSTFTSQASQIREQTLSTIRLVSNMLDMARIQSGGLNLHQEWLLLEELVGSALTQLAAILPRDNV QLALPDGMVWLHGDSTLLERVFINLLENSVKYAGAQTPRGIRAVERAGRLEIEVWDSGPGIPAGQEEKIFDKFTRG DKESAVPGVGLGLAICKAIIETHGGQINARARAEGGASFLISLPQATPPALPEAEQEELK	19~~KdpD (5.76948E122)~~226;X;249~~Usp(1.60439E-36)~~368;X;407~~DUF4118 (6.37052E-20)~~496;X;524~~GAF (0.000000000004223 8)~~639;X;651~~HisKA (0.0000000040967)~~716;X;769~~HATPase_c (5.48273E-28)~~870	KdpD protein

	8E-14	61.2	8	1.3E-13	60.5	5.5	1.4	1	B4E5Q8_BURCJ	Histidine kinase (EC 2.7.13.3)	kdpD BCAL2380	Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) (Burkholderia cepacia (strain J2315))	947	216591	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia cepacia complex, Burkholderia cenocepacia, Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) (Burkholderia cepacia (strain J2315))	>tr|B4E5Q8|B4E5Q8_BURCJ Histidine kinase OS=Burkholderia cenocepacia (strain ATCC BAA-245 / DSM 16553 / LMG 16656 / NCTC 13227 / J2315 / CF5610) GN=kdpD PE=4 SV=1MNRPDPDQLLDKLQRDEEKQRRGQLKIFFGASAGVGKTYAMLQAARQRRQDGVDVVVGIVETHGRSETAALLDGLDVLPPARIDYRGRTLAEFDLDGALARAPQLILVDELAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWETVPDRVFDAADEVTLVDLPAEELLERMRDGKVYLAQQAERAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPTLVRAAARLAASLKADWIAVYVETPRLQRLPDARRQRTLDALKLAAELGAETATLAGADAVAALIGYAKVRNVSKLVAGGSPKVGLARRFARPFGEQLAERAGDVDLMLIRASASDEARAAPLDARARDWRDAFAQFGTHRSPPRHYAYAAAICAAITVVASVVSGRLDLTNLVMLYLLGVVFSAVRLGRGPGVLQSFLSVAAFDFFFVPPRMSFSVSDTQYLLTFFGMLLTSLVISHLTSTLTRQASVAQRRERRTGAIYAMARELGAALTTEQIVEIGSRHVGEVFRARVAFLLPDSADQVRQKIEEPDAAVTLTGAELDSDVGQWVYDQQKPAGRGTDTLPATAALYLPLKAPMRTRGVLAVASREPRELEVPEQQRMLDAFAAQIALALERVHYVEIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLANGRAAAQAGDAAAAARLAQREGELVDAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGAALAACRRVLARHPARVALPADLPLLQMDAVLMERLFTNLFENAAKYTPPDTSLDIGAERVTDDGQPFVRVHVDDHGPGLPAGMETRIFDKFTRGEKESATPGIGLGLAICRAIVEAHGGKIGALNRTAPDGHVTGARFWFTLPVDTPPAAPAVSDDEPDLPGASPPSESLPDHE	21~~KdpD (2.62463E-113)~~230;X;252~~Usp(6.16622E-32)~~374;X;422~~DUF4118 (2.73463E-19)~~510;X;536~~GAF (2.2816E-18)~~659;X;676~~HisKA (0.000000000077190)~~752;X;805~~HATPase_c (1.49668E-21)~~915	KdpD protein
	8E-14	61.2	15.7	1.5E-13	60.3	10.9	1.5	1	A0A068R7B7_9ENTR	Histidine kinase (EC 2.7.13.3)	kdpD XPG1_2374	Xenorhabdus poinarii	895	40577	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus poinarii	>tr|A0A068R7B7|A0A068R7B7_9ENTR Histidine kinase OS=Xenorhabdus poinarii GN=kdpD PE=4 SV=1MAQHEPQRPDPDELLTLANAKPRGKLKIFFGACAGVGKTYAMLQEAQRLLAQGLDVIVGVVETHERQETAALLKGLPQLPAKYVHHHKRRIATFDIDAALARHPAIILMDELAFSNPKGCRHPKRWQDVEELLETGIDVLTTINVQHLESLNDIVGGITGVRVRETIPDHIFDQADDVVLVDLPPDDLRQRLNDGKVYISGQAERAIEHFFRKGNLIALRELALRRTADRVDEQMRAFRDTHGREPVWHTRENLLLCIGDNAGNEKLIRKAARLAAKLNCVWHAVYVETPKLHRLPESKRHAILQSLKLAQDLGAETATLSDPHQEKAILRYAREHNLGKILIGRYYGSQPNILGFKWHRDFSERLGKLGPDLDLIIVALEDKKRGDKELKDNRTSHDKWFVPVQGFLVAVVLCVLITFFSWAFLVTLDQANLVTLYLLGVVMIALFYGRWPSVFAAFINVISFDLFFVQPHWSLAVKDMQYLLTLTVMLIVGAVVGNLTAGIRYQARIARYREQRTRHLYEITRELSKALSEEDIARISYHFLSNSFQAKTGLLLPDCHHHLYQISAHNGGQMRIDEAIAKWCFDKKQPAGAGTDTLPGVPYQLLPIATPAQVFAVLAIESPNLRQLLVPEQQRLLHIFTGLIANALERLHLARKAESAKLDAEREQLHHSLLVALSHDLRTPLTVLFDQSKVLMRDLAGGNSPYTQQVNQIHQQILSTSRLVNNLLDMARLQSGEIQLNLEWHSLEDIVDNAFRSLAYALNHYTVALSLPNDLLLYCDATLLERVFINLLENAIKYTHEKTPLGILATIEKVTSQQLHVEVWDAGTGIPPGQEKHIFEPFSYANQASPIRGIGSGLAICRSIIEIHGGKIWTANNKKGGASFHFLLPLAAPKN	23~~KdpD (1.14697E-119)~~231;X;254~~Usp(7.5118E-35)~~379;X;407~~DUF4118 (5.09004E-22)~~506;X;532~~GAF (5.90852E-16)~~650;X;667~~HisKA (0.000003401 02)~~732;X;784~~HATPase_c (1.72378E-23)~~888	KdpD protein
	9E-14	61	10.9	1.3E-13	60.4	7.6	1.3	1	A0A0A1H5J5_9BURK	Histidine kinase (EC 2.7.13.3)	E1O_24670	Burkholderiales bacterium GJ-E10	917	1469502	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, unclassified Burkholderiales (miscellaneous), Burkholderiales bacterium GJ-E10	>tr|A0A0A1H5J5|A0A0A1H5J5_9BURK Histidine kinase OS=Burkholderiales bacterium GJ-E10 GN=E1O_24670 PE=4 SV=1MADQRPDPDALLARIQNEAERAARGRLKLFFGASAGVGKTYAMLSAARRQRDQGVDVVIGVVETHGRSETEALTLGLERIPLREIAYRDRTFAEFDLDAALQRKPALILVDELAHSNVEGSRHPKRWQDVEELLAAGIDVYTTINVQHLETLNDVVSGITGVRVRETVPDRVFDRADEVVLVDLTPDELLQRLKDGKVYISRQAESAVRNFFRKGNLIALRELALRRTADRVDGEMLQYRRDRAVAPVWQTRDSLLACVTAGADDDRVVRTAGRIASRLEIPWHAIYVETPERTRIGDAARQAVMKALKLAQSMGAETATLADHDEVAATVRYARDHNLSRMIVGHSGPLRRWLPRGWSARTGLSRAGLPIWHRSFADRLAGSAPDLEVTIVSAVDPASAGSRSPAREDRFVFEAGSLPAYAGAAAVCAGAALISAPLQSIFTLPNIVMLFLLAVVLVALRFGRGPAVLASFLSVLEFDFFYVPPKFSFAVSDVQYLLTFAVMLAVGLIAGQLTAGLKYQARVANRREGRVRGLYEMARDLSGALLPDQIAEICERFLDRELHAQATLLLADDQEKVVLPRDDGDRADSVPLEPGIAQWALDHGEAAGMGTNTLPATPALYLPLKAPMRMRGVLVVRPREAARLQGPEQSRLLDTVARLAAIALERVHYVDVAQRVSLQMESERLRNSLLSAISHDLRTPLAALVGLADSLQWSGGTPVQQKAIVERMREQTQRMRSLVENLLDMARLQAGQVALNRQWNAIEEVVERALRAMAHALAAHVVRVQLPADLPMLEMDAALMERVFDNLLENAGKFTPPGSVIDIGARAEPERVVLWVEDNGPGVPRGKEEAIFSKFERGHVESATPGVGLGLAICRAIVEAHGGIIRAENRPGGGARFWIELPRGNPPDVPAESVDLQ	22~~KdpD (7.61416E-124)~~232;X;255~~Usp(5.60216E-29)~~393;X;433~~DUF4118 (8.69707E-21)~~520;X;547~~GAF (2.52212E-16)~~666;X;683~~HisKA (0.000000000000162152)~~747;X;800~~HATPase_c (4.0514E-29)~~901	KdpD protein
	1E-13	60.9	8.3	1.6E-13	60.2	5.7	1.3	1	B5EH77_GEOBB	Histidine kinase (EC 2.7.13.3)	kdpD Gbem_2605	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	892	404380	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	>tr|B5EH77|B5EH77_GEOBB Histidine kinase OS=Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622) GN=kdpD PE=4 SV=1MRDDAARPSPETLLKVAKAEEEAQSGRGKLKIFLGYAPGVGKTYAMLEAAQMRKREGRDVVAAYVESHGRAETDLLLEGLEVIPKLRIEYQGVQLSEMDIDTVLARKPQIALVDELAHTNAVGSRHEKRWQDVEELIYAGIDVYTTVNVQHFDSLNDIVAQITGVVVRETVPDKLLDLALEIRVVDIPPEDLLERLREGKVYIPEKAMLATEKFFKPGNLMALRELSLRRAASRVDDQMRAYMEARSIAGPWPAAEKLLVCVSGSPYSEKLIRTTRRLADEVKARWHTVYIETPGLSKHARENRERVWRDLRLAESLGAEVATLSSASVAQALVEFAVHNNVTKIVVGKPKKPRWREFLRQPLVDEIIRLSGPVDVYVVSIAATGETPKAAQVHPKKPVQWTGYLKGSALVVAVTLLCKVLQGFLAPTNLMMIYLLGLVLAATKLGRRPAVLTALLSVLAFDFFFVPPRLTFAVADTEYLITFIALFTVGFVISTLVSQTRERAESIREREEQTATLYYLSRDLTVASDLRGILLAATLKNIEDSVGGMVAVLLPEGERLELQAASGGLTLDTKEHAVADWSFRNSSPAGRGTETLGSSELLYLPLLTSGDVLGVLGVRLKSETEYTSPLTRRLLHAFATQTAFAIERVLLVKQAEQAQILRARENLERALLNSISHDLRTPLVSISGALGALRDRTTYLEEESRRDLLEAAWEEAGRLNRFVGNLLDMTRLEAGAMKPKRVPSDLQDLIGCALASLEPQLSKLAATLKNIEDSVGGMVAVLLPEGERLELQAASGGLTLDTKEHAVADWSFRNSSPAGRGTETLGSSELLYLPLLTSGDVLGVLGVRLKSETEYTSPLTRRLLHAFATQTAFAIERVLLVKQAEQAQILRARENLERALLNSISHDLRTPLVSISGALGALRDRTTYLEEESRRDLLEAAWEEAGRLNRFVGNLLDMTRLEAGAMKPKRVPSDLQDLIGCALASLEPQLSKRKLTVRVDPGPLVSMDMVLMTQVLVNLLDNALKYAPSNELIELESRALDGKVTLKVADRGPGVPPQDLERIFDKFYRVPVVPEGAGGTGLGLSICKGIVEAHGGTIHAENREGGGLKITVQLPVEGEGHG	25~~KdpD (2.11039E-118)~~235;X;257~~Usp(2.17304E-44)~~380;X;404~~DUF4118 (2.03976E-19)~~503;X;529~~GAF (0.0000000031 94)~~647;X;664~~HisKA (0.000000000410465)~~730;X;785~~HATPase_c (3.9722E-32)~~884	KdpD protein
	1E-13	60.9	8.2	1.8E-13	60	5.7	1.5	1	A0A0E9M6B3_9PROT	Sensor protein KdpD (EC 2.7.13.3)	kdpD OYT1_01123	Ferriphaselus amnicola	506	1188319	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Gallionellales, Gallionellaceae, Ferriphaselus, Ferriphaselus amnicola	>tr|A0A0E9M6B3|A0A0E9M6B3_9PROT Sensor protein KdpD OS=Ferriphaselus amnicola GN=kdpD PE=4 SV=1MDTFHSSSVSKESGLVHQLWAIVACVLMTLVTQPLRDLVDLANIVMLFLLTVAIIAVWLGRKPAITASLVSIGLFDFFYVPPRFSFSVNDAQYLITFTVMLMVALIISHLTAGLRQNAIEAQRREQQIRALYALAQQLAGALTVEQASLDAQRFIRHLGMELHVLVPTLNEVLLTVGGEPVALDVAEMMVAKSVFSNNEAMELRSESPTKLVLPLSGVTRPRGVILVSAEREVLAQRPLLEAVASLMATALDRLHFVEVAQQHRMQMLTERLRSSILAALSHDVRTPLTVLYGLADTLTLPQYALPESAKETACAIRDQSLRLNNLVNNLLDMARLHAGQVQLRKEWQPIEEVIGASIKLLGVALQRHPVKVHLAADLPLIEFDAVLLERVFCNLLENAAKYAPLDTDIVMSARVVGVELEVTVANAGTGFPPDKLLKVFEPFERGIAESPVAGVGMGLAICRAVIEAHGGEISASNPESGGACVRFTLPLGEPPVIEQEAGELP	19~~DUF4118 (3.95158E-17)~~117;X(272);389~~HATPase_c (6.58065E-27)~~490	non-KdpD DUF4118 protein

	1E-13	60.8	9.1	1.7E-13	60.1	6.3	1.4	1	A5V6B3_SPHWW	Histidine kinase (EC 2.7.13.3)	Swit_1465	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	895	392499	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas wittichii, Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	>tr|A5V6B3|A5V6B3_SPHWW Histidine kinase OS=Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273) GN=Swit_1465 PE=4 SV=1MIHPPEPARADPDALLRAAAREARGRLKLFLGAAPGVGKTYEMLSEGAARLREGEDVVVGVVETHGRRETEALTRPFEIIPRRVSEHHGRPLSEMDIDAILARAPQLVLVDELAHSNAPGSRHPKRWQDVEELLAAGIDVYSTINIQHVESLNDVVASFTRVRVRETVPDHVLEQAEIEIVDIPPDELIERLKDGKVYVPEEASRALSHFFSKSNLSALRELALRRAAQAVDAQMLDHLRAHALGGTFAGGDRVLVAVSERPEAEALVRAAKRLADALRAPWTAIHVETGRSSGFGAAERERLARTLALAAQLGGGTASVPATDVVSGLAGYARDYRATQLVLGKSSRSWWFELRHGSVVDRIVRSAEGVAVHVLPIAGQAGAGLAARRTWREGLEARPFLWSLAMVAATVASAVGLRQLLDLNNVAMLFLLPVLAAAGRFGLRPGLFAGLVLAVSALAYNFFLLPPLYTLSISNPENVIAFFVLLIVAVVTSQLAARMRAQAELANRSARQNAALAGFAQRIADAANPDELAQAICGEIARLFNVNAMLFMPSPAGAALVAAVPTGHEPDQLDLAAANWTLEKGKPAGRGSDTLTASDWLFQPIAKGDRTLAALAVAHVDPDGAAIRSDELPLLLSLAHQSALAMDRMQLAEAMRELDVVRSRDRLRAALLSSVGHDLRTPLTTIRSAIGELGQSALAPTDAAIVDALDGEVERLDRFVGNLLDMARAQAGAITLAIEPIDLTDAVASAVHAVRKTLDGHDILLDIPPELPMVRADPQLLHHVLINLLDNAGRYAHPGTPLRIGARRGPDGLSLAIRDEGPGLPEGKETAVFETFTRFDGSDRARGGTGLGLAIARDFAAAMEVDIRAERCADPQGARFTLSWPDRLVVRIDPEALA	28~~KdpD (1.87655E-103)~~231;X;253~~Usp(1.54031E-41)~~376;X;399~~DUF4118 (2.3564E-20)~~499;X;525~~GAF (0.00000255026)~~645;X;662~~HisKA (0.0000000296748)~~725;X;778~~HATPase_c (1.59365E-21)~~880	KdpD protein
	1E-13	60.8	9.7	1.7E-13	60.1	6.7	1.4	1	V6F0X5_9PROT	Histidine kinase (EC 2.7.13.3)	kdpD MGMSRv2__1827	Magnetospirillum gryphiswaldense MSR-1 v2	901	1430440	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum gryphiswaldense, Magnetospirillum gryphiswaldense MSR-1, Magnetospirillum gryphiswaldense MSR-1 v2	>tr|V6F0X5|V6F0X5_9PROT Histidine kinase OS=Magnetospirillum gryphiswaldense MSR-1 v2 GN=kdpD PE=4 SV=1MNDDRHDRPSPDALLAEAQKESRGHLKIFLGAAPGVGKTYAMLETAHERRREGIDVVAGIIETHDRRETEALLADLDILPPRLAEYRGRSFREMDLDGLLRRRPRIALVDELAHSNIPGSRHLKRWQDVEELLAAGIDVYSTLNIQHLESINDIVEQISGVKVRETLPDSVLATADEIELIDLPPQDLIKRLEEGKVYVPEQARRAVHSFFSPGNLTALRELALRHAAERVDRQMVDYMRAHAIPGPWPARERILVCIDERVDAERLVRTAKRSAERRGAAWVAVTVETPAAHGLPEAAKDRIDAALRLAAQMGGDTVTLHGDDVGECVLSYAREHNCTQIVVGRARKAGWLRRWSRSVTDDLISRAGDFTVVLVGGEDETRPKPARPAVNKTDDTWLHLGLGYAVALLATAAATGLGFVIHPWLPIANISVGYLLAVMIVAMKSGLRPGILASAASFLAFNFFFTEPRFTFAITDTQNIVTVVFFLIAAFIISNMAARLRDQIRATRESARRTGNLYDFGRKISAAATQDDVLWAVVHHVSATIHGKSLVLLPGEAGLSIAAGYPPEDQIDDKSAGAADWAWSHGKIAGRGSATLPAAQWLFLPLKTGRGPVGVLGVQMTEDADLPSPGQMRLLETLADQAAVAIERTTMVADIETARVATERERLRAALLSSLSHDLRTPLVSIMGAASSLIAYDDKLDADGRRDLAQTIQDEAERLNRFVQNLLDMTRLGSGALKPRVDWVDLRDVVTAAVKRTERLARRHAIKVDIAPDTPLLCLDAVLMEQVIFNLLDNACKYAPPGSPVKVWAKRTADHIAIEVADQGPGIPPEDREKVFDMFYRVRAADTQEAGTGLGLAICRGIVEAHGGTIKAEPGLHGAGTCIIIHLPPPPDLDLDGKGNP	21~~KdpD (1.23255E-121)~~231;X;253~~Usp(1.09322E-39)~~376;X;419~~DUF4118 (2.07931E-18)~~503;X;529~~GAF (1.44705E-14)~~648;X;665~~HisKA (0.000000000000539)~~731;X;784~~HATPase_c (7.98645E-29)~~886	KdpD protein
	1E-13	60.7	6.8	1.8E-13	60	4.7	1.4	1	Q2SZS1_BURTA	Two-component system, sensor kinase protein KdpD (EC 2.7.3.-) (Universal stress family protein)	kdpD BTH_I1024 DR63_2806	Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	1035	271848	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, pseudomallei group, Burkholderia thailandensis, Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301)	>tr|Q2SZS1|Q2SZS1_BURTA Two-component system, sensor kinase protein KdpD OS=Burkholderia thailandensis (strain E264 / ATCC 700388 / DSM 13276 / CIP 106301) GN=kdpD PE=4 SV=1MNRPDPDQLLDKIQREEEKQQRGKLKIFFGASAGVGKTYAMLLAARARKQEGVDVVVGIVETHGRSETASLLDGLDVLPLMQIEYRGRTIGEFDLDAALARKPQLVLVDELAHSNVPGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGAITGIRVWETVPDRVFDVADEVTLVDLPAEELLSRLREGKVYMAQQAERAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPTLVRAAARLAASLKADWLAVYVETPRLARLPDALRQRTLNALKLAAELGAETATLTGADAVAALIGYAQVRNASKIVAGGSSKTGFLRRFSRPFGERLAERAGDVDLMLIRASAGEDARTPLDAGARAWRDTLSSVVDGRSPPRNYGYAAAICALITGVANLLQGHLDLTNLVMLYLLGVVFSAVRLGRGPGVVQSFLSVAAFDYFFVPPRMSFSVTDTQYLLTFFGMLLTSLVISHLTSSLTRGATIAQRRERRTSAMYAMARELGAALTAEQIVEIGSRHVSEVFRARVAILLPKSAGPNLRQLMVPEQQRLLQTFTSLIANALERLHLARSAELAKLDAEREQLRNSLLAALSHDLRTPLTVLFGQAEILTLDLAAEGSRHAPQANQIRQQVLSTTRLVNNLLDMARIQSGGFNLRKEWQSLEEIVGSALHMLETTLSHHQIRVELPGDMVLINCDGSLLERVFINLLENAHKYAGYDALLGIRATVQGEWLNVEVWDNGPGVTAGQEQLIFDKFSRGNKESAIPGVGLGLAICRAIIDVHGGRIWVEKGQDGGASFHFTLPLEKPPEIDGENIDTEK	21~~KdpD (1.52988E-122)~~230;X;252~~Usp(2.92886E-30)~~374;X;409~~DUF4118 (7.61905E-21)~~508;X;537~~GAF (1.18882E-16)~~658;X;675~~HisKA (6.51991E-14)~~741;X;794~~HATPase_c (2.88073E-22)~~904	KdpD protein
	1E-13	60.5	11.9	2E-13	59.8	8.2	1.3	1	W8TZ56_YEREN	Histidine kinase (EC 2.7.13.3)	kdpD LC20_01655	Yersinia enterocolitica LC20	899	1443113	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yersinia, Yersinia enterocolitica, Yersinia enterocolitica LC20	>tr|W8TZ56|W8TZ56_YEREN Histidine kinase OS=Yersinia enterocolitica LC20 GN=kdpD PE=4 SV=1MVDAEPTRPNPDSLLAVANEKSRGRLKVFFGACAGVGKTYAMLQEAQRLRAQGLDVLVGVVETHGRSETAALLAGLAILPPKRIHHRNRQVREFDLDAALARHPALILMDELAHSNAHGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGGVTGIRVRETVPDHMFDEATEVVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAFRDTQGRERVWHTRDAILLCIGHNSGNEKLVRTAARLAARLGCIWHAVYVETPRLHRLPEAKRRAILRSLKLAQELGAETATLSEPCEEQAILRYAREHNLGKIIIGRRTEKHWKLRGSFADRLGKLGPDLDLVIIALEGDTPSSVVKETDSRTFTEKWRMQLRGCAAAIGLCALITILSQWLIPGFDQANLVMVYLLGVVIIALFYGRWPSVLAAFINVASFDLFFVQPHWSLAVTDVQYLLTFAVMLIVGIVVGNLTAGVRYQARIARYREQRARHLYEMSRGLSRALTADIAKTSRHFLSSSFQAKTDLLLPQEDGRLQQITTDEGGALSVDEAIARWSFDRGAPAGAGTDTLPGVPYQLLPLTASQQTYGVLAIEPANLRQLMVPEQQRLLQTFTSLIANALERLHLARSAELAKLDAEREQLRNSLLAALSHDLRTPLTVLFGQAEILTLDLAAEGSRHAPQANQIRQQVLSTTRLVNNLLDMARIQSGGFNLRKEWQSLEEIVGSALHMLETTLSHHQIRVELPGDMVLINCDGSLLERVFINLLENAHKYAGYDALLGIRATVQGEWLNVEVWDNGPGVTAGQEQLIFDKFSRGNKESAIPGVGLGLAICRAIIDVHGGRIWVEKGQDGGASFHFTLPLEKPPEIDGENIDTEK	21~~KdpD (1.49408E-118)~~231;X;254~~Usp(1.57471E-39)~~374;X;404~~DUF4118 (1.36081E-23)~~502;X;531~~GAF (1.37984E-15)~~646;X;663~~HisKA (0.0000000000886711)~~728;X;781~~HATPase_c (2.98522E-26)~~882	KdpD protein

	1E-13	60.3	9.9	2.4E-13	59.6	6.9	1.4	1	V5U9D6_9BURK	Histidine kinase (EC 2.7.13.3)	X636_00780	Pandoraea sp. RB-44	967	1380774	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Pandoraea, Pandoraea sp. RB-44	>tr|V5U9D6|V5U9D6_9BURK Histidine kinase OS=Pandoraea sp. RB-44 GN=X636_00780 PE=4 SV=1MERPDPDELLDKLHRDEAREQRGRLKIFFGASAGVGKTFAMLQAARKLREEGTDVVVGVLETHGREETASLLEDLEVLPQQSVEYRGRVLREFDLDGMLARKPAVALIDELAHTNVPGGRHPKRWQDVQELLGAGIDVYTTLNVQHLERLNDVVGQITGIRVWETVPDRVFDLADEVKLVDLPPDELLERMREGKVYLPAQAERAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADQSIGHVWQARERLLVAIGPGPEGVTLVRAAARLAASLRADWLAVHVETPAILKQSPERREGTYATLKLAQELGAETLTLDGAHAAATLLAYAQMRNVSKLVVGASGARRWWTAHTPLHEQLVRLARGVEVVLIAPAAGDASADRRVVRGDWRDWVDTAVPELGIVGGPWRAYAWAAAVCGAVSLAAAELTSFLDLANIAMLYLLGVIAVAMRLGRGPGVLASFLSVVAFDFFFVPPKMSLSVSDTQYLLTFAVMLTVALVISHLTTSLRFQARLATWRERRTGAVYAMARELAAALTTTQILEIGARHVREVFQARVALLLPDSQGSVRQPVENVQVETMPAHIDTDVAQWVYDRQQAAGRGTDTLPASDAYYLPLRAPMRTRGVLVVAAQPNADGALGSPEQHRLLDTFAAQIALALERVHYVEIAQDALVTMESERLRNSLLSAISHDLRTPLTSIVGFASMLCRNAQTPGPLRAELVDAIHEEAQRMTGLVTNLLDMAKLQAGGVQLNRQWQMLEEVVGTSLRACRRVLAAHAVTTRLPADLPLLRFDAVLLERLFANLLENAAKYSPPGSHIEIAARVRGDMVEVSVSDDGPGLPAGTEGRIFEKFMRGEKESSKPGIGLGLAICRAIVEAHGGRIHADNVPQGHGARFTFTLPVETPPEAPLGPLAPLAPLAAMRGDAALPGQDDDRASPSGREGLDEDAAGHHDDAHPTREPGTNATREHE	20~~KdpD (4.44561E-123)~~230;X;252~~Usp(2.11988E-21)~~374;X;411~~DUF4118 (2.62975E-22)~~511;X;540~~GAF (6.35048E-16)~~660;X;677~~HisKA (2.04134E-14)~~742;X;795~~HATPase_c (5.55783E-31)~~897	KdpD protein
	2E-13	59.8	6.6	3.6E-13	59	4.6	1.4	1	Q63VS0_BURPS	Histidine kinase (EC 2.7.13.3)	kdpD BPSL1174	Burkholderia pseudomallei (strain K96243)	993	272560	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, pseudomallei group, Burkholderia pseudomallei (Pseudomonas pseudomallei), Burkholderia pseudomallei (strain K96243)	>tr|Q63VS0|Q63VS0_BURPS Histidine kinase OS=Burkholderia pseudomallei (strain K96243) GN=kdpD PE=4 SV=1MNRPDPDQLLDKIQREEEKQQRGRLKIFFGASAGVGKTYAMLLAARARKQEGVDVVVGIVETHGRSETAALLDGLDVLPLMQIEYRGRTIGEFDLDAALARRPRLVLVDELAHSNVPGARHLKRWQDVYELLDAGIDVYTSVNVQHLESLNDVVGAITGIRVWETVPDRVFDAADEVTLVDLPAEELLSRLREGKVYMAQQAERAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGAEAPTLVRAAARLAASLKADWLAVYVETPRLARLPDALRQRTLNALKLAAELGAETATLTGADAVAALIGYAQVRNASKIVAGGSSKTGFLRRFSRPFGEQLAERAGDLDLMLIRASASEDARAPLDARARAWRDFASSVVDGRSPPRHYGYAAAICALITGAANLLQGHLDLTNLVMLYLLGVVFSAVRLGRGPGVVQSFLSVAAFDYFFVPPRMSFSVTDTQYLLTFFGMLLTSLVISHLLTSSLTRGAAIAQRRERRTSAMYAMARELAAALTAEQIVEIGSRHVSEVFRARVAMLLPDSGDKVRQKIENPDEAVTITGAALDIDVGQWVYDQQKPAGHGTDTLPAAAALYLPLKAPMRTRGVLAVVTKDPGELEVPEQRRMLDAFAAQIALAVERVHYVEIARDALVNMESERLRNSLLSAISHDLRTPLTAIVGLSSMLANARGATREGSPAREDELVDAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGAALAACKRVLARHPARVRLPADLPLLQTDAVLMERLFANLFENAAKYTPLDTPIEIGAERIVDDGRPFVRVFVDDHGPGLPAGMEARIFEKFTRGEKESATPGIGLGLAICRAIVDAHGGKIGALNRLGPDGRVEGARFWFTLPVDTPPPEPGAGDEAPDDDAGAAADASGMRDAGRAAGRRIAGERVAGERAFAAAARPVPGQAAAADAPRRDGGAPPLSNEPPHAHE	21~~KdpD (8.35063E-121)~~230;X;252~~Usp(3.79273E-28)~~374;X;409~~DUF4118 (2.34333E-20)~~508;X;537~~GAF (2.79686E-16)~~658;X;675~~HisKA (0.000000000000473468)~~744;X;797~~HATPase_c (1.58082E-22)~~907	KdpD protein
	2E-13	59.8	14.9	3.7E-13	59	10.3	1.4	1	A0A090ADE5_9GAMM	Histidine kinase (EC 2.7.13.3)	THII_1571	Thioploca ingrica	909	40754	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Thiotrichaceae, Thioploca, Thioploca ingrica	>tr|A0A090ADE5|A0A090ADE5_9GAMM Histidine kinase OS=Thioploca ingrica GN=THII_1571 PE=4 SV=1MDDKRPDPDELLNKIQQEEAKQQRGRLKIFFGGCAGVGKTFAMLSAAGAQRQQGIDVVAGVVETHGRSETAQLLADLEVLPPKLIEYRDRQLPEFDLDGALARKPSLILIDELAHSNVAGSRHPKRWQDVEELLTAGISVYTTVNVQHLESLNDIVGQITGIRVWETVPDHVFEKADEITLVDLTPDELLQRLKEGKVYLPQQAEHAIQHFFRKGNLIALRELALRRTADRVDAQMRDYRADRSIHPVWQAKERLMVCIGSSLEGDQLVRSAARLATGLRADWLAVYVETPGLQRLPANHRDRILKTLKLAQELGAETAVLSGSELASTLMSYARSHNVTKWVVGKSSRSSLARLWRTSLADELANRSQDIDVYVVSHTLASETAATLPAANAISLEFEENSERQPQGYVWAIAAGIGVTFIAAGLSNFLDLANVIMLYLLAVVLVTVRFGRGAGVFASILSVVIFDFFFVPPKLSLTIADTQYLFTFVVMLVISLIISHLTASLRYQARVASYRERRASALYALSKELSSALTVAQIIEISTEHLRGMFQAQIALLLPDSREKVRQPVAEMQENPRFSLFDPGIAQWVYDNQQPAGLGTNTLPANPVLYLPLRAPMRTRGVLAMAQANSRQIFQPEQQRLLDTFAAQIALALERVHYVEIAQDVLVSMEAERLRNSLLSAISHDLRTPLTAIVGLSSTLSTQPELPVQTRQELANALYEEALRINGLVTNLLDMARLQSGGLKLNQQWQPIEEVIGSALRASERLLSKHQIATDLPPDLPLLLFDAVLIERVLCNLLENAAKYTPAESCITLHGRVNADEFQFSVIDNGPGLTAGMEEKIFDKFTRGEKKYSQAGVGLGLAICKAIVEAHGGKITAENVQPTGAKFTFTLPLGQSPPLPETELTDDES	23~~KdpD (8.38758E-125)~~232;X;254~~Usp(1.65276E-42)~~377;X;409~~DUF4118 (4.83184E-23)~~508;X;534~~GAF (6.87003E-20)~~655;X;672~~HisKA (0.000000000016470 4)~~737;X;790~~HATPase_c (2.87823E-30)~~891	KdpD protein
	2E-13	59.7	11	4E-13	58.9	7.6	1.3	1	H2IX79_RAHAC	Histidine kinase (EC 2.7.13.3)	Rahaq2_3200	Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	898	745277	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Rahnella, Rahnella aquatilis, Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65)	>tr|H2IX79|H2IX79_RAHAC Histidine kinase OS=Rahnella aquatilis (strain ATCC 33071 / DSM 4594 / JCM 1683 / NBRC 105701 / NCIMB 13365 / CIP 78.65) GN=Rahaq2_3200 PE=4 SV=1MTEDRPDPDSLLALANEKPRGQLKVFFGACAGVGKTFAMLQEAQRLRATGLDVLVGVVETHGRQETQALLPGLSLLPPKRIHHRGRQVQEFDLDAALARRPALILMDELAHSNAAGSRHPKRWQDVEELLDAGIDVFTTVNVQHLESLNDVVSGVTGIIIRETVPDRLFDDASEVVLVDLPPDSLRQRLKEGKVYIPGQAERAIEHFFRKGNLIALRELSLRRTADRVDDQMREYRDDQGVNRVWHIRDALLLCIGHGGGNEKLVRVASRLAARLGCVWHAVYVETPRLHRLPEGQRRAILHSLKLAQELGAETATLSDPQEEQAILRYARAEHRLGKIMTGRRREKRWKFSTSFADKLAEIAPDLDLIVVGLEDAPPNTARKEQDSRTFADRFSRQLWGCALAVALCAVITMMSQWLLPTFDQANLVMVYLLGVVIVALFYGRWPSVLAAVINVVSFDLFFVQPRGSLAVTDAQYLVTFGVMLIVGILIGNLTAGVRYQARIARHREKRAQHLYEMSKGLSQSLTPEAIAQTSRHFISSSLNAKTAILLPQENGELAQPAGEITSIVVDDAIARWSFDKKLPAGAGTDTLPGVPYQLLPLIASGESRGLLAVEPPNIRQLLVPEQQRLLQTFTVLIANALERLHLAASAETARLETEREQLRNSLLSALSHDLRTPLTVLFGQAEILTDLASEGSKHAPQASQIRQQVLSTTRLVNNLLDMARIQSGGFNLRKEWQSVEEITGSALRMLEPVLVHDNIEIDLPKEMVLVNCDASLIERVLINLLENAHKYAGTGATIGIKATPLDEWLEMEVWDNGPGIPAGAEHSIFDKFARGNKESAIPGVGLGLAICRAIIEVHDGRIWAENGPDGGARFRFRLPLEALPEMESDMESDIDEVS	20~~KdpD (6.11302E-115)~~228;X;251~~Usp(8.19021E-36)~~371;X;403~~DUF4118 (1.5826E-21)~~499;X;525~~GAF (1.55738E-15)~~642;X;659~~HisKA (0.000000000540644)~~724;X;777~~HATPase_c (5.79819E-30)~~878	KdpD protein

	2E-13	59.7	11.6	4.2E-13	58.8	8	1.4	1	Q7N6W8_PHOLL	Histidine kinase (EC 2.7.13.3)	kdpD plu1417	Photorhabdus luminescens subsp. laumondii (strain TT01)	897	243265	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Photorhabdus, Photorhabdus luminescens (Xenorhabdus luminescens), Photorhabdus luminescens subsp. laumondii, Photorhabdus luminescens subsp. laumondii (strain TT01)	>tr|Q7N6W8|Q7N6W8_PHOLL Histidine kinase OS=Photorhabdus luminescens subsp. laumondii (strain TT01) GN=kdpD PE=4 SV=1MDQHEPQRPDPDELLTLVNEKQRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGLDVVIGVVETHERQGTAALLDGLPQLPLKQIYYRRRKISVFDLDAAIARHPAIILMDELAFSNPHTNRHPKRWQDVEELLEAGIDVLTTINVQHLESLNDVVGDITGIRVRETIPDHIFDQANEIVLVDLPPDDLRQRLNEGKVYIPSQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAFRDTQGHEPVWHTRDNLLLCIGNSSGNEKLIRTAARLAARLGCIWHAIYVETPKLYQLPEGKRRSILKALRLAHELGAETATLSDPNKEKAVLRYAREHNLGKILIGRRCTSKQKLFGWQWRSGFADRLGKLGPDLDLVIVALEERSHWDKEQDNRSVSEKWRVQIQGCLIAIALCTLITLFSRTFLLTLDKANLVTLYLLGVVVIALFYGRRPSIFAAFINVISFDIFFVQPHWSLAVTDMQYLLTFSVMLIVGVVVGNLTAGMRYQARIARYREQRTRNLYEMTRELSRALNEEDIARTSYHFLTNGFQAKTGLFLPNDDGNLYQLTTNNGGHMLIDDAIAKWSFDKNLPAGAGTDTLPSVPYQLQPIATPSAVLPLAIEPSYLRQLLIPEQQRLLQTFTGLIANALERLQLSRRAESAKLDTEREQLRNSLLAALSHDLRTPLTVLFGQAEILMLDLSAEGSPHTKQVNQIRQQILSTSRLVNNLLDMARIQSGGIQLNLEWQSLEEIVGSTLRSLEYALNRHPVAVSLPSDLLLHCDASLLERVFINLLENAIKYTDEQIPLGIKATTEKNQIHIEVWDAGKGIPPEQEQLIFDKFSRARKESAIPGVGLGLAICRAIIEIHQGKIWASNNEKGGASFHFVLPLEKPPEIITEEM	21~~KdpD (2.17693E-121)~~231;X;254~~Usp(1.08358E-35)~~379;X;407~~DUF4118 (7.96511E-22)~~505;X;531~~GAF (3.2765E-15)~~649;X;666~~HisKA (0.000000000046212 8)~~731;X;783~~HATPase_c (3.04986E-29)~~884	KdpD protein
	2E-13	59.6	11.1	3.8E-13	58.9	7.7	1.3	1	C5BG89_EDWI9	Histidine kinase (EC 2.7.13.3)	NT01EI_2891	Edwardsiella ictaluri (strain 93-146)	902	634503	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Edwardsiella, Edwardsiella ictaluri, Edwardsiella ictaluri (strain 93-146)	>tr|C5BG89|C5BG89_EDWI9 Histidine kinase OS=Edwardsiella ictaluri (strain 93-146) GN=NT01EI_2891 PE=4 SV=1MVDDEQRPDPDTLLAQVGEPARGRLKVFFGACAGVGKTYAMLQEAQRLRAQGLDVAIGVVETHGRSETAALLDGLELLAQKRIQHRGRQIREFDLDRALARAPALILMDELAHTNAPGSRHPKRWQDVEELLAAGIDVLTTVNVQHLESLNDVVGSVTGVQVRETLPDRLFDAASEVVLVDLPPDDLRQRLKEGKVYIPGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAFRSGPGGSRVWHTRDALLLCIGQYADNDKLVRTAARLAGRLGCVWHAVYYVETPHLHRLPENERRAILRSMRLAQELGAETATLSDTAPEHAILRYAREHNLGKILLGRRQREARRLRWPGASFVDRLARLGPDLDLLIVAVEDRPSGPRENDPRPFGEKWRVQIQGFLVAAALCAVISLCGKLIQPTFDQVNLVMVYLLGVVVVALFFGRWPSVFAACISVASFDLFFVQPQWSFAVSDVQYLVTFGVMLIVGILIGNLTAGMRYQARVARYREQRARHMYEMSKALGNALNHDAVVRSACASLNHSFGARTTLLLPDGDGLLRPRHGDEAGVTNVDLAIAQWCLDRRQPAGAGTDTLPGVPYQLLPLSSAQNTFGVLAIEPANLRQLMVPEQQRLLQTYTVMIANALERLHLAHSAAAARLEAEREQLRNSLLAALSHDLRTPLTVLFGQAEILTLDLASERSVHAPQAEEIRQQILNTSRLVNNLLDMARIQSGGFRLRKAWQSLEEIVGSAIHTLEPMLVGHPLALSLPADLPLVNCDGALIERVLQNLLENAGKYAGNTASIAILARVGADGLEVEVSDSGPGIAAEQRPHIFNKFTRGDKESAIPGVGLGLAICRAIIDIHGGRIWVESPPQGGAHFHFTLPLETVPEIDPETDKEMTDNP	20~~KdpD (3.29698E-125)~~230;X;253~~Usp(4.58022E-35)~~376;X;403~~DUF4118 (6.96322E-22)~~502;X;572~~GAF (0.00000000016635)~~646;X;664~~HisKA (0.000000000298677)~~728;X;781~~HATPase_c (9.40899E-31)~~882	KdpD protein
	3E-13	59.5	12.6	4.2E-13	58.8	8.7	1.3	1	E6WH82_PANSA	Histidine kinase (EC 2.7.13.3)	Pat9b_3780	Pantoea sp. (strain At-9b)	891	592316	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. (strain At-9b)	>tr|E6WH82|E6WH82_PANSA Histidine kinase OS=Pantoea sp. (strain At-9b) GN=Pat9b_3780 PE=4 SV=1MNDELPRPDPDALLLNHSDSHRGKLKIYFGACAGVGKTYAMLQEAQRLRAQGLDVLAGVVETHGRDETAALLQGLAVLPRRATGRSRHAEFDLDAALARHPAVILMDELAHTNVQGSRHPKRWQDIEELLDAGIDVITTVNVQHLESLNDVVGGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALRELALRRTADRVDDQMRAWRDQQGRDKVWHTRDAILLCIGDDTGSEKLVRTAARLAARLGSEWHAVYVETPRLNRLPEARRRAILRTLQLAQELGAETATLSDPDEARAVLRYAREHNLGKIVTGRQPQRRWRRDSFAQRLGELGPDLDLLVVALDEPVRDAPSLMNGQRASAEKWRMQLRGCLMALVLCILVTAAGRWLLVEFDPANGVMIYLLAVVIVALRFGRWPSVFATVINILAFDLFFVAPTGTVAVSDLQYLVTFAVMLAVGVIVGNLTAGVRYQARVARYREQRARHLYEMAKSLGSALTPQDIASTSQRVIEVTLQARSLLLLPDEQGELRAVGESSMGTPPDLAIAKWSYSKGQPAGAGTDTLPAVPYQILPLKSGNHCRGLLVVEPENLRQLMIPEQQRLVETFTVLIANALERMALSQSEAASRLAAEREQLRNALLSALSHDLRTPLTVLFGQAEMLMLDLASEQSKYVAQANQIREQTLSTIRLVSNMLDMARIQSGGLNLREEWVALDEVIGGALSSMGPSLKGHDFTLDLPAELVLIKGDSSMLERVFTNIIENSLKYAGNAAQHGIHAWRENARLEIAIWDSGPGIAPDALTRIFDKFTRGDKESAVPGVGLGLAICKTIVESHGGRIWAENRAEGGASFRLSLPLPPAPEISEDGLK	20~~KdpD (2.6381E-123)~~228;X;251~~Usp(1.70469E-41)~~370;X;402~~DUF4118 (2.49572E-22)~~498;X;524~~GAF (6.63755E-15)~~641;X;658~~HisKA (0.00000000065319)~~723;X;776~~HATPase_c (2.28662E-29)~~877	KdpD protein
	3E-13	59.4	9	5E-13	58.6	6.2	1.5	1	D9SK28_GALCS	Histidine kinase (EC 2.7.13.3)	Galf_2441	Gallionella capsiferriformans (strain ES-2) (Gallionella ferruginea capsiferriformans (strain ES-2))	505	395494	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Gallionellales, Gallionellaceae, Gallionella, Gallionella capsiferriformans, Gallionella capsiferriformans (strain ES-2) (Gallionella ferruginea capsiferriformans (strain ES-2))	>tr|D9SK28|D9SK28_GALCS Histidine kinase OS=Gallionella capsiferriformans (strain ES-2) GN=Galf_2441 PE=4 SV=1MKFLRFFSTFPQPHSPCARMLWAVIACVIATLLAWPWRDFLDPANTAMLYLLAVAVVAARAGKGAAIAAALLGTALLDFFFIQPRFTFTVGDVQYAVTLAVMFAVALIIGNLTQGLQREKEAAQERERQSNALYQLASQLAGALTLEQIEGMTRRFLHETQSCQSQLLMRHGEEMSPVIPGQTPLSGKPYYAVKAALQQGAAQATLDGALHWLILPLHDTPQARGVLVLSFYDVGLLGNERRPLFKAIAALVAASVERLHFVEIAQQAQLQMTDERLRNSILSALSHDIRTPLTVLYGMADTLAQSALPQALHEMADAMRQQTFRLNSMASNLLDMAKLRAGDIRLRNLEWQPVEEVIGASIKLLGPALAQHPVSVVLPADMPLLRFDAVLMERVLCNLLENAAKYAAPGSSIRIAVRADQKFAHLSVCNEGSQFPIDRLERLFELFERGDIESNVPGVGLGLAICRSIVSAHGGSIYADNDAGACVTFTLTLGEPPVIETEDEYE	non-KdpD DUF4118 protein
	3E-13	59.3	12.3	5.2E-13	58.5	8.5	1.3	1	D2TNK5_CITRI	Histidine kinase (EC 2.7.13.3)	kdpD ROD_07011	Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	895	637910	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter rodentium, Citrobacter rodentium (strain ICC168) (Citrobacter freundii biotype 4280)	>tr|D2TNK5|D2TNK5_CITRI Histidine kinase OS=Citrobacter rodentium (strain ICC168) GN=kdpD PE=4 SV=1MVNEEPLRPDPDRLLEQTAAPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQGLDVLVGVVETHGRQETAALLEGLVLLPLKRQAHRGRHISEFDLDAALARRPALILVDELAHSNAPGSRHPRRWQDIEELLDAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLHQRLKEGKVYFAGQAERAIERFFRKGNLIALRELALRRTADRVDEQMRAWRARPGEDKVWHTRDAILLCIGHNTGSEKLVRAAARLASRLGSVWHAVYVETPALHRLAEKQRRDILSALRLAQELGAETATLSDPCADKAAVRYAREHNLGKIVLGRPSSRRWWRKDNFAERLAKRAPELDVLIVALDEPPRRALPAVPDTRSVKDKWRVQIQGCLVAVALCAITTVIASQWLAAFDEANLVMLYLLGVVVVSLFYGRWPSVFATVISVISFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVVGNLTAGVRYQARVARYREQRARHLYEMSKALAMGRSEQDIAAISERFIASTFHARSQVLLPDEHGRLVPLTRQQGITPWDDAIARWSFDKGLPAGAGTDTLPAVPYQFMPLRCAEKTYGLVIVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEEQARLASERESLRNALLAALSHDLRTPLTVLFGQAEILTLDLASEGSAHAKQASEIRQQILNTTRLVNNLLDMARIQSGGFNLHKEWLTLEEVVGSALKMLEPGLLQPVNLSLPAPLTLIHVDGPLFERVLINLLENAIKYAGPQAEIGIDAQVTNNRLQLEVWDNGPGIPEGQQQQFIFDKFARGNKESAVPGVGLGLAICRAIVEVHGGTLTVRNRPQGGACFRVTLVQEPPPALEDFHEAM	21~~KdpD (3.49823E-120)~~231;X;254~~Usp(7.15015E-40)~~374;X;404~~DUF4118 (2.7511E-21)~~502;X;528~~GAF (0.000000000000309992)~~645;X;662~~HisKA (0.000000000480142)~~727;X;779~~HATPase_c (2.0453E-33)~~880	KdpD protein

	4E-13	59.1	9.6	5.9E-13	58.3	6.6	1.4	1	A9AXU7_HERA2	Histidine kinase (EC 2.7.13.3)	Haur_2273	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	895	316274	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Herpetosiphonales, Herpetosiphonaceae, Herpetosiphon, Herpetosiphon aurantiacus (Herpetosiphon giganteus), Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	>tr|A9AXU7|A9AXU7_HERA2 Histidine kinase OS=Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785) GN=Haur_2273 PE=4 SV=1MEHQRPNPDQLLERIQSANQQAQRGRLKVFFGAAAGVGKTYAMLQAAQQRRAEGIDVLVGYIETHGRAETDALLVGLPQLPALQVEYRGTSLREFDLDAALERKPSLILVDELAHSNAPNLRHAKRWQDINELLHAGIDVYTTVNVQHLESLNDLVAQVTGVIVRETVPDAVLESADEVELIDLPPDELLGRLNEGKIYIASQAAQAARNFFRKGNLIALRELALRRTADRVDAQMQRYRHDHAIPTTWPTRERLLVGVGPSPLSERLVRATRRMANDLKAEWLVVYVETPKHLRLSEADRDRVTATLRLAESLGAQIVTLGGINPGEEMLRYARQRNVSKIVVGKPAQPRWRELLFGSIVDQLIRQSGEIDVYVISGEHDDTHKPNAKPSLQPHSPKINYVKSSGVVLACTMVCYGIFPHLELSNLIMLYLLGVTWVAARYGRGPAISASILSVAAFDFFFVQPYLTFAVSDVQYILTFMVMLIVALTISTLTVQIQAQAETARQRERRTAALYAMTREFASIRGLDNLLQTAAQHISSVFEGQTAILLPNPKGQLRPIVGQQWPFISDQRELITAQWVYDHQQKAGMHSDTLPSAQAMYLPLIATRGVVGVLALQPEQPRRLLDPSHVHLLETFANQTTVAIERAHLAEEAQAASVQIETERMRNSLLSSVSHDLRTPLAAISGAASTLLDQTNQLDQHIQHELIQTIADEGQRLNRLLSNLLDMTRLEAGAVQVHKEWQALEEVLGTALARLAPQIDQRSISIELPNQAFVPFDSILIEQVLVNLLENSLKYSPSSSPIEIRAVERIGLIEVQIADHGPGIPPSALETIFEKFFRVQARKRSASSGVGLGLTICRGIIEAHGGTIWAENRPAGGAIFAFTLPIEGQPPQIRGE	22~~KdpD (5.6864E-124)~~232;X;254~~Usp(9.06379E-45)~~377;X;400~~DUF4118 (1.02681E-19)~~494;X;527~~GAF (4.89745E-15)~~646;X;663~~HisKA (0.0000000372216)~~715;X;781~~HATPase_c (8.08471E-30)~~883	KdpD protein
	4E-13	59.1	10.7	5.8E-13	58.4	7.4	1.3	1	E1SHK7_PANVC	Histidine kinase (EC 2.7.13.3)	kdpD Pvag_3065	Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	892	712898	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea vagans, Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	>tr|E1SHK7|E1SHK7_PANVC Histidine kinase OS=Pantoea vagans (strain C9-1) GN=kdpD PE=4 SV=1MNHDEPQRPDPDALLQANRESHRGQLKIYFGACAGVGKTYAMLQEAQRLRAQGLDVLIGVVETHERPETAQLLTGLTLLPRRATGRSRHAEFDLDAALARHPAVILMDELAHTNVQGSRHPKRWQDIEELLEAGIDVLTTVNVQHLESLNDVVGGVTGIQVRETVPDPFFDSADEVVLVDLPPDDLRQRLKEGKVYIGDRAERAIENFFRKGNLFALRELALRRTADRVDDQMRAWRDQQGRDRVWHTRDAILLCIGDDSGSEKLVRTAARLAARLGSEWHAVYVETPRLNRLPEARRRAILRTLQLAQELGAETATLSEPDEAEAVLGYARERHNLGKIVTGRRPLRRWRRDSFAERLGQLGPDLDLLVVALDEPLKDAPHPLPDGRVTSEKWRIQLRGVMMALVLCIVVTAAGQSVLINFDPANCVMIYLLAVVIVALRYGRWPSVIATVMNIVAFDLFFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRYQARVARYRYEQRARQLYEMAKSLGSALTPQDIAATSQRVLDATLQARCLLLLPDEQGELQPVGEALPASEPDRAIAKWSYSKGQPAGAGTDTLPAVPYQILPLKSGAHCRGLLVVEPQNLRQLMIPEQQRLVETFTVLIANALERMALSHSEAASRLSAEREQLRNALLSALSHDLRTPLTVLFGQAEMLMLDLASDNSKYVPQASQIREQTLSTIRLVSNMLDMARIQSGGLNLREEWLALEEVIGGALSSMAPSLKGHEVQLDLPDDIVLIKGDSTLLERVFTNLIENSLKYAGNSAPRGIRAWRAATRLEIAVWDSGPGVAEDDLTRIFDKFWRGDKESAVPGVGLGLAICKTIIESHGGQIWAENRPEGGAAFRLSLPLPPVPEISDEGLK	21~~KdpD (5.5175E-120)~~229;X;252~~Usp(8.85194E-36)~~371;X;403~~DUF4118 (2.02809E-21)~~499;X;525~~GAF (0.000000000000110258)~~642;X;659~~HisKA (0.000000000546041)~~724;X;777~~HATPase_c (1.16064E-29)~~878	KdpD protein
	4E-13	58.9	11	5.6E-13	58.4	7.6	1.2	1	D1CGX7_THET1	Histidine kinase (EC 2.7.13.3)	Tter_2095	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	539	525904	cellular organisms, Bacteria, unclassified Bacteria, Thermobaculum, Thermobaculum terrenum, Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	>tr|D1CGX7|D1CGX7_THET1 Histidine kinase OS=Thermobaculum terrenum (strain ATCC BAA-798 / YNP1) GN=Tter_2095 PE=4 SV=1MREAWSTLITPRVAQPTTDNWQRLLRALSRYLFTVGSVALVTALIWLMTDRVRLANISMLYLLAVMVVAVTCGSVPAIIASVLSFLAFDFFFVQPTWSLTIRDPDEWLALLLFLITAIVTGQLAALLRRRAEEASRREREANLLYELLRVLGEEEIGVALESAAEQIRRELRLEGVGIEISSLDNGGPIRVFSGSKRARLQLLTLSGSRRYVLEDGAPTNGGAPRSTWLHVAPNLPQMGRAHRDLLRVVYIHTEGRRLGSINLVGGGSLSDADVRLLSAVAQQLGRTLERAALRRRAMEMEAIKRADELKTSLINAVSHDLRTPLATISAAADSLLRQDVEWSEEERRGFVRDIAEESRRLGRLVDNLLDMSRLEGGSLRPHKSWCDLGALVEETIDRLGSLTAHHQLHLEVEEDLPPVLLDYVEIGQVVSNLLENAIKYAPQGTTIDIQVRRQGDEVRVAIADRGPGIPPQDLSRIFDKFYRVQGSSPAPQGMGLGLSVAKGLIEAHGGRIWGENRPGGGAVFSFTLPLSPAGVPPPC	30~~DUF4118 (1.17737E-17)~~127;X(180);307~~HisKA (0.000000000000342763)~~373;X;426~~HATPase_c (3.33158E-33)~~528	non-KdpD DUF4118 protein
	4E-13	58.8	13	8.7E-13	57.8	9	1.5	1	G0AB27_COLFT	Histidine kinase (EC 2.7.13.3)	kdpD CFU_1320	Collimonas fungivorans (strain Ter331)	926	1005048	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Collimonas, Collimonas fungivorans, Collimonas fungivorans (strain Ter331)	>tr|G0AB27|G0AB27_COLFT Histidine kinase OS=Collimonas fungivorans (strain Ter331) GN=kdpD PE=4 SV=1MSSPYSNDDLRPDPDALLARLQVQESLVGRGKLRIYFGASAGVGKTYAMLSAAHKLHGEGRDVLAGVIESHGRAETAALLNGLELLPMKQVAYRDKHLPEFDLDAALQRKPSLVLVDELAHSNAAGSRHPKRWQDVEELLNAGIDVFTTLNVQHLESLNDVVGGITGIRVAETLPDTVFDAADEVVLVDLPADELLNRLKLGKVYKLPQAERASRNFFRKGNLIALRELALRRTADRLQGDVQAYRIEKSIGAVWQTDAALLACVGPSPNAEHVIRGTARLATQLNAEWHAVYVETPKLQRLPSAKRERILKLTLKLAQDLGATTAVLAGSEVAEVVAGYARSHNFSKIIIGRSQRRFPWQASHSARIAAQARDIDLIAIGASSASTAEKAEEGVGGILPRHLPMQGRIEWWGYAWALAVCVLVTLLATPILPFFDLANIVMLYLLAEVLIAIRYGRGPAIFVALLSIASFDFFFVPPRFSFAVSDFQYLLTFGVMLAVGLTITHLTSGLRYQARIASDREARSRALFEFARALSGVLQTEQIFETSGQFLQRSFQAKTLLLIPDEAGRLSLPAVIPDDVAHVAAALDMGIAQWAFDNASSAGIGTDTLPASSYLYLPLVAPMRTRGVLVILPHNRRWILIPEQQQQLYTFATLTAIALERVHYVEVAQDALVRMESERLRNSLLSALSHDLRTPLTALIGLSESLVLSKPPLQQHQQVLATALHSEMLRMSALVTNLLDMARIQSGEVKLNLQWQPFEEVVGSALRASGSALHGHQVEIRVAHELPLVHFDAVLIERVLCNLLENAAKYTPAGSHIVLAAAVNARFLTVTIADDGPGLPSGMEDTIFEKFTRGERESAKPGVGLGLAICRAIVEAHGGTIRAHSGRHGTSGAEFIFTIPLGAPPSMPDLEEHEPSAGSMEKDSEKT	29~~KdpD (1.96499E122)~~238;X;261~~Usp(8.89021E-39)~~380;X;413~~DUF4118 (6.75712E-21)~~512;X;539~~GAF (6.05406E-15)~~660;X;677~~HisKA (0.000000000013828)~~742;X;795~~HATPase_c (1.21208E-27)~~898	KdpD protein
	5E-13	58.7	5.1	1E-12	57.6	3.5	1.6	1	A0A0A7I4I4_9BIFI	Nucleoside-diphosphate sugar epimerase	AH68_02230	Bifidobacterium kashiwanohense PV20-2	735	1447716	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium kashiwanohense, Bifidobacterium kashiwanohense PV20-2	>tr|A0A0A7I4I4|A0A0A7I4I4_9BIFI Nucleoside-diphosphate sugar epimerase OS=Bifidobacterium kashiwanohense PV20-2 GN=AH68_02230 PE=4 SV=1MEVLLVGNTDFITKQWIQHAFPRDHVVIAEREDTVDGNDRLRIVNMSDANTLAETITTYEFDRIVFFSENLTPRSDRDGDLGALRRLLHAIRNRQTQMLMVSGPESEFTYPENVDVRDTSKSLMSRASEELCLYYARTYRLEAKIIRSPYLYASDRNGVTAYFNHLFEQAESGTLSFCEQKNQQTCFLCADDLAELIYRMFDDWTAESEIFHVPNVFNFTYGDLADVISAAFPGLSVIFGEDRTQCYPADDHVLRLRYGWSPRYSLKQDLPPILQRWKEARAQEQSGKHPIWDFLRNHSKPWIAFEICVTFILEEMLRTAVQGNSQLGTVDLRLFFVVIVGTMYGLNAGVFAAALACAGMALSYASNGASFAPLFYDTSNWITFVVYFVAGAVCGYVQMRNRENLRFMRDENGLLRERLAFLRDLYHDVLDDRRMLRGQIIGRRDSFGKMYAMTRELDEVLPRKLYHATIRIMQDTLGGDSFGIYRIDNGGRFARLMAASPQTESLFSKSALLENYANIVTALDHGGLWVNRNLEQNLPMYAAGVHADGKLAVVIVLAKAQPDQMNLYFQNLFTIMCGLVESAMVRAFDYENVARQTMLVPGTEFLNTQVFLSKVLAANELKHDHMSNHLLLRVEDAWQDDGSRLMGAIRQTDEAGVLQDGNVYVLMNQASEHELPIINRRLIQAGLHVKLVSGHEEDSLLAEASEQVAIESQADETPRSNVAQNDSASHEGGAA	1~~NADB_Rossmann (0.00000322576)~~231;X;301~~DUF4118 (0.000000000002360)~~404;X;462~~GAF (2.69797E-15)~~586	non-KdpD DUF4118 protein

	5E-13	58.7	2.6	8.9E-13	57.8	1.8	1.5	1	A5GDP4_GEOUR	Metal dependent phosphohydrolase	Gura_0079	Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	320	351605	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter uraniireducens, Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	>tr|A5GDP4|A5GDP4_GEOUR Metal dependent phosphohydrolase OS=Geobacter uraniireducens (strain Rf4) GN=Gura_0079 PE=4 SV=1MSKQNGSRNKIIVLASVIGIIALLHYLTPTEPHAYHKLHIILRKLYFLPPVMAAAWFGLRGACATALAVSLLFIMH AFLDWPGNYMEQANQVGELAGFWVAGVIPGWLFDRQRSLLQELANANEETLLCLVSALDLREHNTRLHSQRVRE YTELIASRFGVDEKTRREIGFGALLHDVGKMAVPDQILLKPDKLTDEEWQEMRKHPEAGYRIVKRIGFLRDAAEIVH AHHERYDGGGYPRGLKGDEIPLGARLFMVADVYDALTSQRPYRSPLSHEEAAAEIRKQSGYHFDPAVVATFMAIA PEELRLIAERYWNGELPD	11~~DUF4118 (0.0000000447544)~~113;X;139~~HDc (6.22073E-22)~~282	non-KdpD DUF4118 protein
	5E-13	58.6	7.5	8E-13	57.9	5.2	1.4	1	F2LE20_BURGS	Histidine kinase (EC 2.7.13.3)	bgla_1g29620	Burkholderia gladioli (strain BSR3)	996	999541	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia gladioli (Pseudomonas marginata) (Phytomonas marginata), Burkholderia gladioli (strain BSR3)	>tr|F2LE20|F2LE20_BURGS Histidine kinase OS=Burkholderia gladioli (strain BSR3) GN=bgla_1g29620 PE=4 SV=1MNRPDPDQLLDKIQREEERQQRGRLKIFFGASAGVGKTYAMLQAARARADEGVDVLVGIVETHGRRETAAL VEGLELPPPLAVSHRGRELAEFDLDAALARRPQLVLVDELAHSNLPGSRHLKRWQDVHELLDAGIDVYTTVNVQH LESLNDVVGAITGIRVWETVPDRVFDAADEVTLVDLPAEELLERMRDGKVYMAQQAERAVRNFFRKGNLIALRELA LRRTADRVDAQMREYRADRSIARIWQARERLLVCVGAGPEAPTLVRAAARLAAGLKADWIAVYVETPRSQRLDDA RRRRPLDALKLAAELGAETVTLAGADPVAALIGYAQVRNVSKLVAGGSPRTGLLRRLARPFGERLAERAGDLDLML LRTSAQDDPRHGESDAGVRAWREAFSRLAGERSPPRHYVTAALICAALTGVAAIAQARLDLTNLVMLYLLGVVFS AVRLGRGPGVMQSFLSVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLLTSLVISHLTSSLTRSAGVAERRERRTGA MYAMARELAAALAAEQIVEIGSRHVAEVFRARVAMLLPDGADQVRQKIENPDEAVTLTGASLDTDVGQWVYDQQ KPAGRGTDTLPAALARYLPLKAPMRTRGVLAVVTQDSRELDAPEQQRMLDAFAAQIALALERVHYVEIARDALVS MESERLRNSLLSAISHDLRTPLTTIVGFSSMLAGMHADAARAKAGAKAAADPVALPAAAGAHEAAAGDQPTDREH ELVEAIHDEALRMTGIVTNLLDMARLQAGSLQLKRQWSLLEETVGAALAACKRVLARHPVQVRLPADLPLLQTDAV LMERLFANLFENAAKYTPPGTGLTIGAEAVEEDGKPFVRVSVDDHGPGLRAGMEARIFDKFTRGEKESATPGIGL GLAICRAIVDAHGGRIGARNRLAPDGSVAGASFWFTLPVDAPPPVPDVDEADAIDEAEDVDAIDAPRRDDHAAGS RHVPGAAEAGAPLSPSPKNVDHE	21~~KdpD (3.30506E-120)~~230;X;252~~Usp(1.24581E-29)~~374;X;410~~DUF4118 (2.64271E-20)~~509;X;539~~GAF (1.87408E-15)~~659;X;676~~HisKA (0.00000000857314)~~772;X;825~~HATPase_c (6.41867E-22)~~935	KdpD protein
	5E-13	58.6	11.3	7.8E-13	57.9	7.8	1.3	1	D4GDC9_PANAM	Histidine kinase (EC 2.7.13.3)	kdpD PANA_3787	Pantoea ananatis (strain LMG 20103)	891	706191	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea ananas (Erwinia uredovora), Pantoea ananatis (strain LMG 20103)	>tr|D4GDC9|D4GDC9_PANAM Histidine kinase OS=Pantoea ananatis (strain LMG 20103) GN=kdpD PE=4 SV=1MNHEPLRPDPDALLQTSSDSHRGKLKIYFGACAGVGKTYAMLQEAQRLRAQGLDVLVGVVETHERPETAQL LNGLVLLPRRATGRSRHAEFDLDAALARHPAVILMDELAHTNVKGSRHPKRWQDIEELLEAGIDVLTTVNVQHLES LNDVVGGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLKEGKVYIGDRAERAIENFFRKGNLYALRELALRR TADRVDDQMRAWRDSQGRDRVWHTRDAILLCIGDDTGSEKLVRTAARLAARLGSEWHAVYVETPRLNRLPEAR RRAILRTLKLAQDMGAETATLSDPDEAQAVLRYAREHNLGKIVTGRRPARRWRRDSFAERLGQLGPDLDLLVVAL NEPIQDAPHPLAEDRVNSDKWRLQLRGVLMALVLCIVVTAAGQSVLISFDPANCVMIYLLAVVIVALRYGRWPSVIA TVMNIIAFDLFFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRYQARVARYREQRTRQLYEMAKSLGSGLT PEDIAATSQRVLEATLQARCLLLLPDEQGELHTLGNALPGNEPDWAIAKWSFSKGQPAGAGTDTLPAVPYQILPLK VGDLCRGLLVVEPQNVRQLMVPEQQRLLETFTVLIANALERMALSQSEAASRLSAEREQLRNALLSALSHDLRTPL TVLFGQAEMLMLDLASDNSKYVPQASQIREQTLSTIRLVSNMLDMARIQSGGLNLREEWLALEEVIGGALSSMAPS LKGREVELDLPEDIVLIKGDSTLLERVFTNLIENSLKYAGNCAPRGIRAWCENTRLEIAIWDGGPGIAQNDLTRIFDK FSRGDKESAVPGVGLGLAICKTIIESHGGQIWAENRAEGGACFRLSLPLPPVPEISPEGLK	20~~KdpD (4.49495E-122)~~228;X;251~~Usp(1.6975E-35)~~370;X;402~~DUF4118 (2.14445E-21)~~498;X;524~~GAF (2.47732E-14)~~641;X;658~~HisKA (0.000000000438066)~~723;X;776~~HATPase_c (1.79512E-28)~~877	KdpD protein
	5E-13	58.5	11.5	1.1E-12	57.5	7.9	1.5	1	X4Z2T7_9BORD	Sensor protein KdpD (EC 2.7.13.3)	kdpD D560_0215	Bordetella holmesii ATCC 51541	884	1247649	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella holmesii, Bordetella holmesii ATCC 51541	>tr|X4Z2T7|X4Z2T7_9BORD Sensor protein KdpD OS=Bordetella holmesii ATCC 51541 GN=kdpD PE=4 SV=1MADPGNDRLDPDRLLQTLEQAQSDARRGRLRIYFGACAGVGKTYAMLAAARAQAAQGVDVVAGLVETHGR ADTAALLDTLPALPLQTLDFQGRRLREFDLQATVARRPRLLLLDELAHTNAPGARHAKRWQDVEELLAAGIDVWTT LNVQHLESLNEAVGGITGVRVRETVPDSVFDAADEIILVDLSADELLRRLREGRVVYVPEQARHASRHFFRKGNLIAL RELALRRTAEHVDDDVRAYRHERAIEPVWRTREAVVACIDADPHAEHVLRSAHRLAQQLDCEWHAITIEAPRVAPL PRAGRARLDQALALAETLGAHVETVAGTDMVDAATRYMRRHNITKAVVGRDAWRRRGLSGLLDAALTPGRLLRR RSFADALASACPEADIVRVGAPSAATAAPRRDPRSWRNASAPAGHAAAGAYLWALAYCAAATLASRLAFPVLHQ TNIVMIFLLAVVAAALRHGRGPAALASVVSVALFDFFFVQPLASFAVSDVQYLLTFAVLLTVGLLVGQLTAGLRQQA RAAARREADARGLYEFARELSAALQPEQIAGAASAFLNAAFGARGALYILGLDDRLRLAPGAGDAALEPTLAQWA FDHGQACGAGTDTLSNSPVLYLSLRAPMRVRGVLALHHAGPPLYSAAPARRQLDAYATLIAIAIERLHYVEVAQQA LLSIESERLRNALLTAVSHDLRTPLTSLLGMAETLQRSPAAMTPAALETVAAMDQARRMHALVVNLLDMARLQSH DAPLRRQWQSVEELVGSALAAMNAALQDRPVTVAPLSALPLVKCDGILIERVLCNLLENAAKYTPPGSAIHIDALAD RQRIFEKFARGQRESAPPAQASGWRYAAPSWTPTRAASGSSRPGACAAPASSSRCR	25~~KdpD (1.04039E-110)~~235;X;258~~Usp(3.80447E-33)~~378;X;424~~DUF4118 (8.2903E-20)~~518;X;550~~GAF (0.000000000013875)~~665;X;682~~HisKA (0.000000000005274)~~747	KdpD protein
	5E-13	58.5	4.9	1.3E-12	57.3	3.4	1.6	1	D4BLH7_BIFBR	Uncharacterized protein	BBBR_0023 BIFBRE_02912	Bifidobacterium breve DSM 20213 = JCM 1192	735	518634	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium breve, Bifidobacterium breve DSM 20213 = JCM 1192	>tr|D4BLH7|D4BLH7_BIFBR Uncharacterized protein OS=Bifidobacterium breve DSM 20213 = JCM 1192 GN=BBBR_0023 PE=4 SV=1MEVLLIGNTDYITEQWIQHAFPRDHVVIAEREGTVDGNDRLRIVNMSDANTLAETLTTYEFDRIVFFSENLTPR SDRYGDLGALRRFLHAIRNRQTQMLMVSGPESEFTYPENADVRDTSKSLISRASEELCLYYARTYRLEAKIIRCPYL YAPERNGATAYFGRLFEQASAGSISFRREREQQQTCFLCADDLAELIYRMFDDWTAESDIFHVPNVFNFTYGDLAD VISAAFPGLSVTFGEDRPQSYPADDHVLRLRYGWSPRYSLKQDLPLVLQRWKEARAQEQSGKHPIWDFLRNHSK PWIAFEICVTFILEELLRTAVQGDSQLGTVDLRLFFVVIVGTMYGMNAGVFAAALACAGMALSYASNGASFAPLFY DTSNWLAFVVYFVAGAVCGYVQMRNRENLRFMRDENSLLRERLAFLRDLYDDVLDDRRMLRGQIIGRRDSLGKM YAMTRELDEVLPRKLYHATIRIMQDTLGGDSFGIYRIDNGGRFAHLVAASPQTESLFSKSVLLENYANIVTALDHGG LWVNRNLEQNLPMYAAGVRADGKLAVVIVLAKAQPDQMNLYFQNLFTIICGLVESAMVRAFDYENVAWQTMLVP GTEFLNTQVFLSKVLAANELKHAHMSNHLLLRVEDAWQDDGSRLMGAIRQTDEAGVLQDGNVYVLMDQASEHEL PIINGRLAQAGLHVKLVSGHEEDSLLAEASEQVAAESQADETPRSDAAPNDSASHEGGAA	120~~NADB_Rossmann (0.0000455574)~~271;X;301~~DUF4118 (0.000000000041241 2)~~404;X;462~~GAF (1.41651E-15)~~586	non-KdpD DUF4118 protein

	5E-13	58.5	11.5	1.1E-12	57.5	7.9	1.5	1	Q7VVZ6_BORPE	Two component sensor protein	kdpD BP2483	Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	904	257313	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella pertussis, Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251)	>tr|Q7VVZ6|Q7VVZ6_BORPE Two component sensor protein OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) GN=kdpD PE=4 SV=1MADPGNDRLDPDRLLQTLEQAQSDARRGRLRIYFGACAGVGKTYAMLAAARAQAAQGVDVVAGLVETHGR ADTAALLDTLPALPLQTLDFQGRRLREFDLQATVARRPRLLLLDELAHTNAPGARHAKRWQDVEELLAAGIDVWTT LNVQHLESLNEAVGGITGVRVRETVPDSVFDAADEIILVDLSADELLRRLREGRVVYVPEQARHASRHFFRKGNLIAL RELALRRTAEHVDDDVRAYRHERAIEPVWRTREAVVACIDADPHAEHVLRSAHRLAQQLDCEWHAITIEAPRVAPL PRAGRARLDQALALAETLGAHVETVAGTDMVDAATRYMRRHNITKAVVGRDAWRRRGLSGLLDAALTPGRLLRR RSFADVLASACPEADIVRVGAPSAATAAPRRDPRSWRNASAPAGHAAAGAYLWLAAYCAAATLASRLAFPVLHQ TNIVMIFLLAVVAAALRHGRGPAALASVVSVALFDFFFVQPLASFAVSDVQYLLTFAVLLTVGLLIGQLTAGLRQQAR AAARREADARGLYEFARELSAALQPEQIAGAASAFLNAAFGARGALYILGLDDRLRLAPGAGDAALEPTLAQWAF DHGQACGAGTDTLSNSPVLYLPLRAPMRVRGVLALHHAGPPLYSAAPARRQLDAYATLIAIAIAIERLHYVEVAQQAL LSIESERLRNALLAAVSHDLRTPLTSLLGMAETLQRSPAAMTPAALETVAAMQDQARRMHALVVNLLDMARLQSH DAPLRRQWQSVEELVGSALAAMNAALQDRPVTVAPLSALPLVKCDGILIERVLCNLLENAAKYTPPGSAIHIDALAD AHTLQVRVADDGAGVAQADRQRIFEKFARGQRESAPPPAQASGWRYAAPSWTPTRAASGSSRPGACAAPASS SRCR	25~~KdpD (2.31029E-110)~~235;X;258~~Usp(6.66891E-34)~~380;X;424~~DUF4118 (6.39791E-20)~~518;X;550~~GAF (0.000000000000535 48)~~665;X;682~~HisKA (0.000000000001177 47)~~747;X;800~~HATPase_c (0.000000000000251 722)~~862	KdpD protein
	6E-13	58.4	11.5	1.1E-12	57.5	7.9	1.5	1	A0A0H3M1M8_BORBR	Two component sensor protein	kdpD BB3920	Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	931	257310	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella bronchiseptica (Alcaligenes bronchisepticus), Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) (Alcaligenes bronchisepticus)	>tr|A0A0H3M1M8|A0A0H3M1M8_BORBR Two component sensor protein OS=Bordetella bronchiseptica (strain ATCC BAA-588 / NCTC 13252 / RB50) GN=kdpD PE=4 SV=1MRAACARPFPTRHTHPMADPGNDRLDPDRLLQTLEQAQSDARRGRLRIYFGACAGVGKTYAMLAAARAQA AQGVDVVAGLVETHGRADTAALLDTLPALPLQTLDFQGRRLREFDLQAAVARRPRLLLLDELAHTNAPGARHAKR WQDVEELLAAGIDVWTTLNVQHLESLNEAVGGITGVRVRETVPDSVFDAADEIILVDLSADELLRRLREGRVVYVPE QARHASRHFFRKGNLIALRELALRRTAEHVDDDVRAYRHERAIEPVWRTREAVVACIDADPHAEHVLRSAHRLAQ QLDCEWHAITIEAPRVAPLPRAGRARLDQALALAETLGAHVETVAGTDMVDAATRYMRRHNITKAVVGRDAWRR RGLSGLLDAALTPGRLLRRRSFADALASACPEADIVRVGAPSAATAAPRRDPRSWRNASAPAGHAAAGAYLWAL AYCAAATLASRLAFPVLHQTNIVMIFLLAVVAAALRHGRGPAALASVVSVALFDFFFVQPLASFAVSDVQYLLTFAV LLTVGLLIGQLTAGLRQQARAAARREADARGLYEFARELSAALQPEQIAGAASAFLNAAFGARGALYILGLDDRLRL APGAGDAALEPALAQWAFDHGQACGAGTDTLSNSPVLYLPLRAPMRVRGVLALHHAGPPLYSAAPARRQLDAYA TLIAIAIERLHYVEVAQQALLSIESERLRNALLAAVSHDLRTPLTSLLGMAETLQRSPAAMTPAALETVAAMQDQARR MHALVVNLLDMARLQSHDAPLRRQWQSVEELVGSALAAMNAALQDRPVTVAPLSALPLVECDGILIERVLCNLLEN AAKYTPPGSAIHIDALADAHTLQVRVADDGAGVAQADRQRIFEKFARGQRESATPGAGLGLAVCRAILDAHQGRI WVEPARRLRGACFVFALPLTPPPAVPPEPA	41~~KdpD (6.11683E-110)~~251;X;274~~Usp(1.1443E-32)~~394;X;440~~DUF4118 (1.49392E-19)~~534;X;566~~GAF (0.000000000000796 096)~~681;X;698~~HisKA (0.000000000001871)~~763;X;816~~HATPase_c (1.38296E-28)~~918	KdpD protein
	6E-13	58.3	7.7	1E-12	57.6	5.4	1.4	1	C5AAP0_BURGB	Histidine kinase (EC 2.7.13.3)	bglu_1g26250	Burkholderia glumae (strain BGR1)	976	626418	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia glumae (Pseudomonas glumae), Burkholderia glumae (strain BGR1)	>tr|C5AAP0|C5AAP0_BURGB Histidine kinase OS=Burkholderia glumae (strain BGR1) GN=bglu_1g26250 PE=4 SV=1MNRPDPDQLLDKLQREEEKQRGRLKIFFGASAGVGKTYAMLRAARSRADEGVRVLVGIVETHGRRETAAL LDGLDLLAPRVIEHRGRRLEEFDLDAALERRPQLVLVDELAHSNLPGSRHLKRWQDVHELLDAGIDVYTTVNVQHL ESLNDVVGAITGIRVWETVPDRVFDAADEVTLVDLPADELLERMRDGKVYLPQQAERAVRNFFRKGNLIALRELAL RRTADRVDAQMREYRADRSIARIWQARERLLVCVGPGPEAPTLVRAAARLAAGLKADWIAVYVETPRSQRLDDA RRRRPLDALKLAAELGAETVTLAGGDAVAALIGYAQVRNVSKLVAGGSPRTGFARRLARPFGERLAERAGDLDLM LLRTSAQDEARRAPSDAGALAWRDAFLRLAGERSPPRHYAVAAAICAVLTGIASLAQTRLDLTNLVMLYLLGVVFS AVRLGRGPGVMQSFLSVAAFDFFFVPPQMSLSVSDTQYLLTFFGMLLTSLVISHLTSSLTRAAGLAERRERRTGA MYAMARELAAALTAEQIVEIGSRHVAEVFRARVAMLLPDSADQVRQKIENPDEALTLTGAALDSDVGQWVYDQQK PAGRGTDTLPAAQARYLPLKAPMRTRGVLAVVTQDARELDMPEQQRMLDAFAAQIALALERVHYVEIARDALVSM ESERLRNSLLSAISHDLRTPLTTIVGFSSMLAGLHEAAGQGGAGAAGAAESAASRERELVEAIHDEALRMTGIVTNL LDMARLQAGSLQLKRQWSLLEETVGAALGACKRVLAHHPVQVRLPADLPLLQTDAVLMERLFANLFENAAKYTPA GAALVIGAERIDEDGAPFVRVTVDDHGPGLRAGMEARIFDKFTRGEKESATPGIGLGLAICRAIVDAHGGRIGARN RLAPDGSILGAQFWFTLPVDAPPPVPESDEAGEAHAERTAAAGSAPDEDGPGGAGQTRARVARAAFEPPLKPDH E	21~~KdpD (3.95153E-113)~~230;X;252~~Usp(3.66143E-30)~~374;X;410~~DUF4118 (1.21926E-20)~~510;X;538~~GAF (2.85908E-15)~~659;X;676~~HisKA (0.000000000118797)~~755;X;808~~HATPase_c (3.89575E-21)~~918	KdpD protein
	6E-13	58.2	5.9	1.2E-12	57.4	4.1	1.4	1	A0A0D5V8M9_9BURK	Histidine kinase (EC 2.7.13.3)	OI25_467	Burkholderia fungorum	944	134537	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia fungorum	>tr|A0A0D5V8M9|A0A0D5V8M9_9BURK Histidine kinase OS=Burkholderia fungorum GN=OI25_467 PE=4 SV=1MNRPDPDELLDKLQRDEEKRQRGRLKIFFGASAGVGKTYAMLQAARRRADEGTDVVVGIAETHGRGETAA LLEGLDVLPLAMIEYRGRKLGEFDLDAALARKPQLILVDELAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQH LESLNDVVGQITGIRVWETVPDRVFDRADEVTLVDLPAEELLDRMRDGKVYLPQQAERAVRNFFRKGNLIALRELA LRRTADRVDAQMREYRADRSIERIWQARERLLVCVGPGPEAPMLVRAAARLAASLKADWIAVYVETPALQRLPDA RRERTLNALKLAAELGAETATLAGTDAVAALIGYAQARNVSKLVAGASARSGFQRWVRRPLGERIAERAGDLDLTL IRASSERDGGEQRRLLNTTANAWREALSAARERRSPPRAYGIALTICAAITLLSSQLIDHIDLTNLVMLYLLGVIFTAV KLGRGPGVVLSFMSVAAFDFFFVPPRMSLSVSDTQYLLTFLGMLLTSLVISHLTSSLRREASVARRREQRTGAMY AMARELAAALTTEQIVGIGSRHVSEVFGARVAILLPDSADQVKQKIEDPDAAITLEGEMLDSDVGQWVYDQQKPA GHGTDTLPAAAALYLPLKAPMRTRGVLAVVMRDERELDVPEQQRMLDAFAAQIALALERVHYVDIARDALVNMES ERLRNSLLSAISHDLRTPLTTIVGFSSMLAQSREAHPGAQPGDDLVEAIHEEALRMTGIVTNLLDMARLQAGSLQLN QQWTLLEETVGAALRACKRVLANHPVQVKLPADLPLLHLDAVLMERLFSNLFENAAKYTPPDTPLTIGAQRLDADG KSFVRVAVDDNGPGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEAHGGTIGALNRMSPDGRVEGARF WFTLPVETPPEAPDALEDEGADALPDRDPTSNLLSKPSHE	21~~KdpD (7.73995E-122)~~230;X;252~~Usp(1.07462E-31)~~374;X;415~~DUF4118 (1.10304E-19)~~512;X;538~~GAF (5.76711E-18)~~661;X;678~~HisKA (0.000000000002223 45)~~745;X;798~~HATPase_c (1.76987E-22)~~908	KdpD protein

	7E-13	58.2	14.8	1.3E-12	57.3	10.3	1.4	1	D3UX99_XENBS	Histidine kinase (EC 2.7.13.3)	kdpD XBJ1_1070	Xenorhabdus bovienii (strain SS-2004)	905	406818	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus bovienii, Xenorhabdus bovienii (strain SS-2004)	>tr|D3UX99|D3UX99_XENBS Histidine kinase OS=Xenorhabdus bovienii (strain SS-2004) GN=kdpD PE=4 SV=1MDQIEPLRPDPDDLLALANEKPRGKLKIFFGACAGVGKTYAMLQEAQRLLSQGLDVIAGVVETHERQETAALLTGLPQLPLKHIRYHERRIAAFDIDAAIARYPAIILMDELAFSNPHSSRHPKRWQDVEELLEAGIDVLTTINVQHLESLNDVVGAITGIRVRETIPDHIFDHADDVVLVDIPPDDLRQRLNDGKVYISGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAFRDTRGKEPVWHTRDNLLLCIGCNAGNEKLIRTAARLAAKLGCEWHAVYVETPKLHRLPEIKRRTILKALKLAQELGAETATLSDPHEERAILRYAREHNLGKILVGRYHGSHSTSFSDKWLGFKWRPDFVERLGKLGPDLDLIIVALEDKKRWDKEQRDNRAFHEKWRIQIHGFLIAIILCTLITLFSHTFLLTLDKANLVTLYLLGVVIIALFYGRWPSVFAAFINVISFDIFFVQPRWSLAVTDMQYLLTFTVMLIVGVVVGNLTAGIRYQARVARYREQRTRHLYEITRELSRALNEEDVARISYHFLSNSFQAKTGLLLPDNNARLYQVKSNNGGQMQIDEAIAKWSFDKKQPAGAGTDTLPGVPYQLFPIATASQVFAVLAIESPNLRQLLVPEQQRLLQTFTGLIANALERLHLSRRAESAKLETEREQLRNSLLAALSHDLRTPLTVLFGQTEILMLDLSTENSPHTQQVNQIRQQILSTSRLVNNLLDMARIQSGGIQLNLEWHSLEEIVGSALRSLEYTLSRYTVELSLSANLLLHCDACLLERVFINLLENAIKYTHEQTPLGIRATTEYKQVHIEIWDAGSGIPQGQEQVIFDKFSRVRKESAIPGVGLGLAICRAIIEIHGGHIWAANNKKGGASFHFVLPLEEVPKIEEVIEEM	23~~KdpD (2.55199E-108)~~231;X;254~~Usp(2.86673E-35)~~384;X;412~~DUF4118 (3.18142E-21)~~511;X;537~~GAF (6.74244E-17)~~655;X;672~~HisKA (0.0000000000192553)~~737;X;789~~HATPase_c (1.82897E-26)~~890	KdpD protein
	7E-13	58.2	7	1.2E-12	57.4	4.8	1.4	1	G2IMI9_9SPHN	Histidine kinase (EC 2.7.13.3)	kdpD SLG_31030	Sphingobium sp. SYK-6	891	627192	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingobium, Sphingobium sp. SYK-6	>tr|G2IMI9|G2IMI9_9SPHN Histidine kinase OS=Sphingobium sp. SYK-6 GN=kdpD PE=4 SV=1MSSQPPPEDLRPNPEALLRQAAQEGRGRLKVFLGAAPGVGKTYEMLTEAVARKREGTDVVIGVVETHGRAETEALVHGLEVIARRPVDYQGRTLSEMDVDAILARRPQLVLVDELAHTNAPGSRHDKRYQDVEELLAAGIEVYSTVNVQHLESLNDVVASFTRVRVRETLPDRVIENADIEVIDIPPDELIERLKQGKVYVPAEATRALGNYFSKSNLTALRELALRRAAQAVDAEMLDYLRAHALAGNWAAGERIVVAVSEQSGAAELVRAAKRIADALRGPWTVVHIETPRSSQLGDADNARLAATLHLASQLGAQVATVPAETVVDGVIRFAAEARATQLIVGKSQRSRWFELRHGSVVDRLVRETPGITVHVLPMEEQAPVAAPTGRKKAQWGRPADYVISFGLIALVTLVGEVVFTAASIANVGLLFLLPVMIAASRYGLRLGIVCSLVASLAYNFFFIPPTHTFTIQDPQNILTVLVLLGVAVVSSQLAARARDDQALLAQRSAAQNSSLAGFARQLTAVSNAEELARLLCGEVGRLLGVHTLLLLPEEEELVLRAAVPPDARLETIELAASRWAFDHNQPAGRGSDTLTASEWLFHPLAAGGQVLGVFGIARPDAGTPIRSDRLPLLLSLLDQAALALERIALEGEMASITQLKERDRLRAALLSSVSHDLRTPLTTILGMLGELRPATDEQRRQLGEMRGEAERLNRFVDNLLDMVRIETGALLQSVEPVDLAEAVVAAVHDMRAVLRGREVELDVSPDLPFVRVDPRLFHHCLINLIDNAVKYGSPDTPVTITARRSATGLALSVLDEGAGFPSGEERRIFETFARIEGSDRKGGTGLGLAIVKGFAEAMGIEVHAMNRPDRSGARFDLFMPEAILVKGARDE	24~~KdpD (5.27075E-120)~~233;X;255~~Usp(4.44739E-39)~~378;X;402~~DUF4118 (0.000000000000248037)~~478;X(185);663~~HisKA (0.000000000029775)~~724;X;777~~HATPase_c (1.73547E-22)~~875	KdpD protein
	7E-13	58.1	10.8	1.1E-12	57.4	7.5	1.3	1	A0A0A0Z0J6_9ENTR	Histidine kinase (EC 2.7.13.3)	PSNIH1_04915	Pantoea sp. PSNIH1	891	1484158	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea sp. PSNIH1	>tr|A0A0A0Z0J6|A0A0A0Z0J6_9ENTR Histidine kinase OS=Pantoea sp. PSNIH1 GN=PSNIH1_04915 PE=4 SV=1MNDELPRPDPDALLLSHSDSHRGKLKIYFGACAGVGKTFAMLQEAQRLRAQGLDVLAGIVETHNRAETAALLHGLTLLPRRTTGRSHHTEFDLDAALARHPAVILMDELAHTNVQGARHPKRWQDIDELLDAGIDVITTVNVQHLESLNDVVAGITGIQVRETVPDPFFDSADEVVLVDLPPDDLRQRLKEGKVYVGDRAERAIENFFRKGNLFALRELALRRTADRVDDQMRAWRDQQGRDRVWHTRDAILLCIGDDTGSEKLVRTAARLAARLGSVWHAVYVETPRLHRLPEAQRRAILRTLQLAQELGAETATLADPDEVRAVLRYAREHNLGKIVAGRQPHRRFRRDSFAQRLGELGPDLDLLVVALDEPLRPALHAASSKPVSSDKWRLRLRGCIMALLLCLAVTFIGRGLLAEFDSANAVMIYLLSVVLVALRYGRWPSVFATVINIVAFDLMFVAPTGTVAVSDLQYLVTFGVMLAVGVIVGNLTAGVRYQARVARYREQRARYLYEMAKSLGSALTPQDIAATAQRVIEVTLQARSQLLLPDEQGELQATGPDLRGTPPDAGIAKWSYSKGQPAGAGTDTLPAVPYQIVPLKSGQQCRGLLVVEPENLRQLMIPEQQRLVETFTVLIANALERMALTQSEAASRLAAEREQLRNALLSALSHDLRTPLTVLFGQAEMLMLDLAHAQSPFVAQAGQIREQTLSTIRLVSNMLDMARIQSGGLQLREEWVALDEVIDGALRSMGPMLKGHAFELALPSELVLIKGDSAMLERVFSNLIENSLKYAGNAAQHGIRAWRDGSRLEIGVWDSGPGIAGDSLTQIFEKFARGDKESAVPGVGLGLAISKTITEAHRGRIWAENRASGGAEFRLSLPLPAPPEISEAALK	20~~KdpD (2.20877E-120)~~228;X;251~~Usp(2.72445E-39)~~370;X;402~~DUF4118 (1.87347E-20)~~498;X;524~~GAF (8.08039E-14)~~641;X;658~~HisKA (0.00000000552893)~~723;X;776~~HATPase_c (8.97483E-27)~~877	KdpD protein
	8E-13	57.9	11.7	1.4E-12	57.1	8.1	1.3	1	B2VJK1_ERWT9	Histidine kinase (EC 2.7.13.3)	kdpD ETA_33620	Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	890	338565	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Erwinia, Erwinia tasmaniensis (strain DSM 17950 / Et1/99)	>tr|B2VJK1|B2VJK1_ERWT9 Histidine kinase OS=Erwinia tasmaniensis (strain DSM 17950 / Et1/99) GN=kdpD PE=4 SV=1MNDELQRPDPDALLRQAVESHRGKLKIYFGACAGVGKTWSMLQEARRLRAQGLEVLVGVVETHDRPETAALLSGLTVLPRRATGPQRRPEFDLDAALARHPAVILMDELAHSNTPGSRHPKRWQDIDELLEAGIDVMTTVNVQHLESLNDVVGGVTGIRVRETVPDPFFDAADEVVLVDLPPDDLRQRLKEGKVYIGESAERAIENFFRKGNLIALRELALRRTADRVDDQMRAWRDTQGREKVWHTRDAILLCIGDNSGSEKLVRSAARLAARDLSVWHAVYVETPRLYRLSETRRRGILRTLQLAQDLGAETATLSDPSEASAVLRYAREHNLGKIIIGRRPTRRWWRESFAERVGELGPDLDILIVALDDPPPDSVSSLAERVDSQEGKRGSQLRGCAAALLLCMLVTLAGRWLLPAVDSVNLVMVYLLSVVIVALRYGRWPSVVATLLNILAFDLVFVAPTGTMVVSDVQYLVTFGVMLAVGVIVGNLTAGVRYQARVARYREQRAHHLYETAKALSRALTQRDIASTLQRSVESTLQARSELYLPDEHGELVPVGAAHLSAVPDRAIARWSFDKGQPAGAGTDTLPGVQWQMLPLKSGSDMLGLLILEPLNLRQLMIPEQQRLVETFTVLIANALERMALSQREAASRLAAEREQLRNALLSALSHDLRTPLTVLFGQAEILTLDLASANSPYAGQASAMREQTLNTIRLVNNLLDMARLQSGGFSLRREWMALDELIGSALRQLAPLLADRPVTLDLPAELLLIDVDGPLMERVLVNLLENALKYAGDKAQIGIRARAVAQRLELEVWDTGPGIAPDQQQLIFEKFSRGDKESTVPGVGLGLAICQAIVTLHEGKIHAENRPQGGVSFVISLPLTAPPMLEEYT	20~~KdpD (1.2538E-118)~~228;X;251~~Usp(2.16181E-37)~~370;X;401~~DUF4118 (6.80192E-21)~~499;X;525~~GAF (0.000000000161844)~~642;X;659~~HisKA (0.00000000284288)~~724;X;777~~HATPase_c (9.74458E-31)~~878	KdpD protein
	8E-13	57.8	12.2	1.6E-12	57	8.5	1.4	1	K8WAH7_PRORE	Histidine kinase (EC 2.7.13.3)	OOC_07093	Providencia rettgeri Dmel1	854	1141663	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia rettgeri, Providencia rettgeri Dmel1	>tr|K8WAH7|K8WAH7_PRORE Histidine kinase OS=Providencia rettgeri Dmel1 GN=OOC_07093 PE=4 SV=1MLQEAQRLRAQGLDVLIGVVETHEREETAALLDGLSLLPRRITHHGRRLNGFDIDAAIARHPAIILMDELAFSNPHGSRHPKRWQDVEELLDAGIDVLTTINVQHIESLNDIVGSITGIRVRETVPDHIFDAADEVVLVDLPPDDLRQRLKEGKVYIPGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMREFRDGKGQAPVWHTRDGLLLCIGHNTGNEKLVRTAARLAAKFGSVWHAVYVETPSLHQLPETQRRAILKALRLAQDLGAETATLSDPSEEKAILRYAREHNLGKILIGRRNKVNKWFKLNLRPGFADRLGKLGPDLDLVIVALEEKSEWDKEPERKPFSEKWRSDMNGYLMAIVMCAAITLFSRTFLLALDKANLVTLYLLGVVLIALFYGRRPSVFAALVNVISFDLFFVQPHFSLAIMDMQYLVTFTVMLIVGVVVGNLTAGMRYQARIARYREQRTRHLYEMTKELGQAITTDDIGRTGYHFLNNAFQAKSCLLLPDENDQLSPLKCEGHSEMLIDKAIAKWCFDKRQPAGAGTDTLPSVPYQLQPITTADQTLAVLAIEPRNMRQLLIPEQQRMLQTFTGLIASALARLQLTKQAESAKLDIEREQLRNSLLAALSHDLKTPLTVLFGQTEILMNLLSAEKSPLTEQVNQMRQQVLSTSRLVNNLLDMARLQSGSIQPNLAWESLQEITSSAVRTLDYTLHSHPLEIDIPADLLLYCDANLIERVLINLLENAVKYSHDDTPIGIRATVEGQKIHIEIWDASNAIPNGQEKTIFDKFSRAQKESAIPGVGLGLAICRAIIQLHEGEIWAQNNNKGGASFHFVLPLKQLPDIEVET	1~~KdpD (1.52117E-108)~~190;X;213~~Usp(1.15841E-36)~~337;X;364~~DUF4118 (1.6219E-20)~~463;X;489~~GAF (3.75348E-16)~~607;X;624~~HisKA (0.000000000293357)~~689;X;741~~HATPase_c (1.57077E-23)~~842	KdpD protein

	8E-13	57.8	3.1	1.4E-12	57.1	2.1	1.3	1	A0R7M2_PELPD	Metal dependent phosphohydrolase	Ppro_3640	Pelobacter propionicus (strain DSM 2379)	320	338966	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Pelobacteraceae, Pelobacter, Pelobacter propionicus, Pelobacter propionicus (strain DSM 2379)	>tr|A0R7M2|A0R7M2_PELPD Metal dependent phosphohydrolase OS=Pelobacter propionicus (strain DSM 2379) GN=Ppro_3640 PE=4 SV=1MSNYSDTQKKVIILAALVGIIALLHYATPTEPHYFHKIHIILRKLYFLPPVIAAAWFGFRGAIITTTTVSVLFLLHAFLDWPGNYMEQANQLGELAGFWLAGLISGRLFDRQRSLLMDLATANEETLIGLVSALDLREHNTRMHSQRVRDYTELIADRLGVDEKMKREIGFGALLHDVGKIAVPDQILLKPGKLTDEEWIEMRKHPEAGYRIVKRIGFLKDAAEIVHAHHERYDGKGYPRGLKGNEIPWGARMFMVADAYDALTSKRPYKSPLPYEEAVIEILNQKGKQFDPEVVAIFLIIAPDELRLIAERYQDGDLPS	13~~DUF4118 (0.0000000918596)~~113;X;139~~HDc (3.08852E-22)~~278	non-KdpD DUF4118 protein
	8E-13	57.8	6.9	8.4E-13	57.8	4.8	2	1	C3K5J9_PSEFS	Histidine kinase (EC 2.7.13.3)	kdpD PFLU_1679	Pseudomonas fluorescens (strain SBW25)	883	216595	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens (strain SBW25)	>tr|C3K5J9|C3K5J9_PSEFS Histidine kinase OS=Pseudomonas fluorescens (strain SBW25) GN=kdpD PE=4 SV=1MSDSGRADALLADLPRDGRGRLKVFLGAAPGVGKTYAMLQAAHTQLRQGVRLVAGVVETHGRAETEALLSGLPQQPLLRSEYRGVMLEEMDLDGLLAAKPRLVLVDELAHSNAPGSRHEKRWQDIQELLAAGINVFTTVNVQHLESLNDQVRGITGVQVRETLPDWVLQEADELLLIDLPSRELLERLRDGKVYVPEQARAAIDAFFTQTNLMALRELAMQTAAAHVDDDLAQGYRQLGQSAPAVRGRLLVGVDGDAQAERLVRHASRVAQRRHLPWSLVHIDNGRARDEQSRLRLQNAQQLAERLGGEVVLLRAGEVAKTLIQHAAERRASLLLVGQSRMRWRRRLFGGGLAARLLRHARGLEINILDSDDMPASPRLPEVRGLVWFDYALAVVATVVAAAVAWAVSSVLPLPNISLVFLAAVLLVAVRSSLGPSLVCAGLSFMTYDFLFIPPNFSFSIQREEDVLTLLFFLLMAALTGNLAARQRRQLQALRDTQEETSELLDLSRKLTAATDRQAVISAAAHHLEGWSDLDLCLVNRDGQGGWAIETGGPLTLTEAERAAADWAWQHDQPAGMGTGTLPFGRWWWWPLSGEEGPLGLLGVSPKPGLELSGQRRRLLTALSQPLAQALARAQLAQELESARLHGETEQLRSALLASVSHDLRTPLTSMRGSIDSLLALGEAIPLEDRRELLEGTRDEAERLDRYIQNLLDMTRLGHGALKLARDWVSPGDIVGSALGRLRAVLAPLQVSADVPPELPLLYVHAALIEQALVNVLENAARFSPPQGRLQLSAGVLDNQLFFAVADEGPGIPEDERAKIFDMFYTAARGDRGGQGTGLGLAICQGMVGAHGGHISVADGIDGRGTCITLFLPLPTQPGLEREA	18~~KdpD (9.98527E120)~~227;X;248~~Usp(2.58562E-32)~~368;X;411~~DUF4118 (0.000000144168)~~489;X(160);649~~HisKA (0.000000000000255101)~~715;X;768~~HATPase_c (1.34478E-24)~~871	KdpD protein
	8E-13	57.8	14	1.5E-12	57.1	9.7	1.4	1	A0A090UEC1_9ENTR	Histidine kinase (EC 2.7.13.3)	kdpD CIFAM_08_00560	Citrobacter farmeri GTC 1319	895	1114922	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter farmeri, Citrobacter farmeri GTC 1319	>tr|A0A090UEC1|A0A090UEC1_9ENTR Histidine kinase OS=Citrobacter farmeri GTC 1319 GN=kdpD PE=4 SV=1MVDDDVLRPDPDRLLEQAVSPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQGLDILIGVVETHGRKETAALLDGLSILPLRRQTRHGRHISEFDLDAALARRPALILMDELAHSNAPGSRHPKRWQDIEELLDAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAWRGRPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRLGSVWHAVYVETPALHRLPEKQRRNILHALRLAQELGAETATLSDPSEDKAVVRYAREHNLGKIVLGRTTTRRWWHRDSFADRLAKRAPELDLMVVALDDPPVRTLTSMPDTRAFKDKWRVQIQGGLVAVALCALTTFIASQWLSAFDAANLVMLYLLGVVVIALFYGRWPSVFATFISVISFDLFFIAPRGTLAVSDVQYLLTFGVMLTVGLVVGNLTAGVRYQARVARYREQRTRHLYEMSKALAMGRSAQDIATTSEQFIASTFHARSQILLPDEEGKLTALTHQHGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLRSADKTHGLVVVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEELARLASERESLRNALLAALSHDLRTPLTVLFGQTEILTDLASEGSPHARQASEIRQHVLNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALKMLEPGLVHPVNLSLPAPLTLIHVDGPLFERVLINLLENAIKYAGPQAEIGIDAHVENDHLQLDVWDNGPGIPQGQEQRVFDKFARGNKESAVPGVGLGLAICRAIVEVHGGAIAVYNRPQGGACFRVTLVQETPPELEDFHEDM	21~~KdpD (2.22426E127)~~231;X;254~~Usp(3.23078E-40)~~374;X;404~~DUF4118 (6.35432E-22)~~502;X;530~~GAF (2.01807E-15)~~645;X;662~~HisKA (0.00000000190457)~~727;X;779~~HATPase_c (6.0935E-32)~~880	KdpD protein
	9E-13	57.8	12.6	1.5E-12	57.1	8.8	1.3	1	W0HXN9_9ENTR	Histidine kinase (EC 2.7.13.3)	kdpD Sant_3534	Sodalis praecaptivus	894	1239307	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Sodalis (tsetse S-endosymbionts), Sodalis praecaptivus	>tr|W0HXN9|W0HXN9_9ENTR Histidine kinase OS=Sodalis praecaptivus GN=kdpD PE=4 SV=1MTDEPLRPDPDVLLAQADNDGRGKLKIYFGACAGVGKTWAMLQEARRLRAQGLDVVAGVVETHGRQETAALLEGLEMLKPRATGRRRHQAFDLDAALARRPAVILMDELAHSNAPGARHPKRWQDIEELLEAGIDVLTTVNVQHLESLNDVVSGVTGVRVRETVPDPFFDAAAEVVLVDLPPDDLLVRLKQGKVYVGDRAERAIENFFRKGNLFALRELALRRTADRVDGQMRAWRDARGREEKVWHTRDAVLLCIGASTGSEKLVRTAARLAAKLGSEWHAVTVETPTLYRRGEARRRATLRTLQLAQKMGAVTATLSDPDEAKAVLRYAREHNLGKIILGRPPQRRWRFANRFHRRLSRLGPDVDLLIVALDDDVPDTSLARAEDGRGMGNGWRQNMRGALAAAALCALITLVCQWLPGVSPINLVMIYLLGVVLIAIVFGRLPSVAAALLNIVAFDLFFVAPAGSFAVSDAEYLVTFTVMLAVGLLTGNLTAGVRYQARVARHREQRARYLYEMADGLSRVRRPEAIAHICQRVVSAALLARCEIWLPDRQGELQGPAQSMMHTVPDAAIVKWSFDKGQPVAGAGTDTLPGVPYKILPLPTSSGRTLGLLIIEPSNVRHLMIPEQQRLLETFLVLIAGALERLELTRREQLSRLAAEREELRNSLLAALSHDLRTPLTVLFGQAEILMLNLSAEGSRYVHQADELRRQTLSTIRLVNNMLDMARIEADGFRPQTDWIALEEIIGSALKSLEGVVSARHVRLDLPREMILLRADGPLLERVFVNLLENAQKYAGQGAEIGIRAEKRTDTLTITVWDNGPGLPVGKENQLFDKFTRGHQESAIPGVGMGLAICRAIVEMHQGEIYAANRPSGGACFTIILPLPPAPALEEPLQEDA	21~~KdpD (1.211~~Usp(1.01327E-34)~~372;X;411~~DUF4118 (1.67777E-18)~~499;X;527~~GAF (0.000000000042235)~~642;X;659~~HisKA (0.00000000314452)~~724;X;777~~HATPase_c (1.24907E-29)~~878	KdpD protein
	9E-13	57.7	13.2	1.7E-12	56.9	9.1	1.4	1	I0DX86_PROSM	Histidine kinase (EC 2.7.13.3)	S70_15695	Providencia stuartii (strain MRSN 2154)	906	1157951	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia stuartii, Providencia stuartii (strain MRSN 2154)	>tr|I0DX86|I0DX86_PROSM Histidine kinase OS=Providencia stuartii (strain MRSN 2154) GN=S70_15695 PE=4 SV=1MDNQDPVRPNPDELLAKANESGRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGLDVLVGVVETHEREETAALLDGLSQLPPRRLNHRGRRMSAFDIDAAIARHPAIILMDELAFSNPAGSRHPKRWQDVEELLDAGIDVLTTINVQHIESLNDIVGSITGIHVRETVPDHIFDAADEIVLVDLPPDDLRQRLKEGKVYIPAQAERAIEHFFRKGNLIALRELALRRTADRVDDQMREFRDGKGHVPVWHTRDGLLLCIGHHNGNEKLVRAAARLAAKLGSVWHAIYVETPKLHRLPEGHRRAILKALRLAQDLGAETATLSDPYEEKAVLRYAREHNLGKILVGRRTKRRRWLDFGTHTNFAERLGALGPDLDLVIVALEERNDWVKEPERKPFSEKWRSDVNGFLVAIAICTVITLFSRTFLLALDKANLVTLYLLSVVLVALFYGRRPSIFAALINVISFDLFFVQPHFSLAIMDMQYLVTFTVMLIVGVVVGNLTAGMRYQARIARYREQRTRHLYEMTKELSRALTEQDIGKTGYHFINNAFQAKTCLLLPDENNQLSPLLCEGHSPMQIDQAIAKWSFEKRQPAGAGTDTLPSVPYQLQPITTADQTLAVLAIEPNNLRQLLIPEQQRMLQTFTGLIASALARLQLSKQAESAKLDIEREQLRNSLLAALSHDLKTPLTVLFGQAEILTLNLSAENSPYTEQVNQMRQQILSTSRLVNNLLDMARLQSGSIQPNFEWQSLQEITGSAVRTLDYTLHSHPLSIDIPANLLLYCDGNLIERVLINLLENATKYSDKDTPMGICAQIEDNQVHIEVWDASNAIPDGQEKIIFDKFSRAQKESAIPGVGLGLAICRAIIQLHDGNIWAENNKKGGASFHFVLPFKQLPDIEELDNYCESPSNTDH	21~~KdpD (3.23652E126)~~231;X;254~~Usp(2.09863E-26)~~378;X;406~~DUF4118 (1.91295E-21)~~504;X;530~~GAF (3.51258E-16)~~648;X;665~~HisKA (0.000000000048678 9)~~730;X;782~~HATPase_c (1.9011E-21)~~883	KdpD protein

	9E-13	57.7	7.1	1.6E-12	56.9	5	1.4	1	Q142K6_BURXL	Histidine kinase (EC 2.7.13.3)	Bxe_A3249	Burkholderia xenovorans (strain LB400)	944	266265	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia xenovorans, Burkholderia xenovorans (strain LB400)	>tr|Q142K6|Q142K6_BURXL Histidine kinase OS=Burkholderia xenovorans (strain LB400) GN=Bxe_A3249 PE=4 SV=1MNRPDPDELLDKLQRDEEKRQRGRLKIFFGASAGVGKTYAMLQAARRRHDEGADVVVGIAETHGRSETAA LLEGLDVLPLAQIEYRGRKLGEFDLDAALARKPQLILVDELAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQH LESLNDVVGQITGIRVWETVPDRVFDSADEVTLVDLPAEELLDRMRDGKVYLPQQAERAVRNFFRKGNLIALRELA LRRTADRVDAQMREYRADRSIRRIWQARERLLVCVGPGPEAPMLVRAAARLAASLKADWIAVYVETPALQRLPDA RRERTLNALKLAAELGAETATLAGADAATALIGYAQARNVSKLVAGASARTGAERWLRRPLSERIAEKAGDLDLTLI RASSGRDGGEHRHLLNTTANAWREALSAARERRSPPRAYAFALAICAAITLLASQLSDHIDLTNLVMLYLLGVIFAA VKLGRGPGVVLSFMSVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLLTSLVISHLTSSLRREASVARRREQRTGAM YAMARELAAALTTEQIVGIGSRHVSEVFGARVAILLPDSVDQVKQKIEDPDAAVTLEGEMLDSDVGQWVYDQQKP AGHGTDTLPAAAALYLPLKAPMRTRGVLAVVTRNEGELDVPEQQRMLDAFAAQIALALERVHYVDIARDALVNME SERLRNSLLSAISHDLRTPLTTIVGFSSMLAQSPDAQPNAELVEAIHEEALRMTGIVTNLLDMARLQAGSLQLNQQ WTLLEETVGAALRACKRVLANHPVQVKLPADLPLLHLDAVLMERLFSNLFENAAKYTAPATPLTIGAQRLDTDGKS FVRVTVDDNGPGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEAHGGTIGALNRVSANGHVEGARFWFT LPVETPPEAPDALEDEGADALTHVDTDSESTPNPFAKPSHD	21~~KdpD (8.66115E123)~~230;X;252~~Usp(1.9741E-30)~~374;X;412~~DUF4118 (6.56566E-20)~~512;X;538~~GAF (2.89995E-17)~~661;X;678~~HisKA (0.000000000000534028)~~741;X;794~~HATPase_c (7.64922E-23)~~904	KdpD protein
	1E-12	57.6	12.9	1.9E-12	56.7	8.9	1.4	1	A0A089UJW6_9ENTR	Histidine kinase (EC 2.7.13.3)	LH23_11605	Cedecea neteri	895	158822	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cedecea, Cedecea neteri	>tr|A0A089UJW6|A0A089UJW6_9ENTR Histidine kinase OS=Cedecea neteri GN=LH23_11605 PE=4 SV=1MTEEPLRPNPDKLLEKVNRQPRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGLDVLVGVVETHGRKETAEL LKGLTIQPPRRIHHRGRLVQEFDLDAALARSPALILMDELAHTNAPGSRHPKRWQDVEELLEAGIDVLTSVNVQHL ESLNDVVGGVTGIQVRETVPDPIFDAADEVVLVDLPPDDLRQRLHEGKVYISGQAERAIEHFFRKGNLIALRELALR RTADRVDDQMRAWRDNQGQEKVWHTRDAILLCIGHSNGNEKLVRTAARLAAKLGSIWHAVYVETPQLHRLPEHQ RRTILSALRLAQELGAETATLADPNEEKAVLRYAREHNLGKIIIGRHTTRRWWHRTSFADRLAKRAPDLDLLIVALD EKPLPSPARAPDTRTLSEKWRIQLRGCAVAVVLCAFITFIANQWLVAFDAANLVMIYLLGVVMVALFYGRWPSVLA TVINVISFDLFFIAPRGTLAVSDVQYLLTFGVMLTVGLVIGNLTAGVRYQARIARYREQRTRHLYEMSKALADDRTP QDVAATSVQFINNTFQARSLLLLPDDHGKLSRIAAEGEPAQWDEAIARWSFDKGQPAGAGTDTLPGVPYRILPLST TERTLGLLVVEPENLRQLMIPEQQRLLETFTLLVATALDRLLLTASEEQARLSSEREQIRNSLLAALSHDLRTPLTVL FGQAEILTLDLASEGSKHAPQANEIRQHVLNTTRLVNNLLDMARIQSGGFNLRKEWLTLEEVVGSALKMLEPGLGG RHIALNLPDPLMLIEVDGPLFERVLINLLENAVKYAGYKANIGIKATSTADKLDLEVWDSGPGVPAGKELLIFDKFAR GNKESAIPGVGLGLAICRAIVEVHGGTIYALNRPEGGASFHVVLPLSPPPELPEMIEVL	22~~KdpD (2.7805E-125)~~230;X;253~~Usp(1.44838E-39)~~373;X;403~~DUF4118 (2.64488E-20)~~501;X;527~~GAF (2.49708E-16)~~644;X;661~~HisKA (0.00000000219598)~~726;X;779~~HATPase_c (1.32769E-25)~~878	KdpD protein
	1E-12	57.6	14	1.6E-12	57	9.7	1.3	1	A7IKC2_XANP2	Histidine kinase (EC 2.7.13.3)	Xaut_3236	Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	900	78245	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Xanthobacter, Xanthobacter autotrophicus, Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	>tr|A7IKC2|A7IKC2_XANP2 Histidine kinase OS=Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2) GN=Xaut_3236 PE=4 SV=1MPDDRAAPVRPSPDALLAAAEQETRGRLKIFLGAAPGVGKTYEMLASGHARRNDGADVVIGVVETHGRRET EALVAGLEVIPRRSIPYKGRMIEEMDLDAILARRPALVLVDELAHTNAPESRHAKRYMDVEELLAAGIDVYTTLNIQH VESLNDVVAQITRVRVRETVPDAIIDRADDIEVIDITPGDLLQRLKEGKVYVPETARRAVENYFSPGNLTALRELALR RTAERVDEQLLSHMRAHAISGPWAAGERVLVCLSEDPRSAALVRYTKRLADRLRAPWVALYVETERALRLDTAER DRIADFLRLAERMGGEAVTIPGGTRIADDVLSYARSANVTHIVIGKSDRSRWFEILHGSVVHDLVRRSGNISVHVIA GDKETPAPGRSGAAVPTARRETWPYLASLVIVALATLVGFGLQKVLALQNIALVFLTAVLVSAVRFGLAPALVASGA AMLAFNFFFIPPLYTFTITDPENVVALFFFLVVAIIASNLTARVRAQALAARARAKTAEDLYLFSKKLAGAGTLDDLLW ATAFQIASMLNVRVVIVLPDGDTLAVKAAYPPEDAIDAADLAAARWAFENNRWAGRGADTLPGAKRLFMPMQTG RGAVGVIGIDRDKEGPLLTPEQRRLMDALADQAALAVERVNLVADVEKAKLDAATDRLRTALLTSISHDLKTPLASI MGAAGTLRSFFSALTEEARSDLLSTVEEEAERLNRFIANLLDMTRLESGAIVPNAGLCDVSEVVGSALDRARSILRH HRLEIDLAPDLPMLSIDPVLFEQALFNLLDNAAKYAPEGALVRIEGWSDGAFVTLRVLDEGPGIAEEDRERVFDKFY RVRKGDQVRAGTGLGLGISRGFLEAMGGTLTADGRPDRRGAAFTIRMPVPPQARALKALP	25~~KdpD (1.52261E122)~~233;X;255~~Usp(1.51442E-43)~~379;X;403~~DUF4118 (1.24455E-19)~~497;X;529~~GAF (0.0000837882)~~648;X;665~~HisKA (0.000000000008896 13)~~731;X;784~~HATPase_c (5.96041E-24)~~886	KdpD protein
	1E-12	57.4	9.3	2.1E-12	56.5	6.4	1.4	1	D2R314_PIRSD	Histidine kinase (EC 2.7.13.3)	Psta_4097	Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	909	530564	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Pirellula, Pirellula staleyi, Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	>tr|D2R314|D2R314_PIRSD Histidine kinase OS=Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) GN=Psta_4097 PE=4 SV=1MTDSRPNPDALLALAEDEQKLDDTTTGKRGSLRIFFGYAAGVGKTYGMLEAAQAARREGRDVVVGYIEPHA RKETQALAADFETLPTKQLSYRGVTLREFDVDAALARKAEITLVDELAHTNAEGSRHEKRWQDIEELCASGLHVW TTLNVQHLESLNDVIGQITGVQVRETIPDHVFDAADQLELIDITPEELLGRLEAGKIYLPEQAKRAIQSFFQRSNLSAL RELSLRQAARRVHTDVESARRARSVRQPWATTDRLLVCVGPSPTTARVIRTAKRMASALDAPWIAVSVDLTGASS TSPASQQIAEHFRLAERLGAETVTLPGQRMTETILEYARTRNVTKILIGKTDQPRWKRLLMGTVVDEILEQSGEIDV YVIHGEKDQAARVATPPARPPIDYWLYGKAAVPVGLAGLAALAMKRWHFADAEANTVMIFLAAVAWAAFRFGRG PAIVASLLAVTIFDFFFVPPFHTFAVADTQYIVTFAVMLAIALLISTLTSRLRAQLEAMRDRQRRTAALYELGKQLSSL YGSSFLAKAAGEKIAEMVGGEVAIYLDRHAPSPELVFGARSSIALQHGSSAVAHWVIQHGQMAGAGTSTLPSAVG LFLPLIGSQRVHGAMAVAVASAARLQQPELRQLLESCASQLAISIERDALVVEAADARVKAEAEQVRSSLLSSVSH DLKTPLAAIAGASSTLLEASSLPPSTREQLLQTVAEEAVRLGRLLENILQMSKLDAGASPPHLEWHMLEEIVGSSIR RIEKSLTQHQLIIQIPEQLPLLRLDGLLMEQVFVNLLENAARYTTAGSTISVRAVVEGQEVRVTVADNGPGLPAGAE EKVFDKFYRAFPSADGGRGSGLGLAICRAIVKVHGGRIEAANLPAGGAEFVIHLPLAQDIPQVPLSPSDSSRAS	27~~KdpD (1.21932E117)~~237;X;259~~Usp(2.5635E-39)~~380;X;407~~DUF4118 (1.09889E-18)~~506;X;536~~GAF (0.0000183883)~~652;X;681~~HisKA (0.00000000506713)~~734;X;787~~HATPase_c (5.1623E-29)~~889	KdpD protein

	1E-12	57.3	8.3	2E-12	56.6	5.7	1.4	1	W0A6Z8_9SPHN	Histidine kinase (EC 2.7.13.3)	NX02_05670	Sphingomonas sanxanigenens DSM 19645 = NX02	889	1123269	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sanxanigenens, Sphingomonas sanxanigenens DSM 19645 = NX02	>tr|W0A6Z8|W0A6Z8_9SPHN Histidine kinase OS=Sphingomonas sanxanigenens DSM 19645 = NX02 GN=NX02_05670 PE=4 SV=1MTSAPDRPDPEAFLRQAAQEGRGRLKLFLGAAPGVGKTYEMLSEGRQRREAGIDIVIGVVETHGRRETEALVAGYEVIPRIDVDHRGHNLGEMDIDAILARRPQLVLVDELAHTNAPSSRHPKRYQDVEELLDAGIDVYSTVNIQHVESLNDVVASFTRVRVRETVPDAMLEAAEIEVVDIPPDELIERLKEGKVYVPEEASRALGHFFSKSNLTALRELALRRAAQAVDAQMLDYVRQHALAGSFAVGERIIVAISEHPSGPGLVRAGKRLADALKAPWTVVHIETQRSQSLSDFERQRVADAMALASRLGAVTASIPAQRVVVDGLRRDFATEARATQIVIGKSTRSWMFELRHGSVVDQLVRAIDGVAIHVLPGDGEVAREMPGAAAPRRPRGDLSDYLWTLAAVALCTAIARGLVELIDLGNVGMMFLVPVMFAAASFGLRAGLFAGVTASLAYNFFFLPPTGTLTVSNPENIISIFVLLGVALVTSQFAARVRTQADLAQSSARQNAALAGFSRLLTGAADQEALMQAICAEVARLFDVRTVLLLPSATGPQLRAAYPPEDRLDQIELAAAAQWAIDNEQPAGRGSSTLTASDWLFHPLATTRGVLGVLGLARAEDAGEPLRSDQMPLLMSLLDQAAIAFDRMALEGEMQDARQLRERDRLRSALLSSVSHDLRTPLTSILSAVQQMRIEPRPDLVETVEDEAQRLNRFVANLLDMARVEAGALPLRIEATDLTDAVASAVHDTRRALAGHEIRLEIPPDMPLVRIDPQLFHHCLINLLDNTGRYADPDTPVTIAARRDAQGIALSIIDQGPGIPPGKESKLFETFTRLEGSDRAKGGTGLGLAIVKGFAEAMGLAVSARNVDPPGACFTITIPESAVISALDDQDLP	20~~KdpD (2.90433E-120)~~229;X;251~~Usp(1.02457E-35)~~374;X;399~~DUF4118 (2.55963E-18)~~498;X;524~~GAF (0.00000000103928)~~643;X;660~~HisKA (0.000000000951360)~~719;X;772~~HATPase_c (1.14471E-23)~~874	KdpD protein
	1E-12	57.3	16.6	1.2E-12	57.3	11.5	1.6	1	B2V898_SULSY	Uncharacterized protein	SYO3AOP1_05531	Sulfurihydrogenibium sp. (strain YO3AOP1)	426	436114	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Hydrogenothermaceae, Sulfurihydrogenibium, Sulfurihydrogenibium sp. (strain YO3AOP1)	>tr|B2V898|B2V898_SULSY Uncharacterized protein OS=Sulfurihydrogenibium sp. (strain YO3AOP1) GN=SYO3AOP1_0531 PE=4 SV=1MFLTKFLKELNLKILIAEIFIFTLALLFIGMYTNPSDPLFIESKFGYLFYLLPLLVFTLYYGLVAGIISFFAIVLIAFFFYKEFPTVYILWLFLFVLVASEFNYYWSENVKKAEEKFKYADGKLRDLARELMLLKISHDQLEKQYIIKPISIREVIYQIKQKIISNFEENEVFNMLMNLLIQSFNIEKAAFVYIDLKKNNFKIISSTHDDFDFNIKDVLVSKAIEDRSISYLSKIEEESKYYAAIPVFISETQVYLFIIEEIGFLSLNMDTLLMINLFIYYVISEKITLEKIKDIVKNFDMFDIDFIKELYKMSEIKKNLGIESSLVIFQIKGSIEDENIKNLLRNNLRGLDIMDSLFLQEENLLIIPILLPFTPISGANSFVERVKNILVENLSLSFFEKNIKLKIEPVDINPAKNLQSILETIK	16~~DUF4118 (0.000000000093739 2)~~109	non-KdpD DUF4118 protein
	1E-12	57.3	8.4	2.2E-12	56.5	5.8	1.4	1	D8IRC8_HERSS	Histidine kinase (EC 2.7.13.3)	kdpDHsero_3776	Herbaspirillum seropedicae (strain SmR1)	939	757424	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herbaspirillum, Herbaspirillum seropedicae, Herbaspirillum seropedicae (strain SmR1)	>tr|D8IRC8|D8IRC8_HERSS Histidine kinase OS=Herbaspirillum seropedicae (strain SmR1) GN=kdpD PE=4 SV=1MLRLGSTGLLPLQCSNPDNPDMTTRPDPDDLLERVMRDEERQARGRLKIFFGFSAGVGKTFAMLEAAQALAAQGGDVVAGVVETHGRAETEAQLAGLARLPMRMVAYRDRQLPEFDLDAALERKPGVILVDELAHSNVPGSRHAKRWQDIDELLRAGIDVYTTLNVQHIESLNDVVGQITGIRVFETVPDHVFDEADDVMLVDIPPDELLARLQQGKVYLPQQAEKAGRNFFRKGNLIALREIALRRTADRVDADMRQYRADRSIAQLWQARECIVVAIGSGSGEERLIREAARLAAKLQAQWLAVHVDLPGQRQAMEARERVVSYLKLAHSLGAETASISGEELAAALLQFARSRNAGKLVIGQEEGGLRRLLRWPRGTLAQRIARSGGEIDLYTIARSRTRHQHEPASPDSAASAAEALLTRRRRTRGTLWAVASCAITTTLAFLLDGKLHPANVIMLYLVGVMLVAMRYGRAASALVSVLSVLSFDFFFVDPRFSITVSDAQYLLTLAVMLAVSLFISSLAARLRRQASVAMQREARAANLYMLGKELSALLTLDQILEIGRRHLAAVFGARIAFFLPDSADQLRLAEPEQDSGAAHVFRNVDAGVAQWVYDNGQAAGKGTATLPSAAALYLPLTATMRTRGVLAFAIEAPSEEERQLAAAQLALPENRQMLEIFCSQIAMAIERLHYAEVAQDALVTMESERLRNSLLSAISHDLRTPLTSLVGSADVLAANARLDDDARAMARTISEQSQKMVGLMNNLLDMARLQAGVVTLNRQWNALEELAGSALRLLAKALEGRQVDTRIAPELPLLRVDAVLLERVLANLVENAIKYSPPGTPIGISAHVEHGDGAPQVKVCVMDQGRGFPPTMTQHAFEKFTRGDNESATPGVGLGLAICRAIIEAHQGRIWIAPQEAGQGATVCFTLPVETQPAPPEE	43~~KdpD (1.65755E-111)~~252;X;275~~Usp(8.21562E-28)~~398;X;433~~DUF4118 (1.48669E-19)~~530;X;556~~GAF (3.19239E-16)~~688;X;705~~HisKA (0.000000000013677)~~769;X;822~~HATPase_c (1.34905E-27)~~928	KdpD protein
	1E-12	57.3	5.8	2.5E-12	56.3	4	1.5	1	A1A0E1_BIFAA	Nucleoside-diphosphate-sugar epimerase and GAF domain	BAD_0393	Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a)	721	367928	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Bifidobacteriales, Bifidobacteriaceae, Bifidobacterium, Bifidobacterium adolescentis, Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a)	>tr|A1A0E1|A1A0E1_BIFAA Nucleoside-diphosphate-sugar epimerase and GAF domain OS=Bifidobacterium adolescentis (strain ATCC 15703 / DSM 20083 / NCTC 11814 / E194a) GN=BAD_0393 PE=4 SV=1MRRVEILLIGNTDFVTKQWIEHAFPHDKVVVALRKGTESSGEDLKIIDMPDRDAMSEVFSNYEFDRIVYFSEDLTPRSERDGDLGYLRRLLHTVRNRKVQMLMVSGPESEFTYPQETDVHETSKSLMSRAGEELGLYYARTYDLEVKIVRCPYLYAPQRNGVTAYFNGLFEQAQAGELRFHERAEQRTCFLCADDLAELIYRIFDDWTADSELFHVPNVFDFTYGDLGTLIAGYFPGTKVVYGEDRPQAYPADDHELRLRYGFSPRYSLREDFPHVIEGWLKLRENKTDKHPVWDFLRSHNKWWTVLEIIGAFLLTEWLRTFTQGNSQLETVDLRLLFVVIVGTIYGLHAGVFAAVLACAGVAMSYASQGASFAPLFYDTSNWLAFVIYFVAGSVCGYVQSRNQESVRFVRDENGLLRNRLDFLRGLYQDMLDDRRQLRDQIIGRRDSFGKLYAVTRELDEVQPQKLYHTAIRIMQESLDSDSLAIFRVDNGGQFARLVAASPRFDVGSFRSVRVSDYGEIITALEHNGIWVNRTLKDKFPMYAVGVRDRGELAVIITMGEAKPDQMNLYFQNLFSIMCGLVESAMIRAFEYEDVARRSMLVPGTNLLKPEAFLPKVLAANDLKHDHMGDHLLLKVECEGNLEDVDSLLMQSIRQTDEAGMLTDDGVYLLMNQAGEKELPIILKRLTRSGLHCSYVPQTQEDALLSEARSHIAQADDGGES	105~~NADB_Rossmann (0.00000104936)~~217;X;307~~DUF4118 (4.08928E-16)~~405;X;464~~GAF (0.000000000000022943)~~588	non-KdpD DUF4118 protein
	1E-12	57.2	6.3	2.3E-12	56.4	4.4	1.4	1	B2JE24_BURP8	Histidine kinase (EC 2.7.13.3)	Bphy_2054	Burkholderia phymatum (strain DSM 17167 / STM815)	949	391038	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia phymatum, Burkholderia phymatum (strain DSM 17167 / STM815)	>tr|B2JE24|B2JE24_BURP8 Histidine kinase OS=Burkholderia phymatum (strain DSM 17167 / STM815) GN=Bphy_2054 PE=4 SV=1MPRPDPDELLDKLQREEEKRQRGKLKIFFGASAGVGKTYAMLQAARRRMEEGIDVVVGIAETHGRGETAALLEGLDVLPLARIEYRARSLAEFDLDAALERKPQLILVDELAHSNVPGARHAKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETVPDRVFDRADEVTLVDLPAEELLDRMRDGKVYMPQQAERAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPLLVRAAARLAASLKADWIAVYVETPKLQRLSDARRERTLDALKLAAELGAETATLAGADAVTTLVGYARVRNVSKLVAGGSSATGVTRWLRRPFGERLAERASDLDLTLIRASSDEAGPAGTTRERIADAEGRAWRDALIAARDRRSPPRSYAWAVAICAGVTLIASQLIDRIDLTNLVMLYLLGVIFTAVKLGRGPGVMLSFLSVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLLTSLVIGHLTSSLRREARVARRREQRTGAMYAMARELAAALTTEQIVGIGSRHVSEVFRARVAVLLPDSADQVKQKIDDPDTTIMLDSASLDVDVGQWVYDQQKPAGHGTDTLPAARALYLPLRAPMRTRGVLAVVMEDERELDVPEQQRMLDAFAAQIALALERVHYVDIARDALVSMESERLRNSLLSAISHDLRTPLTAIVGFSSMLAAQRDARTDAQGELVDAIHEEALRMTGIVTNLLDMARLQAGSLKLNRQWSLLEETVGSALRDCRRTLARHPVTVSLPADLPLLQLDAVLMERLFANLFENAAKYVPPDTPLMIGAQCIEENGTPFVRVTVDDTGPGLPPGMEARIFEKFTRGEKESAKPGIGLGLAICRAIAEAHGGKIGAANRIAADGRVEGARFWFTLPIDTPPPVPDVSDLPDEAAAEPDPEPHRRQQADTHPHTHS	21~~KdpD (3.04068E-123)~~230;X;252~~Usp(8.16192E-28)~~374;X;416~~DUF4118 (1.12355E-19)~~512;X;541~~GAF (2.51224E-17)~~664;X;681~~HisKA (3.81537E-14)~~746;X;799~~HATPase_c (3.93794E-22)~~909	KdpD protein

	1E-12	57.2	14.6	2.2E-12	56.5	10.1	1.4	1	B6IQY6_RHOCS	Histidine kinase (EC 2.7.13.3)	kdpD RC1_04 33	Rhodospirillum centenum (strain ATCC 51521 / SW)	917	414684	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum centenum (Rhodocista centenaria), Rhodospirillum centenum (strain ATCC 51521 / SW)	>tr|B6IQY6|B6IQY6_RHOCS Histidine kinase OS=Rhodospirillum centenum (strain ATCC 51521 / SW) GN=kdpD PE=4 SV=1MARPEDQDRPSPDALLEHARREQRGKLKIFLGAAPGVGKTYAMLEAAQSARRDGVALVVGIVETHGRAETERLVHGLEVVPRSRIDYRGRSFEEMDLDAILVRRPALVLVDELAHTNIPGSRHLKRWQDVEELLAAGIDVWSTLNVQHLDSLNDVIERIAGIKVRETVPDSVLRGADEIEMIDLPPQELRKRLGEGKVYVPAQARMAVEKFFSVGNLTALREMALRQAAERVDAQMLSYMRRNGIAGPWPTRDRILVAIGPEPNAATLVRSARRMADRRQAPWTVAYVETHRHQTLSETRKAHVTEALRLAHQLGGETVVLPGDDIAGELIGWARANNVSQIVLGRSRQRRRFGLTSTDDMLKRATAYDLLLVGGTEEKPEPSGQGAAGQALAGPAGSDRRGWRAYAWAGVALILATALSWGVFSVLPVANVSLVYLLAVLLIATRFGLVPSIVTAVLAFFAFNFFFTEPRQTFLVNTSEDLLTIGFFLVAAVFTGHLASRLRAQIELSRTSQRRTANLYDFARKVASAASEDDVLWAVVHHVAATLKAKALVLLPLDGELAIRAGYPPEDRLDQRAAAAAQWAWSNGERAGRGSDTLPASEWLFLPLKTQRGTVGVLGVQGYEGGSRLSADQARLLDALVDQAALVLERTQLVRDIEAAQIAGEKEQLRAALLSSLSHDLRTPLVSILGSASSLLTLEHELDDDARRELARTIQEEAERMNRFVQNLLDMTKLGSGGLKPKTDWTDLADIVGRALARAKPLLKGRRIKVDLAPDLPLLQLDPVLMEQVLFNLLDNAARYSPAQGAITVWARRRGDRVVAEVCDQGPGIPVADRDRVFDMFYRVAGGDQQTAGTGLGLAIAKGIVEAHGGSIGVLDGMHGVGACLVLRLPVPEEAPPAPAEMSAEVAVAVPAGGGPA	22~~KdpD (1.9841E-117)~~232;X;254~~Usp(4.93477E-39)~~374;X;405~~DUF4118 (6.72864E-16)~~505;X;531~~GAF (0.000000000000146492)~~650;X;667~~HisKA (0.000000000000120441)~~733;X;786~~HATPase_c (1.47873E-25)~~889	KdpD protein
	1E-12	57.1	13.1	2.5E-12	56.3	9.1	1.4	1	D5SYH6_PLAL2	Histidine kinase (EC 2.7.13.3)	Plim_18 74	Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	895	521674	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Planctopirus, Planctopirus limnophila (Planctomyces limnophilus), Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	>tr|D5SYH6|D5SYH6_PLAL2 Histidine kinase OS=Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) GN=Plim_1874 PE=4 SV=1MPDARPNPDDLLAKVQAEDTESTRGSLKVFFGYAAGVGKTYTMLENAQRAKAAGREVVVGYVEPHGRPETEALLAGLEVLPLREFEYRGVRLRDFDVDAALARNPDLLLVDELAHTNAVGCRHEKRWQDVEELLEAGINVWTTLNVQHIESLNDVIGQITGVTVRETVPDRAFDLADDLELVDITPEELLHRLKAGKVYVPDQAQRAIQSFFQKSNLTALRELSLRQAARRIHTDVESARREKAAIQPWATAERLLVCVGPSPTTARVIRTARRMAAALDAPWLAVSVDLTGEPASSPRKQQVSQHFRLAERLGAETVTLAGQNVSETILDYARSRNVTKILIGKTNQPRWRRLLAGTVVDDLLEKSGDIDVYVIRGEEEKTAHAPARTASTTQKLPYFWAVGLVSLTGLLAYGLRFLHLADAEANTVMLFLAAVAWTAFRYGRGPAVFASVLAVLVFDFFFVAPFHTFAVADTQYVVTFAVMLTIGLVISTLTSRLRAQIENTRLRERRTSSLYELGKQLSSLYGNVFLVGAAGGKVAEMVGGEVAIYLRQPSGPPELAFGHDTTIVKHSVSLPVAQWVIEHDQLAGAGTNTLPNAAALFFPLTGSQGTHGAIAIRVPDTERLLDPEFRRLLDACANQLALALERDQLAIEAANARIQAEAEQVRSSLLSSVSHDLKTPLAAIAGASSSLLEATSLDEETRRQLLETVADEAARLNRLLENILQMSKLDAGAAVPLCQWHVLEELVGSALHRTRREVLAQHDVAVQLSSELPLLYVDGLLMEQVFVNLFENAARYTPEGTKVTIRAALDGDHVRIGISDNGPGLPAGAEERIFDKFYRASPTADGGRGSGLGLAICRAIIKAHGGTLVAANRPGGGAEFVIRLPVSKDAPQVMVE	24~~KdpD (5.9295E-119)~~232;X;254~~Usp(8.54151E-42)~~375;X;397~~DUF4118 (2.00072E-20)~~500;X;530~~GAF (0.000000000029285)~~646;X;675~~HisKA (0.000000000153179)~~728;X;781~~HATPase_c (1.21722E-31)~~883	KdpD protein
	2E-12	56.9	10.2	3.8E-12	55.7	7.1	1.6	1	A0A0F5JWY6_9BURK	Membrane protein	WM40_17845	Burkholderia andropogonis	452	28092	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia andropogonis	>tr|A0A0F5JWY6|A0A0F5JWY6_9BURK Membrane protein OS=Burkholderia andropogonis GN=WM40_17845 PE=4 SV=1MRKTGAFGNVGRIRRMIAPAVQRPFALVESAAFMLIVLTILAMLRPHDPLALAAAFPWIWLAPMVLALRYGTLLGLFGGAFMLVEWVLIGHSGVGSGAFPVGFFAGGMVQVIVVGHFGDTWGARAIQAGAKNDYLSDRLVALTNNHYLLRMSHDRLEKDLLSQPTTLRDSIVELRRMSVQGGLQDPGESKMSAEQLMRYIAPICRLEQAAFYTVRNGRVSTVAMAIVGDPFDLVPGDALITHALENGALAHLKMDEGELPDSLYLVCAPLLAADGSIRGVLVIRRMPFLSLTFDNLQLIQVLLGYFGDGLEHAELVRHVIDVVPDCPVEFALELSRLGRMAARTGVHSSLVSLTFPRTEASDSLFEHVSRRRRALDVFWEIQTAEHSIVVNLMPVTDMGGINGYLARIESSLRAQFAMDLETARVAVHTQLLGDLDPALALQRILTLSGVDD	26~~DUF4118 (0.000000000958908)~~124;X;194~~GAF (0.000000000661677)~~312	non-KdpD DUF4118 protein
	2E-12	56.8	11.6	3.2E-12	56	8	1.4	1	U1ZQF9_9BURK	Histidine kinase (EC 2.7.13.3)	N879_04 860	Alcaligenes sp. EGD-AK7	889	1386079	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Alcaligenes, Alcaligenes sp. EGD-AK7	>tr|U1ZQF9|U1ZQF9_9BURK Histidine kinase OS=Alcaligenes sp. EGD-AK7 GN=N879_04860 PE=4 SV=1MSLEDRPDPDELLQVIGEDPHQPRRGQLKIFFGACAGVGKTYAMLKEAHQRQSEGVSVAIGIVETHGRQETQALIDGLPVLPRKEYQRQGRAVTEFDLDAALASGYQLLLVDELAHSNIEGSRHAKRWQDVEELLDAGIDVYTALNVQHLDSLNEVVGGIVGVRVRETVPDRIFDRAADVLLVDLPPDDLLSRLSAGKVYLADSVAHARQNFFRRGNLIALRELALRRVADRVNADVHVYRISHAIRTVWPTRELLMVCVSADSAQEALIREGARLAQQLQTPWIVLHVDTPQESGQIKAQEALVRLAASAQHAGAEFANIAGQDVAHTILAYARQRNATKLILGNSSARSIWPWRTRLSERLARSNPEIGLLLLRMDTVQRPIRPLELEQPMAQGKALSIASIICVVTTLLAEKLLPFFELSNVIMLFLITVVFIALRLGRLAGVWASLLSVAFFDFFFVEPRYSFSVTDTQYVFTFGVMLGVALIIGQLAAKLQAEARAARDGERRAAALTRVSRDLAGALALAEQVLAVCRDTLEPLFEMQVVLVVPDQQNQLVATRHTGFVELSVAQWVFDHMEAAGNGTETLSGASALYLPLKGPMAPRGVLVVQSGGAASLRTPDGRRLLDACCFTLAQALERIHYVEIAQDTVLRMEGEKMRNTLLSAVSHDLRTPLTVIRGLAETLEQPKGLSETERTDIARSIRIESDELRRQVSNLLDLARMQSEGVKLHKEWHALGEIVGIAVARCSAALQPRKVVTEFAADLPLIEVDGVLLERVVTNLLDNAAKYTPVTSTISLRGLCSGQFMYLMISDDGPGLPPGDPERLFDTFTRGQKESSVAGVGLGLGLCRTIIAAHGGTISAKPRMPHGVIFEIRLPWKAAPRMDDDELLT	23~~KdpD (1.96843E-106)~~233;X;256~~Usp(6.62438E-27)~~375;X;404~~DUF4118 (3.22239E-18)~~498;X;525~~GAF (0.0000000715266)~~638;X;655~~HisKA (0.000000000002204 53)~~720;X;773~~HATPase_c (7.85144E-24)~~874	KdpD protein
	2E-12	56.8	0.2	3.5E-12	55.8	0.2	1.5	1	D4Z1X1_SPHJU	Uncharacterized protein	SJA_C1-17690	Sphingobium japonicum (strain NBRC 101211 / UT26S)	315	452662	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingobium, Sphingobium japonicum, Sphingobium japonicum (strain NBRC 101211 / UT26S)	>tr|D4Z1X1|D4Z1X1_SPHJU Uncharacterized protein OS=Sphingobium japonicum (strain NBRC 101211 / UT26S) GN=SJA_C1-17690 PE=4 SV=1MLKKRPMLLQCAEMLLLFAALVAVDQGLMKGDAFSDLNPNPYWLPVLVMATTYGTGSGLAAAAISSAIWFHWSNLWSGATDHIEQQLRLSIQPMLWMVTALVTGEVTASRRNRLADQERQHQAMDRNWKKLAEIIARLTDTNRKLQVRIATEQRTIVQAMAAGLAFSKADPESQADALARLIALAAQTEDFTFYDVRGAQVTARFGGRAAMGQPPDLSRSSMAQAMLATPRPLRADRAADCPLLSESGILAVPVAGTDEGLAAIILVHSAVGIRITEAYVAQLLQVADLLGQSPALFGREQASAAKWLVPEGKVA	12~~DUF4118 (0.000000000350308)~~113	non-KdpD DUF4118 protein

	2E-12	56.7	8.5	3.9E-12	55.7	5.9	1.5	1	A0A089M9Z7_9BACL	Histidine kinase (EC 2.7.13.3)	PGRAT_25575	Paenibacillus graminis	899	189425	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus graminis	>tr|A0A089M9Z7|A0A089M9Z7_9BACL Histidine kinase OS=Paenibacillus graminis GN=PGRAT_25575 PE=4 SV=1MEINQTGDGSILEQLTGMKAGKRRGRLKIFIGYAPGVGKTCAMLNAAHEEQKEGTDVVGGYIETHARPDTQAMLEGLELVPPMKVSYEDSVIPEFDLDRAIQRSPELILLDDLAHANTAGCRHKKRYQDVEELLRAGIHVYTTINVQQIESLTDIVYSITGMTVQERIPDSVFDSADQVELVDIEPNDLIDRLNKGKIQRENADEQGIEQLFTKEKLTALREIALRNTASQLNRIAVQISEQAKKNDYDTKDHILVCLSSAASNKKVIRAAARMAEAFHGQFTALFVETPQTQKLTPKNKTELRDNLRLAEQMGANIATVYGEDVPGQIAEYVKTSRVSKIVLGRSPFKKRGYAKSNLVDKLTTLLPNIEIYIIPYTHPSFYKRLPLYVRYPKLSLADTNKTIAILLVCTLIGIWFRYLGFLESNIITVYILGVLLSAIVTKGRVYSAVSSVMSVLVFNYFFTEPYYSLNAYDSGYPVTFLVMLTASFITSTLTMRVSEQARQSAQKAYRTEVLLETSRKLQQAKDSPAIIDEMAHQMVKLLDRTVIFYAVQEGALTEPLIFPKEGSEADPHMYTGSNERAVADWVFKNNKRAGATTDTFFGANCLYHAVRGGDTVFAVAAIVMEQEEPLEVFEKGLMIAMLGECALALEKEKLNEKQKEISLQIQQEHLRANLLRSISHDLRTPLTSISGNAGILVGNSGVLSEEQKKGLYTDIYDDSIWLIHLVENLLSISRIENGTLNLNFQAELLEEVISEALLHVNRNSEKHVIQTELADELLMARMDSRLIVQVLINIVDNAIKYTQQGSHITVSAKQDGQRVIVEISDDGPGISEEAKARLFEMFYTVDNIRGDGRRGLGLGLSLCKSIVNAHGGTIGVMDNVPKGTVFYFTLHAEEVNIHE	22~~KdpD (1.2419E-104)~~232;X;253~~Usp(4.11289E-34)~~375;X;402~~DUF4118 (8.29466E-20)~~500;X(168);668~~HisKA (0.00000000103348)~~734;X;787~~HATPase_c (9.51555E-23)~~890	KdpD protein
	2E-12	56.7	10.9	3.3E-12	55.9	7.6	1.4	1	E3HLX8_ACHXA	Histidine kinase (EC 2.7.13.3)	kdpD AXYL_01191	Achromobacter xylosoxidans (strain A8)	928	762376	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Achromobacter, Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans), Achromobacter xylosoxidans (strain A8)	>tr|E3HLX8|E3HLX8_ACHXA Histidine kinase OS=Achromobacter xylosoxidans (strain A8) GN=kdpD PE=4 SV=1MADIAGERPDPDALLKTLDDAARQAVRGKLRVYFGSSAGVGKTYAMLVAARAQAAQGVEVLAGIVETHGRRETATLLEGLPVLPLQDVPYRSHVLKEFDLDGALARHPDLVLVDELAHSNAPGSRHAKRWQDIQELLAAGIDVWTTLNVQHLDSLNEAVGSITGVRVWETVPDEVFDAADEVILVDLSADELLRRLKEGKVYLPEQARHATRNFFRKGNLIALRELALRRTADHVDDDVQAYRRDRAIEPVWRTREAVVACIGPDVDAEYVIRSAHRLSQQLECDLHVVTIDTPRAAPPPQAEQERIQRSLALADALGARSETLAGGDMVDAVVRYVRRHNITKAIIGRTRASGLQRLRLSLSAVLTAAISPGWLWRRHSFADMLAAGCPEIDIIRLGAPPLPAAAAPGRDPLTLGQRARLGADERNPRPLAGYAWALCYCAAATALSALAFPALHQTNIVMLFLLAVVAVALRHGRGPAALASVISVGLFDFFFVQPLASFAVSDVQYLLTFGVLLSVGLLIGQLTAGLRLQAQASVKREADARSLYEFARELSSALLPEQIVTLAGAFVHATFGSRCALYILGMDDDRLKLASPAADDMPPLESALAQWVYDHGQPAGAGTATLSNSELLYLPLKAPMRTRGVLALAAPRRSLFSNPDSRRQIEAYATLIAIALERLHYVEVAQQALVSMESEKLRNSLLAAVSHDLRTPLTSLVGMTDTLMRQQAALPPGIHDTIRAMRDQAQRMHALVVNLLDMARLQNRDTPLRLEWQSIEELVGASLAAMREPLAAHRVAVDSLSQLPLVECDGVLIERVLCNLLENAAKYTPAGSTLRVHADVHEGELRVAVSDNGPGVPPGAERRIFEKFTRGDRESATPGVGLGLAVCEAIIAAHHGKIWVEHAPGQESGAQFVFTLPLGTPPPIQSETP	27~~KdpD (2.14842E119)~~235;X;258~~Usp(3.29748E-30)~~394;X;457~~DUF4118 (7.126E-17)~~531;X;560~~GAF (4.93711E-14)~~677;X;694~~HisKA (0.000000000015115 2)~~759;X;812~~HATPase_c (6.63165E-29)~~915	KdpD protein
	2E-12	56.6	12.5	3.5E-12	55.8	8.7	1.3	1	G9Z513_9ENTR	Histidine kinase (EC 2.7.13.3)	HMPREF0880_02597	Yokenella regensburgei ATCC 43003	894	1002368	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Yokenella, Yokenella regensburgei, Yokenella regensburgei ATCC 43003	>tr|G9Z513|G9Z513_9ENTR Histidine kinase OS=Yokenella regensburgei ATCC 43003 GN=HMPREF0880_02597 PE=4 SV=1MTDEPLRPDPDRLLEQTASLHRGKLKVFFGACAGVGKTYAMLAEAQRLRAQGLDILIGVVETHGRKETAAMLTGLATQPLKRISHRGRYVLEFDLDAALARRPALILMDELAHSNAQGSRHPKRWQDVEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIGGQAERAIENFFRKGNLIALRELALRRTADRVDDQMRAWRDRQGQEKVWHTRDAILLCIGHNTGSEKLVRTAARLAAKLGSVWHAVYVETPALHRLPEHQRRAILSALRLAQELGAETSTLSDPSEELAVLRYAREHNLGKIVIGRYNKRQWFHSRTFADRLSAHAPDLDVMIVALDEKPVPAPRTNDTRPWMEKWRVQLRGCAVAVALCAAITMVAMQWMYAFDAANLVMIYLLGVVVIALFYGRWPSVLATVINVISFDLFFIAPRGTLAVSDVQYVLTFGVMLTVGLVIGNLTAGVRYQARIARYREQRTRHLYEMSKALAVGRSAKDIATTSEQFIHSTFDARSQVLLPNDAGKLMPLTQQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLRSADRTHGLVVVEPSNLRQLMIPEQQRLLETFTLLVASALERLSLTESEEQSRLASERESIRNSLLAALSHDLRTPLTVLFGQAEILTLDLASEGSKHAPQANEIRQHVLNTTRLVNNLLDMARIQSGGFNLRKEWLTLEEVVGSALKTLEPTLGGRHIALSLPDPLMLVHVDGPLFERVLINLLENAAKYAGYRAQIGIKAETVGEHLQLDVWDNGPGIPPGQEQAIFDKFARGTKESAIPGVGLGLAICEAIVDVHGGTISAWNRPEGGACFRVTLPLETPPQLEDFHEDL	21~~KdpD (6.82162E126)~~230;X;253~~Usp(3.57569E-37)~~373;X;426~~DUF4118 (7.63595E-19)~~500;X;529~~GAF (1.76516E-15)~~643;X;660~~HisKA (0.0000000045085)~~725;X;778~~HATPase_c (3.29438E-30)~~879	KdpD protein
	2E-12	56.6	11.1	3.6E-12	55.8	7.7	1.4	1	Q605R4_METCA	Histidine kinase (EC 2.7.13.3)	kdpD MCA2214	Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	910	243233	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylococcus, Methylococcus capsulatus, Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath)	>tr|Q605R4|Q605R4_METCA Histidine kinase OS=Methylococcus capsulatus (strain ATCC 33009 / NCIMB 11132 / Bath) GN=kdpD PE=4 SV=1MAAERPDPDALLARVEREQARARRGRLKIFFGAAAGVGKTYAMLEAARERRAEGIDVVVGLVETHGRKETEALLEGLEMLPVRTVEYRGTVVGEFDLDGALKRRPSVILVDELAHTNTAGSRHPKRWQDVEELLRAGIDVYTTLNVQHLESLNDDVGQISGIRVWETVPDTVFEAADEVELIDLPPDELLVRLKEGKVYLPQQAELAAENFFRKGNLIALRELALRQTAARVDAQMQDYREDHTIREVWQVGERILVCIGPNPMAERLIRAGKRLAASLKAEWLVVYVETPALQRLPAERRDAVLRMLRLAEQLGAETVTLSAPDMSEAIIDLARERNVTKIVMGKPRRRGWKRWLLGSVVDTIIAEAHNINVYLLGSPPGEDRGQESLQAPQPGLSAKPDRGGAEYRGYLGAATATFLCTLTAKAMFGRFELTNLVMVYLLGVIFVATRYGRGPSILASILGVLAFDFFFVVPYHTFSVADTQYLFTFAVMFSVALVTANLMANVRSQAKVASHRERRATVLYAMSKELAASRSEAEIVRIAVRQIETEFGGRAVLLFPDESGRIGYPVSPLAEEFLPGIDMSVAQWVFDHDEMAGRGTNTLPGASGVYIPLTGAEKTIGVLVMKPVNLRRVFLPEQQKLLQTFVNLIVQAIERVRLAEQARINQVRMESERLRNSLLSSISHDLRTPLATIVGSASTLVEGDYALEPEDRRELCRAIYDESRRMASLVNNILDMAWFDAGVVKLHLQWHVLEEIVGTVLTRLKKQLERRPVTVRLPRDAPFVYVDSVMLEQVLANLMENAIRYTPENSPIEIAAEATPFTMTITVSDHGPGIPKGQEELIFEKFYRVHREGPQSGVGLGLAICRAIVEAHGGYIRARNRAGGGAVFTIVLPLRESPPRIEPEAEPAE	22~~KdpD (5.26949E124)~~232;X;254~~Usp(9.88461E-51)~~377;X;411~~DUF4118 (2.68387E-19)~~510;X;536~~GAF (0.000000000000478912)~~656;X;673~~HisKA (0.000000000000102 15)~~738;X;792~~HATPase_c (9.38647E-32)~~893	KdpD protein
	2E-12	56.5	10.3	3.6E-12	55.8	7.1	1.4	1	G2J4F5_PSEUL	Histidine kinase (EC 2.7.13.3)	kdpD NH8B_2135	Pseudogulbenkiania sp. (strain NH8B)	503	748280	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Pseudogulbenkiania, Pseudogulbenkiania sp. (strain NH8B)	>tr|G2J4F5|G2J4F5_PSEUL Histidine kinase OS=Pseudogulbenkiania sp. (strain NH8B) GN=kdpD PE=4 SV=1MFTGQWFSKLRVSPAARYGLVVLCCLLITGLTVPFRDTLELANAVMLFLLVVFLVALRLGRGPAIFAAFLGVALFDFFLVPPHYTFAVHDGMYLITFAVMLAVGLLTTQLTTSLQDETEQVRQHERETRELYDLARTLTGAATLDQVEAAVATYADCQHCAARCFWLTDAGQLDVRHSAVLESHLLQMAITRQEPVLGDAEAGLPPIYLPLKAPMGMRGVLAVYPDPSISDLPQLKERFVTPASLLAIAVERLHYVDVARQTEIQINAEKLRSSILSALSHDLRTPLTGLVGMAEDLAGRELPAAEHETARLIRDQAEAMHKLMTNLLDMAKLQAGKVRLHLEWQLYEDVISTSLQLLKPVLDVHPLELRIEPGLPLVQFDAVLIERVLCNLLENAAKYSPAGSPIRIRAYIDNGFACLAVSDQGLGIDPAHIQRLFDLFERGETESSTPGVGLGLGISKAIAEAHGGSITLSSSTGGGTTAQLRLPLGNPPIVVTEDDHDRV	17~~DUF4118 (4.85222E-16)~~104;X;145~~GAF (0.000128527)~~252;X;269~~HisKA (0.000000000131073)~~332;X;385~~HATPase_c (2.83366E-30)~~486	non-KdpD DUF4118 protein

	2E-12	56.5	9.7	3.9E-12	55.7	6.7	1.4	1	D5X2Y5_THIK1	Histidine kinase (EC 2.7.13.3)	Tint_0068	Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	914	75379	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Thiomonas, Thiomonas intermedia (Thiobacillus intermedius), Thiomonas intermedia (strain K12) (Thiobacillus intermedius)	>tr|D5X2Y5|D5X2Y5_THIK1 Histidine kinase OS=Thiomonas intermedia (strain K12) GN=Tint_0068 PE=4 SV=1MTDPDIRPSPDALLAQVQQDAEQAQRGRLKLFFGASPGVGKTYAMLMAARRLRDEGVDVCVGLVETHGRAETARLLEGLEQIPLREVRHGAHLLREFDPAAALARRPAVLLVDELAHSNAPGSRHPKRWQDVEELLDAGIDLYTTLNVQHLESVSDIVGGITGVQVRETLPDRIFERADEVVLVDLPPDDLLQRLKDGKVYLPEQAAHAVRNFFRKGNLLALRQLALRLTAEQVEGEMRDYRSRRVGGAVWDAAEALLVCAGPRDDIGLVRAAARLADALHARWHVITVETPALQGASEAQRDHALALLQRARDLGAQTAMLAGPHAAEAALAYARTHNLNRVVLGRASRWPWWRRVLGRSTTAVLARQAPDLDLILITRDARSPLTALAGLHPALPSADALMRRYLAALLISGAITLLASPLRSYFDLSNTVMLFMLGVVAVALRFGRGPAALAAVVNVLAFDFFYVPPRFSFAVSDVQYVFTFSVMLGVGLLIGHLTSHLHFQARVAGQRERRTHDLYELSRELSGALTVDQVAEIGTRVVQASFRCRATLLVLGLDERLQPSADVAADALLPFDAELARWCLQRGAPAGQGTDTLPGAPLFYLPLKAPMRVRGVLVVDPGNTRLSTIPELRRLLETCATQIAIALERIHFVSVAQDTLLAMQAERMRNSLLSALSHDLRTPLTALVGTAEVLSTRLAAHPPGDAATLHGQALSLLQQSRRLARMVDDLLDMARLQSGQVTLRQDWQSVEELVGSALRAVDAAALAQHPLQIDLPADFPLVRADAVLLERVLVNLLDNALKFTPPGTPLGVRARVRGAEAEITVWDRGPGLPAGRERAVFETFTRGDPESPIPGVGLGLAICRAIVEAHGGRVTAANAPEGGAAFNVRLPLHEMPPLDAAAELGTEPAGPTP	24~~KdpD (1.65042E-103)~~234;X;284~~Usp(1.49644E-14)~~379;X;405~~DUF4118 (2.9765E-19)~~502;X;531~~GAF (2.25699E-14)~~650;X;667~~HisKA (0.000000000163765)~~736;X;790~~HATPase_c (5.11699E-28)~~891	KdpD protein
	2E-12	56.4	7.5	5.1E-12	55.3	5.2	1.6	1	A0A077LKJ0_9PSED	Histidine kinase (EC 2.7.13.3)	PSCI_3959	Pseudomonas sp. StFLB209	880	1028989	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. StFLB209	>tr|A0A077LKJ0|A0A077LKJ0_9PSED Histidine kinase OS=Pseudomonas sp. StFLB209 GN=PSCI_3959 PE=4 SV=1MSDSSRADAILAQLPRDGRGRLKIFLGAAPGVGKTYAMLQAAHSRMRQGVNLLAAVVQTHGRAETEALLVGLPQLPMLRREYRGMTLEEMDLDGVLRAAPALVLVDELAHSNVPGSRHDKRWQDVHELLAAGIDVYTTVNVQHLESLNDQIRAITGVQVRETLPDWVLQEAFELVLIDLPPRELLERLRDGKVYVPEQARAAIDAFFSQTNLTALRELAMQTAAAQVDNDLAQGYRQRGEQAPAVRGRLLVGIDGDIQADLLVRHASRVAERRHLPWSLVHVDADRPLDEQGRAYLQGAQQLAERLGGEVVTLRAGEVARTLLQHAVERRASVVMVGQSRHLWRRRLFGGGVAGRLLREAHGLEIISVLDSQALPDRPRQRAPIKGLDYALAVLATALASGVAWGIAGILALPNISLIFLMAVLLVAVRSSVGPALFCALLSFLAYDFLFMPPNFSLSIQREEDVLTLVFFLLMAALTGQLASRQRRQFKALRATQEQTSTVLDLSRKLTAATDRQAVLSAAEQHLSGWPELQLCLLGRDQNASWVVELGGPLTFSEAERVAADWAWQHDQAAGLDTGTLPSGRWWWWPVSAEEGPLALLGVCPRPGHRFTAQHRRLLSALSQPLAQALARAQLVQDLESARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALGEAIPLDDRRELLEGTRDEAERLDRYIQNLLDMTRLGHGSLKLARDWVAPADIVGSALGRLRAVLAPLQVEVQMAAELPLLYVHAALIEQALVNVLENAARFSPVGGVLRVHSRVSEGELQLLVSDQGAGIPEAERAKIFDMFYTAARGDRGGPGTGLGLAICQGMVGAHGGRVTVAEGIDGLGTCMTLHLPLPAQPQADSE	18~~KdpD (8.53863E-117)~~227;X;248~~Usp(1.05552E-29)~~365;X;400~~DUF4118 (1.17323E-16)~~487;X(160);647~~HisKA (0.000000000000282075)~~713;X;766~~HATPase_c (1.29711E-23)~~869	KdpD protein
	3E-12	56.3	12.2	4E-12	55.7	8.4	1.3	1	D5MJR3_9BACT	Histidine kinase (EC 2.7.13.3)	kdpD DAMO_0414	Candidatus Methylomirabilis oxyfera	900	671143	cellular organisms, Bacteria, unclassified Bacteria, candidate division NC10, Candidatus Methylomirabilis, Candidatus Methylomirabilis oxyfera	>tr|D5MJR3|D5MJR3_9BACT Histidine kinase OS=Candidatus Methylomirabilis oxyfera GN=kdpD PE=4 SV=1MTVMSEHRPDPEALLARVKEEAAREKRGKLKVFLGAAAGVGKTYAMLEAAREQRAEGVDVVAGLVETHGRPETEALLQGLEILASHRLEYRGTTLKEFDLDTALTRHPTVILVDELAHTNAPGSRHTKRWQDVMELLGAGIHVYTTLNVQHLESLNDIVTRITGTVVRETIPDSVLEQADEIELIDLPPDDLLQRLKEGKIYVPELAKEAIGNFFRKGNLTALRELALRRTADRVDAQMRAYMSDQAIPTTWPVTERLIVLVGPSPHSAQTVRGAKRMAAALRAEWIAVYVETEAYARLSETDRRRVAENLRLAEQLGAEVVTLSGSQTNESAAVLRYANERNVTKIILGKPTRSLWRRIVAGSIVDALVRGSGDIDIYVISGTGIPHAPVARVERAPEPDWSAYGRAATVVALCTAVAWLMYPYFELSNLIMVYLLGVTGVAARSGPGPSVLASILSVAVFDFFFVVPHFTFRVADAQYLVTFAVMLVVALVISGFTVRIRIQAESARQRERRTAALYALSRELASARGVEHVLRAAGRHIADVFGGQVAVLLPDPSGHLGLQVGPSAQFEVTPSERGVAQWVYEHGQTAGCGTSTLPGAKVLYLPLVASQGILGVLGLLPADPHSLEAPEQLHQLETFANQTALALERTQLAAAAQEAQVRAEAEKLRSSLLSSVSHDLRTPLATITGAASSLLEGDKILDDQTQQDLLESLLEEAERLNRLVNNLLEMTRMESGTLQVRKEWHVLEEVVGAALGRLTKLLCDRPVTTSLPADLPLVPIDDVLIEQVLINLLDNAIKHTPDGGPLEITVRAHNSMVTVEVADRGPGLPPGDERVFEKFYRGYGLTSRGTGLGLAICRGIVEAHGGRIRAENRPGGGVAFRFTIPLTGTPPELEGIDV	25~~KdpD (2.81586E-123)~~235;X;257~~Usp(3.8415E-41)~~382;X;411~~DUF4118 (0.000000000000012724)~~502;X;531~~GAF (1.48595E-14)~~650;X;679~~HisKA (0.0000192606)~~733;X;786~~HATPase_c (2.26518E-32)~~886	KdpD protein
	3E-12	56.3	14.2	3.7E-12	55.8	9.9	1.2	1	R6PD75_9FIRM	Histidine kinase (EC 2.7.13.3)	BN627_01442	Lachnospiraceae bacterium CAG:364	489	1262983	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	>tr|R6PD75|R6PD75_9FIRM Histidine kinase OS=Lachnospiraceae bacterium CAG:364 GN=BN627_01442 PE=4 SV=1MKKRDILWCIVSLALSTAVAFVFSALGFSDANLIMIYILGVLMVALLTGGYVWGIISSILGVLTFNFFFAEPIFTFSVYNPDYLITFVVMFATSITCSVLTKRVKNYAAENARKSYRSELLLQASRSLQEASTSQEILQKTVKQLGKLLEKKIYCLMGKPENWKMPKELLKEDRATALWCYQHGEDAGFSTDVLRESPYMFLAVKGKQKTFAVIVVDTKKEAIGTFERGIVGTIIHECVFALEKEELLNKQREAEMRLEKEQLRANLLRSISHDLRSPLTSISGNAENLLANEEKLPAGRRREIYRDIYDDSKWLINLVENLLSITRIENGNMKLDMQGEIVEEVIEEALKHVNFRGKDQSVRIECDEILMAKMDLKLMLQVIINLVDNAVKYTPKNAEIMIKAEAEGEKVILSVRDNGTGLTPEQKEKVFDMYYTVNRGIGDARRGMGLGLPLCQAIVKAHGSRLEVCDNTPKGTVFKFALSKEEILL	6~~DUF4118 (3.37189E-20)~~105;X(156);261~~HisKA (0.000000000005268066)~~327;X;381~~HATPase_c (6.00937E-25)~~482	non-KdpD DUF4118 protein
	3E-12	56.3	9.2	4.2E-12	55.6	6.3	1.3	1	Q2KWC3_BORA1	Two component sensor kinase (EC 2.7.3.-) (Fragment)	kdpD BAV2704	Bordetella avium (strain 197N)	922	360910	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella avium, Bordetella avium (strain 197N)	>tr|Q2KWC3|Q2KWC3_BORA1 Two component sensor kinase (Fragment) OS=Bordetella avium (strain 197N) GN=kdpD PE=4 SV=1VPHSFPASMTVPGANRPDPDLLLHTLDQAAAAARRGRLRIYFGASAGVGKTYAMLAGARAQIAQGVQVLAGVIETHGRKETQQLLDGLPLLPPKTLAYRGHVLREFDLEGALQRRPALLLLDELAHSNAPGSRHAKRWQDVQDLLHAGIDVWTTLNVQHLDSLNEAVGGITGVRVWETVPDDIFDQADEIILVDLSADELLRRLKDGKVYVPDQARHATHHFFRKGNLIALRELALRRTADHVDDDVQAYRRDAAIQPVWRTRETVAACIGPDADAAHVVRNAHRLAQQLDCEWHVITIEGLNIRPGQPHGGLEQALALAETLGAHAEILAGADRVEAAARYARRHNVTKMVVGRGQARRRLAPQLDRLLAPGWLWQRHSFADELARACPDIDILRVAAPAHAPVAPVQHDPLTASGSRQAATPAPRRWPDYGWALAYCLFATAVSKLAFPLLHQTNIVMFYLLAVVGVALRHGRGPAALASVISVGLFDYFFVQPISSFAVSDVQYLLTFAVLLGVGLLIGQLTAGLHAQAETSVKREADARALYEFARELSSALLPEQIVQAADTFLKAAFDADSALYILGMDDRLQLAATPPPSMAAPEPSLAQWVQDHGQAAGAGTATLSNSPLLYVPLAAPMRVRGVLVLQTSHPIASAPASWRQVQAYATLIAIGLERLHYVEVAQHALLNVESEKLRNSLLAAVSHDLRTPLTGLIGMTETLARSATDAAVQEQANAIRDQARRMHRMVVNLLDMARLQSQGTPLKREWQSVEELAGAALANMRETLRGHQVRVLPLSELPLVECDGMLIERVFCNLLENAAKYSPEGGTITLEGRVSDDALQVSVSDQGPGVAPGSEDRIFQKFTRGERESALPGVGLGLSVCRAIVQAHQGRIWVEPAPGGQGARFIFELPLGQPPTIDHELS	40~~KdpD (3.92454E-105)~~243;X;266~~Usp(3.71294E-27)~~395;X;432~~DUF4118 (2.17903E-19)~~526;X;558~~GAF (0.000000000000208694)~~674;X;691~~HisKA (9.28004E-14)~~754;X;807~~HATPase_c (3.31234E-30)~~909	KdpD protein

	3E-12	56.2	8.7	4.2E-12	55.6	6	1.3	1	R7C3W0_9BURK	Histidine kinase (EC 2.7.13.3)	BN641_00699	Sutterella sp. CAG:397	907	1262976	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Sutterellaceae, Sutterella, environmental samples, Sutterella sp. CAG:397	>tr|R7C3W0|R7C3W0_9BURK Histidine kinase OS=Sutterella sp. CAG:397 GN=BN641_00699 PE=4 SV=1MPDNASNTKTADQILKEVQKERRGKLKLFFGAAPGVGKTYAMLQEVQEKRAQGLDVLVGWVDTHARKDTEAMLAGLEVLPRKTIVHRGFKYQEFDIDEVLKRRPGLVVVDELAHSNAPGSRHPKRWQDVEELLDAGINVYTALNVQHLESLNNVVERMIGVTVNETVPDRLFDEANEVRLVDLPPADLIARLKAGKVYLRQTIEAALGSFFKQGNLLALRELSLKRMAERADAETNARRVLSQTPDLTTEGIVLWLGNASGAEELVRSCSRLSATQQRNWHVVWYDDGTAGEKRRLEMMHCLALAEELGAATQVLSGFEEERAVCDYARTHGASTIAVSKAYMNFWRRRRLMNEAEDLRILEMTALPTETEKDTVQTTGLFAITERDGWWQSCVVTAVVALILMWLEPYIKPANAVMVLLIPTLIISMRYGRAPGVLTALLSSAAFIVLFVEPPFSFAVDDPSYLIVPFVMLLVAAGTGTLFARLRRISDQANDRTAHMRMLFTLSRELGKSLMVEEVAEILEKHAFSDLGAKIELWSSGGTVSDVKRLTANIKNVDRAIVLWCVEHGDEAGRGTHTLPYSPYLYLPLRGQMRVHGVIVFSVDEPDRWLDPEMRRVATAVADLAALALERLHYIDVSQKTLVEMESDRFRHALIQELGDELQVPLSDLTEGAEALSAKLSVQNSPEAAEGRKLLSDVRRMSRLTGNLLEMSRLQSSGFELEAKKTPIAELFEESLDEIAPSQRQQFHIVTNIAKDCPAEVSVDPALIRRLLVNLLDNAVKYCSAGCTIELSAEASAGNVLISVSDNGPGLPGGDVNRLFDPFKRGVKTGNGAVAGVGLGLAISRTIARVHGAQLIGKNNADGPGCTFTLILPLPEEEEAEEEAKEKETEKDGKPLVTAPAEVAADKA	21~~KdpD (5.20914E-114)~~230;X;261~~Usp(0.0000000182837)~~361;X;392~~DUF4118 (1.1472E-17)~~487;X;556~~GAF (0.0000330077)~~615;X(152);767~~HATPase_c (1.95256E-24)~~871	KdpD protein
	3E-12	56.2	7.3	2.7E-12	56.2	5	1.8	1	Q4K8P7_PSEF5	Histidine kinase (EC 2.7.13.3)	kdpD_1 PFL_4294	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	883	220664	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	>tr|Q4K8P7|Q4K8P7_PSEF5 Histidine kinase OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=kdpD_1 PE=4 SV=1MSDSGRADALLAELPRDGRGRLKVFLGAAPGVGKTYAMLQAAHSQLRQGVKVLAGVVETHGRAETEALLSGLPQQPLVRSEYRGVLLEEMDLDGLLKAKPKLVLVDELAHSNAPGSRHAKRWQDIQELLAAGIDVFTTVNVQHLESLNDQVRGITGVQVRETLPDWVLQEAYELLLVDLPPRELLERLRDGKVYVPEQARAAIDAFFTQTNLTALRELAMQTAAAQVDNDLAQGYRQLGQAAPAVRGRLLVGIDGDAQAERLVRHASRVAQRRHLPWSLVHVDNGRLRDEQARLRLQAAQQLAERLGGEVVLLRAGEVAKTLIQHAAERRASLLLVGQSRRRWRRRWFGGGLAARLLRNADGLEINVLDSEPQPHQPGLRVKHSLIWFDYVLAVLATLLASALAWGVASVLPLPNISLVFLAAVLLVAVRSSLGPALACAALSFLSYDFLFIPPNFSLAIQREEDVLTLLFFLLMAALTGNLAARQRRQLQALRDTQEETGELLDLSRKLTAATDRQAVISAAAQHLNGRDELRVCLINRDGQGGWKVETGGSPQFSEAERAAADWAWQHDQPAGLGTGTLPFGRWWWWPLSVDDGPLGLLGVCPREGEEFSGQRRRLLTALSQPLAQALARARLAEDLEAARLHGETEQLRSALLASVSHDLRTPLTSMRGSIDSLLALGEAIPLEDRRELLEGTRDEAERLDRYIQNLLDMTRLGHGALKLARDWVAPGDIVGSALNRLRAVLAPLQVATELPADLPLLYVHAALIEQALVNVLENAARFSPLQGHLQLKVSASEQELSFAVSDEGPGIPEDERAKIFDMFYTAARGDRGGQGTGLGLAICQGMVGAHGGHISVAEGIGGKGTCITLHLPLQTQPELESDL	18~~KdpD (5.22387E-121)~~227;X;248~~Usp(7.03407E-28)~~365;X;405~~DUF4118 (0.00000000274391)~~489;X(160);649~~HisKA (0.000000000000184095)~~715;X;768~~HATPase_c (1.31607E-25)~~871	KdpD protein
	3E-12	56.1	11.6	5.1E-12	55.3	8.1	1.4	1	B4ETV7_PROMH	Histidine kinase (EC 2.7.13.3)	kdpD PMI1227	Proteus mirabilis (strain HI4320)	900	529507	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Proteus, Proteus mirabilis, Proteus mirabilis (strain HI4320)	>tr|B4ETV7|B4ETV7_PROMH Histidine kinase OS=Proteus mirabilis (strain HI4320) GN=kdpD PE=4 SV=1MEQAPQWQRPSPDDLLALTRAPHRGRLKIFFGACAGVGKTYAMLQEAQRLHQQGIDVLAGVVETHQRQETAQQLEGLPLLPPLKLHYRGRKLSAFNLDAALARHPAVILMDELAFSNPHKCRHPKRWQDVEELLDAGIDVLTTINVQHIESLNDIVGSITGIRVQETIPDYIFDNADEVVMVDLPPDDLQQRLNEGKVYLAGQAERAIEHFFRKGNLIALRELALRRMADRVDSQVKEFRDSQGGTPVWHTTDSLMVCLGAHGRNDKLVRTAARYAAAFGCQWHAIYVETPKLHQIGEHKRRAILHSLKLAQHLGARTAILSDNQAEKAVIRYAREHNLGKVIIGQRPYQKWQWLKRWVRMRFAERLARYAPDLHVISVALNEEEPRYKTKTFVPQNDKWRQNLKGYLTAIGLCLAITLFSRTFLLALDKANLVTLYLLGVVLIALFFGRRPSIFAALINVISFDLFFVQPHFSLAVLDMQYLVTFSVMLIVGLVVGNLTAGMRYQTRVARYREQRTRHLFEMTRELSRALTLEEVVRTSYHFLSSAFDAKVCLLMPNHHGELTPYNAEGMGQLPIDSGIARWCWDKDQIAGAGTDTLPSVPYQLHPISASQQVLAILAIEPNNLRQVLIPEQQQLLQTFNGLIANALERLQQAEMAEQSRINIEREQLRNALLAALSHDLKTPLTVLFGQSEILLLDLSAEGSAHTEQVSQIRQQILTTSRLVNNLLDMARIQSGGIQVNLQWNLLQEIAGSAVRSLSYLLDKHPLQIDIPADLLLYCDSLLIERVLTNLLENAVKYTASQTKLGIKATVEEDQIHVEVWDEGAGIPTEQLQLIFNKFSRAVKESAIPGVGLGLAICSAIIHLHEGKIWAENNKKGGASFHFVLPLKSLPNIDEIEIKQ	22~~KdpD (1.10468E-114)~~232;X;255~~Usp(3.89623E-29)~~378;X;408~~DUF4118 (4.00104E-20)~~506;X;532~~GAF (1.67033E-17)~~650;X;667~~HisKA (0.000000000061811 4)~~732;X;784~~HATPase_c (3.80488E-28)~~885	KdpD protein
	3E-12	56	8.8	5.5E-12	55.2	6.1	1.4	1	A0A0C9M332_SPHPI	Histidine kinase (EC 2.7.13.3)	kdpD SP6_31_00020	Sphingomonas paucimobilis NBRC 13935	888	1219050	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas paucimobilis (Pseudomonas paucimobilis), Sphingomonas paucimobilis NBRC 13935	>tr|A0A0C9M332|A0A0C9M332_SPHPI Histidine kinase OS=Sphingomonas paucimobilis NBRC 13935 GN=kdpD PE=4 SV=1MTAGEPRPDPDALLRAAEREGRGRLKIFLGAAPGVGKTFEMLSEGAARRRDGVDVVVAVVETHGRVETEALVRGQEVMPRRAVPYEGRTLHEMDLDAVLARAPRLALVDELAHTNAPGSRHPKRYQDVEELLDAGIDVYTTVNIQHIESLNDVVASFTRVRVRETVPDRILEAAEIEVVDIPPDELIERLKAGKVYLPQEATRALSHFFSKSNLSALRELALRRAAQAVDAQMLDHVRSLGVGGQWAAGERLVVAVSELPGADELVRAAKRTADALRAPWTALFIDTPRTATLGEAQHRRLAATMTLATQLGAAVATVPAPSVVEGIRAFLTDARATQLVVGKAKRSRWFELRHGSVVDRLVRETPGVTVHVLPVGEAPVERERTKRRGQWGSPIGYGLTLLGVAAVTALASALFHILNLGNVALLYLLPVMAAASLYGLRTGLFAGIASSLAYNFFFLPPVGTLSVSNPENVISIFVLLGVAVATSQLTSRVRAQADLAAASARDNATLAGFLHRLSGLADPAEAARVICEDIALLFEVQAVLLTPSPAGLAVQAATKPDYRLETMEMAAAHWAFDTGTPAGKGSATLAASEWLFQPLKAGNRTLAVLGLAREAGGEPVRADRLPLLTGLIDQAALILERLRLESEVRDVDAVRTRDRLRAALLSSVSHDLRTPLTAVMAAAAQLRQGATPELVSTIEGEAARLNRFVANLLDMARVEAGALKLKIEAIDLSDAVTGAAHDARRALEGHAVRLDVPPDLPLVRADPQLLHHCLLNLLDNAGRYGDPGTEIVIEGRHRHGSLRLSVLDHGPGLPPGREAEVFETFRRLEGSDRVAGGTGLGLAIVKAFAEAMGLTVEAGNREDGAGAAFALCFPRELIMRDGAPEGMA	20~~KdpD (8.32001E-111)~~229;X;251~~Usp(1.10636E-34)~~374;X;397~~DUF4118 (6.47769E-18)~~494;X;522~~GAF (0.0000098731 9)~~641;X;658~~HisKA (0.000000001301 3)~~717;X;779~~HATPase_c (5.19554E-17)~~873	KdpD protein

	3E-12	56	6.6	5.4E-12	55.2	4.6	1.4	1	E5ASX3_BURRH	Histidine kinase (EC 2.7.13.3)	RBRH_02494	Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454)	938	882378	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia rhizoxinica, Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454)	>tr|E5ASX3|E5ASX3_BURRH Histidine kinase OS=Burkholderia rhizoxinica (strain DSM 19002 / CIP 109453 / HKI 454) GN=RBRH_02494 PE=4 SV=1MERPDPDELLDKLQREEEKKQRGKLKIFFGASAGVGKTFAMLQAARRCRDEGVDVVVGVAETHGRRETLALLDGLPSIPAARYPYRGKVLPEFDLNAALARRPQLILVDELAHSNVPGARHLKRWQDVQELLDAGIDVYTTLNVQHLESLNDVIGQITGIRVVWETIPDRIFDLADEVTLVDLPADELLARLRDGKVYLPQQAEHAVRHFFRKGNLIALRELALRRTADRVDAQMREYRADQSIERVWHARERIIACVGPGSESATLVRAAARLAASLKADWLAVYVETPTLQRLPDTVRKRTLDALKLAAELGAETVTLDGPDAARTLLAYARMRNVSRLVAGVPRTRRWLAPSVGERLLQSASDIDVTLVGAGRAHQRRGARGDVRSFASLLGDERRSKLRYYAYAAAISAGITVVATELLHRIDLANLAMLYLLGVIFAAARLGRGPGVLISFLSVASFDFFFVPPRISLSVSDTQYLLTFAVMLLTSLTISHLTSSLRRQARIATLRERRTSAMYAMTRELGAALATDQIIEIGMRHVAEVFQARVAILLPDSHDKVRQKVEEPDPAIMLQPPALDTDIAQWVYDQQKPAGQSTDTLPAADALYLPLKAPMRTRGVLALVVSRFEDLAVPEQRRMIDTFAAQIALALERVHYVEIAQDALVSMESERLRNSLLSAISHDLRTPLTAIVGFASMLAEQQSGGAPPRPQAERDLIEAIHEEALRMTRLVTNLLDMARLQAGAVRLNRQWLMLEEMVGAALAACRRSLAAHPVHTRVPAELPLLRLDPVLMEHLFANLFENAAKYTPTGAPLSIDAGVVEDGARRYVKVAIEDSGPGLPPGMQARVFDKFTRGEKESAKPGIGLGLAICRAIVDAHGGRIGAENRVDVQGRVLGARFWFMLPADEVPPGSGEVLDEAQEQDADAARSGHVVSEITPKS	20~~KdpD (1.44534E-107)~~230;X;252~~Usp(3.74418E-28)~~372;X;413~~DUF4118 (1.04157E-18)~~503;X;530~~GAF (8.59139E-18)~~652;X;669~~HisKA (3.27942E-14)~~738;X;791~~HATPase_c (9.43875E-23)~~901	KdpD protein
	4E-12	55.7	7.6	6.9E-12	54.9	5.3	1.4	1	A0A089WM28_9PSED	Histidine kinase (EC 2.7.13.3)	LK03_14250	Pseudomonas cremoricolorata	894	157783	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas cremoricolorata	>tr|A0A089WM28|A0A089WM28_9PSED Histidine kinase OS=Pseudomonas cremoricolorata GN=LK03_14250 PE=4 SV=1MTDSSGAAASGAAALRADALLTALPAQGRGRLKVFLGAAPGVGKTYAMLQAAHERQRQGVRLLAAVVQTHGRSETEALSLGLPQVPLLRHEYRGVLLEEMDLDAVLAAAPQLALVDELAHSNVPGSRHAKRWQDVQELLAAGIDVYTTVNVQHLESLNDKVCGITGVQVRETVPDWVVQEAFELVLIDLPPRELLERLRQGKVYVPEQARAAIDAFFSQTNLGALRELAMQTAAAQVDADVAQGYRQRGEQAPALQGRLLVGVDGDDQAEALVRHASRVAQRRHLPWSVVHVERGAARDEGSRQCLQAAQQLAERLGGEVVVLRAGEVARTLLGHAAERRASVLLVGQSRRRWWRRWLSGGVAQRLLREPSGLEISVLDGQAARPARVRGEPGRWVAGHYLLAILATALAAGLAWAVSSVLELPNISLVFLAAVLLVAVRSSLGPALVCALLSFLAYDYLFIAPSYSLSIRREEDVLTLLFFLLMAALTGKLAARQRRQLQVLRDTQDETRQLLELSLQHLALATDRKAVLAAAVTHLEQAAGQPVTVVQRLADGGFSPLSGPAQALPVSAQAAAHWAWQHGQAAGAGTDTLPDSPFWWWPLRVEDRPLALLGVKVAPSAALSRRRLRLLRGLAQPLAQALARVELAEQLEAARLQGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALDQALSGADRRELLEGTRDEAERLDRYIQNLLDMTRLGHGSLALARDWVAPADIVGSALHRLRTLLAPLRVERQMAGDLPLLYVHAALIEQALVNVLENAARFSPRDGRILLQVAVEGEQLRLAISDQGPGIPLAERSKIFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGRIEVDDGADGQGTCITLCLPLPAQPDADAEAP	28~~KdpD (2.68676E-112)~~232;X;258~~Usp(1.21939E-25)~~375;X;425~~DUF4118 (0.000000197815)~~499;X(160);659~~HisKA (0.000000000000099518)~~725;X;778~~HATPase_c (9.90575E-26)~~881	KdpD protein
	4E-12	55.7	5	6.8E-12	54.9	3.5	1.4	1	A0A0C5LBU1_9SPHN	Histidine kinase (EC 2.7.13.3)	TS85_00375	Sphingomonas sp. WHSC-8	884	1609977	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. WHSC-8	>tr|A0A0C5LBU1|A0A0C5LBU1_9SPHN Histidine kinase OS=Sphingomonas sp. WHSC-8 GN=TS85_00375 PE=4 SV=1MTDDRPDPEALLRATAQEGRGRLKLFLGAAPGVGKTYEMLREGVARLRAGVDVVIGIVETHGRAETEAQVQGLEIVPRRAVDYEGRSLDEMDVDAILARAPQLVLVDELAHTNVPGSRHDKRYQDVEELLAAGIDVYSTVNIQHLESLNDVVASFTKVRVRETLPDRVLENAEIEVVDIPPDELIERLREGKVYIPEEATRALGHFFSKSNLSALRELALRRAAQAVDAQMLDYLRAHALAGTWAGGDRVVVAVHELPGAAELVRAAKRVADALRAPWTAVHIETPRAAQFSDAENARLAATLHLASQLGAQVASVPAESVLAGLKKRFTVEARATQLIVGKSARSRWFELRHGSVVDRLVRETPGIAVHVLPMAEGAPAPRQRPRRGPGHGWGKPMGYAVSLGLTGLVTLVGASMGNVTNIGLLYLLPVMVAATRYGVRTGVVTGLASSLAYNFFFIPPTHTFTIQDPQNILTVLTLMAVAVVSSQLAARVRAQAVLAQRSAGQNSALAGFARLLTGTSKRDELGQILCAEVGRLLDASTVLLLPEHGELALVAAFPPEDRLEAIEQAAARWAFDHNQPTGRGSDTLTASEWLFHPLAAGGRVLGVMGLARPDATTVLRSDQLPLLLSLLDQAALALERMALEAEMATVTQLKERDRLRAALLSSVSHDLRTPLTTVLGMLAEMEPASPEQAGQLAAARSEAERLHRFVANLLDMVRIESGALHQAIEPVDLAEAAASAVHDLRRALEGHAIRLDVSPELPFVSVDAQLFHHCLINLLENAAKYGDSGSPITISARRQPSGMTLSVLDEGPGLAAGEEKRIFETFARIEGSDRKGGTGLGLAIVKGFAEAMGLRVDAANRADGAGACFTLRIPESHLRKGGGGE	18~~KdpD (4.3667E-119)~~227;X;249~~Usp(7.03692E-35)~~372;X;398~~DUF4118 (5.99172E-17)~~494;X;522~~GAF (0.000000223896)~~613;X;656~~HisKA (0.000000000851413)~~717;X;770~~HATPase_c (6.52398E-24)~~872	KdpD protein
	4E-12	55.6	10.9	6.7E-12	54.9	7.6	1.3	1	F4A0C6_MAHA5	Histidine kinase (EC 2.7.13.3)	Mahau_2863	Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	535	697281	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family IV. Incertae Sedis, Mahella, Mahella australiensis, Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	>tr|F4A0C6|F4A0C6_MAHA5 Histidine kinase OS=Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON) GN=Mahau_2863 PE=4 SV=1MLKKHMDKQIYNDAVEFQHYCDLKPRNIILRALKNISIVIGIMIIATLISYGFRALGFHESNYIMIYILGVMIIASITDGYLYGIMASALSVLTFNYFFTEPYYTLLAYSPEYPVTFIIMLIVALITSTLAARIKHESQRAELREMRIRILYQIEKDLLAVKNIEQVAQVAAKDISKIFRLPVMLSLADMDGGLTIDHIEGDDIFNSYSEMMARTETFQSGNACGARTRLFADSRAYFQPISGQNGVLGVIGILGLGNADMLTEGQKSFIDTIATQIAPVLERERLYEKQQRAKIEMEHERLRSDLLRAISHDLRTPLTSILGSSSTVIENYDVLTDEMRRDFLQDIYDDAEWLSILVENILSMTRFSEGRIELKKEMEAVEEIVAEAVSRVNKRAKQHEISVSVPKELIMIPVDGILIEQVLINLLDNALKYTLPDSKINVSVKKEDGKVMFQVSDNGPGIPEEELPFIFNRFYTKNLNNTSRPGMGLGLAICKSIVEAHGGEISADNDPAGGAVFRFTIPIREEDHESIDTDSR	40~~DUF4118 (8.86787E-19)~~135;X;163~~GAF (0.0000211305)~~282;X;299~~HisKA (0.000000000007512)~~365;X;418~~HATPase_c (4.11047E-34)~~520	non-KdpD DUF4118 protein
	4E-12	55.6	14.3	7.3E-12	54.8	9.9	1.3	1	E0SEX6_DICD3	Histidine kinase (EC 2.7.13.3)	kdpDDda3937_01552	Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	909	198628	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Dickeya, Dickeya dadantii, Dickeya dadantii (strain 3937) (Erwinia chrysanthemi (strain 3937))	>tr|E0SEX6|E0SEX6_DICD3 Histidine kinase OS=Dickeya dadantii (strain 3937) GN=kdpD PE=4 SV=1MTDEEQRRPDPDSLLSQIEEQPRGKLKIFFGACAGVGKTYAMLQEAQRLKAQGLDVLVGVVETHGRSETAALVEGLPHLPMRKISHYGRHHHEFDLDAALARCPALILIDELAHSNIRGSRHPKRWQDVQELLDAGIDVFTTVNVQHLESLNDIVGGVTGIRVVRETVPDPIFDDANEVVLVDLPPDDLRQRLNEGKVYLPMQAERAIENFFRKGNLLALRELALRRMADRVDDQMRAMRASQGRERVWHTRDAILLCIGRGVGNEKLVRTAARLAARLGSIWHAVYVETPRLHRLPEGERRAILRALKLAQDLGAETATLSDPSVERAVLRYARDHNLGKIVIGRHTEQKLGWWRRTRFAEKLGKLGPDLDLVVVSVQDDAAPPPPKTPDIRGITDKWRLQFYGCGVAALLCTLITLLALWSPFSMLEPVNLVMLYLLAVVIIALFYGRWPSVLAAFINVASFDLFFVVPKGTFAVADVQYLVTFAVMLTIGILVGNLTAGVRYQARVARYREQRVRHLYEMSKALNRSLSVQDIAKASHHFLRSTFQAKIAILLAEPVSSPTAELQQAALDEPDQLIVDQAIARWSYDHAAPAGAGTTTLPGVPYQLLPLATPQLTFGVIALEPNNVRQLMIPEQQRMLETFTVLIANALERLHLVKSTENARLDAEREQLRNSLLAALSHDLRTPLTVLFGQAEILTLNLASEGSPYAPQASQIRQHILSTTRLVNNLLDMARIQSDGFNLRKEWQTLEELAGSALRQLENSLANNTIQLRLPQDMTLVYCDASLIERVLINLLENAIKYAGEQATITVSASPISSPASGDMLEVQVRDNGPGIPDGQEKVIFDKFARGHKESSIPGVGLGLAICRAIVEIHGGRIWATNADDGGAVFHFTLPLAPPPALEPEEMES	23~~KdpD (4.53979E-115)~~231;X;254~~Usp(6.69166E-39)~~376;X;408~~DUF4118 (8.89996E-21)~~505;X;531~~GAF (4.87879E-14)~~653;X;670~~HisKA (0.000000000827158)~~735;X;788~~HATPase_c (2.4396E-30)~~893	KdpD protein

	4E-12	55.5	6.6	6.8E-12	54.9	4.6	1.3	1	A0A068SL95_RHIGA	Histidine kinase (EC 2.7.13.3)	RG540_CH02720	Rhizobium galegae	901	399	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Neorhizobium, Rhizobium galegae	>tr|A0A068SL95|A0A068SL95_RHIGA Histidine kinase OS=Rhizobium galegae GN=RG540_CH02720 PE=4 SV=1MPDDSRESENRPSPDALLEHAEREARGRLKIFLGAAPGVGKTYEMLMSGRARKVDGLDVVIGVVETHGRQETEALVEGFEIVPRKAIDYRGQQLDEMDLDAILARRPALVLVDELAHTNAAGSRHPKRYMDVQEILGQGIDVYSTLNIQHVESLNDVVAQITRVRVRETVPDSIIDRADDVEIIDITPDDLIKRLNDGKVYVPQTARRAIENYFSPGNLTALRELALRRTAQRVDEQLLNHMQAHAISGPWAAGDRVLVCLDHGRNGASLVRYARRQADRLRAPWAALHLETPQSVNLPEQDKDRLAANMRLAEQLGGETVTLPALQPSREIIAYANANNFTHIVVGRPARPRWRQILQGSVTYDLIRYAGDISVHVISGDTKEGEPKRGLKAAQLPKAFRFKPYVKSTIFVALAIIAGAALDQTLDVRNLALVFLMAVLAAAVRGGLGPGLFASVAGALSFNFFFLEPRYTFTVRDPESLVALFFYLGVAVVASNLTAAVQRQAAAARQRARTTEDLYLFSKKLAGTGTLDDVLWATAFQIASMLKVRVVILLPENGSIAVKAGYPPDDTLVDADIAAAKWAWEHNRPAGRAADTLPGAKRLYLPMRTGREAVGVIGLDNDKQGPLLTPEQQRLFDALTDQAALAIERIQLVSDVDKAKLAAETDRLRTALLTSISHDLKTPLAAIMGSAGTLKDFGADIPEEARAELLTSVVDESERLNRFISNLLDMTRIGSGAMEPNYAFHFAGDIVGTALSRAAKIVSAHKLNVGIPADMPMLKVDPVLFEQVLFNLIDNAAKYAPEDTVIDIRGWQDGGSILISVMDEGPGIPPDDLERIFDSFYRVRKGDHVRAGTGLGLSICRGFIEAMGGTIRASNRSDRPGAIFTIRMPVPAETPILGEQE	24~~KdpD (7.47799E-121)~~234;X;256~~Usp(1.30578E-44)~~379;X;404~~DUF4118 (0.000000000000296186)~~497;X;530~~GAF (4.08986E-16)~~649;X;666~~HisKA (0.000000000001873 52)~~732;X;785~~HATPase_c (1.60674E-29)~~887	KdpD protein
	5E-12	55.5	4.9	7.1E-12	54.9	3.4	1.3	1	A0LPE2_SYNFM	Histidine kinase (EC 2.7.13.3)	Sfum_3624	Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	344	335543	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophobacteraceae, Syntrophobacter, Syntrophobacter fumaroxidans, Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	>tr|A0LPE2|A0LPE2_SYNFM Histidine kinase OS=Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB) GN=Sfum_3624 PE=4 SV=1MNDLRESRKGRNVCRIVLVFSIIAVLSVLHYGTATRHMEYHILYRELYFVPIVMVSLWYGLRAGVYFSLLVVILYTPHVMMTWSGQPGVNVGNLSQIIVFILVSAITGTLSDRERKRQLEIREAQNLASLGKASLAMTSELREVLDALKELMKDREMPASPNFSQRLKNQVDRITTLDHTLSHFTLERSEAQKDFAEVDSSVERVKSKLKPLAERSGVTVETRLEPALGLLAVNELDFVWMIEELTTNAIESSTAGSTVTIASRWSEGQCEVEVHDRGIGIPPENLSKIFVPFFTTKERGTGLSMAVCKKIMKDCDGEIRVDSDRAEGTRLVLVFRRIHPQTRG	18~~DUF4118 (6.65677E-15)~~117;X(124);241~~HATPase_c (1.56374E-20)~~335	non-KdpD DUF4118 protein
	5E-12	55.5	9.7	7.4E-12	54.8	6.7	1.4	1	A0A0A7PJB0_9SPHN	Histidine kinase (EC 2.7.13.3)	SKP52_16045	Sphingopyxis fribergensis	889	1515612	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingopyxis, Sphingopyxis fribergensis	>tr|A0A0A7PJB0|A0A0A7PJB0_9SPHN Histidine kinase OS=Sphingopyxis fribergensis GN=SKP52_16045 PE=4 SV=1MTGNDRPSPEAFLRQAAQEGRGRLKVFLGAAPGVGKTWEMLTDGRQRREAGVDVVIGVVETHGRRETEALVHGHEIIPRRDVDHQGHSLGEMDIDAILARRPQLVLVDELAHTNAPGSRHPKRYQDVEELLGAGIDVYSTINIQHVESLNDVVASFTRVRVRETVPDSILENAEIEVVDIPPDELIERLRDGKVYIPQEATRALTHFFSKSNLTALRELALRRAAQAVDAQMLEHVRSHALAGSFAVGERIVVAVSELPVAAELVRAGKRLADALKAPWSAVYIETRRSQGMTDDDRRQLADTLALASRLGASTATVPAASVVEGLRAFAADARATQVVIGKSSRPWWFEMRHGSVVDQLVRTIDDVAVHVLPGEPDAKAVSRSAVAIPGRWGKPSDYLLALAMVALMTALGRLLLAVIDLGNISLLYLVPVMFAAATFGLRAGLFAGLASSLAYNFFFLPPTGTLTVNNPENVVSILVLLGVAVVTSQFAARVRAQADLAQSSARQNAALASFSRLLIAAPDQESLMQAICAEVGRLLDVRTALLLPSADGPMLRAAVPPEDRLEQIERAAAQWAMDNEQPAGRGSSTLTASDWLFHPLRTTRGVLGVLGLTRDDAREPVRSDQVPLLMSLLDQASIALDRMELEEASLRTRQVDERDRLRSALLSSVSHDLRTPLTTILSAAQEMRRHPSENLAETIETEALRLNRFVSNLLDMARVEAGALPMKVEATDLFDAAASAAHDTRASLLGHEVKVDISPNIPLVRVDPVLLHHCLINLLDNAGRYADPGTPIVIRARRAADAIFMSIIDQGPGIAPGNEKRVFDTFTRLEGSDRAKHGTGLGLAIVKGFAEAMGLSVEAGNNDDPLGACFTIRIPETLIITHLDDKEVP	19~~KdpD (7.27575E-118)~~228;X;250~~Usp(3.5662E-36)~~373;X;398~~DUF4118 (4.29687E-18)~~497;X;523~~GAF (0.000000000624399)~~642;X;659~~HisKA (0.000000000068137 3)~~718;X;771~~HATPase_c (3.39612E-22)~~874	KdpD protein
	5E-12	55.4	7.9	8.4E-12	54.6	5.5	1.4	1	G8Q1U4_PSEFL	Histidine kinase (EC 2.7.13.3)	kdpD PSF113_1668	Pseudomonas fluorescens F113	883	1114970	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens F113	>tr|G8Q1U4|G8Q1U4_PSEFL Histidine kinase OS=Pseudomonas fluorescens F113 GN=kdpD PE=4 SV=1MSDSGRADALLANLPRNDRGRLKVFLGAAPGVGKTYAMLQAAHTQLRQGVKVIAGVVETHGRSETEALLGGLAQQPLVRSEYRGVMLEEMDLDGLLAAHPTLVLVDELAHSNAPGSRHAKRWQDIQELLTAGIDVYTTVNVQHLESLNDQVRGITGVQVRETLPDWVLQEADELLLIDLPPRELLERLRDGKVYVPEQARAAIDAFFTQTNLTALRELAMQTAAAQVDNDLTQGYRQLGQAAPAVRGRLLVGVDGDVQAERLVRHASRVAQRRHLPWSLVHVDNGSARDEPSRQRLQNAQQLAERLGGEVVLLRAGEVARTLIQHASERRATLLLVGQSRPRLRRRLFGGGLASRLLRDARGLEINVLDSDEQPRPARVRSNAVQTGFDYVLALTATVAASALAWGISGWLALPNISLVFLMAVLLVAVRSSLGPALACAALSFLAYDFLFIPPNFSFTIQREEDVLTLVFFLLMAALTGNLAARQRRQLQALRDTQQETGELLDLSRKLTAATDRQAVISAAAQHLNGWHDLQLCLLNRDNQGGWKIESGEPLTFTEAERAAADWSWQHDQPAGAGTGTLPSGRWWWWPLSAEGGPLALLGVCPKEGKPLSGQRRRLLAALSQPLAQALARAQLAQDLEAARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALGEAIPLADRRELLEGTRDEAERLDRYIQNLLDMTRLGHGALKLARDWVSPADIVGSALNRLRAVLAPLALSLVEVPAELPLLYVHAALIEQALVNVLENAARFSPAQGQLLLSAGATDSEVFFAVADEGPGIPEEERAKIFDMFYTAARGDRGGQGTGLGLAICQGMVGAHGGRISVADGLDGRGTCITLHLPLQAQPGMDDEA	19~~KdpD (2.12087E-120)~~227;X;248~~Usp(1.69667E-30)~~365;X;390~~DUF4118 (7.16204E-20)~~489;X(160);649~~HisKA (0.000000000000436485)~~715;X;768~~HATPase_c (9.74591E-26)~~871	KdpD protein
	5E-12	55.3	6.8	7.7E-12	54.7	4.2	1.7	1	Q97L35_CLOAB	FUSION: Nucleoside-diphosphate-sugar epimerase and GAF domain	CA_C0731	Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	725	272562	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium acetobutylicum, Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	>tr|Q97L35|Q97L35_CLOAB FUSION: Nucleoside-diphosphate-sugar epimerase and GAF domain OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) GN=CA_C0731 PE=4 SV=1MRILIVGGCGFIGSHVVERLYKEGHKTYIIDNLSTGNLKNVTVPHKFYNLSIESESCEEVFKANKFDAVIDLSSPVVNTNAEASSFELTPSVKGITNLLNFSSKYGVKRFIFASSASVYGNNNLTIKEEAEINPLSPYAVNKYVGEFYTQKWFEIYGLKTISLRISNVFGPRQSIKGEGNVVALFINKALKSSEIDRFGDGTQTRDFIYVEDVVDAIYKALESDYTGVLNISTNTEHSLNELIDTLEEFHPIRKVNYRLNRSGDIKKSKLDNSKAKTELGWDTKYSFRAALEKTYDWYKKNCSLSETVSDTSKAKTKKRTLFKYLPYFENILFMLLIFFLTFSILKVKDPFSSGFADICYMYIIIMSIMYGMKQASLSVIFSCGLYFYLLLNTGYSVVTILYDPTNLPHVLSYIIIGAVCGYAADVYKRNSKIKELKIDTLNNKYKFLETIYNETRNAKEELEEQIIGSENSFVNIYNTTKALDSLEVNDIYFGSIRIIDKLLNTLKSSIYILDRDGKYLRLKAKSSSENFSLPYSVNLDQFREINQAIKSKTVFINRTLNPKLPTMVAPVIINDNVKAIISVYDVKFEKLTLHYENLFKALVDLISNAIGKALKYDEIAARNKYIPNTEILTTKEFKKVLTDKIRNKEISGINFTLLRIKDNNLSYEENFNKLSLSIRDDDDLIGLGEGNYIYVILSNTDKIKSEKVLMRISKSGLNAEVMEDLY	2~~NADB_Rossmann (8.59873E-92)~~298;X;326~~DUF4118 (3.12081E-18)~~430;X;487~~GAF (5.24939E-18)~~610	non-KdpD DUF4118 protein

	5E-12	55.3	14.2	9.1E-12	54.5	9.9	1.4	1	A8AJC0_CITK8	Histidine kinase (EC 2.7.13.3)	CKO_02466	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	895	290338	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter koseri (Citrobacter diversus), Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	>tr|A8AJC0|A8AJC0_CITK8 Histidine kinase OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=CKO_02466 PE=4 SV=1MVNEEPLRPDPDRLLEQTAAPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQGLDILTGVVETHGRKETAALLDGLSILPLKRQTHHGRHLSEFDLDAALARRPALILMDELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRARLKEGKVYIAGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAWRSHPGEEKVWHTRDAILLCIGHNTGSEKLVRAAARLAARLGSVWHAVYVETPALHRLPEKQRRAILSALRLAQELGAETATLSDPAEEKAVVRYAREHNLGKIVLGRPATQRWWRRDSFADRLAKQAPDLDQVVVALDDPPTRPLNQTPDTRAFKDKWRVQIQGCLVAIALCAVTTVIAVQWMVAFDAANLVMLYLLGVVIIALFYGRWPSVVATFINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGVRYQARVARYREQRTRHLYEMSKALAVGRSRQDIAATSEQFIASTFQARSQVLLPDENGTLTPLTHQQGITPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSADKTHGLVVVEPGNLRQLMIPEQQRLLETFTLLVASALERLTLTASEELARLASERESIRNALLAALSHDLRTPLTVLFGQAEILTLDLASEGSPHARQASEIRQHILNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLSHPINLSLPAPMTLVHVDGPLFERVLINLLENAVKYAGSQAEIGIDAHVEDEHLQLDVWDNGPGIPDGQEKSIFDKFARGNKESAVPGVGLGLAICQAIVEVHGGTISAHNRPQGGACFRVTLPQETAPELEDFHEDM	21~~KdpD (1.91642E127)~~231;X;254~~Usp(3.02169E-31)~~374;X;404~~DUF4118 (2.69858E-21)~~502;X;530~~GAF (1.22344E-15)~~645;X;662~~HisKA (0.00000000124227)~~727;X;779~~HATPase_c (2.10556E-32)~~880	KdpD protein
	5E-12	55.3	13.9	9.6E-12	54.4	9.6	1.4	1	L0M5A0_ENTBF	Histidine kinase (EC 2.7.13.3)	D782_3155	Enterobacteriaceae bacterium (strain FGI 57)	896	693444	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, unclassified Enterobacteriaceae, unclassified Enterobacteriaceae (miscellaneous), Enterobacteriaceae bacterium (strain FGI 57)	>tr|L0M5A0|L0M5A0_ENTBF Histidine kinase OS=Enterobacteriaceae bacterium (strain FGI 57) GN=D782_3155 PE=4 SV=1MMTDEPQRPNPDRLLEQTASPHRGKLKIFFGACAGVGKTWAMLAEAQRLRAQGLDILAGVVETHGRKETSEMLKGLTVLPQKRLSWQGRYLHEFDLDAALARRPALVLMDELAHSNAPGSRHPKRWQDINELLEAGIDVFTTVNVQHLESLNDIVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLNEGKVYLAGQAERAIENFFRKGNLIALRELALRRTADRVDEQMRAWRDTQGQEKVWHTRDAILLCVGHHTGSEKLVRTAARLAARLGSVWHAVYVETPTLHRLPEAQRRAILSSLRLAQELGAETATLSDPSEEKAVIRYAREHNLGKIVIGRQEKRHWWSGERFGDRLARHAPDLDLLVVAMDEKPDPLPSSTRDPRSFFDKWQVQIRGYAVAFTLCTAITLIAAQWLMAFDAANLVMLYLLGVVIVALFYGRWPSVLATVINVISFDLFFIAPRGTLAVSDVQYLLTFGVMLTVGLVIGNLTAGVRYQARVARYREQRTRHLYEMSKALAVGRSAEYIARTCEQYIQSTFHARSQVLLPDENDKLTPSTQQDGLTPWDDAIARWSFDKGLPAGAGTDTLPGVPYQILPLKSASKTLGLVVVEPLNLRQLMIPEQQRLLETFTLLAASALERLALTASEEQARFASERESLRNSLLAALSHDLRTPLTVLFGQAEILTLDLASSGSPYAPQANEIRQHVLNTTRLVNNLLDMARIQSGGFNLNKEWLTLEEVVGSALRMLEPGLNGQQIALSLPDPLMLIHVDGPLFERVLINLLENAVKYAGPQARIGINAREQNHQLFLDIWDNGPGIAQGQEIRIFDKFSRGNKESAIPGVGLGLAICRAIVDIHGGTLSASNRPEGGACFHVTLPLESPPELEEFHEDM	21~~KdpD (5.93048E127)~~231;X;254~~Usp(2.88315E-40)~~374;X;405~~DUF4118 (6.95123E-21)~~502;X;532~~GAF (9.75649E-15)~~645;X;662~~HisKA (0.00000000251172)~~727;X;780~~HATPase_c (3.72252E-30)~~881	KdpD protein
	5E-12	55.3	13.2	9.4E-12	54.5	9.2	1.4	1	A6T6D6_KLEP7	Histidine kinase (EC 2.7.13.3)	kdpD KPN_00714	Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	895	272620	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Klebsiella, Klebsiella pneumoniae, Klebsiella pneumoniae subsp. pneumoniae, Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578)	>tr|A6T6D6|A6T6D6_KLEP7 Histidine kinase OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=kdpD PE=4 SV=1MSDEPLRPDPDRLLQHTAAPHRGKLKVFFGACAGVGKTWAMLAEAQRLRAQGLDILIGVAETHGRKETAAMLQGLSTLPPRRLAHRGRYVYEFDLDAALARRPALILVDELAHSNAPGSRHPKRWQDVDELLEAGIDVFTTVNVQHLESLNDVVSGITGVQVRETVPDPFFDAADDVVLVDLPPDDLRQRLNEGKVYIGGQAERAIENFFRKGNLIALRELALRRTADRVDEQMRAWRDRQGQEKVWHTRDAILLCIGHNTGSEKLVRAAARLAARLGSVWHAVYVETPSLHRLPEARRRAILAALRLAQELGAETATLSDPSEEKAVLHYARERHNLGKIVIGRQSKRRGWDRSGFADRLARHAPDLDLVVIALDEKPSPLPARGNDSRTALEKWRLQLQGCAVAVALCAIITLVAMQWLMAFEAANLVMLYLLGVVLIALVYGRWPSVLATVINVISFDLFFVAPRGTLAVSDVQYLLTFGVMLTVGLLIGNLTAGVRYQARVARYRERRTRHLYEMSKALAVGRSQQDIATTSERFIASTFQARSQLLLPDAQGKLLLPLTHQPGLTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSAARTWGLLVVEPENLRQLMIPEQQRLLETFTLLVASALERLTLTASEEQARLTSERESLRNSLLAALSHDLRTPLTVLFGQAEILTLDLASEGSKHAPQANEIRQHVLNTTRLVNNLLDMARIQSGGFNLHKEWLTLEEVVGSALRMLEPSLGGQHIQLDLPDPLQLVHVDGPLFERVLINLLENAHKYAGARASIGIRAEADARQLSLEVWDNGPGIPAGQEQTIFDKFARGNKESAIPGVGLGLAICQAIVDVHGGTISASNRPEGGASFRVTLPGETPPELEELPEEL	20~~KdpD (6.27628E126)~~230;X;253~~Usp(1.50931E-28)~~373;X;403~~DUF4118 (7.47591E-20)~~501;X;527~~GAF (2.54147E-14)~~644;X;661~~HisKA (0.00000000443041)~~726;X;779~~HATPase_c (4.17225E-30)~~880	KdpD protein
	5E-12	55.2	14	9.6E-12	54.4	9.7	1.4	1	A0A024HIT0_PSEKB	Histidine kinase (EC 2.7.13.3)	kdpd5 PKB_3065	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	901	1301098	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas knackmussii, Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	>tr|A0A024HIT0|A0A024HIT0_PSEKB Histidine kinase OS=Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13) GN=kdpd5 PE=4 SV=1MSDTQRPDPDQLLAQIRQDEAQQQRGRLKIFFGACAGVGKTYAMLSAARAALAQGTQVLVGVVETHGRAETEALLQGLERLPLRQVEYKGRRLGEFDLDGALARHPPLILIDELAHSNVAGSRHPKRWQDVEELLAAGIHVWSTMNVQHLESLNDIVGSITGIRVWETVPDRIFDGADEVVMVDLPPDDLLQRLKEGKVYLAHQAERAVRNFFRKGNLIALRELALRRTADRVDSEMLEYRGRILSQPVWGTRGSLLVGVGINEQDEKTVRSSARLASQLDVPWHAVYVETPRLQRLPEARRQRTLRTLKLAQELGAEIAVLAGQDEAEVLVKYARQHNLSKVVLGRRGGSRSWRWRAGLADRIAAQGADLDLLQIALPATRGGRTEEAPRGPGSPPYLPGYLMAVLAVGAITLVATPLTEVFERTNIVMLFLLAVVAVAVRCGRGPAVLAAFLAVASFDFFFVPPRFTLAISGVQYLVTFAVMLVVALVIGQMAAGLTYQARVAQGGEDRMRGLYEMSRQLSAALMIEQVADIASQFLASELNARSALFVTDLQDRLRPPVPTDLAEVDAAVAQWCFDKEEPAGHGTDTLPAGPTLYLPLTAPMRVRGVLAIQPRENARLAIPEQRRLLDTCASLLAISLERIHYIEVAQSSTLQMESERMRNSLIGAISHDLRTPLTSLVGLAEALVQAQPPLGGAHLELANGIRELTLRMNNLLNNLLDMARLESGAVELKRAWQPLEETIGSALATCRLALGERQVEVALPADMPLVQVDAVLFERVLVNLLENAAKYTPPGTPIHIGAAARRKSFELWIDDWGPGVPPGRETIFNKFERGRKESAIPGMGLGLALCRTIIEAHGGSISASNRPGGGARFLITLPRGEPPQVPVEDEPDDTQRQP	24~~KdpD (4.53937E124)~~233;X;256~~Usp(2.93452E-33)~~377;X;403~~DUF4118 (0.00000000001061 95)~~501;X;528~~GAF (2.69668E-16)~~644;X;661~~HisKA (0.00003422)~~714;X;779~~HATPase_c (1.05668E-25)~~880	KdpD protein

	6E-12	55.2	14.3	9.5E-12	54.5	9.9	1.3	1	Q8X9G1_ECO57	Sensor for high-affinity potassium transport system	kdpD ECs0723 Z0842	Escherichia coli O157:H7	894	83334	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli O157:H7	>tr|Q8X9G1|Q8X9G1_ECO57 Sensor for high-affinity potassium transport system OS=Escherichia coli O157:H7 GN=kdpD PE=4 SV=1MNNEPLRPDPDRLLEQTAAPHRGKLKVFFGACAGVGKTWAMLAEAQRLRAQGLDIVVGVVETHGRKDTAAMLEGLAVLPPKRLAYRGRHISEFDLDAALARRPALILMDELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADDVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRKLALRRTADRVDEQMRAWRGHPGEEKVWHTRDAILLCIGHNTGSEKLVRAAARLASRLGSVWHAVYVETPALHRLPEKKRRAILSALRLAQELGAETATLSDPAEEKAVVRYAREHNLGKIILGRPASRRWWRRETFADRLARIAPDLDQVLVALDEPPARTINNAPDSRSFKDKWRVQIQGCVVAAALCAVITLIAMQWLMAFDAANLVMLYLLGVVVVALFYGRWPSVVATVINVVSFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGVRYYQARVARYREQRTRHLYEMSKALAVGRSPQDIAATSEQFIASTFHARSQVLLPDDNGKLQPLTHPQGMTPWDDAIAQWSFDKGLPAGAGTDTLPGVPYQILPLKSGEKTYGLVVVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEEQARMASEREQIRNALLAALSHDLRTPLTVLFGQAEILTLDLASEGSPHARQASEIRQHVLNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLSSPINLSLPEPLTLIHVDGPLFERVLINLLENAVKYAGAQAEIGIDAHVEGENLQLDVWDNGPGLPPGQEQTIFDKFARGNKESAVPGVGLGLAICRAIVDVHGGTITAFNRPEGGACFRVTLPQQTAPELEEFHEDM	20~~KdpD (3.97046E-129)~~230;X;253~~Usp(8.59003E-42)~~373;X;403~~DUF4118 (6.10853E-21)~~501;X;527~~GAF (2.92186E-17)~~644;X;661~~HisKA (0.000000000260724)~~726;X;778~~HATPase_c (1.21374E-31)~~879	KdpD protein
	6E-12	55.2	14.3	9.5E-12	54.5	9.9	1.3	1	KDPD_ECOLI	Sensor protein KdpD (EC 2.7.13.3)	kdpD b0695 JW0683	Escherichia coli (strain K12)	894	83333	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Escherichia, Escherichia coli, Escherichia coli (strain K12)	>sp|P21865|KDPD_ECOLI Sensor protein KdpD OS=Escherichia coli (strain K12) GN=kdpD PE=1 SV=2MNNEPLRPDPDRLLEQTAAPHRGKLKVFFGACAGVGKTWAMLAEAQRLRAQGLDIVVGVVETHGRKDTAAMLEGLAVLPKRQAYRGRHISEFDLDAALARRPALILMDELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADDVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRELALRRTADRVDEQMRAWRGHPGEEKVWHTRDAILLCIGHNTGSEKLVRAAARLASRLGSVWHAVYVETPALHRLPEKKRRAILSALRLAQELGAETATLSDPAEEKAVVRYAREHNLGKIILGRPASRRWWRRETFADRLARIAPDLDQVLVALDEPPARTINNAPDNRSFKDKWRVQIQGCVVAAALCAVITLIAMQWLMAFDAANLVMLYLLGVVVVALFYGRWPSVVATVINVVSFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGVRYYQARVARYREQRTRHLYEMSKALAVGRSPQDIAATSEQFIASTFHARSQVLLPDDNGKLQPLTHPQGMTPWDDAIAQWSFDKGLPAGAGTDTLPGVPYQILPLKSGEKTYGLVVVEPGNLRQLMIPEQQRLLETFTLLVANALERLTLTASEEQARMASEREQIRNALLAALSHDLRTPLTVLFGQAEILTLDLASEGSPHARQASEIRQHVLNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLSSPINLSLPEPLTLIHVDGPLFERVLINLLENAVKYAGAQAEIGIDAHVEGENLQLDVWDNGPGLPPGQEQTIFDKFARGNKESAVPGVGLGLAICRAIVDVHGGTITAFNRPEGGACFRVTLPQQTAPELEEFHEDM	20~~KdpD (1.73015E-129)~~230;X;253~~Usp(9.20189E-42)~~373;X;403~~DUF4118 (5.76547E-21)~~501;X;527~~GAF (3.21301E-17)~~644;X;661~~HisKA (0.000000000276051)~~726;X;778~~HATPase_c (1.27434E-31)~~879	KdpD protein
	6E-12	55	5.9	9.3E-12	54.5	4.1	1.2	1	A0A0F2NLE8_9DELT	Phosphohydrolase	VR65_04035	Desulfobulbaceae bacterium BRH_c16a	305	1629713	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, unclassified Desulfobulbaceae, Desulfobulbaceae bacterium BRH_c16a	>tr|A0A0F2NLE8|A0A0F2NLE8_9DELT Phosphohydrolase OS=Desulfobulbaceae bacterium BRH_c16a GN=VR65_04035 PE=4 SV=1MRTKGKIVVLILLTVTIAFLHFLVPTDRHTFHILHIILRKLYFLPPVMAAVWFGLRGAVHVTLSISVLFSFHAILDWPENYMEQANQWGELVSFWAVGLVAGLLFQRERALLRDLLRANEETLLGLVSALDMKEHNTNLHSQRVRKYTLLLADKFGFDETGKRAIGFGALLHDVGKIAVPDEILLKPGTLTDEEQKVMRNHPSAGYGIVNRIEFLREAAEIVHAHHERFDGSGYPRGLKGEDIPLGARLFAVVDVYDALTSARPYRPAMSHEEALIEIKKGSSRHFDPKAVDAFLAIPREELNTA	7~~DUF4118 (0.000000876788)~~109;X;140~~HDc (2.85251E-20)~~278	non-KdpD DUF4118 protein
	7E-12	54.9	9.5	1.1E-11	54.3	6.6	1.3	1	H8GH08_METAL	Histidine kinase (EC 2.7.13.3)	Metal_3636	Methylomicrobium album BG8	903	686340	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomicrobium, Methylomicrobium album (Methylobacter albus), Methylomicrobium album BG8	>tr|H8GH08|H8GH08_METAL Histidine kinase OS=Methylomicrobium album BG8 GN=Metal_3636 PE=4 SV=1MRELDPEFFSAHANRTEIRKRRGRLKIFFGAVAGVGKTFTMLEVARAHQAEGCEVVAGLVETRGRADTAAQLQGLELLPPQIRYHQGTRRAEFDLDAALARHPDLILVDDLAHTNLPGSRHPKRWQDIRELLDGGIDVYTTLNVQHLESLHEDVGRFAGIRVWETVPDTVFEEADEVELVDLPPDDILARLHEGKIYPPEKAERALLNLFRKGNLIALRELALRRTAEWVSTQLREYRQAYAIREVWNVDERILVCVAPDARAKRLVRAAKRLAASLHADWLALYVETPALQRLSARRRDGVLKALRLAERLGAETVTLSAPDMAEAILTFAHEHNVNKLVLGKPGRKGWRRWFLGSVVDSLISQAHDLNFYLLGDEETPRLQSSAPSPSKSFDRQLVEHKYGHWLWSLAIPLLLTAIEWPFRDLLTPANILMFYLLGVFFVAIRFGFWPSILASLANAAAFAYFFAPPIFSFAIAEPENLAGLAVTLVIGAVTGNLAENVRHQARVAESRERRASALHRLSKGLAEARSEREITEIGVYHIHAQFGGRNTFLFPDRNGRLHYPNEPPLAISLRGADLDVARWVFEHGQLAGRGTDTLPDAPAVYLPLNGSTGTIGVLALEPVELRRIFLPEPYQLLNTFVNQIVHTLERANMAEHAKEATLKMQAEALRNSLLSSISHDLRTPLATIVGAASTLETDAARLEESSKRKLVSAISEEARRMSDLTSKILEMARLEAGEVRLNRQWYAPEEIVGSALRRLDKKLKARRINVRMADGPALIHVDAVLLQQVLVNLLDNADKYSPPELPIDITIESAPSGVSIAVADRGPGIPEGLEQKIFDKFFRVHAESAQSGVGLGLSICRAVVEAHGGTIRASQRSGGGTVVQLHLPMLERPPTIDLEEKTL	20~~KdpD (5.17967E-107)~~230;X;252~~Usp(7.11079E-42)~~375;X;404~~DUF4118 (0.000000000024450 1)~~504;X;530~~GAF (0.000000000036622 7)~~650;X;667~~HisKA (0.000000000011680 4)~~733;X;795~~HATPase_c (2.58078E-23)~~887	KdpD protein
	7E-12	54.9	13.3	7.1E-12	54.9	9.2	1.8	1	Q47A44_DECAR	Histidine kinase (EC 2.7.13.3)	Daro_3558	Dechloromonas aromatica (strain RCB)	512	159087	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Dechloromonas, Dechloromonas aromatica, Dechloromonas aromatica (strain RCB)	>tr|Q47A44|Q47A44_DECAR Histidine kinase OS=Dechloromonas aromatica (strain RCB) GN=Daro_3558 PE=4 SV=1MENNASLLDESPERITPKQGWVLTILACVGTTIIATPLLGYLDLANIVMLFLLTVLLVAVKLGRNAAILASILSVLLFDIFFVPPRFSLAVSNIQYLVTFAVMLVTALITAHLAAGLRQRARESQSREKRTQALYQFARELAGTLTTEQVVEISRSFIKTQLNAQSAVLMPHPENERLMVVSSSESPLLEMHLAQVALKSGQLVRSDEVGGMGYAPLYLPLRASMRIRGVLAIRFADDVAEPSSETTSLLETLASLIAVAVERLHYVDVAQASEVKMLTERLRSSILSALSHDLRTPLTAMVGLADSLFLIKPALPATALETAQALHEQADRLAGLVGNLLDMARLNAGEVTLRREWQPLEEVVGAGIKLLGSALASHPVKVELPRDLPLLEFDAVLIERVLCNLLENAAKYSPDGTPLLLAAEQEMDVVRVSISDHGPGFPAKRRDDLFKMFVRGESESGKPGTGLGLAICKAIVEAHGGTITADNRPDGGACVSFTLPKGVPPVVEEELA	21~~DUF4118 (1.63188E-20)~~120;X;146~~GAF (0.0000000234376)~~263;X;280~~HisKA (0.000000000558615)~~345;X;398~~HATPase_c (1.36889E-29)~~499	non-KdpD DUF4118 protein

	7E-12	54.9	5	1.1E-11	54.2	3.4	1.3	1	G8PHE2_PSEUV	Uncharacterized protein	PSE_4510	Pseudovibrio sp. (strain FO-BEG1)	342	911045	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Pseudovibrio, Pseudovibrio sp. (strain FO-BEG1)	>tr|G8PHE2|G8PHE2_PSEUV Uncharacterized protein OS=Pseudovibrio sp. (strain FO-BEG1) GN=PSE_4510 PE=4 SV=1MRPTKKKKSAPEKRFHLLEIAVLFAPFPVLTSMHPELLIWSISPSPLWIPIIIASSIFGTRSGILSALTALALTLWY VPPQPIGGQNFFEYFTTTGLEPTLWLLTAIIFGEFRTSLLRKNQRLQNQLTQALGQRDTISDYCTTLTMEAENLQSR IASMETTSPVSVFKSIDRLSTLNLKSNPKQLDIALGNLIGATKFSLFSYTNDHLDLVHSNIATSSGVTSPSAQQEQTW LINHLEMTEITGNTQQVITHTPKGSLVLLLKASDVTNPKPDHEVLQGAIIFHQLEQHILEEDTTIFLETIGKSLTQSLAS HNAEKAPDNLISLYSINTPPKSNRLDNTVL	16~~DUF4118 (4.26277E-16)~~119	non-KdpD DUF4118 protein
	7E-12	54.8	12.5	7.2E-12	54.8	8.7	1.9	1	A1TJ27_ACIAC	Histidine kinase (EC 2.7.13.3)	Aave_0358	Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	932	397945	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Acidovorax, Acidovorax citrulli (Acidovorax avenae subsp. citrulli), Acidovorax citrulli (strain AAC00-1) (Acidovorax avenae subsp. citrulli)	>tr|A1TJ27|A1TJ27_ACIAC Histidine kinase OS=Acidovorax citrulli (strain AAC00-1) GN=Aave_0358 PE=4 SV=1MPTDLRPDPDALIAQMRAEEQRVQRGKLRIYFGANAGVGKTWSMLGAAQRERQAGRDVLVGVVETHGRA ETAALLEGLPVLPRRTLEHSGRKRTEFDLDAALQRRPAVLLVDELAHSNVPGSRHAKRWQDVQELVAAGIEVWTA LNVQHLESLNGTVGAITGVRVHETVPDTVLDEADEVVLVDATPDELAARLAAGKVYLPQQAERAAQNFFRKGNLIA LREIALRRTAEHVEDDVRGWRVEQSGGGHGVPPAWNTSGALLACVGPHEDAAHTVRTAARLAGQLNVRWHAA YVETPRLQRLPARERDRILAVLQLAEGLGAETAVLTGDAVAPPLAEHARQLNCATVVVGRARRRTGLGRWWPVP GTAQAIGAAAAPTLEIVEAGEPGSSRRLPAAPWRPAGDPAGAGAQEDGGRPSVRWPGYGAAVAASVAVTLLALPL SGVLELTNIVMLYLLGVVGVAMRFGRVPAALAALLNVAAFDFVFVSPQLSFAVSDVQYLVTFGVMLGVGLLVGQLT AGLRFSAGVSAGREQRMRSLFELTRELSAALEASQVVDIGVRAVQQHFGGQAVVLPLDDTDRLAVPAVPPAGFD PSVADWTLRHGRSAGLGTATLAAQGWRYVPLTAPMRVRGVLALAPARPRWLLIPEQAQHLETLARQVAIALERV HYVEVAQRAVLDMESERLRNALLGAISHDVRTPLTALIALAESLPAQPDEALPAASQAIVQQAHQLHALVSNLLDMA RLESGLAGGSVRLRRDWQSVEEVVGSAIRAARPALGALEVRTALPADLPLVEFDAVLIERVLVNLLENAAKYGALPI DIAAEALPGTLRIRVRDHGPGLPAALRGREHTLFDKFTRGQSESPTPGVGLGLAICRAVVLAHGGDIAASGAGAGP GAEFTVTLPRRNPPAVGEAAELPDEDASDSPGADRNLS	24~~KdpD (1.99069E-115)~~233;X;261~~Usp(5.4299E-25)~~356;X;434~~DUF4118 (0.000000000004587 02)~~520;X;551~~GAF (0.000000000001281 67)~~663;X;680~~HisKA (0.000000000547159)~~742;X;799~~HATPase_c (3.52845E-18)~~881	KdpD protein
	7E-12	54.8	11.2	1.3E-11	54	7.7	1.4	1	A8GB59_SERP5	Histidine kinase (EC 2.7.13.3)	Spro_1245	Serratia proteamaculans (strain 568)	897	399741	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia proteamaculans, Serratia proteamaculans (strain 568)	>tr|A8GB59|A8GB59_SERP5 Histidine kinase OS=Serratia proteamaculans (strain 568) GN=Spro_1245 PE=4 SV=1MVEEEQQRPDPDSLLALANEKPRGRLKVFFGACAGVGKTYAMLQEAQRLRAQGLNVLVGVVETHGRSETA ALLGGLDLLAQKRIQYRGRMVQEFDLDAALARHPALILMDELAHSNAHGSRHPKRWQDVEELLDAGIDVLTTVNV QHLESLNDVVGGVTGVRVRETVPDHVFDEATEVVLVDLPPDDLRQRLNEGKVYIPGQAERAIEHFFRKGNLIALRE LALRRTADRVDDQMRAFRDTQGRERVWHTRDSILLCVGHNSGNEKLVRIAARLAARLGCHWHAVYVETPKLHRL PESQRRAILRALRLAQELGAETATLSEPDEERAVLRYAREHNLGKIIIGRRSEQRWKLRGSFADRLGKLGPDLDLVI VALENDSPPQPGKEHDSRNFGEKWRMQLRGCAVAVALCALITLLSQWLLPGFDQANLVMVYLLGVAIVALFFGR WPSVLAAVINVASFDLFFVQPEWSFAVSDMQYLLTFGVMLTVGITIGNLTAGVRYQARVARYREQRARHLYEISR GLSQALTTEDIAKTSRHFLSSSFQAKTVLLLPQEDGKLQQMVGETGGLLSVDEAIARWSFDKGMPAGAGTDTLPG VPYQLLPLATSKQTFGLLAIEPSNLRQLMVPEQQRLLQTFAVLIASALERLHLARSAEEAKLDAEREQLRNSLLAALS HDLRTPLTVLFGQAEILTLDLAAEGSNHATQASQIRQQVLSTTRLVNNLLDMARIQSGGFNLRKEWQSLEEIVGAS LHMLEPLMTQHQIKVELPAELVLVNCDGSLLERVFTNLLENANKYAGYDATIGIRAHTLPEWLEVEVWDDGPGIPE GKMQLIFDKFSRGNKESAIPGVGLGLAICRAIIEVHGGRIWAENGANGGASFRFVLPLEKPPEIDSEAFDL	23~~KdpD (1.04268E-108)~~231;X;254~~Usp(1.15088E-40)~~374;X;404~~DUF4118 (4.3445E-21)~~502;X;528~~GAF (3.2978E-16)~~646;X;663~~HisKA (0.000000000437894)~~728;X;781~~HATPase_c (8.2579E-31)~~882	KdpD protein
	8E-12	54.6	8.5	8.4E-12	54.6	5.9	2.4	1	A5N1X9_CLOK5	Histidine kinase (EC 2.7.13.3)	CKL_3117	Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	617	431943	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium kluyveri, Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	>tr|A5N1X9|A5N1X9_CLOK5 Histidine kinase OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=CKL_3117 PE=4 SV=1MKPVTKDMSVMLSMIKIAIIIFIAVIIYINLPNYWIYLYIKENINFSLYTTAFLSGILALICIMWLIINTKIERSSNVFRK SWLIETILFTLLISLPIYMSNSYENEYKYLFLLLIIASVIQYGSRYGIITAFFSSFFILGVDLLYAPTINDINVYFQKDLILVG IFIFISWILGYYMDIEAENNRNKDNKLDLLNCKLKEQNIKRKNIEFSLFKNEMCFHMLFEDSVNSIIVHDNGRIIYANQS ASRLLGCEDPLKLNDKSLYDHYRDEDISSIRKKYINIIDEKLSKIVNEENILNCKGNTISVKNTSSFFIYDGKPVILTFLL DLTSQKQMESLKNTAEKNLKLLLNETKEFNTLIMDFFINMSHEFKTPINVIFVAIQTMDIYLNKYDSEDMKKCKSYLKT MKQNCLRLIRLINNITDITRVDSGFISLNKKNMDIVSVVEDITQSVASHIDSKNIELIFDTNTEEKIMAFDPNKMERIML NLLSNAFKYTNSQGTIYVNVEDRGDTVLITVEDDGDGIPEDKLQVIFERFGQANRSLSREHEGSGVGLYLVKSFVT MHNGKIEVTSVQGRGSKFSIELPVEIIDKNEFENNTPFKTSVEKIDIEFSDIYSLTK	8~~DUF4118 (5.08748E-20)~~184;X;231~~PAS (0.000134253)~~281;X;355~~HisKA (0.000000027065)~~424;X;479~~HATPase_c (2.21061E-31)~~582	non-KdpD DUF4118 protein
	8E-12	54.6	12.8	1.6E-11	53.7	8.8	1.5	1	A0A068QT51_9ENTR	Sensor protein kdpD (EC 2.7.13.3)	kdpDXDD1_1326	Xenorhabdus doucetiae	738	351671	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus doucetiae	>tr|A0A068QT51|A0A068QT51_9ENTR Sensor protein kdpD OS=Xenorhabdus doucetiae GN=kdpD PE=4 SV=1MAQNEPQRPDPDDLLTLANKKPRGKLKIFFGACAGVGKTYAMLQEAQRLLAQGLDVIVGVVETHERQETAA LLQGLPQLPPKYFHYHERRIAAFDIDAALARHPAIILMDELAFSNPKGCRHPKRWQDVEELLEAGIDVLTTINVQHLE SLNDVVGGITGIRVRETIPDHIFDQADDVVLVDLPPDDLRQRLNDGKVYISGQAERAIEHFFRKGNLIALRELALRRT ADRVDDQMRAFRDTQGREPVWHTRENLLLCIGYNAGNEKLIRKAARLAAKLDCVWHAVYVETPKLHRLPKNKRR TILQALKLAQDLGAETATLSDSHEEKAILRYAREHNLGKILIGRYYNSHTNFFGFKWHRDFSERLGKLGPDLDLIIVA LEDKKRGDKEPKDNRTFNDKWRISIQGFLMAIVLCALITLFSRTFLLTLDQANLVAIYLLGVVIIALFYGRWPSVFAAF VNVISFDIFFVQPHWSLEVKNMQYLLTLTVMLIVGAVVGNLTAGIRYQARVARYREQRTRHLYEITRELSKALNEED VARISYHFLSNSFQAKTGLLLPDSNHHLHQVRSHNGGQMQIDNAIAKWCFEKKQPAGAGTDTLPGVPYQLLPIAN PSQVFAVLAIESPNQHQLLVPEQQRLLQIFTGLIANALERLYLARSAESAKLEIEREQLRNSLLAALSHDLLTPLTVLF GQTEMLMLDLSAENSPHTQQVNQIRQQILSTSRQVNNLLDMVPKEIPKQ	23~~KdpD (1.99942E-121)~~231;X;254~~Usp(1.00105E-36)~~379;X;410~~DUF4118 (1.03154E-20)~~506;X;532~~GAF (2.33522E-15)~~650;X;667~~HisKA (0.0000000189343)~~730	KdpD protein

	9E-12	54.6	12.6	1.7E-11	53.6	8.8	1.4	1	A7MQV1_CROS8	Histidine kinase (EC 2.7.13.3)	ESA_02644	Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	894	290339	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Cronobacter, Cronobacter sakazakii (Enterobacter sakazakii), Cronobacter sakazakii (strain ATCC BAA-894) (Enterobacter sakazakii)	>tr|A7MQV1|A7MQV1_CROS8 Histidine kinase OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=ESA_02644 PE=4 SV=1MTEEPMRPDPDRLLIQTQGRTRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGLDILVGVVETHGRQETAALLKGLAIQPLKRIHHRGRVVQEFDLDAALARNPALILMDELAHSNAPGSRHPKRWQDVDELLDAGIDVFTTVNVQHLESLNDVVGGVTGIQVRETVPDPIFDAADEIVLVDLPPDDLRQRLHEGKVYIAGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAWRDRQGQEKVWHTRDAILLCIGQGAGNEKLVRTAARLAARLGSVWHAVYVETPRLHQLPETSRRAILSALHLAQELGAETATLADPVEEKAVLRYAREYNLGKIVIGRRNKRRWWSQDTFAERLARHAPDLDLLIVALDDKPTPATAKAADNRPFMEKWRVQLRGCAVAVALCALITLVAHQWLIAFDAANLVMVYLLGVVLVALFYGRWPSVVATVINVVSFDLFFIAPRGTLAVSDVQYLLTFAVMLSVGLIIGNLTAGVRYQARIARYREQRTRHLYEMSKALAVGRSARDIAATSQQFITSTFHARGLLLLPDEHGKLQAPQPLAEITPWDEAIARWSFDKGLPAGAGTDTLPGVPYQILPLRTAGKTLGLVIVEPGNLRQLMIPEQQRLLETFTLLVASALERLFLTESEEQARLASEREQLRNSLLAALSHDLRTPLTIHVDGPLFERVLINLLENAAKYAGPRAQTGVRTSWRDDRLDLEVWDNGPGIPAGQEQAIFAKFARGNKESAIPGVGLGLAICQAIVEVHGGEIYARNRPEGGASFHVLLPNETPPELDIHEVM	22~~KdpD (4.27246E126)~~230;X;253~~Usp(4.61098E-37)~~373;X;403~~DUF4118 (1.79613E-20)~~501;X;529~~GAF (2.65919E-14)~~644;X;661~~HisKA (0.00000000277971)~~726;X;779~~HATPase_c (4.16095E-27)~~880	KdpD protein
	9E-12	54.5	7.1	1.6E-11	53.7	4.9	1.4	1	K4KZA8_9FIRM	Histidine kinase (EC 2.7.13.3)	kdpD DCF50_p401	Dehalobacter sp. CF	515	1131462	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Dehalobacter, Dehalobacter sp. CF	>tr|K4KZA8|K4KZA8_9FIRM Histidine kinase OS=Dehalobacter sp. CF GN=kdpD PE=4 SV=1MKKMNERGNLATPYLMSTILTSALTLLLSPMKEILGQVNISMLYLLPVLLSAACWGRWPAVFTAGIGVITFDYFFVPPYFTFTVDDFRYLISFTILMLVGFSTGTLSARLKDQIINSRQREQQVSTLYSLSRELTAVDNLEVVLDNIARKIADTLDAQVVILLPDERGELILRQSSNPEHFLNENELAAAAWVYAKGLKAGLGTEVFESPSSLYLPLLMEQGNQGVLGISLNHINRGEHINAELIRFLEAFAGLTAIAVNRIKLADEAKKAHTLAESERLRTALFNSLSHDLRTPLSSIIGAATGLIEDHDGLYSSDARHDLLQTILQGAERMKRFVNNLLDMARLESGMIKLNKDWCDMQDIMGVAVSSLGTMLTGRKLEINIPEDLPLVQADCVLIEQVIVNVLDNAVKYSEQDSAITIHVRLQSNNLEIAIANRGNPIPEADLSKVFHKFYRLSSPLQVSGSGLGLSICKGIIEAHHGNIWAENNKLSGVTITFSLPLSNECSEKVPLYEGG	37~~DUF4118 (0.000000000000168792)~~113;X;139~~GAF (0.00000000224808)~~261;X;278~~HisKA (0.000000000000882417)~~345;X;398~~HATPase_c (5.6849E-26)~~499	non-KdpD DUF4118 protein
	9E-12	54.5	12.4	1.5E-11	53.8	8.6	1.3	1	F0TA31_METLA	Osmosensitive K channel His kinase sensor	Metbo_1758	Methanobacterium lacus (strain AL-21)	651	877455	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium lacus (strain AL-21)	>tr|F0TA31|F0TA31_METLA Osmosensitive K channel His kinase sensor OS=Methanobacterium lacus (strain AL-21) GN=Metbo_1758 PE=4 SV=1MKPQYSRPDPDELLRKIKEEERSNKSKKGHLKIFLGYVAGVGKTYRMLSEAGFLCQKGYDVVAGVVETHGRADTEKLLQGLNIIHKKEIEYNGITIGELDIDKILDVRPEFVLVDELAHTNVPGSRNLKRYQDVEELLKAGINVYSTLNIQHIESINDIVYQITGVKVKETVPDKIIDLADKIELVDLPIDELIDRLKDGKVYIPEKAKDAMNKFFTKRNLVALREMALRYATVHVDYDMDHYLKKENILGPWETSNKIMACISPNNSSRRLIRIAHRFSDRFNAEWFAVYVEPSYKIRQSPDELRKLEINLQLAEKLDGKVFRLTGSISDEITKFADSENITLIMMGHSRRSRLKELIEGSIINQVIQKSDAQVLVVENEKQETEVTDTVNSMDFKPYGRNIKPYLFSFLSISFTVFLCYLIRPFIEAINIPMIFIIPVVFTSLIYGRKAGILASILAVISFDFFFVLPYYSLSVADVRFIPTFLVLLIVGIITSLLADSVRNQVRVTRQREKFISALYDFSKDLLSSQDLNDIVDRSTKYISETFNSDVLIMLPDEEGRLVTYMNSEDSDFNDNDMGVSNWVFKQDKSAGYGTDTLSSSRWYQVPLGVQNTTIGVIAIAPKGPMGNEQKHLVEAFARVVALALSNSIQT	26~~KdpD (2.09484E113)~~236;X;258~~Usp(1.13074E-33)~~378;X;405~~DUF4118 (7.10739E-20)~~505;X;531~~GAF (0.000000000027024)~~647	KdpD protein
	9E-12	54.5	14.6	1.8E-11	53.6	10.1	1.4	1	Q6D7I6_PECAS	Histidine kinase (EC 2.7.13.3)	kdpD ECA1339	Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	910	218491	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pectobacterium, Pectobacterium atrosepticum (Erwinia carotovora subsp. atroseptica), Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) (Erwinia carotovora subsp. atroseptica)	>tr|Q6D7I6|Q6D7I6_PECAS Histidine kinase OS=Pectobacterium atrosepticum (strain SCRI 1043 / ATCC BAA-672) GN=kdpD PE=4 SV=1MIDGEDRRPDPDSLLAQVGTPPRGKLKIFFGACAGVGKTYAMLQEAQRLRAQGLDIIVGVVETHGRSETAALLDGLPQLPLKHLRHHGRHTVEFDLDAALARCPALILIDELAHSNVNGSRHPKRWQDVQELLDAGIDVFTTVNVQHLESLNDVVGGVTGIRVRETVPDPIFDQASEVILVDLPPDDLRQRLNEGKVYLPLQAERAVENFFRKGNLIALRELALRRMADRVDDQMRAMRAGQGREQVWHTRDAILLCIGHGTGNEKLVRTAARLAARLGSAWHAVYVETPRLHRLPEPQRRAILRALKLAQDLGAETVTLSEPDEELAVLRYAREHNLGKIVIGRHVEQRFGWWWRTRFAERLGRLGPDLDLVVVAVQDDAPAAPIKTPDARGLVEKWRMQLFGCGLATLLCAFITLLASWSPFAMLEPVNLVMIYLLAVVIVALFFGRWPSVFAAVINVASFDLFFILPSGTFAVSDAQYLVTFAVMLGVGLLVGNLTAGVRYQARVARYREQRVRHLYEMSKALNRSLSSADIVEASQHFLSTTFQAKIAVLLADSLHHTSPDLPQPARDNQQLIVDNAIARWSFDHRAPAGAGTSTLPGVSYQILPLATTQQIFGVLAIEPSNARQLMIPEQQRLLETFTVLIANALERLHLVQSTENARLDAEREQLRNSLLAALSHDLRTPLTVLFGQAEILTLNLASEGSPYAQQANQIRQHILNTTRLVNNLLDMARIQSDGFNLRKEWQTSEELIGSALQQLESALAKNTIQVNLPDEMVLVYCDAGLVERVFINLLENALKYAGEQATIVITAHVVPQTDTQENALEIIVMDNGPGIEHGQESIIFDKFSRGHKESSIPGVGLGLAICRAIVEIHGGRIWATHVESGGAAFHFTLPLSAPPDLEPEDIEEH	23~~KdpD (3.26839E124)~~231;X;254~~Usp(9.25612E-42)~~376;X;407~~DUF4118 (6.28753E-20)~~505;X;534~~GAF (3.64645E-15)~~652;X;669~~HisKA (0.00000000030517)~~734;X;788~~HATPase_c (7.2271E-27)~~894	KdpD protein
	9E-12	54.5	12.4	1.4E-11	53.9	8.6	1.3	1	A9F786_SORC5	Histidine kinase (EC 2.7.13.3)	kdpD sce1355	Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	910	448385	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Sorangiineae, Polyangiaceae, Sorangium, Sorangium cellulosum (Polyangium cellulosum), Sorangium cellulosum (strain So ce56) (Polyangium cellulosum (strain So ce56))	>tr|A9F786|A9F786_SORC5 Histidine kinase OS=Sorangium cellulosum (strain So ce56) GN=kdpD PE=4 SV=1MADASDERPDPEALLAAAREEEERGKVGKLKIFFGAAPGVGKTYAMLEAARSLRGEAVDVVVGWVETHGRAETEALLDEPPPLPRLPAVEVEHRGRTLREFDLEAALKRRPKLLVVDELAHTNAPGLRHPKRWQDVMDLLDAGIDVHTTVNVQHIESLNDVVAQVTGVVVRETVPDSMIERADEIELIDLPPDDLLERLREGKVYLSEQIERAASNFFRKGNLIALRELALRRTAERVDDQMRGYMRAHGIQKTWAVAERIAVCVGPSPMSARLIRATRRMAGGLKAEWHAVYYVQTPAQARLSEADRERVDRNLALAERLGATTVQLHGAEVAGEVLRYARQHNVNKIVVGKPTHPRWKDLIYGSLLDDLVRQSGDIDVHVIQGAAEAAKPEPGAPERRGLRPLAYAWGACVAVICTLVSWLMHPFSDLANLIMVYLLGVVFVASRFGAGPSVLASVLGVAAFDFFFVRPYLTFAVGDLRYLVTFAIMLGVGLVIASLTARIRGQAESASEREQRTAALYAMSREGIDELSLSAARHVREVFGADAVVLLPGADGRLAARAGTAEDLVAGERERAVAEWAYARGKAAGAGTDTLPSASAMHLPLQGSAGPIGVLSVRPSRPWPFLDLSRRELLGAFATQTALALERALLARQAQRARLEAQAEELRNALLSSVSHDLRTPLATITGAAGALLDDGNDGAALDLAARRDLTQTVLEEAQRLERLVRNLLDMTRLESGALAVRKEWLPLEEVVGAALNRVEEHLRGREISIELDRATELVPMDGVLIEQVLINLLENALKYSPAGSPIGIRGFTEGNVATLEINDRGPGIPPPGEEEAIFEKFYRGRGHTQRGIGLGLTICRGIVTAHGGRVAAENRPHGGAAFRVTLPIEGRPPPNLARPELPAAAGA	25~~KdpD (3.63389E111)~~238;X;260~~Usp(7.25764E-46)~~382;X;405~~DUF4118 (4.9917E-20)~~505;X;532~~GAF (0.000000000060270)~~645;X;668~~HisKA (0.000000000000531594)~~737;X;790~~HATPase_c (2.8771E-27)~~890	KdpD protein

	9E-12	54.5	5.7	2E-11	53.4	3.9	1.6	1	A0A089YR56_9PSED	Histidine kinase (EC 2.7.13.3)	LT40_01790	Pseudomonas rhizosphaerae	878	216142	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas rhizosphaerae	>tr|A0A089YR56|A0A089YR56_9PSED Histidine kinase OS=Pseudomonas rhizosphaerae GN=LT40_01790 PE=4 SV=1MSDSGRADALLAALPRNGRGRLKVFLGAAPGVGKTYAMLQAAHARQRQGIEVLAAVVQTHGRAETEALLVGLPQQALRRSQYRDVILEEMDLDAVLAARPALALVDELAHSNAPGSRHAKRWQDVQDLLAAGIDVYTTVNVQHLESLNDQVQSITGVQVRETLPDWVVQEADDLLLIDLPPRELLERLREGKVYVPEQARAAIDAFFTQTNLSALRELAMQTAAAQVDDDLHEGYRSLGQQAPSVRGRLLVGIVADEQAERLVRHASRVARRRHLPWSVVHVDNGRLLDETARQRLQLAQQIAERLGGEVVELRDAEVARTLLQHAGDRRANLILVGQSRRRRFGAGLAERLLRSHSGVEINVLARAQVQPSKPRRPRPVGRWREYVLALLATLLASGLAWAVAQVLDNPLSVLFLAAVLLVAVRSSPGPALSCAALSFLAYDFLFIPPNFSLSIQRQEDVLTLLFFLLMAALTGNLAARQRQQLSALRETQAHTAQLLELSRLLAAATDRQAVFSAAAQHLHGWPGLDICLLERGEQGWKVAHGSAAPFTTTELAAAQWAGNHAQPAGLGTATLPAGRWWWLPVTLEGRVLALLAVAERQPGRLDGHGRRLLGALVQPVAQALARADLAHDLEAARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALGSALAPDDRQALLEVTRDEAERLDRYIQNLLDMTRLGHGALKLARDWVAVGDIVASAVGRLRAPLAPLQVQVQVPAQLPLLYVHAALIEQALVNVLENAARFSPVGGRLQVSARVRDDSLLLAVSDEGPGIPEAERTKIFDMFYTAARGDRGGQGTGLGLAICQGMVGAHGGRVEVSSGIDGQGTCIALCLPLRAQPGADADT	18~~KdpD (3.30946E-116)~~227;X;248~~Usp(7.03663E-24)~~365;X;401~~DUF4118 (0.000000141823)~~485;X;511~~GAF (0.00090766)~~627;X;644~~HisKA (0.000000000000353906)~~710;X;763~~HATPase_c (1.79044E-25)~~866	KdpD protein
	1E-11	54.5	8.4	1.6E-11	53.7	5.9	1.4	1	M4S5E9_9SPHN	Histidine kinase (EC 2.7.13.3)	G432_12260	Sphingomonas sp. MM-1	888	745310	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. MM-1	>tr|M4S5E9|M4S5E9_9SPHN Histidine kinase OS=Sphingomonas sp. MM-1 GN=G432_12260 PE=4 SV=1MALSGDGRPDPDALLRAAAQEGRGRLKIFLGAAPGVGKTYEMLSDGAAQRQEGRDVVVGVVETHGRVETEALVRGHELIPRREVPYQGRILHEMDLDALLERAPELVLVDELAHTNAPGSRHPKRYQDVEELLAAGIDVYTTVNIQHIESLNDVVASFTRVRVRETVPDGILEMADIEVVDIPPDELIERLKAGKVYLPREATRALTHFFSKSNLSALRELALRRAAQAVDAQMLEHVRALGVGGTWAASERIVVAVSELPGADGLVRAAKRIADALHAPWTAVYIETPRAQTFGAGEHRSLAAVMNLATQLGGVVATVPATSIVAGLKAYLTDARATQLIVGKSQRSRWFELRHGSVVDRLVRETPGVAVHVLPLESPPPRTGGFRIHNAWGSRSGYAWTAAMVAGVTAIASGLFHVLDLGNVALLYLLPVMAAATLFGLRTGLFAGLTSSLAYNFFFLPPTGTLTVNNPENVISILVLLGVAIATSQLTARVRAQADMASSSARTNAALAGFLRRLTGIGDPMELARAICEDIARLFDLRVVLLVPNGGGLSLQAASHPGCDLETMELAAARWAFDTSAPAGRGSGTLASSDWYFQPLRAGDRTQGVLGLAKEDGGDPLRADQLPLLTSLVDQAALVMERFRLEEEMRDVESVRTRDRLRQALLSSVSHDLRTPLTAVIAAADQLDHGATPDLIGTIKAESARLNRFVSNLLDMARVEAGALKLNIEAIDLSDAVTGAAHDARRALEGHPVRLDVPPDLPLVRADPQLLHHCLLNLLDNAGRYGDPGTEIVIEGRHLFGHIRLAVLDNGPGLPPGREAEVFETFRRFEGSDRAIGGTGLGLAIVKAFAEAMGMSVEASNREDGSGASFALMFPSPLIVRDVAQGSV	21~~KdpD (4.77072E-119)~~230;X;252~~Usp(9.13073E-37)~~375;X;398~~DUF4118 (4.52933E-17)~~497;X;523~~GAF (0.000000000429041)~~642;X;659~~HisKA (0.00000000116109)~~718;X;780~~HATPase_c (1.90369E-18)~~874	KdpD protein
	1E-11	54.4	11.7	1.8E-11	53.6	8.1	1.4	1	D3VAM2_XENNA	Histidine kinase (EC 2.7.13.3)	kdpD XNC1_1395	Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	904	406817	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Xenorhabdus, Xenorhabdus nematophila (Achromobacter nematophilus), Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6)	>tr|D3VAM2|D3VAM2_XENNA Histidine kinase OS=Xenorhabdus nematophila (strain ATCC 19061 / DSM 3370 / LMG 1036 / NCIB 9965 / AN6) GN=kdpD PE=4 SV=1MLQNELQRPDPDDLLTLANENPRGKLKIFFGACAGVGKTYAMLQEAQRLLAQGLDIIVGTVETHERQETAALLQGLPQLSPKYLRHNNRRVAAFDIDAALARHPAIILMDELAFSNPQGCRHPKRWQDVDELLEAGIDVLTTINVQHLESLNDIVGTITGIRVRETIPDHIFDQANDVVLVDLPPDDLRQRLKEGKVYIAGQAERAIEHFFRKGNLIALRELALRRTADRVDEQMRAFRDTKGKEPVWHTRDNLLLCIGYNAGNEKLIRTAARLAAKLDCAWHAVYVETPKLHRLPEGKRRTILKALRLAQDLGAETATLSDSSEEKAILRYAREHNLGKILIGRYHDSHSNLFSRKWRPDFAERLGKLGPELDLIIVALENRKHWDKEPKDNRSFNEKWRVQIQGCIMAIILCTLTTLFSRTFLLTLDKANLVTLYLLGVVIIALFYDRWSSVFAAFINVISFDLFFVQPHWSLAVKDMQYLLTFTVMLIVGVVVGNLTAGIRYQARVARHREQRTRYLYEITRELSRALNEEDVARISYHFLSNSFQAKTGLLLPDIHHHLYQVKSNNGGQMQVDEGIAKWCFEKKQPAGAGTDTLPGVPYQLLPIATPSQVFAVLAIESANLRHLLVPEQQRLLQTFTGVIANALERLHLTRSAESAKLETEREQLRNSLLAALSHDLRTPLTILFGQTEILMLDLSAENSPHTQQVNQIRQQILSTSRLVNNLLDMARIQSGGIQLNLEWYPLEEIVGSALRSLDYSLHRYNVELTLSTHLFLHCDAALLERVFINLLENAIKYTHEQTPLGIQATIEQETEKKQVHIEIWDAGSGIPSGQEQLIFEKFSRASKESVIPGVGLGLAICQAIIEIHGGNIWATGNQKGGASFHFVLPLEDPPKIEDVQEDM	23~~KdpD (3.36359E-117)~~231;X;254~~Usp(3.22768E-37)~~379;X;410~~DUF4118 (3.97282E-19)~~506;X;532~~GAF (5.72811E-15)~~650;X;667~~HisKA (0.000000000046269)~~732;X;784~~HATPase_c (2.99107E-26)~~889	KdpD protein
	1E-11	54.4	7.8	1.9E-11	53.5	5.4	1.4	1	E1T3S2_BURSG	Histidine kinase (EC 2.7.13.3)	BC1003_2353	Burkholderia sp. (strain CCGE1003)	957	640512	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. (strain CCGE1003)	>tr|E1T3S2|E1T3S2_BURSG Histidine kinase OS=Burkholderia sp. (strain CCGE1003) GN=BC1003_2353 PE=4 SV=1MNRPDPDELLDKLQRDEQKRQRGKLKIFFGASAGVGKTYAMLQAARRRRDEGADVLVGIAETHGRGETAALLEGLELLPLAQIEYRGRKLGEFDLDAALARKPQLILVDELAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETVPDRVFDRADEVTLVDLPAEELLDRMRDGKVYLAQQAERAVRNFFRKGNLIALRELALRRTADRVDAQMHEYRADRSIERIWQARERLLVCVGPGPEAPTLVRAAARLAASLKADWIAVYVETPALQRLPDARRERTLNALKLAAELGAETATLAGTDAVAALTGYAQARNVSKLVAGASTRTGIARWLRRPLGERLAEQGSHADITLIGLSSAGGSGEQRRLLDTTANAWRDALSAARERRSPARAYAFALAICAGITAVASQLLARIDLTNLVMLYLLGVIFAAAKLGRGPGVLLSFLSVAAFDFFFVPPRLSLSVSDTQYLLTFFGMLLTSLVISHLTSSLRREARVARRREQRTGAMYAMARELAAALTAEQIVGIGSRHVSEVFGARVAILLPDSADRVRQKIEDADAAITLEGELLDTDVGQWTYDHQKPAGHGTDTLPAAAALYLPLKAPMRTRGVLAVVLRDERELSVPEQQRMLDAFAAQIALALERVHYVDIARDALVSMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAQSREQAGDARRDDELVEAIHEEALRMTGIVTNLLDMARLQAGSLQLNRQWTLLEETVGAALRACRRVLAGHPVRVELPADLPLLHLDAVLMERLFSNLFENAAKYTPPGTPLTIGAQRVEDEDGKSFVRVSVDDNGPGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEAHGGSIGAINRVSAQGAGPLAAAGAGGRVEGARFWFTLPVDTPPDVTHAADALEEESADNLRPDPPPTEPARPAHE	21~~KdpD (8.20815E-113)~~230;X;252~~Usp(5.91381E-30)~~375;X;412~~DUF4118 (1.84092E-18)~~509;X;540~~GAF (2.45705E-18)~~661;X;678~~HisKA (0.000000000000640732)~~745;X;798~~HATPase_c (6.09437E-21)~~892	KdpD protein

	1E-11	54.4	11.4	1.8E-11	53.6	7.9	1.3	1	K0CGR3_ALCDB	Histidine kinase (EC 2.7.13.3)	B5T_02498	Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	880	930169	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Alcanivoracaceae, Alcanivorax, Alcanivorax dieselolei, Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5)	>tr|K0CGR3|K0CGR3_ALCDB Histidine kinase OS=Alcanivorax dieselolei (strain DSM 16502 / CGMCC 1.3690 / B-5) GN=B5T_02498 PE=4 SV=1MKDPTTPDPDALLAVNDDTGRGRLKIFIGAAPGVGKTYAMLQAARELARQGQPVLLGVIESHGRGETEALC ANLPRLPLRPIQYRGHSFHEFDLQEALQQRPSLILVDELAHRNIPGSLHPRRYQDIEDLLAAGIDVWTTVNVQHLES LNDHIARITGVRMRETVPDALVQSARDLILVDLPPDQLLERLRQGKVYVPEQARAAMDHFFNRSNLTALRELALQT VANRIDHDVFTSMASQGVDGPWPVRPRLLVLVDGRGNDKAVVRAAARMAQRRRAPWTTLWVDTGQAPPDTQK QNLAAVFRLTEQLGGDTVTLHGHDVVGMALDHARHHNVTGIVFGRSRHRPLAGLFGRTLSQKLMRRGQDFELTCI ASAPPHHRRRWRAPGWPPARQLWLALSVVAASVLAAAVADHFLALPNLSLIFLTGVLLVASRTGMRAATFAAVLS LLTYNFFFTEPFFSLAMYHTQDILTVAFFLVIALVTGRLASRLRNQVVNLRRVGDHNRSLLRLSRKLGGATGIQDVQ REAGEYLSREFATVVKVVPSQDLDQDKGLTGSLRTAAQWALESGKQAGRGTDTLGDLPQRIFPLRFRDQSLGVL LLSADKLEGLDTAVLSHMETLANQVALALWRVQLSATLEASRVAEETERLRSALLSSISHDLRTPLSSMIGAASSLR DQASLLSEEHRRELLDAILNEGHRLNSYIQNLLDMTRLGHGTLKLARDWIAPADLIAAALKRTAPLTANLTLHRQVE ADLPLLFVHPALIEQALVNLIENAAKFSPTGGEITLVARADTDRIVVEISDQGPGIPEDQREKVFDMFFTGGDGDRG PYGSGLGLAICRGMVGAHGGTIEALPPVNGSGAHIVITLPLMEQQPDGPNHV	20~~KdpD (3.80141E-114)~~229;X;279~~Usp(3.9345E-21)~~372;X;421~~DUF4118 (2.96587E-16)~~492;X;542~~GAF (0.000000887666)~~626;X;645~~HisKA (0.000000000000083371)~~711;X;764~~HATPase_c (2.17409E-26)~~867	KdpD protein
	1E-11	54.3	13.4	1.8E-11	53.5	9.3	1.4	1	A9MK91_SALAR	Histidine kinase (EC 2.7.13.3)	SARI_02238	Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	894	41514	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica subsp. arizonae, Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980)	>tr|A9MK91|A9MK91_SALAR Histidine kinase OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=SARI_02238 PE=4 SV=1MNDEPLRPDPDRLLEQTPPPHRGKLKIFFGACAGVGKTWAMLAQAQRLRAQGLDVVIGVVETHGRKETAAL LDGLTILPPKRHSHRGRQIREFALDAALARRPALILMDELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLE SLNDVVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIAGQAERAIEHFFRKGNLIALRELALRR TADRVDDQMRAWRAHPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRLGSVWHAVYVETPTLHRLPEKQR RAILSALRLAQELGAETATLSDPAEEKAVVRYARERHNLGKIVMGRPASRRWWRRDAFADRLARRAPDLDQVIVAL EEPPARALTQAPDNRSFKEKWRGQIQGCLVAVALCAITTLIAMQWLVAFDAANLVMLYLLGVVVIALFYGRWPSVV ATVINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGVRYQARVARYREQRTRHLYEMSKALAVGR SEHDIAVTSEQFIASTFQARSQILLPDAHGKLLPLTHQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPL KSADKTHGLAIVEPGNLRQLMVPEQQRLLETFTLLVANALERLTLTASEEQARLASERESIRNALLAALSHDLRTPL TVLFGQAEILTLDLASAGSPHARQASEIRQHILNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGL LHPITLSLPQQLTLIHVDGLLFERVLINLLENAVKYAGPQASIGIDAAVKDDRLQLDVWDNGPGIPAGQEQTIFDKFA RGNKESAVPGVGLGLAICHAIVEVHGGTLTAYNRSQGGACFRVTLPQGKPPELDDFHEDM	20~~KdpD (4.65186E-126)~~230;X;253~~Usp(1.23725E-42)~~373;X;403~~DUF4118 (5.44168E-21)~~501;X;537~~GAF (0.000000000001040 32)~~644;X;661~~HisKA (0.00000000255221)~~726;X;778~~HATPase_c (2.36633E-30)~~879	KdpD protein
	1E-11	54.2	16.2	2E-11	53.4	11.2	1.4	1	C4LDL9_TOLAT	Histidine kinase (EC 2.7.13.3)	Tola_1195	Tolumonas auensis (strain DSM 9187 / TA4)	897	595494	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Tolumonas, Tolumonas auensis, Tolumonas auensis (strain DSM 9187 / TA4)	>tr|C4LDL9|C4LDL9_TOLAT Histidine kinase OS=Tolumonas auensis (strain DSM 9187 / TA4) GN=Tola_1195 PE=4 SV=1MPLDNDDQRPDPDELLAEVRSPRGRLKIFFGACAGVGKTYAMLQEAKRLRAEGLDVLVGVVETHGRSETAA LLEGLTPLPLKQVHYRKHTFHEFDIDGALSRAPALVLVDELAHSNMPGSRHPKRWQDVEELLAAGIDVLTTLNVQH LESLNDIVGSITGIRVRETVPDRLYEEADEIVLVDLPPDDLRRRLDEGKVYLPQQAERAIEHFFRKENLIALRELALRC TADRVDDQMQAYRHSGEPVWHTRDAILVCIGPGSGNEKLVRVAARLASRLGCVWHAVYVETPRLHRLPEQERR SILSTLHFAQELGAETSTLPAQDEADAILYYAREHNLGKILIGRHQKKPWYRWGQSRFAHRLGTKGPDLDLLIVSLT DTEHAASTLLPADIRHKDEKWQREATGIGAALLSCIVITFLSTILVSYLAPLNIVMLYLLGVVFVALQYGRMSASIAAIL NVASFDFFFIAPHFSFAVSDVQYLLTFAVMLLVGLLIGQLTAWARYQARVARYREERARHLFEMAKELSSALTAEDI AHISAHFLNRSFRANSMLLLPDDQKILHCVGKKPLQVDHAIAQWCFDHNAHAGMGTDTLPAAAQRYVPLITPLQTL GVLMLEPANLRLLMIPEQQRLLDTYALLISVALERLKFARVAETAKLQSETERLRNALLAALSHDLRTPLTVLFAQAEI LMQSLALEQSPHIQQANAIRTQVLGTTRLVNNLLDMARLESEGVHLRKEWQSLQEIAGSALATLNIPLTGHPLNINIP PDLPLLHCDGVLIERVLVNLLENGCKYAGDGITIGIDVTESKDFLQVTVWNLGPELPVGKEKLIFEKFARGEKESSIP GIGLGLAICRAIVETHGGKIWAENRVGGGVNFHFTLPLQPLPELEPELVNNNE	23~~KdpD (7.10733E-125)~~231;X;252~~Usp(2.2779E-41)~~374;X;407~~DUF4118 (2.23453E-21)~~503;X;531~~GAF (0.000000000004174 2)~~644;X;661~~HisKA (0.00000000419789)~~726;X;779~~HATPase_c (6.71829E-25)~~880	KdpD protein
	1E-11	54.2	7.5	2.1E-11	53.4	5.2	1.4	1	Q2IPD8_ANADE	Histidine kinase (EC 2.7.13.3)	Adeh_0892	Anaeromyxobacter dehalogenans (strain 2CP-C)	902	290397	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Anaeromyxobacteraceae, Anaeromyxobacter, Anaeromyxobacter dehalogenans, Anaeromyxobacter dehalogenans (strain 2CP-C)	>tr|Q2IPD8|Q2IPD8_ANADE Histidine kinase OS=Anaeromyxobacter dehalogenans (strain 2CP-C) GN=Adeh_0892 PE=4 SV=1MTSPDQRPDPDALLAHARAEEDRARRARFKVFFGFAPGVGKTYRMLQVARDLVAEGVEVVIGAVETHGRY DTAGLMLGLEVLPRRALPHHGRVVEEFDLDAALARRPRILLLDELAHANAPGSRHAKRWQDVVELLAAGIEVYTTL NVQHVESLNDVVAQITHVQVRETIPDSILDRADEVELVDVAPEELLERLREGKVYVPEQAALAREHFFKRGNLLALR ELALRRMADRADVDVLAFREAHGVRRAWATAERVLVCVGHAPDSARIVRAGRRIAAGLRAPWFAAAVEATGQPP LPQEDRDRLEAHLRLAESLGAEVVRLSGVRVSDGILDFARRRNVSRIVLGKPRHPRWRDRLRGSLVDEVIRGSGDI EVHVLAGTDGDGPGRAAPARREGPTPLREHLRAVAIMGVTTALAAAAARALLHVPDVEMLFLLGVMVVALTSGRRA SVVAAVLAVTCYDFFFVPPSFTLGVTDARYLLTFAMMLGVGVVIGTLTLRLREQQQAAVARERRTSAVYALGKELA AAADAAGVGAACVGAVAEAFDCAAVFLVAKDRETLEPLAAVPAGEALTAGARAVAQWAHEHGRPAGRGTDTLP GEPVLCLPLRTSGDVLAILALRAPRERTLDGEQRELVESLGRHAAVALDRVRLADEARRSALRARTEELRSGLLSA VSHDLRTPLAAITGASTLLLDAAVADPAVRRELVATVVEEAERLERLVSDLLDMTRLDSGVVEPRREWVPLVEVVG AAMNRVERALGNRPVAIALRDDLPLLSIDPILIEQLLVNLLENATKYTPPGTEISVAAVREGGTLVIEVADRGPGIPAG EEERIFERFHRAARPGVRGVGLGLPIARAIAQAHGGRLTAASRPGGGSVFRLTLPVQSPPPAPPEPAPPRGGPA	24~~KdpD (6.30911E-101)~~218;X;256~~Usp(9.47298E-40)~~379;X;429~~DUF4118 (0.0000000005307)~~502;X;536~~GAF (9.87157E-16)~~647;X;664~~HisKA (2.41127E-14)~~729;X;782~~HATPase_c (1.26335E-29)~~882	KdpD protein

	1E-11	54.2	6.8	2.4E-11	53.2	4.7	1.5	1	A7HF03_ANADF	Histidine kinase (EC 2.7.13.3)	Anae109_3103	Anaeromyxobacter sp. (strain Fw109-5)	522	404589	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Anaeromyxobacteraceae, Anaeromyxobacter, Anaeromyxobacter sp. (strain Fw109-5)	>tr|A7HF03|A7HF03_ANADF Histidine kinase OS=Anaeromyxobacter sp. (strain Fw109-5) GN=Anae109_3103 PE=4 SV=1MRGSLPVAIDTTTQRPRPRAPRTRAGYLNAVAAMAATTAVATAARALGLPDVEMLFLLGVMITALSSGRRAALLAAALAVVSYDFFFVPPPYTLDISDARYLLTFAMLFGLSVVIGTLTLRLREQRQAAVERERRTAALYALSRELGAALDEESVANVSVLAVAHAFEAEAVFLRARGGELAAIAASPPAAVLGPSERALAQWVAEHGQAAGRGTGTLTGEEVLCTPVRAWGDALAVLAVRTPEPRDLDLEQRGLLEAVARQAALALDRVRLAAEARQAELRARTEALRSGLLSSVSHDLRTPLAVITGAASTLRADLALEPETRRDLSDAICEEAERLERLVANLLDMTRLDAGAVEPRREWVPLVEVLGGALTRLDRRLAGRRVVTALPDDLPLVSLDPVLVEQLLVNLLENAAKYTPAGSTVEIGARSEGDTLCVEVGDRGPGIPPGDEERIFERFHRGAHAGVRGVGLGLPIARAIAQAHGGRLVAANRPGGGAVFRLTLPMSSEPPRAAEPAGESSA	52~~DUF4118 (0.00000000213715)~~125;X;151~~GAF (0.000000000150579)~~269;X;286~~HisKA (0.000000000000109955)~~351;X;405~~HATPase_c (1.97329E-29)~~504	non-KdpD DUF4118 protein
	1E-11	54.1	8.3	1.9E-11	53.5	5.7	1.3	1	A0A052IKP7_9BORD	Histidine kinase (EC 2.7.13.3)	L539_3539	Bordetella hinzii 5132	907	1331257	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Bordetella, Bordetella hinzii, Bordetella hinzii 5132	>tr|A0A052IKP7|A0A052IKP7_9BORD Histidine kinase OS=Bordetella hinzii 5132 GN=L539_3539 PE=4 SV=1MAEPGARRPDPDRLLQSLRQEEQAARRGRLRIYFGASAGVGKTYAMLAGAHAQMAQGTDVLAGVVETHGRQETRRLLEGLPQLPPRQLPYRGRELPEFDLEGALRRRPGLVLLDELAHSNAPGAQHAKRWQDVQDLLHAGIDVWTTLNVQHLESLNEAVGGITGVRVWETVPDDIFDQADEIILVDLSADELLRRLKDGKVYVPEQARHATRNFFRKGNLIALRELALRRTAEHVDEDVQAYRRDAAIQPVWRTREALAACIGPDGDAEHLVRSAHRLAQQLDCEWHAITIEGLRVQPPPEGQARRLERALALAESLGAHCETLAGTDRVEATARYARRHNVTKIVVGRAQGGWARVPWLDRLLTPGRLWHGRGFAEQLARACPDIDILRVAAPAHAPAPPAGREPPSPARAAPRRWSGYGWALAYCALATGVSQAAFPLLHQTNIVMFYLLAVVGVALRHGRGPAALASVVSVPLFDYFFVQPISSFAVSDVQYVLTFAVLLGVGLLIGQLTAGLRAQAETSVKREADARALYEFARELSSALQSEQIVQAAETFLKAAFDADSALYILGLDDRLRLAASCRMAPEPALAQWVQDHGQPAGAGTRTLANSPLLYLPLAAPMRVRGVLVLRTARPVAASPAAWRQAQAYATLIAIAVERLHYVEVAQQALLNVEYEKLRNSLLAAVSHDLRTPLTGLIGMTETLARGSPDAATQEQALAIRDQARRMHLMVVNLLDMARLQSHGAPLKREWQSIEELVGAALATMRETLRAHRLRVLPLSDLPLVECDGILIERVLCNLLENAAKYSPPGGAITLEGQVRGEVLQVSVTDQGPGIAPGREELVFQKFTRGERESPLPGVGLGLSVCRAIIQTHHGRIWVEPAPGGQGARFAFELPLGQPPAIETETP	25~~KdpD (2.55611E117)~~235;X;258~~Usp(1.48904E-32)~~389;X;420~~DUF4118 (1.33613E-19)~~519;X;547~~GAF (1.24569E-14)~~659;X;676~~HisKA (0.000000000000267863)~~739;X;792~~HATPase_c (4.02449E-28)~~894	KdpD protein
	1E-11	54.1	10.8	2.3E-11	53.2	7.5	1.5	1	I0HQX2_RUBGI	Histidine kinase (EC 2.7.13.3)	kdpD RGE_20680	Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	901	983917	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Rubrivivax, Rubrivivax gelatinosus (Rhodocyclus gelatinosus) (Rhodopseudomonas gelatinosa), Rubrivivax gelatinosus (strain NBRC 100245 / IL144)	>tr|I0HQX2|I0HQX2_RUBGI Histidine kinase OS=Rubrivivax gelatinosus (strain NBRC 100245 / IL144) GN=kdpD PE=4 SV=1MNEPSRPDPDSLLRDVQQDEARARRGRLKIFFGASAGVGKTWAMLAAARDALAHGVPLTVGLVETHSRRDTAAMAEGLPQLPRKRCTYRGRELEEFDLDAALAFGATHEDALVLVDELAHSNVAGSRHPKRWQDVEELLAAGVDVWTTMNVQHLESLNDVVGGITGIRVRETVPDRVFDEADEVVVVDLPPDELLARLKAGKVYLPPQAERAATNFFRKGNLLALRELALRRTADRVDGEMLAWRRRNRVETVWPNREALLAAVAPGGHGETVVRRCARLAAQLDLPWHAVMVETPALQRLGPEARREALQQLKLAESLGATTATPSAPDAADGLVRYAREHNLSRLVLGRGRRRRLPWQRPTVERVAALAGELDVVQVGTAGAPAPRAAGPAPAAEGAGWAGYAAAAGACVLTALAATPLRDVLELSNIVMIFLLAVVGVGLRFGRGPAVAAAFFGVALFDFFFVQPRFSFAVSDVQYLLTFGVMLAVALAIGQLTAGLKVQAAAAMQRERRVRRLYEMTRDLSAALLPAQVAEIGARFVAAEFGARCALYATDEHDELQRLPGGEAEADEGVVSWAFRHGRAAGAGTDTLPASRCLVLPLKAPMRQRGVLAIEAGDTAALGPETMRLMETCASLLAISLERLHYVDVAQQSALQIESERLRNSLLSAISHDLRTPLAALVGLADTLALAPPGPAPRGLVDAIRESARRMAALVGNLLDMARLQAGAVRLRRAWQPLEEVVGSALAACRPVLQGRPVTVVLADGLPLLSLDAVLFERVLVNLLENAARYTPAGSALAIRAEALDQTVRLVVDDQGPGLPPGREEALFEKFERGERESATPGVGLGLAISRAIVQAHGGTIHGANRLEGGRVAGARFTIELPRGTPPEDDGSAAAAADEDIR	23~~KdpD (3.23512E106)~~237;X;260~~Usp(1.64411E-22)~~379;X;410~~DUF4118 (0.000000000001178224)~~502;X;529~~GAF (3.30803E-14)~~642;X;659~~HisKA (0.000000000000783684)~~722;X;775~~HATPase_c (4.17839E-25)~~880	KdpD protein
	1E-11	54.1	12.4	2.2E-11	53.3	8.6	1.4	1	G7W7P5_DESOD	Histidine kinase (EC 2.7.13.3)	Desor_0406	Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	917	768706	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus orientis, Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	>tr|G7W7P5|G7W7P5_DESOD Histidine kinase OS=Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) GN=Desor_0406 PE=4 SV=1MLENNNDDVLENDEGDVFLAKGKLTIFLGAASGVGKTYAMLEAALGRVSEGMDVIVGLVETHGRADTEAMLQELTVVPPKARDVSGRIAHELDLDAILARHPQLVLIDELAHSNIEGSRHQKRYMDVKELLAAGINVYTTLNIQDLETLNDIVTQITGVKVRETVPDQILETAAQIQLIDIPPEELIQRIKDGKVHVPEEETDSLKNFFRPGNINALRELALRYTAQRVDRQLESYRRDHGINGPWRTGEKILVCISASPFSAQLIRIAKRMTEKVQGELLAVHVETLRRFPSNEAEKDSMAKNLRLAEEMGAEVIGLTGNSVAEAIVELARKRNVSEIIIGKPEHTRFWELIHGSVVDKVIRQSQGISIHVIPGSQQDAGTTRIHAGWSWNDDKDEVPWWKSPQVIPYLASSLLVILLTFSISLVSSFLGLVNISLIYILPILMIAARWGILPAIVTALMGTLAFDLFFVPPLFKFTVADLRYLISFAIFMLVGLITGTLSDRLKKQVSYSRQRENSISALYSLSRDIAAVDNLEAVLECIVSNVSKTLEGQVMLLLPNENAQLVLKKKDSGINNLFDDREFQVASWVYERGLKAGRGTESWGKAKALFLPLSTEQGTQGVLGIYSNARNYQLASEQIGLLEAFAGLAAMAINRIKLAEQARVSLSLVESERLRTALFNSLSHDLRTPLASIIGASTGLLEDQNVYSPEVRKELLKTILHGAERMNRFISNLLDMARLESGMLRLNKEWCDLQDIIGVAINRLGELLTRRPLEINIPEGLPLVQADGILIEQVLINLLDNALKYSEVGSKIIISIRQNEKSLEIVVANRGHSIPEADLSKVFDKFYRLSSPLQVSGSGLGLAICKGLIEAHGGEIWADNNKLGGVTITFTLPLNDQFFGMVPEMLKESLEFRERNDS	20~~KdpD (8.59164E106)~~229;X;251~~Usp(1.96981E-37)~~374;X;408~~DUF4118 (7.09616E-18)~~508;X;534~~GAF (0.0000000155456)~~654;X;671~~HisKA (0.000000000002054)~~737;X;790~~HATPase_c (1.65055E-27)~~891	KdpD protein
	1E-11	54	7.2	2.6E-11	53	5	1.5	1	R6Q164_9FIRM	Uncharacterized protein	BN792_01760	Faecalibacterium sp. CAG:82	420	1262898	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, environmental samples, Faecalibacterium sp. CAG:82	>tr|R6Q164|R6Q164_9FIRM Uncharacterized protein OS=Faecalibacterium sp. CAG:82 GN=BN792_01760 PE=4 SV=1MDKLRQSTRLLRIVEILAAWLLSEVLVRATGTDAQFQMIDFRLMFVMLIGTVYGLNAGVLAAVLASVSLAAGYLRQGTTLMLLFYEPSNWLAFIVYFVVGASCGYVQLRNTEAARFVREENNLLRDRLRFTQRLYQDTLEDKQMFRRQILGRRDSFGKIYTVTQQLDMLQPQEIYRKTVQVMEDVLENHSLTIYRLEQNHTFARLTAASAGLEPAPAHSIEVAQRLDVLRGIEQEGLWVNRELRPGLPMYAAGVRQNGTLVVLIGLRTATEEQMTLYYQNLFRILCGLVEIALVRAFEYENAVRESWYLPGTCLLRPAVFAQKLESACTLQEDKMAHHLLLRVTGEFKNQDDLNARVERSIRSTDVAGVGPDNAIYLLMNQAEEANLPLLTKRMGEKGLHVISVPLDEQLRLVSAAKQEV	12~~DUF4118 (1.03229E-15)~~113;X;171~~GAF (2.36688E-14)~~295	non-KdpD DUF4118 protein

	1E-11	53.9	12.9	2.6E-11	53.1	9	1.4	1	B5R668_SALG2	Histidine kinase (EC 2.7.13.3)	kdpD SG0700	Salmonella gallinarum (strain 287/91 / NCTC 13346)	900	550538	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella gallinarum, Salmonella gallinarum (strain 287/91 / NCTC 13346)	>tr|B5R668|B5R668_SALG2 Histidine kinase OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=kdpD PE=4 SV=1MNDEPLRPDPDRLLEQTPPPHRGKLKIFFGACAGVGKTWAMLAQAQRLRAQGLDVVIGVVETHGREETAALLDGLTILPPKRHSHRGRQIREFDLDAALARRPALILMDELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIAGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAWRAHPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRLGSVWHAVYVETPTLHRLPEKQRRAILSALRLAQELGAETATLSDPAEEKAVVRYARREHNLGKIVMGRPASRRWWRRDAFADRLARRAPDLDQVIVALEEPPARALAQTPDNRPFKEKWRGQIQGCLVAVALCAITTLIAMQWLVTFDAANLVMLYLLGVVVIALLYGRWPSVVATVINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGVRYQARVARYREQRTRHLYEMSKALAVGRSEHDIAATSERFIASTFQARSQILLPDANGKLLPLTHQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSADKTYGLAIVEPGNLRQLMVPEQQRLLETFTLLVANALERLTLTASEEQARLASERESIRNALLAALSHDLRTPLTVLFGQAEILTLDLASAGSPHARQASEIRQHILNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLLHPITLSLPQQLTLIHVDGPLFESVLINLLENAVKYAGPQASIGIDAAVKDDRLQLDVWDNGPGIPAGQEQKIFDKFARGNKESAVPGVGLGLGLGLAICHAIVEVHGGTLTAYNRPQGGACFRVTLPQGKPPELDDFHEDM	20~~KdpD (5.97384E127)~~230;X;253~~Usp(8.48231E-43)~~373;X;403~~DUF4118 (9.35386E-21)~~501;X;530~~GAF (2.89573E-14)~~644;X;661~~HisKA (0.00000000227628)~~726;X;778~~HATPase_c (4.57784E-23)~~885	KdpD protein
	2E-11	53.9	1	1.9E-11	53.5	0.7	1.2	1	R5IWR1_9CLOT	Uncharacterized protein	BN757_01532	Clostridium sp. CAG:7	181	1262832	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:7	>tr|R5IWR1|R5IWR1_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:7 GN=BN757_01532 PE=4 SV=1MIEKENLEKNTIRKKYGWFPKISILEDLKDQYQDFLDRRQKRENWYRLILSRITGHAAVIKWGEILLFGFSEILHRVLGNSVQFRYIDVRLLYVVIIGSIYGLNEGVAAAFLAVCALTVSYIREGINGLTLFYEPSNWLPYILYFVVGAVCGYSQMKNRKDIAFANEENALLKDKFLFIL	61~~DUF4118 (0.000000000000146684)~~162	non-KdpD DUF4118 protein
	2E-11	53.8	12.9	2.6E-11	53.1	9	1.4	1	Q8ZQW4_SALTY	Histidine kinase (EC 2.7.13.3)	kdpD STM0703	Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	894	99287	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Salmonella, Salmonella choleraesuis, Salmonella enterica I, Salmonella typhimurium, Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720)	>tr|Q8ZQW4|Q8ZQW4_SALTY Histidine kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=kdpD PE=4 SV=1MNDEPLRPDPDRLLEQTPPPHRGKLKIFFGACAGVGKTWAMLAQAQRLRAQGLDVVIGVVETHGRKETAALLDGLTILPPKRHSHRGRQIREFDLDAALARRPALILMDELAHSNAPGSRHPKRWQDIEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDAADEVVLVDLPPDDLRQRLNEGKVYIAGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAWRAHPGEEKVWHTRDAILLCIGHNTGSEKLVRTAARLASRLGSVWHAVYVETPTLHRLPEKQRRAILSALRLAQELGAETATLSDPAEEKAVVRYAREHNLGKIVMGRPASRRWWRRDAFADRLARRAPDLDQVIVALEEPPARALAQTPDNRPFKEKWRGQIQGCLVAVALCAITTLIAMQWLVTFDAANLVMLYLLGVVVIALLYGRWPSVVATVINVASFDLFFIAPRGTLAVSDVQYLLTFAVMLTVGLVIGNLTAGVRYQARVARYREQRTRHLYEMSKALAVGRSEHDIAATSERFIASTFQARSQILLPDANGKLLPLTHQQGMTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSADKTYGLAIVEPGNLRQLMVPEQQRLLETFTLLVANALERLTLTASEEQARLASERESIRNALLAALSHDLRTPLTVLFGQAEILTLDLASAGSPHARQASEIRQHILNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALQMLEPGLLHPITLSLPQQLTLIHVDGPLFERVLINLLENAVKYAGPQASIGIDAAVKDDRLQLDVWDNGPGIPAGQEQKIFDKFARGNKESAVPGVGLGLGLAICHAIVEVHGGTLTAYNRPQGGACFRVTLPQGKPPELDDFHEDM	20~~KdpD (2.60408E127)~~230;X;253~~Usp(8.68063E-43)~~373;X;403~~DUF4118 (1.02757E-20)~~501;X;530~~GAF (2.81335E-14)~~644;X;661~~HisKA (0.00000000225602)~~726;X;778~~HATPase_c (1.22562E-31)~~879	KdpD protein
Disagreement between HMM and CDD prediction	2E-11	53.8	9.2	2.9E-11	52.9	6.4	1.5	1	D5CME2_SIDLE	Histidine kinase (EC 2.7.13.3)	Slit_2388	Sideroxydans lithotrophicus (strain ES-1)	503	580332	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Gallionellales, Gallionellaceae, Sideroxydans, Sideroxydans lithotrophicus, Sideroxydans lithotrophicus (strain ES-1)	>tr|D5CME2|D5CME2_SIDLE Histidine kinase OS=Sideroxydans lithotrophicus (strain ES-1) GN=Slit_2388 PE=4 SV=1MKYFSVLAATPRSLFGRMLWAVAACGIATLLAWPWRGLLDPANTAMLYVLAVALVAARAGKGAAIAAALLGSALLDFFFIYPHFTFTIGDAQHIVTAVMLAVALIIGNLTLGLQREKEAALERERQSRALYQLASQLAGALTLEQVDELTRRFLRETQACHGLLLMRHGEDALPVAQEQQPLSGKPYYAAQSALHQGAMQATLDEPGQWLFLPLHGSTYIRGVLALSASGTELLSNERRPLFEAIAALLAASVERLHFVEVAQRAQLQMTDERLRSSILSALSHDIRTPLTVLYGMADTLAQSALPDALHEMADAMRQQTLRLNSMVSNLLDMAKLRAGDIKLNMEWQPVEEVIGASIKLLGPALARHPVNVILPPDMPLLRFDAVLMERVLCNLLENAAKYALPGSPIRIAAKVDKKLACISVCNDGSQFPPDRLEDLFELFERGDAESNVPGVGLGLAICRSIVTAHGGCIHADNDNGACVTFTLPLGEPPVIELEFEHE	179~~GAF (0.000845761)~~256;X;273~~HisKA (0.0000000008736671)~~336;X;389~~HATPase_c (1.4209E-24)~~488	No DUF4118 detected by NCBI CDD
	2E-11	53.8	10.6	3E-11	52.8	7.3	1.5	1	A0A097EJN6_9SPHN	Histidine kinase (EC 2.7.13.3)	MC45_17045	Sphingomonas taxi	886	1549858	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas taxi	>tr|A0A097EJN6|A0A097EJN6_9SPHN Histidine kinase OS=Sphingomonas taxi GN=MC45_17045 PE=4 SV=1MSDAAARPDPDALLRHAAQEGRGRLKIFLGAAPGVGKTYEMLSEGAARAREGVDVVIGVVETHGRSETEALTRGYTIVPRRIVPHEGHGLAEMDIDAILARAPRLVLVDELAHSNAPGSRHAKRYQDVEELLAAGIDVYSTVNIQHVESLNDVVAGFTRVRVRETVPDRILELAEIEVVDIPPDELIERLKAGKVYLPQEATRALAHFFSKTNLSALRELALRRAAQAVDAQMLDHVRALGVGGTWAGGERVVVAVSEAAGVESLVRAAKRLADALHAPWTAVFVETPRTQAFAAVEHRQVAKVMTLATQLGGAAAAVPAQTVLAGLKAYVGEARATQLIVGKSTRSRWFELRHGSIVDRLVRETPDIAIHVLPMPAAVRGRRAAPVDRWGSRSGYVWTGAMVAAVTGVASALFHILDLGNVALLYLLPVMMAASLFGLWTGLFAGLASSIAYNFFFLPPTGTLTISNPENVVSVLVLLGIAIATSHLTARVRAQADIAAASARTNAALAGFLRQLTRLNDPVAVAQAICDEVGQLFGLHTVMLVAEGAGLAVQAANGSDYRLETMEMAAAQWAYDGGAPAGRGSATLAASQWFFQPLVTGERTLGVLGLANEAGGDPLRPDQIPLFLNLIEQATLAFERLREIETRDLGAMRERERLRTALLSSVSHDLRTPLTAVIAAAAQLHHGATPDLIATIEGEAARLHRFVANLLDMARVEAGALTLRMEAVDLADAVAGAAHDARRALDGHAVQLDVPPDLPLVRADQQLLHHCLLNLLDNAGRYADPGTPIRVEARHRYGVILLSVEDEGPGLPPGREAEVFDTFRRFAGSDRAIGGTGLGLAIVKAFAAAMGIGVEAANRQDRPGARFGLSFPAALIVRDMVEEGD	20~~KdpD (9.34891E114)~~229;X;251~~Usp(4.51817E-33)~~374;X;396~~DUF4118 (5.25962E-17)~~493;X;521~~GAF (0.00000184882)~~640;X;657~~HisKA (0.0000001075)~~716;X;778~~HATPase_c (9.87198E-18)~~872	KdpD protein
	2E-11	53.7	8.6	2.8E-11	53	6	1.4	1	T1ZG94_STRIT	Uncharacterized protein	SIR_1599	Streptococcus intermedius B196	593	862967	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus anginosus group, Streptococcus intermedius, Streptococcus intermedius B196	>tr|T1ZG94|T1ZG94_STRIT Uncharacterized protein OS=Streptococcus intermedius B196 GN=SIR_1599 PE=4 SV=1MKTLLFGNTGYVTEEFIQEAFPKDMVYLLGETHLKNSKKLKLTVFSEAEKTDMEEILRTYRFDRILYFSNSLTYKNHQVGELERLQSFLNVVKGLVYSKILYITGPEVLNRPQELEIAAESLCQHWVKVNRQSLKIVRSPYLYSARLPEDYFYRLFDKVHENRAISIEEHPDEIANFINSEDLAELISKIFDSWDDQTEILNIYNPFEITFQHVAEKLEELAFSKSKIVIDSKSPEPCLYHSTDKDNLRHRYGWFIHYSLLDDLADLYKDFVKENKASKHLEFNRLKAVVYTMRSHKTSQKIAEILLAFFLSEVLSAMLNGFNQLKMLDVRLLFITLVSTIFGTIYGIFASFLSIIGLFAATILAGGNWQSIVYNTDRWITFAAYMFVALICGIIQMKYQDEKEMLEKENQLLNDRNEFLSISYEDAVYDREQLAQQVVSNQTGTSKLFSIFQQLDKPTVEAVLNETKKIVAEQLETNSVNIYSLSEFSGFNLNRYPILAEEELKNDEVWVNKNLIPDYPVVYALKIESASGLSYLLWIEDVSYSHLSLSRMHFLQMIGGATASMLDKAGYHQAFVNLKKTTVLGTTPNGIKYGG	1~~NADB_Rossmann (0.00000000598403)~~229;X;301~~DUF4118 (1.04897E-15)~~402	non-KdpD DUF4118 protein

	2E-11	53.7	2.9	2.8E-11	53	2	1.4	1	C6BZA3_DESAD	Diguanylate cyclase with GAF sensor	Desal_2686	Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763)	469	526222	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio salexigens, Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763)	>tr|C6BZA3|C6BZA3_DESAD Diguanylate cyclase with GAF sensor OS=Desulfovibrio salexigens (strain ATCC 14822 / DSM 2638 / NCIB 8403 / VKM B-1763) GN=Desal_2686 PE=4 SV=1MFKVNTEAKRYKLSKYYETLLGLVAITAVNLIFYRHDPGFLSVSPHPYWIVILLTSTRYGFAGGLFSGIMAGLFLIVFKSLSIPDIELVDFKTLSMWGKPILFFIVGVVLGETRQLHLKEYSDVCEERDAYHDAFDKVKTKYDILSEAKQELDSKILSQESTLGTLYEAAQGLRTLSIDSIYPAVLDILREFMDVEECSIYLLDGTEFRLDTALRHGKSYLPEVVPWGESLMSIAAAQKRAVSIRDIASNESMPSGIIISAPILADNHQHVVGVLNVEKMPFLKFTSDSVRVAGLVADWCGSSVENATVFAETKDKLIADEITDAYTFDYFLRRRLREEFVRARRYELDLSLIMLEFPGLSNASDEGRDEVLMAFSMILKNQVREIDILFISDEPGAFYLILPTTPTAGARVVVNNLLSSFKALSVMAFETDQNLVELRAGVAGYTLGMEDPAELVKNVKEDMVSVLFAE	15~~DUF4118 (0.000000000113421)~~112;X;177~~GAF (7.66488E-15)~~306;X;320~~Nucleotidyl_cyc_III (0.000000000030065)~~457	non-KdpD DUF4118 protein
	2E-11	53.6	13	3.1E-11	52.8	9	1.4	1	A4W858_ENT38	Histidine kinase (EC 2.7.13.3)	Ent638_1207	Enterobacter sp. (strain 638)	895	399742	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Enterobacter, Enterobacter sp. (strain 638)	>tr|A4W858|A4W858_ENT38 Histidine kinase OS=Enterobacter sp. (strain 638) GN=Ent638_1207 PE=4 SV=1MTDEPVRPDPDRLLEQTAAPHRGKLKVFFGACAGVGKTYAMLAEAQRLRAQDLDILIGVVETHGRKETAALLEGLATQPARRTSHRGRLVTEFDLDAALARRPALILMDELAHSNAPGSRHPKRWQDVEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIQVRETVPDPFFDSADEVVLVDLPPDDLRQRLHEGKVYITGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAWRDRQGQDRVWHTRDAILLCIGHGSGNEKLVRTAARLAAKFGSVWHAVYVETPHLHALPEHQRRAILSALRLAQELGAETATLSDPAEDKAILRYAREHNLGKIVIGRRHHRRWFSRESFADKLAKRAPDLDLVIVALDDKPAPLPNRTTDVRPFGEKWRIQLRGCLVATVLCALITFVASQWLIAFDAANLVMIYLLGVVIVALLYGRWPSVLATVINVASFDLFFIAPRGTLAVSDVQYILTFAVMLTVGLIVGNLTAGVRYQARIARYREQRTRHLYEMSKSLAVGRTPRDIVQTSEQFIRSTFHASSLILLPDEHGKLRPLTSASGMTPWDDAIARWSFDKGLPAGAGTDTLPGVPYLILPLRSADKNLGLVIVEPTHLRQLMIPEQQRLLETFTLLVASALERLALTASEEQARMASERESIRNSLLAALSHDLRTPLTVLFGQAEILTLDLAAENSPHAPQASEIRQHVLNTTRLVNNLLDMARIQSGGFNLKKEWLTLEEVVGSALKMLEPGLGGRHISLNMPEPLALIHVDGPLFERVLINLLENAAKYAGSKAEIGLNADVANQALRLEIWDDGPGIPVGQEAAIFEKFARGNKESAIPGVGLGLAICQAIVEVHGGTIAAHNRPEGGACFCVTLPLDTPPELDELPEDL	20~~KdpD (1.39872E-124)~~230;X;253~~Usp(1.77942E-39)~~373;X;403~~DUF4118 (2.4022E-20)~~501;X;527~~GAF (4.33268E-15)~~644;X;661~~HisKA (0.00000000356241)~~726;X;779~~HATPase_c (3.00534E-28)~~880	KdpD protein
	2E-11	53.6	11	3.2E-11	52.7	7.6	1.4	1	A0A089PQV0_PLUGE	Histidine kinase (EC 2.7.13.3)	LG71_21445	Pluralibacter gergoviae (Enterobacter gergoviae)	893	61647	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pluralibacter, Pluralibacter gergoviae (Enterobacter gergoviae)	>tr|A0A089PQV0|A0A089PQV0_PLUGE Histidine kinase OS=Pluralibacter gergoviae GN=LG71_21445 PE=4 SV=1MTDDPLRPDPDRLLADAGRRHRGKLKVFFGACAGVGKTYAMLSEAQRLRAQGLDIVVGVVETHGRRETAALLDGLATLPPRRQHHRGRKVTEFALDAALARRPALILMDELAHTNAAGSRHPKRWQDVEELLEAGIDVFTTVNVQHLESLNDVVSGVTGIRVRETVPDPFFDAADDVVLVDLPADDLRQRLREGKVYIGGQAERAIEHFFRKGNLIALRELALRRTADRVDSQMRDWRDRQGEEKVWHTRDAILLCVGHGGGSEKLVRTAARLAAKLGSAWHAVYVETPDLHRLPEHQRRSILAALRLAQELGAETATLADPQEDRAILRYAREHNLGKIIIGRRPQRGWRRASFADRLARLGPDLDLVIVALEERPPYPGRSSDMRPWHDRWRAQLRGCGVALALCALITLVASQFLTAFDAANLVMLYLLGVVIVALRYGRWPSVLATVVNVVSFDLFFIAPRGTLAVSDVQYVLTFGVMLTVGLTIGNLTAGVRYQARVARYREQRTRHLYEMSKALARGRSARDIAATSEAFIQSTFHARSLLLLPDGEDRLAPLTEGAAVAGWDEAIARWSFDKGQPAGAGTDTLPGVPWLSLPLKTAEKIHGVLIVEPGNRRQLMIPEQQRLLETCTLLVASALERLALTSSEEQARLASERESVRNALLAALSHDLRTPLTVLFGQAEILTLDLAAAGSPHAAQASEIRQHVLNTARLVNNLLDMARIQSGGFNLRKEWLTLEEVVGSAIRTLEPGLGGRHIALSLGDPLTLIHVDGPLFERVLINLLENAVKYAGPDAQLGIRAAGQPEQLRIEVWDSGPGIPAGQEQAIFAKFARGHKESAIPGVGLGLAICQAIVEVHGGTLSAHNRPAGGASFVVTLPPETPPALDDFTEDA	21~~KdpD (1.01702E-123)~~230;X;253~~Usp(9.52751E-39)~~372;X;402~~DUF4118 (9.50497E-19)~~499;X;527~~GAF (0.000000000000154695)~~642;X;659~~HisKA (0.00000000621311)~~724;X;777~~HATPase_c (1.00729E-28)~~878	KdpD protein
	2E-11	53.6	12.8	2.9E-11	52.9	8.9	1.3	1	C1D7X3_LARHH	Histidine kinase (EC 2.7.13.3)	kdpD LHK_01575	Laribacter hongkongensis (strain HLHK9)	877	557598	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Laribacter, Laribacter hongkongensis, Laribacter hongkongensis (strain HLHK9)	>tr|C1D7X3|C1D7X3_LARHH Histidine kinase OS=Laribacter hongkongensis (strain HLHK9) GN=kdpD PE=4 SV=1MDDLRPDPDRLLAALQADEQRAARGKLTIFFGACAGVGKTFAMLQALRQQREAGCEGLVGIVETHGRQETARLLEGLPMLPSRRVAYRGHDLAEFDLDAALALHPPLIVVDELAHSNVEGSRHRKRWQDVAELLAAGIDVYTALNVQHLESLNDIVAGITGIPVRETVPDRVFDEADEVRLVDLPPDELLSRLAAGKVYLPDAAERARQHFFRKGNLIALRELALRRTADRVDAQMRAYRADRDIQPVWEARDRLLVCVGGEGGDRLVREAARLAARLQTDWIAVHVDAPRGGRRVREEALQALKLAASLGAEITTLSGGQVEEVLAAYARSRNATKLLCGVRPQSGRRWRWQRALPERIVARHPDLDVILVSSGEAARTAPRIWHPGRPVWRDYGWATLACAATTVLSALLLQVFAPANVIMLLLLTVVLVAIRWGRGPGAWAALLAVGCFDFFFVPPYWSFTVNDTQYLFTFVLMLGVALLIGQLAASLRQAADIAQLREFRAKALARLARELSGALQTEQIVSIATEQLEPLLTVRIAVLLPDAHETLKAVGALPVDREVAQWVYDNQQEAGAGTQTLSATDIRYVPLKAPMRTRGVLALQLTDSRMPDEPEWRHLLDGCCAQIALALERVHYVEVAQDALVSMEGERMRNTLLSAVSHDLRTPITAIAGLAGTLEKKLADPAQQELAHAIHGEATQMNRLVSNLLDMARLQSGGVKLRLDWQSLEEVVGSALGQLRPVLARHPVQVALPAELPLLEFDALLIERVLVNLLDNAAKYTPVGSGIRISARLDNGWLRLRVDDEGPGLPEPAESLFQPFVRGVRESATSGAGLGLALCRLIVEAHGGTIATENRHEGGARFVVALPVKTAVPEEIE	22~~KdpD (1.91906E-115)~~232;X;254~~Usp(1.18538E-28)~~373;X;395~~DUF4118 (7.83815E-14)~~494;X;521~~GAF (0.00000000302988)~~633;X;650~~HisKA (0.000000000014614 9)~~713;X;766~~HATPase_c (9.19811E-29)~~866	KdpD protein
	2E-11	53.6	9.2	3E-11	52.8	6.4	1.4	1	Q88FD9_PSEPK	Histidine kinase (EC 2.7.13.3)	kdpD PP_4158	Pseudomonas putida (strain KT2440)	884	160488	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas putida (Arthrobacter siderocapsulatus), Pseudomonas putida (strain KT2440)	>tr|Q88FD9|Q88FD9_PSEPK Histidine kinase OS=Pseudomonas putida (strain KT2440) GN=kdpD PE=4 SV=1MSDSARADALLANLPRTGRGRLKVFLGAAPGVGKTFAMLQAAHAQQRQGVQVLAGVVETHGRAETEALLGGLHQQPLLRSQYRGVTLEEMDLDGLLRAAPALALVDELAHTNAPGSRHAKRWQDVQELLAAGIDVYTTVNVQHLESLNDKVRDITGVQVRETLPDWVLQEAFELVLIDLPPRELLERLREGKVYVPEQARAAIDAYFSQTNLTALRELAMQTAAAQVDADLAHGYRQRGQEAPALRGRLLVGIDGDDQAERLVRHASRVAQRRHLPWSLVHVDNGRLRDETARHRLQAAQQLAERLGGEVVLLRAGEVARTLIQHAVERRASLVLVGQSRNRLRRRLFGAGVAARLLRESRGLEINVLDRDVQPPAPRSAVRRVWVWRHYLLALATVMAAGLAWAVSSVLALPNISLVFLAAVLLVAVRSSLGPALACAALSFLVYDFLFIPPNFSFTIQREEDVLTLVFFLLMAALTGNLAARQRRQLQALRETQAQTSQLLDLSRRLTVATDRQAIFKAAGQHLDGWQDAQVCLLERNAEGQLQVASGEACTFSDTERAAADWAWQHGQAAGHGSDTLPNGRWWWWPLAVDDQPLALLGVRPRNGQPLSDPRRRLLTALGQPLAQALARARLAEQLEAARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALGDAIPAEDRRELLEGTRNEAERLDRYIQNLLDMTRLGHGGLKLARDWVAPADIVGSALNRLRVVLAPLRVHTDVPTELPLLFVHAALIEQALVNVLENAARFSPANGRLELQVAVHDDQLRLTVSDQGPGIPEADREKIFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGQILVGEGIDGQGTSITLCLPLPPQPEAESETP	18~~KdpD (8.60373E-111)~~227;X;248~~Usp(1.87446E-29)~~365;X;389~~DUF4118 (1.36702E-19)~~489;X(160);649~~HisKA (0.000000000005195 65)~~715;X;768~~HATPase_c (2.32701E-26)~~871	KdpD protein

	2E-11	53.5	10.3	3.2E-11	52.8	7.2	1.4	1	I3Y596_THIV6	Histidine kinase (EC 2.7.13.3)	Thivi_0076	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	907	765911	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiocystis, Thiocystis violascens, Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	>tr|I3Y596|I3Y596_THIV6 Histidine kinase OS=Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) GN=Thivi_0076 PE=4 SV=1MSDGRPDPDALLERIKEDEQRAARGRLKVFFGASAGVGKTYAMLSAARAQAEQGVDLVVGVIETHGRRETEALLTGLERLPLKELEYRGRVLREFDLDGALARHPSLILIDELAHSNLTGSRHPKRWQDVEELLSAGIDVYSTVNVQHLETLNDVVGGITGIRVWETVPDHVFDAADEVVLVDLAPDELLQRLKEGKVVLPHQAERAIQNFFRKGNLIALRELALRRTADRVDRQMLDYRRDQSVAPVWQTRESVLACIGPGESAERIIRRAARIAARDDVPWHALYVETPSLQRRSRAQRQCILKRLKLAQELGAETATLSGGDPVEVVIGYARSHNLFRILLGRDHPRRWRPWYRSFADRIGGQAPELEVMLVAHDEARPPSPDQDRTDESWLERLKAPWRSYAMSLLICATAAVATAPLHSMFDLANIAMLFLLAVVVVAARYGLGPSVMASFLNVAAFDFLHVSPRFSFSISDIQYLLTFVVMLGVGLVIAQLTTGMKYQARVASRRERRARALYELSRDLSGALLPEQIAQIGQRFAESEFGARSVIMLANDSERFSALVLPAPGELPVDVGIGKWAFDHGAEAGCGTDTLPGSPLLYLPLQAPMRVRGVLALEPRDPRQIMVPEQRRLLDTFARLIAIALERVHYVEVAQTTTLQMESERLRNAFLAAISHDLRTPLTALVGLADALAMTRPPPTAEQAELAAAMREEALRMSSLVNNLLDMARLQSGSVRLNRQWQPLEEVVGSALGAVHSIIAGHRVRVDLPGDLPLLEFDAVLIERVLVNLLENAAKYTPPGSRIGIGAAPATPDRIEIWVEDNGPGLPVGKEEAVFQTFERGQTAGATPGIGLGLALCRAIMEAHGGTIRAERRPAGGARFVFSLPRGTPPVVETADEASPVEASPR	22~~KdpD (6.89278E-126)~~232;X;255~~Usp(1.31103E-24)~~376;X;405~~DUF4118 (1.20513E-18)~~504;X;531~~GAF (3.55443E-18)~~648;X;665~~HisKA (1.2578E-15)~~730;X;783~~HATPase_c (2.89319E-28)~~885	KdpD protein
	2E-11	53.5	5.6	2.9E-11	52.9	3.9	1.3	1	G8NP50_GRAMM	Histidine kinase (EC 2.7.13.3)	AciX8_3966	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	391	682795	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	>tr|G8NP50|G8NP50_GRAMM Histidine kinase OS=Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8) GN=AciX8_3966 PE=4 SV=1MSSLLKALRSTEAFLLQRKSRRAAASVGFIAVLVLLLAPLQSRVNTTTIGFALLLGVLFTAIRMGSRPALAASVVAMLGYNFFFLPPILRLTIEDPQNWVALVAFSITAVVTGQLSASAKERAIEALAAKEEIERLYSELQIAFENASQAEAIKRSDLMKSALLDAVTHDLRTPLTSIRAAATTLRKAQRSGQTLEPDLREELIALVDEESSHLDQIISGFVELARIEAGDLLLKTTWSLLQDVVQAAIRRAQSLLTKHTVAIRIPESLPLMHIDVRALAEVLYTLLDNARKYSPDSSTITISACTVGGDVEVSVEDQGKGFHSEDVPRVFDKFYRGKDVSNSRSNSPGGLGIGLSIAKALVEAHRGRIWVSNSPSSSGAIVTFQIPIRED	46~~DUF4118 (0.000000000000205554)~~122;X;159~~HisKA (0.0000000231065)~~226;X;279~~HATPase_c (1.01392E-24)~~386	non-KdpD DUF4118 protein
	2E-11	53.3	6.1	3.4E-11	52.7	4.2	1.3	1	A5MZH9_CLOK5	Histidine kinase (EC 2.7.13.3)	CKL_2263	Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	663	431943	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium kluyveri, Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	>tr|A5MZH9|A5MZH9_CLOK5 Histidine kinase OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=CKL_2263 PE=4 SV=1MSKEENTSIESSEQIMACISPSPSSEKVIQTAVKMAKSYNSKFIVLYVESIKSQTLSREEKKRLNSYFNLVEQLGGEMVTVYGDSVDKQIIQYAELRNVTKIIIGKNHKKFTSISHFYKRDLVDKIMDSNDYIDVYIIPSPFYKKEKSNFISEFSNEMLSFREIIETIIIMTIVTVIAKFLNYMGFTDVNEIMIFILGVIVVYIKTKGYLMGIISSIVGVLIFNYLFVQPKGSLQFYDKNYITTFAIMLIVSFVIGSLTNRIQKEAYNSYIREKRTEILYRASSKLLSTVGTYDVISTGIEYISRLINRNVVGYLEEKDKLSSLLIYNENKSDSKSIFLNNEKIVYWTFLNGKESGKGTDVFGQCDVYYTPVKVHNKVLGVIGISSSQGIIDREQKFIVQTIVGQMAVALDREILSSQQEASKVQIERERLRSNLLRSVSHDLRSPLAGIKGSVSTILENGAFIDENTKKDLLIGIYNDTEWLIRLVENLLSMTRFDEGNVNIAKNMELVEEVVSEAVQRSSKCFKYHRVKVNIPEKIIMVSMDGSLIEQVLINLFDNAVKFSPKHSLVEIKVYEESEDVIFEVADNGNGIPEKILPYIFDRFFTNGSKVSDSRRGVGLGLAICKSIVELHGGKITAYNKKEGGAVFKFNIPKEKREEINYER	37)~~139;X;180~~DUF4118 (0.000000000036713 6)~~265;X;294~~GAF (0.000122776)~~412;X;429~~HisKA (0.000000000040464 8)~~495;X;548~~HATPase_c (1.20418E-28)~~651	non-KdpD DUF4118 protein
	2E-11	53.3	8.3	3.2E-11	52.7	5.8	1.3	1	R6QGF8_9FIRM	Histidine kinase (EC 2.7.13.3)	BN583_01052	Anaerostipes sp. CAG:276	365	1262699	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, environmental samples, Anaerostipes sp. CAG:276	>tr|R6QGF8|R6QGF8_9FIRM Histidine kinase OS=Anaerostipes sp. CAG:276 GN=BN583_01052 PE=4 SV=1MKTGKNKESAGSRILITAGFLLLASAVGICFRELHFQESNIVIVYMLSVLLTSRFTEGYVFGLTASVIATFLFNWLFTKPYYSFAVYNPGYLITFVIMTITAICTSALTTRVKEDAVRAQEKEAEIEQERYRGNLLRAISHDLRTPLSGIMGTSEMLIGMTSEDDPRHEMAVGIHKDADWLHSLVENILSLTRLQDGRLKIKKEPEALEEVIGGAIALILKRAPEQKIQVEMPEEVLMIPMDARLMEQVFVNLLDNAVKHSEPSDQITITVEAPERESGIRIEVADRGEGISDADLPNIFETFYTSSTRDADSKQGIGLGLAICDTIIKAHGGSIRAENRADGKGAVFTLKIPVNKEEGSNGALS	18)~~115;X;129~~HisKA (0.000000000001972 02)~~193;X;246~~HATPase_c (7.36891E-27)~~352	non-KdpD DUF4118 protein
	2E-11	53.2	7.6	4.2E-11	52.4	5.2	1.4	1	F6D4T4_METPW	Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD	MSWAN_1124	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	651	868131	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	>tr|F6D4T4|F6D4T4_METPW Osmosensitive K+ channel signal transduction histidine kinase, sensor subunit KdpD OS=Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1) GN=MSWAN_1124 PE=4 SV=1MTEIKRPDPDELLSQIKEEESKQDQNKGYLKIFLGYVAGVGKTYRMLSEARVLNENKKDVVVGIAETHGRKETQDLLKGLEVIPQRKIKYKEILLEEFDIDAVLKRKPDYVMVDELAHTNVPGSRHLKRYNDVEELLSQGITVYTTLNIQHIESVNDIIKQITGVQVKETVPDRIIQMTDKIELVDLPTGELIERLKEGKVYIPEKAKQAMERFFRERNLVALRELALRYTTTHIDYDMDYFLKQEKIIGPWDASNRIMVCISSNSSSEKLIRVAHRFSDLFNVEYFAVYVDPSYKFNMKSEEVIQLDKNLKLAEELDANLFRLAGNKISDEIVSFAKSKNITLIIMGHSRRSRFQKIFEGSVINKVIQKSQAQVLILENENKEFIKTKNVKKPYFSLKKELKPYTVSILSIGLTSLICFVIRPYIEAINIPMIFIIPVVISGLVSGRKAGILSSVLAVGVFDFLFVQPYYSFSVSDVRFVPTFLVLLIVGIITSFLADVVKKQVENTRQREQFIASLYDFSKDLLISQSLRDILGRSTQYISELFNYDVIILMQDDQKRLNIVSRFGDHVSFDDNECGVSNWVFEHQKSAGRTTETLSSSKWYHIPLKVPSGILGVLAIATDESIDNEKKHLIESFASIVSLTMSNSIKE	35)~~373;X;404~~DUF4118 (1.10651E-18)~~504;X;530~~GAF (0.000000000525271)~~647	KdpD protein
	2E-11	53.2	12.4	4E-11	52.4	8.6	1.4	1	W0LHX2_9ENTR	Histidine kinase (EC 2.7.13.3)	Z042_19825	Serratia multitudinisentens RB-25	895	1441930	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Serratia, Serratia multitudinisentens, Serratia multitudinisentens RB-25	>tr|W0LHX2|W0LHX2_9ENTR Histidine kinase OS=Serratia multitudinisentens RB-25 GN=Z042_19825 PE=4 SV=1MVDDERPNPDSLLALANEKPRGKLKVFFGACAGVGKTYAMLQEAQRQRAQGLDVLVGVVETHGRGETAALLAGLTVLPQKRIQHRGRLLHEFDLDAALARHPALILMDELAHSNASGSRHPKRWQDVEELLDAGIDVLTTVNVQHLESLNDVVGGVTGVRVRETVPDHVFDEATEVVLVDLPPDDLRQRLNEGKVYLPGQAERAIEHFFRKGNLIALRELALRRTADRVDDQMRAFRDSQGREKVWHTRDSILLCVGHGSGNEKLVRIAARLAARLGCHWHAVYVETPKLHRLPEHQRRAILRALRLAQELGAETATLADPFEEQAVLRYAREHNLGKIIIGRRSEQRWKIRGSFADRLGHLGPDLDLVIVALENDTPLPLSKEHDSRTFTEKWRFQLRGYAVAVALCAMITLLSQWLLPGFDSANLVMVYLLGVAIVALFFGRWPSVLAAVINVASFDLFFVQPEWSFAVSDMQYLLTFAVMLTVGITIGNLTAGVRYQARVARYREQRARHLYEMSHGLSQALNHDDIAKTSRHFLSSSFQAKTALLLPQEDGSLRQMAGEDGGLLSVDEAIARWSYSKGTPAGAGTDTLPGVPYQLLPLSTPKQTFGLLAIEPSNLRQLMVPEQQRLLQTFAVLIASALERLHLAHSAEKAKLDAEREQLRNSLLAALSHDLRTPLTVLFGQAEILTLDLAAEGSSHAPQASQIRQQVLSTTRLVNNLLDMARIQSGGFHLRKEWQSLEEIVGASLHMLEPLLVQHQIKVELPSEMVLINCDGNLLERVFTNLLENANKYAGTEAIIGIRARAVPEWLEVEIWDNGPGIPTEQLQLIFDKFSRGNKESAIPGVGLGLAICRAIIEVHGGRIWAENGAHGGASFRFMLPLETPPALEGEGFDL	21~~KdpD (1.08473E-118)~~229;X;252~~Usp(7.51325E-39)~~372;X;401~~DUF4118 (1.87035E-20)~~500;X;526~~GAF (3.06957E-17)~~644;X;661~~HisKA (0.000000000337651)~~726;X;779~~HATPase_c (3.84237E-31)~~880	KdpD protein

	3E-11	53	8.3	4E-11	52.4	5.7	1.2	1	R5WYE7_9FIRM	Integral membrane sensor signal transduction histidine kinase	BN568_00206	Blautia sp. CAG:257	282	1262756	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	>tr|R5WYE7|R5WYE7_9FIRM Integral membrane sensor signal transduction histidine kinase OS=Blautia sp. CAG:257 GN=BN568_00206 PE=4 SV=1MMMKKKEILQSLLKLVVIVFAATVLGKIFTGLGFPETNIVVMYLLAVLLVARFTSGYQYGILSAVVSLLCYNYFFTEPYHTLAVNDPGYLITFSIMLTTSILTSALTTKEKLLTEEANERGKESQILYMLSSKLSDAADMEAVLRIAAESISHLLQVNVGCIYVGRQSEPIFIQQSGKEQIHRSVPDADEIRKRYTNLRTEYLEEEDTYGYPVNGREHLLAVVKIDKTVNEEHLQEKKKLLHSIMENVSMAMDRIEVTIERVRDRESMERERTCESFACNLS	12~~DUF4118 (2.59424E-18)~~111;X;139~~GAF (0.00114113)~~254	non-KdpD DUF4118 protein
	3E-11	52.9	10.1	6.3E-11	51.8	7	1.6	1	Q2RV86_RHORT	Histidine kinase (EC 2.7.13.3)	Rru_A1158	Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	897	269796	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Rhodospirillum, Rhodospirillum rubrum, Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1)	>tr|Q2RV86|Q2RV86_RHORT Histidine kinase OS=Rhodospirillum rubrum (strain ATCC 11170 / ATH 1.1.1 / DSM 467 / LMG 4362 / NCIB 8255 / S1) GN=Rru_A1158 PE=4 SV=1MAPADRENRPSPDALLAEAHREGRGKLKIFLGAAPGVGKTYAMLEAARERARDGVDVAVAVVETHGRRETEALVHGLDVVPKRTLEYRGRDFEEMDLDGVLARRPALALVDELAHTNISGSRHLKRWQDVQELLDVGIDVYTTLNVQHLESLNDVVERISGVRVRETLPDSVLQQADEIKLIDLAPEDLLKRLEEGKVYVPDQARRAANAFFSRGNLTALREMALRQAAERVDAQMISYMHAHAIQGPWPARERLMACIGDDLAAESVVRLAARSAERRQAPWIAVYIETARHLSLSEEVKDRIARALRLAEELGGEATTVQGDDVVAEVLSFAKARNITQIIIGRPRRHRQRWFGGGDTAKALLARAEAFNVTVIGRENASPSPIARIRRDMPKDWLGYGLATLAVALATGFSVLIDMWMPVPNISVAYLMAVLLVAMRLGLAPSIFASLLSFLIYSFLFTEPRLTLAITDSHNILTMVFFLVAAVIVSNLGSRLREQVQATRLSARRTGTLYDFSRKIAAAATQDDVLWAVVHHVASTIHGQSLILLPENDRLAIKAGYPPEDTLDDKAAAAAEWAWTHGTRAGAGSATLPTSPWLFLPLKTVRGPVGVMGVQMAGAGIPPPSEARLLETLADQAAVAIERTALVADIEAARVAGERDRLRTALLSSLSHDLRTPLVSIMGSASALVNYQDTLSDDAERELALTIQDEAERLNRFVQNLLDMTKLGAGALKPRIDWADFRDIVGGALERAKRLIGQRKVRIDLSDDFPLLCVDSVLMEQVVFNLIDNACKYTPPGSAITVWGRPRRDKVVVEICDQGPGIPEADREQVFDMFYRVKAQDAQIAGTGLGLAICRGLVEAHGGTIAAEPGINDCGTCIVITLPLLVEPELLGAEEKV	22~~KdpD (1.43916E-114)~~232;X;254~~Usp(2.01334E-40)~~377;X;400~~DUF4118 (6.33756E-19)~~499;X;525~~GAF (0.000000000013904)~~643;X;660~~HisKA (0.000000000015710)~~726;X;779~~HATPase_c (3.74927E-26)~~881	KdpD protein
	3E-11	52.9	7.1	6.4E-11	51.8	4.9	1.6	1	D5W5H5_BURSC	Histidine kinase (EC 2.7.13.3)	BC1002_0922	Burkholderia sp. (strain CCGE1002)	951	640511	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. (strain CCGE1002)	>tr|D5W5H5|D5W5H5_BURSC Histidine kinase OS=Burkholderia sp. (strain CCGE1002) GN=BC1002_0922 PE=4 SV=1MNRPDPDELLEKLQRDEEKRLRGRLKIFFGASAGVGKTYAMLQAARRRNEEGADVLVGIAETHGRSETAALLAGLDVLPLAHIEYRGRKLGEFDLDAALARKPQLILVDELAHSNVQGARHLKRWQDVYELLDAGIDVYTTVNVQHLESLNDVVGQITGIRVWETVPDRVFDHADEVTLVDLPAEELLDRMRDGKVYMAQQAVRAVRNFFRKGNLIALRELARRTADRVDAQMREYRADRSIQRIWQARERLLVCVGPGPEAPALVRSAARLAASLRADWLAVYVETPALQRLPDARRARTLNALKLAAELGAETATLAATDALDALIGYAQARNVSKLVAGASSRAGISRWLRRPLGERIAEKSGDLDLTLIRVTSERDSGEQRRLLNTTANAWREALSAARERRSPPRAYAFALAIGAAITMLSSQLIDRIDLTNLVMLYLLGVIFTAVKLGRGPGVVLSFASVAAFDFFFVPPRMSLSVSDTQYLLTFFGMLLTSLVISHLTSSLRREASVARHREQRTGAMYEMARELAAALATEQIVGIGTRHLSEVFGARVAILLPDSADQVKQKIEDPDPAITLEGDALDLDVGQWVYDQQKPAGHGTDTLPAAAALYLPLKAPMRTRGVLAVVVRDERELTVPEQRRMLDAFAAQIALALERVHYVDIARDALVNMESERLRNSLLSAISHDLRTPLTTIVGFSSMLAQGRGGQGPTDPQSAAHRNDELVEAIHEEALRMTGIVTNLLDMARLQAGSLQLNQQWTLLEETVGAALRACRRVLADHPVQVTLPADLPLLHLDAVLMERLFSNLFENAAKYTASGTPLAIGAQQIDAGGVPFVRVTIDDNGAGLPAGMEARVFEKFTRGEKESAKPGIGLGLAICRAIVEAHGGTIGALNRIAADGHVEGARFWFTLPVKTPPEAPETFDTLEDEDTPADTAADLNPLTRPAHE	22~~KdpD (1.72192E-117)~~230;X;252~~Usp(4.54522E-28)~~374;X;412~~DUF4118 (3.36527E-18)~~512;X;539~~GAF (1.05209E-17)~~661;X;678~~HisKA (0.000000000016398)~~751;X;804~~HATPase_c (1.60813E-20)~~914	KdpD protein
	3E-11	52.9	12.3	5.5E-11	52	8.5	1.4	1	A1VTB9_POLNA	Histidine kinase (EC 2.7.13.3)	Pnap_3601	Polaromonas naphthalenivorans (strain CJ2)	899	365044	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Polaromonas, Polaromonas naphthalenivorans, Polaromonas naphthalenivorans (strain CJ2)	>tr|A1VTB9|A1VTB9_POLNA Histidine kinase OS=Polaromonas naphthalenivorans (strain CJ2) GN=Pnap_3601 PE=4 SV=1MNLPAGQRPDPDELLQRLQQQEAQRARGRLRIYFGASAGVGKTYAMLGAAQRERKDGRDIVVGVIETHGRSETAELLAGLEQLPLREVAYRGRTLREFDLDAALARKPAVLLVDELAHSNVEGSRHPKRWQDVQELLDAGIDVWSAINVQHLESLNGTVGAITGIRVNETVPDTVLDAADEIILVDVTPDELTARLKAGKVYLPQQAERAAQNFFRKGNLIALREIALRRTAEHVEDDVRSYRVEKSISPVWNTEGALLACIGPHEGAEQTVRTAARLAGQLNVRWHAAYVETPRLQRLKEAERDRILAVIKLAGELGATTAVLAASDAAAELVAQAQALNCATLVVGRPALPDWRTLWSGRSMTRRLARLAPTLDIVEVADARSSRRLAPAVPRSDDDAASAWHGSLPRYAWAVASSVAITLLATPLLNVFDLANIVMLFLLGTVLVALKLGRGPAALAAFLNVAAFDYFFVAPRLSLAVSDVQYLVTFAVMLVVGLLTGQLTAGLRFQARISSSRERRAQSLFELTRDLSAALMPSQVAELGEAAVQRDFGGQALVLTTDARDQLVLPVHAPPGFDASVADWAFRHAQAAGLATSTLSAQTWHYVPLKATMRVRGVLALQPARPRWLLIPEQLQQLDTLARQIAIALERVHYVDIAQQAVVEMESERLRNTLLAALSHDVRTPLTALIGLAESLQRSQPPLEPQQAGMAQAMAQQARQLNALVSNLLDMARLQNGAVSLHRDWQSVEEVAGSAIRAAQPALNGRTVRTDIAPDLPLVEFDAALMERVLVNLLENAAKYGAPPFEIHARAAPDSLVLSVRDHGPGLPPALRGREAELFEKFTRGQAESATPGVGLGLAICKAIVDAHRGKIVAGNAQGGGAQFTITLPRGSPPEPAPE	26~~KdpD (2.27268E-120)~~235;X;258~~Usp(2.98048E-24)~~381;X;410~~DUF4118 (1.61027E-19)~~510;X;537~~GAF (0.000000000086372)~~651;X;668~~HisKA (0.00000000603536)~~733;X;786~~HATPase_c (3.07328E-26)~~888	KdpD protein
	3E-11	52.7	6.9	6.2E-11	51.8	4.8	1.5	1	A0A077F967_9PSED	Histidine kinase (EC 2.7.13.3)	PSAKL28_17460	Pseudomonas alkylphenolia	886	237609	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas alkylphenolia	>tr|A0A077F967|A0A077F967_9PSED Histidine kinase OS=Pseudomonas alkylphenolia GN=PSAKL28_17460 PE=4 SV=1MSDSNSERADALLAGLPREGRGRLKVFLGAAPGVGKTYAMLQAAHAQVRQGVQVLAAVVETHGRAETESLLAGLAQQPLVRSKYRGVQLEEMDLDGLLKAAPQLALVDELAHSNAPGSRHAKRWQDVQELLAAGIDVYTTVNVQHLESLNDQVRGITGVQVRETLPDWVLQEAFELVLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELAMQTAAAQVDADLAHGYRQLGQDAPSLRGRLLVGVDGDAQAERLVRHASRVAQRRHLPWSLVHVDNGKLRDETARQRLQAAQQLAERLGGEVVLLRAGEVAKTLIQHALERRANLVLVGQSRDRLRRRLFGAGVATRLLREAHGLEINVLDRDERPEPQSAAVKKVWVWRHYLLALVATVLAAGISWGVSGVLALPNISLVFLAAVLLVAVRSSLGPALACAAMSFLTYDFLFIPPNFSFSIQREEDVLTSLFFLLMAALTGNLAARQRRQLQALRETQEQTNQLLDLSRKLTAATDRQAVFNAAGQHLDGWNDLQVCLLERDVEGRLQVASAASVQFNDNERAAADWAWQHDQAAGLGSDTLPNGRWWWWPLSVEEQPLALLGVRPRQGQSLTAQRRRLLKALSQPLAQALARARLAEQLEAARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALGEAIPQADRQELLEGTRNEAERLDRYIQNLLDMTRLGHGGLKLARDWVAPTDIVGSALNRLRVVLAPLQVSTEVPDGLPLLFVHAALIEQALVNVLENAARFSPVNGRLQLQVSADDEQLRFAVSDEGPGIPAADREKIFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGHILVGEGIDGHGTCITLCLPLPTPPEPESEAP	19~~KdpD (5.11795E-118)~~229;X;250~~Usp(2.79571E-28)~~367;X;391~~DUF4118 (1.27522E-18)~~491;X(160);651~~HisKA (0.000000000012709 6)~~717;X;770~~HATPase_c (1.69162E-24)~~870	KdpD protein

	3E-11	52.7	12	5.9E-11	51.9	8.3	1.4	1	D3P2B3_AZOS1	Histidine kinase (EC 2.7.13.3)	kdpD AZL_b02700	Azospirillum sp. (strain B510)	912	137722	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum sp. (strain B510)	>tr|D3P2B3|D3P2B3_AZOS1 Histidine kinase OS=Azospirillum sp. (strain B510) GN=kdpD PE=4 SV=1MAEPDSDERPSPDALLEEANRERRGRLKIFLGAAPGVGKTYAMLEDAHARRRDGTDLVVGVVETHGRHDTEALLDGLDILPRRRIDYRGRPFQEMDLDAILARRPRLVLVDELAHTNIPGSRHLKRWQDVEEILDAGIDVCSTLNVQHLESLNDVVERIAGIKVRETLPDSVLHRADEIALIDLPPQELIRRLQEGKVYVPEQAKRAADHFFSAGTLTALREMALRQAAERVDAQMLRYMRAHAIAGPWPTRERILVCIGDGPQALRLVRTAKRAAERRDAPWVVLYVDTHRNHALSEEDKDGIAQALRLAAQLGGETAVVPGERAAAEILAFARARNVSQIIVGRAHPRRRLRALHQSVTTDLLARNEDFDVLVVAGEDERPARSLETRAPSVVFDWLAYVVATLTVASATAIGLAIDVWLPLPNISVAYLVGVLLVAIRHGLAPSIYASVLSFLTFNFLFTEPKYTFAITDAQNIMTVFFFLVAAVITSNLAARVRAQVETTRLSARRTANLYDFNRRRISAAVGLDDVLWAVVHHVASTMNGHSLVLLPREGRLEVAAGYPPEDTLDEKSMAAARWSWENGKTAGRGSTTLPAADWLFLPLRTGRGPMGVLGVQMTGEQQLLSPEQGRLLDTLADQAAVAIERTALVADIETARVAAETERLRSALLSSLSHDLRTPLVSILGASSSLTSYGETLAPPERMELVQTIQEEAERLNRFVQNLLDMTRIGSGALKPRTDWVDLADVIGAALERAKRMLGDRPVRLELEPGLPLLRLDPVLTGQVFFNLIDNACKYSPDGSPILLQASRAGGEVLIELCDQGAGIPEADREIFDMFYRVEAGDAQTAGTGLGLAICRGIVEAHGGTIRALPGRHGVGTCIAILLPVPAGPEIADIEGDSARGEDSGTPDSGR	22~~KdpD (1.71494E-123)~~232;X;254~~Usp(1.20723E-39)~~377;X;400~~DUF4118 (1.84251E-20)~~500;X;527~~GAF (1.01171E-14)~~645;X;674~~HisKA (0.00000000504122)~~728;X;783~~HATPase_c (1.1709E-24)~~884	KdpD protein
	4E-11	52.6	12.6	5.7E-11	52	8.7	1.3	1	R5AT69_9FIRM	Histidine kinase (EC 2.7.13.3)	BN455_00104	Firmicutes bacterium CAG:103	595	1262999	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:103	>tr|R5AT69|R5AT69_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:103 GN=BN455_00104 PE=4 SV=1MRLAQQLGAEIVTTHGEDVATQIAEYVRLSDVTKIVIGRSGVQRRHFWSEPTLTERLITLAPEVDIHIIPDVEGYKSYRRKRLLPIRPAFPTAWELLLTIGILAAATVIGWAFLRLGFANANIIMVYLLGVLLTSAFTSGYTCGVLSAFLSVILFNYFLTEPRLSLAAYGSKYPITFAVMFAAALLTGTLAAKLKAHAQLSARDAYRTKLLFDMNRQLQKAETPDEVYQMTATQIQKLMQRDVLIYPAQGDVLLDGNVYPADGSSPYCIPDTDQEQNVIQWVWQNRKRAGATTQNFPKAKRLYLAIRTGQQVFGVVGIPMEKQTQPDAFTSSVLFSILGECALALESLRNAEEKEKAAVLAKNEQLRANLLRSISHDLRTPLTSISGNADTLLHSYNVLDEQTRKQIFTDIYDDAQWLTGLVENLLSITKIADGNVKLHLSDQVVDDIVSESLRHIDRRSAEHHIAVDCGDVPLLVRVDAGLIMQVLINLVNNAVKYTPAGSNIRITAIPRDNMAEICVSDNGPGIPDELKEHVFEMFFTGGNPIGDSRRSLGLGLTLCQAIIHAHNGEMTLKENLPHGCIFSFTVPLSEVNLNE	17)~~70;X;96~~DUF4118 (7.38116E-18)~~197;X;223~~GAF (0.0000883627)~~346;X;364~~HisKA (0.000000000012192)~~430;X;483~~HATPase_c (3.47707E-27)~~586	non-KdpD DUF4118 protein
	4E-11	52.6	6.5	8.1E-11	51.5	4.5	1.6	1	Q883V3_PSESM	Histidine kinase (EC 2.7.13.3)	kdpD PSPTO_2245	Pseudomonas syringae pv. tomato (strain DC3000)	887	223283	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas syringae group, Pseudomonas syringae group genomosp. 3, Pseudomonas syringae pv. tomato, Pseudomonas syringae pv. tomato (strain DC3000)	>tr|Q883V3|Q883V3_PSESM Histidine kinase OS=Pseudomonas syringae pv. tomato (strain DC3000) GN=kdpD PE=1 SV=1MSDSGRADALLAQLPREGRGRLKVFLGAAPGVGKTYAMLQAAHAQLRQGVRVMAGVVETHGRAETEALLNGLPQQPLLRTEYRGMTLEEMDLDALLKAAPSLVLVDELAHTNAPGSRHTKRWQDIQELLAAGIDVYTTVNVQHLESLNDQVRGITGVQVRETLPDWVLQEAFDLVLIDLPPRELLERLRDGKVYVPEQARAAIDAFFTQTNLTALREMAMQTAAAQVDNDLAQGYRQLGQSAPAVRGRMLVGIDGDMHAERLVRHASRVAQRRHLPWSAVHVDDGQTLDEQSRARLQNAQQLAERLGGEAVSLRAGEVARTLVQHAIERRASVVLVGQGSRRHWRRRVFGGGVAARLLREGHGLEISVLDDSEELPDQPPRARPAREVVWFDYGLAFVATLIASLVAWGVAGVLALPNISLIFLAAVLLVAVRSSMGPALACAGLSFLAYDFLFIPPPSFSLNIQREEDVLTLLFFLLMSALTGKLAARQRRQLQALRDTQEQTSELLDLSRKMTAATDRKAVLNAAEQHFSGWKELYLCLVDRDTQGGLVVETGGPLTFSEAERAAADWAWQHDQPAGSGTGTLPSGRWWWWPITAEEGPLALLGVCAREGQSFTDQHRRLLAALTQPLAQALARAQLAQELEAARLHGETEQLRSALLASVSHDLRTPLTSMRGSIDSLLALGEAIALEDRRELLEGTRDEAERLDRYIQNLLDMTRLGHGALKLARDWVSPADIVGSALNRLRAVLTPLQVSTQVTGDLPLLYVHAALIEQALVNVLENAARFSPLGGRLQVTAGVVDSELFFSVSDEGPGIPEDERAKIFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGRLTVEEGIDGLGTRITLFLPLQAQPDAEMEEPA	17~~KdpD (2.31834E-121)~~227;X;248~~Usp(7.97106E-36)~~365;X;392~~DUF4118 (4.11961E-18)~~491;X(160);651~~HisKA (0.000000000000282655)~~717;X;770~~HATPase_c (1.35716E-24)~~873	KdpD protein
	4E-11	52.6	9.2	6.4E-11	51.8	6.4	1.3	1	B9M2Y5_GEODF	Histidine kinase (EC 2.7.13.3)	kdpD Geob_2988	Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	661	316067	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter daltonii, Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	>tr|B9M2Y5|B9M2Y5_GEODF Histidine kinase OS=Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32) GN=kdpD PE=4 SV=1MVAMTECIAKDDIQETEFPVSYGPIPFGERLMVCVSGSPFSDKLIRTTHHLAKGMNSPWMVVYIETTAGGRHLQENRERVWNNLRLAETLGAQIETVTAASVAEAIVDFAVSHKVTKIVVGKPKKPRWLEFLRPPLVDRIIYLSGYIDVYVVSIDQVETKRERNFFRKTPPWAGYATGVALVTAATLISKLVHNHIAPTNLVMIYLLVVVLAAVRLGRRAAILTATFSVLAFDFFIVPPHLTLAVSDSEYLITFLALFMVGVVISSLVATANERADAVRQREVQTSALYRLSRSLAAAVDVDSIVEAVVNNVGESLKAEVAVFLPDENRLKLHGVSHDSRWGDKEQIAAESAFYSTRTEEGEVMIPDGSNHLYLPLQTKGAVRGILGIKLNVEEEHQNQQVRRLLDAFAAQTAMALERAHLARQAEHAQILQARKELERALLNSVSHDLRTPLVSITGALSTLRNEGCAPHEKGRLELVDAAWEEAERLNRFVGNLLDMTRVEAGELKLKKEPCDIQDLVGCALAPLDARLQDREVLIDLSDDLPLVQMDMVFMTQVLVNLLENGMKYSTPRTPLAIWAKTDDDLIILAVEDRGPGVPEKELVKIFDKFYRVPVPEGAGGTGLGLSICKGIVEAHGGTIRAENIEGGGLRVLVAIPLNKEA	42)~~153;X;179~~DUF4118 (1.18011E-16)~~274;X;300~~GAF (0.000000000006326684)~~418;X;435~~HisKA (0.000000000476253)~~501;X;556~~HATPase_c (7.16357E-26)~~653	non-KdpD DUF4118 protein
	4E-11	52.5	13.7	6.8E-11	51.7	9.5	1.3	1	G8QN97_DECSP	Histidine kinase (EC 2.7.13.3)	Dsui_0272	Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	898	640081	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azospira, Azospira oryzae, Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	>tr|G8QN97|G8QN97_DECSP Histidine kinase OS=Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) GN=Dsui_0272 PE=4 SV=1MSDPLQRPDPDALLARLEAEEIQARRGRLKIFFGASPGVGKTYAMLAAARTLQSQGVDVAVGVVETHGRRETAELVQGLELLPSRQVEHRGRRLQEFDLDGALQRAPDLVLVDELAHSNAPGSRHPKRWQDVEELLAAGIDVFTTVNVQHLESLNDVVGRITGARVWETVPDRLFDAADEVVLVDLPPEELLTRLKAGKVYVPQQAERAMANFFRKGNLLALRELALRRTADRVDDDVRAYRRDQSVSTVWPTRESLLVCIGPGPGSERLVRSAARLATQLEVPWHALYVETPRYQRLPEGERGRVLKSLRLAQELGAETANRPGQDAAAAAIQYARERHNLGKVLLGRELPGDWRRWLPWRTSLARRLARQAPDLDVMQVASDGVDGEAPPLPDGPARPAAVNVRGYGLAAAAVAAVTLVATPLHGALDLANIVMLFLLAVLFAAVKLGRNPAILAAFLSVAAFDFFFVSPRLSFAVSDVQYLLTFSVMLAVALITAQLTAGLRFQVDVAQSRERRSDALYEMARELSAALTVEQIDDITRRFVQQGFQARALLLVPGQQERLSLPEGLPADLPVDLGIAQWAADHGEAAGHSTDTLPSAPMRYLPLKAPMRTRGVLAVLPREQPWLPSPEQERLLETCATLVAIAVERVHYIEVAQEALVQMESERLRNGLLAALSHDLRTPLTALVGLADSLSLGGALPPAQAELAQAIRGEAMRTSALVHNLLDMARLQSGQVTLKKEWQPLEEVVGAALQARASVLAQHRVRVDLPADLPLLEFDAVLMERVFCNLIENAAKYTPPGSLIEIGARREAERVLVSVSDNGPGLPPGKEAGLFEKFTRGQDESAIPGVGLGLAIVRAIVDAHKGKVWAENRSDGPGARFVFTLPLGQPPALPTELL	24~~KdpD (4.74322E-115)~~234;X;257~~Usp(5.27777E-38)~~381;X;432~~DUF4118 (9.68767E-19)~~506;X;532~~GAF (2.22936E-15)~~649;X;666~~HisKA (0.000000000001496)~~730;X;783~~HATPase_c (9.15842E-30)~~885	KdpD protein

	4E-11	52.5	12.8	6.9E-11	51.7	8.9	1.3	1	I2BB58_SHIBC	Histidine kinase (EC 2.7.13.3)	kdpD EBL_c26830	Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005 74) (Escherichia blattae)	894	630626	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Shimwellia, Shimwellia blattae (Escherichia blattae), Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) (Escherichia blattae)	>tr|I2BB58|I2BB58_SHIBC Histidine kinase OS=Shimwellia blattae (strain ATCC 29907 / DSM 4481 / JCM 1650 / NBRC 105725 / CDC 9005-74) GN=kdpD PE=4 SV=1MTGEPDRPDPDQLLHQLSRPPRGKLKIFFGACAGVGKTYAMLQEARRLHQQGLNILVGVVETHGRQETAALLASLPLLPPRRLLHRGRRIGEFDLDGALSRNPALVLVDELAHSNAPGSRHPKRWQDVEELLAAGIDVFTTVNVQHLESLNDVVGGVTGVQVRETVPDPIFDAADEVVLVDLPPDDLRQRLHEGKVYISGQAERAIEHFFRKGNLIALRELALRRTADRVDEQMRAWRAERGREKVWHTRDAILLCIGHTGDNDKLVRTAARLAGKLGSDWHAVFVETPRLHQLPPAQRRRILNALRLAQELGAQTATLSDPSEEKALVRYARDHNLGKMITGRRTLHRWWPRPPFADRLARLAPDLDIMVVAVDEKAPADPRKTPDNRPFGEKWRVQIQGCLVAVALCALITLFARQFMMGFDAANLVMIYLLGVVVVALFYGRWPSVLATVINVLSFDLFFIAPHGTLAVSDVQYLLTFSVMLVVGLTIGNLTAGVRYQARIARYREQRTRHLYEMSRALATTRSVRDIAATSEHFLGNSFRARCQVLTPDEHGKLTALTAPDSDPFWDDAIARWSFDKGLPAGAGTDTLPGMPWRVLPLSTPSQTLGLVVIEPENLRQLMVPEQQRLLETFTLLCATALERQLLATSEEQARIASEREQIRNALLSALSHDLRTPLTVLFGQAEILTLDLACAGSPHARQASEIREYILNTTRLVNNLLDMARIQSGGFNLHKEWLTLEEVVGSALKTLEPLAAGHPVTLDIPDPLALIQVDGPLFERVLINLLENAIKYAGPGAHISLHARCPQAMLEVDIRDNGPGIPSGQEQTIFDKFARGSKESAIPGVGLGLAICRAIMDVHGGTITAENAPEGGAVFHLRVPQPPAPELDENEVM	22~~KdpD (3.40878E-105)~~230;X;253~~Usp(4.58602E-36)~~373;X;403~~DUF4118 (9.33227E-21)~~501;X;527~~GAF (0.000000000079460 3)~~644;X;661~~HisKA (0.0000000158814)~~726;X;779~~HATPase_c (3.81209E-30)~~880	KdpD protein
	4E-11	52.4	2.5	7.4E-11	51.6	1.7	1.5	1	R6RZ54_9FIRM	Uncharacterized protein	BN586_01073	Dorea formicigenerans CAG:28	703	1263073	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea formicigenerans CAG:28	>tr|R6RZ54|R6RZ54_9FIRM Uncharacterized protein OS=Dorea formicigenerans CAG:28 GN=BN586_01073 PE=4 SV=1MRVLLVGNTGYITKEFVQEAFPESEVFIMGNSLLKTERKKHLIVRPFPEQDEELEDIFHTYDFELMVYFSNYITFHGTMEGEAEKLRKVLSYCKRSKEIHVIYLTGPEAGYAATTGKTLLVRGAENLCCQYGKMYQIPVKIVRIPYLYSGVYKEDYFYRMFAAIRSGEPVEIQESPDQPLQFLNSMDLAELLEKMSDNWDEEYHYLNVPNVFSNTFRELEQKIKEIDASVRIENRGLTPVEKIPPDDKVVRFKYGWFPKISLLEDFSDIYDQYLDAIGEKERRIDRWKIWLDKHRPIVKIVELVVGFFLFEFLNHLAGNQAQFKMIDLRLVFIVLFGSLYGINYGIAAAALETVSLLAAYEREGVGWTTLFYEPSNWIPFIFYFAVGAICGYVRMKNKENIEFVTDENKLIQEKFLFMRDMYQDSIYDKRTYKKQIMGSRDSFGKIFDITRKLDTVLPQELFIETIHVMEDMLENHAVAVYSLGKNSEFGRLEIASKEIRSEFPNSIRISKYQAAISELEDGNVWVNRELLPDYPAYMAGIRKNKELVMIVCIKEVRSDQMTLYYMNLFKILCGLVEVALLRALEYQEAAKNMQYVEGTHILKTSYFMERLETFHAMQDEMVASYILLRLEHPGKSKEEADQILQHLIRANDVWGISEEGELYLILSQTDKESLPIVSGRLKKAGIITYETGIAQIARGGGEV	1~~NADB_Rossman (0.0000000169412)~~226;X;299~~DUF4118 (2.49491E-17)~~400;X;458~~GAF (2.59753E-16)~~582	non-KdpD DUF4118 protein
	4E-11	52.4	1.5	8.4E-11	51.4	1	1.5	1	Q098C6_STIAD	Conserved uncharacterized protein (GAF domain protein)	STAUR_3671 STIAU_5075	Stigmatella aurantiaca (strain DW4/3-1)	471	378806	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Cystobacteraceae, Stigmatella, Stigmatella aurantiaca, Stigmatella aurantiaca (strain DW4/3-1)	>tr|Q098C6|Q098C6_STIAD Conserved uncharacterized protein OS=Stigmatella aurantiaca (strain DW4/3-1) GN=STAUR_3671 PE=4 SV=1MRSTTGAGALLEKQRGSLGEHARKNQPGGWSGWVETGLFVAAVPLLGSQLRPEDLFLLMAPFPWSCMAVLLIALRYGGFHGMACALSLVLGEIAAWRLGVPGARLALEPSVGLLIVGCVAGEFRDGWLRRQLQAEHQGEELRIRLTHLSRSHHLLRASQERMEQRLAGGAPSLRQALSALHERLSTLPFGKSRLETLGAELLGLMANHGGVQAAAVYAVDESGRWKDVPVATFGKCPAHAEDPLVEEALRLGRMVSVRTFSAAAPASALLAAIPLVDVDGHIWGVVAVSEMPFIAFNEDTLRLLAVLAAHVGDSLAQEQEAPARESAAALVQLEKGLRAAQRDGQPAGVVALHLEGLLEPARLEALTTQQRVLNQMWHLQRPDGGTTVLFLLPLTPAPGVKRFLQRIEEALHPDTLYPSQRWVRSWPYQPHEPVEPLLAELRRTCEADEMENRAPQCNRPGTVELGLSLEL	33~~DUF4118 (0.000000000000122 68)~~130;X;194~~GAF (0.000000284302)~~316	non-KdpD DUF4118 protein
	5E-11	52.3	11.2	8E-11	51.5	7.7	1.4	1	F8GKK6_NITSI	Histidine kinase (EC 2.7.13.3)	Nit79A3_1973	Nitrosomonas sp. (strain Is79A3)	889	261292	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales, Nitrosomonadaceae, Nitrosomonas, Nitrosomonas sp. (strain Is79A3)	>tr|F8GKK6|F8GKK6_NITSI Histidine kinase OS=Nitrosomonas sp. (strain Is79A3) GN=Nit79A3_1973 PE=4 SV=1MTDERPDPDHLLAEIKKEEIAAQRGKLKIFIGACAGVGKTYTMLNAAQQRLAEGIDVVIGVVETHGRSDTIKLLEKLTLLPLHEIKYREKSLLEFDIDAALQRAPQLIIIDELAHTNIEGSRHAKRWQDVDELLASGIDVYTTLNVQHLESLNDVVGSITGIRIWETVPDRFFDSADDVTLVDLPPDELLERLREGKVYVPEQVEHAAKNFFRKGNLIALRELALRRTADRVDSQMRAYRADHAIANVWQTRERIIACIGPGPLGNKLVRSAARLAKELKADWHAVYVETPALQRLSKIDRQRILDHLTLAEELGAETATLAGSDLIATLIAYAQSRNASKLVVGRPVDLPWFQHWRPRFIDALARFAPDIDIYVVVGNEKPTRIKNREIKPGTIKWWNYAWATIACGVTTILAAGLLHIFDLSNVVMILLLTVVGISIKFGRGPGAWAAALSVMLFDFFFVPPRFSFSVSDVQYLFTFALMLLVALTIGQLAAKLRFEATIANLRERRAQALAALSKELSGALTVEQVVEIANRNVSGTFNSAVALLLPSSQEKTKVAGTSSSQPTTDIAVAQWVYDHQLPAGFGTHTLSAAVSHYLPLKAPMRTRGVLVLEAKDLLFLNEPEEKRLLDTFAAQIALALERVHYVEVAQDALVSIEGERLRNSLLSAISHDLRTPLTALVGLASTLTDTNLPENSQKELALAIRNEAQQMTELVTNLLDMARLQAGGVKLKKDWQSIEEIVGSACMQLHRVMTTKKLIISIPANLPLCECDPILIQRVIVNLLDNADKFTPPGSTISVCATAGIDELAIVIEDNGPGLPLGQETKVFDKFARGETESNKPGVGLGLALCKAIVEAHGGKISAENRVDGGARFTLTLPLGIAPIPEELL	22~~KdpD (7.27575E-118)~~232;X;254~~Usp(9.558E-42)~~376;X;399~~DUF4118 (7.56348E-19)~~497;X;525~~GAF (0.000000000002496 58)~~642;X;659~~HisKA (1.14742E-14)~~723;X;776~~HATPase_c (6.31311E-29)~~877	KdpD protein
	5E-11	52.2	14.1	8.2E-11	51.4	9.7	1.4	1	H0PS38_9RHOO	Histidine kinase (EC 2.7.13.3)	kdpD AZKH_1662	Azoarcus sp. KH32C	513	748247	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azoarcus, Azoarcus sp. KH32C	>tr|H0PS38|H0PS38_9RHOO Histidine kinase OS=Azoarcus sp. KH32C GN=kdpD PE=4 SV=1MENDSLERHSPVTRHLFAVFACALMTAICLLLRGVFDITNIAMLMLLPVVFVAARLGRGPAILASFVTVALFDFFFVPPQLSFAVSDVQYLVIFAVMLAVSLFISHLTASLKASARDAQQREQRSQALYTLARTLAGAVSADEAVTQVVRFVREQAGGEARLFVPDADDKIHEFPHSTGPLSMDKFLTIEAVYLGGDTVGASATVNLDGACLILPLIGSTRRRGVLFVAAHVDDDHIYELRSMLEAVASLTAIALERLHFVEIAQASQLETEAERLRSSILSSISHDIRTPLTVLFGQADALALASSHLDDQEREAAQAIRDQAGRLHEMVDKLLDMARLQAGKVHLSKEWQPIDEVIGASIQLLGDALRDHPVTVTLAPELPLVAIDAVLMERVCCNLLENAAKYSPPGAPIAVTVTDVAGSLLVEVRDRGPGFPPASLKRIFNLFERGTTESTAPGVGLGLAICRAIVEAHGGQIDASNAPEGGACVRFSLPCGQAPQLEPEPVDPAGARP	10~~DUF4118 (9.56266E-17)~~112;X;142~~GAF (0.00060543 7)~~257;X;286~~HisKA (0.0000000932135)~~339;X;392~~HATPase_c (1.77072E-29)~~493	non-KdpD DUF4118 protein

	5E-11	52.2	6.8	7.5E-11	51.6	4.7	1.3	1	S6AQD9_PSERE	Histidine kinase (EC 2.7.13.3)	kdpD PCA10_22360	Pseudomonas resinovorans NBRC 106553	882	1245471	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas resinovorans, Pseudomonas resinovorans NBRC 106553	>tr|S6AQD9|S6AQD9_PSERE Histidine kinase OS=Pseudomonas resinovorans NBRC 106553 GN=kdpD PE=4 SV=1MSDTRRADALLADMPQGGRGRLKVFLGAAPGVGKTYAMLQAAQAQLRQGVDLRAGVVETHGRAETEAMLAGLPQQPLRRFDYRGMALTEMDLDGILAQPPKLVLVDELAHTNAPGSRHAKRWQDVEELLDAGVDVYTTVNVQHLEALNDQVHDITGVQVRETLPDWVLQEADEILLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELAMQTAAARVDADLNRRYRQRGLEAPAVRGRLLVGIDGDHQAERLVRHASRVAERRHLPWSVVYVDTGGARSEEVRSRLQGAQQLAERLGGEVVTLRGESVAKGLVQHAAERRASLLLVGRSRQRLRRRLLGRGLAERLLRLGEGLEVSVLDTEVDRRPPSPRATHHTRLLDYGLAVVAAITASLVAWAVAHTLELPNISLVFLAAVLLVAVRSSLGPALLCAGLSFIAYDFLFIPPTFSLTIARQEDVLTLLFFLLMAGLTGNLASRQRRQLDALRDTQSETTALLDLSRKLTAATDRQAVLNVAVQQFETWRDVEVCLLSRGRDGVWKVEAGAQRLLADQERAAAEWSWQHDQPAGLGTDTLPGGRWWWLPLSGEEGPLVLLGVSPRDEAPLPVGRRRLIAALGQPLAQALARAQLAEELEAARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLSLGEAIPMDDRRELLEGTRDEAERLDRYIQNLLDMTRLGHGGLKLARDWVAPVDIVASALQRLRPVLAPLQVETGVPEQLPLLYVHAALIEQALVNLVENAARFSPSGGRLRVAVEADEAELRFSVADQGPGIPPDERERIFDMFYTAARGDRGGQGTGLGLAICQGMVGAHGGRVTVGEGLDHRGATLTLHLPLHPQPQLEEE	17~~KdpD (6.15347E-123)~~227;X;248~~Usp(4.92714E-21)~~365;X;390~~DUF4118 (3.88034E-17)~~489;X(160);649~~HisKA (0.000000000000277641)~~715;X;768~~HATPase_c (1.38497E-26)~~871	KdpD protein
	5E-11	52.2	11.4	8.7E-11	51.4	7.9	1.4	1	A0A0D5EAT5_9BURK	Histidine kinase (EC 2.7.13.3)	BW23_4442	Burkholderia ubonensis MSMB22	567	1249668	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	>tr|A0A0D5EAT5|A0A0D5EAT5_9BURK Histidine kinase OS=Burkholderia ubonensis MSMB22 GN=BW23_4442 PE=4 SV=1MNVNETQRHTNRLREIAAREPARRGPGRWRTILDACAGGAASLAWADPGGGPARPDSGTRAHVRTRLHDRASPYYAPLAWATVICGSATVAASALLRVFDLSNVVMLFLMTVVFVSLRLGRVAGAWAAFLCVGCFDFFFVEPRWSFAVSDTQYVFTFALMLAVALAIGQLAARLRAEARAARANEKRSATLARVARDLSAAIETEQIVSVCTGTIAPLLGVHVALVLPDADDRLRIARDAWFVDPSAARWTYDRAQAAGRGTPTFDGAVALYLPLKAPMRVRGVLALLADAQPIPTSPDDRRLLDALCSSIAMALERVHYVGVAQHTMVRMEGERLRNALLAAVSHDLKTPLTAIRGLAETLEQPERLAPGQPAGLARAIRDQAEALRGLVVNLLDLARMQSEGVRLNREWHMLDEIVGSALAHSACVLAGRDVKADLPADLPLIDVDAALLVERVLMNLLDNAAKHAGADASVAVRARVSGDAMVVCVDDDGPGFAARDAERLFEPFERGRAASPVAGVGLGLALCRSIVNAHGGSIRAVPLEPHGARFEIRLPLGAPPDIEHESRA	non-KdpD DUF4118 protein
	5E-11	52.1	11.1	8.8E-11	51.4	7.7	1.4	1	C4KDD1_THASP	Histidine kinase (EC 2.7.13.3)	Tmz1t_3503	Thauera sp. (strain MZ1T)	387	85643	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Thauera, Thauera sp. (strain MZ1T)	>tr|C4KDD1|C4KDD1_THASP Histidine kinase OS=Thauera sp. (strain MZ1T) GN=Tmz1t_3503 PE=4 SV=1MALPTPRDRLPDRAPLRNYLLAALAAGAVALVGAPLLGQFDLANIAMLFPLAVLFAAIRLGRGPAVFAAFLAVALFDFFFVHPHFTLAVSDLQYLLTFAVLLAVALTTAELAARLRRERDSAEARAEEAAQARLAADTERLRNTLLASLSHDLRTPLTALAGLAESLPLAGPPLPPAQAELAEAIRAEALRTHALARDLLDLSRLQSGAPRLALDWLAVDELLGSALQARAHALRAHVFALELPEELPLLHADAVLMERVVCNLLDNAIAHTPEGGHIVLAAQVGADWIRISLCDDGCGLPPGREQAIFERFVRAPHPRGAADATTATGDAGTGLGLAIVHAIVAAHGGSVSAHNRAGGGACFVLQLPLPRQPDRPPPEDEAGAPPR	44~~DUF4118 (0.00000000490737)~~118;X;139~~HisKA (0.000000000147519)~~204;X;257~~HATPase_c (1.25171E-28)~~367	non-KdpD DUF4118 protein
	5E-11	52.1	8.1	8.1E-11	51.5	5.6	1.3	1	Q89FC5_BRADU	Histidine kinase (EC 2.7.13.3)	bll6776	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	907	224911	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium diazoefficiens, Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	>tr|Q89FC5|Q89FC5_BRADU Histidine kinase OS=Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110) GN=bll6776 PE=4 SV=1MVRERRDSEQRPSPEALLEAARREESASGKLKIFVGAAPGVGKTYEMLQSAHAKRKAGIDVVVGFVETHGRAETEALVRGLEVVPRKRLDYRGQTIEEMDLDAVIARRPQIALVDELAHTNAAGSRHPKRYLDVEELLSHGIDVYTAVNIQHTESLNDVVAQITHVRVRETVPDSVFDRADAIELIDLTPDDLIQRLREGKVYVPRQAERALEHYFSPGNLTALRELALRRTAERVDEQLLTHMQANAIAGPWAAGERILVCVSEDPRAAGLVRYTKRLADRLHAPFTAISIETRRSLQLSDDERDRLADTLRLAEALGGEALTIPAVGRRIADDVVNFAQGNNVTQIVIGKKSTRSRWFEITRGSVVHDLVRRAGNITVHVIAGDDVPGEAAPKTAVQTAARTEPFDPLPYLKALGIVLIGLGAAELIQPRFGIENVDLVLLTAVVAVAVRYGLWPSLLATVAASLSYNFFFLPPIYTFTITDPTNVAAFVLFMVVAMIVSNVAARVRTQADTAIGRIRTTEQLYAFSRKLAGTATLDDVLWATAYQIALMLKVRVVLLLPEDGLLTVKSGYPPEDQLDQADLAAANWAWSNDRPAGRGSDTLPGAKRLFLPMRTGRGPIGVIGIDNDRTGPLLTPDQRRLLDALVDQGALAIERVLLVEDMDRVKRTVESERLRSALLTSISHDLKTPLASVLGAASTMRDLAGALSDTEKRDLLATVIDESERLNRFIANLLDMTKLESGAIVPNTALHDLSEIVGSALRRAAKILTAHKVELVLAADLPMLQLDAVLFEQVLFNLLDNAAKYSPAETTISIKSQRERDQVVLQIADEGSGIPPDEVESVFDKFYRVQKGDHVRPGTGLGLAISRGFVEAMHGTISAANRSDRSGAVLTIRLPVPAQTHALDTAA	29~~KdpD (3.94257E-122)~~236;X;258~~Usp(1.60415E-44)~~383;X;410~~DUF4118 (1.0032E-17)~~510;X;536~~GAF (0.000000000011958 6)~~655;X;672~~HisKA (0.000000000017059 4)~~738;X;791~~HATPase_c (7.93415E-26)~~894	KdpD protein
	5E-11	52	12.3	9.5E-11	51.2	8.5	1.4	1	W0UXS5_9BURK	Histidine kinase (EC 2.7.13.3)	kdpD GJA_695	Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	910	1349767	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Janthinobacterium, Janthinobacterium agaricidamnosum, Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628	>tr|W0UXS5|W0UXS5_9BURK Histidine kinase OS=Janthinobacterium agaricidamnosum NBRC 102515 = DSM 9628 GN=kdpD PE=4 SV=1MLPNDSQRPDPDALLAQVQAQEKKASRGKLRIYFGASAGVGKTCAMLAAAHKMQDDGQQLLVGIVETHGRRDTAALLEGLPLLPLKQIVYRGKNLAEFDLDEALLRRPPLILMDELAHSNAPGSRHPKRWQDVEELLDAGIDVLSTVNVQHLESLNDVVGGITGVRVAETLPDTVFDRADEVVLVDLPADELLTRLKLGKVYQPQQAERASQNFFRKGNLIALRELALRRTADRIQDDVQAYRVVEKSINPIWKTGAALLACIGPRPGAEHVIRSTARLASQLNAEWHALYVETPQLQHLPPAERERILKLTKLAQDLGARTAVVSNSDIAGAIVDYARAGNISKVIVGRGRRNWPWRIAHARRIAQLAPDVDLIEIGQPAAQAGAASQPAARDGEEGADAGRRPSRHWRYLVAAGASVLTALLVLPMLAYLDLANIAMLFLLTVVLVAVRFGRGPAALASLVGVACFDFVFVPPRYSFAVGDFQYVITFGVMLAVGLIIGHLTAGLRFQARVASHREARARALYEFARELSGVLQTEQIFEITRDFIQRAFQARATLLIPDDDGRLQMTQQAGDIHAQQLALLDLGIAQWSFDHAEAAGIGTDTLPAASVFYLPLIAPMRTRGILALLPDNRRWLLVPEQRQHLDTFAALAAIALERVHYIDVAQGALVQMESERLRNSLLAALSHDLRTPLTSLVGLSESLVMSKPGLAPEQLTMARSLQEETLRMSALVSNLLDMARIESGQVRLNLQWQALEEVVGSALRASRSQLTCHQVQTRLERDLPLVSYDAVLIERVLCNLLENAAKYTPPGSSITIAADVRGAWLQVSVYDDGPGLPAGREEAIFEKFTRGERESNKPGVGLGLAICRAIVEAHGGKIRAGQSPIHGAAIEFTLPLGTPPAMPELDLELPH	25~~KdpD (2.20101E-110)~~235;X;258~~Usp(1.20344E-37)~~376;X;409~~DUF4118 (3.97917E-19)~~509;X;536~~GAF (3.2791E-16)~~657;X;674~~HisKA (0.000000000038952 4)~~739;X;792~~HATPase_c (1.86482E-28)~~893	KdpD protein

	6E-11	52	11.5	9.1E-11	51.3	8	1.3	1	A4SZG6_POLSQ	Histidine kinase (EC 2.7.13.3)	Pnuc_1667	Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1)	897	312153	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Polynucleobacter, Polynucleobacter necessarius, Polynucleobacter necessarius subsp. asymbioticus, Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1)	>tr|A4SZG6|A4SZG6_POLSQ Histidine kinase OS=Polynucleobacter necessarius subsp. asymbioticus (strain DSM 18221 / CIP 109841 / QLW-P1DMWA-1) GN=Pnuc_1667 PE=4 SV=1MPESRPDPDQLLAQIQSQEIQSGRGKLKIFFGANAGVGKTYAMLSAAHEQSKNKRVIAGVVETHGRKDTIAMLDGIEVLPLKEIDYRGKKLKEFNLDQALIEKPDLILMDELAHSNAAGSRHPKRWQDVEELLAAGIDVYSTINVQHIETLNDIVGGITGVRVWETVPDHIFDSADEVVLVDLPPDELLQRLKDGKVYLPQQAERATQNFFRKGNLIALRELALRRSADRLDGEIIKYRKDNSVSNVWKTRESILACIGPGDEAENVIRSAARVAAQLQIPWHAIYVETPKLQNLSQKSRERILKTISMAEEMGAKVVTVGGNDAVESIISYARERHNLSRVIVGTGALSRWQIWRRAFSESISRRAPDLDILKIAQGTNSTSIARDSFDIESWMWQLKAPWQSYALSLLICGIAGVVATPLNSIVELPNIAMLFLLAVVLVSVKYGLGPSFMASAVNVLVFDFFFVPPRFSFSVSDAQYVFTFAVMLVVGLITAKLTTGLTYQAKVANRREQRVKSLYEMSRDLSGALMPEQVAEISQHFVEIEFKAKSILLLADDDNQLSEIIINKKSNLQADLSIAQWAFDKSKEAGNGTDSLPGAPLLYIPLRAPMRTRGILVIDAPSSTRLKSPEQRRLLDTFARLLAISLERIHYVSVAQSSTVQIESERLRNSLLSAISHDLRTPLTALVGLTDALEMLDAPLTSEQKEIAVLLREKALKMSSQVSNLLDMARLQSGAVQLNKQWFLIEEAIGAAIKSVESASEGRHITVTLPPDLPLLNFDAVLIERVFINLLENAYKYTPKNSSVSIGASVSSPQSVEIWVQDDGPGLPKGKEEDIFRKFERGNKEGAISGVGLGLTICRAIIEAHGGKITGKTMAGGGARFTFSLPRGNPPKIDIEDQ	22~~KdpD (7.94073E-121)~~231;X;254~~Usp(1.12818E-37)~~375;X;404~~DUF4118 (1.45708E-19)~~503;X;530~~GAF (2.03459E-16)~~647;X;664~~HisKA (0.0000000000780934)~~729;X;782~~HATPase_c (2.31643E-25)~~884	KdpD protein
	6E-11	51.8	11.6	1.2E-10	50.9	8	1.4	1	A0A0F2JLF4_9FIRM	Osmosensitive K+ channel histidine kinase KdpD	UF75_0351	Desulfosporosinus sp. I2	881	1617025	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	>tr|A0A0F2JLF4|A0A0F2JLF4_9FIRM Osmosensitive K+ channel histidine kinase KdpD OS=Desulfosporosinus sp. I2 GN=UF75_0351 PE=4 SV=1MAKGKLTIFLGAASGVGKTYAMLEAALGRLSEGIDVVVGLVETHGRADTEAMLKELTVIPWGTRDYLGRTFHELDLDAVLTRRPQLVVIDELAHTNIEGSRHKKRYMDVKELLSAGINVYTTLNIQNLETLNDIVTQITGITVQETVPDQVLEAASQIQLIDIPPEELIQRLKDGKVYVPGQETEGFRNFFRPGNIALRELALRYTAQRVDRQLESYRRIHGIDGPWATGEKILVCISASPFSAQLIRIAKRMTEKVQGELLAVHVETLRRFPSSESEKDSMAKNLRLAEELGAEVIGLTGNSVAEVILGLARKRNVSQILIGKPQHTRLWEIIHGSVVDKVIRQSQGVSIHVIPGNQQEAGSAQIQTLEIRNSPKLIPYLASSLMVIVMTLVLTLVSPFLGLVNISLAYLLPILLSAARWGTLPAIATAFMGTIAFDLFFVPPIFKFTVADLRYLISFVIFMLVGLITGTLSERLKKQVNYSRQRENSISALYSLSRDIAAVDNLEAVLDCIVSNVSETLEGQVMLLLPNEKAQLVLRKHSGLNDFLDQPEFSVATWVYERGLKAGYGTETLGTAKALYLPLRTEQGTQGVLGIYIKERKAQFDPEGMRLLEAFTGLSAVAINRVKLAEQARETLTLVESERLRTALFNSLSHDLRTPLASIIGAVTGLLEDQNVVYSPEVRKELLKTILHGAERMNRFISNLLDMARLESGMLSLKKDWCDLQDILGVAINRLGDTLTRRPLDIDIQEGLPLVQADGILIEQVLINLLDNALKYSEAASKILISIRQQERQLEIVIANRGPNIPETDLSKVFDKFYRLSSPLQVSGTGLGLAICKGLIEAHGGDIWAENNKLGGVTITFTLPLTDQCFGIVPEMDEGE	1~~KdpD (7.92257E-108)~~211;X;233~~Usp(6.85486E-38)~~356;X;380~~DUF4118 (1.79028E-16)~~480;X;506~~GAF (0.00000000148999)~~626;X;643~~HisKA (0.000000000001921)~~710;X;763~~HATPase_c (7.01755E-28)~~864	KdpD protein
	6E-11	51.8	8	1.2E-10	50.9	5.6	1.5	1	Q9I389_PSEAE	Histidine kinase (EC 2.7.13.3)	kdpD PA1636	Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	885	208964	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	>tr|Q9I389|Q9I389_PSEAE Histidine kinase OS=Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228) GN=kdpD PE=4 SV=1MTDTARADALLADLPADGRGRLKVFLGAAPGVGKTFAMLQAAQAQLRQGVKLRAGVVETHSRAETESLLAGVPQQPLRSLEYRGMKLQEMDLDGLLADPPALALVDELAHSNVPGSRHAKRWQDIQELLAAGIDVYTTVNVQHLESLNDQVRDITGVQVRETVPDWVLQEAYEIVLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELAMQTAAARVDADLNHRYRQRGEEAPALRGRLLVGIDGDEQAERLVRHACRVAERRHLPWSVVHVDTGGLRGEQARMRLQGAQQLAERLGGEIVVLRAGEVARTLLQHARERRASLVLVGQSRRRWYRRAFGGGLAGRLLRDGQGLEISALDSEADLRPAEPRPRYPVVWNDYLLALLATALASGLAWIVAHLLELPNISLVFLMAVLLVAVRSSLMPALLCAVASFLAYDFLFIPPHFSFAIHRHEDLLSLAFFLFMAGLTGNLAARQRRQLEALRDTQEETSLLLELSRKLTAATDRQAVLAAAAQQFDDWKDVEVCLLGQVNGEWKTEAGVQRQLADQERVAADWAWAHDQPAGLGTGTLPGGRWWWWPLSAEEGPLALLGVAPLDGQPLSPQRRRLLAALGQPLAQALARARLAEDLEAARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALGEAIPPADRRELLESTRDEAERLDRYIQNLLDMTRLGHGGLKLARDWVAPGDIVGSALNRLRAVLAPYRVVQAIVANDLPLLYVHAALIEQALINVLENAARFSPNHGRLRIEVSQDAAELRFAVSDEGPGIPEAEREKIFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGRISVGEGLDGRGTTLVLHLPLHPQPDLGQLEGDE	18~~KdpD (1.02212E-120)~~227;X;248~~Usp(1.7193E-31)~~365;X;405~~DUF4118 (4.53798E-14)~~489;X(159);648~~HisKA (7.63804E-14)~~714;X;767~~HATPase_c (9.46546E-27)~~870	KdpD protein
	6E-11	51.8	0.9	1.1E-10	51	0.6	1.4	1	G7ZA57_AZOL4	Uncharacterized protein	AZOLI_p10209	Azospirillum lipoferum (strain 4B)	466	862719	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum lipoferum (strain 4B)	>tr|G7ZA57|G7ZA57_AZOL4 Uncharacterized protein OS=Azospirillum lipoferum (strain 4B) GN=AZOLI_p10209 PE=4 SV=1MSSQPPAVPAATIPADGAPRRRWFGLRPVALLELVLFFGVVLGLDVWLGSGHRFEGVQPHPFWIPVLLLAIQYGTNEGVLAALAATVALRLGNVPDAGITQDLYDHLFTLTREPILWLVAAVLFGELRMRHLREREELRAGLAAARQEAEAIARSYRALKSVKESLETRVAGQLRTVFTLYQAAKSIDRLDEGEVMLGVADLVRTVMKPEKFSLFLLNNDVLESVTNEGWDDDTDTYARWFDSGTALFQQVIARQRQVCVNRAEDERILAGEGILAGPLASSDTGEVVGMVKIESLGFTDLSVNTVENFRILCEWIGTALAKARQYRTANEQRVFTDDALYSSSYIGRQAEFLALLGRRMGFETTAITIRPVGISRLSVGQRAELAAAIGEAVRGSLRDTDLACDFGHQGTSFGVVLAGTPLDGARLVEAKLERAVRQALPAALADITIGFTTRRIEAPADGQAAQ	30~~DUF4118 (0.0000001016 04)~~134;X;191~~GAF (0.000000000462222)~~322	non-KdpD DUF4118 protein
	7E-11	51.7	10.1	1.2E-10	50.9	7	1.4	1	J7SKK9_MORMO	Histidine kinase (EC 2.7.13.3)	MU9_3392	Morganella morganii subsp. morganii KT	895	1124991	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Morganella, Morganella morganii (Proteus morganii), Morganella morganii subsp. morganii, Morganella morganii subsp. morganii KT	>tr|J7SKK9|J7SKK9_MORMO Histidine kinase OS=Morganella morganii subsp. morganii KT GN=MU9_3392 PE=4 SV=1MYDEPLRPDPDQLLAQVTERPRGKLKIFFGACAGVGKTYAMLKEAQRLREQGIDVLAGVVETHGRSETAALLEGLRILPLKKHNYRGRQVAGFDLDRALAIHPAVILMDELAHTNIPGARHPKRWQDVEELLNAGIDVLTTINVQHLESLNDIVGGVTGVRVRETVPDPVFDAADEIVLVDLTPDDLLDRLREGKVYLPAQAERAIEHFFRKGNLLALRELALRRTTDRVDEQMRAWRERKGQEKVWHTRDAILVCLRPDGGNEKLVRAAARLAARLGSDWHAIFVETPARHKLPSPQRRTILTTLSLAQQLGATTATLAEPEESRAVIRYARENNLGKIMIVRHERTSWWRRDKLQEQLSRSAADLDVVMIAPQDRQPENREKFSDNRPFLDKHKTDLQGCVVAALICAVTTLMAHHWLMAFDNANLVMLYILGVVVVARFYGRWPSVFATIINVISFDIFLINPKGTLAVSDMQYLLTFAVMMTVGLVIGSLTAGVRYQARVARYRYEQRTWHLYEMSKALAVARESDDIASVSCHFISHSLHARCEMLLPDEQGNLIPAGGGVADNGRDDAIIRWSYDKGQPAGFGTGTLPGVPYQILPVCTTEKVYGVVIVEPYNRRQLLIPEQQRLLETLILLAAGALERRTLTEREAQSRLVSEREQVRNSLLAALSHDLRTPLTVLFGQAEILTLDLTSEGSPYAAQANEIRQHILSTTRLVNNLLDMARIQSGGFNLNKEWLPLEEVIGSALQMLKPRFDTDSVQIDLNDPMQLICADGPLFERVLINLLENAIKYAGPQAQIGIRSRLSDNMIDIEVWDNGPGIPAGQEAQIFEKFSRGQKESAIPGIGLGLAICRAIAEVHGGTILAGNRDGGGASFHIRLPCEDPPVIDEDDNPL	22~~KdpD (5.01135E-113)~~214;X;253~~Usp(1.3453E-21)~~373;X;403~~DUF4118 (2.32937E-18)~~501;X;529~~GAF (0.000000000045652)~~644;X;661~~HisKA (0.000000000248982)~~726;X;779~~HATPase_c (3.82244E-30)~~880	KdpD protein

	7E-11	51.6	9.3	1.1E-10	51	6.4	1.3	1	E3GLH5_EUBLK	Histidine kinase (EC 2.7.13.3)	ELI_1562	Eubacterium limosum (strain KIST612)	907	903814	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium limosum, Eubacterium limosum (strain KIST612)	>tr|E3GLH5|E3GLH5_EUBLK Histidine kinase OS=Eubacterium limosum (strain KIST612) GN=ELI_1562 PE=4 SV=1MDFQDERPNPERLLKEINEEERRSREDEEGIGHLKIFFGYCAGVGKTYAMLEEAQQLYKKGVDVLVGYVEPHTRPETMAMLEGLPAIPPQVVDYKGITLRDFDLDKALEKKPKVIIVDEFAHTNPEGFRNKKRYQDIEELLNAGIDVYTTVNVQHIESLNDVVGSITGIIVHERVPDYVFDKADKIKLVDIDPEELLKRFEEGKVYAPEKADLAKRRFFTVENLNALREIAMRKAADRIVSGAGNKKKKVPFSKMLVCVGPSPSSAHCIRTTARIADAFHIPWVALYVKTSDRTYADISERKNLQDNMNLAEQLGAEIVTMQGDDMAMVISEYIKQSGITNVVIGKGRNKPNPFKEDLEDQLLSMNPGIEIHIVPDSQAEKTSGGIPKKRLSWLSKRILSLHFSLKDFGKTVLTLVLATAISFGLRELNLGDQNIIMVYLLSILVISRLTVGYLYGICASVFGVLLFNFFFTEPYFTFNATNPTYPVTFIVMLLVALMTSALTNGIKVQAKMAVMNERRTEILYELSKKLLITRGLENIVTLTNESLTSIFERSVIFYTQNPDEKNRGTFMQGPEETSGAFMQSKEEEAVAHWVFQNKKAAGNGTDTLVGAKGFYMPVVSQGRVLGVIGISCVEEMLPPKRRAFLKMIVSQVAMALERQRLSDEQGKARLETEKEKMRSNFLRAISHDLRTPLTGILGSSSALLENIGELDISTQKKLLRDIKDDSEWIIRMVENLLSVTRIGEGKVDLKKHPEAVEEIVGEAVAIIRKRFDHTDIKVEVPDTLLMVSMDGTLIEQVMINLMENAIKYAGSHPVLDVKVQNLGKKARFIVGDNGEGISETMLPHIFEGYMGDEEKSSDSRRGMGIGLTICKSIVDAHGGTLKARNKQEGGAEFSFELPVEEDDNNES	32~~KdpD (9.79353E-117)~~239;X;254~~Usp(1.22663E-37)~~375;X;411~~DUF4118 (1.98482E-18)~~509;X;536~~GAF (0.000000144342)~~658;X;675~~HisKA (5.04448E-14)~~741;X;794~~HATPase_c (1.14503E-23)~~897	KdpD protein
	7E-11	51.6	13.6	1.5E-10	50.6	9.4	1.5	1	C0QR35_PERMH	Uncharacterized protein	PERMA_1362	Persephonella marina (strain DSM 14350 / EX-H1)	415	123214	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Hydrogenothermaceae, Persephonella, Persephonella marina, Persephonella marina (strain DSM 14350 / EX-H1)	>tr|C0QR35|C0QR35_PERMH Uncharacterized protein OS=Persephonella marina (strain DSM 14350 / EX-H1) GN=PERMA_1362 PE=4 SV=1MERKRFKILVESLTLSILFVLFGFVWNNDDPLFLNIGGNITYYIFVIILLTLYYGLLSGIVSMFVFGISAFFLYEQFPYETFFWYLLITFVLGEFFQYWNRRKERLEEENSFLKEKIEELGRNFFMLKISHDQIEKNYVLKPLSIRSVLRDIRMMILNKEVDLFKNFLMLISRFTNIDGGALYINEDNGFKKVAQIGKGAELNRDDPLVKQAFIDKTSTYLAVNRLEGDVKSEYLAVVPAVDINGNINGLLLITDMPFLSLNKDNLLTINVFLTYLFDEYNLAKGLEETVVKFPNIHLSFIKELRKLIHLKSKFGIESSIVVFFMLKQDFLDAAFTEIERGLRGFDISTRCSEVEKEKLIILLPFTGDVAAVEFVNRIKEKIEDIFGEEVEGKIKSRILTVENDLEQTLTKVKEL	9~~DUF4118 (0.000000000005999 55)~~102	non-KdpD DUF4118 protein
	7E-11	51.6	3.9	1.3E-10	50.9	2.7	1.4	1	Q2GBD8_NOVAD	Histidine kinase (EC 2.7.13.3)	Saro_0387	Novosphingobium aromaticivorans (strain DSM 12444 / F199)	502	279238	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Novosphingobium, Novosphingobium aromaticivorans (Sphingomonas aromaticivorans), Novosphingobium aromaticivorans (strain DSM 12444 / F199)	>tr|Q2GBD8|Q2GBD8_NOVAD Histidine kinase OS=Novosphingobium aromaticivorans (strain DSM 12444 / F199) GN=Saro_0387 PE=4 SV=1MDLFAETSLRDELRRTMISKASAWRAPAVIFAVTAVLVIVLKPILDGEVSSGMLFMLGITLVGARSGLTPALISALLASAIFNFFLADPVLTFRMSSGEDLAPPLIFTACALVSGLLAGRLKDKTFQLGRTNLQLESLLETSRLLQAAPDVAAIEAALATTVPGRLGFRLSLYGLKDGTTEALPASDRRPEALALARQAIEGDGIVRHRDSIAFRLDGSRSCVGALVVENVSGAQVDPAFLEALASLVGLALERARFASVIAEAEANVRTEELKSALLSSVSHDLRTPLTAISASASSLIEFGSRFDRETSKALLQGIVDECDRLNRFTANLLELSLRLQAGGPSIAGQVLSVNDVVRAVVQRLRTRFAGREISVSSTDPEILVTADTALFELAVTNVIQNALIYSEPDMPVLVQSSCDRNQCVLTVTDQGCGVPEAEQTRVFERFYRVKRSEPSPQGSGLGLAIAKGFVEAFEGTVKLMSPVIGGKGTTVTITLPVVSEVKA	23~~DUF4118 (1.1469E-15)~~124;X(147);271~~HisKA (0.000000000089594)~~337;X;390~~HATPase_c (1.67835E-20)~~494	non-KdpD DUF4118 protein
	8E-11	51.6	11.6	1.3E-10	50.8	8	1.4	1	A0A0A2UBK2_9BACL	Histidine kinase (EC 2.7.13.3)	P364_0106830	Paenibacillus sp. MAEPY2	515	1395587	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. MAEPY2	>tr|A0A0A2UBK2|A0A0A2UBK2_9BACL Histidine kinase OS=Paenibacillus sp. MAEPY2 GN=P364_0106830 PE=4 SV=1MKLKRVPKYIWVTLGIALLTMLLHTIGMSEDLVNVGLIYLFPVLVSAVYWGLGPAIYAASLSVVAFDFFFVPPYLSFTVEDLRYIFSFAVYLAVAVLTASLAGRLRQQLEMVKQRENTTNSLYALSRQMTAVTDLDTLLNNIASQVSLTLGAPAALYLPNSDGELAVTSSSGEPDFAGWGKSESEAAIAKWVYIHGEVAGRGSSSLRESSGLYVPLRTEDQIHGVLAVNLESSDLYEQREELRLLEACGGLAASAIARVKLAEEARLAQMTAESERIRTALLDSVSHELRTPLTAIIGSATGLLENDSLFTAEDRKELTANIRDGALRMNRLVTNLLGMVKLESGMLQLRRKWCDVGDMIGIVLGQVQQFIQHRSIRVDLPDQPPFISGDEVLLEQVLVNVISNAIKYSPVDSEIVITVKVDESLGRMTIEVADAGVGIPEADRERVFEKFYRSESSSRHVTGTGLGLAICRGIVEVHGGTITAEPNPGGGTRVCICLPTEEPEASFPYMGQGEEE	8~~DUF4118 (2.76739E-18)~~108;X;134~~GAF (0.000000000000329147)~~258;X;275~~HisKA (0.000000000001169 65)~~341;X;394~~HATPase_c (6.23314E-34)~~497	non-KdpD DUF4118 protein
	8E-11	51.4	11.3	2.1E-10	50.2	7.9	1.6	1	J7J0P9_DESMD	Osmosensitive K+ channel histidine kinase	Desmer_2979	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	671	768704	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	>tr|J7J0P9|J7J0P9_DESMD Osmosensitive K+ channel histidine kinase OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=Desmer_2979 PE=4 SV=1MKKEKRIDPDELLASLEKEGLGKLTIFLGAAAGVGKTYAMLEAAKEKLSEGMDVVVGLAETHGRAETKALLEGLPVIPTKPQDYKGKTFYEMDLDAILARRPQIALVDELAHTNVAGSRHKKRFMDVQELLAAGINVYTTLNIQHLETLNDIVAQITGVTVRETVPDQILETAFQIQLIDIPPEELIQRLKDGKVYVAGQATEALKNFFRPGNINALRELALRYTAKKVDRQLESYMRVHGIAGPWPTGEKVLVCISASPFSAKLIRVAKRMAASQNAEWFAVHVEPHLHRLSGNEADRDSMAKNLRLAEQLGAEIIGLTGDDIAEEILHLAAKRNVSQIIIGKPEHTRFWTFVHGSVVDKVIRHSQGISIHVIPGSQQETGQRNYPAERVKKKGISPQLVHSSSVPYILAPLLMTLMISIITPISSFLGIVNISMLFLLPVLISAARWGRLPAVITAAMGAITLDFFFVPPIFTFTVADIRYVLSFAIFMLVGIITGTLSDRLKKQINYSRQRENRVSALYALSRDIAAVSQLDDVLESIVNNVSSTLEGQVVLLLPNEKGKLVLQRDSGLNNFLNDSELAVASWVFDKGRKAGKGTETLGAATALYLPLSTEQGVQGVLGICFNTTEVQFDSERIRLLEAFAGLTAMAINRIKLSEQARRTLCQSHSCY	22~~KdpD (3.47822E-122)~~229;X;251~~Usp(2.35415E-39)~~375;X;407~~DUF4118 (1.25163E-16)~~507;X;534~~GAF (6.04295E-14)~~653	KdpD protein

	8E-11	51.4	11.2	1.4E-10	50.7	7.8	1.4	1	C1DIF6_AZOVD	Histidine kinase (EC 2.7.13.3)	kdpD Avin_24520	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	874	322710	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Azotobacter group, Azotobacter, Azotobacter vinelandii, Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	>tr|C1DIF6|C1DIF6_AZOVD Histidine kinase OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) GN=kdpD PE=4 SV=1MTHAMNEARDVPERTAAQSSHGEGGGRLRRGRLRIYLGAAPGVGKTLAMLQAATELLRQGVDLRVGSLDC ADDAARGELRMRLAALPGGREAAGELDLDALLARPPALLLVDRLARANPPGSRHAQRWQDVQELLAAGIDVHATL DVSHLESLKNRVEALTGQPVTETLPDWLLEEAHEVLLIDCLPGELRDFAPTTLAALRALALQVVAGRADSEVQRRY RPSGREAPAVLGRLLVAVDGDEQSEQLVRHASQVARRRQLPWTLVHVDDGRARGEESRRLLQAAQRLAERLGG EVVGLLGDEVADTLLRHARERRASVLLVGGHRRRWFGRGVVERLLRRARGLEIGVLAAEEEAVSVPSFAVRGFVA GPLDYALALLATLLASAVAWGFSRMLALQNISLVFLAAVLLVAVRSGFGPALCCALLSFFAYDLLFIAPTFSLIVAHR VDVLGLLFFLLMAALTGNLATRQRRQMQALRETQAETAALLDLTRKLSAATDRRAVLAAAVEQFAAWRDLDVRLL GPDGAGALRVEAGVAGDLGKSERAAAEWVWQHELPAGLGTDTLPDGRWWWWPLSGERGPLALLGIAPRDGR PLPASRRHRLVALCQPLAQALARAQLAEELQAARLRGETEQLRSALLASVSHDLRTPLTVMHGAIDSLLTLDGQIAA ADRRELLESTRDEAERLDRYIQNLLDMTRLGHGGLKLERDWVAPADIVASSLQRLRPVLASFRLETRIAGELPLLHV HAALIEQALVNVLENAARFSPPGGRLRVAVDSDGGELRLSVSDQGPGIPPAEREKIFDMFYTAARGDRGGPGTGL GLAICQGILGAHGGRVTVGEGLDGQGATLTLHLPLQPQPPGESERDDEAPVLP	35~~KdpD (1.32951E-42)~~192;X;234~~Usp(1.61452E-25)~~351;X;388~~DUF4118 (0.000000181966)~~472;X(160);632~~HisKA (0.000000000000268729)~~698;X;751~~HATPase_c (2.9579E-27)~~854	KdpD protein
	8E-11	51.4	9.6	1.3E-10	50.8	6.7	1.3	1	Q7CTB1_AGRFC	Histidine kinase (EC 2.7.13.3)	kdpD Atu3787	Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	900	176299	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Agrobacterium fabrum, Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	>tr|Q7CTB1|Q7CTB1_AGRFC Histidine kinase OS=Agrobacterium fabrum (strain C58 / ATCC 33970) GN=kdpD PE=4 SV=1MPDDISDMPSRPSPDALLENAQREARGRLKIFLGAAPGVGKTYEMLMSGRAKLADGVDTVIGVVETHGRRE TEALVEGLSVVPRKRIDYRGQVLEEMDIDAILARRPALVLVDELAHTNAAGSRHPKRYMDVQEILAQGINVYTTLNI QHVESLNDVVAQITRIRVRETVPDSIIDRADDVEIIDITPDDLIKRLQDGKVYLPRTARRAIENYFSRGNLTALRELALR RTAQRVDEQLLNHMQSHAISGPWAAGDRVLVCLDHGRNGPGLVRYARRQADRLRAPWTALHLDTPRSQQLSEA EKDRLAGTMRLAQQLGGETVTLPALDLTREIIAYANANNFTHIIIGRPRKSWWQRIFQRSLTHDLIDHAGDISVHVIS GDKNEEKPGQAVKLAPARSPQSFRSYLNSTLFVGLAIIVGIVLDQTLDVQNLALVFLMAVLAAAVRGGLGPALYASL LGALAFNFFFLEPRYTLTVSSPDSLVALLFYFGVALVASNLTVAVQRQAASARSRARTTEDLYLFSKKLAGTGTLDD VLWAAAYQMASMLKVRVVLLMPENGAIAVKAGYPPDDTLVDADIAAAQWAWEHNKAAGRGADTLPGAKRLYLPL RTGSGAVGVVGLDDDRSGPLLTPEQQRLFDALADQAALAVERIQLASDVDRARLAAETDRLRTALLTSISHDLKTP LAAILGSAGTLKDFADDIPPDARAELLSTIVEESERLNRFISNLLDMTRIGSGAMEPNYGLHFLGDMVGTALSRAAKI VVRHEVVLDIPSDLPMLKVDPVLFEQVLFNLIDNAAKYAPEHTTIAIRGWRQGKNIFLSVADEGPGIPPDDLERVFD SFYRVRKVDHVQAGTGLGLSICKGFIEAMGGSIRAENRADRGGAQFTIGLPVAVDTPVLDHD	24~~KdpD (3.9992E-122)~~234;X;256~~Usp(5.81186E-48)~~379;X;405~~DUF4118 (6.25228E-19)~~504;X;530~~GAF (0.00000000706499)~~649;X;666~~HisKA (0.000000000000384966)~~732;X;785~~HATPase_c (2.87113E-28)~~886	KdpD protein
	9E-11	51.4	11.5	1.3E-10	50.8	8	1.3	1	A4Z015_BRASO	Histidine kinase (EC 2.7.13.3)	kdpD BRADO5827	Bradyrhizobium sp. (strain ORS278)	905	114615	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium sp. (strain ORS278)	>tr|A4Z015|A4Z015_BRASO Histidine kinase OS=Bradyrhizobium sp. (strain ORS278) GN=kdpD PE=4 SV=1MAHQRRDPDQRPSPEALLEAARREESPAGKLKIFVGAAPGVGKTYEMLSSAHAKLKAGIDVVIGFVETHGR VETDALVRGLEVIPRKRIGYKDQVIEEMDLDAVIARRPKLAIVDELAHTNAAGSRHPKRYLDVEELLSHGIDVYTAVN VQHIESLNDVVAQITHVRVRETVPDSILDRADAIELIDLTPDDLIQRLKEGKVYVPKQAERALEHYFSPGNLTALREL ALRRTAERVDEQLLNHMQANAIAGPWAAGERILVCVSEDPRAAGLVRYTKRLADRVHAPWTAVTIETRRNLQLSD KQRDRLADTLRLAESLGGEALTIPSAGRRIADDLIGFAQANNVTQIIIGKSQRSRLFEIIRGSVVHDLVRRAGNISIHVI PGEETPGETGTSVQTRARSEPLQAKPYIMALLITAVGLGLAELIQPFFGIENVDLVFLTAVVGVAARYGLWPSLLAS LMASLCYNFFFLPPIYTFTITDPTNVAAFFFFMLIALLVSNVASRVRVQADSATQRIRTTEQLYAFSRKLAGTATLDDI VLWATAYQAALMLKVRVVLLLPQDGKLIVMAGYPPEDQLDDADLAAASWAWSNDRAAGRGSDTLPGAKRLFLPM RTGRGLIGVIGIDDDRSGPLLTPDQRRLLDALVDQGALAIERVLLVEDMDKVKRTMEQDRLRSALLTSISHDLKTPL ASVLGAASTMRDLATRLSDKEKLDLLATVIDESERLNRFIANLLDMTKLESGAIKPNTAPHDLGEIVGSALRRASKIL AGHKISLELAADLPMLELDAVLFEQVLFNLLDNAAKYAPADTTIELRSRRDGAWVVLDVRDEGDGIPPDEVEHVFD KFYRVQKGDQVRPGTGLGLAISRGFVEAMQGRMTAGNRADRSGAVLTIRLPVPPQAKTLETAA	29~~KdpD (1.87078E-121)~~236;X;258~~Usp(5.58343E-45)~~383;X;408~~DUF4118 (7.35903E-19)~~508;X;534~~GAF (0.000000000003112 52)~~653;X;670~~HisKA (0.000000000090343 6)~~736;X;789~~HATPase_c (1.14859E-26)~~892	KdpD protein
	9E-11	51.3	10.6	1.3E-10	50.8	7.4	1.2	1	Q8RGC5_FUSNN	Uncharacterized protein	FN0379	Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131)	295	190304	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Fusobacterium, Fusobacterium nucleatum, Fusobacterium nucleatum subsp. nucleatum, Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131)	>tr|Q8RGC5|Q8RGC5_FUSNN Uncharacterized protein OS=Fusobacterium nucleatum subsp. nucleatum (strain ATCC 25586 / CIP 101130 / JCM 8532 / LMG 13131) GN=FN0379 PE=4 SV=1MKTIFRCLLESIVYTILVLLIFYFLPYTKKEFLILNLHPLEVVVAFMSLRYGTYLGILSSFIAIFGYIFAYLHSGNDMI LFLLKFQYYKFFLMFLFTAMVLGKFKLNYKNREEDLKKGFEHLENNFQEEKEKNQQLLDINISLKNQIIRSGGSIVSF HNLKKGLLQLKKEELYEKVLEIFRQLLACEVCSIYTLVDNKLIRRFEMGKSKMEKEILLNSEAGKKFLEVSKKNISLNF PFDIAGKQPIFIGPLYNEKNITGFLEIESFSYTTGEKYNFELFKILMEEINEILQKRRD	8~~DUF4118 (0.000000000000255261)~~111	non-KdpD DUF4118 protein

	9E-11	51.3	11.8	1.5E-10	50.6	8.2	1.3	1	B6JA61_OLICO	Histidine kinase (EC 2.7.13.3)	kdpD OCA5_c03360	Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	901	504832	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Oligotropha, Oligotropha carboxidovorans (Pseudomonas carboxydovorans), Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	>tr|B6JA61|B6JA61_OLICO Histidine kinase OS=Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5) GN=kdpD PE=4 SV=1MSDDPIREHSRPSPDALLESAQRETRGHLKIFLGAAPGVGKTYEMLMSGRAQRADGVDVVIGVVETHGRAETEALVDGFEIVPRRTVPYRGHVLDEMDIDAILARKPALVLVDELAHTNAPGSRHPKRYLDVEELLANGIDVYSTLNIQHVESLNDVVAQITRIRVRETVPDSIIDRADDIEIIDITPGDLIKRLNEGKVYLPKTAKRATQNYFSPSNLTALRELALRRTAQRVDDQLVTHMQAHAITGPWSAGERVLVCINERPGATALVRYGRRQADRLRAPWAAVHVETSKDARLSEHQKDKIASALRLAEQLGAEAVTLPGENVAQEILTYASTNNYTHVIVGMPTSPRWRELFAGSVSHDLIRAKTDVSVHVISPGNGEDTRRPATVSARSKKRPDVGHYLWSTLYVAVALGLGTALSRFLDVRNIALVFLMAVLASAMGGGLWPALFASVLSALAFNFFFLDPLYTLVIGDPESVVAFAFFLVVAVIASNLASRVQRQAVTARERAKTTEGLYQFSKKLAGAGTLGDVLWATVYQIASMLHVRVVALLPENGRIAVQAGYPPDDTLDDADIAAAHWAWEHDKPAGRGADTLPGAKRLYLPLKTGRTQVGVIGLDNDKQGPVLTPAEQRLFDSLADQAALAIERIQLVADVDNARLAAEADKLRSALLTSLSHDLKTPLASILGSAGALRDYSTSLTDSGRVELLTTIVEEAERLNRFIANLLDMTRLESGAAAVSLTPLFIGDSVGSALRRAEKILACHRVDLAVPPDLPMVRLDPVLFEQVLFNLLDNARKYAPAGSLILIRAWAEEDHVVLQIVDEGPGIPSDDLTRIFDSFHRVRKKDHVQAGTGLGLSICKGFVEAMGGTIFATNRADRPGAIFTLRFSIGPEPSPMEGRI	26~~KdpD (2.64966E-112)~~234;X;256~~Usp(1.61787E-39)~~379;X;404~~DUF4118 (3.06211E-20)~~504;X;530~~GAF (1.65672E-15)~~649;X;666~~HisKA (0.000000000057394 3)~~732;X;785~~HATPase_c (8.45486E-28)~~888	KdpD protein
	9E-11	51.3	7.7	1.9E-10	50.3	5.3	1.5	1	D4K1L8_9FIRM	Uncharacterized protein	FP2_28970	Faecalibacterium prausnitzii L2-6	706	718252	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii L2-6	>tr|D4K1L8|D4K1L8_9FIRM Uncharacterized protein OS=Faecalibacterium prausnitzii L2-6 GN=FP2_28970 PE=4 SV=1MEILLTGFTAFLTQEWIETAFPDDHVLTTRAKGEAPPDTRIKTVTLEGGQLLDQIAETYQFDRVVYFSEYLLPHGNQEGELDRLRRVLQSCREREVELLYLSGPEAAFVPSSGKTLLANAAEELCFHYARTSKLQVKVFRLPYLYAVSASGADQFARLFEQMPAGTVQMEEQAAQPLLALCAEELADLVARVFDTWTPEPERFTLPDVFGSTQGQLGEVLQKLQPGLKVLYGTDTIQTYPAADNAVRRRYGWFQRYSILDDLPAIYHAWCARKTEKKSSIRKMVDKLRRSPLLLRLAEIAAAWLATELLVRITGTDAQFRMIDFRLMFVVLIGTVYGLNAGVLSAVLASVSLAAGYLRQGTTLMLLFYAPANWLAFIVYFVVGASCGYVQLRNTETARFVQEENDLLRKRLEFTRKLYQDTLEDKRLFRRQILGRRDSFGKIYAVTQQLDMLQPQEICRKTVQIMEDVLENHSLTIYRMEKNQGFARLTAASAGMTPEPAYSLEVDQWLDVLRAIEQEGLWVNRGFLPGRPMYAAGVRQNGSLVVLIGLHTASEEQMTLYYQNLFRILCGLVETALVRAFEYESVVRENWYLPGTCLLRPAVFAEQLATACTLQEDKMAHHLLLQVTGKFKNRAEINDRVRRSIRSTDAAGVGTNNAIYLLMNQTDEENLPLLTQRLGEKGLHVTAVPLDEQLRLISAAKQEASHA	73~~NADB_Rossmann (0.000777578)~~145;X(152);297~~DUF4118 (3.81538E-15)~~395;X;454~~GAF (5.24361E-16)~~578	non-KdpD DUF4118 protein
	1E-10	51.2	7.3	1.7E-10	50.4	5.1	1.4	1	A6V7F6_PSEA7	Histidine kinase (EC 2.7.13.3)	kdpD PSPA7_3637	Pseudomonas aeruginosa (strain PA7)	885	381754	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	>tr|A6V7F6|A6V7F6_PSEA7 Histidine kinase OS=Pseudomonas aeruginosa (strain PA7) GN=kdpD PE=4 SV=1MTDTARADALLADLPGDGRGRLKVFLGAAPGVGKTFAMLQAAQAQLRQGVKLRAGVVETHSRAETEALLAGVPQQPLRSLEYRGMKLQEMDLDGLLADPPALALVDELAHSNVPGSRHAKRWQDIQELLAAGIDVYTTVNVQHLESLNDQVRDITGVQVRETVPDWVLQEAYEIVLIDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELAMQTAAARVDADLAHRYRQRGEEAPALRGRLLVGIDGDEQAERLVRHACRVAERRHLPWSVVHVDTGGLRGEQARMRLQGAQQLAERLGGEIVVLRAGEVARTLLQHARERRASLVLVGQSRRRWYRRAFGGGLAGRLLRDGQGLEISALDSEADLRPAEPRPRYPLAWNDYLLALLATALASGLAWGVAHLLELPNISLVFLMAVLLVAVRSSLMPALLCAVASFLAYDFLFIPPHFSFAIHRHEDLLSLAFFLFMAGLTGNLAARQRRQLEALRDTQEETSLLLELSRKLTAATDRQAVLAAAAQQFEGWQDVEVCLLGQVNGEWKTEAGAQRPLTDQERVAADAWAWSHDQPAGLGTGTLPGGRWWWWPLSAEEGPLALLGIAPLDGQPLSPQRRRLLAALGQPLAQALARARLAEDLEAARLHGETEQLRSALLASVSHDLRTPLTAMRGSIDSLLALGEAIPPADRRELLESTRDEAERLDRYIQNLLDMTRLGHGGLKLARDWVAPGDIVGSALNRLRAVLAPYRVQAIVGNDLPLLYVHAALIEQALINVLENAARFSPSQGRLRVEVSQGDAELRFAVSDEGPGIPLAERERKIFDMFYTAARGDRGGQGTGLGLAICQGMIGAHGGRISVGEGLDGRGTTLVLHLPLHPQPDLGQLEADE	18~~KdpD (1.99307E-121)~~227;X;248~~Usp(1.30925E-31)~~365;X;405~~DUF4118 (7.94576E-14)~~489;X(159);648~~HisKA (7.14152E-14)~~714;X;767~~HATPase_c (4.4664E-26)~~870	KdpD protein
	1E-10	51.1	13.4	1.7E-10	50.4	9.3	1.3	1	B8ET99_METSB	Histidine kinase (EC 2.7.13.3)	Msil_2823	Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	901	395965	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Methylocella, Methylocella silvestris, Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	>tr|B8ET99|B8ET99_METSB Histidine kinase OS=Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906) GN=Msil_2823 PE=4 SV=1MSERRDFDKRPSPDALLGAAEQETRGRLKVFFGAVPGVGKTYEMLTAAHARKAEGVDVVIGVVESHGRPETEALIRGLEIVPLRQIAYKGRTIGEVDLDAILKRRPQLVLMDELAHTNAPESRHPKRYLDVEELLNAGIDVYTTLNVQHLESLNDVVAQITRVRVQEKIPDSILDRADEIELIDLTPKDLIQRLHEGKVYAQDTAGRALENYFSIGNLTALRELALRRTAQRVDEQLLTHMQAHAISGPWAAGERILVCVNDSPNAIGLVRYGRRVAERLRAPWAAINIETGASVRLDQAARDRLAETLRQAERLGAEAIVLPGRTITEEILRYAAETNVTHIVIARSQRPRWQELLQGSVTHSLIRGAGDISVHVIAPREAATQPAKTADPKGGAAPSLGWKQALAVIGLVGLATAVGAVLRQYLDVHNVALVFLMGVLTSAVSFGLWPALFASIVSMLSFNFFFLRPLYTFTIADPESVVALVFFFIVAVIASNLTASVRSQAVVARKRAKTTEDLYLFSRKLAGVGALDDVLWAAAAFQIASMLSVRVVILLPAADGSLEVRAGYPPEDQVEPADIAAARWAFESNRPAGRGADTLPGAQRLFLPMWTGRGSIGVVGLDSDREGALLTPESRRLLDALIDQTALAIERVNLVEDLDRARLVSETDRLRSALLTSISHDLRTPLASIMGAAGALSDFAGQLTDESKRELTDTIQEEAERLNRFIANLLDMTRLESGAVHPNAAPHDLSDVVGAVLKRARKILAAHRVEVALAPDLPMLDIDAVLFEQALFNLLDNAAKYAPAGSLIRLQAVKDDGFVVLQILDEGPGIPAADVERIFDKFTRAQKGDQVGAGTGLGLAVCRGFIEAMHGTIAAGNRSDTHGAVFTIRLPALEPASGELSA	25~~KdpD (1.16729E-120)~~233;X;255~~Usp(2.73528E-41)~~378;X;406~~DUF4118 (4.78966E-18)~~504;X;531~~GAF (0.000000000000388034)~~650;X;667~~HisKA (0.000000000000234191)~~733;X;786~~HATPase_c (1.44054E-25)~~889	KdpD protein
	1E-10	51	4.2	1.9E-10	50.3	2.9	1.3	1	R4K6B5_CLOPA	Histidine kinase (EC 2.7.13.3)	Clopa_3992	Clostridium pasteurianum BC1	880	86416	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium pasteurianum, Clostridium pasteurianum BC1	>tr|R4K6B5|R4K6B5_CLOPA Histidine kinase OS=Clostridium pasteurianum BC1 GN=Clopa_3992 PE=4 SV=1MRGKLKIFFGYAAGVGKTYEMLREAQEIKESGEDIVIGYIEPHARPETIALTKGLEKIELKTIRYKGSTFREFDIDKALIRKPKIILVDELAHTNGIGQRNRKRWQDIEELLAAGIDVYTTVNVQHIESLNDVVENITHISVRETIPDKIFDEAEKVEIVDIEPDELLNRFKSGKIYRIEQVKRALLNFFTRNNLYALREIALRRIADRVNYEVESGRLAKREITVIPASEQILACISPSPSSAKVIRTAARMAENYHSKFVVLYISTTKAENLSKEDKKRLNLNFSLAEKLGGEIAQLYGDNVADQIIQYAKFRNITKLVIGKNYKRSSKILHFYAKDVVDKLMDSNAYIDVYVIPNSLYKKKREKLIRKLNRWNNFSLKEISESILIIGIATGIAQIFDYMGLNDTNEIMILILGVIIVYIRTTGYFIGVIASIVGVLMFNFLFTEPKYSLEIYDKNYLITFTIMLIVAFIVGNLTNRIQKESNNSYTREKRTQTLYMVSSKLLSAVGASDVISIGIKYTSRLINRTVVAYLSEDNKLSASFVYNNKSENENEINLNRDENAVAYWCLLNGKEAGKGTDTFYGAKGYYVPIKIQEKILGVIGVSCLQGFLEPEQKFIVQTITGQIAIALDREILSSEQETSKVQIERERLRSNLLRSISHDLRSPLAGIKGSISITILEKGKVISEKTKEELLNGIYDDTEWLIRLVENLLSMTKFDEGNMDIIRNMELVEEVVSEAVQRSSKYSKDHKIKVNVPEKIIMVPMDGNLIEQVIINLLDNAAKFSPKYSIIEIKVYESEEDVIFQVIDNGCGIEEKILSNIFERFFTNGSKISDSRRGVGLGLAICKSIVEAHGGKITAANKKGGGAIFTFNIPKKHENLKK	2~~KdpD (4.15928E-123)~~210;X;233~~Usp(8.00178E-41)~~357;X;385~~DUF4118 (2.69554E-16)~~484;X;513~~GAF (0.0000943404)~~632;X;649~~HisKA (0.000000000099328)~~715;X;768~~HATPase_c (1.02193E-28)~~871	KdpD protein

	1E-10	50.7	5.7	2.6E-10	49.9	4	1.5	1	E3EJM1_PAEPS	Histidine kinase (EC 2.7.13.3)	kdpD3 PPSC2_12225	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	898	886882	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus polymyxa (Bacillus polymyxa), Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	>tr|E3EJM1|E3EJM1_PAEPS Histidine kinase OS=Paenibacillus polymyxa (strain SC2) GN=kdpD3 PE=4 SV=1MAAKQNDAGSILNRITDMSVRKRRGRLKIFIGYAPGVGKTCAMLNAAYEEQKEGMDIVVGCVEHDARPYTA ALLEGLELLPYIKISSEESSTKEFDVDQALQRSPELILLDDLAHANAAGCRHRKRYQDVEELLRAGIHVYTTMDIQQI ESLTDIVYSITGISVEERIPDSVFNRADQVELVDIEPDDLIERFYRGKIYRENENIQAHLFTKEKLTALREIALRNTASQ LNRIALQISDQTKTNECNTKEHILVCLSSADSNKKVIRTAARMAAAFHGHFTALFVETQEARELTTKNKSELRENLRL AEQMGAQIATMYGDDIPGQIAEYVKTSHVSKIVLGRSPYKKRGLAKSNVMDKLTTLLPNIEIYIIPSTVPSFYKKMNY YAKYPNLSLADTIKTIAILAVCTVIGLWFKYLEFREANIITVYILGVLLNAIVTKGRMYSAISSIMSVLVFNYFFTEPYYS LQAYDSGYPVTFLVMLAASFMTSTMTMRIREQARQSAHKAYRTEVLLETSRKLQQAKDSPGIINEMAYQLVKLLDR TVIFYSVHQGALLAPQVFSKKESACDPGVYTGGNERAVAEWVYKNNKRAGATTDTFFGAKCLYHAVRGGDQVLA VAAIVMDQEEPLEVFDNSLMLAMLGECALALEKEKLNEKQQEISMQIQQEQLRASLLRSISHDLRTPLTSISGNAGIL LGNSEVLNDEQKKGLYTDIYDDSMWLINLVENLLSISRIENGTLNLNFQAELMEEVISEALLHVNRNSVKHVIQTELD DELMMARMDSRLIVQVLINMIDNAIKYTQDGSHITISARRERHRVVVEISDDGPGISSEEVKDRLFDMFYTADNIHG DGRRGLGLGLSLCKSIVNAHGGNIGVKNDVPKGAVFYFTLQAEEVNVHE	22~~KdpD (9.66339E90)~~230;X;251~~Usp(1.37296E-31)~~373;X;398~~DUF4118 (8.26775E-16)~~498;X(168);666~~HisKA (0.000000000133389)~~732;X;785~~HATPase_c (4.11605E-20)~~889	KdpD protein
	2E-10	50.6	10.2	3E-10	49.6	7.1	1.4	1	E8RRF1_ASTEC	Histidine kinase (EC 2.7.13.3)	Astex_0655	Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	886	573065	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Asticcacaulis, Asticcacaulis excentricus, Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	>tr|E8RRF1|E8RRF1_ASTEC Histidine kinase OS=Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48) GN=Astex_0655 PE=4 SV=1MKAETRPDPDKLLALFSHDTGGLSRGRLKIFFGASAGVGKTFAMLSEARRLLAEGRNVIIGVAEHHNRPETL ALFDGLPVLPQKTIDHRGVSVREFDLDAAALQLKPDLILVDEYAHTNAPGSRHPKRWQDIEELLENGIDVFTTLNVQH LESLNDVVARLTGVWVKETVPDVAFDEADEIALIDIPPEDLLQRLSEGKVYVAEGAPQRAADNFFKKGNLGRLREL ALRRAAERVDADNDAFSAAMGQSEAATGDKILVLVGPDALSERLIRHTKRMADRSRAPWSALYLQTDRHETLSDK ARLRVEHHLRLAEKLGGRVVRLIAGGAAATILGYARHNGFTRLVLGHSRPVWWRFGLPSLSQKLMAQGAGLEITT LTADQIEVGSRDPIGHTLLATPPRTYLMAGVAVGVSTLLGLPFREMIDPDSLVMLYLTGVVIVAARYGIGPSVLASVL SVAAFNWFFIKPYYSFTFDNISYVLTFAVMLATSLIVGSLTARLSLHVRLARRGEAESRLLYDLSRALSAARGLEDIG DAVQRGLTAAFDVEVALWNNGAQITGVPEIDPRELGAMQWVAQNRQIAGRHTDTLPSARALYVPLPSEPGVLGL TPRDRDRQFTGAEWLVFETVASLIASALQRARQSLEAESARVETENEKLRNVLLASVSHDLKTPLTVMNGAVASLL KMRKKLPREAVDELTSLWGHLTGLQKFVANLLRMAAITSGQLKLNFGPYLIQEIAGAALQRIDPQKGDRQLRTLTA GQIPMVNIDGALIEQVLINLLENAIAHTSDDGIITLSFEGDADRVRVRVSDNGPGLPAGEEAQIFEKFHRAGGLSSDR LSTDRSGQSNGLGLAICKGIIEAHGGLIYAKTNPTGGASFIFTLPAYTHPV	25~~KdpD (2.9732E-115)~~234;X;255~~Usp(1.27535E-31)~~374;X;401~~DUF4118 (4.46976E-17)~~497;X;527~~GAF (0.00000325614)~~635;X;652~~HisKA (0.000137175)~~716;X;770~~HATPase_c (1.29841E-28)~~879	KdpD protein
	2E-10	50.6	10.8	1.5E-10	50.6	7.5	1.5	1	R7N524_9FIRM	Osmosensitive K+ channel histidine kinase	BN816_01860	Firmicutes bacterium CAG:95	443	1262988	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:95	>tr|R7N524|R7N524_9FIRM Osmosensitive K+ channel histidine kinase OS=Firmicutes bacterium CAG:95 GN=BN816_01860 PE=4 SV=1MQNIVNKTEREHILVCLSPSPSNERIVRMAGNMAQAFCGSFTALYVQTPGYASMNAEDTVRLQAHMYLAKQ LGAEIVTTHGEDVPTQIAEYARLSDVTKIVIGRSGIQRRHFWSEPALTERLITLAPEVDIHIIPDAEVYKSYRGKRLSTI RPILPTARELLLTLGILAAATIIGWLFLKLDLASANIIMVYLLGVLLTSSFTNGYTCGILCAFLSVVLFNFFLTEPRRLSLG AYGSKYPITFAVMFAAALLTGTLATKLKAHALLSARDTYRTKLLFDMNRKLQKAEAPEEVYQMTAMQIQKLLQRDIL VYPVQGDALSTGILYPTDGSCPHPAPADDQEQDVIHWVWQNRKRAGATTETFPKAKRLYLAIRTGQQAYGVVGI PMEKKTQPDAFTSSILFSILGECALTLESLRNAREKEETAVLAKNEQLRANLLRSISHDL	12~~Usp(4.21628E-36)~~135;X;161~~DUF4118 (1.84701E-17)~~262;X;289~~GAF (0.000386729)~~404	non-KdpD DUF4118 protein
	2E-10	50.5	3.2	2.9E-10	49.7	2.2	1.4	1	A5GDP9_GEOUR	Histidine kinase (EC 2.7.13.3)	Gura_00084	Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	372	351605	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter uraniireducens, Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	>tr|A5GDP9|A5GDP9_GEOUR Histidine kinase OS=Geobacter uraniireducens (strain Rf4) GN=Gura_0084 PE=4 SV=1MEKSSIVRPLILISFIGISLLHYLTPLHLPYLHAIFQRFYYLPIILAALWYGFRGGLLCSLIVSVAYAPHLLFQWG GCLTMEMEKYLEILLYNTVGGVTGLLSQRERERTVELQRTARGLEESYQKLQYQSERIIVIEEQLRRAEKLSTLGE MAAVLAHEIRNPLGSIRGTAEILKDDYNPGDPKHEFIEIQIKETERLNRVVEDFLHMARPQPADLRPCPVQDELETIV TLVANDARDRQIKLVLQPPPFPVIIRADGEKLRQAFLNIIINALQATPPSGSVIISTTIYQAALCEIRFRDSGPGIDAETL GRIFEPFFTTKPDGTGLGLAITRKIIESHGGTMMVESESGHGTTVTVRLPMQDEAGGGAL	10~~DUF4118 (0.000000000000035987)~~110;X;148~~HisKA (0.000000000000020348)~~212;X;263~~HATPase_c (6.94904E-29)~~361	non-KdpD DUF4118 protein
	2E-10	50.5	7.4	2.7E-10	49.8	5.1	1.4	1	A8AV33_STRGC	Uncharacterized protein	SGO_0324	Streptococcus gordonii (strain Challis / ATCC 35105 / CH1 / DL1 / V288)	593	29390	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus gordonii, Streptococcus gordonii (strain Challis / ATCC 35105 / CH1 / DL1 / V288)	>tr|A8AV33|A8AV33_STRGC Uncharacterized protein OS=Streptococcus gordonii (strain Challis / ATCC 35105 / CH1 / DL1 / V288) GN=SGO_0324 PE=4 SV=1MKTLLFGNTGYITKEFIEEAFPNSDVYIFGETNLTGLKRVTVFKKTEAIGIAEILENYRFDQILYLSNFLTYKNQQ IGELERLQDFLKNTSKLTWSKIIYLTGPEIINLPQDLERAAENLCLHWAHTYSGSLKIIRSPYVYSATQPEDYFYGLM SNIRRNQPIRFDELPDEVANFINSEDLAELVYKVFNSWTDEIEVLTIPSPFQDTFQQLATKLQNLELSHSTIGFQSSN KLSPLYQTMDKNNLRGRYGWFIHYSILDDLSDLYCQFASESKPLRRLEFRGLKKNIYRLRGHNDFQKTAEILLAFLL SEVLSFVVARFNQLGMIDVRLLFVTLISTIFGTVYGVFAGILSVLGLFVTSIAAGNKWQSIVYNTDRWLPFAAYIFVAL ICGIIQMKYQDEKELLEKENQLLNEQNDFLTLSYEDAAHDRDALVQKVVSSSNGNSQLYAVHKRLNKKTVEEVIAE AEKIIGEEFSTDEVHFYPLSPFSNFKIELYPQLKEGLEKEAVWINKKMLPDYPVFAVEMKSASGLHYLIWVDEVSYD QLTFSKLHFLQMVSELTASMVDKAGYYQVFSSMNKDSGLTTHSSPGEMRQGN	1~~NADB_Rossmann (0.000000960848)~~189;X(112);301~~DUF4118 (1.90712E-15)~~400	non-KdpD DUF4118 protein
	2E-10	50.4	7.3	3E-10	49.6	5.1	1.4	1	M4WUS5_PSEDE	Histidine kinase (EC 2.7.13.3)	H681_10020	Pseudomonas denitrificans ATCC 13867	885	1294143	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas pertucinogena group, Pseudomonas denitrificans, Pseudomonas denitrificans ATCC 13867	>tr|M4WUS5|M4WUS5_PSEDE Histidine kinase OS=Pseudomonas denitrificans ATCC 13867 GN=H681_10020 PE=4 SV=1MTDPNRADALLADLPGMGRGRLKVFLGAAPGVGKTYAMLLAAQGQLRQGVNLRVGIVETHGRAETEALLA GLPQQALKRSVYRGITLEEMDLDGLLADPPQLALVDELAHSNAPGSRHAKRWQDIQELLSAGIDVYTTVNVQHLE SLNDQVRDITGVQVRETVPDWVLQEAYDLLLVDLPPRELLERLREGKVYVPEQARAAIDAFFSQTNLTALRELTMQ TAAARVDADLAHRYRQQGGEAPAVRGRMLVGVDGEHNAERLVRHACRVAERRHLPWSLVHVDTGDARSEESR MQLQNAQQLAERLGGDVVELRGGEVARTLVEHAKERRATLLLVGRSRQRWHRRLFGGGLAARLLRLGDGLEVS VLDSEADLAPPKARPQSPWPWGSYLLAALAAAGASALAWAVASVLELPNISLVFLAAVLLVAVRSSLGPALACAVL SFLAYDFLFIPPHFSFSIQREEDVLTLLFFLLMAGLTGNLAARQRRQLQALRETQEETSQMLELSRKLTAATDRKAV MAAAAQQLGGWEGLDICLLGQAHGEWKVEGGLSRPLDDQERAAADWAWQHDQPAGLGTGTLPGGRWWWW PLSGEEGPLALLGVSPRDRQPLPGSRRRLLAALGQPLGQALARARLAEDLEAARLHGETEQLRSALLASVSHDLR TPLTSMRGAIDSLLALGDAIPPDDRRELLESTRDEAERLDRYIQNLLDMTRLGHGGLKLSRDWVSPGDIVGSALNR LRAVVAPYRVETRVPPELPLLYVHAALIEQALVNVLENAARFSPPQGRLRVAVEANEEELRFSVSDEGPGIPPAER EKIFDMFYTAARGDRGGQGTGLGLAICQGMVGAHGGRITVEDGIDGRGTTLVLHLPLQQQPDLEQLDAAV	17~~KdpD (1.78584E117)~~227;X;248~~Usp(1.22304E-31)~~365;X;415~~DUF4118 (3.01385E-15)~~489;X(159);648~~HisKA (2.92303E-14)~~714;X;767~~HATPase_c (3.04539E-28)~~870	KdpD protein

	2E-10	50.4	9.4	3.1E-10	49.6	6.5	1.3	1	I3THQ2_TISMK	Histidine kinase (EC 2.7.13.3)	kdpD TMO_0451	Tistrella mobilis (strain KA081020-065)	915	1110502	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Tistrella, Tistrella mobilis, Tistrella mobilis (strain KA081020-065)	>tr|I3THQ2|I3THQ2_TISMK Histidine kinase OS=Tistrella mobilis (strain KA081020-065) GN=kdpD PE=4 SV=1MTRDADRPAPEALIEDAKRERRGRLKIFLGAAPGVGKTYAMLEEAQRRRAEGTDVAVAVVETHGRAETEALLRGLEVIPRRILTHRGRSFPEMDLDAVLARRPALALVDEFAHTNIPGARHEKRFQDVAELIDAGIDVLTTLNVQHLESLNDIVQRITRIRVVRETLPDDVLAMADEIELIDLPPDDLIRRLREGKVYLGDQARRAVLHFFSRGNLTALRELALRAAAERVDEEMIRYMRAHAVPGPWPARERLMVCIGTGAEAEAVVRAGRRMADRARLPWIAVHVETGTGAASAGDYTPQDRANRALRLAERLGAEVTVLPRPVHARRLADELVALARERNVSRIVIGRAPRRPWWRRLGAGGGLAEALVSRATGFELTVIAAEAGTTAAAAEPGRLQAEAPGPHFGPRELALIGVSVAAAALVSTLVEMILPLPNVSLVFLIAVLVVAVRGGLWPSIAASVLSFFAYNFFFTVPHHTFQVSRTEDILTIVFFLIAAALTGNLAGRLRERVQAERQAARRVGNLYDFARKAAGAADVDDVAWAVVSHVARTLQCDAVLLLPEPDGGLRIGAGFPPEDRLTPANRAAAEWAWRHERPAGWSSDTLPASDWLFVPMKAARGPVGLVGVSFGGRDGRPKQLGPEQRRLLEAVVDQAALAVDRTLLAADIERERLKGEADALRAALLSSISHDLRTPLVSIIGAASSLKSLGEALDPGARGELADTIHDEARRLDAYVQNLLDMTRLGHGALALRRDWVDLAELAGRVRGRLARQLGGRQLDVVVPEGLPLLHVDAVLMEQVLVNLVDNAVKHGGPDGRITIAAALADRGRSIDIRVEDDGPGIPEADREAVFDMFHRVKAGDSQPAGTGLGLAICRGFVEAHGGTIRAEAGAGGQGTRIVIRLTVAEPPAPPPEDAE	20~~KdpD (2.1142E-117)~~230;X;252~~Usp(3.41336E-22)~~382;X;412~~DUF4118 (6.87556E-19)~~511;X;537~~GAF (0.000000000000326)~~660;X;677~~HisKA (0.000000000013609)~~743;X;796~~HATPase_c (6.38362E-27)~~901	KdpD protein
	2E-10	50.4	6.6	2.8E-10	49.7	4.5	1.3	1	Q39VD0_GEOMG	Cyclic diguanylate phosphodiesterase	Gmet_1560	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	317	269799	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter metallireducens, Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	>tr|Q39VD0|Q39VD0_GEOMG Cyclic diguanylate phosphodiesterase OS=Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) GN=Gmet_1560 PE=4 SV=1MKKSYLIHGAKGRVVILVLLTAVIALFHFVVPTESHVYHALHIVLRKLYFLPPVMAGAWFGLRGAVYTTSAVTILFSLHAFLDWPGNYMEQANQMGELASFWVVGLVSGWLFDRQRALLAELATANEETLLALVSALDMRAKNSRLHSLRVREIALRLADHLGVTENERKAIGFGALLHEVGKVSIHDSVFTLLKRVGLPELELKEMRSYPEAGYNLLRKIGFLREAAEIVRAHQEHFDGSGYPRGLRGEEIPLGARLLLIADTFEKLITGIGAVQCEEEAVRIIREGSGGEFDPGLVDLFTGIGCDELSHVASAKDE	14~~DUF4118 (0.00000564927)~~116;X;147~~HDc (7.27187E-16)~~286	non-KdpD DUF4118 protein
	2E-10	50.4	6.2	2.1E-10	50.1	4.3	1.1	1	R5DVB8_9FIRM	ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	BN462_00738	Ruminococcus sp. CAG:108	171	1262950	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:108	>tr|R5DVB8|R5DVB8_9FIRM ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein OS=Ruminococcus sp. CAG:108 GN=BN462_00738 PE=4 SV=1MIGRSSATRKSIFSKPTLTEKLIANAPNLDVHIIPDAGGKNAAYRAKKARRKSKSVFSVSDLLKNVAILILASCIGMLFRQLGVAEANIITVYVLGVLVTSVVTRHRIYSLISSIVSVLVFNFFFTNPQFTLRAYDQGYPVTFLIMFLAALLTSSLAVKLKEHAKQSAKAA	62~~DUF4118 (0.000000000010531 8)~~163	non-KdpD DUF4118 protein
	2E-10	50.3	12.6	3.4E-10	49.5	8.7	1.4	1	A0A0F2SJA7_9FIRM	Histidine kinase	VR66_04095	Peptococcaceae bacterium BRH_c23	891	1629714	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c23	>tr|A0A0F2SJA7|A0A0F2SJA7_9FIRM Histidine kinase OS=Peptococcaceae bacterium BRH_c23 GN=VR66_04095 PE=4 SV=1MVKGKLTIFLGAASGVGKTYAMLESALGRLSEGVDVVVGLVETHGRADTEAMLNGFTVIPRRSQEYMDRIFFEMDLDAVLTRRPQLVLIDELAHTNVDGSRHKKRYMDVKELLSAGINVYTTLNIQDLETLNDIVTQITGVAVRETVPDQVLEIASQIQLIDIPPEELIQRLKDGKVYVSDQETEGLKDFFRPGNINALRELALLYTAQRVDRQLESYRQDHGINGPWPTGEKILVCISASPFSAQLIRIAKRMTEKVQGQLFAVHVETLRRLPSSEAEKDSMAKNLRLAEELGAEVIGLTGNGVAEAILELARKRNVSQIIIGKPAHTRFWELIHGSVVDKVIRQSQGISIHVIPGRPPEAGKAQIKAVKNGEEAGTKPQGWNSPKIIPYLASSLMIIGMTLVFTLVHPFLGLVNISLLLYLPLISAALWGTLPAIVTAIMGTIAFDLFFVPPFFKFTVADLRYLISFAIFMLVGLITGTLSDRLKKQVNYSRQRENNISALYSLSRDIAAVDNLDAVLDCIVSNVSKTLEGQVMLLLPNEKAQLVLRKDSGLINSLDKCELSVATWVYERGLKAGHGTETLGTAKAQYLPLSTEQGTQGVLGININESNTQFDPERIRLLEAFTGLAAMAINRVKLAEQARESLSLVESERLRTALFNSLSHDLRTPLASIIGAVTGLLEDKNVIYSPEVRKELLKTILYGAERMNRFISNLLDMARLESGMLRLNKEWCDLQDIIGVAINRLGDTLTRRPLDIDIQEGLPLVQADGILIEQVLINLLDNALKYSEAASKIMISIRQQGNQLEIVVANRGHGIPEADLSKVFDKFYRLSSPLQVSGTGLGLAICKGLIEAHGGDIWAENNKLGGVTITFTLPLTDQFLGIVPEMNEGE	3~~KdpD (7.85169E-110)~~211;X;233~~Usp(5.78677E-40)~~356;X;390~~DUF4118 (2.07696E-17)~~490;X;516~~GAF (0.000000000154838)~~636;X;653~~HisKA (0.000000000004490 46)~~720;X;773~~HATPase_c (3.05232E-30)~~874	KdpD protein
	2E-10	50.3	2.7	2.2E-10	50.1	1.3	1.6	1	B9M0Q8_GEODF	Histidine kinase (EC 2.7.13.3)	Geob_2560	Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	376	316067	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter daltonii, Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	>tr|B9M0Q8|B9M0Q8_GEODF Histidine kinase OS=Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32) GN=Geob_2560 PE=4 SV=1MQIQKLSITAFRPIILACFLVCISLLHYLTPLHLPYLHDIFQRLYYLPIILAALWFGLRGGLICSILVSIAYAPHLLFQWGGHLTLEMEKYLEIMLYNIVGGVTGLLSQRERERTVELQKTARGLEESYQKLQNQSERIIIIEEQLRRAEKLSTLGEMAAVLAHEIRNPLGSIRGTAEILKDDYKPGDPKQEFIDIQIKETERLNRVVEDFLHMARPQPADMQLCPIQEELETIVALLSNDARGRQISLVLKPASAPVIISADGEKLRQAFLNIIINSLQATPPGGSVTITTTPYEAGSCEICFRDSGPGIDAETMDRIFEPFFTTKPDGTGLGLAITKKIIESHGGTMQVESEVGHGTIVNVILPMQNASDGGLR	15~~DUF4118 (0.000000000002178 04)~~114;X;152~~HisKA (7.74441E-15)~~216;X;267~~HATPase_c (2.96E-26)~~365	non-KdpD DUF4118 protein

	2E-10	50.3	9.9	2.9E-10	49.7	6.9	1.3	1	I4D2C8_DESAJ	Histidine kinase (EC 2.7.13.3)	Desaci_0905	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	901	646529	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	>tr|I4D2C8|I4D2C8_DESAJ Histidine kinase OS=Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4) GN=Desaci_0905 PE=4 SV=1MSEKKRVSPDELLADIEDEAKGKLTVFLGAAAGVGKTYAMLEVARERLSEGIKLSAGWVEPHARPETMALM EGIPQIAPKEIEYHGKVLKEMDLDEILSIHPQIVLVDELAHTNVPSSRHLKRYQDVEELLAAGIDVYTTVNIQHVESFN DIVAKITGVTVRETVPDSILEHARIQLIDISTEALIQRLEEGKIYVPNQAKHALDKFFRPGNINALRELSMRFAAQRVD RQLESYMRVHGIEGPWPASERVMVCISSSPFGERLIRMGKRIAVGMKAELLVVYIDTPSNPLKNENQKDQLSKSLH LAQELDAETISLSGNDVVEELLEVAQKRNVTQIIIGKPGQLKIRERFSSSIVEKVLRQSQNISVHVIPGDGPKTKEER ENKKTGVKKTNDLVPYLTTFVSLAVITVVAWLGSSELGLVNTAMLYLLPVLLSAGRYGKRVGIFTSIVSVITYDFFTIP PVLTFTVADLRYLVSFAIMILIGYYLGNLSTRLRIQLINSRQRESQTAALYSLSREIAAVSDLDFVLESVVKKVSDIIRG EVVILVPETNGQLSLRSCSNLETAFEENERAVATWVFENNQTAGKGTDTLGGAKGFYLPLVSEQGICGVLGVQQS SSERYLSAEKRRLLDAFASLTALAIARISLVEKAREAQLLNESEKLRTALLNSISHDLRTPLASMIGAVTSLIENDKLF DVTSRQDLLETIKIGAMRMNKLVNNLLDMARLESDMLKLNKEWCEIDEIIKEAIKHIDEGLENKREIICEISNKELLVNV DFILIKQVLTNLLDNAMKYSKPDSRICIIVRNNEKQVEVSVRDWGLPIPPEDLEHIFDKFYRVRSPRQISGTGLGLAIS KGIVELHGGKIQAENNSEIGGVTISFTIPLSKIPPRIPVEVGDDNE	19~~KdpD (1.66082E-111)~~228;X;250~~Usp(4.79868E-40)~~373;X;398~~DUF4118 (7.41053E-17)~~496;X;524~~GAF (0.000000000062246)~~644;X;661~~HisKA (0.000000000052660 7)~~727;X;781~~HATPase_c (2.48232E-27)~~883	KdpD protein
	2E-10	50.3	10.7	3.7E-10	49.3	7.4	1.5	1	Q187D8_PEPD6	Histidine kinase (EC 2.7.13.3)	kdpD CD630_18290	Peptoclostridium difficile (strain 630) (Clostridium difficile)	900	272563	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptostreptococcaceae, Peptoclostridium, Peptoclostridium difficile (Clostridium difficile), Peptoclostridium difficile (strain 630) (Clostridium difficile)	>tr|Q187D8|Q187D8_PEPD6 Histidine kinase OS=Peptoclostridium difficile (strain 630) GN=kdpD PE=4 SV=1MDRPNPDILLEKIKNEEEKLSRGQLKIFFGYAAGVGKTYSMLESAQNLKKVGVDVVVGYIEPHTRPETLALLD GLEILPVKEIEYKSIKLKEFDLDAALERKPEVILVDEFAHSNVAGLRHTKRWQDIEELLLAGINVYTTVNVQHLESLND IVEIITNVSVKETIPDKFLDTNTQLELIDVEPDVLLERFNEGKIYKKEQATRAKNNFFIKDNLVALREIALRKTAERVNK EVQMTRLSKGDVTVIPTSDTLLACISPSPSSAKVIRTASRISDSTFAKWIALYVETPNTARLPFDEQKQLQNNLKLAK KLGGEIIVLHGENIIEQILRIAKLRNVTKIVIGRNHSSNKRFSKRFKKDIVDKLIDEVDYIDIHIIPYKFASDVKYKTKKDK SSIKSKFKISKVDFIKLIFITLMISILAYAVQSMGFIRENILLIYMLGVVLVSMWTKGYSTGIISSVFNIVLLNYFFTAPLYT LSIADSNYIVTLVVFSIVGIITSTLTSKIQHEAETAAKREENTKMIYQIIKGFLRLSNKDDIVNKGIELLSLSLSRDVICYL NVDKHNKSKLYKKNTNNKDKNDLDSEDEKAVASWVLSNSTVAGNDTDTLPGSKGYYIPIVGMNLTLGVVGISCIDS KLDTEDISLIETIIAQMAIALDREILSEAKENTNLEIERERLRSNLLRAVSHDLRTPLAGISGAVSTIIKNKGTIGQDIIDE LLSGVYEDTQWLIRLVENLLSMTKIDEGKLEVKKHSELVEEIISEALQKIKKRIENALIDINIPEQILFVPMDAKLIEQVLI NLIDNSLKYSKEDCKIEINVYEKDDYVWFEVSDNGPGISKELKKHIFDRFFTGEEGAKDSRKGVGLGLSICKSIIQAH KGEIMVENNKDKGSTFKFSLPKENE	22~~KdpD (1.14233E-108)~~230;X;253~~Usp(6.18197E-42)~~377;X;406~~DUF4118 (1.31302E-16)~~505;X;533~~GAF (0.0000126306)~~656;X;673~~HisKA (0.0000000027628)~~739;X;792~~HATPase_c (1.10753E-29)~~895	KdpD protein
	2E-10	50.2	5.3	3.2E-10	49.5	3.7	1.3	1	R5RKN9_9FIRM	Universal stress family protein	BN747_02091	Firmicutes bacterium CAG:646	672	1262995	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	>tr|R5RKN9|R5RKN9_9FIRM Universal stress family protein OS=Firmicutes bacterium CAG:646 GN=BN747_02091 PE=4 SV=1MEENRPDSEQLLKRLQYEEREKQKKNKGKLKIFLGYAAGSGKTYAMLEAAHEAQKNGVDVVAGYIEPHARP DTQALVKGLEVIPPLFVKYKGVRLREFNLDAALERKPRLLLVDELAHTNARGCRNEKRYQDVKELLRAGIDVYTTINI QHLESLNDLVGNITRIEVRERIPDTIFDHADQVEVIDIEPDELIQRMKDGKIYKEQQAERALQNFFRKEKLAALREIAL RRTADRVNRIAQEERSLQENQDYHTGEHILVCISAAPSSARVIRTAARLAGAFHGELTALCVETPGMQEADEKTKT ALRRHMELARLFGAKVVTVFGSDVAAQIAQYAVVGNVSKIVLGKTNHFSVRPWRRSEFLEKLTYLAPNIDVYIIPDM KQTGKYRPEKKRRRTPGDTWKKIIRDLFMITGVMGGATLLALGFRQMEFSEANTIMIYLLAVLLSSYIANRKIYALYS SMLSVLLFNFFFTEPYYSLKAYDKGYPTTFLMLFIVGLFTGTMTRKLKQQNQESAKTAYRTEILLENSQKLRRCKSR RAVWDQVAVQVGKLLNLAILIYPVSESGLVDQPLLFPRKGMTVEELEKCVNFREKGVVQWVVANHHRAGACTHT LPDAMAMYLPVQSEKEVKGVMGILLEERRPVDEFEYGLLIAMLNETGVKLQDPFVAEESKTS	32~~KdpD (2.09455E-119)~~235;X;256~~Usp(2.53555E-33)~~379;X;411~~DUF4118 (4.06471E-15)~~509;X;539~~GAF (0.000198843)~~661	KdpD protein
	2E-10	50	13	4E-10	49.2	9	1.4	1	Q20XR7_RHOPB	Histidine kinase (EC 2.7.13.3)	RPC_4547	Rhodopseudomonas palustris (strain BisB18)	907	316056	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Rhodopseudomonas, Rhodopseudomonas palustris, Rhodopseudomonas palustris (strain BisB18)	>tr|Q20XR7|Q20XR7_RHOPB Histidine kinase OS=Rhodopseudomonas palustris (strain BisB18) GN=RPC_4547 PE=4 SV=1MADHRRNADQRPSPDALLDAARREDDGRGRLKIFVGAAPGVGKTFEMLQSAHAKRKAGVDVVVGVVETH GRSETEALLAGLEVIPRRRLDYKDHVLDEMDLDALIARRPRLALVDELAHSNAPGSRHPKRYLDVEELLSHGIDVYT AVNIQHIESLNDVVAQITHVRVRETVPDSIFDRADAIELVDLTPDDLIQRLREGKVYVPKQAERALEHYFSPGNLTAL RELALRRTAERVDEQLLNHMQANAIAGPWAAGERILVCINEDTRSAGLVRYTRRLADRLHAPWSAICVETRSAQR LTEVERDRLADTLRLAEALGGEGMTIPGSGRHVADDVISFAHNNNVTQIVVGKSTRSLWVELLRGSVVHDLIRRAG NISVHVIAGEELAADPVARKTVKTLERNDSFDPRPYLMAVLMVAAALGLAILIEPTFGVVNVDLVFLTAVVSVAVRYG LLPSLLASVTASLCYNFFFLPPFYTFTIAEPTNIAAFLFFMLIALLVSNLAGRVRSQAVSAIGRVRTTESLYAFSRKLA GTAALDDVLWATAYQAALMLHVRVVLLLPEDGRIVVKAGYPPEDQLDDADLAAANWAWSNDRPAGRGSETLPGA KRLFLPMRTGRGPIGVIGIDDDRSGPLLTPDQRRLLDALVDQGALAIERVQLVEDMDRVKRSAESDRLRQALLTSIS HDLKTPLAAVLGAASTLRDLSPKLSDAQRAELIGSIVEESERLNRFIANLLDMTRLEAGAVVPNAALHDLGDVVGSA LRRAATILAHHNVQLDLEAELPMLQIDAVLFEQAIFNLLDNAAKYAPLGTTITVRAARHGDAVLLQIIDEGEGIPPEDL ETVFDKFYRVRKSDQVRAGTGLGLAISRGFIEAMQGSMTAANRSDRSGAVLSIRLPVPPARAALDTAA	27~~KdpD (1.97186E-114)~~236;X;258~~Usp(1.50911E-41)~~383;X;410~~DUF4118 (2.88526E-18)~~510;X;537~~GAF (0.000000000033318 6)~~655;X;672~~HisKA (0.000000000039900 9)~~738;X;791~~HATPase_c (1.28756E-25)~~894	KdpD protein

	2E-10	49.9	10.5	4E-10	49.2	7.3	1.4	1	J7IUW2_DESMD	Histidine kinase (EC 2.7.13.3)	Desmer_0442	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	891	768704	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	>tr|J7IUW2|J7IUW2_DESMD Histidine kinase OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=Desmer_0442 PE=4 SV=1MPKGKLTIFLGAAYGVGKTYAMLEAAIGRLSEGIDVVVGFVETHSRTDTEAMVQKLTVIPTRYLNYKGKISRE MDLEAVLTRHPQLVLIDELAHTNAEGSRHKKRYMDVKELLSEGINVYTTMNIQDLETLNDIVAQITGVTVGETVPDQ MLEIASQIQLIDIPPEELIQRLKDGKVHVPDQETEGFKNFFRMGNINALRELALRYTAQRVDRQLESYRRVHGIAVP WPTGEKILVCISASPFSAQLIRIAKRMTEKVQGELLAVHVETLRRFPSSEAEKDSMAKNLRLAEELGAEIIGLTGNGV AEAILEAAKKRNVSQIIIGKPEHTRFWEILHGSVVDKVIRQSQGISIHVIPGNKQEVGLSQIHRLKKNEDTGAKTQQRI FPQIIPYLVSGLMITLMTLFFRGLSPFFGLVNISLAYVLPILISAARWGTLPAIATALMGTIAFDLFFVPPIFKFTVADLR YLISFAIFLWVGVITGTLSDRLKKQVNYSRQRQNSISALYSLSRDIAAVDDLEAVLDSIVSNVSKTLEGQVMLLLPNE QAQLALRKNSGSDDFLDRQELSVATWVYERGLKAGSGTETLGTAKALYLPLRTEQGMQGVLGIYSSDRKANLDP ERFRLLEAFTGLAAMAINRVKLAEQARESLSLIESERLRTALFNSLSHDLRTPLASIIGGVTGLLEDQNLVYSPEVRK ELLKTILHGAERMNRFISNLLDMARLESGMLRLKKDWCDLQDIVGVAIKRLGDTLTRRPLDINIQENLPLVQADGILIE QVLVNLLDNALKYSEAASKIKVSIRQQENHLEIVVSNRGQSIPETDLSKVFDKFYRLSSPLQVSGTGLGLAICKGFIE AHGGNIWAENNTLGGVTITFTLPLTNQFLGIVPEMDEGE	3~~KdpD (5.61857E-106)~~211;X;233~~Usp(7.32271E-40)~~356;X;390~~DUF4118 (9.51436E-16)~~490;X;516~~GAF (0.000000000017350 9)~~636;X;653~~HisKA (0.000000000007895 23)~~720;X;773~~HATPase_c (2.26649E-28)~~874	KdpD protein
	3E-10	49.9	11.8	4.7E-10	49	8.2	1.4	1	I3UFD2_ADVKW	Osmosensitive K+ channel histidine kinase kdpD	TKWG_19630	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	634	1036672	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella kashmirensis, Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	>tr|I3UFD2|I3UFD2_ADVKW Osmosensitive K+ channel histidine kinase kdpD OS=Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) GN=TKWG_19630 PE=4 SV=1MLGAGIDVWTTLNVQHLESLNDVISGITDIRVTETVPDQVFDDADEVILVDITTEALLARLQAGKVYMAEQVPL ARQHFFRKGNLIALREIALRRTAERIHKDVRQYRHETYVEAIWRTAEGILVVVDTALTPNAAQALIRHGSRLSGQMS CPMHVMFLREAANSRGPARSNGDWQLLLQQAEQLQATTTEHYCNGDVMPDIVAYCRSQNLSRLLDRSVLRRY WWRLSPLVRVGQLGPDIDVIIYGGVSNRQRQAAARAQDHAFARREPVDWGKVGLALMFVCATTALLWPFSSILAI TNIAMLYLALTMVVALRLGRWPGLVCAVSSVALFDFSFIPPLLSFSVADIQYLITLLVMLAVSTLISQLAAQQRFQGR LALQQTQRVHSLFELAKRLSGSLQKEQIVQESQKLLLSDLGEDVFVILPDAHESLLLPEAEAGHEAAGLDMVAAQW AFDNEDKAGFGADTLSANAFRYFPLHAPVRIRGVLAVRMQGAPHLLSPEWQQQLEIYAHVIAIALERIHFVEVANEF LRQVESEKLRVTMLNIISHDLRTPLTVLIGEAEVLAAESNDNHVRQKAAIILDRARCMHDMMSKLLDMARIDSGQQH ISKSWQSIEELVGAPSGTRMCPPGVMS	1~~KdpD (5.04547E-48)~~100;X;123~~Usp(0.00000175388)~~245;X;279~~DUF4118 (1.20446E-15)~~375;X;403~~GAF (0.00000023488)~~520;X;537~~HisKA (0.0000000870569)~~600	KdpD protein
	3E-10	49.7	5.6	4.9E-10	49	3.9	1.4	1	Q2G7V9_NOVAD	Uncharacterized protein	Saro_1624	Novosphingobium aromaticivorans (strain DSM 12444 / F199)	337	279238	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Novosphingobium, Novosphingobium aromaticivorans (Sphingomonas aromaticivorans), Novosphingobium aromaticivorans (strain DSM 12444 / F199)	>tr|Q2G7V9|Q2G7V9_NOVAD Uncharacterized protein OS=Novosphingobium aromaticivorans (strain DSM 12444 / F199) GN=Saro_1624 PE=4 SV=1MQIKSLLLGIPPAGENVSPGMRTSGLRPANATSARPFVETLLFFVLLVVVDHAVAAGDAFAALEPHPFWLPVI LMAVAYGSGPGLLAAILASLIWVLDGEQVQTGDHLERMLSLSILPMLWVTTALVTGEITSSHLGAMRRLARHRNRL TREQNKLTEIIGELAETNRALQVRIALEERTIADAIAAAVELVDMRPSQQLAGIERLVNVATKGGAFTFYVVVGDQLL PLLRGNGARGDLRSDGVIADIWRGAIPGDQPIVQVSPRCAVVPVYADGDPYLRGLLSLEGMGEEVLTQSMRAALI HIAYSLGQLANEVPAPAEPMKLPQRPWLLAQEHAA	65~~DUF4118 (0.000000000685012)~~133	non-KdpD DUF4118 protein
	3E-10	49.7	9	4.5E-10	49.1	6.2	1.3	1	Q6N5H3_RHOPA	Histidine kinase (EC 2.7.13.3)	kdpD RPA3001	Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	907	258594	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Rhodopseudomonas, Rhodopseudomonas palustris, Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	>tr|Q6N5H3|Q6N5H3_RHOPA Histidine kinase OS=Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009) GN=kdpD PE=4 SV=1MPDPRVEPPSRPSPDALLEQARRQEPGTGRLKVFLGAAPGVGKTYAMLQSAHARAKAGVDVVIGYAETHG RAETEALLAGLETVPRRRIPYKGQVLEEMDLDAVLARRPQLAIVDELAHSNAPGSRHPKRYLDVLELLANGIDVYTA VNIQHIESLNDVVAQITTVRVRETVPDSAFERADAIELVDLTPDDLIQRLKEGKVYVPKQAERALEHYFSPGNLTALR ELALRRTAERVDEQLLSHMQANAIPGPWAAGERVLVCVSHDQRSQGLVRYTKRLADRLRAPWTAINIETRRSLSL TEQQRDRLADTLRLAEALGGEALAIPGGDRSLAHDILAFARANNITQIVVGKAPRSFWYEALRGSTVHELVRGSGN ISIHVMTGTAVSIEESQTGSLRPAEGTEPFNPWPYPMALVLVGIGLGVAKLIEPFFSIENVDLVFLTAVVGVAVRYGL GPSLLASVVASLCYNFFFLPPVYTFTITDPTNIVAFFFMLIAILVSNLAGRVRAQATAAAQRVRTTESLYAFSRKLA GTAALDDVLWATAYQIALMLKVRVVLLLPEQGRIAVKAGYPPEDQLDPADLAAANWAWENDRVAGRGSDTLPGA KRLFLPMRTGRGPIGVIGIDDDRAGALLTPDQRRLLDALTDQGALAIERVHLVEDMDRVKRDAESDRLRQALLTSIS HDLKTPLAAVLGAATTMRDLASHLSDAQRTELIGTIVEESERLNRFIANLLDMTKLESGAVVPNSAAHDLGELVGAT LRRATSILAQHTVKLDLGHDLPLIEVDPVLFEQALFNLLDNAAKYAPAGSAIQLRAAQSGGQVELQVRDEGEGIPPA ELETVFDKFYRVRKGDHIRPGTGLGLAIARGFIEAMGGRLSAGNRSDRSGAAMTIRLPIASRGDALISAA	29~~KdpD (5.65846E-123)~~236;X;258~~Usp(1.45799E-43)~~383;X;414~~DUF4118 (7.13981E-16)~~504;X;537~~GAF (0.000000000000976868)~~655;X;672~~HisKA (0.000000000099681 2)~~738;X;791~~HATPase_c (1.54813E-24)~~894	KdpD protein
	3E-10	49.7	10.2	5.2E-10	48.9	7	1.4	1	A0A0F5K0K5_9BURK	Sensor protein KdpD	WM40_09820	Burkholderia andropogonis	944	28092	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia andropogonis	>tr|A0A0F5K0K5|A0A0F5K0K5_9BURK Sensor protein KdpD OS=Burkholderia andropogonis GN=WM40_09820 PE=4 SV=1MTERPDPDELLSRIQRDEARQQRGKLKIFFGASAGVGKTYAMLQAAHRLADEGLDVVAGVVETHGRRETIA LLSGLEVLPAAYFEQRGRRLAEFDLDAALARRPALILIDELAHSNVAGARHAKRWQDVQELLDAGIDVYTTVNVQH LETLNDIVGQITGIRVWETVPDRIFDLADEVTLVDLPPEELLERLRDGKVYMPAQAERAIENFFRKGNLIALRELALR RTADRVDAQMREYRADQSIERLWRARERLIVCVGPGPDSAAMVRTASRLASSLKADWLAVYVDTPRLHRLADVE RKPTFEALKLAGELGAETVVLDGANAAESLAAYALMRNVSKVLVGKSSRGRLRALLQPPFAACLAQAAPQVELTLI APSSDVRHADKRARRPLLRRGESSGDPRSPLSAYVIATIIAAAITAVVTLSLSQANLSNLVMLYLLGVVFAAVKLGR GPGAYLSFLSVFLFDFFCVDPRFSFAIADTQYLLTFVVMLTTSLTISHLTSSLRRQARAASARERRTAAMYAMVKEL GAALTEGQIIEIATRHTHEVFGARVAVLLPDSEDQVRQKIDHPDPMTALPEESLAIDVAQWVYDRQQPAGAGTNTL PASTAYYLPLKAPMRTRGVMALVSNRNTQWASPEQNRLLETFASQIALALERVHYVEIAQDALVSMESERLRNSLL ATISHDLRTPLTAILGLAATLAAQLRESTSSRNDQGIDLANTIHGEAQHMVSLVSNLLDMARLQGGIKLDLQWLMLE EAVGAALALCRRILDGRPVTVTIASDVPMIRLDAVLMERVFVNLFENVCKYATPGTTIGIVGTVVVHDGARRFVKVAV NDIGPGLVPGTEGKIFDKFTRGVKESATRGVGLGLAICRAIVEAHGGQMQARNRISATGERIGASFSLTLPADVQP PAIEEMGEDDMRDEECSGRLIAADAKRGDGEHE	22~~KdpD (2.08458E-122)~~231;X;253~~Usp(1.56852E-33)~~376;X;432~~DUF4118 (0.000000000000345 06)~~505;X;537~~GAF (1.1766E-18)~~657;X;674~~HisKA (0.000000000001301 07)~~743;X;795~~HATPase_c (5.00623E-16)~~905	KdpD protein

	3E-10	49.6	11.3	5.2E-10	48.9	7.8	1.4	1	H6NGY1_9BACL	Histidine kinase (EC 2.7.13.3)	PM3016_1498	Paenibacillus mucilaginosus 3016	509	1116391	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus mucilaginosus, Paenibacillus mucilaginosus 3016	>tr|H6NGY1|H6NGY1_9BACL Histidine kinase OS=Paenibacillus mucilaginosus 3016 GN=PM3016_1498 PE=4 SV=1MIQQRSYLWVTLSIILLTFVLNMLGPAFDLVNIALVYLLPVLISAVYGGKGASFYAAVLGVLAFDFFFVPPQLSFSVSDLRYVVSFGIFLFVASLTGGLAAKLKNQLHYSKQREAYTASLYALSKEMNAIADFQALLQHITLKVSHTVQSESVIYLPNERDELEPASYSMPVPAWAQSEAEMVIAKWVYQHGEHAGKGAGTLREASGRYIPLKIEEKIYGVLSVNLGSSAPSSDMLKLLEALGEIAASAIARVKLSEEAKLAHLTAESERLRTAILDSVSHELRTPLATVIGSATALIEGEGMFSPQDRMELLVTIRDGSLRMNRLVSNLLGMVQLESGMLRLRKRWCDVEDIIGVALKQVKDFQQHRKIRVQFLKQVPLILGDEVLLEQVLVNIISNAIKYSPDGSEINIMVNKEEDAVFFSVSDQGIGIEVSERERIFDKFYRADKSKHITGTGLGLAICKGIVELHGGTISAKPNGEKGLSIVISLPISDEDKIFFIHEEGEQAPV	7~~DUF4118 (0.000000000001102 44)~~106;X;132~~GAF (0.0000000316129)~~252;X;269~~HisKA (0.00000000147375)~~331;X;388~~HATPase_c (1.0317E-30)~~489	non-KdpD DUF4118 protein
	3E-10	49.6	8.3	5.9E-10	48.7	5.7	1.5	1	A5N880_CLOK5	Histidine kinase (EC 2.7.13.3)	kdpD CKL_1469	Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	898	431943	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium kluyveri, Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680)	>tr|A5N880|A5N880_CLOK5 Histidine kinase OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=kdpD PE=4 SV=1MGIHQTNSNLLTEQLLNMSTEKRQGRLRIYFGYAAGVGKTCAMLNDAHEMKKDGIDVVAGYIEPHARPETMVLLNGLELLPPLEVLYNGIMLKEFDLDSALKRKPQLVLVDELAHSNAVACRHKKRYQDVEELLHAGIDVYTTINVQHIESLNDVVASITGISVRERIPDSVFDSADQVELVDIEPDDLIDRLNKGKVYGREQAQRALVNFFTKEKLVALREIALRRTADQVNRVAVLNNKQSKNGGHYTNEHILVCLSSAPSNAKVIRTAARMADAFHGTFTALLVETPQIKELSEKNMIKLRENLRLAEQLSAQIATVYGEDIPMQIAEYATASRVSKIVIGRSNHVKKWFAKTNFVDRLITLAPNLDIYIIPDTQSSFYVKIYKFTKPLELSLPDIFKSAGILFICTLIGLWFDSLGFSESNIIMVYILGVLFNAMVTKGKIYSAVASILSVLVFNFYFFTYPYFSLLAYDPGYPVTFLVMLMASFIVSTLTKRVKEQARYSAQKAYRTEVLLETNRKLQQARDKSEIFSETAHQLVKLLDRTVIFYPEQHNTLSEPLVFPKDGWEDYFKIYLKTDERAVAEWVYKNNKRAGATTNTLSAAKCLYLAVRSSDMVFAVVGIVMDKKVPLEAFEKSLMIAMLGDCALSLEKEKLNERQKQISMQIQQEKLRGNLLRTISHDLRTPLTSISGNAGILMGNSKVLSEAQKKGLYTDIYDDSMWLINLVENILSITRIEDGKINLNLQPELLEEIIAEALCHINRNSVNYHIETIVEDELIMAKVDSRLIIQVIINIVDNAIKYTPPGSHIVISAKRRKQFILVEIADDGPGIEDEAKDRLFDMFYTVDNIHGDSRRGLGLGLSLCKSIVHAHGGTIYVKDNIPOGTVICFTLQAQEVKLS	22~~KdpD (2.17125E-119)~~232;X;253~~Usp(5.96982E-37)~~375;X;399~~DUF4118 (3.46786E-16)~~500;X(168);668~~HisKA (0.00000000124787)~~734;X;787~~HATPase_c (3.33696E-28)~~890	KdpD protein
	3E-10	49.6	4.4	4.5E-10	49.1	3.1	1.2	1	R6EWZ4_9FIRM	Uncharacterized protein	BN538_00486	Lachnospiraceae bacterium CAG:215	285	1262985	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	>tr|R6EWZ4|R6EWZ4_9FIRM Uncharacterized protein OS=Lachnospiraceae bacterium CAG:215 GN=BN538_00486 PE=4 SV=1MKAEQRTTKKVMFCKPKNGWKTVLLDLAEITAVMAVTTVAAHGMQMWNLSESNIIMIYILGVLLSSYIADNRLYALYSSLLGVLSFNFFFTEPYLSLKAYDRGYPTTFLMLFIVGLFTANMTRKLKVQNKENAKKAYRTEILLENSQKLRRCKSEAEVWEQVASQSEKLLDLSVIVYPIAKNGLPQKPLLFPRQGAEKKDLLQYVNPQEKAVVQWVIANRHRAGACTHTLPTAKAMYLPIQDEEEVKGVMGVVLEERREIQEFKYGLLIAMLNETGVKLQDKFLE	27~~DUF4118 (5.1688E-16)~~128;X;154~~GAF (0.0000000320302)~~280	non-KdpD DUF4118 protein
	3E-10	49.5	7.4	5.1E-10	48.9	5.1	1.3	1	R5DTN5_9FIRM	Histidine kinase (EC 2.7.13.3)	BN462_00446	Ruminococcus sp. CAG:108	658	1262950	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:108	>tr|R5DTN5|R5DTN5_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:108 GN=BN462_00446 PE=4 SV=1MKVQTEQSKFDTDEHILVCLSSSPSNARIIHTAAKMAKVLHARFTAIYVQTDTVINDEDQSRLSQNIQLAQRLGAEIVMTHGENVALQISEYVRLSDVTKIVIGQSSARRRGLFGRPTLTEKLISSAPNVDIHIIPDALNYTKSHRRRLFFGAEIPSLRDIAVTVLALVVCTAIGFLFDHLDFPDTNIVTVYILGVLMISVLTKGYLCSIAGSLLSVVLFGFFLTEPRLSFQTYAVGYPVTFAVMLASSVLTGTLASKLKDHARLSARSAFRVQVLFDTDRLLQKAKSNDDVLSVTCMQLSRLLDRSIVAYTKGENGMLSGRLYAEKKDTHAEKLLSDAERQTAEWVLQNGHRAGAATAQFGKSECLYLAIRAGGRVYGVIGIPMKPEKPDSFESSIVLSVVNECALAMDNAHNAAEKERAADLAKSEQLRADLLRSISHDLRTPLCSVSGNADTLLHNGNCLDEATKQQIYKDIYDDSEWLIGVVENLLYVTRLNDGRLKLELTDQLVDEVVNEAVSHLKKKSVGHKVTVRCDDLILARMDAQLIVQVIVNLIDNALKYTEQGAEICVSAEKQGGDAVIRVTDNGNGIADDMKPHIFEMFYTGKNTVADSRRSFGIGLTLCKSIVELHGGTLTLTDNVPHGCIFTFTLPLSEVTLNE	15~~Usp(1.21159E-32)~~136;X;161~~DUF4118 (6.31088E-15)~~262;X(166);428~~HisKA (0.00000000999011)~~494;X;546~~HATPase_c (1.34721E-28)~~649	non-KdpD DUF4118 protein
	3E-10	49.5	9.9	5.4E-10	48.8	6.8	1.3	1	Q2K0Q3_RHIEC	Histidine kinase (EC 2.7.13.3)	kdpD RHE_PE00263	Rhizobium etli (strain CFN 42 / ATCC 51251)	902	347834	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium etli, Rhizobium etli (strain CFN 42 / ATCC 51251)	>tr|Q2K0Q3|Q2K0Q3_RHIEC Histidine kinase OS=Rhizobium etli (strain CFN 42 / ATCC 51251) GN=kdpD PE=4 SV=1MPDDNRDQAGRPSPDALLEKARAEMRGRLKIFLGAAPGVGKTYEMLISGRAKIADGHDVVIGVVETHGRKETEALVAGFEIIPRVEIDYKGRLLEEMDLDGILARRPDLVLVDELAHTNAEGSRHPKRYLDVKELLDRGIDVYTTLNIQHVESLNDVVSQITRVRVRETVPDSIIDLADDVEIIDLTPDDLIKRLHDGKVYMPKTAERALTNYFTPGNLTALRELALRKTAQRVDDQLLTHMQAHAIAGPWAAGERVLVSIDHHPRSASLVRYAARMASRLRAPWAAVYIETNRSINLSEAERDTIASTLRLAEQLGGEAITIPGREVAEELVRHASANNVTHIVIGAPKKPTWRDWWGRSVTDELIRKTGEISVHVISGTEKDGTTARGIKAAAVAPQLDIRAYLLATVYVAIALGVSIVLDQVLDVRNLALVFLMAVLTSAVLHGLRPALYSCILGALSFNFFFLPPRYTLTISDPESVLAFFFFLGVAIIASNLTATVQRQAAAARQRARTTTEDLYLFLSKKLAGTGTLDDVLWAETAFQLASMLKVRVVLLLPEEGSIAVKAGYPPDDTLDDADIAAAGWAWEHNHAAGRGADTLPGAKRLYVPLRTGRTAVGVIGLDSDRRDGPLLTPEQQRLLDALADQAALAIERVQLVADVDRARLAAEADRLRSALLTSISHDLKTPLAAILGAAGTLRDYFASMPEEDRSDLLSTVVDESERLNRFIANLLDMTKIESGAMEPNSALHYAGDIVGTALARAAKILEHHKTEMSIPAELPMVRVDPVLFEQVIFNLLDNAAKYAPEGSVIQIEGWADADNVVVQISDEGPGIPPADLARVFDTFYRVRKGDQVRAGTGLGLSICRGFIEAMGGTITAGNRRGRPGAVFTIRLPKPNDIPKLDELK	26~~KdpD (4.86902E-117)~~234;X;256~~Usp(3.66035E-44)~~379;X;404~~DUF4118 (1.39026E-17)~~499;X;530~~GAF (0.0000000298134)~~650;X;667~~HisKA (0.000000000042327676)~~733;X;786~~HATPase_c (9.44449E-29)~~889	KdpD protein
	3E-10	49.5	12.4	3.4E-10	49.5	8.6	2	1	R5HER1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN555_00576	Firmicutes bacterium CAG:24	717	1263012	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:24	>tr|R5HER1|R5HER1_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:24 GN=BN555_00576 PE=4 SV=1MKDVILIVGMALTLFGWFLMKQLDRFLYENQKRIRLDTIETAAFWCYNTIKRGGETVQNNENNLSKEHILVCLSSSPSNERIVRMAGKMAQAFCGSLTALYVQTPGYSGMNAEDIARLQANIRLAQQLGAEIITTHGEDVPTQIAEYARLSDVTKIVIGRSGVQRRHFWSEPTLTEQLITLAPEMDIHIIPDAEVYKSYPRKPLFAVRPALPTARELLLTVGILTAATIIGWLFLRLGFADANIIMVYLLGVLLTSAFTSGYTCGVLSAFLSVILFNYFLTEPRLSLVAYGSKYPITFAVMFMAALLTGTLAAKLKAHAQLSARDAYRTKLLFDMNRQLQKAETSEEVYRMTATQIQKLMQRNILIYPAQEGALSKGILYPADASSPYSAPDADPEQDVIDWVWQNRKRAGATTQNFPKAKRLYLAIRTEQQIYGVVGIPMEKQTQPDAFTSSVLFSLLGECALALDNLRNAREKEEAAVLAKNEQLRANLLRSISHDLRTPLTSISGNADTLLHSYDMLDDQTRKQIFTDIHDDAQWLTELVENLLSITKIADGSVKLRLSDQVVDDIVSEALRHIDRRSTEHHITVDCGDVPLLIRVDAGLIVQVLINLVNNAVKYTTAGSNICITAIQQKKAVEICVSDNGPGIPDELKERVFEMFFAGGNPIGDSRRSLGLGLTLCQAIIHAHHGEITLKNNSPHGCIFSFTLPLSEVNLNE	69~~Usp(1.07055E-35)~~192;X;218~~DUF4118 (2.66777E-17)~~319;X(167);486~~HisKA (0.000000000059931 8)~~552;X;605~~HATPase_c (3.88699E-26)~~708	non-KdpD DUF4118 protein

	4E-10	49.3	9.6	6.1E-10	48.6	6.7	1.3	1	G7ZDP0_AZOL4	Histidine kinase (EC 2.7.13.3)	kdpD AZOLI_p20517	Azospirillum lipoferum (strain 4B)	917	862719	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum lipoferum (strain 4B)	>tr|G7ZDP0|G7ZDP0_AZOL4 Histidine kinase OS=Azospirillum lipoferum (strain 4B) GN=kdpD PE=4 SV=1MTDDQGGRNQRPSPDALLRQAEREGRGRLKIFLGAAPGVGKTFAMLLTAQAKRRDGADLVVGVVETHGRADTEALVAGLEIVPRRIVRHKGHALAEMDLDAILARRPKIVLVDELAHTNAPGSRHAKRYLDVQELLDAGIDVYSTLNIQHVESLNDVVAKITRVRVRETVPDSVIDRADDIEVIDLTPEDLIQRLKEGKVYVPRTAEQAIRHYFSPGNLTALRELALRRTADRVDDQLLTHMQAHAISGPWAAGERLLVCIDQDANCGALVRYARRQAERLRARWGAIHVETSRDLRLSEAERDRIADTLRLVERLGGEAVTIPGRDVADAVVEYARANNITHLVIAKSGRPRWSELLHGSVAHSLIRRAGDISVHVIAAANPGANPGDTVPPKTVRTETDGRWSFHGLPYLAATGYVAAALGLGHLLHLALGLSNIALVFLTAVLASAVTGGLGPSLYACIASVLSFNYFFLPPLYTFTISDPENIVALLVFAVVAAIASNLTARVRAQALTARQRAKTTEDLYRFSRKLAGVVTMDDLLWATAYQIAAMLKAHVVLLMPDGDGQADRLTVRAGYPPEDVLEEADLAAAMWSWQNNKPAGRGADTLPGARWLFLPMRTGRGPVALVGVDTGGGDRSRKSGLLSPDQRRLLDALGDQAALAIERVMLAEDVDRAKLAAETERLRSALLTSISHDLRTPLASILGSATSLTRYGSTLDEAGRLDLATNIQEEAERLNRFIANLLDMTRLESGAVRPRSGPVDLSELVGSALERTGRILAGHHVEVDLAPDLPMVDLDPVLFEQVLFNLLDNAAKYAPAGSRVTVRARRLGDAVEVRLMDEGDGIPPADVDRIFDKFYRVHAQDRQRAGTGLGLAICRGFVEAMGGAIAAGNRSDRSGAVFTLTIPAAADLPALEDSSL	24~~KdpD (2.16574E121)~~234;X;256~~Usp(4.23018E-43)~~379;X;435~~DUF4118 (2.25885E-15)~~510;X;536~~GAF (0.000000000005429 64)~~664;X;681~~HisKA (0.000000000042085 6)~~747;X;800~~HATPase_c (3.01098E-27)~~903	KdpD protein
	4E-10	49.3	12	6.9E-10	48.5	8.3	1.4	1	C4XK61_DESMR	Histidine kinase (EC 2.7.13.3)	kdpD DMR_09250	Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	889	573370	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio magneticus, Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	>tr|C4XK61|C4XK61_DESMR Histidine kinase OS=Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1) GN=kdpD PE=4 SV=1MHDEDNRPDPDALLAMVQREEENKRRGQLRIFLGMAPGVGKTYAMLEAARLKMTEGVEPLVGIVETHGRQDTEALLYGMSILPRQRIDYRGHALEEFDLNTALAKRPSLILVDELAHTNAPGCRHPKRWQDVEELLEHGLDVWTTLNVQHLESLNDIVAQITGVRVRETVPDAVLAKAQSVILVDLPPEDLRQRLTEGKVYLPKQAEWAGENFFRVGNLNALRELALRQTANRVGTEVLVYRRGHAIETTWPTAERILVCVGPSPYSATLVRTAKRLADGLHADWHALFIQKSPEGTSTDQAMANLRLAQELGAQTHVLTGADVAKLVVGFARQHNVTRIVIGKKPLTRNLLDVLRGSPVDQLVRESGEIDVHVIKGQDPRLPAARRPPPALAKGRWKDLPAALGIVAASTAACFAMYPYFELANLIMVYLVGVLAASIWLSRRASAAASVLSVLAFDFCFVPPRFSFSVTDVAYLVTFAVMFLVALVLSSMASRVKAQADSAVQLERQASELSDFSRNLATTRGAANLLLVAHEHITRIFGCTTFALLPNTEGKLEDAFVSEANETLTDKDVGVAQWVFDNGKPAGLTTQTLAESDALYLPLPGTEAILGVMGLRPDSPDAADSLELPDRRRLLEAVVHQTALALDVDRLEERAKKTLVEAEREKLRAALLSTVTHDFKTPLSAIAGSAESLLALGEATTPEVRRSLEENIAQEASRLERLVDNLLRIAALESGSVVPDIKLIPIEDVVGSALARLDATLAGHAVHLDIPPDDLPPIPMDEVLMEQVLINLLENAAKHTPLGTEILVSAAIRGHKAVIEVRDAGPGLPPGDPEKLFERFQRGDRSSTSGYGLGLAICRAVVKAHGGSITADRNRPAGAAFTVILPLYANE	24~~KdpD (3.11374E114)~~234;X;256~~Usp(1.72234E-39)~~374;X;401~~DUF4118 (1.40316E-16)~~498;X;528~~GAF (0.000000187099)~~646;X;664~~HisKA (0.00000000011512)~~729;X;783~~HATPase_c (1.96573E-29)~~883	KdpD protein
	4E-10	49.3	7.1	8.2E-10	48.2	4.9	1.5	1	G2T3Q4_ROSHA	Uncharacterized protein	RHOM_08785	Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	723	585394	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, Roseburia hominis, Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	>tr|G2T3Q4|G2T3Q4_ROSHA Uncharacterized protein OS=Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183) GN=RHOM_08785 PE=4 SV=1MNILLVGSKCRFLQLLTDKLDKEGHRVFLLTAEDKSVRTSKKIFETYHFAYDNPCIREVLEGVRPDVTVFMGAYDTGFLWGKGSSTASAYTSGLFQLLMNETAGNVGRFLYLSSEEVFGGEYTQDISCEENCAAYTVRAQAIAAGEELCRSYFNMGYETIVLRLDHLYGEPLTGAEARDICARMSVEGLETGEIRVNPHNRVALLHYSDAVEFLYAVITAKKMTYGVYQISSGETISVRSAAEFVAAELEGVKVVEDTGRERMEPVLSNQRFAEEFGIRIVHKPETEIGREAAYIRQHASSFVRTQSRKKGWSRFGERSREAVRAMIPFAENLLCFLPFFLLNNWMAGSAYFQNIDFYLLYVLLFAITYGQQQATFSSILAVAGYLAVQMYQRSGFDVVLDVNTYIWIAQLLILGLVIGYMRDRLHAVEEEERHEVDFLSRQVEDISDVNGSNVRIKEILSNQIVNQNDSFGKLYEITSSLDKYEPSEVLFYAAEVLAKLMDSQDVAIYTVANHSYARLFSATSPKARMLGNSIHYVQMEELYEKLREKKVFINKTMDERYPLMADAIYSEDEMQLILMLMVWGIPWERMTLGQANMLTVIGYLIQNAVVRANRYLSALEQQQRYIHGTRILEADAFASLVKAYLNAREKKLTECALVVFEEGEISREEAAGVLSGMMRQSDYLGELSDGKMYALLANTSAEDAGMVVERFRSAGFPCRMKEEMEL	58~~NADB_Rossmann (0.00000000838727)~~231;X(114);345~~DUF4118 (0.000000000000120062)~~425;X;485~~GAF (0.000000000155527)~~609	non-KdpD DUF4118 protein
	4E-10	49.2	9.6	6.4E-10	48.6	6.7	1.3	1	B9JKR0_AGRRK	Histidine kinase (EC 2.7.13.3)	kdpD Arad_9466	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	903	311403	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Rhizobium radiobacter (Agrobacterium tumefaciens) (Agrobacterium radiobacter), Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	>tr|B9JKR0|B9JKR0_AGRRK Histidine kinase OS=Agrobacterium radiobacter (strain K84 / ATCC BAA-868) GN=kdpD PE=4 SV=1MPDDSRDTLNRPSPDALLEKARQETRGRLKIFLGAAPGVGKTYEMLLSGKAKIADGVDVVVGVVETHGRRETQALLEGYEIIPRVNVDYKGRALDEMDLDAILNRRPGLVLVDELAHSNAHGSRHPKRYLDVKELLDRGIDVYTTLNIQHVESLNDVVSQITRVRVRETVPDSIIDLADDVEIIDLTPDDLIKRLHDGKVYVSRTAERALTNYFTPGNLTALRELALRRTAQRVDDQLLTHMQAHAIPGPWAAGERVLVSIDHHPRSASLVRYAARMASRLRAPWAAVYVETNRAISLTEAQRDTIAATLRLAEQLGGEAITIPGREVAEELLRHSASNNVTHIVIGSPKVGTWRDWSRASVSYELIRKAGDISVHVISGSDAEASPASRGVKSAPAPTPFQLRGYILATLYVAVALGVCVILDQVLDVRNLALVFLMAVLATAVTQGLRPALYSCLLGALAFNFFFLPPRYTLTISDPESVLAFFFFLGVAIIASNLTATVQRQAASARQRARTTEDLYLFSKKLAGTGTLDDVLWATAFQLASMLKVRVVLLLPEDGTIAVKAGYPPDDTLDDADIAAARWAWEHNHAAGRGADTLPGAKRLYVPLRTGRTAVGVIGLDSDRRDGPLLTPEQQRLLDALADQAALAIERVQLVADVDRAKLAVEADRLRSALLTSISHDLKTPLAAILGAAGTLRDYLETMSHEDRVDLLSTVVDESERLNRFIANLLDMTKIESGAMEPNYALHYGGDIVGSALRRGAKLLARHRVETQMPADLPMVKVDPVLFEQVLFNLLDNAAKYAPEESTIRLEAWADVDNVVFRIMDEGPGIPPADLERVFDTFYRVRKGDQVRAGTGLGLSICRGFIEAMAGTITAGNRTDRQGAVFTIRLPKPTDLPKLDELK	26~~KdpD (2.14017E106)~~234;X;256~~Usp(5.49212E-40)~~379;X;406~~DUF4118 (5.58151E-17)~~505;X;531~~GAF (0.00000001332)~~651;X;668~~HisKA (0.000000000010120 4)~~734;X;787~~HATPase_c (2.03949E-29)~~890	KdpD protein
	4E-10	49.2	11.4	7.5E-10	48.4	7.9	1.5	1	R7B4I2_9CLOT	Histidine kinase (EC 2.7.13.3)	BN653_02088	Clostridium sp. CAG:43	660	1262805	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:43	>tr|R7B4I2|R7B4I2_9CLOT Histidine kinase OS=Clostridium sp. CAG:43 GN=BN653_02088 PE=4 SV=1MQNKGSEIPKEHILVCLSSSPSNERIVRMAGKMAQAFCASLTALYVQTPGDADMNAEDTVRLQANMRLGQQLGAEIVTTHGEDVATQIAEYVRLSDVTKIVIGRSGVQRRHFWSESTLTEQLITLAPEVDIYIIPDVEAYKNCRRNQPLTIRPAFPTARELLLTIGILAATTVIGWIFLRLSFANDNIIMVYLLGVLLTSTFTSGYTCGVLSAFLSVLLFNYFLTEPRLSLAAYGSKYPITFAVMFAAALLTSTLAAKLKAHAQLSARDAYRTKLLFDMNMQLQKAETPEEVYRMTATQIQKLMQRDVLIYPTQGSALLDGNIYPADGSSPYSIPDTDREQNVVQWVWQNRKRAGATTQNFPKAKRLYLAIRTGQQIYGVVGIPMEKQTQPDAFTSSVLFSILGECSLALDNLRNAREKEEAAVLAKNEQLRANLLRSISHDLRTPLTSISGNADTLLHSYDVLDEQTRKQIFTDIYDDAQWLTGLVENLLSITKIVDGSVKLRLSDQVVDDIISEALRHIDRRAAEHHIAVDCGDVLLLARMDAGLIMQVLINLVNNAVKYTPVGSNIWITAIPRENMAEICVSDNGPGIPNELKERVFEMFFTGGNPIGDSRRSLGLGLTLCQTIVHAHHGEMTLKDNSPHGCIFSFTIPLSEVNLNE	12~~Usp(1.47476E-33)~~135;X;161~~DUF4118 (2.09381E-17)~~262;X(167);429~~HisKA (0.000000000011097 7)~~495;X;548~~HATPase_c (1.8968E-26)~~651	non-KdpD DUF4118 protein

	5E-10	49.1	5.9	7E-10	48.5	4.1	1.3	1	R5R460_9FIRM	Histidine kinase (EC 2.7.13.3)	BN747_02095	Firmicutes bacterium CAG:646	528	1262995	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	>tr|R5R460|R5R460_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:646 GN=BN747_02095 PE=4 SV=1MKKIKENREDGEEFSLGIRKKELVFSLADVLKSVAILAAASCLGCIFQKVGFAEANIITVYVLAVLIISVVTVNRV YSLISSLVSVLVFNFLFTEPRFTFQAYDKEYPITFLIMFTSALLTSSLAAKLKNSAKESAQAAFRTKVLFDTSQLLQRA KNEEEILSGTADQLVKLLNRDIVVYPSEKGKLKEPMVFPAEETKDRDLLLSAREKETAQWVLEHNRHGGATTPNM PDADGLYLAIRVKDAVYGVVGIAVGEHHMDVYENSILLSILGECALALENQKNAREKEEAAILAKNEQLRANLLRTIS HDLRTPLTSISGNASNLLSNGTSFDENTKKELYQDIYDDSMWLINLVENLLSVTRLEEGRLNLHISAELVDEVIEEAL RHVNRKRSEHEITVENQDDLLLARMDAKLIVQVLINLVDNAIKYTPVGSKIQVMSRREGEWVVISVADDGPGISDEK KKNVFDMFYSGANLVADSRRSMGLGLSLCKSIVAAHGGTIRVTDHVPHGAEFTFTLPVEEVELHE	31~~DUF4118 (3.05978E-14)~~129;X(168);297~~HisKA (0.000000000088580 7)~~363;X;416~~HATPase_c (3.43453E-30)~~519	non-KdpD DUF4118 protein
	5E-10	49	7.8	9.6E-10	48	5.4	1.5	1	A0A098GEI3_TATMI	Uncharacterized protein	LMI_1070	Tatlockia micdadei (Legionella micdadei)	444	451	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Tatlockia, Tatlockia micdadei (Legionella micdadei)	>tr|A0A098GEI3|A0A098GEI3_TATMI Uncharacterized protein OS=Tatlockia micdadei GN=LMI_1070 PE=4 SV=1MDYSVPIAPVVKFLMLNKKEVEHVMTGWVESFVITALFIFVSEILQNPLFLESSFPWIWFAPVLVGLRYGLWP AMMSIILFLSTYLYDHPEQLYTIPFQLYLLGGFLLTLLCVIYQRIGEKKIRYSEEISTYLQNRIQTTAHAYKVVLFAYQH LEHSLISNPVTLRSSLAELRELLAKGHDKLEPELMYRFLNILASHCGLEATAIFPVENNHVFAQPIASIGFVKTPSQED FLIRECIERQAITYITTQQILKEYWGNYLIVAPFLDQNNEVYALLVVQEMPFLKLNMDNLDSIDLFLNYFTEGNCDVN ADKILEKFPDCHVDFANELQRLVKLEKNTKHDSALCAFLFLDNPHREEYIYVIKNEIRGIDTYWETSKEGQKILLIIMP LSNRLAIESYKNRIVSLLLEKFNIELNGKEIRFKSCLLSSFKNPVDLIDDMLNIK	28~~DUF4118 (0.0000000105033)~~96;X;186~~GAF (0.00000325103)~~301	non-KdpD DUF4118 protein
	5E-10	48.9	9.4	8.2E-10	48.2	6.5	1.3	1	R5HD40_9FIRM	Histidine kinase (EC 2.7.13.3)	BN469_02101	Firmicutes bacterium CAG:114	755	1263001	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:114	>tr|R5HD40|R5HD40_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:114 GN=BN469_02101 PE=4 SV=1MYTTVNVQHLESLNDVVASITGISVSERVPDNVFDSAYQVEVVDLEPADLLERLREGKIYRGPQAAQALDHF FSLKNLASLREIALRRTADQLESSPRFQGEVKPKAGEHILICLSGAPSNAKVIRTAARMAKAFHGAFTALFVETSDF ASQSEQDRKRLRDHVHLAEELGARIATAYGDDPAVQIAEYARISGISKVVLGRSPRKRGFTSPKNLVDRLNELAPD LDLYIIPDQTARQSKRLRRLRQSQEKFSPKDLAKMLGILLLCTLGGALFSHWGFANSNVIMLYILGVLGIAMVTTGR SYSVAASVLSVLIFNFFFTHPYFTFMSDPSYIATFGVMFVVAFLGSSLTTRMKRQARLNAEKAYRTAILLETSQKLQ KAEGSQAILALTAHQLNKLLDRDLVIYQREENGELSPTLFPVSPGTDLSEFLTESERGVAEWVFKNNKHAGATTNT LPSAKCLYMSIRGTGGALAVAAIVTKNREKPEAFEKNFMVAILDECGLALEKEMTVREKQAVEERAHQETLRANLL RAISHDLRTPLTSISGNANILMEGRGQLCQEKLQALYTAIYDDSMWLIDLVENLLSITRIEDDKLGLKTQPELLEEIFQ EALQHLDRNASQHQISVELEDDLLMANVDARLLVQVVINIVNNAIKYTPEGSHITLSAHREGDQVEVEIADDGPGID QDAKDRIFDMFYTADKKRGDSRRGLGLGLSLCKSIINAHGGTIQAVDNHPQGTIFRFTLGAVEETNHE	2~~KdpD (9.59517E-44)~~93;X;110~~Usp (1.54991E-34)~~232;X;257~~DUF4118 (7.11021E-17)~~357;X(167);524~~HisKA (0.00000000466702) ~~590;X;643~~HATPase_c (5.85488E-32)~~746	KdpD protein
	5E-10	48.8	11.9	1.1E-09	47.9	8.3	1.5	1	D3F9I5_CONWI	Histidine kinase (EC 2.7.13.3)	Cwoe_0719	Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	463	469383	cellular organisms, Bacteria, Actinobacteria, Thermoleophilia, Solirubrobacterales, Conexibacteraceae, Conexibacter, Conexibacter woesei, Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	>tr|D3F9I5|D3F9I5_CONWI Histidine kinase OS=Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577) GN=Cwoe_0719 PE=4 SV=1MRDTRPPLWAGVVAGAAAVAFTTLAIYPLREIVPAVSTGVIYLLAVLLVASWFGLWVGLGTAVASALAFNWF HIPPTGRFTVSDPQNWVALAVFLVAAAIASTLAEIARARTREAELRRREADLAADLARLLLGGSDMRSALRPAADRL ARALALPGATIELGDGDGDGGDADGAIPLLAQGERIGTLRLDAPATDEALGRVVPGLEAILGVALEREALQQDIVET QALRRTDVIKTSLLRAVSHDLRSPLTAIATAGEALTSPNLTDAERAELAAAVTGESQRLSRLVDKLLDLSRLQGGAA DPRREWCSVEEVLRVAIDETPHPAGFNVGIDRDLPLVRADAVQLERAFANLLENAARYGGDHPVAVRARVVVGHRL LIRIVDRGPGIHGRELERIFEPFHRAPETRNDGHVGSGLGLAVVRGFIEANDGRVWAESLPGQGTTFVVELPVEEV REPVVEGVG	21~~DUF4118 (0.0000000061146 1)~~111;X(125);236~~HisKA (0.000000000046402 57)~~297;X;347~~HATPase_c (1.14537E-26)~~449	non-KdpD DUF4118 protein
	6E-10	48.7	7.4	8.9E-10	48.1	5.1	1.3	1	E8TDR5_MESCW	Histidine kinase (EC 2.7.13.3)	Mesci_1804	Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)	909	765698	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium, Mesorhizobium ciceri, Mesorhizobium ciceri biovar biserrulae, Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)	>tr|E8TDR5|E8TDR5_MESCW Histidine kinase OS=Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271) GN=Mesci_1804 PE=4 SV=1MPDDRSSDTRPSPDALLDHAEREGRGRLRIFLGAAPGVGKTYEMLMSGRARLADGVDVVIGVVETHGRKE TLALVEGYEVIPRRKVDYKGRILDEMDIDAILARRPALVLVDELAHTNAPGSRHPKRYLDVQEILTHGIDVYTTLNIQH VESLNDVVAQITKVRVRETVPDSIIDQADDVEIIDLTPDDLIKRLEEGKVYFPNTAQRAIENYFSPGNLTALRELALRR TAQRVDDQLLIHMQAHAIPGPWAAGERVLVCLDARPGGAARVRYARRLADRLRAPWTALHVDSTRSASMPEDDK DRLATNLRLAQQLGAEVTTIPGQNVAQDIVRYATANNFTHIVVGRPTRSRWRELIEGSLTYDLIRNAGDISVHVISG SERGTEAASRSVKAADEQRQFEIRPYLKATAFVIGSLAFAVLLDQFLDVRNLAIILLIGVLASAVTGGLWPALYACFV SALAFNYFFLEPRYTLTIRDPESIVALGVFLVVAVIASNLTARVQRQAVAARSRARATEDIYLFSKKLAGAGTLDDVL WATAFQIASMLKLRVVLLLPEDGTITVKAGYPPDDTLAEADIAAARWAWEHNRAAGRGADTLPGAKRLYLPLRTG RTAIGVVGLDNDKQGPLLTPEQQRLLDALADQAAVAIERIQLVADVDRAKLAAEADRLRSALLTSISHDLKTPLAAIM GAAGTLRDFSAALPEPDRAELLSTVLDESERLNRFIANLLDMTKIESGAMEPNYAFHYVGDIVGSALQRARKIIGEH KIETDIPRDLPMLKVDPVLFEQALFNLLDNAAKYAPAGSTIRVQGWTDNGSVLLQIMDEGPGIPPGDLERIFDTFYR VRKRDQIRAGTGLGLSICRGFIEAMGGTITAANRTDGSGAVFTIKMPKPANPPNFDASNTDDVGDLA	23~~KdpD (2.4857E-114)~~233;X;255~~Usp(4.12845E-47)~~378;X;404~~DUF4118 (9.01356E-17)~~502;X;530~~GAF (1.89017E-16)~~649;X;666~~HisKA (0.000000000001269 1)~~732;X;785~~HATPase_c (5.51704E-28)~~887	KdpD protein
	6E-10	48.7	8	1.1E-09	47.8	5.5	1.4	1	I4D558_DESAJ	Histidine kinase (EC 2.7.13.3)	Desaci_1955	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	891	646529	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	>tr|I4D558|I4D558_DESAJ Histidine kinase OS=Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4) GN=Desaci_1955 PE=4 SV=1MKNQGKLTVFLGAVAGVGKTYAMLEAAKERLSEGTDVVIGFVETHGSLETETVLKGIPYISSKTQEFLGKLV QEMDLEVLLERHPQLVVVDELAHTNIPGSRHRKRYQDVEELLASGIDVYTTLNIQHLESLNDVVAQITGVTVSETVP DRILEIASQIQMVDITPDELIQRLKEGKVNVPGVAAEAIEKFFRPGNINALREMSLRYTAKRVDCQMESYMRNHGIA GPWPSGEKVMVCVSGNPFSTKLIRTAKRMAARQNAEWLAVHVVLPGEMQKNENEKDLMEENLRMAEKLGAEIV TPHGDDIVEELLTLARKRNVSQIIIGKPERARFQELFHGSVVDKVIRRSHGISVHVISGRKNAADRKRETIAEDNNTS LGHLSRRQRYSATPYLMSVLMMSALTVAVSPIETFLGPVNIPMLYLLPVLLTAARWGRLPALITAGMGVIIFDYFFVP PFYTLHVDDFRYVISFVILMIAGIVTGTLSGRLTDQINYSRQREQQVSALYSLSRDLTAVDKLERILDSIARKIGETLD GQVVLLLPDERNNLVLSQSSSTDHFMTESEMNVASWVYERGQKAGRGTETLRSAKALYLPLITEQGTHGVLGICF FHQNDIVSPQQIRFLDAFAGLAALAINRIKLADEARQAHALAESERLRTALFNSLSHDLRTPLSSIIGAATGLLEDEDV VYSPDARHDLLQTILQGAERMNRFVNNLLDMARLESGMLKLHKDWCDIQDIIGVAINRLDIVLAKRLLDINIPAGLPL VQADYALIEQVIVNLLDNAVKYSEPVSKIVISVKQVGQNLEISVANRGNPIPETDLSKVFDKFYRLTSPLQVSGSGLG LSICKGIIESHNGDIWAENNELGGVTIIFTLPLEYELSDKLPIEGGD	105)~~212;X;234~~Usp(2.11613E-41)~~357;X;396~~DUF4118 (2.44603E-15)~~491;X;518~~GAF (0.000000000004251 06)~~637;X;654~~HisKA (0.000000000000209 321)~~721;X;774~~HATPase_c (1.97571E-27)~~875	KdpD protein

	6E-10	48.7	14.9	9.7E-10	48	10.3	1.3	1	R6R0R9_9FIRM	Histidine kinase (EC 2.7.13.3)	BN652_02435	Firmicutes bacterium CAG:424	520	1263022	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	>tr|R6R0R9|R6R0R9_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:424 GN=BN652_02435 PE=4 SV=1MKQKKSILNTGRSLFALSFGDIWKSILILVLATLIGFFFYGCGFTEANIIAVYILGVLIISVVTTHRAYSLIASLVSVLIFNFFFTYPKFTFLAYDQGYPVTFLIMFIVAFITGSLAIRLKNTASQATRAAYRTQILFDTNQMMQQAQDRNQIITAMANQLGKLLGKNIIVYLEQEGNLGEPHLFWQEGKEENQSCTGEKERQVAQWVWEHNRRAGAFTRNFPECQCLYLAIRINEQVYGVVGIVMEDSRMDDFVNSIVLSILGECALALESEKNAREKEEAAILAKNEQLRANLLRAISHDLRTPLTSISGNASNLMANGKEFDEETKMGIYTDIYDDSMWLINLVENLLSVTRIEKGRMNLKASAELVDEVIMEALRHVNRKSVEHTITVSSEEEFLLVKVDARLMVQTIINIVDNAIKYTPPGSEIWIHTRQKENLVEIQIADNGPGIPDEVKAHVFEMFYSGANKVADSRRSLGLGLSLCKSIINAHEGEITVSDNQPHGTIFTITLPAGEVQLHE	(4.51105E-16)~~121;X(168);289~~HisKA (0.00000000314201)~~355;X;410~~HATPase_c (2.04439E-28)~~511	non-KdpD DUF4118 protein
	6E-10	48.6	7.6	6.2E-10	48.6	5.3	2.4	1	C4IHP9_CLOBU	Histidine kinase (EC 2.7.13.3)	CLP_27 80	Clostridium butyricum E4 str. BoNT E BL5262	615	632245	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	>tr|C4IHP9|C4IHP9_CLOBU Histidine kinase OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_2780 PE=4 SV=1MENNKKKLSDMLLIIKVSMIIFTVIIVYMHLSEYWMNTKVEVVGKINIFTAMFFLLITIVVYMLCILMSPKVEMYHNVFKLKWLIENILCILFISLPVHFFVTYTNEYKYIFLLLILSSTIQYGSKYGMITSLFSSIAILSTDLLYAPIKDGINMIFQQDIIMTGIFIVIGWIFGYYVDLVSEEDRKKENKLNVLNNKLEEKIKQRKEIQKILVNNETCYDILFENSINAVIVHKDGKILYANRSAINLLGYDYIDDFNVKTICEFYTEKQREYINSKYRKIEKEHMSKVIEEETIIDMFGKVIPVSNTSSFFLYKEESAILTVLTDVTNEKKIESLKLDMEKNIKILNETKEFNMLIRSFFINMSHELKTPITVMYSAIQAIDLNIQKYNSDSVERDREYIKNMKQNCLRMIRLINNFVDATRLEAGEMKISKENADIVDAVESIIQKTAQYIHDKSIELIFDTNVEEKLMAFDKEVMKRILLNLISNAIKFGDKKQKIQIDLNSVDDYVFINVKDEGRGIPRNKLDVIFERFGQVDNSLSRECEGSGVGLYLVKCFVELHNGKIKIISSEGEGTEVIICLPVEVLDDMEFSSKRIVESDEEKIQREFSDIYSI	83~~DUF4118 (6.57282E-17)~~184;X;220~~PAS (0.000218742)~~281;X;355~~HisKA (0.000000000334576)~~424;X;479~~HATPase_c (4.94935E-27)~~582	non-KdpD DUF4118 protein
	6E-10	48.6	7.7	1.1E-09	47.9	5.4	1.4	1	G8M761_9BURK	Histidine kinase (EC 2.7.13.3)	BYI23_A008920	Burkholderia sp. YI23	925	1097668	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. YI23	>tr|G8M761|G8M761_9BURK Histidine kinase OS=Burkholderia sp. YI23 GN=BYI23_A008920 PE=4 SV=1MPRPTPDELLDKLHREEEKRHRGTLKVFFGASAGVGKTFAMLQAARRRRDEGVDVVIGIVETHGRKETLALLEGLETLPPARIEYKHRVITEFDLDAALQRKPQLILVDELAHSNVQGSRHLKRWQDVQELLDANIDVYTTVNVQHLESLNDIVGRITGIRVWETVPDRVFDLADEVTLVDLPPEELLDRLREGKVYLPQQAEHAVRNFFRKGNLIALRELALRRTADRVDAQMREYRADQSIERIWRARERLIACIGPGPESATLVRAAARLAAALKADWLAVYVETPKLQRLSDDIRKRTLDALKLASELGAETVTLDGADAAATLIDYAHMRNVSKLVAGASGKAGWRRRFERTVSERIIGQGSDIDVTLVSTGTRDANRRTLAEAFGTWRDGAHSSPRAYGYALAIGAGITLVAQGLAARQIAITNLVMLYLLGVIFAAVKLGRGPGVMLSFLSVAAFDFFFVAPELSFSVTDTQYLLTFVVMLLTSLTISHLTSSLRREARIASQRERRTGAMYAMTKELAAALMTEQIIEIGTRHVAEVFQSKVAILLPDAADKVRQKVGEPNPDVTLDAACLDLDIAQWVYDQQKPAGRGTDTLPASQALYLPLKAPMRTRGVLALSTGREAELAVPEQRRMIETFASQIALALERVHYVEIAQDALVNMESERLRNSLLSAISHDLRTPLTSIVGFASVLEEQAREAGGGEQASQELVHAIHEEALRMSGLVVNLLEMARLQAGAIRLNRQWSMLEETVGAALATSRRVLAGRAVQAHVPANLPLLRLDAVLMERLFANLLENAAKYTPPGTPIRIGAALEHDGDARFVRVCIDDEGPGLPSGMQHRLFDKFTRGEKESAQPGIGLGLAICRAIVETHGGQIGAENRADANGRIEGARFWFTLPANDAAPEDVPPDEDVESKAAGDV	21~~KdpD (6.20217E124)~~230;X;252~~Usp(5.23638E-29)~~375;X;403~~DUF4118 (8.42113E-17)~~504;X;531~~GAF (1.7134E-17)~~653;X;670~~HisKA (0.000000000004556)~~738;X;791~~HATPase_c (1.94523E-23)~~901	KdpD protein
	6E-10	48.6	11	1.3E-09	47.6	7.6	1.5	1	C7RUD9_ACCPU	Histidine kinase (EC 2.7.13.3)	CAP2UW1_1681	Accumulibacter phosphatis (strain UW-1)	509	522306	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, unclassified Betaproteobacteria, Candidatus Accumulibacter, Candidatus Accumulibacter phosphatis, Accumulibacter phosphatis (strain UW-1)	>tr|C7RUD9|C7RUD9_ACCPU Histidine kinase OS=Accumulibacter phosphatis (strain UW-1) GN=CAP2UW1_1681 PE=4 SV=1MKTGLPSRWRRAPYLVAAALCTLTTLGTLPLRGLLDLANIVMIFLLTVFVAAVWLGRGPSVMAAFLGVALFDFFFVPPHLSFDVADGQYLVTFAVMLAVGLISSHLAALLSERTAEAQSREQETRVLYQLARDLGGALTADQVADITRHFLGAVELDVTLLVAEASGKGVAFHEFHEYGSHRLNDLEYGFARSAYERGTIVETDPLAGMGVAIVFLPLVVPTRVLGVLALVPRSDDVDRVRALRPLLEAVASLLAITLERLHYADAAQDSELQVSAERLRTSILSSLSHDLRTPLTSLVGLADTLVHRQPALDEGAIETAAIIRDQAHAMHHLMSNLLEMARLQAGSITLNKEWQPFEEIVGSSTRLLAGLLASRKLDIQVPRDLPLVDFDAVLLERVLCNLLENAAKYSPPGARIEVLARTRGEALEIAVGNDGRGFPVDRIDQVFDLFARGEREPAVAGTGLGLAICKAIVEAHGGTIVAENRPGGACVRFTLPLGTPPAMDEEGTS	39~~DUF4118 (3.41684E-14)~~113;X(164);277~~HisKA (0.00000000106301)~~342;X;395~~HATPase_c (4.41174E-29)~~495	non-KdpD DUF4118 protein
	6E-10	48.6	9.9	1.1E-09	47.8	6.9	1.3	1	B8I9I9_METNO	Histidine kinase (EC 2.7.13.3)	Mnod_0197	Methylobacterium nodulans (strain ORS2060 / LMG 21967)	907	460265	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium nodulans, Methylobacterium nodulans (strain ORS2060 / LMG 21967)	>tr|B8I9I9|B8I9I9_METNO Histidine kinase OS=Methylobacterium nodulans (strain ORS2060 / LMG 21967) GN=Mnod_0197 PE=4 SV=1MSEPRRDPTRPSPDALLAAARREEGRRGRLKVFLGAAPGVGKTYEMLTIGRARRKAGADVVVGIVETHGRAETEVLLEGFEVIPRRRVPYRGTLLEEMDLDALLARRPALALVDELAHTNAPGSRHPKRYQDVEELLDAGIDVLTTLNIQHVESLNDVVASITRIRVRETVPDSILDRADDIEVVDLNPDDLIQRLKDGKVYVPQNAERALKHYFSRGNLTALRELALRCTADRVDDELLSHMRANAIAGPWGAGERVLVCVGEDPRAAGLVRYAKRLADRLHAPWTALTVEGPRSPSLSEAERDRIADTLRLADRLGGDTVTIPGGRRIAEDILAYARSANVNHVVVGKSDRSWLFELMHGSVVHDLVRRSGTISVHVVAGEAAEAAPVPRKTVATMAATPAWGPRPYAVALLAVAAALGVALLGQPYVGVENSNLFLLSSVVAVAVRYGLGPSLLAVVAASLSYNFFFLPPVYTFTIADPTNVAAFVLFTVVAVLVSNLAARSQRVAAVAQARARATERLYGFSRKLASCGTLDDVLWATCAQVAAMLKVRVVLLLPEQDGLAVRAGYPPEDMLDDADVAAAKWAFDNDRSAGRGADTLPGAKRLFLPMRTGRGTIGVIGLDADGTGPILTPEGRRLLDALADQGALAIERVRLVEDLDRAERAAETDRLRQALLTSMSHDLRTPLASVLGAATTLRDLDEALAPEAKRDLLATIIAESERLNRFIANLLDMTRLEAGAVAPNLAPHDIGETVGTALRRTEAMLAGHRVAIDVPADLPALRLDPVLFEQVLVNLLDNAAKYAPEGSTVTIRGWREGSLVRLQVLDEGEGGLPEAEIERVFDKFYRVRKGDRVRAGTGLGLSIARGFVEAMGGALVAANRPDRPGAAFTLTLPVPAKDRDAAPEIAA	30~~KdpD (5.33967E118)~~235;X;257~~Usp(4.62757E-40)~~378;X;434~~DUF4118 (0.000000000000493868)~~504;X;534~~GAF (0.000000000004783 61)~~653;X;670~~HisKA (0.000000000000995726)~~736;X;789~~HATPase_c (6.34984E-26)~~892	KdpD protein

	7E-10	48.5	6.9	1.2E-09	47.7	4.8	1.4	1	G5KAR6_9STRE	Histidine kinase (EC 2.7.13.3)	STRPS_2029	Streptococcus pseudoporcinus LQ 940-04	881	875093	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus pseudoporcinus, Streptococcus pseudoporcinus LQ 940-04	>tr|G5KAR6|G5KAR6_9STRE Histidine kinase OS=Streptococcus pseudoporcinus LQ 940-04 GN=STRPS_2029 PE=4 SV=1MQTGKLRIYFGYAAGVGKTYAMLNEAQKAKKAGVDVLAGYIEPHNRPETMALLAGLEQLSPKSITYKGITLK EFDIDAALKRQPRIILVDELAHTNCFGSRNKKRYQDIRELLCAGIDVYTTVNVQHIESLNDVIETITGIQVNERIPDAVF NQADQIELVDIEPLDLLERLDKGKIYAKSQANLAKHHFFTEEKLIALREIALRKAADQINQSAIRSEKVKASLVTKEHV LVCVSPSPYASHVIRAASRLASAFNADFTALYIGSLDRESPNQKADNKLRQHLELAEQLGAKVSIVDADNVSKQIVD YAKLSHVSKLVVGKSSDKTIWPKENIVEVLSQSVPDLDIFVIPNARGKKEPYHDKFSFVSWIPKWQFSFSDLLKTLA MLLLVTLTGLLFRYWNFSVDNIITIYILGVQVNAVWTKGKLSSVVSSILSVLCFNYFFTEPYYTFVAFSPNYPITFIIMLI AGLITSSLIKRIQEQARLSTEKSYRTELLLQTNKGLSQADTIPAILEELAVQVKKLLDRDVVIYPVIAGTLEDPKYFSAS QSLQTLTDYDQLNERGVVEWVLHNNKRAGATTNTLSAAKFLYLSVREKDHVFAIIGILMDDKATVDLFEKSVILAVL GEAALALEKERLREEQQKIELKMQKEQLRANLLRAISHDLRTPLTSISGQARLMMETGETLEKQQLTELATYIYDDS MWLINLIENLLSITKLDNDMTLSLSTNIFDEMVEEALKHVDRHLKHHNFILDLSDDLLMAKMDGPLIVQVLINIINNAVK YTPEGSRITLTSKRKDQNLVVEVSDDGPGISDQAKEKIFDLFYTSENASADGKRGLGIGLSLCKSIITAHGGTIYVHD NIPKGVIIGFTLPLVGVPVLHEK	4~~KdpD (2.08745E-117)~~211;X;230~~Usp(3.53111E-30)~~351;X;439~~DUF4118 (0.00000209771)~~481;X(168);649~~HisKA (0.000000000450689)~~715;X;767~~HATPase_c (2.91535E-26)~~870	KdpD protein
	7E-10	48.5	3.5	1.3E-09	47.6	2.4	1.5	1	A0A089N5N8_9BACL	Histidine kinase (EC 2.7.13.3)	PSTEL_14205	Paenibacillus stellifer	888	169760	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus stellifer	>tr|A0A089N5N8|A0A089N5N8_9BACL Histidine kinase OS=Paenibacillus stellifer GN=PSTEL_14205 PE=4 SV=1MRLDDQPAAAKGRGKLSIFIGYAPGVGKTSAMLSAAQEEHKDGIDVVAGFVDAHSRPDTTALVEGLEQLTP RILSGQGSPVHEFDLDRALSRGPEILLLDDLAHSNAAGCRHKKRYLDVEELLRAGIDVYTTLNVQQIESLADIVAAIT GFPVQERIPDSVFDSADQVKLVDIEPDDLIDRLNKGKIYPDIEAQRAAEVLFTREKLTALREIALRSTASQLNRIAIQIS EQASRNEYDTKDHILVCLSSAESNKKVIRTAARMAEAFHGRFTALFVETPETMALSAKNKEELRSNLRLAEQLGAQ IATVYGEDIPAQIAEYVKTSQVSKIVLGRSPNKKRGFAKASVVDKLTALVPGVETYIIPYQQPAGSGKLSRHSKPLRL SPADLGKTAVIIAGCTLIGLDFQYLEVKEANIITVYILGVLLNAMITKGRLYSVVSSLLSVLVFNYFFTKPYYSLRVYDS GYPVTFLVMLAASFLTSTLTMRVRDQARQSAQKAYRTEVLLETSRNLQQAQDFQAIVGETARQMVKLLDRTVIFYT ASDVGLSKPMIYLKNDLSSLPDIYIDENERAVADWVYTNNKRAGATTDTFFGARCLYHAVRGGETVFAVAGVVME QEEPLDVFEKSLLIAMLGECALALEKDRLNEKQQEISMQIRQEQLRANLLRGISHDLRTPLTSITGNAGILIGNSGVL SDEQKTSLYTDIYDDSMWLINLVENLLSISRIENDSIHLNLQAELVDEVISEALLHLNRNREKHIIETDVEDELLMARM DPRLIIQVLINLVDNAITYTQVGSRIRISARREGRWVNIEVADDGPGITDDTKTRLFEMFYTANNIRGDGRRGLGLGL SLCKSIVNAHGGTINVRDQVPRGAVFYFTLQAAEVNVYE	11~~KdpD (3.71086E98)~~221;X;242~~Usp(6.65956E-35)~~364;X;388~~DUF4118 (0.000000159068)~~489;X(168);657~~HisKA (0.00000000472978)~~723;X;776~~HATPase_c (2.99476E-20)~~879	KdpD protein
	7E-10	48.4	9.4	1.4E-09	47.5	6.5	1.5	1	I4B150_TURPD	Histidine kinase (EC 2.7.13.3)	Turpa_0348	Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) (Leptospira parva)	893	869212	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Turneriella, Turneriella parva, Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) (Leptospira parva)	>tr|I4B150|I4B150_TURPD Histidine kinase OS=Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) GN=Turpa_0348 PE=4 SV=1MSYQRKGHFRPDADLLLSAVNKTETERRGRLRIFFGMAAGVGKTCAMLRAAHRLKDEGVDVVLGFVETHG RKDTAVLMEDLELIPRVSLPYQNVLLEEFDLEGALRRKPHTIVVDELPHTNAPGSRHPKRYQDILELLDAGINVMTA FNVQHLESVADSVEAITSVHVQERVPDSFVDMASDIELVDLVPEELIRRLEEGKIYAADKAVLAANNFFRKGNLTAL REMALHFTASFVDNELQHYRTLKNIGETWKTAERILVAVSPSANGENLIRLARQRAFELKARWIAVYIDSGASLKSE AQKSLAQNMSLARELGAEVISVRDTDVVTGILRLARQKNITQVIVGKPPDTLWQRLTGRSILDRLVRSSGNLEIHAA GVAVRSKSAADFLSLQNLTSSRRQYLAAIATTCATTLICMPFLETIGYSAVSLIYLTVVIVLGLFVGRGPLVLAAAISAL GWDYFFIPPKYTLHVAQLEDYLTLIIYFAVALAMGTLMARLRQRERALMAREERVAAVYSFSRLLSRSTSLDETLQN CIEFIAQFFGARVSINLREKSGKLALEPAAASTRRISAKEASVAFWVFEHKKPAGRYTDTLPLAAATYYPLISTGGIV GVLGLRLPAKARLTPDKEEILFAFVNHAAITIERDFLASERRRLRVAEESEKLHEAILNSISHELRTPIAVILGAVSAMQ LKSTENNFAVQSELLSEVDIAARKLNVLVSNLLDMSRIEANKMRLNRQSYDLRNTITEATERLRSEIRNASLSVDFQ GDDFTCECDNTLLQQAIMNIVVNSVLHNENGVAIQLTCSATEPGNLTVVISDDGVGLPPELIDSVFDKFVRSAQANS GGTGLGLPIAKAIVELHGGSITASNLPTGGACFRLTLPRCIPTGEK	26~~KdpD (2.88884E111)~~233;X;258~~Usp(1.16754E-35)~~376;X;431~~DUF4118 (0.000000000010266 1)~~502;X;528~~GAF (0.000000000000104408)~~647;X;671~~HisKA (0.0000000301524)~~730;X;783~~HATPase_c (2.10368E-25)~~884	KdpD protein
	7E-10	48.4	9.5	1.1E-09	47.8	6.6	1.3	1	W6RZV1_9RHIZ	Histidine kinase (EC 2.7.13.3)	kdpD LPU83_4162	Rhizobium sp. LPU83	905	348824	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium sp. LPU83	>tr|W6RZV1|W6RZV1_9RHIZ Histidine kinase OS=Rhizobium sp. LPU83 GN=kdpD PE=4 SV=1MTRMPEDNRDKVGRPSPDALLEKARQETRGRLKIFLGAAPGVGKTYEMLESGRAKISDGVDVVIGIVETHG RKETQALVDGFEVIPRVKIDYKGRPLEEMDIDAILARHPSLVLVDELAHTNAEGSRHPKRYLDVKELLDGGIDVYSTL NIQHVESLNDVVSQITRIRVRETVPDSIIDMADDVEIIDLTPDDLIKRLHDGKVYVPKTAERALTNYFTPGNLTALREL ALRKTAQRVDDQLLTHMQAHAIPGPWAAGERVLVSVDQHPRSTSLVRYASRMAARLRAPWAAVYVETNRSINLT EADRDTIAATLRLAEQLGGEAITIPGREVSEELVRHAAANNVTHIVIGAPSKPSWRDWLHRSIADDLIRKSGNISVHV ISGSEKEGTSTRGVNAAPSSPAFNIQAYLSATTYVAIALIVGVVLDQVLDVRNLALVFLMAVLTSAVIHGLRPALYTCI LSALSFNFFFLPPRYTLTISDPESVLALFFFLGVAVIASNLTATVQRQAAAARQRARTTEDLYLFSKKLAGTGTLDDV LWATAFQLASMLKVRVVLLLPEEGTIAVKAGYPPDDTLDEADIAAARWAWEHNHAAGRGADTLPGAKRLYVPLRT GRAAVGVIGLDNDRRDGRLLMPEQQRLLDALADQAALAIERIQLVADVDRARLAAEADRLRSALLTSISHDLKTPLA AILGAAGTLRDYLDSMSQEDRVDLLSTVIDESERLNRFIANLLDMTKIESGAMEPNYALHYPGDIAGSALRRAEKILA HHKTVVTIPADLPMVRVDPVLFEQVLFNLLDNAAKYAPQGSSIRIDGWADGYNVMIQVSDKGPGIPPADVDRVFDT FYRVRKGDQVRAGTGLGLSICRGFVEAMGGTITAANRSDRSGAVFTIRLPKPNEIQKLDELQ	29~~KdpD (8.36929E119)~~237;X;259~~Usp(1.18289E-41)~~382;X;407~~DUF4118 (6.46568E-17)~~502;X;533~~GAF (0.00000013287)~~653;X;670~~HisKA (0.000000000029283)~~736;X;789~~HATPase_c (1.16693E-28)~~892	KdpD protein
	7E-10	48.4	6.9	1.1E-09	47.8	4.8	1.3	1	R6MS94_9FIRM	ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	BN531_00832	Eubacterium sp. CAG:202	391	1262884	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:202	>tr|R6MS94|R6MS94_9FIRM ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein OS=Eubacterium sp. CAG:202 GN=BN531_00832 PE=4 SV=1MPQELIERLQAGKVYSPTQAERATENFFTVENLTVLREIALRRCADRVNLLTETVRTKSHSDYHTDEHILVCL SSSPSNAKIIRTAARMANAFKGAFTALFVETPDYQVMSEEDVKRLRSNMRLAEQLGAKIETVYGEDVSYQIAEFAR LSGVSKIVIGRSSATRKSIFSKPTLTEKLIANAPNLDVHIIPDTDGKNTAYRAKKARKRNGIVFSVSDLLKSIAILILASCI GMLFRQLGFAEANIITVYVLGVLVTSVVTRHRVYSLISSIVSVLVFNFFFTDPQFTLRAYNQGYPVTFLIMFLAALLTS SLAVKLKEHAKQSAKAAYRTKVLFDTNQLLQQAKDKNEIVSATANQLIKLLGKDIVFYLTEGETLGEPIFLQFREIKQ TKK	2~~KdpD (9.80695E-19)~~48;X;68~~Usp(4.15249E-42)~~191;X;218~~DUF4118 (1.68135E-14)~~319	KdpD protein

	8E-10	48.3	8.9	1.4E-09	47.5	6.2	1.4	1	A0A0E9MTX1_9SPHN	Uncharacterized protein	SCH01S_52_01010	Sphingomonas changbaiensis NBRC 104936	500	1219043	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas changbaiensis, Sphingomonas changbaiensis NBRC 104936	>tr|A0A0E9MTX1|A0A0E9MTX1_9SPHN Uncharacterized protein OS=Sphingomonas changbaiensis NBRC 104936 GN=SCH01S_52_01010 PE=4 SV=1MDDASALLKLFANSRRSDAWSYALGALGAALITLLDMGLLGRLNVASLALLYLLPVMLASAQGGLAPGLVTSALAALAFNFFLVPPRFTLRIFDPDHLVTMILLFAVAAVISEFAARLRAAADRAEAAAEDSRLLASFGHKLANTRSAEQVDTILCLQLAATFRASTAVLDVDGPAVACRVASGDTPDLSDLDLAAVRWAQANGEITGRGQPTMASAEWLFVPLAAVGTPFGVAALARPDARPPIPPARMPLLTGLVTEAAQALARLRAAEAAELEQQREHERLRDALLSSVSHDLRTPLTVILGELALIEGEGAARVRAEARRLDRRIGNLLEMSRLEAGALRLAVVPTDLSDAVAVALDDMGRELDGIAVALDLAPDLPMVRADPRLLHHILINLLDNARKFARSAIRIEGRAADTVTLAVIDDGPGLPPGADALVFDRFRQLQGSDRLGGSGLGLGIVRSFAEAMDAQVSARNRPGGGAEFRIAFPDAAVTRLAAE	22~~DUF4118 (0.000000000000492186)~~114;X(169);283~~HisKA (0.00000117348)~~338;X;400~~HATPase_c (0.000000000006260 54)~~489	non-KdpD DUF4118 protein
	8E-10	48.3	11.3	1.4E-09	47.5	7.8	1.4	1	A0A0F2RQU5_9PROT	Histidine kinase	VR70_06055	Rhodospirillaceae bacterium BRH_c57	899	1629718	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), unclassified Rhodospirillaceae, Rhodospirillaceae bacterium BRH_c57	>tr|A0A0F2RQU5|A0A0F2RQU5_9PROT Histidine kinase OS=Rhodospirillaceae bacterium BRH_c57 GN=VR70_06055 PE=4 SV=1MNDDRDDRPSPEALLAEAQREGRGRLKIFLGAAPGVGKTYAMLEAAHERMRESVDVVAGVVETHGRKETGALLKGVDTLAPRMVEYRDKTFREMDLDALLKRRPKIALVDELAHTNIPGSRHVKRWQDVEELLAAGIDVYSTLNIQHLDSINDIVEQISGVKVRETIPDSVLSTADEIELIDLPPEDLIKRLEEGKVYVPEQARRAVHSFFSLGNLTALREMALRHAAERVDRQMVDYMRAHAIPGPWPARERVLVCIDAGVDADRLVRFAKRAAERRGAAWVAVTVETSQAHALTDAEKNRIDAAMRLAAQLGGDSATLQGDNVADAVVGFARDRNCTQIVVGRARKAGWFGRVGKSVTESLIDKAGDFTVVLVGGDENEKPKPSAPLPKPQTGWRVWLGYAFALVAAAAATGVCLLIDLYLPIANISVTYLLAVMIVAMKSGLRAGIMASVLSFLSFNFLFTEPRYTFAIADIHNITTVVFFLLAAVIVSNLAARLRTQVEATRESARRTTNLYDFGRKITAAATLDDVLWAVVHHVATTIHGKSLVLMPGEAGLYIAAGYPPEDQIDDKSAGAADWAWTHGNLAGRGSATLPTANWLFLPLLTTGRGPVGVLGVQMMEDADMPSPTQLRLLETLADQAAVAIERTTLVADVETARVATERERLRAALLSSLSHDLRTPLVSIMGAATTLGSYDEKLEAEGRQDLIQTIQDEAERLNRFVQNLLDMTKMGSGALKPRVDWVDLGDVVSAAVKRTERLARRHTIRIEIAPEMPLLCLDAILMEQVFFNLLDNACKYAPPGTPIKVWAIKTAKHIAIEVADQGPGIPPEDREKVFDMFYRIDQADSQTAGTGLGLAICRGIVEAHGGSIHVEPGLHGIGTCIVIHLPLPPELSLDGAGTA	21~~KdpD (5.32019E122)~~231;X;253~~Usp(6.13892E-35)~~376;X;413~~DUF4118 (2.12928E-15)~~501;X;527~~GAF (9.09509E-15)~~646;X;663~~HisKA (0.000000000000676 59)~~729;X;782~~HATPase_c (1.74452E-29)~~885	KdpD protein
	8E-10	48.2	9.2	1.6E-09	47.3	6.4	1.4	1	C1DNS4_AZOVD	Histidine kinase (EC 2.7.13.3)	Avin_10590	Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	488	322710	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Azotobacter group, Azotobacter, Azotobacter vinelandii, Azotobacter vinelandii (strain DJ / ATCC BAA-1303)	>tr|C1DNS4|C1DNS4_AZOVD Histidine kinase OS=Azotobacter vinelandii (strain DJ / ATCC BAA-1303) GN=Avin_10590 PE=4 SV=1MTLHKLLPAILVSVGLTLLMLPLQEAIDLSNTALLYVLAVVVIGSHYGRGPAIATALLSALLYAHVFVPPLFSLAITEVQYLLAAVVMLVVALLVGHLTASLKGQAEQVQARETQTHALYDLARHLTAAQKPTEVEEIASRFLRTALQAEHTRILPESALAAPPAPLTAALLQSALASRHPLMSAGSDPQHTLALVPLIASGPQHVLACELPATQAGSDATRTFLETASSVLTVALERTHFAEIARETELRRAAESLRSSILSALSHDLRTPLTVMVGLADTLALGKASPERQKNMLNALRNQALSINQLVTNLLDMARLRSGNIELNEAWQPIDEVIGATLRQVRTQWKDREITLDIPLGLPPLCFDAVLVERVLWNLLENAIKYSPADTPVELVVRRFGDWLDVMVCDWGPGLPPEGAEELFGLFRRGQTESNIPGVGLGLAIARSIAEAHGGQVLAENRMGGGACFRLRLPLGSAPTLSDLKDET	5~~DUF4118 (0.00000114451)~~105;X(150);255~~HisKA (0.000000000017486 1)~~319;X;373~~HATPase_c (1.55256E-29)~~473	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	8E-10	48.2	12.1	8.4E-10	48.2	8.4	1.7	1	A0A0B4Y426_9PROT	OmpR family two component system sensor histidine kinase	TH3_16300	Thalassospira xiamenensis M-5 = DSM 17429	883	1123366	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Thalassospira, Thalassospira xiamenensis, Thalassospira xiamenensis M-5 = DSM 17429	>tr|A0A0B4Y426|A0A0B4Y426_9PROT OmpR family two component system sensor histidine kinase OS=Thalassospira xiamenensis M-5 = DSM 17429 GN=TH3_16300 PE=4 SV=1MTDEEDRPSPEALLEQTRKDDRGKLKIFLGAYPGVGKTYAMLQAAQERRKEGRDVIVGIVETHGRVETENLLRGLEALPRKRLLHRGRVFGEMDIDAIIWRKPEIALVDELAHTNVPGSRHEKRYQDIDELLDAGIDVYTTLNIQHLESLNDIVARISRVRVRETLPDSFLEKANEIELIDLPPDDLLQRLRDGKVYVIDQVGRALRHFFSKGNLTALRELAMRIAAERIDAQMLEYMRTHAVSGPWPTQDRLMVCLNESPVAKKLVRTAKRMAERQRVPWIALHVETPRDDRMANAEKDDIAEALRLAEQLGAEIVTLQAESHLAREISALASKRNVTRLLIGRPRRRRWTGLLRENVARKLLENAEGFDVTVIAADADEKKRSLISDNPFEPGSWRSRSLSWVFGSVTVATAAALFADRYVPLGNLSLIYLLAVLLTAIRCGMWPSIAVSLLSFISYNFFFTVPYYTLSVFHHEQLITIVFFLIVSVIVGNLAGRLRLQVDAMKTSGKRTANLYDFSRKIAAAASLDDVLWAAVHHVAATLDCQSMVLQPSTDGSLEITAAYPPEDQLGLKDWGAAEWAWEHSKPAGWRSETLPTAEWLFMPVNTPQGPLGVLGVRFREDARTLGPSQRRLLEALVDQVAVAVERTRLATDIEEARLLSSTEQLRAALLSSVSHDLRTPLVSIIGSATTLSSYGDSMGEEDRGQLTQTILEESERLNRFVQNLLDMTRLGYGALQPKKEWSDLAEIIGRAVKHVRKYAGSRSFDVQVSPDLSPIQLDPVLIEQVLFNVLDNAVKHTADDGRITVKAKADKTRMVVEISDNGRGIPTEARQAVLMFSTVCAQAIARWRARGLDCRSAVVLSRRMAEVSLHTTGRRGWAQRLS	22~~KdpD (1.35825E119)~~230;X;252~~Usp(1.7618E-36)~~376;X(151);527~~GAF (2.60977E-14)~~647;X;664~~HisKA (0.000000000014100 1)~~730;X;783~~HATPase_c (0.000000000001074 08)~~877	KdpD protein
	9E-10	48.2	6.9	1.5E-09	47.4	4.8	1.4	1	D3RSE1_ALLVD	Histidine kinase (EC 2.7.13.3)	Alvin_1161	Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	891	572477	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Allochromatium, Allochromatium vinosum (Chromatium vinosum), Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	>tr|D3RSE1|D3RSE1_ALLVD Histidine kinase OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) GN=Alvin_1161 PE=4 SV=1MNATADDRPDPQALLSAIERERHGALKIFLGASPGVGKTYKMLEAARERREGADIIIGIIESHGRQETEALCEGLESIPLMQMAYRGAQFRELNLDAILKRAPAVVLIDELAHRNIPGTRHLRRYQDIEELLEHGIDVWTTVNIQHLESLNDVVARITGVRMRETVPDTVLSEARDVVLVDLTPRELIERLKQGKVYIPEQARAALDGFFSPTNLAALRELALQTVAERIDRDVREVMRSQGVTGPWPVRARIVVAIDGIGNGEELVRLGRRLAERRRAPWSAVFVDRGDTGPEQQAGVERTFDLAARLGGETLTLRGHDPVEELLAFAREQNATTLVVGRSRHRPLAGFFSQSLSQRLLRCGEDFEITFVSSRVARVRRRRHWFRRLEPMRDYVLTLAVVAAATGIAAVIEPLVPLPNLSLVFLTAVLLVAVRTAIRPALIAAVLSAAAYNFFFTEPRFTLAMHRTHELATVGFFLIMGLIGGQLAGRLRHQVLALRGTNEQTQRLLSLSRRLATAVDLPTIHRESTTAIAEHLHVPVLLAPGDSGRLAQAAASQDEVVLNDKAWSAAQWAYDHRQPSGFQTQTLSAIDWRFLPLAIEQECFGVLGVYRPNPGFQSEQLAAIDALITQVTMAMARTRLTTTLEQAKVAEETERLRSALLSSVSHDLRTPLASMIGAASSLRSLDEALSTDDRRELLDSVISEGERLNRYIQNLLDMTRLGHGTLKLERDWIGIDDILNSALRRTRELLHHCRLIRHIEPGLPLLYVHPALIEQALVNVIENAAKFSPEGSEVRVAAMRDDGELLITVADEGPGIPADHREKVFNMFFTGGEGDRGKHGSGLGLAICSGMIGAHGGRIEALPGPGGRGTTIATHLPLIEPPDDDNEERA	21~~KdpD (1.93826E113)~~231;X;253~~Usp(8.8133E-33)~~370;X;395~~DUF4118 (4.13849E-17)~~494;X;531~~GAF (0.0000638361)~~638;X;655~~HisKA (7.64142E-14)~~721;X;774~~HATPase_c (4.15674E-23)~~873	KdpD protein

	9E-10	48	7.3	1.7E-09	47.2	5.1	1.4	1	F6AJZ9_PSEF1	Histidine kinase (EC 2.7.13.3)	Psefu_4136	Pseudomonas fulva (strain 12-X)	508	743720	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas fulva, Pseudomonas fulva (strain 12-X)	>tr|F6AJZ9|F6AJZ9_PSEF1 Histidine kinase OS=Pseudomonas fulva (strain 12-X) GN=Psefu_4136 PE=4 SV=1MPTAAHRPTHRTPAPARDYLLAALAAGLGCLLALAVSRWLDLPNISLVFLAVVLVVAVRSSVGPALLCALLSFAAYGFCFLPPTWSVVVHREQDVLTLMFFLLIALLTGNLAARQRQQFRDLQVAQRQTESLLGFAGKLSSAQDQRDLLAAMLSQLDLPAERLCLLSRDAQGNWYQADGSRLALSELERISAEHAWQSRHPRGYDSHSLTHPHWWWWPLMDNDQPLALLGMRTAQGDPPAGEQRQLIDVLLPLLAHALARVQLVETLGHTRLQHETERLRSALLASVSHDLRTPLTAMRGNIETLQLFIDSLDAATRDDLLQSTASEASRLDRYIQNLLDMTRLGHGGLHLERDWVAASDLLAAALQRLQPVLQHLQVRMDVPADLPLLWVQGALIEQALVNVLDNAARFSPPGGVIDIRLSHDGETFSFAIADQGPGIPADEQTQIFDLFYTAARGDRGGQGTGLGLAICLGMLNAHGGTARVESTPGQGTTLILQLPLQAPDENPA	63~~DUF4118 (0.00000000132352)~~118;X(159);277~~HisKA (0.000000000001812 47)~~343;X;396~~HATPase_c (2.36006E-29)~~498	non-KdpD DUF4118 protein
	1E-09	48	12.1	1.7E-09	47.2	8.4	1.3	1	H6LIZ9_ACEWD	Histidine kinase (EC 2.7.13.3)	kdpD Awo_c05630	Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	903	931626	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Acetobacterium, Acetobacterium woodii, Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	>tr|H6LIZ9|H6LIZ9_ACEWD Histidine kinase OS=Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655) GN=kdpD PE=4 SV=1MAIFSDTRPNPDDISAGLFIKEQNKKGRLEIFFGYAAGVGKTYAMLDDAQEQIKCGVDVLVGYVEEHTHPETVQLISGLPALPPKIVEYRKIRLKEFDLDAALERKPDLILVDELAHTNAPGTRNKKRYQDIEELLNAGIDVFTTVNVQHLESLNDVVQKITWVDVKETIPDYIFNQADKIRLIDIEPDELLRRFEGGKIYRTERTQKSQDDFFIRENLRLLREIAMRKAANRISTDNQNEPRLSKKMANTKLMVCISASPSSARCIRWTNRTAEAFRAPWTAVYVEAMDSDVMTDAEKDAVRDNLVLAERLGAEIVTLNGHDVATVIAEYAKLSGITNIVIGKSRNKKSLLSYLKASLEEKLIAMLPSIEIHIIPGDPGKNNSALYQQRRLRISGSLFFTWQDGLKTLLIIVIATAISLILQALNISDQNIIMVYILSVLIVSRVTTGYVYGILTSCLTVLVFNYFFTIPYYTLHAIQPGYPITFVIMLLVALITSALTVRIKTQAHLAVEREHRTEVLYEINKKLLASRDLKETIQLINVYMVKIFGRSAIFYHQDPKDLESETFQQSALDSDASFLMSESERAVAHWVFMNKKCAGAGTDTLMGAGAFYMPIVSQSKVLGIIGLSCADGVLNQNNRLFLRMIASQVEMALERHYLSNEQRRMIVEAEKEKMRSNLLRGISHDLRTPLTGILGSSSAILENGQTMDQDTQDTLLFNIREDSQWLIRMVENLLSVTRINEGPMNVTKTPEAVEEIVAEAISRIRKRFVNRKIKVKVPEQLLIVPMDGTLIEQVLINLLENAIKYSPEDSVIEVEVKKNENAAEFEVKDQGKGISDQDFPYLFETAVPDGKRSSDSSRGMGIGLSICNSIVKAHHGEMAAQNRLSGGSIFQFTLPLEEESKNG	25~~KdpD (9.54261E-111)~~234;X;252~~Usp(3.67505E-39)~~376;X;406~~DUF4118 (8.83403E-17)~~506;X;532~~GAF (0.0000171635)~~655;X;672~~HisKA (0.000000000036393)~~738;X;791~~HATPase_c (2.65656E-26)~~894	KdpD protein
	1E-09	48	6.4	1.8E-09	47.1	4.4	1.5	1	Q21VE5_RHOFT	Histidine kinase (EC 2.7.13.3)	Rfer_2541	Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) (Albidiferax ferrireducens)	503	338969	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Rhodoferax, Rhodoferax ferrireducens, Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) (Albidiferax ferrireducens)	>tr|Q21VE5|Q21VE5_RHOFT Histidine kinase OS=Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) GN=Rfer_2541 PE=4 SV=1MNSPELSASNRPPARGWVIVVLLLTAATACSFLLDRYVSLTSQAMIYVLAVVIASYKLDWIESAVCAVAAVTALNFFFVPPRWTFEVENQEHFIALGTMLVLALVISHLAKGVRRETELAHLNERRARQLQALATNLSNVNSPADIEALGHKALDAAFAGPCSLALTRDGRELDFAADLDPAVRDGMRCCVKEEAVLGPGTGRWPGLLAWYLPLGERGHVTGAACVRPALAADEAGREHAQALCALLAQALWRLRVTASMLAAQSEAQRQQLQSTFLAAISHDLRTPLAAIVGAASSLQTQRDKLSEPEQDRLLGSIVSEASYLSTVTENTLQLVQLTGAAQALKRDWESMEEIVGAVLARVRQRDSQRRIKSNVPENLPLVKADPVLLAQLISNLLDNALQYSDGAIDLSVSVEAQELLVSVKDRGPGIPEAEQKVIFEAYTRGDQSGQRGAGLGLALCRAIALAHGGRLTLRPRRGGGSNFVLALPLDAQQPGQELNQELP	17~~DUF4118 (0.00000000001578 91)~~116;X(154);270~~HisKA (0.000000000123695)~~334;X;389~~HATPase_c (2.28563E-27)~~487	non-KdpD DUF4118 protein
	1E-09	48	6.7	1.5E-09	47.4	4.7	1.3	1	G2T0Z0_ROSHA	Histidine kinase (EC 2.7.13.3)	RHOM_04310	Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	669	585394	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, Roseburia hominis, Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183)	>tr|G2T0Z0|G2T0Z0_ROSHA Histidine kinase OS=Roseburia hominis (strain DSM 16839 / NCIMB 14029 / A2-183) GN=RHOM_04310 PE=4 SV=1MYNETKKAVKPMQIQTEQPKNGADEHILVCLSSSPSNARIIHTAAKMAKVLHAKFTAIYVQTDSVESEKNRLRLEQNIQLAQGLGAEIIMTHGEDVPLQISEYVRLSDVTKIVIGQSSARRRGLFGKPTLTEKLISVAPNVDIHIIPDALNYVRPHRRRLLFGAETPSLRDIGVTVLSLAVCTAIGFLFDHLDFPDTNIVTVYILGVLMVSVLTKGYLCSMAGSLLSVVLFGFFLTEPQLSFKTYAVGYPVTFAVMLVASVLTGTLASKLKDHARLSARSAFRTQVLFDTDRLLQKAKSNDDILSVTCMQLSRLLDRSIVAYTKSENGMSTGRLFAEKKYTYSENLLNAAEQKAAEWAFQNGRRTGATTAQFGKSECLYLAIRAGSRVYGVIGIPMRPEKPDSFENSIVLSVVNECALAMDNTHNAAEKERAADLAKSEQLRADLLRSISHDLRTPLCSISGNADTLLHNGNCLDETTKQQIYKDIYDDSEWLIDVVENLLYVTRLNDGRLKLELTNQLVDEVISEAVSHLKQKSVGHTVTVKCDDLILARMDAQLIVQVIVNLIDNALKYTEQGSEICVSAEKQGKYAVIRVADNGSGIPDDMKSHIFEMFYTGKSTVADSRRSFGIGLTLCKSIVELHGGTLTLRDNVPCGCVFTFTLPLSEVTLNE	26~~Usp(8.1375E-35)~~147;X;175~~DUF4118 (1.27228E-14)~~273;X(166);439~~HisKA (0.000000000974135)~~505;X;557~~HATPase_c (4.72655E-29)~~660	non-KdpD DUF4118 protein
	1E-09	47.9	13.2	1.8E-09	47.2	9.2	1.4	1	C7JIB3_ACEP3	Two component sensor histidine kinase KdpD	kdpD APA01_40530 APA01_43130	Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)	895	634452	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acetobacter, Acetobacter pasteurianus (Acetobacter turbidans), Acetobacter pasteurianus subsp. pasteurianus, Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153)	>tr|C7JIB3|C7JIB3_ACEP3 Two component sensor histidine kinase KdpD OS=Acetobacter pasteurianus (strain NBRC 3283 / LMG 1513 / CCTM 1153) GN=kdpD PE=4 SV=1MEAHLIRPDPDALLRQTVLDGESRKRGRLKVFLGAAPGVGKTFEMLTVAHQLQRDGVDVVIGVVETHGRAETAALVNGLELVPLRTMTYRDRMAQEMDLDAVLRRAPCVAAVDELAHTNVPGSRHPKRWMDVEELLAAGIDVLTTVNIQHLESLNDIVASITRIRVRETVPDHVIGDADEVELIDLTPNDLLQRMRDGKIYAEHTAGRAMLHYFSPGNLTALRELALRQTAQQVDAQLVDHMKANAIVGPWAAGERIMVCLTLQDGDASLLRYGKRLADHLHAPWIVLHVETNRDLSDAARATMASQMHLAQSLGAELVTIPGQDVALDAVAYARTQNVTQIVAAHPVGRGWSARVRQWLGRSTTERLIQFAQGGFPVHVVVPRSPGENAPTEQLLNIAPFTARPYVVGTLIVLGALVVALLLRQSFEVSNVSLAFLTAILGVAVAYGLWPSLWASLMAMLCFNFFFLPPFYTLTIAAPDNVVALFFFLVTALIASNLGARVRNQAVVARHRADITQSLYHFSRTITGILQLEDLLWSASHQIATMLDCDVAMLLPDGEILKVKASYNGGKAVGAADLAAATWAWKNNKVAGRGSDNLPGGRWLFIPLRTGRGPVAVIGLHAERTGPILDLEQQGLLDALADQTASAIESILLAGELDQARLDVETDKLRGALLTSISHDLRTPLASILGATSSLESYGEELDENARKELLSTIHDEADRLNRFVANLLDMTRLEAGALQPRKERVDIGEVIASALCRAARLLSDHETEMVIEPDLPMLLLDDVLLEQALFNILDNAGKYTPVGTKIVVTASVAADTLLIRVTDEGEGFAAHDPETAFSKFKRFKSADRSRPGTGLGLAISRGFIEALGGKIVSRNRKDCSGAELVMTFPLDEKNTK	25~~KdpD (1.05915E-107)~~234;X;256~~Usp(3.28833E-32)~~381;X;428~~DUF4118 (0.000000000000011521)~~503;X;530~~GAF (0.000000000033295)~~647;X;665~~HisKA (0.000000000000404 47)~~731;X;784~~HATPase_c (4.77293E-20)~~887	KdpD protein

	1E-09	47.7	9.6	1.9E-09	47.1	6.6	1.3	1	R5RG13_9FIRM	Histidine kinase (EC 2.7.13.3)	BN521_01702	Coprobacillus sp. CAG:183	624	1262853	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:183	>tr|R5RG13|R5RG13_9FIRM Histidine kinase OS=Coprobacillus sp. CAG:183 GN=BN521_01702 PE=4 SV=1MANAFFGEFTAVFVETPNFEKMPTKVKQALRANTKLASQLGANIVNLYGDNVPEQISEYARFAGVSKIVLGRTNTKRRFSHNSFADQLIALTPTIDIYIIPDKIRNNYKHTSLKPRQFFSLSIKDTILSIVIILIVTLLGIWFRDLGFGEANIIMVHILGVLATSLLTENLIYTLLSSLVSVLSFNFFFTIPMHSFTAYGKGYPITFVIMFLTAFITGTLTKRVKEQARLSAIKAFRTEVLLKSSQKLQRAKTKKEIIDEISKQLFKLLDKTIIFYPVENHELSEPLVFKSNEQEDEKIYLNKDEEAVASWVFNNNKHAGASTTTLPGAKCLYLAVRCEDSVLGVIGIYLDKTAIDDFENNLLMAILNEGAMALEKEASNSKKREVEIKANQEELRANLLRSISHDLRTPLTSISGNAGVLLDSADKLSNERKIEIYSDIYEDSMWLIDLVENLLSITRIENGNIQINKEAQLINEIVLEAMHHISKDSADHIIQLDLSDEFIFVKIDARLIMQVIINIVNNAIKYTPLGSTIKITTKKLNQVLSLEISDDGEGVPPDDQKEKLFEMFYTRNNLNGDSRRGLGLGLALCKSIVEAHDGKIKVIDNYPRGSIFVINLPLEEVDIHG	1~~Usp(5.20072E-24)~~101;X;137~~DUF4118 (0.000000499634)~~227;X;256~~GAF (0.0000456324)~~376;X;393~~HisKA (0.00000000011269)~~459;X;512~~HATPase_c (1.02126E-25)~~615	non-KdpD DUF4118 protein
	1E-09	47.4	5.5	2.6E-09	46.6	3.8	1.5	1	R6NMI4_9FIRM	Histidine kinase (EC 2.7.13.3)	BN627_00061	Lachnospiraceae bacterium CAG:364	515	1262983	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	>tr|R6NMI4|R6NMI4_9FIRM Histidine kinase OS=Lachnospiraceae bacterium CAG:364 GN=BN627_00061 PE=4 SV=1MRKLKEKSKLQKSVKDILKTLGILSAATAIGVFFRWGGLNEANIITVYILGVLITAVSTSQRIFSLVSSFISVLLFNFWFTEPRFTFKAYDPSYLTTFPIMLAAAFITSSLAERIKKQAAQSAKTAYRTQILFDTNQQLSNEQDIEGIISVTCGQLKKLLKRDIIFYKATENKLDKPVFFPFQEGKAEAEYRTEEERSVAKWAFDNNKHAGAGTKTYPDAKCQYLSVRVGQSVFGVLGIVMGEWPLDSFEKSIVLSILGECALAMQNEKVTRERAAAALMAKNEQLRANLLRSISHDLRTPLTSISGNAGILISNADSMGKEKQQQLYEDIYEDSLWLINLVENLLSVTRIEDGTMKLQLNAELLEEIVQEAVHHVEKRCKKHKLRVQLSENLILVKADARLIVQVLVNLVDNAVKYTPKGSEILIETRQEGTNAVVSVSDNGSGISDEVKEYIFEMFYTGNSHAADSRRSLGLGLALCKSILHAHGGDIFVEDCQPHGARFTFTLPAKEVQLHE	17~~DUF4118 (1.29758E-14)~~118;X(166);284~~HisKA (0.000000000004051 99)~~350;X;403~~HATPase_c (1.25365E-28)~~506	non-KdpD DUF4118 protein
	2E-09	47.4	10.2	2.5E-09	46.7	7.1	1.4	1	Q8Y3Z9_LISMO	Histidine kinase (EC 2.7.13.3)	lmo2679	Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	896	169963	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, Listeria, Listeria monocytogenes, Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	>tr|Q8Y3Z9|Q8Y3Z9_LISMO Histidine kinase OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e) GN=lmo2679 PE=4 SV=1METNRPSPDALLVNLQEETDSSVGKLKIYFGFAAGVGKTYAMLSDAKDQLAAGVDVVAGYIEPHARVETLRMLEGIPIISPKAINHKNIALKEFDLDEALKRKPELILVDELAHTNAAGVRNKKRFQDVEELLQAGIDVYTTVNVQHIESLNDIVEGITKVAVRETIPDYVFDEADRVKLIDIEPDELLKRLEQGKIYQPERAQTAMQNFFTRENLKLLREIAMRKAADRISHEYDQTGVYPEKRASSKWLVCIGTSPSSAKLIRWTARTAEAFRAPWTALYIENEENDYMTKAEKKCLRETMELAERLGAEIVTLAGHDIAETVAEYARLTGVTNIVVGKSRRRMGLRSLFEEDFEDRLITHLDNVDMHIIPSSHPKAKKRRMKMRFKSFLTWHDMAKMVLLLALATAICVGLSEFGIGDQNVIMVYILSVLIISRVTSGYVYGVLGSIIGVMLFNFFFTSPLYTFNTIQAGYPVTFGIMLLVALITSALTVRIKTQASLAVERERRTEVLYEINKQLLVTRNLKGIINLTNEYILHLFSRSVIFYSADPAKSNEGIFVQAEGKEDASALLSADEEAVAHWVFKNKKRAGAGTDTLMGAFGYYMPVMSQGKVLGVIGVSCSPEEGPLTQDNRIFLRMISSQVALALERQYLSEEQRQIVIESAKEKMRSNLLRAISHDLRTPLTGIIGASSALLEKEDELDKETERNLIRGIKDDSGWLIRMVENLLSVTRISEGLVSLERAPEAVEEIVGEAVGRIKKRFRDRTIHVKVPRDLLMVPMDGTLIEQVLINLMENALRHGGTGAEVWVDVTKTKQSAIFSVRDNGKGIPENRLADLFDTFAVEARERSDMSRGLGLGLSICMSIIRAHDGTLEAKNNKHGGATFWFTLPLDGGDGK	24~~KdpD (5.92334E125)~~231;X;249~~Usp(2.01335E-46)~~373;X;397~~DUF4118 (2.18454E-16)~~498;X;534~~GAF (0.0000000219942)~~649;X;666~~HisKA (0.000000000015242 6)~~732;X;785~~HATPase_c (3.66867E-26)~~888	KdpD protein
	2E-09	47.4	13	2.6E-09	46.6	9	1.4	1	E3I288_RHOVT	Histidine kinase (EC 2.7.13.3)	Rvan_3284	Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	905	648757	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Rhodomicrobium, Rhodomicrobium vannielii, Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	>tr|E3I288|E3I288_RHOVT Histidine kinase OS=Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299) GN=Rvan_3284 PE=4 SV=1MADARETNRPSPDALLELARNENRGRLKIFLGAAPGVGKTYEMLLSARAKCTEGADVVVGVVETHGRPETAALLAGYEIVPRRPVTYKGRIIEEMDLDAVLARRPQVALVDELAHTNAPGSRHPKRYMDVEELLAAGIDVYTTLNIQHVDSLNDVVAQITRIRVQETVPDSVLDKADDIEVIDLAPDELIQRLREGKVYVPEQARRALQHYFSPGNLTALRELALRRTAQRVDEQLLTHMKAHAIEGPWAAGDRVLVCISEDPRSAGLVRYTKRLADRLRAPWTALYIETLRSQDLSIAERDRIADTLRLAERLGGVAATLPGRGRVADDVMDFARSNNVTQIVIGKSERSRWFEALYGSVVHDLVRRSANISVHVIAGDALNKETIPRKTVRTATSSDASALGYVAAIVATAGAVLAARLAQPYLGAETIPLMFLMGVLGIAYYFFGLGASLFAAIAAMLSYNFFFIPPLYTFTIADPINISALFFFLFTALAVSNLTARVRRQAELARNRAAITSALYAFSKNLASNATFDDLLWAAVSQIATSLKADVVILLPETSGQLNVAAAFPPGDMIEDSDVGAAKWSLDNGFAAGRGADTLPGARRLFLPLRTGRGVIGVVGLGPGLRSDILLTPDERRLLDALMDQTAVAIERIKLAKEMDDARVAAEAERLRGALLTSLSHDLRTPLAHCTVEFDIERDLPLLNLDPVLMEQVFVNLLDNAGKYAPPGSTITLRARTVGSSVRICVMDEGPGIPEDKLSLVFEKFHRADNGDRQRAGTGLGLAICRGFVEAMGGAISAANRSDRTGAILAISFPASSTVRLPHERSVT	22~~KdpD (6.34138E124)~~232;X;254~~Usp(4.72062E-45)~~378;X;405~~DUF4118 (1.59839E-17)~~504;X;530~~GAF (0.000000000000401 64)~~651;X;668~~HisKA (0.000000000022221)~~734;X;787~~HATPase_c (5.58176E-25)~~890	KdpD protein
	2E-09	47.3	12.5	2.6E-09	46.6	8.7	1.3	1	A0A060B975_9GAMM	Histidine kinase (EC 2.7.13.3)	FF32_12940	Halomonas campaniensis	894	213554	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas campaniensis	>tr|A0A060B975|A0A060B975_9GAMM Histidine kinase OS=Halomonas campaniensis GN=FF32_12940 PE=4 SV=1MYSADQRPDPNTLLKAARREARGCLRVFLGAAPGVGKTYTMLRTARERAEEGEDIVIGVVESHGRADTEALCDGVARLPLAPLKHHGRTFYEFDIDAALARRPTILLVDELAHRNIPGSRHPRRYQDIEELLDAGIDVWTTVNVQHLESLNDDVARITGIRMRETVPDALLERARDVSLVDLTPDELLERLRRGKVYIPEQARAAMEGYFNESNLNALRELAIQTMAERVDADVKVAMDAGGRAGPWPVRPHLLVVINGSEDDVSLVRAAHRMAERRLAVWRAVYVDKGIASPEQQLAIEQVFSLVTRLGGDSIRLQGHSQLSEVLNYARSINATTIVVGREAKRRWWKWSRPLAQRLMAHAEAFDIVVVAKGAVKQHANRWRHGWKLRPPQLLATSLAVTASLGVAVMLEPWLELANLSLVFLVAVLFSAVWAGTAMAMFSAIASFLVFNFFFTEPRLTFAMVERGQLLTAVFFLLVAVVVGQLAGRGRRRLIALRASRDQTQLLLRYAEQLSTATDSASAAKIGVDTLVQCFAVPTVFIESAESANEVRVVHALPDSVRLDMTAKQAAVWSWQHQKPSGQGTDTLSQQAWRLIPLTVQGEKVGMLALKLSESLKALTYERESLIDTLVRQLSMALERTRLVAELNTTRVSEENERLRSALLSSVSHDLRTPLSSIIGSASSLIELKPQLSDSDQRELLDGILSESERLNRYIQNLLDMTRLGHGTLKIERDWVAFDDVINSALKRLGQSLKHVVVRKSWPPSLPLLYVHPALVEQALVNVLDNAQRFSPPGGELSIKAHFTEGDPATLVITVEDQGPGISPELREQVFDMFYSGGDGDRSAHGSGLGLAICRGMIGAHGGTIMAGTGESGRGTAIIITLPLLGADIRRSDEE	20~~KdpD (1.91697E113)~~230;X;252~~Usp(2.33846E-24)~~371;X;392~~DUF4118 (0.00000000635309)~~492;X;548~~GAF (0.00000776492)~~639;X;656~~HisKA (5.18047E-14)~~722;X;776~~HATPase_c (1.44543E-23)~~881	KdpD protein

	2E-09	47.3	10.3	2.6E-09	46.6	7.2	1.3	1	A0A0B4XAK7_9RHIZ	Histidine kinase (EC 2.7.13.3)	kdpDRGR602_PC00988	Rhizobium gallicum bv. gallicum R602	902	1418105	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium gallicum, Rhizobium gallicum bv. gallicum, Rhizobium gallicum bv. gallicum R602	>tr|A0A0B4XAK7|A0A0B4XAK7_9RHIZ Histidine kinase OS=Rhizobium gallicum bv. gallicum R602 GN=kdpD PE=4 SV=1MPDDRSDQAARPSPDALLVKARAETRGRLKIFLGAAPGVGKTYEMLVSGRAKLADGVDVVVGVVETHGRKETQALLDGFSTIPRAKVQYKGHTLEEMDLDAILARKPDLVLVDELAHTNAEGSRHPKRYLDVKELLDRGIDVYTTLNIQHVESLNDVVSQITRIRVRETVPDSVIDLADDIEIIDLTPDDLIKRLHDGKVYVPKTAERALSNYFTPGNLTALRELALRKTAQRVDDQLVSHMQAHAISGPWAAGERVLVSIDQHPRSASLVRYATRMASRLRAPWSAVYIETNQSVSLTEEQRDTIAATLRLAERLGGEALTLPGAGVAEELLRHASANNVTHIVVGSPVKAPWRQWFQHSPVDELIRRAGGISVHVISGNEKGGNAGRGVKPAPALPAFNIKAYVLATIYVAAALAFSTVLDQVLDVRNLALVFLMAVLTSAVLHGLRPALYSCILGALAFNFFFLPPRFTLTIRDPESVVAFFFIGVAVIASNLTATVQRQAAAARQRARTTEDLYLFSRKLASTGTLDDVLWATAFQIASMLKVRVVLLLPEGGTIAVKAGYPPDDTLDDADIAAARWAWEHNHAAGRGADTLPGAKRLYVPLRTGRTAVGVIGLDSDRRDGPLFTPEQQRLLDALADQAALAIERIQLVADVDRAKLAAEADRLRSALLTSISHDLKTPLAAILGAAGTLRDYFGSMPVEDRNDLLATIIDESERLNRFIANLLDMTKIESGAMEPNDGLHYPGDIAGSALRRAAKILEGHEAQMIMPADLPMVRVDPVLFEQALFNLLDNAAKYAPEGSAIRIEGFVDAGNVVIQIADEGPGIPPPDLTRVFDTFYRVRKRDQVRAGTGLGLSICRGFIEAMGGTIDAGNRKDRCGAVFTIRLPEADDIPKLDELK	26~~KdpD (1.09535E110)~~234;X;256~~Usp(1.91647E-43)~~379;X;404~~DUF4118 (1.85888E-16)~~499;X;530~~GAF (0.00000000560502)~~650;X;667~~HisKA (0.000000000008234 56)~~733;X;786~~HATPase_c (3.88757E-27)~~889	KdpD protein
	2E-09	47.3	11.9	3.2E-09	46.4	8.2	1.5	1	Q0BVR9_GRABC	Histidine kinase (EC 2.7.13.3)	GbCGDNIH1_0185	Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	899	391165	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Granulibacter, Granulibacter bethesdensis, Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1)	>tr|Q0BVR9|Q0BVR9_GRABC Histidine kinase OS=Granulibacter bethesdensis (strain ATCC BAA-1260 / CGDNIH1) GN=GbCGDNIH1_0185 PE=4 SV=1MQDIRPERPDPDALLRQAEKEGQEGRRGRLKIFLGAAPGVGKTCEMLTTAHHLLRDGVDLVIGVVETHGRAGTAALVEGLEIIPLRSVPYRDRTMTEMDLDAILNRAPQMVLVDELAHGNVPGSRHPKRWMDVEELISAGIDVMTTVNIQHLESLNDIVASITRIRVRETVPDRVLSEADEIELVDLTPNDLLQRMRDGKIYAPQAAGRAMLHYFSPGNLTALRELALRQTAQQVDAQLLDHMKANAISGPWAAGERIMVWLTLQDRDVSLLRYGRRLADHLHAPWIVLHVETGRDITEDARARMAGQMHLAQSLGAETVTIPGQDEALDALAYARAHNVTQIVAAHPDGHAGRMHWYQRVARWFSRSMTNRLIRAGGSFPIHIVARSRDDDQDVVTPFAPEPRQAMPYVSSTLIIGVATGAAMLLRQILEVGNVSLTFLTAILWVAVAYGLWPSLWASVLGMLCFNFFFLPPLYTFTIAAPENVVAMFFFLTTALIASHLGARVRNQAVVARHRADITQSLYQFSRRLSGIVTLDDLLWTACHQIATALERNAVILMPEGDRLILRASYTPDEQIDADDLAAASWAWKNDRMAGRGSDTLPGVGWLFIPLRTGRGPVAVIGLDAHAEDHLLYPEQQQLLDALGDQAALAIERIGLAKDLDEARLTAETEKLRGALLTSLSHDLRTPLASILGAASSLHEYDALLTEQDRRELLLTIREEAERLNRFVANLLDMIRLEAGALQPRRERVDLAEVAASALSRAARILSDHPVRLEVAPDLPMPLLDDVLLEQVLFNLLDNAAKYTPPGTPISIVIGQGPGVLTIRVLDEGAGLATQDTESVFEKFTRFRAADRSRPGTGLGLAIARGFIEAMGGGIAARNRSDRSGAEFTITLPVEAENR	25~~KdpD (1.75134E118)~~235;X;257~~Usp(2.04471E-27)~~386;X;408~~DUF4118 (5.0037E-19)~~508;X;534~~GAF (0.000000000005478 9)~~653;X;670~~HisKA (0.000000000003649 6)~~736;X;789~~HATPase_c (1.05321E-24)~~892	KdpD protein
	2E-09	47.2	10.1	2.7E-09	46.6	7	1.3	1	R6WBS7_9FIRM	Histidine kinase (EC 2.7.13.3)	BN605_00327	Dorea sp. CAG:317	514	1262873	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea sp. CAG:317	>tr|R6WBS7|R6WBS7_9FIRM Histidine kinase OS=Dorea sp. CAG:317 GN=BN605_00327 PE=4 SV=1MDEKKHLKRAVRFAMADIAKSVLLLIAASCIGYIFETLGFAEANIITVYVLAVLIISVVTINRIYSLISSVVSVLVFNFLFTYPKFTLHAYDQGYPVTFLIMFTAAFLTGTLAARLKDSAKQSAQSEFRTKVLFETNQLLQQAKDREGIVSDTAYQLLKLLNRDIVFYNEEGGALKNPKFYPANADSKLAGYQGGEEIKVARWVLEHNRQAGATTKVYPDAKCLYLAIRVNEAIYGVIGIAVEGKPLDEFEHSILLSILGECALALENDKNAREKEETAIIAQKEQLRANLLRAISHDLRTPLTSISGNASNLLSNGESFDGEIKERLYQDIYDDSMWLINLVENLLSVTRLVDGRLNLHMSAELVEEVVKEALRHVNRLKSEHYISVEHEDDLLLARMDARLIVQVLINLIDNAIKYTQKDSHITVKTKREGTQAVISVMDDGPGIAHKDQVFDMFYCGTNKVADSRRSMGLGLCLCKSIVEAHGGEICVKDHKPRGSVFIFTLPVEEVDLHE	10~~DUF4118 (3.73793E-14)~~118;X(167);285~~HisKA (0.000000000227553)~~351;X;404~~HATPase_c (2.56166E-24)~~505	non-KdpD DUF4118 protein
	2E-09	47.1	11	3.2E-09	46.3	7.6	1.3	1	D9R746_CLOSW	Histidine kinase (EC 2.7.13.3)	Closa_2942	Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	506	610130	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	>tr|D9R746|D9R746_CLOSW Histidine kinase OS=Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1) GN=Closa_2942 PE=4 SV=1MAERNWMEHRSYVLTVIFFIAAATGICWLFRLLHFPETNLVVVYILSVLLTARFTKGYIYGIAATVIAICTFNYFFTEPYYTLSVNDPTYFVTFGIMTVTSIITSALTTKVKQNALEAREKEAEASALYQLTSHLTDAADISDIAAITIKTSIDLNCRAACLCFDESGQPEQCFIQQKNAKEQTRRNVADKEVLRHRMENLKTAYYAGEEFYDWPIYGREAILGILRIPNEAAERMSDAQLRLLRSMMESTALAMDRFRSAQERILSKEEIAQERYRSNLLRAISHDLRTPLSGIMGTSEMLMGMTDQEDGRYALAEDIYKDADWLHSLVENILGLTRLQDSRLVLNKQMEAVEEVISVAVMAIGKRAPEREIAVHIPDSVMLVPMDAKLIDQVLVNLLDNAVKHTPPEGEISVTVIENKEEEAAVFTVADRGMGIAPVDLSHVFQMFYTTHEKGADSQRGVGLGLAICESIVKAHGGTISAQNRRGGGAEFTFTLPLEVEKNDK	12~~DUF4118 (1.54073E-14)~~114;X;140~~GAF (0.00000143649)~~258;X;275~~HisKA (0.000000000195463)~~339;X;392~~HATPase_c (4.16458E-28)~~497	non-KdpD DUF4118 protein
	2E-09	47	9.8	3.1E-09	46.4	6.8	1.3	1	R6P495_9CLOT	Histidine kinase (EC 2.7.13.3)	BN578_00327	Clostridium leptum CAG:27	898	1263068	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium leptum CAG:27	>tr|R6P495|R6P495_9CLOT Histidine kinase OS=Clostridium leptum CAG:27 GN=BN578_00327 PE=4 SV=1METQRPSPEELLYHIHQQQDQSTHGKLKIFFGYAAGVGKTYTMLEAAHQAQKEGRDVVVGYVERHVRPETLALLDGLEQMPCKEVPYKGVMLKEFDLDEALARKPQLILVDELAHSNAPGCRHAKRYQDVEELLRAGIDVYTTVNVQHLESLNDLVASITGVSVSERIPDRIFDSADQVELVDIEPADLIIRLQAGKVYREGQAQRALNHFFSEENLTALREIALRRTADRLNRTAQKRGSETAARAGEHILICLSSAPSNAKVIRTAARMAEAFHSGFTALFVETPETKELKGDNLKRLRDHLRLAEQMGAQIATVYGDDPAVQIAEYARVSGVTKIVLGRTNHRSLLFFKGKSLADRLTDLAGNLEIYIIPDTQPLYKKRIAFHKNDEPWFRWQDLVKTLVITLLSTLVGFAFFAAGLRDANIIIIYILGVLVTAIWTHGHVYGAIGSLLSVVAFNFFFTVPRFTLEATAPDYPVTFLIMLIASVISSTLATRVKKQARQSAQKAYYTELLMSSSQKLQQGKNEQEIIQLAAEQVSILLERPVLYALAKGKGELQFQVTPAERREELLKSMTIEERGVADWVVKNNKRAGATTNTLSHAQNLYLAVRGLQGVMGVVGIPSKYYPVPEVFEKNLMVSILNECGLILERRRFREEKQAIELETQQERLRSNLLRAISHDLRTPLTSISGNAGVLMEKSIVLDEEKKQELYRSIYDDSMWLVNLTENLLSITRIENGTMHLQMGAELMDDVFQEALAHVDRQSKDHHISVELPDDLLLAKMDVRLIVQVIINIVNNAIKYTPAGSHIILRAEKQGAKVAVSISDDGPGISDEAKIHLFDMFYTASQGKPDNRRGLGLGLNLCRSIVTAHGGEITVTDNIPHGSIFTFTLPLEEVELNNV	25~~KdpD (3.05563E120)~~232;X;250~~Usp(1.56126E-34)~~373;X;398~~DUF4118 (1.43963E-16)~~499;X(167);666~~HisKA (0.000000000208726)~~732;X;785~~HATPase_c (6.75769E-27)~~888	KdpD protein

	2E-09	46.9	14.3	3.8E-09	46.1	9.9	1.4	1	Q2W609_MAGSA	Histidine kinase (EC 2.7.13.3)	amb1912	Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	898	342108	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum magneticum, Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	>tr|Q2W609|Q2W609_MAGSA Histidine kinase OS=Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) GN=amb1912 PE=4 SV=1MIGMSEPQRPSPDALLAQARREGRGRLKIFLGAAPGVGKTYAMLCAAHERLKDGVDVVAGVVETHGRKETEALVKGLDVLPARLVEYRGREFREMDLDALISRRPAIALVDELAHANVPGSRHLKRWQDVEEVLAAGINVYATLNIQHLESLNDVVERISGVKVRETLPDGVLAGADEIELIDLPPADLIKRLNEGKVYVPEQARRAVGHFFSPGNLTALREMALRHAAERVDAQMVDYMRSNAIAGPWPARERIMVCIDERADSDRLVRVAKRAADRRGAAWVAVTVETSHTLTLPEADKDRVAAAMRLAAQLGGETAHLQGDDVVAVVLACAAERNATQIVVGRPRRLRLLDHFAATVTDRLVERGGAFNVLVVGDDSEDARKVPKPTAVQPEPQDWPGLALALAAAGAATGLGFAIDLWLSVASISVAYLLAVMVVAMWIGLRPGILASVASFLAFNFFFTEPRFTFAVSDVQNLLTLAFFLIAAFIVSGMASRLRAQVQASRESARRTVNLYEFGRKVTGAATQDDVLWAVVHHVADTIRGRSLVLMPVEGRLSVMAGYPPEDHLDDKSAAAAAEWAWSHGKPAGRGSATLPAALWLFLPLRTGRSAVGVLGVQMSEDADLPSPAQMRLLETLADQAAVAIERTTLVSDIEAARVATERERLRSALLSSLSHDLRTPLVSIMGAASSLISYDDILGPADRRDLAQTVQDEAERLNRFVQNLLDMTRLGSGTLKPRIDWADLSDIVGGAVERAARLTRSHAVKVDIDPDMPLLCVDAVLLGQVFFNLLDNACKYSPPGTGIKVWARRAADHISIEVADQGPGIPEADREKVFDMFYRVGLTDSQPAGTGLGLAICRGIVEAHGGTIRAEAGLHGSGTAIIIRLPLPPSPDVAGEEA	22~~KdpD (7.78604E-112)~~232;X;254~~Usp(4.2646E-35)~~377;X;432~~DUF4118 (1.06973E-15)~~501;X;527~~GAF (0.000000000006462 8)~~646;X;675~~HisKA (0.00000000105173)~~729;X;782~~HATPase_c (1.44647E-29)~~885	KdpD protein
	2E-09	46.8	7.8	4.6E-09	45.8	5.4	1.4	1	Q2G871_NOVAD	Histidine kinase (EC 2.7.13.3)	Saro_1511	Novosphingobium aromaticivorans (strain DSM 12444 / F199)	478	279238	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Novosphingobium, Novosphingobium aromaticivorans (Sphingomonas aromaticivorans), Novosphingobium aromaticivorans (strain DSM 12444 / F199)	>tr|Q2G871|Q2G871_NOVAD Histidine kinase OS=Novosphingobium aromaticivorans (strain DSM 12444 / F199) GN=Saro_1511 PE=4 SV=1MTRAVAAYPKALLAVAAVTWITAAQLPLLGLASSAMLFLLPVLISAVRGGVGPGLTAALTGAAAYNFFLLEPRYTFRVHQLDNLVSLLVLVAVALVTSRLASRLMMREAEAVERARLSDELAELSGLLSSHPAQPALERGIALLEARYGKLELLLPHAGRIQENEAFSSLDASAAAWSAHNGDITGHGTATMPVADWTFLPLSPRNRHDISVMALARPMDGTVRAASELDHLRQLAMLLGQCLDRDALEAERRERELLEERDRLRRTLLASLAHDFRTPLTIITGRLAELASGNPAATDALAAAQRMDRMMNDLIGAARIEAGALEPVLESIDLVDVVGAACEGLIQPHGVALKQSIPADLPFVRGDPVLLQHLIANLIDNGICHARSTVVVSAAKQSGLVLLRVSDDGPGIPEGERQRIFERFARIEGTDRTQGSGLGLAIVKGFGDVMGMAVTVTSAPSGGALFTVAMPRAGRAGT	268~~HisKA (0.000187626)~~319;X;371~~HATPase_c (5.50992E-26)~~468	No DUF4118 detected by NCBI CDD
	3E-09	46.6	7.6	4.5E-09	45.9	5.3	1.4	1	A1K9B0_AZOSB	Histidine kinase (EC 2.7.13.3)	kdpD1 azo2799	Azoarcus sp. (strain BH72)	472	62928	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azoarcus, Azoarcus sp. (strain BH72)	>tr|A1K9B0|A1K9B0_AZOSB Histidine kinase OS=Azoarcus sp. (strain BH72) GN=kdpD1 PE=4 SV=1MTAAPPVPPTPLQRARPYLAAVAGSVLVTVCAAPLRHVLDPANIAMLFLLAVFLAALRLGRGPAVAMAFANTVLLDYVIVPPHFAFIPTDLQYLVTLVVMLTVGLVTARLSTGLGRQTRLSASQERDTSALYELAHELAGCITLEQIRRALDGYLTRQPREVRLLLPDDPPAAAASVAIFPLQGTDPSRGELHVRLAPREAALPAPDSERFRTVASLLATAIERVRYVELAESHAVAISSERLRTSVLAALSHDLRTPMTVLIGLADSLVMSRDPLPPEAHQTATSLLHQARALSGILNNVLDMARLHSGTIRPRREWHLLDDVIAASVRLLKPQLSDHPIRVRLEPDLPLVEFDATLLERVVCNLIDNAAKYSPAGAPIEITAFVDAGGNQACIEVCDQGEGFPAGNIDRLFELFERGNTESSVPGMGLGLSICQRIMAAHGGSIAVRNRERGACVQLRLPLGTPPVIYEE	17~~DUF4118 (3.30638E-14)~~117;X(124);241~~HisKA (0.00000000230926)~~306;X;359~~HATPase_c (5.34562E-28)~~461	non-KdpD DUF4118 protein
	3E-09	46.6	5.1	5.2E-09	45.6	3.5	1.5	1	X4ZL98_9BACL	Histidine kinase (EC 2.7.13.3)	PSAB_12660	Paenibacillus sabinae T27	885	1268072	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	>tr|X4ZL98|X4ZL98_9BACL Histidine kinase OS=Paenibacillus sabinae T27 GN=PSAB_12660 PE=4 SV=1MEGIPAEKKRGKLNIFIGYAPGVGKTYAMLSAGKEEQKDGIDVVAGFIESHDRPDTMALLEGLELMPPLTISGAGAAIEEFDLDLALQRKPDLILLDDLGHTNAAGCRHKKRYRDVEELLRAGIHVYTTINIQQIESLTDIVASITGISVHERIPDSVFDSADQVKLVDIEPDDLIDRLHKGKIYRNDEAEEAQAQLFTREKLTALREIALRSTASQLNRIAIQISEQAKRDEYNTKDHILVCLSSAASNKKVIRTAARMAEAFHGRFTALFVETPETMALASKNKEELRGNLRLAEQLGAQIATVYGEDIPGQIAEYVKTSGVSKIVLGRSENKKRGLAKSNVVDKLTALVPNIETYIIPYSQPPSPRKFHLNAKPLHLSASDIAKTTAIIAGCTIIGLCFQYFGLKEANIVTVYILGVLLNAMITRGRLYSVFSSVLSVLVFNFCFTEPYFSLRVYDSGYPVTFLVMLAASFLTSTLTMRVRDQASQSAQKAYRTEVLLETSRKLQQAQDFPAIIDETARQMVKLLNRTVIFYSVQQKGLSAPIIFPKKDSGSTPAVYMDENEQAVADWVYKNNKRAGATTDTFFGAHCLYHAVRGGETVFAVAAIVMDQEEPLDVFEKSLVFAMLGECGLALEKEKLNGQQQEIFMQIRQEQLRANLLRAISHDLRTPLTSISGNAGILIGNSNVLSEEQKKGLYTDIYDDSMWLINLVENLLSISRIENGSINLNLQAELIEEVISEALQHVNRNSVKHSIQSIVDDDLLMARVDSRLIVQVLINLVDNAIKYTQEGSCITLSAIRDGQMVLIEVSDDGPGISDESKTRLFEMFYTGDNIRGDGRRGLGLGLALCKSIVNAHGGTIGVRDHFPRGTVFYFTLQAAEVSVYE	8~~KdpD (5.72652E-106)~~218;X;239~~Usp(9.46295E-35)~~361;X;385~~DUF4118 (5.18793E-15)~~486;X(168);654~~HisKA (0.000000000617172)~~720;X;773~~HATPase_c (3.74462E-22)~~876	KdpD protein
	3E-09	46.4	7.8	4.9E-09	45.7	5.4	1.3	1	R5AGZ3_9CLOT	Histidine kinase (EC 2.7.13.3)	BN452_00246	Clostridium sp. CAG:1013	888	1262769	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:1013	>tr|R5AGZ3|R5AGZ3_9CLOT Histidine kinase OS=Clostridium sp. CAG:1013 GN=BN452_00246 PE=4 SV=1MEVAFNGHIENQRQGSLKIFFGYAAGVGKTYAMLEAAHQAQKQGIDIVVGYVERHTRPDTLALLEGLEQLPNREIEYKGIKLKEFDLDAALKRHPQIMLVDELAHSNAAGCRHAKRYQDVEELLRAGIDVYTTVNVQHLESLNDLVASITQVAVSERIPDSVFDSADQVELVDIEPDDLIARLQSGKVYRKNQASRALNHFFTRDNLAALREIALRRTADRLSRNAQKSGNETVAKAGEHILICLSSSPSNAKVIRTAARMAEAFHSGFTALFVETPETKELKGESLKRLRDNLRLAEQLGAQIATVYGDDPAVQIAEYAKVSGITKIVLGRTNHQSKIFLRSKTLADKLTKLAGDIDIYIIPDAQPFYKRKFNLLRKEEQKFRWIDLLLKVVLITLLTTIISFGFYATGLREANIIIVYILGVLITAIWTHGHLYGALASLLSVISFNFFFTVPRFTLEATDPDYPVTFLIMLTASIISSSLATRVKKQARQSAQKAYYMELLMNSSQKMQQGRDEQEIIALAAEQIRALLDRPVLYSLAMKGKELEFQVCPQSETNKMIGAMTAEEIGVADWVVKNNKHAGATTNTLSHAQNLYLSVRGNQEVMGVIGIPSKYYPPLEVFEKNLLISLLNECGLILERRRLRAEKQAIEMETQRERLRSNLLRAISHDLRTPLTSISGNAGVLMEKSILLDEDKKQEIYSSIYDDSMWLVNLTENLLSITRIENGTMHLQMNAELIDDVFREAISHIDRKASEHELSVELADDLLMAKMDVRLIVQVIINIVNNAIKYTPEGSHICLSAQKEKKMVRIRISDDGPGISDEAKQHLFDMFYTADIGKADSRRGLGLGLSLCKSIVDAHGGELSVSDNKPHGAVFSFTLPLEEVNFDHV	13~~KdpD (9.67315E-124)~~222;X;240~~Usp(9.26068E-36)~~363;X;388~~DUF4118 (1.05129E-16)~~489;X(167);656~~HisKA (0.000000000715072)~~722;X;775~~HATPase_c (3.41519E-28)~~878	KdpD protein

	3E-09	46.4	11.9	5.5E-09	45.6	8.3	1.4	1	B8GEQ9_METPE	Osmosensitive K channel His kinase sensor	Mpal_2485	Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	637	521011	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanosphaerula, Methanosphaerula palustris, Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	>tr|B8GEQ9|B8GEQ9_METPE Osmosensitive K channel His kinase sensor OS=Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c) GN=Mpal_2485 PE=4 SV=1MTGDDGRPLPDDLLSLAREDDRRRTEGKLTVYLGYASGVGKTYTMLADALGWRTAGTDVVIGYVETHGRPETDALAARLEAVQPKVVDYLGIHLNEMDLDAVLARNPAVVLVDELAHTMAPGQRHTKRYQEIEELLRAGISVCTTVNIQHIESEHDAVARITGIQVHETVPDTFLELAGDLRLIDLPPDQLVERLHAGKVYIQDMAALAVARFFTPANLIALRQLALRFVAGSTDRELVGLMHSQAIAGPWPAAERVLVGVRTGPYADQMVRAGYRVASRLQAEWIVLSVETEDDLGAPVKDQAHLREALETARRLGGRVVRYRAEDVAGEIIRHAKRNNVTTILLGKPRGLGLFLSPVYRVMRHTQGIALHLVDPIERTRIPIRRQLPIPSIPDAGIALVLIGGVAAVNVTLRDTLSPSNLLIIQLIPVVIAALFLGRAASVFAVAVSILLFDILFVPPYYTIAISDWQYFISFIGYLVVALVISNLASRLRYLLPQIRESEATVAAMSGLSKDLDVATTRQEVFERLVDHLHQVTGGPVTVLIPKGGELARTAGDPTYPLDEKEEAIAAWVYENRRPAGQGMETLPAGHGRYLPLVVSGRALGVVGVMPEEHGGPADEVLEGMVRLGSLVLDRLA	27~~KdpD (1.93624E-97)~~231;X;256~~Usp(8.30027E-29)~~374;X;399~~DUF4118 (3.42679E-14)~~494;X;523~~GAF (0.00072878)~~635	KdpD protein
	3E-09	46.3	9.2	5E-09	45.7	6.3	1.3	1	C3KRJ3_RHISN	Histidine kinase (EC 2.7.13.3)	kdpD NGR_b12490	Rhizobium sp. (strain NGR234)	901	394	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Sinorhizobium fredii group, Rhizobium fredii (Sinorhizobium fredii), Rhizobium sp. (strain NGR234)	>tr|C3KRJ3|C3KRJ3_RHISN Histidine kinase OS=Rhizobium sp. (strain NGR234) GN=kdpD PE=4 SV=1MPGDRPDVDTRPSPDALLENAEREARGRLKIFLGAAPGVGKTYEMLVSGRARKSEGVDVVIGIVETHGRQETQALVDGLEAIARRNVEYRGHVLDEMDLDAILARRPQLVLVDELAHTNVEGSRHSKRYLDVEEILAKGIDVYSTLNVQHIESLNDIVAQITRIRVRETVPDSIIDRADDVEIIDLTPDDLIKRLHEGKVYLPTTAKRAIANYFSPGNLTALRELALRRTAERVDDQLVSHMQAHAIPGPWAAGDRVLVCIDHGSRGAALVRYAKRQADRLRAPWSAIHVETTGSINLPDADKDRLASHLRLAEQLGGEAITIPGQSVARDILRHAAAHNFTHVVTGKPNKPRWRELIEGSVSHDLIRHAGEISVHVVSGAARAASAARGVKTAPPPKQVKLQAYLLSTLYVSIALAFSALLDQVLDVRNLALVLLIGVLTSAVTAGLGPALYACFVSALAFNFFLEPRYTFTIRDPESVLALVFFLVVAVTASNLTARVQRQAAAARQRARTTEDLYLFAKKLASTGTLDDVLWATAHQIASMLKVRVVILLPESGSIAVKAGYPPDDTLVDADIAAARWAWENDRPAGRGADTLPGAKRLYLPLRTGRAAIGVVGLDNDRQGPLLTPEQQRLFDALADQAALAIERVQLVADVDRARLAAEADRLRSALLTSISHDLKTPLAAIMGSAGTLRDYSGAMPEEDRTDLLSTVVDESERLNRFIANLLDMTRIESGATEPNASLHDVGDVVGTALRRAAKMLARHKTAIDAPGDLPMLKLDPVLFEQVLFNLLDNAAKYAPPGSTVRIRAWVDDNSVALQVMDEGPGIPSGDLERVFDSFYRVRKGDHVRAGTGLGLSICRGFIEAMGGTIAAGNRTDRSGAVFTITMPIPVGAPNVEDLT	24~~KdpD (1.45837E-120)~~234;X;256~~Usp(6.51996E-42)~~377;X;404~~DUF4118 (9.49864E-14)~~498;X;530~~GAF (0.000000000677602)~~649;X;666~~HisKA (0.000000000034239 6)~~732;X;785~~HATPase_c (2.42336E-26)~~887	KdpD protein
	3E-09	46.3	10.4	5.1E-09	45.7	7.2	1.3	1	R4T157_AMYOR	Histidine kinase (EC 2.7.13.3)	kdpD AORI_5977	Amycolatopsis orientalis HCCB10007	861	1156913	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis orientalis (Nocardia orientalis), Amycolatopsis orientalis HCCB10007	>tr|R4T157|R4T157_AMYOR Histidine kinase OS=Amycolatopsis orientalis HCCB10007 GN=kdpD PE=4 SV=1MDENTTKPRRGELRIYLGAAPGVGKTYAMLGEARRRLDRGTDVVIGLVETHGRKKTAELVEGLETVPRRRSAHREHEFEEMDLDALLARAPEVAVVDELAHTNVPGSRNEKRWQDIDELLDAGIDVLSTVNVQHLQSLNDVVERITGVTQQETVPDEVVRRAEQLELVDITPEALRRRLAHGNVYPAERIDAALGNYFRPGNLTALRELALLWVADQVDVALQRYRAEQKITDTWEARERVVVSITGGPESETLIRRASRIANRAGAELQVLHILRGDGLAGMGPTAVGKYRKLTEEVGATFHTVVGDDVPTALLDFAQGVNATQLVVGTSRRSRVARLFDEGIGAAVVQRSGPIDVHMVTHAEAGGRLRARFNRSPLPSTRRLAGWALAFVLPVLSTLLGVLLKEQLDFSTDMVAYMLATVLVALVGGLGPALLAAVLSAGLLNFFFTPPLYTLTVHEPRNVITLIAMVLVAILVAAVVDTAARRATQAARARTEAALLASYARTVLTHTNPIERLLEKVRENFGMTSVTLLEKRDGKWKRVANAGTDPCADPDQADADIAVTADVHLTLRGRALPASDRGVLEAVAGQALLALRQQRTAKAAIRAERKAEATELRTALLSAVGHDLRTPLTSIKAAIGSLRATDISLSEEDTDELFEAIEESADRLAGLIDNLLDSSRLATGAVRPHLRPVGYDEVVSHALSNVDNSASVVVAIDSRLPSVCADPGLLERVVANVIDNALRHGASGEPVSARASTHSEYVELRIIDHGRGLKKGTADSAFAPFQRLGGDRDSVPGVGLGLSVAKGFTEAMGGRIRAEDTPGGGLTVVISLPAYVVGQDPEKSLLAFDDEGLENEEERVR	8~~KdpD (1.50294E-121)~~218;X;240~~Usp(5.50508E-31)~~361;X;387~~DUF4118 (5.97688E-16)~~481;X(134);615~~HisKA (0.000000000023612 5)~~680;X;730~~HATPase_c (7.69372E-22)~~832	KdpD protein
	3E-09	46.3	12.5	6.1E-09	45.4	8.6	1.5	1	A0A0F2S4I1_9RHOB	Histidine kinase	VR71_00125	Roseovarius sp. BRH_c41	884	1629709	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Roseovarius, Roseovarius sp. BRH_c41	>tr|A0A0F2S4I1|A0A0F2S4I1_9RHOB Histidine kinase OS=Roseovarius sp. BRH_c41 GN=VR71_00125 PE=4 SV=1MTDDARPSPDALLREAQREGRGTLKIFLGAAPGVGKTYEMLLEGAEKIEAGADVVIGLVETHGRDETEALVAPLPVIPRRKIDYKGQTLTEMDLDAVLERRPKIVLVDELAHTNAPGSRHPKRWQDIEELRAAGIDVMTTVNIQHVESLNDVVGSFTHVRVRETVPDKVFEEAEIELIDLPPEDLISRLGDGKVYVPDQARHALDHFFSKGNLLALRELALRHAAQYVEARIQEHKSVTGKDIGYAGGQRILVAISQEAGGEQVIRAAKRLADALKAPLIALYVETPSAERFGDAEKTQLAGNLSLAASLGATLQSVPATSVQDAILAHCRDVSATQLVLGKSRRQGGWWRRRDPIVQDILDRTTGVAIHVIPFDEQVRGRDWRNFVPRGSWTGDAVAIGSVAALTLAAFLAQGWISRGPIDLLYLLPVIVSASLYGFRAGLIAAIAAGIAYNFFFLPPFYTVIIYGPANIITAVLLVVVAIITGQLAARARAAAALAMRSARENAGLARFATRLGAASNTQETAQLIRDELRSLLAVQTIVLHPSADGVTISAFGQTKPQLSPVDRAAAEWVMDHGEEAGIGTNTLTASAWQFRPLKTSLGTLAVLGFRGPHGRDPIPTERAALAESLIDQAALAHERLKLEADMRDMEVVRQRDNLRAALLASLSHDLRTPLTAVTAAAEALSATGDEAELVETVRSEARRLNRFLSDLLDLTRIEEGAVTPDLVPTDLTDVIASALGDLSKSLTGRKVLTSIDPNLPLVRADAVLLNHALLNLVDNAAKYSPQDAPIEIIARMGRRGPVIDVLDSGPGIPQGSEQRIFDRFARGETSDRTGGSGLGLAIVKGFAAAMGFTVEAARRQGGGSRFTIRIPSTAIIQVSLEDIA	19~~KdpD (1.00552E-109)~~212;X;250~~Usp(8.95754E-31)~~373;X;421~~DUF4118 (0.000000113901)~~487;X(169);656~~HisKA (0.000000000025781 5)~~716;X;769~~HATPase_c (5.25386E-26)~~870	KdpD protein
	3E-09	46.3	8.3	5.4E-09	45.6	5.7	1.3	1	R6Q206_9CLOT	Uncharacterized protein	BN618_00210	Clostridium nexile CAG:348	664	1263069	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	>tr|R6Q206|R6Q206_9CLOT Uncharacterized protein OS=Clostridium nexile CAG:348 GN=BN618_00210 PE=4 SV=1MEEMRPNSEQLLRRLKYEEEQKQTTRGKLKIFLGYAAGSGKTYTMLEAAHEAKKHGIDVVAGYIEPHDRPDTLKLTEGLEMIPPLWIEYKGVRFREFDLEQALKRKPKLILVDELAHTNVAGCRNHKRYQDVKELLRAGIDVYTTINIQHLESLNDLVGTITHIEVRERVPDRIFDHADQVEVIDIEPEDLIRRMQEGKIYQKQQAQRALDHFFRREKLAALREITLRRTADRVNRIAEEERNIMGDMEYHTGEHVLVCISAAESSPKVIRSAARLAYAFHAKFTGIYVETPEMQEAGEKTKQSLQNHMELARSLGAKIVTVFGSDIGFQIAEYAVVGNVSKVVLGRTNHNRFIQKPRPELLEKLNNRAPNIDVYVIPDIKQKKIHTRMNIRSERWEKKWKRIFWGFAAITVVMILTTMVAFVLQKWNLPESNIIMVYILGVLLSSYISDNKLFAVYSSMFSVLAFNFFFTEPYLSLKAYDKGYPTTFLMLFIVGLFTAVQTRKLKLQNRESVKKAYRTEILLENSQKLRRCKSELEVWNQVAGQVGKLLNLSLIIYPVNEKGLLNDALVFPKKGVTKEQLEFLLDSQERAVAQWSAANHHRAGTCTHTLPTAKAMYIPIQNEKEVKGILGIYLEERRKLQEFEYGLLIAMLNETGVKLQDTFH	26~~KdpD (3.70712E-123)~~234;X;255~~Usp(6.04674E-32)~~378;X;407~~DUF4118 (6.86056E-16)~~504;X;537~~GAF (0.0000482837)~~660	KdpD protein

	3E-09	46.3	7.9	5.2E-09	45.6	5.5	1.3	1	Q98GX8_RHILO	Histidine kinase (EC 2.7.13.3)	mll3127	Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	907	266835	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium, Rhizobium loti (Mesorhizobium loti), Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	>tr|Q98GX8|Q98GX8_RHILO Histidine kinase OS=Rhizobium loti (strain MAFF303099) GN=mll3127 PE=4 SV=1MPDDRSNENRPSPDALLEHAEREGRGRLRIFLGAAPGVGKTYEMLMSGRARLADGIDVVIGVVETHGRRETQALVEGYEVIPRRKVDYKGRVLEEMDIDAILARRPALVLVDELAHTNAPGSRHPKRYLDVQEILARGIDVYTTLNIQHVESLNDVVAQITRVRVRETVPDSIIDQADDVEIIDLTPDDLIKRLEEGKVYFPNTAQRAIENYFSSGNLTALRELALRRTAQRVDEQLLNHMQSHAIQGPWAAGERVLVCVDARPGGAARIRYARRLADRLRAPWTALHVDTPRSAGMSEEDKDRLAALMRLAEQLGAEVTTIPGQSVAQDIVRHATANNFTHIVVGRPTRSRWRELIEGSLTYDLIRNAGDISVHVISGTERDAEAASRRVKAAAEQKQFQIWPYLLATTYVAGSLALSAVLDQFLDVRNLAIVFLLAVLTSAVAGGLWPALYACFLSALAFNYFFLEPRYTLTIRDPESIVALAVFLAVAVIASNLAARMQRQAVAARSRARATEDIYLFSKKLAGAGTLDDVLWATAFQIASMLKLRVVLLLPEDGTITVKAGYPPDDTLAEADIAAARWAWEHNRAAGRGADTLPGAKRLYLPLRTGRTAIGVIGLDNDKQGPLLTPEQQRLLDALADQAAVAIERIQLVADVDRAKLAAEADRLRSALLTSISHDLKTPLSAIMGAAGTLKEFAPDLPEQDRAELLSTVIDESERLNRFIANLLDMTKIESGAMEPNYALHYVGDIVGTALNRARKITSEHKIEVDIPPDLPMLKLDPVLFEQVLFNLLDNASKYSPPGSTIRLQGWADNGSVIVQIMDEGPGIPSHDLERVFDTFYRVRKGDQVRAGTGLGLSICRGFVESMGGTISAANRTDRPGAAFTIRMPVPTEAPDRGEETSMDRPS	23~~KdpD (2.69126E-122)~~233;X;255~~Usp(8.50241E-48)~~378;X;404~~DUF4118 (1.53422E-16)~~502;X;530~~GAF (1.66533E-16)~~649;X;666~~HisKA (0.000000000001785)78)~~732;X;785~~HATPase_c (1.2963E-26)~~887	KdpD protein
	3E-09	46.3	4.7	3.3E-09	46.3	3.3	2.3	1	C6Q1S1_9CLOT	PAS/PAC sensor signal transduction histidine kinase (EC 2.7.13.3)	CcarbDRAFT_4989	Clostridium carboxidivorans P7	628	536227	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium carboxidivorans, Clostridium carboxidivorans P7	>tr|C6Q1S1|C6Q1S1_9CLOT PAS/PAC sensor signal transduction histidine kinase OS=Clostridium carboxidivorans P7 GN=CcarbDRAFT_4989 PE=4 SV=1MNNFMDVKNMYNIDKNRQQNIYNIVSIVKLASLCFCGIVIYNEFFMRNKGIANENDNYFYIIELGLLICLMFLIYWGWSFFSIRIFKSKNIKKMQLMENAVFIMIFSFSIFLSNSYTSQYKFLFLFLIITSTLQSGMKYGMSIALISSVIILAIDLVYGSNNSVNLYFENDLILVGVFILTAWPLGHYVKIEKENLKQKDMQLKTLNSKLSKQEKHRKYIEGMLLNNEACYNLLIENSRDAIFVHRDDKVIFTNESAAKLVGFTKTEDLNEKSILDFTTSNEKDNVKEKFKQIYDKKITRLVFEEKIMRSNGDIVIVKNTSTYFIYEGKQTILSILSDITSEKQVEKLEKDVEKNIKLLNETREFNKMITEFFSNISHELKTPLNVIFSAVQVLNLYINKNEGENIEKQHKYLKVVKQNCYRLLKLINNLLDITRADSGFLKLHTGRYNIVSVVEDITLSVVSYVESKGINLIFDTDVEEKVINFDADKIERIILNLLSNSIKFTNPGGKIYVNMSDIGNGVTISVKDTGVGIPEDKLQMIFERFGQVDKTLRRNSEGTGIGLCLVKSFVEMHGGTIEVKSKLGEGSEFIIKFPEIITEQQQSEENSMYETNTERINIEFSDIYSQDT	95~~DUF4118 (3.2198E-16)~~195;X(171);366~~HisKA (6.68501E-15)~~435;X;490~~HATPase_c (2.46665E-30)~~593	non-KdpD DUF4118 protein
	4E-09	46.1	3.9	7.8E-09	45.1	2.7	1.5	1	R5TGY0_9FIRM	NAD dependent epimerase/dehydratase family protein	BN683_01990	Roseburia sp. CAG:50	669	1262949	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:50	>tr|R5TGY0|R5TGY0_9FIRM NAD dependent epimerase/dehydratase family protein OS=Roseburia sp. CAG:50 GN=BN683_01990 PE=4 SV=1MNVLLIGGSGSLINSLIVKFKKEGHRIFLLTGDRYKKQKYEPVFERYNFAYSSENLQEIMESVRPDITIYTGAFDPNYRWMSEERETVRFTSDLMNVLVAYSTIRMGKFIFLSSHEVYEGYHENALTEDIPPETTGYRGTTLIQAEEICNNYRKNWKLDLLILRLDHLFCIPESAPEIHSVCARMCLESMRDGCISADSNHEFAMLYEQDAVEFIFQIVKSREHKFYLYHLSSDCVISEVELAGRIQKCLNNGSSIVTVSKYDKRCILSGKRFQEEFGMHTIFELDEIIGQTIDYMRKHEERFDKYQESRDSWWKILWKKWKWVFQVIVPFVENLLCFIPFFMLNNRMTDSAYFTNLDPYLLYVLVFAIIYGQQQATFSAVCAVAGYLFRQMYQRTGFEVVLDYNTYVWIAQLFILGLIVGYMRDQIRMIRRESLEMEEHLTGQIADLQEINATNVRIKAAMEQQLIGHQDSIGKIYQITSRLEQQQMPDIYQELAERRVYINKAMAEEYPLMATAIYEEEEIRLIIMVWGLSWEHMTLGEANFLTVVSYLIQNAVLRAQRYIKALEEARYREGSEILEPEAFESLVRAYEHAQGRNLTQYTLLCVSEQPERYKKICSDMRGLLRSTDYMGMRADEKLYVLLTNTGRTDAVFVEQRFEKKGYPVVAVEIE	108~~NADB_Rossmann (0.0000305154)~~232;X;330~~DUF4118 (3.07447E-16)~~428	non-KdpD DUF4118 protein
	4E-09	46	10.3	8.3E-09	45	7.2	1.5	1	A1KA55_AZOSB	Histidine kinase (EC 2.7.13.3)	kdpD2 azo3094	Azoarcus sp. (strain BH72)	509	62928	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azoarcus, Azoarcus sp. (strain BH72)	>tr|A1KA55|A1KA55_AZOSB Histidine kinase OS=Azoarcus sp. (strain BH72) GN=kdpD2 PE=4 SV=1MGVGRLAGLSVPVRHLVAATLCALAAAAVYPLRQLLEPANVVMLLLLVVAFNAAWLGRGPAVLGTVVSVALFDFLFVPPQLSFAVSDVKYLITFAVMLLVSLLIGQLTVSLRASADEAALRERRSHALYALARSLAGAMLPAQVMEQVAAFVRTEAGAEVHFHLPDEDDGALHPQPAGVPAPGVAETTAAAGIFFTPAEGQAGCVAVAGVGLMLPLHGATRCRGVMVVQPGAAAAPLESLRPLLEAVASLAAIALERLHFVAVAQASQFEAEAERLRNSILASISHDIRTPLTVLFGLADALSEGRLGSEEREAAHAIRDQAGRLHDMVDKLLDMARLQAGTVRLRKEWQPLDEILGAAIALLGDALRAHPVTLVQAAETPLVAVDAVLLERVFCNLLDNAARCSPAGTPITVDLAREGDMLVVGVRDHGPGFPAGGERAFELFERGRASGVAGVGLGLAICRAVVEAHGGWIRAGNAADGGACVRFALPCGEAPVIEPEAGVEAQA	33~~DUF4118 (0.0000000045323)~~112;X;141~~GAF (0.0000466479)~~257;X;274~~HisKA (0.000000000041942)7)~~339;X;392~~HATPase_c (5.63912E-24)~~491	non-KdpD DUF4118 protein
	4E-09	46	9.7	6.7E-09	45.3	6.7	1.4	1	R7APY1_9BACE	Histidine kinase (EC 2.7.13.3)	BN656_00295	Bacteroides pectinophilus CAG:437	501	1263051	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides pectinophilus CAG:437	>tr|R7APY1|R7APY1_9BACE Histidine kinase OS=Bacteroides pectinophilus CAG:437 GN=BN656_00295 PE=4 SV=1MFKNIIKSIAILAGATALGMVFYRIGFSSANIIMVYILGVLITSIATSHRVYSLISSIASVFVFNYLFTAPRFSLSAYETGYPVTFVVMFITAYVSGTFSLRYKEQARQSEKLADTTRILFDTDKLLTAAKGRDAIIKAAAGQISRLLERNIVIYLNVDGKLSEPYMLNVSDSSCAGNAGVMDEKNVAEWVLANNHYAGASTDRFADSVYVYYAVRVNDRVYGVIGIEAKDKILDSSSQSILLSILGECALALENEKNQRDKEEAAILAESEQLRANLLRSISHDLRTPLTTIAGNASSLLSNGKSFDEQTRYQIYQDIYNDSVWLNNLVENLLYATRIEEGRMVLNTSTELLADVIDDAVRHVKQHSGEHSIFVESDDEYILVTADARLIVQVIINIVDNAVRYTPPGSHITIRSCSENNMAVVYIEDNGNGISDEDKEHVFDKFYSGTNRIADNRRRSIGLGLYLCKAIIEAHGGTITVRDNNPAGAVFVFTLPLADNAF	4~~DUF4118 (3.10233E-15)~~106;X(166);272~~HisKA (0.000000000045803)9)~~338;X;391~~HATPase_c (3.76083E-28)~~494	non-KdpD DUF4118 protein
	4E-09	46	5.4	9.6E-08	41.6	1.7	2.5	2	C0ZK82_BREBN	Conserved hypothetical membrane protein	BBR47_05560	Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	734	358681	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus brevis (Bacillus brevis), Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	>tr|C0ZK82|C0ZK82_BREBN Conserved hypothetical membrane protein OS=Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599) GN=BBR47_05560 PE=4 SV=1MKVLITGGYGFIGSFVAERFYKEGYKVFILDNLSSGNQRNVTFPHKAYELDVADKKCDEVFKSNKFDVVIHLAAQVSVAASMEDPLLDTNTNILGLVNMLKLSSKYGVSKFIFASSAAVYGMNECTPLLEDSGCDPVSVYGINKHIGEMYCRKWTEMYGLQTVAFRLANVYGPRQSAGGEGGVISTFLTQINHGKEIVLHGDGSQTRDFIYVEDVADAIFRSVTTDDTGVMNLSTNQESSINELIDILGANQPLQGISRREKRPGDVDKSVLDNTWAKRRLDWIPMYSLAEGLEKTAQWYQETVAEKEQEQESEAKKAIHWLRSWDARPYLENILAFLLVVFATVGTVNSGVFDLKLIYIVLIGAIYGTKQSLLSVILACGLFIGESLHNGRDVVSLLYDANVLFHIAVYFIIGIAVGYSIDKRNRDVLSKELQKQALEDKYDFLKDIYNDVLMVKQELQQQIVNSEDSFGKIYNITKELDSLEPERVLQKSVKVLERIMKSDEIAIYTMNQNGSFLRLMAKSNKAGFDLPRSLKMSEHAYLTELMTMKKIIVNKELRHDMPLIAAPIFDKGKMVAVVTLQQLGFENFTMYTQNLFQVAVQLISSALSRSLRYLNSTQKDRYLDDTPILIPAYFSAMVKNKRDAKQQLNTDFTLLAVDFAQMDHHTLATYIASSLREADYMGMDEAGNVYIILSNSNEQEARIVIDRLGRLGIASRIVQEKDQDRFSLKDGAYV	non-KdpD DUF4118 protein

	4E-09	46	8.8	6.6E-09	45.3	6.1	1.3	1	R5IX00_9CLOT	Histidine kinase (EC 2.7.13.3)	BN757_01589	Clostridium sp. CAG:7	657	1262832	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:7	>tr|R5IX00|R5IX00_9CLOT Histidine kinase OS=Clostridium sp. CAG:7 GN=BN757_01589 PE=4 SV=1MEERILVCLSSSPSNGKIIRTAAQMAEAFNGTLTALFVETPLAGKMGKEDQERLKGNIKLAKQSGAEIETVYGDDISFQIAEFARLSGITRIVIGRSAAKKKGVFAGTSLVEKLIDHAPEMEIYIIPDSQMGPEVIRKWNRLAQKNAFSFKAAVKSAGILFAATAVGWLFEKLKLTDANIITVYILGVLLISIVTEGWFYSFSSTIASVLVFNFLFTAPRFTLRAYDRSYPFTFAVMFLAALITGSLASRLKQHAGQAARDAYRLKVLLDTNQLLQQAKGKTEILEGAAQQIVKLLKRETVIYDVKDGKLEHPLRRVPQGEEDITIEDEACEEQAAAWALENNRHAGTGTDHFKQAKRQYLAIRVNSTVYGVVGIMIQKQPLDAFENSVLLSILGECALALENDKNVREKEEAAILAKNEQLRANLLRTISHDLRTPLTSISGNANNLLYNESCLDAQMRRQIYGDIYDDSMWLIDLVENLLSVTRIEEGRMQIRQSAELVDEVIKEALKHTGQSRTGRTIKVEEEDELILAKMDARLIVQVLINLIGNAVKYTPQGTDITVRVKKEKAENAERSQVIISVCDLGNGIPDDRKERVFDMFYTGSDQVADSRRSLGLGLGLCRSIINAHGGKIWISDNIPHGAVVTFTLPAEEVALNE	4~~Usp(1.78086E-35)~~127;X;154~~DUF4118 (5.41959E-14)~~254;X(166);420~~HisKA (0.000000000640569)~~486;X;539~~HATPase_c (1.28957E-22)~~648	non-KdpD DUF4118 protein
	4E-09	45.9	4	8.2E-09	45	2.7	1.5	1	D4KWS1_9FIRM	Nucleoside-diphosphate-sugar epimerases	RO1_11640	Roseburia intestinalis XB6B4	713	718255	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, Roseburia intestinalis, Roseburia intestinalis XB6B4	>tr|D4KWS1|D4KWS1_9FIRM Nucleoside-diphosphate-sugar epimerases OS=Roseburia intestinalis XB6B4 GN=RO1_11640 PE=4 SV=1MRLMINRLNKEGHRVFVLTEEPKKGYSLKKVFEVYHFSYEDACVREVLESIMPQVVVFLGAYDHNFSWNRVENTAASYAAGLTNILMNYTALKKGRFVYLSSESVFGGGSAQFMTEDDPTGAYSKKGQAIAIGEDICKNYARMGNDVVILRLDHLYGEIRKKEDTDTICADMCLEAVQTGEIIASQNEKIMLLHEADAVEFIYQIMVAKDHKHTLYQLSSGEKMSRYELAQAVAAGMENEVSIVEEENKKYREVMLSGKRYDEEFGSRVLHHAETDVEKIAAYFSRHVSEFTDAGQKKGHLFRRLGSRTKEIITNLIPFMENLICFIPFFMLNNRAVGSEYFQNIDFYLLYVLLFALVYGQQQATFSALLAVAGYCFRQMYHRSGFDVMLDYNTYVWIAQLLILGLAVGYLRDQLRAMREEQRHEVSYLTKQLDDISDINVSNVRVKEILANQIVNQNDSFGKLYEITSSLEQYEPCEVLFYAAEVLAKLMGSKDVAIYTVANRSYARLFSATSEKARSLGNSINYSEMDAMYTVLAGKKVYINKNMDERYPLMANAIYSEDEMQLILMIWGIPWERMTLGQANMLTVIGYLIQNAVVRANRYISALEQQRYIKGTNILEPEAFLALVKAYLNARDKGLTQCALLSVDTKENDRDEVGKRLIKLLRQSDYVGELEGGKMYALLANTSAKDATMVKERFEKEGVSCQIQEDVFV	4~~NADB_Rossmann (0.000000000165992)~~216;X(102);318~~DUF4118 (2.39706E-17)~~416;X;475~~GAF (0.000000000001537 87)~~599	non-KdpD DUF4118 protein
	4E-09	45.9	11.5	7.1E-09	45.2	7.9	1.4	1	A0A060QKY1_9PROT	Histidine kinase (EC 2.7.13.3)	ASAP_2241	Asaia platycodi SF2.1	923	1382230	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Asaia, Asaia platycodi, Asaia platycodi SF2.1	>tr|A0A060QKY1|A0A060QKY1_9PROT Histidine kinase OS=Asaia platycodi SF2.1 GN=ASAP_2241 PE=4 SV=1MNRRSRQTEPGNAMTRQDYDRPDPDALLRQGCGERRRGRLKIFLGAAPGVGKTFEMLSSARHLMQEGVDLAIGVVETHGRAETQALVEGLPVIAAGSVAYRGQILREMDLDAILARRPTLALVDELAHSNAPGSRHPKRWMDVEELLNAGIDVFTTVNIQHLESLNDIVASITRVRVRETVPDHVIESADELELVDLTPGDLLQRMRDGKIYAAHTAGRALLHYFSPGNLTALRELALRQTAQQVDAQLVDHMKANAIAGPWAAGERVMVCLTLQDGDAGLVRYGKRLADRLHAPWIVLHVETSRDLTEEARARMASQMHLAQSLGAETVTVPGHDIALDALAYARAQNVTQIVAAHPAGTGWLGRLRQLIGRSTTERLIQRSENFPVHVVPRSGEAMDHRIYENPPPRFSPYLASTAIVLCALGLALLLRQGFEVSNVSLAFLTAILGVAVAYGLGPSLWASIFGMLCFNFFFLPPLYTLTIAAPDNVVALFFFFATALIAGNLGARVRSQAVVARHRAEITQSLYRFSRTITGMSTLDDLLCSVTRQIATLLDCHVVLLMPDGGRLAVQAQSDKAHPPGEDDLAAASWAWKHSRLAGRGSDSLPGVQWLFIPLRTARGPVAVIGLYREKPGQLLDAEQQSLLDALADQTASALESLLLTRDLDRVRLEAETDRLRGALLTSISHDLRTPLASILGAASSLRDYGEVLGEEGRSELLSTLTDEAERLNRFVGNLLDMTRIEAGALPLRHDSVDCAEVAATALARAAKLLEHHHVTLDTASTLPMLDLDAVLLEQSLFNILDNAAKYTPAETAITLRLAMRHSRLVIAIEDEGPGFGDRDPAEIFGKFTRFAAADTARAGTGLGLAIARGFVEAMGGDIEAANRTDRQGAVFTLRFPLPASQAMRQIVPDRTGPETRDGRKSL	36~~KdpD (4.70974E118)~~245;X;267~~Usp(1.05595E-34)~~392;X;437~~DUF4118 (0.000000000000082 98)~~512;X;538~~GAF (0.000000000001173 41)~~656;X;674~~HisKA (0.000000000000982559)~~740;X;793~~HATPase_c (4.76741E-22)~~896	KdpD protein
	4E-09	45.9	8.2	7.3E-09	45.2	5.7	1.4	1	R6PLD0_9CLOT	Histidine kinase (EC 2.7.13.3)	BN597_00116	Clostridium sp. CAG:306	583	1262794	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:306	>tr|R6PLD0|R6PLD0_9CLOT Histidine kinase OS=Clostridium sp. CAG:306 GN=BN597_00116 PE=4 SV=1MANVFDADFTALYIEMTGTKKLSSENKKRLESNTALARAQGAKVVTLNGDDIAYQVAQYAKTGKVTKIVIGRSGYRANSFFAPPNFVDKLIQQTPEIEIYVIPDKVQAVYLGQKHNKKIFKLPEFSLIDTFKTIVVFLLTTSVCLYFQKLNINESNMIMIYLLGVLITAYITESKLYSIISSVLAVLSFNYFFTRPYMTVVSMDSGYTFTFFIMFFVALFVSSITKKIKEQAKQSYLKAYSTQIMLDMSQKLQQAKNVEEIDEITIEQIKKLLDCDVLLFEPNKEPVSTVYECFPIRNTDTVFLNAAIPAKRYKSATEFEKNLFSAMLRESALAYEKETITQTKNELLLKHKQEELRSTLLRAISHDLRTPLTGISGNADILLNNADVISGEKKHQIYSDIYDDSIWLLNLVENLLSVTRFDKNEINIKKKESEFISDVIQEAVSHIGRRKDNYNIKIEITDESLSAKVDARLISQVVFNLVDNAMKYSPVNTTITIGAYAEGKDIKVFVSDQGNGISDEDKKSIFDMFYTVNNAVSSDSRRGLGLGLALCKAVVEAHGGTICVTDNKPEGTIFEFSLEGDFYE	21)~~103;X;131~~DUF4118 (0.000000000000706085)~~231;X(123);354~~HisKA (0.000000000008723 1)~~420;X;473~~HATPase_c (1.35469E-25)~~577	non-KdpD DUF4118 protein
	5E-09	45.7	2.8	1.1E-08	44.6	2	1.5	1	R5YAU6_9FIRM	Nucleoside-diphosphate-sugar epimerases	BN528_01468	Roseburia sp. CAG:197	725	1262943	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:197	>tr|R5YAU6|R5YAU6_9FIRM Nucleoside-diphosphate-sugar epimerases OS=Roseburia sp. CAG:197 GN=BN528_01468 PE=4 SV=1MNILLVGGKSHFLQLLIEKLNKEGHRIFILTDEPKSGRPTRKVFETYHFSYEESCIREVVESIQPDETIFLGAFDTNYKWAELKSHAGAFSAGLMNVLSAFVGCSTGRFIYLSSEEVFQQEFADAISEDETPAAVTAKGQALAVGEGICKYYRDMGKDVVTLRLDHMYGMPESALEAKNMIGRMCVEALETREILVGKWQRAALLHESDAVEFIYRVVAAKEPKYGLYHISSGEPISQQTMAEALVKGFDGEIAIMENPKEPRWEPVLSNTRYAEEFGIRIFHTPEKELPPIAKHINRNATEFARIEVRPKGIIGKIHRWIKEFLPAVFPFLENMVCFIPFFMLNNRAVGREYFQNIDFYLLYVLLFAIVYGQQQATFSSLLAVAGYTFRQMYHRSGFDVILDYNTYIWIAQLLILGLAVGYMRDRLRVLEDEGKNEVKFLSKQIDDIADINVSNVRIKEMLSTQIVNQNDSFGKLYEVTSSLDKYEPGEVLFYAAEVLAQLMGSKDVAIYSVANRSYARLFSATSQKARSLGNSINYVEMEEMYEQLQERKVYINKNMDERYPLMADAIYSEENMQLILMVWGIPWERMTLGQANMFTVIGYLIQNAVLRANRYMSALEEQRYIEGTNILGQEAFRSLVKAYMNARNKELTECALILIDTGEVPKEEAGHTLSKMIRQSDFLGELEDGNLYALLANTNEKSAEMVETRFQEAGFECSIQEDDVV	3~~NADB_Rossmann (0.000000000000148223)~~231;X;330~~DUF4118 (1.17466E-16)~~428;X;487~~GAF (0.000000000804081)~~611	non-KdpD DUF4118 protein

	6E-09	45.5	8.3	1.1E-08	44.6	5.7	1.4	1	A0A0C2TN58_BACBA	Histidine kinase (EC 2.7.13.3)	SD77_1461	Bacillus badius	898	1455	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus badius	>tr|A0A0C2TN58|A0A0C2TN58_BACBA Histidine kinase OS=Bacillus badius GN=SD77_1461 PE=4 SV=1MEDQRPSPEVFLAKMEAEQEAAAGKLKIFLGYAAGVGKTYAMLDAAHQAKQLGKDVVVGYIERHPRPETLALLEGLEQIPAKSIEYKGKIFQELDIDKVIERQPEIVLIDELAHTNVPVMRHLKRFGDVEELLAKGMDVYTTVNIQHIESLHDVVEDITGIKVRERIPDYVIDQASQIKLVDIEPDELIQRLKEGKVVYPPKQAEKAIDSFFRKQNLVALREIALRRTADTVYYKTAKESFKQNVQIEEHLLVGLSSSPTNAKVIRTAARIAQALHGKFTALYVQRAEKGEASPADVERLQQHMKLSEQLGGHVVIVQEEDVAAALASYAHISGVTKLVIGRTAIKRKWWQPSSKISQRLNEYAPSLAIHIVPDQENEPIYLPEMKAHLYFEWMDGLKMLAVFSLASLMGLFFFQMGYSEANIITIYILGVLILAIWSSGWMMSIISSAAAVLLFNFLFTEPRLSFEAYHRDYPITFFIMFLSGIITSSLTKRIKEQAAAAIRKSYRTEVLLETNRKLHHAKSIDEIITQGVSQIVKLVEKPVNFFEIDHRLIAKSLFFRTDTLSNSENRAIEGLFGNANELGVVNWVANNKRIAGVSTDIFPEAGAYYLPVISGGEVKGVIGIALSKHDPLPAFERHVLHAVINDFSLAFDKWYLQKLHAQVVREAELQQMRANLLRAISHDLRTPLTSISGNADILLTNTEQIPEGDKIRLYQDIYSNSKWLVQMVENLLAVSKLDDGQLAIELQPELVEDIVQEALLHVVRLNNTHNISYQAEPELLLALMDARLIIQVLINIIDNALTYTPAGSDISIVAKEAGDAVLFSISDNGPGIEDSLKAKLFEPFTTGKAQRSDSRRGLGLGLALCQTILHLHGSELTVSDNKPQGTTFSFSLKKGMVAI	24~~KdpD (7.54799E-118)~~231;X;249~~Usp(2.46064E-31)~~372;X;396~~DUF4118 (1.34834E-14)~~496;X(173);669~~HisKA (0.000000000414223)~~735;X;788~~HATPase_c (4.28385E-27)~~891	KdpD protein
	6E-09	45.5	6.8	9.5E-09	44.8	4.7	1.3	1	R6R026_9CLOT	Histidine kinase (EC 2.7.13.3)	BN621_00577	Clostridium sp. CAG:352	900	1262798	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:352	>tr|R6R026|R6R026_9CLOT Histidine kinase OS=Clostridium sp. CAG:352 GN=BN621_00577 PE=4 SV=1MDETRQSPEHFLKEIEKEKQNLNRGHLKIFFGYAAGVGKTYAMLKAAHSVKRHGIDVVAGYIEPHARPQTSALVNGLECLPNLVSEYNGITLSEFNLDAALARHPQLILVDELAHTNAPVCRHTKRYQDIEELLNAGIDVYTTVNVQHIESLNDTVASITSIMVHERIPDSVFDNASQVELVDIEPQELIERLQAGKVYNPTQAERATENFFTVENLTALREIALRRCADRVNLLTETVRTKSHSDYHTDEHILVCLSSSPSNAKIIRTAARMANAFKGAFTALFVETPDYQVMSEEDVKRLRSNMRLAEQLGAKIETVHGEDVSYQIAEFARLSQGVSKIVIGRSSATRKSIFSKPTLTEKLIARVPNLDVHIIPDTGGKNTAYRAKKARKKNGIVFSVSDLLKSVAILILASCIGMLFRQLGFAEANIITVYVLGVLVTSVVTRHRVYSLISSIVSVLVFNFFFTDPQFTLQAYDQGYPVTFLIMFLAALLTSSLAVKLKEHAKQSAKAAYRTKVLFDTNQLLQQAKDKNEIVSATANQLIKLLGKDIVFYLTEGETLGEPHIFTVSGDKTDKEITGTKEEAVAEWVLKNNKHAGATTETLSNAKCLYLAVRVNSRVYGVVGIYIGNEPLDAFEKSILLSILGECALSLENEKNAREKEEAAILAKNEQLRANLLRAISHDLRTPLTSISGNASNLISNGNSFDEATKNQLYTDIYDDSMWLINLVENLLSVTRIEEGRLNLHITEDLVDDVITEALHHVNRKSVEHHITVRHKEDYLLAKMDAKLMVQVVINIVDNAIKYTPKGSNILIKTWKQGDKAVISIADDGDGIPDEMKERVFDMFYSGANKIADSRRSLGLGLSLCRSIVNAHAGKITVSDNTPHGTVFTITLPAGEVEIHE	23~~KdpD (1.2884E-118)~~232;X;252~~Usp(2.76056E-40)~~375;X;402~~DUF4118 (4.07752E-15)~~503;X;529~~GAF (0.00000320239)~~652;X;669~~HisKA (0.00000000227628)~~735;X;790~~HATPase_c (8.99491E-27)~~891	KdpD protein
	7E-09	45.3	3.8	1.2E-08	44.4	2.6	1.4	1	R6QPX1_9CLOT	Uncharacterized protein	BN618_01595	Clostridium nexile CAG:348	587	1263069	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	>tr|R6QPX1|R6QPX1_9CLOT Uncharacterized protein OS=Clostridium nexile CAG:348 GN=BN618_01595 PE=4 SV=1MAVAQGEELCRSYRETSGSNTVVLRFDHLYGEPKKERQEENPCFQMMLEALKTGKISANSRNVFSLLYMSDAVEFTYQIIKAENLLHATYNIASGESITQMELARQIQKYAGTGMELVDNTVGEGYRRVLSTERYKCEFPHKVFVPSEEGVKRTVKYMKKHSRRFLKKEDAGGSIGSRTWKMIKNIVRSLIPYLENLFCFGVFFMLNNRAVSSAYYNKLDFYLLYVLLFAIVYGQQQAIFSALLAVVGYCFRQMYDRSGFEVLMDYGTYVRMAQLFILGMVVGYMRDQIRYIKEKDKEEIGYLNGQLGDVIDINERNVRMKHMFERQIVNQKDSLGKIYAIVSELDQYGPEEVLFYAAHVLSHLMDTPDAAIYTVANGDYARLFSFTSDTAKKMGNSIKYTDMKELYGELKERRVYINRTMDNRYSLMAVGVYAEEQMQIIMMLWGIPWERMNLAESNRLMIIGSLVQNAAVRASRYLEALHENRYVADTNILEQEAFERLVNAFFDAKGKGWTECSLLKIEDAARTYEDTAHAFSSLLRQTDYLGVLQDGLYVLLPNTSEENAKWVIARFQEQGCNCELRNREVTG	4~~NADB_Rossman (0.00000343488)~~93;X;192~~DUF4118 (9.40904E-16)~~291;X;350~~GAF (0.000000000004829 31)~~473	non-KdpD DUF4118 protein
	7E-09	45.3	10	1.2E-08	44.5	6.9	1.4	1	A9HGJ6_GLUDA	Histidine kinase (EC 2.7.13.3)	kdpD GDI1566	Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5)	894	272568	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Gluconacetobacter, Gluconacetobacter diazotrophicus (Acetobacter diazotrophicus), Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5)	>tr|A9HGJ6|A9HGJ6_GLUDA Histidine kinase OS=Gluconacetobacter diazotrophicus (strain ATCC 49037 / DSM 5601 / PAl5) GN=kdpD PE=4 SV=1MMEDRTDRPDPDALLRQAAHDMGGTRGRLKIFVGAAPGVGKTFEMLTTAHRLIRDGVDVVVGVVETHGRSETAALLDGLEVVPRRVVAYRGQTLTEMDLDAILARQPRLVLVDELAHTNAPGSRHPKRWMDVEELLAAGMDVFTTVNIQHLESLNDIVAGITRIRVRETVPDTVIDRADEIELIDLTPADLLQRLREGKVYTAPAASRAMRNYFSPGNLTALRELALRQTARQVDAQLIDHMRSNAISGPWAAGERILVCLTLQDVDGSLLRYGRRLAERFHAPWTVLHVETSREAGETIRQRTASQMHLAQSMGAETITIPGQDVATETLAWARSHNVTQIVAGRPARRPWTSWMTPWTWTSVTRILADRAGDIPVHVVGATNGHEGAEEKPEKRPLAFGPYIAATGIVAGALVLSLVRHGMEVQNVSLTFLTAVLGVALGFGLWPSLYASVMAVLSFNFFFLPPLYTFVIAAPDNIAALAFFSITAVTASHLGNRVRAQAIVARHAEITESLYEFSRKLTGVTSMDELLWTTCQQIATMLDRQVVILLPQDDKLIIRASDPPEKSLDSADLAAATWAWRHDRSAGRGSDNLPGARRLFVPLRTARGPIGVIGLDSDGPGLLLGQEQQRLVDALGDQAALAIERIILSHDLDQARLHAETERLRGALLSSISHDLRTPLSSILGAASSLDSYDALLDKKDRKELLTTIREEAERLSRFVANLLDMTRLEAGALTPARQPCDLGEVAGSALARASVILRHHRVSLKVAPDLPLVPLDDVLVEQALFNILDNAAKYTPEGSMVMIEIAQKGGSLRLRLTDEGPGLPADNPNQIFDKFTRIQFADRQRPGTGLGLAIAKGFVETAGGSITAENRPDRTGAVFTLSFPIVAEVSG	24~~KdpD (6.11271E-115)~~234;X;256~~Usp(1.084E-33)~~381;X;402~~DUF4118 (1.71413E-16)~~502;X;528~~GAF (0.000000000000233829)~~647;X;664~~HisKA (4.70611E-14)~~730;X;784~~HATPase_c (5.03955E-24)~~886	KdpD protein
	7E-09	45.2	9.1	1.3E-08	44.3	6.3	1.4	1	Q02CY0_SOLUE	Histidine kinase (EC 2.7.13.3)	Acid_0070	Solibacter usitatus (strain Ellin6076)	498	234267	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Solibacteres, Solibacterales, Solibacteraceae, Candidatus Solibacter, Solibacter usitatus, Solibacter usitatus (strain Ellin6076)	>tr|Q02CY0|Q02CY0_SOLUE Histidine kinase OS=Solibacter usitatus (strain Ellin6076) GN=Acid_0070 PE=4 SV=1MGQTILAAAGFQPARPLPEPIPVRLKLLHFLTSLLAVAGVLALYLFLLPVNNTTVALSLLLVILAISARWGLAEATLASVIAVLGLNYYFLPPVRTFTIQDPQNWVALVAFLVTAVTASQLSARVRRRAAEAEARRLEIERLYALVQAMILSGNARRTLREFVQTVVKVFACDAAAFYYQPGGEFFRSGPESSPITDHDLLAAAEVDHVSFDPEKHIATAPVRLGGRPLGSMALLGELPSEQTMSAIVNLVAISVEKARALEDASHAEAARQSEVLKSALLDSLAHDIKTPLTSIKAAVTSLLSNSAAADQELLTIINEEADRLNQLAAEVIAMARVEAGKLHLEKRPVNVAELIEGALGELGARSGHAVTVNLSPRLPRASCDPEFVQQVVKQLLENALKYSPEGAEVTVSAERKGAKIVVGVADRGPGIDEEERARVFDKFFRGKRHRFETKGTGMGLAIAKGIIEAHGEKIWVESEPEHGSAFYFSLPLAEGRDA	34~~DUF4118 (0.000000000169599)~~122;X(152);274~~HisKA (0.00000000384763)~~336;X;389~~HATPase_c (1.00305E-31)~~490	non-KdpD DUF4118 protein
	8E-09	45.2	10.8	1.1E-08	44.6	7.5	1.3	1	C4L748_EXISA	Uncharacterized protein	EAT1b_1214	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	408	360911	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	>tr|C4L748|C4L748_EXISA Uncharacterized protein OS=Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b) GN=EAT1b_1214 PE=4 SV=1MIYTQHRTSIKWIEMIVTILLIGILDYTFSLSLSDWAIDPLIFYILLFSLRYGLLGAFVSFALTSLYHFSFLLMEGSDLLLFLYDTNELAWILLHFFVALSAGVFSTSYRERYQSLHIRQEEVVDENEQLKQTIQQLQESQGEMRKRVLDSTYTLSKIYEIGLKLDQDATDLVRDHLIGTFTRVFRARQLALYHVDASRRTLRLHVRSGEVERLPQTLFIDSEQGIFARMFQSKKPTIRLADELDGPLLVAPICYEGTVKEVLVVHEIDILRLRSHEMNMMKLVLDWTGTRIEKADALEWMLVSDQLVDGTHMFRMEAFEQKVAQQVQRHEQYGQPYSTVTLPIEGVDLSLIEMELILRQSMREIDVIGYDEEDRILHFLLPGTPVESAERFKERIEHVFYVKGGKRL	11~~DUF4118 (1.30277E-15)~~112;X;170~~GAF (0.000000000001044 51)~~294;X;318~~Nucleotidyl_cyc_III (0.000551327)~~400	non-KdpD DUF4118 protein

	8E-09	45.1	12.8	1.2E-08	44.5	8.9	1.3	1	E4T7V3_PALPW	Histidine kinase (EC 2.7.13.3)	Palpr_2667	Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	886	694427	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Paludibacter, Paludibacter propionicigenes, Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	>tr|E4T7V3|E4T7V3_PALPW Histidine kinase OS=Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4) GN=Palpr_2667 PE=4 SV=1MNDFEIDRPNPDELLAALAKEEEKNKRGKLKIFFGMCAGVGKTYTMLQAAHVEKKKGNDIVIGYVETHKRKETEALVHGFEIIPRKAIEYKSTSVEEMDLDAIIARHPQIVLVDELAHTNAPGSRHNKRYQDVQELLENGINVFTTLNVQHLESRTDTVAQITGVIIRETLPDFIFETSDDIELVDITPDELLQRLSDGKVYTPERSKEAVNNFFRKGNITALREMSLRIVADRVDNQLHDYMQDKRIRGPWKSGLHFLVAIGVSPSSQGLLKWAKNLAYTMGANVEALYVETSQRLTPRDHEQLDANIELAKELGFKVRIVTNDDLVKAIINYAQKENITHIIVGKSRFSSLKSLLKLGNFVNRLIKYSGNIDVYILGSDTPVEDKINIKSTIPTFTSRSRQYLTVSLIVALTSVLSYLVRDIVGYQVVSVILLFMVSLLALFYGTGPVLFAATASALIWDYFFIPPQFTFLIQKPLDILLLVMFFIVALVNGTLTSRVRRQEKKIRVREERTHALYQLTKDLNSVSGFDEVIKIAYDFINRYFKLECSIVVKNDVNQLEVMPKENSTIQLTESEMSIIHWVEKNSMKAGNLTSTLPSNEFTYYPLIGSNSTLGVIVVKQTKVFTHGEEQFWESSLSQIIGKYERELLRNATRKTYMISESEKLYKTLFNSISHELRIPIAAIMGSSETLLEQQLPEQIQQELYSEINTASIRLNRLVENLLNMSRLESGRITPHPDWCDAHDLVNSVSESLQNELESFTFKIDIPDDLPLIYVDFGLIEQVLHNLVLNATQHSPKGSAIELKIELADDNLFIKVTDRGHGFPEDELSSVFDKFYRGKDAKAGGTGLGLSIVKGFVEAHNGSVSAANGVNGGAVFTLKIPKKEKK	26~~KdpD (2.65945E-120)~~235;X;257~~Usp(3.79093E-29)~~379;X;403~~DUF4118 (1.65767E-16)~~503;X;531~~GAF (0.000516883)~~640;X;663~~HisKA (0.000000000000625423)~~727;X;780~~HATPase_c (6.16469E-26)~~880	KdpD protein
	8E-09	45	7.5	1.4E-08	44.3	5.2	1.4	1	R7HB97_9FIRM	Histidine kinase (EC 2.7.13.3)	BN634_01129	Eubacterium sp. CAG:38	658	1262889	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:38	>tr|R7HB97|R7HB97_9FIRM Histidine kinase OS=Eubacterium sp. CAG:38 GN=BN634_01129 PE=4 SV=1MDKTYTNGSDRTEEHILVCLSSSPSNKKIVHTAAAMAAALHARFTALYVQNRILSDTSDKKRLEEHIHFAEKLGAEIVTTHGENIPVQIAEYAHLSNVTKIVIGQSNAKRSHFFSRAALTEQLIKAAPDIDIHIIPDAVKSEIYPKKQPLLYTNKPSLKDCFLTISIFAICTLIGLLFQKLKFTDTNIVTIYILGVLLTSIVTNGYLCSICSSCLSVVLFCFFLTEPRMSFQTYAVGYPVTFLIMLISSVLTGTLAAKLKTHANISAQLAFRTQILFDTDRLLQKATGSTEILSITCSQLARLLNRNITAYVAEQGTLSKGQLFFNKKETPAEDILTEKEYEIAKWVYENKKRAGATTRHFNDAECLYLAIRIGNNVYGVIGIPVKKDSLDSFEHSILLSVINECALAMENSQNAIEKEKNAILAKNEQLRADLLRAISHDLRTPLCSIYGNADMLLNNDTCLDTSTKHQIYTDIYDDSEWLIGVVENLLSITRLNDGRLKFKFTDQLVDEVIAESLRHINRKHDNHKIIADCNELILARMDVRLIIQVLVNLIDNAVKYTPAGSTIYIHAVKKSAEAQISVTDNGPGIPDPIKPHIFEMFYTGKNTIADSHRSLGLGLALCHSIIEAHNGKLNLTDNVPHGCIFTFTLPLSEVTLNE	27)~~136;X;164~~DUF4118 (0.000000000000052062)~~262;X(166);428~~HisKA (0.000000000931847)~~494;X;546~~HATPase_c (2.5833E-27)~~649	non-KdpD DUF4118 protein
	9E-09	45	11.2	1.6E-08	44.1	7.8	1.4	1	A0A0F5LAG7_9RHIZ	Histidine kinase	VW29_17360	Devosia limi DSM 17137	891	1121477	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia limi, Devosia limi DSM 17137	>tr|A0A0F5LAG7|A0A0F5LAG7_9RHIZ Histidine kinase OS=Devosia limi DSM 17137 GN=VW29_17360 PE=4 SV=1MTDNNDTLRPDPAALLELAARETRGKLTIFLGAAPGVGKTYAMLTRARQRRAEGVEIVIGLVETHGRAETAALLEGLEILPRRAGRQAGRTYDEFDLDAALRRKPAIIIVDELAHSNDADARHPKRYQDIAELLAAGIDVWTALNVQHLESLSDLVARIAGVPVRETVPDIVLQKADEVVLVDLPPSELIARLREGKVYLPENAGRAAEGFFKPANLTALRELALRRTADRVDDQMADIWRQQAVEGPWTTGERLLVCVGPDQLSEKVVRTASRLAVGLNARWIVLSLSGASNPIPPPARAARLEATLHLAERLGAEIRRATVDDFVAEILRIARRENITQIVVGRPRPGLLPRRSLPEALLRAAGDIGVYMVPGQGDAPRNPLRLRRRTLPQWALTLALPFVATGLITVLGLGLSQLVALQNLSMLFLVAVLVSALLGGRFAALLAAGLSFLAYNFFFIDPVRTFTIARPHEVLALAIFVGVAVVTGSLAARLREQMGRARQAVRNTQALYDFSRKLSAAYGLDNVLTATAGHLQTTLGLDTVLLASLDGGELELQVAWPPDQNLDATAMTAARWAHDKREPAGFLTATLPAVPYLFLPIRSEQRLVGVVGLKLNAERGPLTPDEGRQVAAILEQAAIAIDRARLVRDNARIALEKEGEKLQTALLSSLSHDLRTPLASITGAVTTLRQLGDRMNGETRADLLMSIEEETGRLNRFVTNLFDMTRIESGAVKPRRDPVDLLALITNVVERARALDPALVVESTSIADAMPPVLADPALLDPVLFNLLDNARKYAGTALPVTIFVRVDNGMATIAVTDQGKGIPPGELEAIFDKFYRRAKGDHRAAGTGLGLSIARGFVEAMGGTLKAESPAMRRRGTRFTIRLPLAEGARS	24~~KdpD (1.48827E-113)~~232;X;254~~Usp(1.16681E-26)~~374;X;398~~DUF4118 (1.0467E-15)~~497;X;524~~GAF (0.000000000025328)~~643;X;660~~HisKA (0.0000000034094)~~726;X;782~~HATPase_c (5.82922E-26)~~883	KdpD protein
	9E-09	44.9	13.1	1.4E-08	44.3	9.1	1.3	1	A6X5I1_OCHA4	Histidine kinase (EC 2.7.13.3)	Oant_3779	Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	912	439375	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Ochrobactrum, Ochrobactrum anthropi, Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	>tr|A6X5I1|A6X5I1_OCHA4 Histidine kinase OS=Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168) GN=Oant_3779 PE=4 SV=1MICRPSFQELYLTSDPLRFGENRPSPDALLEQAERETRGRLKIFLGAAPGVGKTYEMLMSGRARRADGIDVVIGVVETHGRVETEALTEGLEIIPRAQVAYRGHLLDEMDIDAVLARKPQLVLVDELAHTNAPGSRHPKRYQDVEEILARGIDVYTTLNIQHVESLNDVVAQITRIRVRETVPDSIIDRADDIELIDLTPNDLIKRLNEGKIYLPKTAKRAIHNYFSSGNLTALRELALRRTAQRVDEQLLSHMRAHAIEGPWAAGDRILVADERPRSISLVRYARRLADRLRAPWAAIHIETARSAGLTEEAKDRLATALRLAEQLGGETIIIPGQSVAEDIVRYASTHNFTQIVAGKSIKSRWREMIDGSIARELVRLSGAIDIHITAGVDYENGETPRKVKTASQKATPDITPYLIGMVMTGIALVTGLLLDQFLDVRSIALVFVVGVLGVAVTLGLWPALFASVLSAFAYNFFFLSPLYTLSIADPESVVALVFFLFVSFIASNLASRVQRQAAAARQRARMTEDLYLFSKKLAGTGSLDDVLWATAFQIASMLKVRVVMLLPEGNSITVRGGYPPDDTLDDADIAAAHWTWEHDLPAGRGANTLPGAKRLYLPLKTARTSVGVIGLDNDRMGPILTPEQQRLFEALADQAAIAIERVQLVGDVERAKLAAEADKLRSALLTSISHDLKTPLAAILGAATTLRDYSSSLPDTDRSDLVATVVDQSERLNRFIANLLDMTRIEAGAMKPNLSLHYVGDLIGAALNRAAKILVHHQVNIAVPADLPMVQLDAVLFEQVLFNLFDNAAKYAPENTPITIKAHAAPSRITLEISDRGPGIPPGDLERVFDTFYRVRKGDHVQAGTGLGLSIARGFIEAMGGSIRAGNRHEGTGAVFTIALPVPADEVDKNS	38~~KdpD (1.38656E-124)~~246;X;268~~Usp(1.98789E-45)~~389;X;460~~DUF4118 (0.00000000852311)~~512;X;543~~GAF (0.000000000001373389)~~662;X;679~~HisKA (0.0000000000261673)~~745;X;798~~HATPase_c (9.71094E-27)~~901	KdpD protein
	9E-09	44.8	11.6	1.8E-08	43.9	8	1.5	1	D7A9S8_STAND	Histidine kinase (EC 2.7.13.3)	Snov_1545	Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	903	639283	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Starkeya, Starkeya novella (Thiobacillus novellus), Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113)	>tr|D7A9S8|D7A9S8_STAND Histidine kinase OS=Starkeya novella (strain ATCC 8093 / DSM 506 / CCM 1077 / IAM 12100 / NBRC 12443 / NCIB 9113) GN=Snov_1545 PE=4 SV=1MSVQDPPRADPEALLAAAEREARGKLRIYLGAAPGVGKTYAMLSAARAAKAAGGDVVIGIVETHGRAETEALIEGIESLPRKGVPYRGRLVPEFDLDAALARQPGLLLVDEYAHSNVDGSRHPKRWQDVQDLLAAGIDVWTTLNIQHVESLNDVVQRITGVRVRETVPDTALQKADEIILVDLPSDELIKRLADGKVYVEDTATRAVQSFFKPSNLTALRELALRRVAARVDSDLLERMQGAAIEGPWAAGERILVCVGPDIAAERVVREAKRLADLMDASWFAVTVERPGHVMAGGDRRRLEAGMRLAETLGAETRSLVAADVASELLRFARFENVTQIIIGKARRWWLARLLRGPLADALVKQADGVAIHVVTAEASEVPARRRFQPPPAGQLAGYSAAVLSVGAATVTGLFLTRFVALPNVSMLYLLAVLLPALLYGVWPAILASTLSFLAYNFFFIDPVETFTVARPHELLALLIFLIVAVLISTIAGRAREQARIAAQRMRATRRLYEFTRKLSALPDRSSVAEAAAVELHTVLGRPSVILLSEHGDLSIAAAWPPEDRLDTGSMTAASWAFEHGEAAGAGTGTLPSVPWLFRPLGGMAGGTAGGAPIGVVGIERDPTMPVLDAESESILGTLSEQTAAALVRTMLSAEVTRARTAAETERVRNILLASISHDFRTPLASILGAATSLIDYGPDIPPEVRRDLLAQMRDEAENLDHMVRNLLSMTRLEAGALEIHKDWVDAVELMNRAVSAVRRRGATQRFVVTSAPDLPLIQADQSLMDQALGNVVANAVRYAGKEARIGLAATVIDNELVIAVTDDGPGIPTQTLPHVFEKFVRASRGAADGGDGSGLGLAITKGIVEAHGGRVAGRSPAPGQRNGTRITMKLPLPAHAPEGEGKS	24~~KdpD (1.73542E-112)~~231;X;253~~Usp(1.07585E-37)~~375;X;440~~DUF4118 (0.000000827379)~~497;X(168);665~~HisKA (0.000000000009286)~~731;X;786~~HATPase_c (8.31622E-15)~~890	KdpD protein

	9E-09	44.8	11	1.5E-08	44.2	7.7	1.3	1	R7AXP4_9FIRM	Histidine kinase (EC 2.7.13.3)	BN599_00238	Firmicutes bacterium CAG:308	644	1263016	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:308	>tr|R7AXP4|R7AXP4_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:308 GN=BN599_00238 PE=4 SV=1MNEHILVCLSPSPSNTKIIEAASKMVEAFNANFTALYVKTTKEPSKEDRQRLNDNVKFAQDRGATIESVFGDD VAYQIIEYSRLSHVTKIVVGKSRVKGLSNIKPTLVDKLIAQAGNVDVYIIPDTEDTRPAPKEKEPIDLNALKKDLLKSFV ILSITTLISYLFFEIGFADSSIMMVYILGVMIIAMITQGKAYSLITSALIVVIFNFLFTEPRFTLKAYASEYPVTFLVMFFAA LITGTLAGKLKDFASESTRNSYRTKILFDTNQLLQNSTSSEEIVTIMAKQIQKLLSKSVIVYIKENGKIDRPYVFMYNK EDPSKYLNDHEFKVAQWVCEHNKQAGAFTVRFTDSSCLHLSIRVNQQGYGVVSIPIDEPIEPFENSILLSILGESAL AMENYRNIKDKEESIILAENERTRANMLRSISHDLRTPLTSILGNASNLLSNAHLFDEKTKSQIYLDIYDESWWLINLV ENLLSVTKIEDGDMHLNFSYELINEIVEEALKHVDRHKIEHKISIHSEDDLMLVKVDSRLMVQVFVNLIDNAIKYTPKG SHIDVFILKKEEEVLIRVQDDGPGISDEDKEHIFERYYQKANTLADSRRSLGLGLALCRSIINAHGHEIVVKDNVPHG TIFEFTLSSKEVVLDA	4~~Usp(6.94416E-30)~~124;X;148~~DUF4118 (1.76062E-16)~~248;X(165);413~~HisKA (0.000000000129263)~~479;X;534~~HATPase_c (1.54676E-27)~~635	non-KdpD DUF4118 protein
	1E-08	44.8	8.4	1.5E-08	44.2	5.8	1.3	1	D4KH79_9FIRM	Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain	MHY_04990	Megamonas hypermegale ART12/1	516	657316	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	>tr|D4KH79|D4KH79_9FIRM Universal stress protein family./Osmosensitive K+ channel His kinase sensor domain OS=Megamonas hypermegale ART12/1 GN=MHY_04990 PE=4 SV=1MQLGGAYMPIIRKSPEKILEQIHIEEHESKRGKLKIFFGYAAGVGKTYAMLEAAHEAKKQGIDVVAGYIEPHAR PATAALVNSLEVISPLVINHKDITLNEFNLDAAIKRNPQLILVDELAHTNADGCRHIKRYQDIEELLKAGIDVYTTINVQ HIESLNDIVASITKIIVRERIPDRIFDEAEQVELVDIEPSDLVTRLSEGKIYQKEQADRALGNFFTVENLTALREIALRR MADRVNKISLKVKNENNKDYYTNEHILVCLSSSPSNSKIIRTAARMANAFKAQFTALFVQTSSFEKTSLENKKRLKE NIHLAEQLGAKIEMVVGEDIPFQIAEFARLAGVSKLVIGRSIARNGFMRLMRKSFTDKLIEQLPNLDIHVIPDNKALFY KNFWKKSVNEREICNTSDIITILVILIITSMIGMLFYSMNLGEANIMTVYILGVLIAALKTSKRLYSVVLSVLNVLAFDFLF IEPRYTFTAYDPVYIITFSVMFVSAFVTGGLTNKIKNKLYSLLN	29~~KdpD (2.23349E-127)~~239;X;259~~Usp(2.30323E-37)~~383;X;421~~DUF4118 (0.000000000008856 99)~~510	KdpD protein
	1E-08	44.7	9.3	1.6E-08	44.1	6.4	1.3	1	Q8PCL9_XANCP	Histidine kinase (EC 2.7.13.3)	kdpD XCC0705	Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	886	190485	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas campestris, Xanthomonas campestris pv. campestris, Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	>tr|Q8PCL9|Q8PCL9_XANCP Histidine kinase OS=Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25) GN=kdpD PE=4 SV=1MSDARTQQADALIGELQREHGGRLTVFLGAAPGVGKTYAMLSRARERLRQGVDVVAGVVETHGRSETAAL LDGVPLLPRVQVSYQGHALEELALDALLARKPQLALIDELAHRNVPGSRHERRWQDTVELLDAGIDVYTTVNIQHL ESLNDIVLRITGVRVSETVPDAVFDRLRDIVLVDLPPRELIERLQQGKVYLPEQASQALQAFFSPSNLTALRELAMQ TAADRVDSDLRDTQAARGLPGTAALRRHVVVAIDGRGSSDYLVRVARRLSERRDAPWTVVTVQTRTVADAAWQL EIDRAFALTRRLGGDTALLHGANVADALLDFASQNGVSTLVLGRTRERPLARMFNRTLTQQLLQRGAHYELVIVSS GDARARARQRWRNPGQWLQRYDLAYAAIAAAAAVAVAWVIQRWTDIDDLSMVFIVAVVLVASRTRMAAAVIAALL SFVAYNFFFIEPRFTLHISARQGVVTVCLFLIAALVAGRLASRLRSQVLALRAANAHANALQALARQLSTAADLGQV LEAGRRALASALDAEVWLRLEQCESEAPTSFSALDRNAADWTQRHGQPAGRFTDTLAGAQWWCLPVRHERGT LGVAALRFRQQLQRPGLEQRRLAEAMVEDIGQAALRTRLVADLEGARVSGETERLRSALLSSVSHDLRSPLASMI GSASSLAEYGEAMDATDRRSLLETIQLEGERLDRYIQNLLDMTRLGHTGLTLKRDWIGVDELIGSATRRLQRYQPQ VRLQLDLAPELPAIWVHPALVEQAIFNVLENAAKFSPPGVAVTVQARLQSGALQIEIGDQGPGIPEDERARIFDMFY SVERGDRGRHGTGLGLTICQGMIGAHGGSVEALAGPHGHGTTIRITLPLLVPAASPRPDAD	19~~KdpD (1.67896E-115)~~229;X;251~~Usp(7.9026E-27)~~372;X;424~~DUF4118 (0.000000000023877 5)~~495;X(155);650~~HisKA (0.000000000060482 6)~~716;X;770~~HATPase_c (1.0525E-23)~~872	KdpD protein
	1E-08	44.7	12.4	1E-08	44.7	8.6	1.9	1	Q1QJ49_NITHX	Histidine kinase (EC 2.7.13.3)	Nham_2991	Nitrobacter hamburgensis (strain X14 / DSM 10229)	894	323097	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Nitrobacter, Nitrobacter hamburgensis, Nitrobacter hamburgensis (strain X14 / DSM 10229)	>tr|Q1QJ49|Q1QJ49_NITHX Histidine kinase OS=Nitrobacter hamburgensis (strain X14 / DSM 10229) GN=Nham_2991 PE=4 SV=1MSGEPATRASPDALLALAKKEGRGHLKIFLGAAPGVGKTYAMLAAARSEIAGGRNVVVGLVETHGRRETDQ MLDGFEVLARKPIVYRNQVMHEFDLDAARARKPGLLLVDEYAHTNVPGSRHPKRWQDIDELLRAGIDVWTTLNIQ HLESLNDVVQKISKVRVRETVPDKVFDQADEVVLVDFPPDELLKRLAEGKVYVQDTAARAVENFFKPQNLTALREL AMRRAAERVDASLIERMQAQAIDGPWAAGERILACIGPDPVSPTVVRTAKRLADLMDAPWIAVTVERPGASLNSA ARQRLDEVMKLAESLGAETQTLTGADLPAELLRFAKFENVTQIVVGRSRGGFFSELLRRSLPYELVRRTQDIAIHLV TRESDVSEPASGWLLHNRSPLRPLPVYATLTVAAALAVSKVLTELMPIPNLSMVFMLSVLVSAINFGVWPAIYASV LSFFIYNFFFIPPLYNFTIAEPYELLALVIFLVVAIVTSAMAGRVRDQARVSAGRVRAMRRLYEFTRRLSGLATRDGIA EGAAGEIHASLARPVVVLLAEGDGLALTAAWPPEDALDTATMTAARWAYNHAEPAGADTGTLPIIPWYFVPLRIGD KALGVIGVAKDKDTPPLDSEARTLLDTLSEQTAAALERAALASEMVSARTATETERVRNTLLASVSHDFRTPLSSIL GAATSLLSYGDKIGAAAKTDLLGQIKQETEGLDEMVRNLLAITRIDSGALELRRDWIDLREIVERVASAARRRSAPQ RIDITMPPDLPLVRADAALAEQAIGNVVANAIVHTSKETHIVIDAQSGLSDITVRVTDNGPGIGSDILPHVFNRFVRGN GADDVHDGGEGTGLGLAIARGIMEAHGGSITVDSPVEGQPGARFVMVFPREDGAT	21~~KdpD (1.67569E-116)~~231;X;253~~Usp(1.18621E-38)~~375;X;414~~DUF4118 (4.27321E-15)~~499;X;527~~GAF (0.0000000688941)~~638;X;661~~HisKA (0.000000000178129)~~727;X;781~~HATPase_c (9.00759E-25)~~887	KdpD protein
	1E-08	44.7	11.3	1.1E-08	44.7	7.8	1.8	1	D1CGU8_THET1	Histidine kinase (EC 2.7.13.3)	Tter_2066	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	496	525904	cellular organisms, Bacteria, unclassified Bacteria, Thermobaculum, Thermobaculum terrenum, Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	>tr|D1CGU8|D1CGU8_THET1 Histidine kinase OS=Thermobaculum terrenum (strain ATCC BAA-798 / YNP1) GN=Tter_2066 PE=4 SV=1MRAAQNLSYAYRAAKGRWSWLAPLGRGRWSGYLLAIGGVAAITRLISLVFTRWHIANISMIYLLLVLALAVLY GSGPAVLASVAAFLAFDWFFVQPTWSLTIRDPDEWLALCLFLVTALITGQLAGNLRSREAQLHRRARELEVVNDLT RSILLDVNLEGLLRRLVTNISEMLGLSACKVIIPDENGRLRTVVQWPAPVAGEDPPHRVAVPLMLEDRSRGVLMAY RDAQGLPFSADELRVLRACADQVAVAMERERLMAEEQRAALLEESDRMKSALLSSMSHELRTPLSVIRAAAGGM LEAPEMPPALRELALSIDREASRLDRLVGNLLDMSRIEAGVLRPHPEPQALDEIVGAVLQRLRPLLGERPVLLDFPP DLPLVAFDALQIDQVLTNLLDNACKFSPPGTEIQVGAAVEALQVRVWVRNRTCRPLSDEELRRVFDKFYRAGGEN PGSGLGLTICKAIVEAHGGSVRAARVGEGQVEFSFALPLQGTDGR	74~~DUF4118 (0.0000000949678)~~131;X;157~~GAF (0.0000012029)~~262;X;271~~HisKA (5.17553E-15)~~335;X;388~~HATPase_c (3.16295E-18)~~488	non-KdpD DUF4118 protein

	1E-08	44.5	10.5	2E-08	43.8	7.3	1.4	1	J7Q9H9_METSZ	Histidine kinase (EC 2.7.13.3)	BN69_2486	Methylocystis sp. (strain SC2)	899	187303	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylocystaceae, Methylocystis, Methylocystis sp. (strain SC2)	>tr|J7Q9H9|J7Q9H9_METSZ Histidine kinase OS=Methylocystis sp. (strain SC2) GN=BN69_2486 PE=4 SV=1MARDDGDFDRRPDPDALLALSDKESKGKLRVFLGAAPGVGKTYAMLARAQTAKAEGVDVVVGVAETHGRAETQALLNGLETLPRRKCDYRGRIIEEFDIDAALARKPQLILVDELAHTNAPDSRHPKRWQDVEELLDVGIDIWTTLNVQHLESLADVVSRVTGVAVRETVPDRVLQNAADVILVDITPEELLQRLKDGKVYVPETARRATQNFFTPRNLTALRELALRRTAERVDDQMVDFLRQGAIEGPWATSERLLVCVGRDANSEAVVRAGARLATALNATWIALYVERGGQDESAEVVRSVDQALRLAERLGAEIARTPGDDLAGEALSFARRENITQIVLGRSRARPFSRLLRRSLTDEILRRSTDIAVHVVVQEDGPPQSRQAWKLPTLSQTWLGFGGAAVSVMMTVLVGHGLERWLGLVNPSVVFLLPVVLCAVWLGMWSAIIAAVLSFLACDFFFFSPRYELTISQPQEFLTLVVALVVAVITGMLASKMRTYAQNMRQRSQAVQSLFEFSRKLSTITTLDDILWASTLQIQKAGEASSVIMLIPEEGGLKVSAAWPPVDRMDAGELAAARWALEKSEPAGWRTDTLPNVRFQFRPLATARGVVAVCGIEPKTPEEPLSAAAESTISSLLEQTAIAIDRSMLVGESVKAAALEENEKLRTILLSALSHDLRTPLTSITGAVTSLRELGEKLPPEDRKDLLLSIEEEAGRLSRFIANMLDMSRIESGALAPRSDLVDVAEVIRSVLERAKRSFPGKETSISIAPDLPPIRGDANLLGQVLFNLIDNAHKYGGPAGAIVHARREGGDVVITVTDEGPGVKTADIERIFEKFYRSGRVDGRKAGTGLGLSICRGLVRAMGGTIVAQSPAARRRGTRLIMRFPAAGESRRGVAA	24~~KdpD (8.75768E-123)~~234;X;256~~Usp(1.76971E-38)~~378;X;406~~DUF4118 (0.00000000155291)~~500;X;528~~GAF (0.00000258669)~~648;X;665~~HisKA (0.000000000008631)~~731;X;784~~HATPase_c (2.2824E-25)~~887	KdpD protein
	1E-08	44.5	10.2	1.7E-08	44	7	1.2	1	R5CSS2_9FIRM	Histidine kinase (EC 2.7.13.3)	BN705_01721	Firmicutes bacterium CAG:555	364	1263030	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:555	>tr|R5CSS2|R5CSS2_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:555 GN=BN705_01721 PE=4 SV=1MKNTNFTKADVKIFRLLKNWAITIAVVSVACILCSAIKHISSSDPYVPMIFVLAVLIISLLTDGYFYGVLTSFVSVIVVNWAFTYPYMKLDFSIYGYSTTFLTMLAVSLVISTLTTRVHEQEKLRHDTEQAQLRANLLRAVSHDLRTPLTSIIGSISAVIDGGEALSEEQKAEMLTDAKEDAEWLVRMVENLLSITRISGSTEPNIQKSPELIEEIVGDCVTKFKKRNPDVALKVNVPDTPLMVSVDAMLIEQVLMNLMDNAVHHAEGMTELCVNVTQRKRFAQVAVSDNGKGLDPYILDDIFKGQLVSNDGTSPDSNKFRGIGLAVCKSIITAHGGKISADNKPTGGAVFTFTLPLEPEETEE	19~~DUF4118 (0.000000000109459)~~121;X;132~~HisKA (0.000000000001482)53)~~197;X;251~~HATPase_c (3.74698E-22)~~353	non-KdpD DUF4118 protein
	1E-08	44.4	8.3	2.2E-08	43.6	5.8	1.4	1	B2IIP8_BEII9	Histidine kinase (EC 2.7.13.3)	Bind_1099	Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	896	395963	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Beijerinckia, Beijerinckia indica, Beijerinckia indica subsp. indica, Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712)	>tr|B2IIP8|B2IIP8_BEII9 Histidine kinase OS=Beijerinckia indica subsp. indica (strain ATCC 9039 / DSM 1715 / NCIB 8712) GN=Bind_1099 PE=4 SV=1MKEQPTHSEPNALMVKTGNVRRGRLKVFLGMSPGVGKTYEMLRAARRRKAEGGDVVIGVVETHGRRETEALLRGLEILSRRPIDYRDRSFLEFDIDAALARKPALLIDEYAHSNVPGSRHPKRWQDVQEVLAVGIDVWTTLNVQHLESLVDVVWKITGVRQRETVPDSALSNADEIEVVDITPSELRQRLAAGKVYVPETAQLASEKFFKPENLTALRELALRRAAQTIDDQLMGEMKRAGVEGPWAAGERILVLIGADTMAHSLIRAARRLSDMMMNAPWTVAHVEIANRAPPDTVSVARLNEAFKLAEQLGGSTVVLTGNDLIDSAFAYARQSNITQIMVGKSRRVWWWKWRNRSLAHALLDKATGVALHVITEAAPDHLMPPVPPARPVQNRWSDYVLGIGLVAAATFLSYFLDRAFEHTDLGMIFLSAVLAVGVLFGLRPALVAATLAFLTYNFLFLDPRYSFAIGSPTDVLTLLVFLAVALATGGLAGRVRDQASATARRASAISALLAASRRLSAVSTKDEAAKALAEQVSAAARGKAVVLLPIAETIAPAATASTTTPLSTADMGTADMAAARWAWEKGESAGAGTGTLPNAAWTFRPLQGLRTRSGVVGIEAKATSQEDERFVAALLDQGAVALERAELAAKAAEAEAWKRSDQLRSALLNSISHDLRTPLSTVLGSATTLIDYGKTLDSAVSVDLLESIREEAERLNRYVGNLLNMTRLEGGALNPRSEWTDVRDVLNAAAQRVSRRLGKRKLVTDYPPTLSPITTDAALLEQAVVNILENAIAYSPDDTDVEIAVYEDPRNIVISIEDEGRGIPTAELSRVFEKFRRMEEISDRGKGVGLGLSISKGFVDAMGGRIAAASPIHGDKGTRVLISLPKMAVIPQGST	21~~KdpD (8.82085E-121)~~230;X;252~~Usp(4.2476E-32)~~376;X;400~~DUF4118 (1.01013E-14)~~499;X(163);662~~HisKA (0.000000000028630)~~728;X;781~~HATPase_c (1.26786E-25)~~885	KdpD protein
	1E-08	44.4	7.4	2.3E-08	43.6	5.1	1.4	1	C4IDW5_CLOBU	Histidine kinase (EC 2.7.13.3)	CLP_3545	Clostridium butyricum E4 str. BoNT E BL5262	896	632245	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	>tr|C4IDW5|C4IDW5_CLOBU Histidine kinase OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_3545 PE=4 SV=1MVYERPNPDDVLKAISKEHKKNGKLKIFFGYAAGVGKTFAMLEAAHKSKESGIDVVAGYIEPHTRVETLNLLNGLEMLPNLKVDYKGISLNEFNIDGALERKPDLILVDELAHSNAVGCRHVKRYQDIKELLDNGIDVYTTVNVQHIESLNDIVASITGIIVKERIPDSVFDNADQIELVDIEPEDLIQRLNEGKIYRTDQAKRALLNFFTKEKLVALREIALRRTADAVNKKIDIERERTKNSYYTEEHLLICLSSSPSNAKVIRTAARMADAFHGLFTALFVETTDTKEFQDENRVRLERNLKLAEQLGARIATVYGDDIAWQISEYAKLSGVSKIVLGRSTTKKGLFKTKKTLVDKLTEIAPNIDIYIIPDNSKQKQTKIKLKANLYKFDMVDIAKTFGILFLSTILALIFFEFGYSEANIITIYIFGVLLTSITTSGKRCGILMSILAVLTFNFLFTDPRFTFQAYDKSYPVTFAVMFISSIVTSKLATKVKLEAQQQSTRKAYRTEVLLETSQKLQIAKSKEDIFNKTAYQTKKLLDKTIILYKSEKGVLAEPLVFKHENDKDVLEYISEEEKAVAQWTLKNKKHAGATTNTLPGAKCLYLSIRNHEKAFGVIGIPLEKDEFLEAFEKNLLIAVLGESALALEKEEINQSKNKIYIKAEQEKLRSNLLRSISHDLRTPLTSISGNAGILINNSEILSEEKKKSLYLDIYDDSMWLINLVENLLSITRIENGTMKINTEPELVEEVIEEAICHINRKVSEHKINTVIEDDLLMAKMDSGLIIQVIINIINNAIKYTPKDSIITITSKRKNNMAVIEISDNGKGINEESKEKLFDMFFTDNNKFGDGRRGLGLGLALCKSIIDAHEGCIYVRDNKPNGAIFGFTLHIEEVKINE	20~~KdpD (1.49902E-120)~~230;X;250~~Usp(3.93196E-37)~~373;X;397~~DUF4118 (4.78142E-16)~~496;X;524~~GAF (0.0000292447)~~648;X;665~~HisKA (0.00000000138116)~~731;X;797~~HATPase_c (0.00000000789602)~~887	KdpD protein
	1E-08	44.4	7	1.3E-08	44.4	4.9	2.3	1	M1MBW2_9CLOT	Histidine kinase (EC 2.7.13.3)	resE2 Cspa_c00980	Clostridium saccharoperbutylacetonicum N1-4(HMT)	619	931276	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium saccharoperbutylacetonicum, Clostridium saccharoperbutylacetonicum N1-4, Clostridium saccharoperbutylacetonicum N1-4(HMT)	>tr|M1MBW2|M1MBW2_9CLOT Histidine kinase OS=Clostridium saccharoperbutylacetonicum N1-4(HMT) GN=resE2 PE=4 SV=1MKAFIDKDENNLAIMLSIIKIAIIAFISIIIYINLPKYWGDLNIKDNGQYNLYTMGFLLCITGLCYFLWLIISRKMLQSSNVFKVSWLLENIFFIAIISLPMYLSTVYESENKYLFLLLIISSVIQYGSRYGIITSLFSSIFILGTDLLYAPIKDGINLYLQKDLTMVGVFIFVAWILGYYVDMEVSNNKKKDRTLEILSSELKEKNKERLDIESLLLKNKTCYDMLFENSSNAIIVHENGVIIYANESSAKLLGYENPIELNGKDFYKHYPQNIKLNVEERYLNIISNEDLKVMEEENILNCNGGLIPVRNTSAFFTYKGKSSILTLLLDITSEKKLETLEEDVEKSLKLLLNETREFNNLITDFFTNMSHELKTPVNVIFAAIQTIYVYLDDCKLDNIDKCKSYLKTMKQNCLRMIKLINNLLDITKLDSGFIKINKRNGNIVSVIEDIVQSIASYVKSKDIELIFDTDTEEKIMGFDHDMMERILLNLISNALKYSNPNGHIYVSLVDEQSSLVIKVKDEGKGIPPNKLDVIFERFGQVNNSLSRQCEGTGIGLYLVKSFIEIHGGKITVTSTEGEGSEFIIVLPAKLVENESYEDKAFFETHVERIEIEFSDIYSI	87~~DUF4118 (6.60438E-15)~~185;X(174);359~~HisKA (0.000000000155579)~~428;X;483~~HATPase_c (2.27171E-29)~~586	non-KdpD DUF4118 protein

	1E-08	44.3	12.3	2.1E-08	43.7	8.6	1.3	1	B3E0Q9_METI4	Histidine kinase (EC 2.7.13.3)	kdpD Minf_0758	Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	902	481448	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, unclassified Verrucomicrobia, Methylacidiphilales, Methylacidiphilaceae, Methylacidiphilum, Methylacidiphilum infernorum, Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	>tr|B3E0Q9|B3E0Q9_METI4 Histidine kinase OS=Methylacidiphilum infernorum (isolate V4) GN=kdpD PE=4 SV=1MQEQIDNRPNPDALLEVVQKEEGEKNRGSLKIFLGMCPGVGKTYAMLQAAQVELTNGKDVVIGYVETHGRK ETEQLTRGIPIIPRKIVHYRDMVLEEMDLDAILERKPQLVIVDELAHTNAPGMRHLKRYQDVLEILDAGIDVFTTLNVQ HIESRTDTVSYITGAPIYEKVPDSIVDIAEIELVDLSPEDLLKRLAEGKVYIPDQARAAALNFFREGNLRALREIVLRLA AEKAGKDVQEYMQIMHIQGPWKISHRLLVAISASPSSETLIRWTRRNAESLKCPWYAVYVETSRVLSEEDQQRLS KNMELAKHLGAEIITTADEDIVRGILRIARQWNITQIVFGKPRGRGLLEWFKSRSLLHRLVRESGQIDIHIVGEDEKE EKRKKRKFLLIPESGLSQYGLTCLVIFVITLFCLWANRWIGSRSIGMIYLLGIVIIALFVGRGPVIVAALLSAIIWDFLFL SPKFSLGIQGIENSFVVFSYFVVALVLGQFIARLRAQEKAERRREARISALYMLSQELSQAAGLDEIVIKVIEQLSHFF QAEVAVFLVNPYDNKLSGLPHWASTLKVTEKEAGVAAWAFEHGKAAGRFTENLPLSKAYYVPLSTHKGSVGVLGI NIPGIQSLSFDQKSLIQAFANQIALVIDRQRLAELAEHARVVAESERLSRTLLNSISHEMKTPIAVITTAIESLSKEDQSI KTADRAQLIEEIRSATLRLNRIVRNLLDMARIESGRFKLKKEWTDIHDLFNLSLKETAKELAGREVKVDIQRDIPLIRID FSLMLEALNNLLLNAALHTPASSPVELSASVKKNSLVIRVADRGPGIDPEILNRIFEKFYRGTGAPPGGTGLGLSIVK GVVDAHGGKVLVQNRPEGGAVFSIILPLESVPEVHPMPLEESAKK	25~~KdpD (2.62035E-112)~~232;X;256~~Usp(4.27128E-41)~~378;X;401~~DUF4118 (0.000000000000101674)~~501;X;528~~GAF (6.33053E-16)~~647;X;668~~HisKA (0.000000000096138 3)~~730;X;797~~HATPase_c (2.11018E-18)~~883	KdpD protein
	1E-08	44.3	11.6	2.1E-08	43.7	8	1.3	1	F8JAZ5_HYPSM	Histidine kinase (EC 2.7.13.3)	kdpD HYPMC_3099	Hyphomicrobium sp. (strain MC1)	907	717785	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium sp. (strain MC1)	>tr|F8JAZ5|F8JAZ5_HYPSM Histidine kinase OS=Hyphomicrobium sp. (strain MC1) GN=kdpD PE=4 SV=1MAEENRTPDHRPSPEALLEVLKREERQKGRLKIFLGAAPGVGKTYEMLRTARAKVKEGADVVVGVVETHGR KETKALLRGLDVVPPRQVEYKGRTLEELDIDAVIARRPEIALIDELAHTNAPMSRHPKRYLDVEELLDEGIDVFTTINI QHIDSLNDVVAQITGIRVRETVPDSILARADDVELVDITPEDLIQRLKEGKVYVPDQARRALENFFSPVKLTALRELA LRRTAERVDEQLVTQLRAKAMSGPWAACERVLVCVNEDVRSSGLVRYAKRAADRLHAQWTAVTIETRRSLRFSE GERNRIAEAMRLAELLGGETLTMPGSSKSIADDIISYARAHNVTQIIVGKSDRPRWFEILNGSVVHDLVRQSGNISV HVISGEQLPAEPATAQTVRTARDQPQHRPLNYFITFIAMAAALGVAWVLRPWIGVESVDLIFLTAIVGVAAKLGIGP SLVASVAGALLYNYFFLPPLFTFTIADAKNVAAFLCFVVVAIVVSNIAARMRSQTVIAMNRASTTESLYGFSRKLAGT GTLDDVLWATVFQIASMLKVRVVLLLPENGSIAVKAGYPPEDMLDPSDIAAATWAWTNDRPAGRGSDTLPGSPRL FLPLRTARGIVGVVGIDSDRPGPLLTPDQRRLFDALVNQGALAIERVHLVEDVERAKRSIETERLRAALLTSLSHDLK TPLAAILGAATTMRDLGDKFDAEAQSELLATIIDESERLNRFIANLLDMTKLEAGAIVAKTEIQDVGEIVDAALKRARKI LSRHKVQANLPSEPLKVDADPVLLEQVLFNLLDNAAKYAPENTLIEVGAWNDHGLVVIQIRDEGPGIPDRDVEKIFD KFYRANKADHVRAGTGLGLPISRGFIEIMGGTITAGNRPDRSGALLTVTLPASARSETLENAA	27~~KdpD (1.36501E-123)~~236;X;258~~Usp(2.57614E-42)~~383;X;410~~DUF4118 (9.78214E-16)~~510;X;536~~GAF (3.56799E-14)~~655;X;672~~HisKA (0.000000000002312 45)~~738;X;791~~HATPase_c (3.10067E-26)~~894	KdpD protein
	1E-08	44.3	9.3	2.6E-08	43.4	6.4	1.4	1	A0A0F5P6M8_9SPHN	Uncharacterized protein	WP12_21395	Sphingomonas sp. SRS2	496	133190	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas sp. SRS2	>tr|A0A0F5P6M8|A0A0F5P6M8_9SPHN Uncharacterized protein OS=Sphingomonas sp. SRS2 GN=WP12_21395 PE=4 SV=1MDERDYPPAVKTPAFGRWSIAAALLLVGAATGTGVLLGGWLSLASIAFLLLMPVIVMADRGGLWSGLAAAM LALFCLNFFFIPPTFTLQVARADNIVTLAVFIGVAMTVSSLADRRRHQARLSARIAMESELLAALSQQLAHLSDPALIR EHLRERLGRWTGGDVRFLTSADLDEGAVVEPIDQAAARWAIEHGDAAGKGSAIMPGAEACYLPFRILKDEIWLAQ FWSGGIAPPVPTERTNFVRQALDRGGDALHRALLAARQADIEARQQHDALRETTLLASISHDLRTPLTTVRAALGTI RSDDRGALDSAKQEADRLDRMIGNLLDLARLRTDGGAVENLPVDLTDAVDAALDALRAMLSGRPLSIDIDDDDLPLV LADARMLHHMLINLIENACKYSPDGSAIDIAARREGHRVTLSVGDHGNGIPASDPSELFASFRRGADSDRVPGSGL GLAVVAGFAAAMHLRVDAANRSPAGGPGGGAIFAIHFPETATC	31~~DUF4118 (0.000000000004350 07)~~119;X(154);273~~HisKA (0.000000000006216 85)~~331;X;384~~HATPase_c (1.76096E-20)~~474	non-KdpD DUF4118 protein
	1E-08	44.3	7.6	2.3E-08	43.6	5.3	1.3	1	M1MSZ4_9CLOT	Histidine kinase (EC 2.7.13.3)	kdpD Cspa_c09110	Clostridium saccharoperbutylacetonicum N1-4(HMT)	857	931276	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium saccharoperbutylacetonicum, Clostridium saccharoperbutylacetonicum N1-4, Clostridium saccharoperbutylacetonicum N1-4(HMT)	>tr|M1MSZ4|M1MSZ4_9CLOT Histidine kinase OS=Clostridium saccharoperbutylacetonicum N1-4(HMT) GN=kdpD PE=4 SV=1MLMEAHDMKKMGKDIVIGYIEPHARPETMALVNGIEDIGVKVIEYKGITLKEFDLDKAIARKPQIILVDELAHTN ASTERHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDIVESITHIAVRETIPDKVFDEADKVELIDIEPTELLNRFSEGK VYSKEQTRKAFDNFFTKNNLFALREIALRRTADRVNYEVESVRLAKGQVTVIPTSDVVLACISSSPSSLRVIRTATR MAEAHHSKWIALYVETTKSQNLSKEDRERLNSHFNLAEQLGGEVVTAYGDNTVEQIIQYAKFRNATKIIIGKNHKKP NNLFHFYAKDIVDKLMESNSYIDVYVVPNSSSDKQKKFNIKKNRQKFNISSREILISIFIMIITTIISLFIDYFGFSDANVI MLFILGVIIVNIKTRGYILGFICSIISIFLFNYLFTEPRYSLEVYDKSNLATFPIMLIVTFIIGTLTNKIQREAINSSQRENRT RNLYRVSKKLLSATGTVDVVGIGIKYLSRLLEKTVICYLVQDNKLSTPFIYTATRGEKDRTLLNKDEEAVAHWTFLND KESGAGTNTFHGAKAYYMPLKSHGKILGVLGVSCVNGSLEPEQKYVFETVASQIYIALDREILAETQKKSSLEIESE RLRSNLLRSISHDLRSPLAGIKGSVSTIIETGEFLSEKTKGELLQSVYEDTEWLIRLVENLLSMTRLDGGGLKIKKEM EIVEEVVYEAVQRTSKHFKEHKIKVMVPDEVIMVPMDGSLIEQVLLNLLDNAIKFTPKDSLIEIKVYEENNNIMFEVID NGPGIAEDILPHIFDIFFTDGYKISDSRRGVGLGLAICKSIVEAHGGEICAYNENGAVFKFNIPKEEEKL	1~~KdpD (2.33087E-110)~~190;X;213~~Usp(4.47989E-42)~~337;X;378~~DUF4118 (0.000000000006396 22)~~464;X;493~~GAF (0.0000000780412)~~613;X;630~~HisKA (0.000000000137537)~~696;X;749~~HATPase_c (1.56358E-27)~~850	KdpD protein
	1E-08	44.3	5.5	2.4E-08	43.5	3.8	1.3	1	R6V994_9FIRM	NAD dependent epimerase/dehydratase family protein	BN546_00255	Firmicutes bacterium CAG:227	727	1263010	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:227	>tr|R6V994|R6V994_9FIRM NAD dependent epimerase/dehydratase family protein OS=Firmicutes bacterium CAG:227 GN=BN546_00255 PE=4 SV=1MDIMLVGGASPLMKKLSLKLHKEGHRIFVLSGSRDPQNHYEHVFERYDFSYDKASVEEVFRSVNPDVTILMG AYDSNYPGRDFRREAVAYSAGLQNLLLSWSALKKGRLIYLSSVEVYGGRYPSAVSEQDKPGPRGVRPRMLYQGE ESCRFYQEELSMDVVILRLDWLHDVCCSTKEALSSICGRKCLDAFRDGSVSYQRNYAYALTYIGDAVESIYKVVAC EEHQEALYHISSSEAYSEHDIVKKVGEVLGKKIEQIDNTVGEQHQIILSNERFKAEFGFKVWCRPEETIEKTLQYMK QHSNKFLDADHPGMDIWHKLYYAMTSTLGALVPYLENLILFIPFFMLNNRATDSQYFSKIDFYLLYVLLFAVIYGQR QATFSGILATAGYLFRQMYTRSGLAVVTDYNTYVWIAEIFIVGLVVGYMKDSLLFLKEEKEWEVGFLSEQVTDIGDI NDSNLRVKEGLIDQVINYDNSLGTVYDATEQLEQEQSVEIFFCALNMIQKLMDCPDVAIYRVNKEKYARLFAYSSAK AASMGNTVYLPDKKSLDEACNENRVYINRSMEKEYPMMAYNVESEEQMEILIMLWSIPFERMTINEANRLIVIGKLI QTSVRRADRYLEALSEERYHSESQILKASAFEELVGAYRKASKEKLTEYVLLQIEVEGENEKETVDKFTSMLRESD YIGNLSDGKLYLLLTNTDLKGCSFVQNKLKQNGVASSISEEGRL	non-KdpD DUF4118 protein

	1E-08	44.2	9.1	2.6E-08	43.4	6.3	1.4	1	A0A0A8UWB8_LEGHA	Sensor protein kdpD (EC 2.7.13.3)	kdpDLHA_23382	Legionella hackeliae	894	449	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella hackeliae	>tr|A0A0A8UWB8|A0A0A8UWB8_LEGHA Sensor protein kdpD OS=Legionella hackeliae GN=kdpD PE=4 SV=1MMGADNQRPDPDVLLAQVQSQEKQASKGKLRIYFGASAGVGKTYAMLVEARKLKEDGCDVIVGLVETHGR KETEALLSGLPLLPRKSILYRNKELYDFDIDAAALEKHPQLILVDELAHSNIPGMRHPKRWQDVEELLEAGIDVFTTLN VQHLESLNDAIGGITNIHIAETVPDTIFDKADEVVMVDITADDLLLRLKAGKVYQGPQGELAAQNFFRKGNLIALRELL ALRRTAERLEDDVQAYRIEQSIDKIWKTDTALLACVGERPGAEYVIRNTARLACQLNAEWHVIYVETPALMRLPFSK KQYALNALKLAEELGATTSIVTGDDVALAIADYARNQNFSKIVLGRRRPSLRFWHSSILSRLAAYAPDFDLLVIGDLD KAGNSLDVQDISKPVKEKKEYAHYLVAVGAIFFTVLISKILEPYFSLINISLLLLLTSLLIAIRFGRGPALVASLIAAGSLD FFFIEPRYSFLIADWQQGIMMCLIVAIALITGHLTANLRYQVFIKGQRESRTHVLYKFAYELSSALLTEPILETTRTYIQ HAFSARAWLLLPDDDGQLQLPTDEETFQASEMQNLDMGIAQWAFDHKESAGLGTDTLPGNSFFYLPLVAPMRTR GLLVIQPKISQWLQRPEERQQLDTFAALAAIALERVHFIQVAQEALVHMESERMRNKVLANLSYDLQTPLASLINLS ESLVKSDSLLTPLQQELANSLKNEILHMDSLIKNLFEIARIKTGELKLNLQWHHFDTILINVSHAMNAKMTTHHIETLL EGNLPLVYLDNLLIERVLIALLDSTCKYTPKGTSIILSATSHDNNLKIAIYDKGSILSSGRAKALWKKLKRGFRIDLEIAI CGAIIEAHGGNIQLGHSPEGGTSIICSLPIKPVPELIIEE	25~~KdpD (5.96731E-118)~~235;X;258~~Usp(1.00427E-38)~~378;X;443~~DUF4118 (0.00000000590066)~~504;X;534~~GAF (0.000000000000032389)~~652;X;669~~HisKA (0.00000016472)~~734;X;787~~HATPase_c (0.000000116834)~~882	KdpD protein
	2E-08	44.1	9.5	2.6E-08	43.4	6.6	1.4	1	W0IXI3_9BACT	Histidine kinase (EC 2.7.13.3)	OPIT5_02025	Opitutaceae bacterium TAV5	524	794903	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Opitutae, Opitutales, Opitutaceae, unclassified Opitutaceae, Opitutaceae bacterium TAV5	>tr|W0IXI3|W0IXI3_9BACT Histidine kinase OS=Opitutaceae bacterium TAV5 GN=OPIT5_02025 PE=4 SV=1MPARLHPSIIPASGPDASGDVIDRETRQPPVWREYAEVLLVIAAITTVAWFVPVDYRVFGDIYLLAVIVLCLRV SRWAILFASVASVVAWNFVIVPPRMAFSQLYLHDSMFLGTYFVVAIVAGQLTARLREKEQQERQREQQATAMFHL TRALGSARTLDEAVDVALRQADTLFGAPTALSLLGNNGRLALHPASSFPLDERELALAESACREAGAEEQPAPALP HGQGAHLAVRRGQTVFGVFSVQWSRRGADMPPKYRKLMEVFVGQIGLLVEREQFRAASEREKLLAESERMHRT LLDSVSHELKTPVAVLRSAAEGLAREKGARREILAQEIRTAARRLDHLVANLLDQTRLDAGRLRLRLDWCDVHDLIG AARRAVGEGLTTRPLTIAVPADMPLFMADAVLMEHVLSNLLLNALHHTPAGTAISVYAGMEKREPGGECVFVTVAD RGPGLAPESRAKLFQKFERGDHARAGGLGLGLSIVRGFMLAQGGDVVADDNPGGGARFMIYLPHKVHESVPHE	(0.000000000015560 2)~~129;X;158~~GAF (0.0000399459)~~276;X;293~~HisKA (0.000000000784417)~~355;X;408~~HATPase_c (1.00504E-24)~~513	non-KdpD DUF4118 protein
	2E-08	44.1	10	2.6E-08	43.4	6.9	1.3	1	B1M7D3_METRJ	Histidine kinase (EC 2.7.13.3)	Mrad2831_0205	Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	905	426355	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium radiotolerans, Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	>tr|B1M7D3|B1M7D3_METRJ Histidine kinase OS=Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831) GN=Mrad2831_0205 PE=4 SV=1MPETGRDPTRPSPDALLEAARREERTRGRLKVFLGAAPGVGKTYEMLTIGRARLKAGIDVVVGVVETHGRA ETEALLDGFETIPRRSVPYHGTVLQEMDLDALLARRPALALVDELAHTNAPGSRHPKRYQDVEELLDAGIDVLTTLN IQHVESLNDVVASITRIRVRETVPDGVLDRADDIEVVDLNPDDLIQRLKDGKVYVPTHAERALKHYFSRGNLTALRE LALRRTADRVDDELLGHMRANAIAGPWAAGERVLVCVNEDPRSSGLVRYAKRLADRLHAPWTALSIEGARAAALS EAERDRIAEALRLADRLGGDAVTLPGGRRIADDVLDYARSANVNHIVVGKAHRSWLFELLNGSVVHDLVRRSGAIS VHVVPGEAVPDETPPRRAVAVTAPRPGFDARPYAIALAAIAAGLGAAIVAEPYAGVENADLFLLTAVVAVAVRWGL GPALAAVVAASLAYNFFFLPPVYTLTIADPTNVAAFLLFTLVAVLVSNLASRARRVAVVSQGRARATERLFGFSRKL AACGTLDDVLWATCAQVAAMLKVRVVLLLPDGQAVTVRAGYPPEDMLDEADLAAAQWAFDNDRPAGRGADTLP GAKRLFLPMRTGRGTIGVIGLDSDGTGPILSPEGRRLLDALADMGALAIERVRLVEDLDRAERAAETDRLRQALLTS ISHDLRTPLASVLGAASTLRDLDAALPAEAKAELLATIIEESERLNRFIANLLDMTRLEAGAVAPNLSAQDVAETVDT ALRRTQKILADHRVAVEVEADLPALADPVLFEQVLVNLLDNAAKYAPEGSTVTVRARRAGDRVRIAVLDEGDGLP DADVERVFDKFYRVRKGDRVRAGTGLGLAISRGFVEAMGGTVTAENRRDRGGACFTVSLPVPARNAPRDIAA	27~~KdpD (4.82554E-119)~~235;X;257~~Usp(1.33485E-38)~~381;X;431~~DUF4118 (0.0000000554893)~~507;X;534~~GAF (0.000000000040733)~~653;X;670~~HisKA (0.000000000016489)~~736;X;789~~HATPase_c (3.02216E-28)~~892	KdpD protein
	2E-08	44	4.4	2.6E-08	43.4	3	1.3	1	A0R7M8_PELPD	Histidine kinase (EC 2.7.13.3)	Ppro_3646	Pelobacter propionicus (strain DSM 2379)	372	338966	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Pelobacteraceae, Pelobacter, Pelobacter propionicus, Pelobacter propionicus (strain DSM 2379)	>tr|A0R7M8|A0R7M8_PELPD Histidine kinase OS=Pelobacter propionicus (strain DSM 2379) GN=Ppro_3646 PE=4 SV=1MGKSTLLRTLLLAAFITGISLLHYFTPLHLPYLHDIFQRLYYLPIILAALWFGLRGGLLCSIVVSVAYAPHILFQW GGQMTMEMEKYLEILLYNIVGGVTGLLSQWERERTVELQKTARGLEESYQKLRHQSERIIAIEEQLRRSEKLSTLG EMAAVLAHEIRNPLGSIRGTAEILKDDYKPENPKYEFIEIQIRETERLNRVVEDFLHMARPQPTDMQSCQVLDELEMI STLLLSGARERQITLELKSPPFPVTIQADGDKLRQAFLNIIINALQATPIGGRVLISTTVHASTTCEIQFHDTGPGMDA ATMERMFEPFFTTKPGGTGLGLVITKKIIETHGGTLMVESEVGKGTTVIVKLPMQTAANGGMP	21~~DUF4118 (0.000000000545031)~~110;X;148~~HisKA (4.31098E-14)~~212;X;263~~HATPase_c (5.30347E-26)~~361	non-KdpD DUF4118 protein
	2E-08	44	8.8	2.8E-08	43.3	6.1	1.4	1	G8AUY1_AZOBR	Histidine kinase (EC 2.7.13.3)	kdpDAZOBR_p230081	Azospirillum brasilense Sp245	919	1064539	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum brasilense, Azospirillum brasilense Sp245	>tr|G8AUY1|G8AUY1_AZOBR Histidine kinase OS=Azospirillum brasilense Sp245 GN=kdpD PE=4 SV=1MPNDRTAAAARPSPEALLRAAAREGRGRLKLFLGAAPGVGKTYEMLLTAQAKRRDGVDVVVGVVETHGRR ETEALLAGLTVLPRLKVEYKGRRLDEMDLDAILARRPAIVLVDELAHTNAPGSRHAKRYLDVEEILAAGIDVYTTMNI QHVESLNDVVARITRVRVRETVPDSILDRADDIEVIDITPDDLIQRLKDGKVYVPRTAERAIRHYFSPGNLTALRELAL RRTAQRVDDQLLTHMQAHAIAGPWAAGERLLVCVNEDPACAAVVRYARRQAERLRAHWTALHVETPRSLRLSEA ERDRIADALRLVEKLGGEAVTIPGGDVAGTVVEYARTNNVAHIVIAKSHRGPWAELLRSSVAFRLIRQAGGISVHVI ADDAEEPIPPKTVRTAAPRRPALSWWPYAAATGYVALALGIGEVLQQVLDVSNVALVFLTAVLTSAVTGGLGPSLY ACVASILAFNYFFLNPLYTFSIADPENIVALFFFAVVAVIASNLTARVRAQAVTARLRAKTTEDLYGFSRKLAGVVTM DDLLWATAHQIAAMLKVHVVLLLPEGGTVSVRAGYPPEDELREADLAAAVWAWENNRPAGRGSDTLPGAKWLFL PLRTGRGPVGVVGIDTDTARTGKPGALLTPDQRRLLDALTDQAALAIERVTLAEDVDRARLAAETERLRSALLTSIS HDLRTPLASILGSATSLTAYGAGMDEASRRDLAATIQEEAERLNRFIANLLDMTRLESGAIRPRTGPVDLAETVGSA LGRAGRILAGHRVDVDLAADLPMLEADDVLFEQVLFNLLDNAAKYAPTGSLIQVGASREGDRVRIEVRDEGDGIPA ADVERIFDKFYRVQAQDRQRAGTGLGLAICRGFVEAMGGTIAAGNRKDRSGAVFTLTMPAAAALPDLEGPDLEGP GLEEEGTP	24~~KdpD (1.98001E-110)~~234;X;256~~Usp(1.0769E-43)~~379;X;405~~DUF4118 (2.43082E-16)~~505;X;531~~GAF (0.000000000000116308)~~655;X;672~~HisKA (0.000000000012921 5)~~738;X;791~~HATPase_c (8.16951E-28)~~893	KdpD protein

	2E-08	44	12.6	2.6E-08	43.4	8.7	1.3	1	A0A0D5LMW2_9RHIZ	Histidine kinase (EC 2.7.13.3)	TM49_04465	Martelella endophytica	906	1486262	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	>tr|A0A0D5LMW2|A0A0D5LMW2_9RHIZ Histidine kinase OS=Martelella endophytica GN=TM49_04465 PE=4 SV=1MGSEESTRDTTRPSPDALLEKAEQETRGRLKIFLGAAPGVGKTYEMLLSGRARKSDGDDVVIGVVETHGRKETEALVRGFEIIPRTKIEYKGRILEEMDLDAVLERGPALVLVDELAHTNAPGSRHPKRYLDVLELLDHGIDVYTTLNIQHLESLNDVVAQITRIRVRETLPDSILQKADDVEIIDITPDDLIKRLNEGKVYVPRTAKRAIENYFSPRNLTALRELALRQTAQRVDQQLLSQMRQSAIEGPWPAGERILVCVNEDPCSSGLVRYAKRLADRLHAPWVALHVEGRRTQSLDDDGRDRIAAALRLAQSLEGDAVTVPGGGGRVAADIVAYARANNITHIVIGKSERSRWFEILHGSVVHELVRHAGDISVDVVAGSKPGGVPASRASVAVAEPRSRPDWKAYLKATMVVAMAVGFGLALWPWLGVEHIALIFLTGVVTVAVWFGLLPSLYASVLSAACYNFFFTNPYHTFLISRPREIVSVVFFTIVAVIVSNVAARARAQTIAAKARARTTEALYSFSRKLAGASTLDDVLWASAHQMASMLKARIIILLPENGTVAVRAGVPPDDTLVDADIAAARWALEHNRPAGRGADTLPGAARLYVPLTTGETPVGVVGLDSDRQGPLLTPEEQRLLDALADQAAVAIERIQLVADVDKARLAAEADKLRSALLASISHDLKTPLAAILGAAGNLRDYSAALSEQDRNDMLSTIVDESERLNRFIANLLDMSRIETGAMEPNASLQYLDDMVGSALRRAQKMLSRHHVRTELPADLPMLKVDPVLFEQVIFNLLDNAAKYAPPQTAIRMRAWKDGNWVMIQILDEGPGIPPADLERVFDSFHRARKRDHVLAGTGLGLSICRGFVEAMGGTITSANRTDRSGAVFTIRMPTPANPPRVGDAS	27~~KdpD (3.2409E-120)~~235;X;257~~Usp(1.82051E-43)~~382;X;409~~DUF4118 (2.53559E-17)~~509;X;535~~GAF (6.16221E-18)~~654;X;671~~HisKA (0.000000000000231603)~~737;X;790~~HATPase_c (1.17887E-27)~~892	KdpD protein
	2E-08	43.9	12.7	3.3E-08	43.1	8.8	1.4	1	V5XQE6_ENTMU	Sensor histidine kinase KdpD	kdpD EMQU_1741	Enterococcus mundtii QU 25	873	1300150	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus mundtii, Enterococcus mundtii QU 25	>tr|V5XQE6|V5XQE6_ENTMU Sensor histidine kinase KdpD OS=Enterococcus mundtii QU 25 GN=kdpD PE=4 SV=1MERQDVSEMLHQREKSRGRLRVYFGFAAGVGKTYAMLAEAQELSVLGKDIVVGYIEPHDRPDTNQLLEGLPQIPLKEVTYKGLTLSEPNIDAIIKRQPEIVLIDELAHSNAPGSRNRKRYQDIEELLNAGINVHTTINVQHIESLNDIVEEVTGIEVKETVPDTFFQQATLKVIDVEPDELIDRLAQGKIYADENAKRALQHFFIPKKLEQLRGLAIQRASDHINRVIGKTNGVQSKLITIVQDAFPKMAEKSIRWTARLAQGLGAEWIVLYIRSDDRLQGTNDLAEKLGAEVVVIEEDHSFETIVEYAKLVGATDLIIGKNLAKPWTERLFSEELDVRLLKRLPETELHLIPYKEKRSTILSHSKKLVEGGGKDFAISLICVFVATLLTEVMQYLHFGEQNLMLVYIFFILLVARLTSGYFWSALSSILSVLAFNWFFVEPLYSLTVYKQGYPITLVIMLIVALMISNLMVRLKKQAVHAREKEQQMEILYELNKQFVLAEDQQQIVELSATYLGRLLDREVIFFDKHAIKLSQYTPKDAPFLLDHPEEAAVAYWTAKNQKDSGYGTDTLSGAKGFYLPIVANGKTLAVLGIRRSRGLPIEDSQLNYLRLVLTQLAVILEQTELKNEKEQIELENEREKVRSNLLRAISHDLRTPLTAISGIAETLLQTDEELKQATRQKLLTDIQTESQWLIRMVENLLSITRINMDTMQVKKTTEPIEEIIEAVYEHVTKVYPDKELLVHLPTAVLFVEVDPILIEQAMFNLVENAFRHGSTQGQVEVSVFQEGQQVICEVKNDGEISLKQYEKIQMNLSNEEVPIDSKNGLGIGLSIVKTIIHAHNGKLEMAVSEGKTVVRIYLNKSEEVTLHEESTID	15~~KdpD (1.71436E-114)~~224;X;247~~Usp(3.77604E-26)~~353;X;376~~DUF4118 (7.67496E-17)~~477;X;503~~GAF (0.00000115656)~~621;X;639~~HisKA (0.000000000002576 11)~~705;X;758~~HATPase_c (4.13154E-15)~~858	KdpD protein
	2E-08	43.9	11	3.3E-08	43.1	7.6	1.4	1	C8WRA7_ALIAD	Histidine kinase (EC 2.7.13.3)	Aaci_0250	Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	541	521098	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Alicyclobacillus, Alicyclobacillus acidocaldarius, Alicyclobacillus acidocaldarius (Bacillus acidocaldarius), Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	>tr|C8WRA7|C8WRA7_ALIAD Histidine kinase OS=Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) GN=Aaci_0250 PE=4 SV=1MRHARRTEWMRVRFTPKWQILRVNWPTWWQEGRQGETALPRPARAVWAYAAVCGMDALLTGLVFLLDFHYDRVNIAMLYLIPVVVASGVYGLWPGVFAACLGLMSFDFFFVPPIFSYAVSDLRFLVSFAVFLVVAITTAGLASSMRRRAEEASQRARIAQTLFRMSRALTAAMDEARVVQTALEQVRDLLNTHAYIALKRPHGYDLRALQGDEADPVIDRQVLDWVLRHGDLASFGSKSHGQAAFLYVPIRAQDEVYGAFIVGEPGQFRLATRGEIVDILRAMASLVAIALSRIASERARLADIAAESERIRTAILNSISHELRTPITTMLGAAEALLDPGASLDPADRRELVLTLRNSALRMNRLVTNLIGMARIEGGMLVLNRRPTDLADVIRSALHEVAELTADHPVRVRAPHPSPIAEVDETLFQQAVVNLLSNAAKYSPPGAPTDVTLASCGTEATLEVRDYGIGISDDEIDRVFDKFYRSQRVNKIPGTGLGLAIVRAVVEAHGGHIEVERMNPGTAFHIRLAARPAPKEAENR	57~~DUF4118 (0.000000000000041858)~~148;X;174~~GAF (0.00000000002692)~~293;X;310~~HisKA (0.000000000006324 43)~~376;X;429~~HATPase_c (2.89666E-31)~~529	non-KdpD DUF4118 protein
	2E-08	43.9	9.9	3.1E-08	43.2	6.9	1.4	1	R5XDF0_9FIRM	Histidine kinase (EC 2.7.13.3)	BN568_00631	Blautia sp. CAG:257	893	1262756	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	>tr|R5XDF0|R5XDF0_9FIRM Histidine kinase OS=Blautia sp. CAG:257 GN=BN568_00631 PE=4 SV=1MEKQNQSADILPAASDQMSSTERGHLKIFFGYAAGVGKTYAMLEAAHMEKKHGTDVAVGYIKSNAHPQTRARLNGLKLLPPLYSKHNGTPVEEFDLDKAIKTKPGLILIDELAHTNADGCRHHKRYLDIYELLKAGIDVYTTANVENIESLNDMVTAITGNRILERIPDSVFDNADQVKLVDIEPQELLERLAAEKDSDSSETDSFTFTLETLTALRELALRRCADRVNKRTESARIRNKSDYYTDEHILVCLSSSPSNAKIIRTAARMANAFRGAFTALFVETSQFSAMTEEDRQRLRSNIYLAQQLGATIETVYGDDVPLQIAEFAKLSGVSKIVIGRSTVTGKRLFGRPSLTEQLIANVPNMDVHIIPDQSPNRTPPVHNQKNHIIFSASDILKSIFILSAASCLGYLFQQLGFDEANIITVYVLAVLVTSIVTVNRVYSLITSIVSVLVFNFLFTDPKFTLMAYDRGYLVTFVVMFISAFLTGTLTTRMKTIASQSARAAFRTKILFDTSQILQQATDRDAILTSTAHQLTKLLNRDIVIYPAEKNTLAAPMTFSAGEEDTASDYLTRNESAVAEWVFKNNRHAGATTQTLSNAKCLYLAIRVNDSVYGVVGIAAGKQPLDASENNILLSILGECALAMENEKNAHEKEEAAILAKNEQLRANLLRTISHDLRTPLTSISGNASNLLSNSSSFDENTKRTLYQDIYDDSMWLINLVENLLSVTRLEEGRLNLRISAELADEVVTEALRHVNRLSVEHHITVNHQDDLLLAKMDAKLIVQVIINLVDNAIKYTPQGSEIQISTFREENWAVISVADNGPGIPDENKKQIFDMFYTGSNRVADSRRSLGLGLSLCKSIINAHGGSISVSDNVPHGTVFTFTLPAEEVQLHE	22~~KdpD (5.81954E-88)~~228;X;248~~Usp(1.63279E-38)~~371;X;395~~DUF4118 (1.37566E-14)~~494;X;522~~GAF (0.00000145709)~~645;X;662~~HisKA (0.0000000952866)~~728;X;781~~HATPase_c (1.45643E-31)~~884	KdpD protein
	2E-08	43.9	4	1.9E-08	43.9	2.8	2	1	A6LY71_CLOB8	Histidine kinase (EC 2.7.13.3)	Cbei_3169	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) (Clostridium acetobutylicum)	610	290402	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium beijerinckii (Clostridium MP), Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) (Clostridium acetobutylicum)	>tr|A6LY71|A6LY71_CLOB8 Histidine kinase OS=Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) GN=Cbei_3169 PE=4 SV=1MDNYTNKHNDKLKTMMCFIKIAIIVLSSIIIHMNLPEYWSSLYIHENAQFNIYISIFSSLFIGINFILCLIITGVILQKGILLKNSWLIDNIIFMFIISIPIYLSKAYQSECKYLFLLLIIYSIIQYGSKCGIVTALFSCGIILGADLLYDSLENGVNIYFQKDLIMCGVFILVAWILGYYVNIEAENNKKKDETLSTLSNEKKEMESLLLNNKICYDMLFENSLNSIIVHTNGEVIYANASATKLLGLKGENFYNHYLSEVNKDIKKKYSRISHNKLVKITSEESILNCDGEFIPVINTSSFFTYKGKPSVLTFLRDITSEKKVESLQEDIEKNLKLLNESREFNNLIMNFFTNMSHELKTPVNVIYSAVQTVNIYFGNYNLENIEKCKLYFKTMKQNCLRLIRIINNFLDVTKLNSDSGFIRIKKRNGNIVNIIEEITQSVASYVNDKDITLIFDTNVEEKIMGFDHDMMERIMLNLISNALKYSHSKGNIYVDFIDKQTSVIVKVRDEGEGIPKDKLNFIFERFGKVDNTLSRKCEGTGIGLYLVKSFVEMHGGKISVASVEGQGSEFIIELPVELIKNEEEEDKILFKTNIEKIQIEFSDIYSLQS	87~~DUF4118 (8.72328E-15)~~188;X(158);346~~HisKA (0.0000000093463)~~415;X;472~~HATPase_c (2.84282E-27)~~575	non-KdpD DUF4118 protein

	2E-08	43.8	7.2	2E-08	43.8	5	1.8	1	A0A0F4PGK7_9GAMM	Uncharacterized protein	TW72_16810	Pseudoalteromonas ruthenica	455	151081	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Pseudoalteromonadaceae, Pseudoalteromonas, Pseudoalteromonas ruthenica	>tr|A0A0F4PGK7|A0A0F4PGK7_9GAMM Uncharacterized protein OS=Pseudoalteromonas ruthenica GN=TW72_16810 PE=4 SV=1MPHSKRRGLNAVIRRLLFGSDHQPIAWFELVFITFIALSIWVYQASLAHEHATDYFYWPMLGPLVIALRYGFGRGMMSFVLLLVSGVVDNFIATEVSISLSVSVGTAVVTMLVGEFRDHWHDINQRFELNHRYMEQKLKSFTQNYHLLKISHDQLEQRAAGKQMSLRTGIQLLQQAASGHAENRLANLAQKSLQVFADVITMYQAGLYEIRDGKLVPGALATIGSEHALIADDLMLQDVYTSKAVLSPANFIDSDEYNLNYQLVIPLVDVSGELQGVVLAEKVKFVSLTQSNIALIALLAGYIANFMSHQLFAPILKPEQRQLFRQYLENQLWYKHHYGADSAMVVFYDNSEAQHLDLEHVTDFRRGADIYWSCEREDGRQALCVLLPMTTVMEAEQFVQRIRSILANNAPIAEGDLDVFGPLLVFEQYQQVNTLLEDLGAFDEDLADSSNDSL	26~~DUF4118 (0.000116813)~~121;X;186~~GAF (0.000000703564)~~310	non-KdpD DUF4118 protein
	2E-08	43.7	3.2	2E-08	43.7	2.2	2.4	1	G7LY81_9CLOT	Histidine kinase (EC 2.7.13.3)	CDLVIII_1449	Clostridium sp. DL-VIII	622	641107	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. DL-VIII	>tr|G7LY81|G7LY81_9CLOT Histidine kinase OS=Clostridium sp. DL-VIII GN=CDLVIII_1449 PE=4 SV=1MSKFINEKRDNLSAMLAIIKVSIVMFISIIVYINITRYFININIEKNGQFNVYTTGFFFIIIGICCIAWLIITSRIVQSLNIFKIAWVSWFLENTFYISIISIPMYLLKFSQNEYKYLFLLVIIFSTIQYGSRYGVITSIISSSLITLSGLLYTPLNNGINENLQGELIFSCIAIFIAWIIGYYVDMEKERNKSKDKKLKVLRTELDEVIKERCEIEIERLLLKNKFCYDMIFENSLSALIVHENGVIIYANESAAKLLGYKNPIDLNGRNFYDYYPEDVKKNIEKKYSNIIRDEFLKIVNEENILNCEENLIPVRNTSAFFTYKETSAILTLLIDITSEKKLETLEEDVEKNLKLLNETREFNNLITIFFTNMSHELKTPVNVIYAAVQTISIYLNNYKSDDTIKCKSYLKVMKQNCLRMTRLINNLLDITKLDSGFIKLNRKNDNIVSVIEDIVQSVALYVKSKNINLIFDTDIEEKIMSFDHDMMERIMLNLISNALKYSHSNGNIYIDIIDEKSRIIIIKVKDEGEGMPQNKLDFIFERFGQINNSLSRQCEGSGIGLYLVKSFIEMHNGRINVKSIEGKGSEFTIILPVELADEEAYVNKVLFKTHVERIEIEFSDIYSI	90~~DUF4118 (0.00000308896)~~191;X(177);368~~HisKA (0.000000000354033)~~431;X;486~~HATPase_c (1.89466E-26)~~589	non-KdpD DUF4118 protein
	2E-08	43.7	6.7	3.8E-08	42.9	4.6	1.4	1	A0A0D5LS15_9RHIZ	Histidine kinase (EC 2.7.13.3)	TM49_16175	Martelella endophytica	888	1486262	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	>tr|A0A0D5LS15|A0A0D5LS15_9RHIZ Histidine kinase OS=Martelella endophytica GN=TM49_16175 PE=4 SV=1MPEQTRPDPEALLPAAKREGRGRLKIFLGAAPGVGKTYAMLDAAARLARSGTHVLVGLVETHGRAETEAMLHDLTVLPRRPFFHNGRILHELDVDALIAARPDLALIDELAHSNLSDSRHQKRWQDVEDVLAAGIDVFTTLNVQHVETLNDMVARITGVRVRETVPNRILAEADEIELIDLPPDELIERLRAGKVYVEDQAARAVANFFAKGNLTALRELALRTAADRIDRQLQEHMAAHAIAGPWPTQERIMVVMPQEASGQDVIRAGKRAADRARVEWLALGISRLREGRPSAGGANTLRLAEQLGARISLLEVEDDGATEVIARAGRENVRRILMPRPRRRTLFARLMRPSLHERLYDGLLRKAGDFELTLVSEEAVASPAKAEPVRVSEPFSLRQIAIVTGALGVTTGIAALLRPVFPITSLSLLFMTVVVAVAARMGRKPALVAAGLSFLCFNFFFTEPLYTLRIWDQTQFLTLVLLVISSMLTGNLAARLRERVIAQKAAAERTAKLYEFSRRAAAAASFGDVVWAAVSHVSAVLGGHAVLLAPVGNGRLDIVGSSPAEDHLPAREMTAARYSFEHGEPTGRGSSTLPAVDWLFLPLVASDRCIGVLGVRSEDGNAALAGERGLAEALADQVALALERIRLSEDLAQTRVVSSEAERLRTALLSSVSHDLRTPLVSILGAAESLENPGLTDHARGILTETIRDEGERLDRYIQNLLDMTRLGHGALKLRTSATDLRELAGAARRRLGGPLRDHPLEIGIAEDLPAAIDPLLIEQVLINILDNAAKYSGIGSAIYLGADLTGNAITVWIEDDGPGFPPEAMHHVFDMFWRAEQGDGMPMGAGLGLAICRGIVEAHGGTISAGAAHARGRGARIEFTVPLAGRS	19~~KdpD (2.58061E-112)~~229;X;251~~Usp(1.09983E-14)~~376;X;399~~DUF4118 (5.01557E-14)~~499;X;528~~GAF (0.000000000001903 74)~~644;X;661~~HisKA (0.000000000000352998)~~725;X;778~~HATPase_c (2.13244E-22)~~882	KdpD protein
	2E-08	43.7	5.1	3.5E-08	43	3.5	1.3	1	A0A0D6T9R0_9RHOB	Histidine kinase (EC 2.7.13.3)	SY26_17625	Paracoccus sp. 361	888	1603292	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 361	>tr|A0A0D6T9R0|A0A0D6T9R0_9RHOB Histidine kinase OS=Paracoccus sp. 361 GN=SY26_17625 PE=4 SV=1MTELRPEPDALLAQAEREGRGRLKIFLGAAPGVGKTYAMLEAARRRAAEGVDVVAAVVETHGRAETEALLQGLDLLPKRAQFYRERILHEMDLDALLERRPQLALIDELAHSNIPGSRHDKRWQDVEEVLAAGIDVLTTLNVQHLETLNDRVARISGVRVRETVPDAVLARADEVELIDLPTEELIERLRAGKVYVQDQIARAVQNFFSKGNLTALRELAMRAAADRVDAQLREHMRANAIGGPWPAQERILVALTESPVARTLVRTAKRMADRARVEWVAVTVTSARSEALSDPDRDALAQALRLAERLGGEVATLSAAGPVADEILDYARRRNVSRILLGRPRPRPWWRRIGRQNVARAVTEAGRDFEVTVVSDPQRTPTPPAVRHWSVDRDPRAYAKATLTVIAASLLALSADRIFPVTSLSLIFMTGVIVVAVRQGLWPSLYASCLSFLTYNFFFTDPRNTFLVIRQDQIMTLLLFLIASGLTGNLAARLRDALAQRDIAMRTNLLYDFARQVAGAGSAVEVLRAAAIHVGAALGCDTVVMRPGPLGRPVIEVAEPPRDTLALRDASAADYAWTRGEEAGRGSGTLPASDWLFLPVGTEGRRLAILGIAYPDGRSLAPMDRRLLDAMTDQTGIALERIALQADLEQALVTSEAERLRAALLSSVSHDLRTPLVSIIGAASSLADPALDLAAPARASMAATIRDEGERLDRYIQNLLDMTRLGHGALVPKRVPADLREIAGSARHRLRGALRDHRVEVAVPDDLPQVLVDPLLIEQVVVMNLLDNAAKYAPEGSRIDVTARVDGARAELSVGDDGPGIPPDARGRVFDMFYRVAEGDGQRAGTGLGLAIARGIVEAHGGTIAAHPARADGRGTRITLTLPLDTPA	18~~KdpD (5.40427E-118)~~228;X;250~~Usp(2.08524E-25)~~375;X;397~~DUF4118 (4.10866E-14)~~497;X;526~~GAF (0.00000798145)~~642;X;659~~HisKA (0.000000000532491)~~725;X;778~~HATPase_c (3.48219E-28)~~882	KdpD protein
	2E-08	43.6	12.3	4E-08	42.8	8.5	1.4	1	Q1IUD8_KORVE	Histidine kinase (EC 2.7.13.3)	Acid345_0507	Koribacter versatilis (strain Ellin345)	478	204669	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Candidatus Koribacter, Candidatus Koribacter versatilis, Koribacter versatilis (strain Ellin345)	>tr|Q1IUD8|Q1IUD8_KORVE Histidine kinase OS=Koribacter versatilis (strain Ellin345) GN=Acid345_0507 PE=4 SV=1MRSSARQLGRYVVVVLVLVAVVFIYRHVPANPTTVALTFLILVLLTAAFWGFRVAMALSVLATAAINFFFLPPVGTFTIADPQNWIALLAFLVTAVVASNLAERARNEAEKATEQRQNVEHLYDLSQKLLTVETVPELMNAIPVFVLESFGGSGVALISNVKPTIYRSTADVSIDAETLRNTLARGESTQQNGVNYFPVRLGVRSVGALAIKGLEIPRQTADAIGSLVGTAIERTRAVDELATSRAARESEQLRSALLDSVTHEFRTPLTSIKASVTTLLEGSLADAAARAELLTIINEETDRLNRLVGEAAEMARLDSRVITLQRRQFALSEVVETVLDEQISTLRKHPVTVELPKGLPPVYADFDRIRQVLTHLVENAAKYSPDDTPIRISAELKGDFIVTSVADRGPGIDSFEQTLIFDKFYRGEKQRYAAAGTGMGLAISKVLIEAHGGTLTVVSQIGQGSVFSFTLPISGERS	39~~DUF4118 (0.000000000045544 1)~~108;X(143);251~~HisKA (0.000000000071078 9)~~316;X;369~~HATPase_c (3.0115E-26)~~471	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	2E-08	43.6	0.5	3.7E-08	42.9	0.3	1.4	1	Q1ASP5_RUBXD	Diguanylate cyclase	Rxyl_2666	Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)	487	266117	cellular organisms, Bacteria, Actinobacteria, Rubrobacteria, Rubrobacterales, Rubrobacterineae, Rubrobacteraceae, Rubrobacter, Rubrobacter xylanophilus, Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129)	>tr|Q1ASP5|Q1ASP5_RUBXD Diguanylate cyclase OS=Rubrobacter xylanophilus (strain DSM 9941 / NBRC 16129) GN=Rxyl_2666 PE=4 SV=1MRAGRGEVQRGRSLPALLRRGGPAGKRPARAVAYAETLAALALLVGAGLLLQPQNPGFAGVSPHPFWLVVIPIAALHGSPPGYVAGAASALAYLGLAALQAGSVTDPALLRPGLLAEPVLFLVAGGALGELRQAQRRREEALLRRQEALEGDLQDLAQRYLASVELARELERRIVDQTSTVTTLYEAAKALERLEVEELPPAVLELASSFVDVEACSLYLLRDRMPFLRFTPAAARLFSLLGDWASGAFQRALRFRQTRDRNIEDDLTGAYNHAYLLKRAEDHERIPPVRLPGVLRTLSLVFRHHIRPVDVLGRHEEEGTFLLLLPHLGAEEAGELAERLRREVEGFGFRPFEEDDRTLRLRTGRATLSGKTGGAEGLVEEAVRDLLRGGG	195~~GAF (0.00000000217594)~~326;X;340~~Nucleotidyl_cyc_III (5.36898E-15)~~478	No DUF4118 detected by NCBI CDD

	2E-08	43.6	13.3	3.8E-08	42.9	9.2	1.4	1	R5FPW2_9FIRM	Histidine kinase (EC 2.7.13.3)	BN756_00394	Coprobacillus sp. CAG:698	651	1262856	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:698	>tr|R5FPW2|R5FPW2_9FIRM Histidine kinase OS=Coprobacillus sp. CAG:698 GN=BN756_00394 PE=4 SV=1MEKVLLNNKEHVLVCLSSAPSNIKIIQNAAAMAKAFNATFSAIYVKTPVSESMSSEDSDRLLTNIHFAEMMGASIAIVCGDDIAFQIAEYARLSCVTKIVIGRTVISKRKFIRRPNFTEKLISLAPNVDIHIIPDSDVSIDNRKEKLFEKRNIANIVKEFVISLVIVLLSTLLGFLFSTLGFTEANIITIYMLGVLIIAILTKSKFFWVASSIASVFVFNFLFTEPRFSFLAYGNGYAITFMIMLIASLIIGGTTDKLKTRERQATQTSYRTKILFDANQLIQKSSNEADVFRVTANQLRKLLNKNILVFDENGQKVYSSLVEKNPNIISNYEHIVMQVMKNNAKAGKGTDICPESNYVFFPIRKSNKQYGVIGIFVGNSSIESFNESIALSLIGECAIAVDAIVNAKEREQTAILAKNEQLRANLLRSISHDLRTPLTSISGNASNLISNGNYIDDKTKKQIYEDIYEDSLWLINLVENLLSVTRLEEGKMNINLTTELIGDVISEALKHIHTKSEKQRITVIQSDDLILAKMDARLIVQVLINLLDNAIKYTSSNSQIKIITEQDEKMVRISVADNGNGISDEQKERVFDMFYTGTNKIADCRRSIGLGLSLCKAIINAHGGEISISDNKPHGAVFTFTLPIGEVKINE	11~~Usp(3.15234E-22)~~134;X;160~~DUF4118 (6.05305E-16)~~261;X(159);420~~HisKA (0.00000000017528)~~486;X;539~~HATPase_c (2.80208E-26)~~642	non-KdpD DUF4118 protein
	2E-08	43.6	6.9	3.7E-08	42.9	4.8	1.3	1	G8P0S0_GRAMM	Histidine kinase (EC 2.7.13.3)	AciX8_0323	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	473	682795	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	>tr|G8P0S0|G8P0S0_GRAMM Histidine kinase OS=Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8) GN=AciX8_0323 PE=4 SV=1MRCIGAAACLAGIVTFYRLVVHANQTTVALTLLLLILFIAARWGLRFSIGASLVATACYNFFFLPPLYKFTVSDPQNLVALAVFLITAVFASRLSHRIRAESSDARARQSELEILYSLSRDLLQSEELTQLTNSIPASVTLATGSNSVLFYLLEGNRSYRAGLDTSIAWPPTIDTTELHELAHAPGVSITSDGAAIVPLRTGVKPRGLLILRGVKLSTQTLEALGGLVSVALDRVRAVEEVAHVEAAQESERLRSMILDSITHELRTPVASIKTSIDKLLEANAESAESHELLTEISEQNDRLDQLVTEAVEMAQLDTQQVSMDVSPQQLSDMIDAAIETAGARLADHEIIKRIPEDLPCVVADPLRIEKVIYNLLENAAKYSAPGQPIYISVEVRGQCASCSIADRGIGIDPAEQPLVFDKLYRSRKRTAHIPGTGMGLAICRAIVEAHNGTISVTSQPGQGSVFTFTLPLA	42~~DUF4118 (0.00000000462291)~~101;X(150);251~~HisKA (0.0000000621042)~~315;X;368~~HATPase_c (6.1386E-31)~~470	non-KdpD DUF4118 protein
	2E-08	43.5	13.4	3.4E-08	43	9.3	1.2	1	R7MRQ9_9FIRM	Histidine kinase (EC 2.7.13.3)	BN739_01805	Ruminococcus sp. CAG:624	354	1262965	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:624	>tr|R7MRQ9|R7MRQ9_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:624 GN=BN739_01805 PE=4 SV=1MRILKRDSFKSLLRNVFVSVIIIMCAILICYILRIVDHTAAYAPMIFILAVFIISRLTYGYVYGIISSLLSVLIVNFIFTYPYYDFNFTLSGYPVSILSMLVVAVATSTLTSQIKAQEKIKIEAEREKMRSNLLRAVSHDLRTPLTSIVGASSAMIENDSYISKEQRIEFLQGIKEDSEWLIRMVENLLSITRIDNSENSSAKITKTPEAVEEVVAASVRKFKKRFPDMPIKLTVPDELLFIPMDAMLIEQVIINILENVVMHSKTATQIILSVVAEDDSIMFKISDNGVGISKKKLADIFNDACNMSESYSDAKRNMGIGLSVCNTIIKAHNGTMNAGNNKDGGAFFSFNLPV	15~~DUF4118 (0.00000000003638 68)~~117;X;127~~HisKA (0.000000000000707243)~~193;X;249~~HATPase_c (9.19679E-19)~~352	non-KdpD DUF4118 protein
	2E-08	43.5	10.6	4.4E-08	42.7	7.3	1.4	1	R6N6Z4_9FIRM	Sensor histidine kinase KdpD	BN627_01443	Lachnospiraceae bacterium CAG:364	675	1262983	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	>tr|R6N6Z4|R6N6Z4_9FIRM Sensor histidine kinase KdpD OS=Lachnospiraceae bacterium CAG:364 GN=BN627_01443 PE=4 SV=1MSSDRSTPEEILKRIQAEEKQKENEKRGKLYIFLGYAAGVGKTCAMLDTAQELKKKGIDVVAGYIEPHARWETSMREKGLEKIPPLMVPYKGIELREFNLDAALKRKPQILLVDELAHTNANGLRHKKRYEDIEELLDAGIDVYTTVNIQHLESLNDIVENITKIHVKERIPDGVFDEAEQVKLIDIEPDLLITRLKEGKIYKTVQAERALQNFFAKEKLIALREIALRRMADKVNQIAQQERLLSEKQEEGEGYQGEHILTCISTAPSCERVIRSASRMAYAFHARFTALYVETTRLQNADASVKKIRDDNLHLAEMLGAKIVTVFGDDVAFQIAEYARVSGVTKLVLGRTNHKILFGQKKGNITDEISEYSPNLDIFIIPDMGHTGKKKYFLFSPTNSEKRKKTEKLGADILKEAFMLGIATAVGLLFQKLGFLNADIIMVYLLGILLLSLYTARRYIAVSSAVFSVLLFDWFFVEPFYSFNFYSGKYSATFGIMLLFSIIISAIISTEKHQAKESAKMMYRTELLLDNSRRMRRVESVKELLTELSDKVLKLMNLSVVFYVQKEGKLTGPWLFPKPGISKAELGKTVDTKEKAVVDWVMTNRKRAGCCTHTLPEANAIYLPIKTSDEIYGVMGIVLEEKREIPPFEYGLLTAMLNEAALVFARLIYGRKEKP	25~~KdpD (1.98856E-116)~~235;X;259~~Usp(7.59823E-33)~~382;X;417~~DUF4118 (0.00000235999)~~499;X;540~~GAF (0.000000646184)~~666	KdpD protein
	3E-08	43.5	7.3	2.5E-08	43.5	5	2.1	1	A5HYN0_CLOBH	Histidine kinase (EC 2.7.13.3)	CBO0336	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	615	441771	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum A, Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	>tr|A5HYN0|A5HYN0_CLOBH Histidine kinase OS=Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A) GN=CBO0336 PE=4 SV=1MNLDKIEIRNWSHDKKIYNSMLIVKFIILLFCGGAIYLDYAEKNNKNISQNFYCNALNLVIIIICLVSVYFIWMFISIKAFKFERIKTIQVIENTISIVIFTFIIMMSGSYKSSYKFLFLVAIITATIQLGMKHGIITSLVSSIIILAIDLILAPKAPVNIYFETDLILVGVFIMTAWPLGYYVNIQKEDLRQKEEEVNILANKLDQKEMQKRCMEQLLIKNENCYNLLIRNSKDAILVHRYGKIIFANERLKQMLGYKKEYNFEDIDIKSLIPKDEYNTVKNKLENLYYGSENVVNFQHNVINNKEKTIQNTSTYVIYDGMPTIFSILHDVTSKIQVEKLEQDVKKNIELLNESREYNKLITEFLSNISHELKTPLNVIFTAVQLLDFYEKDVDYEKQDKYLKLIKQNCYRLMKLINNLLDTTKLDSGYLRLNLVNYNIVSLIEEITLSVTSYAESKGINIIFDTEMEERVIAVDTDKIERIILNLLSNAIKFTNPGGNIFVNIKDSEENVYVHIKDTGVGIPSDKLESIFERFFQIDKTLKKNKEGTGIGLHLVKSFVEMHNGKVTINSELGKGTEFIIKLPAIVCEEQIKSKNVVYEANIERINMEFSDITQ	90~~DUF4118 (0.00000000002220 44)~~190;X;226~~PAS (0.000497922)~~288;X;359~~HisKA (5.7687E-15)~~425;X;480~~HATPase_c (1.90098E-29)~~583	non-KdpD DUF4118 protein
	3E-08	43.4	8.9	4.1E-08	42.8	6.1	1.3	1	V6KFF6_STRNV	Histidine kinase (EC 2.7.13.3)	M877_09270	Streptomyces niveus NCIMB 11891	847	1352941	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces niveus (Streptomyces spheroides), Streptomyces niveus NCIMB 11891	>tr|V6KFF6|V6KFF6_STRNV Histidine kinase OS=Streptomyces niveus NCIMB 11891 GN=M877_09270 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHNRPRTEVMLKGLEQIHRRELPHRGTVFTEMDVDAVIERRPAVALVDELAHTNVPGSRNSKRWQDVEELLQAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEMVRRADQIELVDMSPQALRRRMAHGNIYQPDKVNAALSHYFRPGNLTALRELALLWTADRVDEYLQQYRGEHNIRSTWQARERIAVGLTGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGLTSASPKELTLQRTLVEDLGGTFHHVIGDDVPSALLEFARGVNATQIVLGSSRRKSWQYIFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVARGARLGRSRILSGWLAGVVAPVLLTLLLTALDDTLGLANDVLLFLFLTVLAALLGGLRPALASAAVGSVLLNFYFTPPTHTLTIQDPRNIVAIVIFFAVAVSVASVVVDIAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFSMESVALLERTSDVDPWTRAGSVGPRPVDRPEAADVDMPVGDHMALALSGRVLPAEDRRVLSAFAAQAAVVLDRQRLVGEAEGARRLAEGNRIRTALLAAVSHDLRTPLAAIKAAVTSLRSDDVEWSDEDHAELLEGIENGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALLGVPEGSVVLDIPESLPMVAVDPGLLERAVANIVENAVKYSPDGTRVNVSASSLGARVQVRVVDRGSGVPDEAKERIFEPFQRHGDAPRGAGVGLGLAVARGFVDAMDGTLTAEDTPGGGLTMVLDLTAVPGLAPAGPELPAEVSS	1~~KdpD (3.04533E-121)~~211;X;233~~Usp(1.20566E-30)~~356;X;420~~DUF4118 (0.00000381449)~~466;X(146);612~~HisKA (2.68217E-14)~~678;X;727~~HATPase_c (3.00348E-26)~~828	KdpD protein

	3E-08	43.4	5.3	5.2E-08	42.5	3.6	1.5	1	B3E967_GEOLS	Histidine kinase (EC 2.7.13.3)	Glov_3074	Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	378	398767	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter lovleyi, Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	>tr|B3E967|B3E967_GEOLS Histidine kinase OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ) GN=Glov_3074 PE=4 SV=1MTRTADTVHQHSYPPRRQTYARLLLLVLVIAGISLTHYLAPLQLHYLHDIFQRLYYLPIILSAFWFGLWGGVGC ALLVSLLYAPHIVFQWGGSVTLELEKYLEIVMYNVVGGLTGLLTQRDRQQRKELQLTAAGLEQSYRALQEQTERIG AVEEQLRRSERLSTLGEMAAVLAHEVRNPLASLRGTAEILRDDFRPGTPKHEFVEIQIKETERLNRVVEEFLRMAR QQPGELQRCVVAEELETIVTLTSNEARRRKVTLQLEAANRDLAVNADGEKLRQAFLNIILNALQATPEGGRVTIAVQ PQQQNCEIRISDSGPGINDEIRQRIFEPFFTTKPDGTGLGLAVTKKIIEAHGGSLSVESAAGSGTTMVVQLPLSH	20~~DUF4118 (0.000000000013430 2)~~124;X;162~~HisKA (0.000000000004200 26)~~226;X;277~~HATPase_c (2.46082E-31)~~374	non-KdpD DUF4118 protein
	3E-08	43.4	10.5	4.4E-08	42.7	7.3	1.3	1	C5APB1_METEA	Histidine kinase (EC 2.7.13.3)	kdpD MexAM1_META1p0132	Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	905	272630	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium extorquens group, Methylobacterium extorquens (Methylobacterium dichloromethanicum) (Protomonas extorquens), Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	>tr|C5APB1|C5APB1_METEA Histidine kinase OS=Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1) GN=kdpD PE=4 SV=1MPGTGRDPNRPSPDALLEAARREERTRGRLKVFLGAAPGVGKTYEMLTIGRARLTAGADVVVGVVETHGR AETEALLEGFETIPRRAVPYRGTVLEEMDLDALLARRPALALVDELAHTNAPGSRHPKRYQDVEELLDAGIDVLTTL NIQHVESLNDVVASITRIRVRETVPDSILDRADDIEVVDLNPDDLIERLKAGKVYVPANAERALKHYFSRGNLTALRE LALRRTADRVDDELLSHMRANAIPGPWAAGERVLVCVSEDPRSAGLVRYAKRLADRLHAPWTALVVEGPRAASL SEAARDRVAEALRLADRLGGDAVTLPGGRRIADDILAYARAANVNHIVVGKATRSWIFELVNGSVVHDLVRRSGNI SVHVVPGEAAPAETASRRAVATAAPPATFDARSYALALLVTGAGLGLALLLEPSTGVENADLMLLTAVVAVAVRVW GLGPSLAAVVAASLSYNFFFLPPVYTFTIADPTNVAAFLLFTLVAVLVSNLAARARLSAVVSQGRAKATERLFGFSR KLAACGTLDDVLWATSAQVAAMLRVRVVLLLPDAQTVAVRAGYPPEDMLDEADLAAAQWAFDNERPAGRGADTL PGAKRLFLPMRTGRGTIGVIGLDADGTGPILTPEGRRLLDALADMGALALERVRLVEDLDRAERAAETDRLARALLT SISHDLRTPLASVLGAASTLRDLEGALPVESKAELLTTIIEESERLNRFIVNLLDMTRLEAGAVAPNLAPQDVAETIDT ALRRTQKILAGHRVAVEIAPDLPTLRLDPVLFEQVLVNLLDNAAKYAPEGSTVTLRARQDGRTVRIEVLDEGFGLPE ADVERVFDKFYRVRKSDRVRAGTGLGLAISRGFVEAMGGTVTAGNRRDRLGAAFTVMLPVPARTTPRDIAA	27~~KdpD (3.04116E-115)~~235;X;257~~Usp(3.55982E-40)~~381;X;434~~DUF4118 (0.000000000002523 16)~~506;X;534~~GAF (0.000000000085579 8)~~653;X;674~~HisKA (0.000000000045464 5)~~736;X;789~~HATPase_c (9.04499E-26)~~892	KdpD protein
	3E-08	43.4	13.3	4.4E-08	42.7	9.2	1.4	1	K4L432_9FIRM	Histidine kinase (EC 2.7.13.3)	DCF50_p2267	Dehalobacter sp. CF	894	1131462	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Dehalobacter, Dehalobacter sp. CF	>tr|K4L432|K4L432_9FIRM Histidine kinase OS=Dehalobacter sp. CF GN=DCF50_p2267 PE=4 SV=1MKSQGGGGVQDIRARAAKKTGKLKIFFGYAPGVGKTYAMLDDARSQLKSRVDVVVGYLEPHTGSETIQLLD GLPALPPKTVNHKNRYRKEFDLDAALQRKPELLLVDVLAHNNADGMRNKKRYQDIEELLNAGIDVYTTVNVQHIES LRDLVQDITKVNEQDTIPDYMFDSADKVELIDIEPDELMKRYAEKKCPLSLESLRLLRETAMRKVTDRIVNENQNEQ LLSAKTAGIKLLVCISSSPSTAKCIRWTARSAEAFHAPWTALYIEDMESRYFTEEEKKNVQENLDLAELLGAKIVTLN GQGLASIIAEYARLTGITNIVIGKSRNKKTLKTLFDPALEDKLIGLLPNIEIHIIPSSGPRRSYREPRRKRISKDLFLSWP DIWKTIGVLTGATLLSFGLRALEFGNQNIIMVYILSVFFISRLTMGYVYGITASVLSVLVFNFFFVSPLFSFYAIQTGYP VTFVIMLVVALITSTTVRIQTQARLAAEREGRTELLYEINKRLLTTRGLQHIVTLTNEYIVKLFKCSAVFYTRDQYGS ANLHRSSNHHGSSGILTQSSAEPDASFLLSERESKVVQWVFANQKQAGVGTDTHTEAGAYYMPIISQGDVLGVV GISCLKGRLSRNNRLLLKMIISQVAMALERQYLSDEQRQILIESEKEKMRSNLLRAISHDLRTPLTGILGASSAILENG DHLDKETHIQLVSNIKEDSQWLIRMVENLLSVTRIKEGTMNVAKTFEAAEEIVAEAISRTRHRYPDRKITVQVPEDLL LVPMDGKLIEQVLINLLENAVKHSPDDAVTAVRVTKAGAQAVFEVSDNGPGVAEEDFPYLFESYVPCGKRSSDSA RGMGIGLSICMSIIKAHNGKMEAANKEQGGAVFRFTLPLEEENIYE	18~~KdpD (9.99358E-88)~~193;X;234~~Usp(1.31829E-37)~~358;X;388~~DUF4118 (1.08277E-15)~~486;X;513~~GAF (0.00000362756)~~646;X;663~~HisKA (0.000000000049176 7)~~729;X;782~~HATPase_c (2.79539E-27)~~885	KdpD protein
	3E-08	43.4	9.1	2.6E-08	43.4	6.3	1.7	1	R7DCX0_9FIRM	Histidine kinase (EC 2.7.13.3)	BN639_00221	Ruminococcus obeum CAG:39	584	1263107	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus obeum CAG:39	>tr|R7DCX0|R7DCX0_9FIRM Histidine kinase OS=Ruminococcus obeum CAG:39 GN=BN639_00221 PE=4 SV=1MAKTVLVLIVLVMFSIGLFIVSKVGVFLKESKKEASDEREGVQLVKILEGIPGERTKVNMNIQDSAWTKRQKN HHPIYIEKPSIKDYLLTFSIFVGCTVIGLVFQKLHFTDINIVTVYILGVLVTSIVTDGYLCGLVGSFLSVVLFCFFLTEPR MSFQTYAVGYPVTFLIMLISSVLTGTLAAKLKDHARLSEQQAFRTQILFDTDRLLQQAKNSEEILCVTCKQLVRLLNR DIVAYIVKNNDLSEGKMFFNNTNKRNGEYLTSEEQCVARWAYENGQRAGVTTTHFSSAKCLYLSIRSGESVYGVI GIPVKKDAMDSFEYSILLSVINECALAMENSQNAIEKEKNAILAKNEQLRADLLRAISHDLRTPLCSISGNADMLLNN ERCLDDITKQQIYTDIYDDAEWLIGVVENLLSVTRLNDGRLKIKFTDQLLDEVIAESLRHISRKHDAYKIQVECEELILA HMDVRLIIQVLVNLIDNAIKYTPQGSTICIRGLRTDGRAQISVEDNGPGIADEMKSHIFEMFYTGKTTIADSHRSLGLG LALCHSIIEAHEGELTLKDNYPHGCIFVFTLPLSEVTLNE	0.000000000000240 647)~~188;X;216~~GAF (0.0000246811)~~337;X;354~~HisKA (0.000000000123465)~~420;X;472~~HATPase_c (8.05131E-27)~~575	non-KdpD DUF4118 protein
	3E-08	43.3	1.2	1.4E-07	41	1.1	1.9	1	A0A0F2NB41_9FIRM	Uncharacterized protein	VR68_10765	Peptococcaceae bacterium BRH_c4a	729	1629716	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c4a	>tr|A0A0F2NB41|A0A0F2NB41_9FIRM Uncharacterized protein OS=Peptococcaceae bacterium BRH_c4a GN=VR68_10765 PE=4 SV=1MDILVTGGCGFIGSHVAERFYKEGHNVFIIDNLTSGLRSNINFKHKFYEMAVEDMRCEDIFCINKFNVVVHLAA QTSVPASFENPYKDTVSNVTGLINMLSLSERYGVKRFIFISSAAVYGDPDQLPTDEDTETNPMAPYGISKLVGEMY CHKWHEIYGLSTVCLRLSNAYGPRQAAKGEGGVVSVFMKQILDGQSLTVYGDGKQTRDFIYVEDIADAVYRCVES GFCGVMNLSANTEISINDLIDTLAHRADIKEALHKEKRSGDISRSSMDNSRIKRELNWLPKYNFEEGLQKTFDWYA SIYKKQEKETEASKKSETTKPRSKLADYAIPFVESLLGFIAVIFIERLFNRGDHFFIDLKLLYIILMGIAYGTKHSIMAVA LSSSLFIISNAGYGRDLISLFYDPNSLLHIAYYLFAGFSVGYTIDMKNRKVKSQDLKIEATEEKLEFVTKVYDETRIVK NELQKQIMASQDSFGKIYSIIKELDTFEPEDVFSSAVQVMEKILKVNSIAIHVMSRNGLFARLVANSGSLSWHISKSM KVEDSPALKYIMESKEIFVNKKLDPSLPIMMAPITDNGKTVAIISILELDFDNINLYYQNLFKVASDMISSSLSKAHRYQ EATNDSRYISGTAILNRDSFEKLLHGKMQTKEKEMANYVLLCVNAADPADNLEHRISNTIRDRDYIGLGKDNRLYILL SNTSEKEAGAVTKRLTDKGISTSIPAGADLIA	3~~NADB_Rossmann (1.06764E-115)~~300;X;332~~DUF4118 (2.00986E-14)~~432;X;489~~GAF (2.4421E-15)~~612	non-KdpD DUF4118 protein

	3E-08	43.3	11.3	4.8E-08	42.6	7.8	1.4	1	A8HY24_AZOC5	Histidine kinase (EC 2.7.13.3)	AZC_1568	Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	890	438753	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Azorhizobium, Azorhizobium caulinodans, Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571)	>tr|A8HY24|A8HY24_AZOC5 Histidine kinase OS=Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / JCM 20966 / NBRC 14845 / NCIMB 13405 / ORS 571) GN=AZC_1568 PE=4 SV=1MGQEDKPRASPDALLAMVEREGKGKLRVFLGAAPGVGKTYAMLQAARAAKADGLDVVVGIVETHGRRETE AMLEGLPVLPRRPIHYRGRLVPEFDIEGALARRPKLLLVDEYAHSNVPGSRHPKRWQDVEDLLDAGIDVWTTLNIQ HLESLNEVVQRITGVRVRETVPDTAIQEADEVVMVDLPPDELLKRLAEGRVYVQDTAARAIERFFKPTNLTALRELA LRRVAARVDSDLIEHMQGGAIEGPWAAGERILVCVGPDASAQKVVREAKRLADLADAPWLAVTVERPGHPLDAT ARARADAALRLAESLGAETRALVGSDLVEELLKVARFENVTQIVVARARPSRLSRPFVRTLADALVREADGIAVHVL TFEEGERSAPRRRLPPVGGLDGYVAAAMAVSIATLLGEELTKHVALPNVSMIFLLAVLIPALFFGVWPAVFASLFSA LAYNFFFIDPVYTFTIARPHEVLALVIFLVIAVIISAVAGRAREQAKASAQRVKAGRRLYDFTRKLSSLADAPEVAAGA ASEIHAILSRAAVILSSTRGELHIAAAWPPEDRLDTASLSAARWAYEHGEPAGARTATLPSVPWLFIPLKARQGIIGV IGIEALSGEPLDAEGRVLLDALADQTASALERAALAGEMADVRSAAEAERVRNILLASISHDFRTPLSSILGASSSLIE YGARIDPEQRRDLLSQIREEADHLDSMVRNLLSMTRLEAGALDLRRDWVDVGEVVNQSVAAARRRGAIQHLTVRL GENLPLVRADQILLNQVLANIVGNAVRYAGASASIEVSAERVGDEVEIAVTDSGPGIPSGLLGHVFEKFVRAASDRA DGGEGAGLGLAIAKGIVEAHGGTITAESPPPGRASGLRLAFRLPVEPDTGP	21~~KdpD (8.04817E-120)~~231;X;253~~Usp(2.14086E-26)~~375;X;397~~DUF4118 (2.1164E-15)~~496;X;525~~GAF (0.000000000000307449)~~640;X;657~~HisKA (0.000000000002674 04)~~723;X;776~~HATPase_c (1.11634E-18)~~882	KdpD protein
	3E-08	43.3	10.6	4.5E-08	42.6	7.3	1.3	1	R6H926_9FIRM	Histidine kinase (EC 2.7.13.3)	BN490_00090	Firmicutes bacterium CAG:137	900	1263004	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:137	>tr|R6H926|R6H926_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:137 GN=BN490_00090 PE=4 SV=1MEIPRQNPDQLLRAIRNDTESKKRGKLKIFFGYAAGVGKTYAMLQAAHQAKANGTEVVAGYIEPHSRPQTSA LLDGLEQLPVKQVLYGEMILREFDIDSALKRKPQLILVDELAHTNGSGSRHAKRYQDVQELLSAGIDVYTTVNVQHI ESLNDTVASITGVLVRERIPDSVFDQADQVELVDIEPTELLERMASGNIYQGDQAERAAVNFFTVENLTALREIALR RCADRVNLLTESARIQSRGDYHTDEHILVCLSSSPSNAKIIRTAARMARAFRGNFTALFVETPATTEMNEDDKKRLR ENIRLAGQLGAHIETVYGEDVPYQIAEFARLSGVSKIVIGRSTATRKSIFSKPTLTERLIANAPNLDIHVIPDASSGAV CQKRRNHRFHVTAVPVRDLAKSILVLLASTLVGYVFYTMGFSEANIVSVYIFGVLVISVITTSRFCGAVASVVSVLVF NFFFTVPRFTFRFNNPNYLVTFPIMFMVALLTGSLATRLKNNAKQSANAAYRTKILFETNQLLQRETEEQAVVKATA GQLLKLLQKDIVVYLANGQELDAPSIFRTPDSNQCELVSENEKAVAAWVLRNNKHAGATTDTLSSAKCLYLAIRVN QQVYGVVGVAMNDVPLDSFENSVLLSILGECALALENIKNAREKEEAAIMAKNEQLRANLLRAISHDLRTPLTSISG NADNLLANYQKMDDDTRKRTFTDIYEDSMWLINLVENLLAITRIEGGQVHLTQSVELMDEVVAEALRHINRKSREH TIRVSSSEDLILASIDAKLIVQVIINLLDNAIKYTPAGSVIEVHTEKNNASQQVLVSVSDDGPGIPDDQKTHIFDMFYSG ANKIADSRRSLGLGLSLCKSIVSAHGGTIWVTDRDPKGTVFTFTLPAGEVELHE	22~~KdpD (1.35346E-123)~~232;X;252~~Usp(1.60558E-37)~~375;X;401~~DUF4118 (0.000000000325936)~~502;X(165);667~~HisKA (0.000000000265631)~~733;X;786~~HATPase_c (3.95737E-29)~~891	KdpD protein
	3E-08	43.3	7.8	4.9E-08	42.5	5.4	1.4	1	Q123Z6_POLSJ	Histidine kinase (EC 2.7.13.3)	Bpro_4254	Polaromonas sp. (strain JS666 / ATCC BAA-500)	514	296591	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Polaromonas, Polaromonas sp. (strain JS666 / ATCC BAA-500)	>tr|Q123Z6|Q123Z6_POLSJ Histidine kinase OS=Polaromonas sp. (strain JS666 / ATCC BAA-500) GN=Bpro_4254 PE=4 SV=1MMNAPTVQDGDVASARGWVTVALLLVAATLVSMLLDQHVALMSQAMIYVLAVVIASYRLRRIESVVCAVGA VTTLNFFFVPPRWTLVVENRELFIGLATMLVLALVISHLATRLRRESETARLSERRARQLQGLSTDLASAASPAEVL SLGQRALDTAFAGPCTLVLANDRHELPDAAAEPAVLDGLRCCMNEAAVLGPGTGRWPGLNAWYLPLGDKARTV VGAACVRPALSGDTDGREHAQALCALLAQSLWRLRLSASVAEAQGEMQRHQLQSTFLAAVSHDLRTPLAAIMGA ASSLQTQRDRLPLPDQDRLLDSIVNEASYLSEVTENTLQFVRLSSSEQALRRDWESIEEIVGAVLARVRQRDPQRR IKSRVASGLPLIRADPVLLAQMLGNLLDNALKYSDGTVDLTVGVTGVVAAVGTAGVSADNLELEIAVKDRGPGVPE ADQEAIFEPYARGEQSGHRGAGLGLAVCRAIAAAHGGRLALRRRSGGGSCFTVSLPIEAQPIGKDLP	18~~DUF4118 (0.000000000000207694)~~117;X(155);272~~HisKA (0.000000000008270 37)~~337;X;390~~HATPase_c (5.51233E-26)~~502	non-KdpD DUF4118 protein
	3E-08	43.2	12.4	4.9E-08	42.5	8.6	1.4	1	D1BKY0_SANKS	Histidine kinase (EC 2.7.13.3)	Sked_27030	Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	853	446469	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Sanguibacteraceae, Sanguibacter, Sanguibacter keddieii, Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74)	>tr|D1BKY0|D1BKY0_SANKS Histidine kinase OS=Sanguibacter keddieii (strain ATCC 51767 / DSM 10542 / NCFB 3025 / ST-74) GN=Sked_27030 PE=4 SV=1MGDTRTGRLTVYLGAAPGVGKTFAMLDEARRRRARGTDVVVGLVETHGRQATAEQVGDLEVLPRAVVPYR GTELGELDVAGVLARAPEVVLVDELAHTNAPGSTHPKRWQDVADLLEAGIDVVTTVNVQHLESLGDDVHAITGVR QRETVPDHVVRSADQVQLVDLSPDALRRRLAHGNVYRAEQIDASLSSYFRVGNLTALRELALLWLADSVDDALTR YRSDHAIDGTWPARERIVVAVTGGPEGETLLRRGARIAQRTAGSELLAVHVLATDGLPSAPPAAIASDRDLTRALG GTFHTVVGEDVPSAVVDFARGVNATMIVVGVSRHSRVREALLGSSSAQTAQLAGSIDVHLVTHDHARSGSPLRRR WSALSRTRQVSGWALAVVLPAVLTGLVWWFRGDVSLTTELMLFLAGTVGVALVGGLWPAVVTALVSFVCVNWF FTPPTGMLTVSNPENALALVVFVVVAVSVASVVDLAARRTAQAYRARAEASTLAALSRSVLSGDDSADAVVSRLA ETFAVSEVRLEERTGAKAPWVTVAQTHRAGQRGGVDAEASTVRIDDDRRLVVVGRTLPASDQQVLEAFAAQAGI VLEYRRLREAASQAAVLEQADATRTALLAAVSHDLRTPLASIRAAIDGLSAADVQLDAEDQAALLDTIGGSTARLEA LIANLLDLSRIQTGSVRAVLVARSVDEIVPAVDGFAPGGVDLDVPDNLPLVLTDAGLLERAVANVVANAVRFSPAG VPVLVTASARPGEVEIRVVDRGPGLDDDRKQRMFEPFQRLGDTSPDGLGLGLAVAQGLVRAVGATVVVDDTPGG GLTMVLTVPTAEGSTAAPAVPTAESLSDRGGA	5~~KdpD (1.2123E-109)~~214;X;236~~Usp(1.48323E-28)~~358;X;384~~DUF4118 (0.00000000012698)~~459;X(155);614~~HisKA (0.000000000000152865)~~680;X;742~~HATPase_c (7.71771E-16)~~829	KdpD protein
	3E-08	43.2	9.8	5.9E-08	42.3	6.8	1.5	1	U4KQI1_9MOLU	Histidine kinase (EC 2.7.13.3)	kdpD BN8541 0430	Acholeplasma palmae	833	38986	cellular organisms, Bacteria, Tenericutes, Mollicutes, Acholeplasmatales, Acholeplasmataceae, Acholeplasma, Acholeplasma palmae	>tr|U4KQI1|U4KQI1_9MOLU Histidine kinase OS=Acholeplasma palmae GN=kdpD PE=4 SV=1MIGGMCMQRGKLKIFFSYFYKTAKTKAMLSEIIEKYHLKYRVLIIDAQCDDTQMNQEIIHMNHIVIDDQLSFNIN SILKMNPEIVVIDQIENFDLYSIEKLLEVGINIYATLNVFNILSMNQYLSEKFNILTHEKTVPDYFFNQADEVEFIDIPPK ELLLRLEPYEQYQWVTEENLKYFRTIALDKLIDHNKYSHKKLIESNLQFLVCISPSPSAIRSIEWTARNAQAFYASWK ALYITTNKHKNNIQDIKKIEEYENKVHELGGEFVRITANNIDAAIIEYAKLTGVTNMVIGKSRTVNYRFPFRLTTLESKII NAIKGIELHIIPNYDYGTKKYEYKPKKTSSRVWKDILLSVLITLFATAICFLINFNTDEFNEGLIYLMAVLLISRFTKGYIY GIATSFISFLIFLYLFVQPNFTFNVSQVDSWVTFGIIFITSIMTSMITSQIKSDKESNVSAITELEKLYTFNQELLKVDDK LEIINLMKAFFKNEFGGESTFYDIDNNQIVNEPAQNDHIEAVQWMIINHQEVGNATKLFSNIDTTYFPIIISKKIIGAVSI TGLNLQTFKDYDYLIRVILYQTGLAIEKETLKIHRQKLSEIASQEIVRSNLLRSVSHDLRTPLTSIYGMITTIEQETITRD EIVNNLASARDDIQWLIRMIENLLSITRINQETQKVMKNLEVVEEIVSESVIRVRKRFPKAKIKVKIPNDVLLVPMDGTL IEQVIINLLENTIKHGKNVQNIILSVDDEQDKVIFKVSDDGKYIDLNKIENLLKDTQTIEYGDKGTKHSGIGLLICKTIIQA HQGQFSFYKNQENGITFYFTLPKGDHDEFK	22~~KdpD (3.01923E-22)~~190;X;205~~Usp(3.01923E-22)~~327;X;351~~DUF4118 (0.000000000008065 08)~~449;X(158);607~~HisKA (0.000000000469423)~~669;X;722~~HATPase_c (1.67044E-16)~~824	KdpD protein

	3E-08	43.1	7.3	5.5E-08	42.4	5.1	1.3	1	D5AKZ5_RHOCB	Histidine kinase (EC 2.7.13.3)	kdpD RCAP_rcc02255	Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)	897	272942	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter capsulatus (Rhodopseudomonas capsulata), Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)	>tr|D5AKZ5|D5AKZ5_RHOCB Histidine kinase OS=Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003) GN=kdpD PE=4 SV=1MPAGDPEKRPDPDALLALSQRERPGRLKIFLGAAPGVGKTCAMLQEAHRLRAEGVDVVLGLIETHGRAETEALAAGLETLPRRHIDHRGQPLEEFDIDAALARRPALLVVDELAHTNAPQSRHPKRWQDIRELLDAGIDVWTALNIQHLESLADVVARITGAPMRETVPDVLLQEAQDVVLVDIPPDELIARLKAGKVYLPQTARRAVEKFFTPGNLTALRELARRTAERVDDQMTEILRQKAIEGPWAAAERLLVCLVADGSSDALIRQTARLASALNADWIALLLAPPGDPAQPDRRASEALRLVETLGGTAQRRTSADFAADILRVARREHVTQILLGHRPRPGPLARLLRQSLAEALAARAEGIAVHLLPLPGPAPAAARRRLDALRRGLTRPGLPADLALAGLATTGVIAIGHALAAVMELPNLSMIFLAGVLICGTLRGTRAAVLAALLSCLGYNFFFIEPLHTFSIARPHEFLALLIFLVVASLTGSWTGRIRAQARAALAQTRGVEAQAAFSRQLSAASSAEDVAWAMVTQVQGGLGGKAILLLVEGSELVPCAAWPPEEIADPVEMTAARWAFEKGEVAGWRTATLPNLRLRFHPLATPRHVVAVLGYEPPDRDQPLSVADEAKLAVAVEQAAVALDRALLVREAVKAAAMQENENIRDALLASLGHDLRTPLAAITGAVTTLQRGETDLRPDQRTELLDTIGQEAARLNRFVGNLLEMSRIDQGVVKVRRDWVDVGDAIRLAAERARKTHPGRQTRVSLAPDLGFVRGDQDLLSQVIFNLLDNAHKYGESEVSVHARNEGDQVAISVTDDGPGVKPADLERIFEKFFRAGGTDRRKPGTGLGLSICRGLVRAMGGTIKAESPAIRRRGTRLIVRLPLAELPQDEEAR	22~~KdpD (2.10696E117)~~232;X;254~~Usp(7.04055E-21)~~371;X;403~~DUF4118 (0.000000000001065 15)~~498;X(166);664~~HisKA (0.000000000045339 2)~~730;X;783~~HATPase_c (8.06031E-29)~~885	KdpD protein
	3E-08	43.1	7	5.8E-08	42.3	4.9	1.4	1	S5YHT4_PARAH	Histidine kinase (EC 2.7.13.3)	JCM7686_pAMI4p337	Paracoccus aminophilus JCM 7686	905	1367847	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus aminophilus, Paracoccus aminophilus JCM 7686	>tr|S5YHT4|S5YHT4_PARAH Histidine kinase OS=Paracoccus aminophilus JCM 7686 GN=JCM7686_pAMI4p337 PE=4 SV=1MNHDAPRPDPETFLAAADIEAGEPAGTERGRGRLKIFLGASPGVGKTYAMLEEASAVHRAGGDVIVALAETHGRAETAALLSQLDQIPRRLVTYRGRQISEMDLDGLLARQPRLALIDELAHSNVPGDRHPKRWQDVEEVLDAGIDVYTTLNIQHIESLNDVVARITGVRVQETVPDAILQRASEIRLIDLSAEDLIKRMREGKVYMPAEAGRALLNFFSKPNLTALRELALRTAASRVDAEMLALTRGSGRPSAQDRLMVCLEDPATAKALVRAGRRMTDRARIPWIAATVITPDIERQGPGAAGAMTDALALAERLGAEIQILRADHADVVDELLASARRRKVSRLILGRVPRTGWRARVHARFFTPLSERILEQAADLEVTILSPSGEPSPPKVKPRRSAAGWPRLSAEALAVTAVSTLIATPFDRILPVASLAVIYLVGVLSIGMRRGTAGAVLASVMSFLAYNYFFTSPYYSLRVASHESIVALLVFTVSALFTGSLAGRLKRQVEFMRVTQARTETLYDFARKIASASSTTDDVLWAAAAHIAHSLECESLILMPDEGGDLRQVQGFPAIQEDLAPPIFAAALWAYQKNTPAGSGTDTLPALDWMFLPLATQGAPIGAIGVRFFDATRGRDPETRRMLSAVEDQVAVAVERIKIESDLERARLASQTEILRAALLNSVSHDLRTPLVTVIGSLSALDQGDLPPETTAALVRGALSEAERLDRYVANLLSMTRLGHGALVARRAPTDVAELIGRAQSDLAAPLAPFRVAITLPKDLPPIMVDPVLIGQSLINLMENATKYAPEGSTIRLTAQPEDKGVALMIEDEGPGIPQEQRTRVFELFHRAIQGDGQPAGTGIGLAIVKGMIEANDGKVEAIEPPSGKGAAIRLWLPVADSLEESHGA	30~~KdpD (8.03895E115)~~239;X;258~~Usp(2.56366E-23)~~387;X;411~~DUF4118 (5.62012E-14)~~509;X;535~~GAF (0.0000000209232)~~656;X;675~~HisKA (0.0000000401279)~~737;X;790~~HATPase_c (2.14814E-20)~~893	KdpD protein
	3E-08	43.1	7.9	5.1E-08	42.5	5.5	1.3	1	R6YT15_9ACTN	Histidine kinase (EC 2.7.13.3)	BN642_01536	Collinsella sp. CAG:398	537	1262852	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Coriobacteriales, Coriobacteriaceae, Collinsella, environmental samples, Collinsella sp. CAG:398	>tr|R6YT15|R6YT15_9ACTN Histidine kinase OS=Collinsella sp. CAG:398 GN=BN642_01536 PE=4 SV=1MGKVNVRAPRREGRMAARLGSMCVLLASSTAIGLGFHELGFTDSSIISLYILSTLLTATVTSGRMYTLLSSALSVVLYNFYFVVPRFSFESLDTSYLVTFAIMFVAAIVASELTSHIARNAREARRTAYRTSVLLETNQLLQQADGPESIARIALGQLLKLLNGPVAFYPVEGDGLGSPLVGDGVNEVMPASIAENARVNALRALRSSKLARDAASAGAAPASAPPATADALEIVAIPMGDGLFLPVRTHDEVFGVVGIRAAERDIDSFELSIARSIIGECALELARERERAREREEAAVLARNEQLRANLLRSLGHDLRTPLTAISGAAAILRDDSDRLAPEQRRALLDDVYHDSLWLIDMVENLLTITHFDEGTIKLTLNSELIDDIFEAAVSHLANQAGGHRIVIEPAEEILLVHIDASLIIQVLTNLVGNAIKYTPAGSTIQLSARREGAFVRVTVADDGPGVADDDKPHVFDRFYSGAKAERPADAQRSFGLGLALCRSIVEAHGGAIEVHDNVPHGAVFSFTLPAEEVAIHG	23~~DUF4118 (0.000000000037957 2)~~120;X(184);304~~HisKA (0.00000000148423) ~~369;X;423~~HATPase_c (1.1801E-28)~~528	non-KdpD DUF4118 protein
	4E-08	43	12	5.8E-08	42.3	8.3	1.3	1	C6W8N7_ACTMD	Histidine kinase (EC 2.7.13.3)	Amir_3228	Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	854	446462	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Actinosynnema, Actinosynnema mirum, Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	>tr|C6W8N7|C6W8N7_ACTMD Histidine kinase OS=Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971) GN=Amir_3228 PE=4 SV=1MDKRKRGELRIYLGAAPGVGKTFAMLGEAHRRRERGADVVVALVETHGRERTATMVDGLEVLPRKEVQHRGTTITEMDVDAVLARAPEIAVVDELAHTNAPGSRNAKRWQDVEELLDAGIDVLSTLNIQHLESLNDVVRRITRVEQRETIPDEVVRRAEQVELVDLTPEALRRRLAHGNVYAAHKIDAALGNYFRVGNLTALRELALLWVADQVDVALQRYRTEQRITDTWEARERVVVAVTGGAESETLIRRARRIAARAGAELLVVHTMRGDGLAGSAPESIAVLRKLTEDVGATFHMVVGDDVPAALLEFARGVNATQLVLGTSRRTRLARVFDEGIAAVIGQGSGSIDVHMVTHDESRRAPRWKVDRNPLTASRQVLGWSLALLLPVLVTGIGMALQEELDFSTDLVGFFLATVVVALVGGLGPAVVAALVGAVLLNYFFTPPFYSLTIATPENMLTLVVMVTVAVLVALVVDRAARLAAQAARARTEAALLASYARTVLTSPHPLVRLLEKVRENFGMESVAMLERVDGRWRRVACVGPRPCDEPDEADADVPVTADVHLSLRGRPLPAADQRALETAAGQALALRQQRMAVETADAQRRAATTELRTAILSAVGHDLRTPLTSIKAAIGSLRDPALALSEEDTGELLEAVEVSADRLAGLIDNLLDSSRLATGAVAPLLRPVTYDEVVAQALSGLDERAAVSVEVPEDLPPVLADSGLLERVVANVVDNALRHGRMAPRRVVDVDGDGDVITEHEPEVVVRASAHDDRVELRVVDHGSGVPEKSARAVFTPFQRLGDRDSTPGVGLGLSVAKGFVDAMGGAISAEDTPGGGLTMVISLPVADAWAADA	5~~KdpD (5.1185E-120)~~214;X;236~~Usp(1.12953E-21)~~357;X(254);611~~HisKA (0.000000000128028)~~676;X;726~~HATPase_c (3.33817E-24)~~844	KdpD protein
	4E-08	43	1	3.6E-08	43	0.7	2.4	1	R4K8E7_CLOPA	Histidine kinase (EC 2.7.13.3)	Clopa_4093	Clostridium pasteurianum BC1	629	86416	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium pasteurianum, Clostridium pasteurianum BC1	>tr|R4K8E7|R4K8E7_CLOPA Histidine kinase OS=Clostridium pasteurianum BC1 GN=Clopa_4093 PE=4 SV=1MILYIIYFKNRCVNNMEQIQQNGEKRINDIISIVKLASLFFCVIIIYEKVYQNNLFGYTYNNFLKINFTGLLMFLAIFLWWLLSHITSNIYKFKYVIIIRSIENVVLTIIYTALILTTNTYSNQIKCLFLLVIISSTLQLGKRMGMLTAFISSAIILIIDFTYVPSGDINYYFQNDLIIVGVFILTAWPLGHYKEIEDKRIENKDVQLKLLNNKLEKNHEQRKLMEENLLKNKSCYNLLIENSYEAILVHRNNKLIFVNESAAKLLGFSSYSELVGKSILSFLPEEEKIHLKDQFCRIYKEKLPKLVFEEKVLNSSNKIIAIENTSSFFIYEGKPTILSILRNITSEKEVVELQKDVERNSKLLEESISNKTITEFFINISHELKTPLNLIFSALQMIKLYNKDGDCNYIKKRNDYVDIMRTNSYRLLKLINNLLDLTKSDTGFLKIQLENTNIINMIEDITLSIADYVENKGIKLIFDTNVEEKITAVDGDKIERIMLNLLSNAVKFTNSGGQILVNVIDKGETVSIIVKDTGIGIPEDKKNLIFERFGQVDKTLSRNREGTGLGLCLVKSFVELHGGTIAIESQVGLGSSFIINLPVKHVEKNAENKAFYETDTERINIEFSDIYS	102~~DUF4118 (0.000000000080177 8)~~200;X(171);371~~HisKA (0.000000000076760 3)~~440;X;495~~HATPase_c (5.00211E-28)~~598	non-KdpD DUF4118 protein
	4E-08	43	11.6	5.1E-08	42.5	8	1.2	1	R5SLZ1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN483_01059	Firmicutes bacterium CAG:129	373	1263003	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:129	>tr|R5SLZ1|R5SLZ1_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:129 GN=BN483_01059 PE=4 SV=1MKDLLSRIGQWTEKMWRSIPIHLRDAIFTALLLGIAAAICFVLRSIDENGSFTLLIFVLAVVIISRFTEGYFWGVFSSLFGVICVNFVFTYPFWAFNFRLTGYPLTFLTMLAVSLIISAMNTKIKKQERLRTEAERETMRANLLRAMSHDIRTPLTSIVGNTSAILENGDTLSTEQQRELLRDVNEDAQWLIRMVENLLSITRISGEQTAISKEYEAAEEILAASVHKFEKRFKSNIRIAVEVPQEVVLVPMDATLIQQVLLNLMENAVLHGESTTELRLSVEHIGDEACFTVSDNGLGIPRERLATLFDGSLSGEKGGGFDMKKNMGIGLSVCQTIVKAHGGRITAENRPEGGAQFRFYLPLKEEKEDEDQG	27~~DUF4118 (8.96698E-14)~~127;X;137~~HisKA (0.000000000001452 33)~~203;X;257~~HATPase_c (3.63799E-26)~~361	non-KdpD DUF4118 protein

	4E-08	42.9	8.9	6.3E-08	42.2	6.2	1.4	1	R6BNL0_9CLOT	Histidine kinase (EC 2.7.13.3)	BN513_00389	Clostridium sp. CAG:169	900	1262778	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:169	>tr|R6BNL0|R6BNL0_9CLOT Histidine kinase OS=Clostridium sp. CAG:169 GN=BN513_00389 PE=4 SV=1MSENNLMADKLLKAIQEEERDKTRGHLKIFFGYAAGVGKTYAMLKAAHEAKQRGIDVIAGYIEPHARPKTAALLHGLEVLPSKSVPYNGITLREFDIDAALQRKPQLILVDELAHTNADGSRHAKRYQDIKELLYAGIDVYTTVNVQHIESLNDMVASITGVFVRERIPDSIFDQADQVELVDIEPQELIERLKEGNVYRESQAKRAVNNFFTVENLTALREIALRRCADRVNILTENSRIKSHGDYHTDEHILVCLSSSPSNAKLIRTAARMANAFRSDFTALFVETPAFSAMKVEDKKRLQDNVHLARQLGAKIETVYGDDIPLQVAEFARLSGVSKIVIGRSVAAKKHLFSKPTLTEKLIAYAPNLDVYIIPDTTSAPVSYYAKKAKGIRHLVYSPADLAKSIGILLAASGIGFLFQKLGFAEANIITVYVLGVLLTSAITTHWIYSLISSIVSVLLFNFLFTVPRFSLEAYDQGYPVTFIIMFLAALLTGSLATQLKNHAKQSAQAAYRTKVLFDTNQILQQEKNQEDIISATSRQLVKLLGRGIVFYPVENGLLGEARTFSPDGNVLDNSCLSVNEQGVAKWVLKNNKHAGATTDTLSDAKCLYLAVRIMDRVYGVVGIVIGQQPLDAFENSILLSILGECAMSLENEKNAREKEEAAILARNEQLRANLLRAISHDLRTPLTSISGNASNLLSNGKSFDEDTKLQLYTDIYDDSMWLINLVENLLAVTRIEEGRLNIRASANLIDEVIAEALHHVNRKSVEHCITVEHEEDFILAKIDARLIVQVIINIVDNAIKYTPKGSHIQIKTRKQDEHVIVTVADDGEGIPDELKPKVFDMFYSGANKIADSRRSLGLGLSLCKSIIHAHGGTISVSDNIPHGTVFTFTLPAEEAQIHE	24~~KdpD (6.98954E-125)~~232;X;252~~Usp(1.73157E-35)~~375;X;402~~DUF4118 (0.000000000000050691)~~503;X;529~~GAF (0.00014528)~~652;X;669~~HisKA (0.0000000017785)~~735;X;788~~HATPase_c (1.46829E-29)~~891	KdpD protein
	4E-08	42.8	17.8	7.7E-08	41.9	12.2	1.6	1	R7G9M3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN631_00322	Eubacterium dolichum CAG:375	524	1263076	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium dolichum CAG:375	>tr|R7G9M3|R7G9M3_9FIRM Histidine kinase OS=Eubacterium dolichum CAG:375 GN=BN631_00322 PE=4 SV=1MKQEHKRTMGRLVNMHVERKKLYLSLLILTLSTFIGFLFFQLGFNDSNIIMLYLLAVFLIAIITANRIYSIIFSFISVLIFNYFFTFPLLSLSAYDSGYPMTFVIMFTVAFVTSTLAAKIQQNSHFSALIAQRTRILLETNQMLQKEITKEGIIQKGCEQLYKLLKRDIVFYPYSEHELQEVYVYPPQTSEHFKDVLSDEIHVARWVAKHNRHGGASTDYLPNSKYLYLAVRADHNVYGVLGIYLDKEQLDSYENDILLAILGEIAFALEIEHINDEKKQSELKAKNEQLRADLLRSISHDLRTPLTSISGNADMLVSKEQELAQKDRLQLYEDIYDDSLWLINLVENLLSITRMEEGAIRLKLEPQMIEDILYEALKHVSRKKKEHHLHVQIDDDLLMADMEAHLIIQVIINLVDNAIKYTPQGSNITLHAYQKEDMVTIEVYDDGAGIPDDKKEHIFDKFYRGNTKIVDSKRSLGLGLALCKSIVHSHGGEIHVMDRIPHGAMFYFTLPATKLKLEEHGEVS	(8.82569E-15)~~123;X;151~~GAF (0.00000110148)~~270;X;288~~HisKA (0.0000000000156507)~~354;X;407~~HATPase_c (5.73473E-29)~~510	non-KdpD DUF4118 protein
	4E-08	42.8	9.4	8.4E-08	41.8	6.5	1.5	1	A0A0F5PSN8_9RHIZ	Histidine kinase	WH91_19475	Devosia psychrophila	886	728005	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia psychrophila	>tr|A0A0F5PSN8|A0A0F5PSN8_9RHIZ Histidine kinase OS=Devosia psychrophila GN=WH91_19475 PE=4 SV=1MARHTEKERPDPTALLQLAAREGRGKLTVFLGAAPGVGKTYAMLERARGLKAQGVDVVIGLVETHGRGETARLAEGLETLPRQGEGDAYREFDLDAALARRPALLIVDELAHSNAPGSRHPKRHQDIAELIHAGINVWTALNIQHLESLSDLVARIAGIPVRETVPDIVLKTADEVILVDLPPAELIARLNEGKVYLPDNAARALDGFFKPATLTALRELALRRAADRVDDQMVEFLRQSAVEGPWATGERLLVCVGPDTMSEKVVRTASRLASGLNARWLVVSLNRPDAALPSPADAVRLEEVLRLAERFGAETRRESASDFVDAILRIARREHITQIVIGRPTTTRWLRRSLPDALLRQAGEIGVHVVPGATSSAGRKPRRRLTLPEWALTLGLPLVSVGATTIFGLGLTALVALQNLSMLYLAAVLVSAVIAGRGSALVAAALSFAAYNFFFIEPTGALTVAQPQEVLSLVIFVAVAFAAGQLAARLREQADLSRQQARQSQALLDFSRKLSGAHGQDSVFDAIASHLHTSLGRPAVVLVPDDSGDLDPAAAWPPEQALDGTELTAARWAFDKKEPAGFLTGTLPQVRYLFRPIIAAQRILGVAGLGMGPRDVPLAADEERTLIALLDQAAIAMDRARLNRESAMASVAREGEKVQAALLSSLSHDLRTPLASITGAVTTLRQLGEKLPVETREDLLLSIEEESVRLNRFVANLFDMTRIEAGMMKARREAIDLNTVVASSVARAKRLHPDLLIDISLAPNLPSALGDGTLLEQVLFNLLDNARKYGAAEQPVSIFAKAEDGHATISVTDQGKGIPEADLEKIFEKFYRRAKSDGRPAGTGLGLSIARGLMTAMGGTIKATSPAVRKRGTRFTLRLPLATKEE	22~~KdpD (2.67749E-109)~~229;X;251~~Usp(1.1208E-34)~~371;X;398~~DUF4118 (8.13058E-15)~~493;X;521~~GAF (0.0000000266413)~~639;X;656~~HisKA (0.0000000189619)~~722;X;775~~HATPase_c (1.25867E-29)~~879	KdpD protein
	4E-08	42.8	10.4	6.4E-08	42.2	7.2	1.3	1	R6ZQF8_9CLOT	Uncharacterized protein	BN593_00577	Clostridium sp. CAG:299	666	1262792	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:299	>tr|R6ZQF8|R6ZQF8_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:299 GN=BN593_00577 PE=4 SV=1MQEERPDSEQLLKRLKYEEREQEKRTRGRLKIFLGYAAGSGKTYAMLEAAHEAKAHGIDVAAGYIEPHDRPDTQALTKGLEMLPPAFMEYKGMKLREFDLDGALKRKPQLLLVDELAHTNCRGCRNEKRYQDVKELLRAGISVYTTLNIQHLESLNDLVGSITHIDVRERIPDTVFDHADQVEVVDIEPEDLIERMKEGKIYRKEQADRALQNFFRRERLAALREIALRRCADRVNRIAEEERSLLERQDYHTGEHILVCITAAPSSAKVIRTASRLADAFHGTLTGLCVETPDTQEAGEKTKEALRNNMELAKLLGAKIVTVFGSDVAAQIAQYAIVSNVSKIVLGRTNHFTMRPMYRSELLEKLTYMAPNIDIYIIPDMRQTKRWHPRQSAAKRQESWKKCAAGLAAATAVMLAATALALILRMFVFSEANTIMIYMMGVLLASCAASRKLCALYSALLSVILFNFFFTEPLYSLKAYDQAYPITFLMLFLAGLFTATVTGKLKRQNMEISKTAYRTGILLENSQKLRRCKTREDVWRQAAVQAGKLLNLSILFYPVRKDGAVEEPLLFPRKGMDPEELKRCVNAQEKGVAQWTASNRRRAGACTHTLPDAMAMYLPVQDEEQIHAVMGIFLEERRPVAEFEYSLLTAMLNETGVKLKDFFIQS	27~~KdpD (4.41402E-124)~~235;X;256~~Usp(1.60928E-33)~~379;X;431~~DUF4118 (0.000000000023171 4)~~508;X;536~~GAF (0.0000253269)~~657	KdpD protein
	4E-08	42.8	6.4	6.4E-08	42.1	4.4	1.3	1	C9LWX6_SELS3	GAF domain protein (Putative phytochrome sensor protein)	Selsp_2171 SELSPUOL_01982	Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	711	546271	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Selenomonas, Selenomonas sputigena, Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28)	>tr|C9LWX6|C9LWX6_SELS3 GAF domain protein OS=Selenomonas sputigena (strain ATCC 35185 / DSM 20758 / VPI D19B-28) GN=Selsp_2171 PE=4 SV=1MSTWTKKVMFAGLPRFLEQLLAACFRKEAWEVSSLSANEEERSQKGMKTYDCALESAEAGMVFAVENLDLLIYRLERDPVLGVRRLDAMLRFACASKVRRVFLLSGDEVFAPGTEPLEDAALQPQGETGALLARLEAQGLSWRAQGLSVSIVRLPELYAPGQTSDDGFIGRLFGAALMNRPLPRYTDPAAVSCGFLDARDAVYAIYQAAARGFDGAHLHIGAPAATTMEELYAICREFFPRMEEAAVPRETQGRAILKSAIAEKELGWRPVRPFAQGLKETWEAMCAMHDTRVADVRAMSRRARLARLQQRFIPYAENLAGAALTAGVGALQGGTTVNAMTAFDFAFLYIGCMGLLYGKQQALIAAVLSLVLLIHSLLGAGGDLVAMLYNPREFLHFVSYFFVAVLTGYFADRASYQQLADTRIKRRLQNRYSFLENLFKENLAVKDRLYRQIVNSDDSIGRLYRIVSRLDSVETENLFTQATSVTADILDVEDVVVYVVGEGGYYLRQKVRLGSRTGEMPRSLRVDDYPYLQEMLREKKIFVNRDLIKGLPDLAAPISYEGRVIAVLQIYHLDFEQWSLYEQNLLSITARLVSSSLGRAYAWEQETAGRKYIDETRILRIEEFQKVIEEFCERRRMQADYPVALLPVSIKDESYREIDHKIANSIRAEDFIGATADGVALLLPDVAGKTLDMVRERLEKAGIETGESLSL	non-KdpD DUF4118 protein

	4E-08	42.7	5.6	7.9E-08	41.9	3.9	1.4	1	B2TMJ4_CLOBB	Osmosensitive K+ channel histidine kinase KdpD (EC 2.7.3.-) (Sensor protein KdpD) (EC 2.7.13.3)	CLL_A0981 CB17B0916	Clostridium botulinum (strain Eklund 17B / Type B)	900	935198	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum B, Clostridium botulinum (strain Eklund 17B / Type B)	>tr|B2TMJ4|B2TMJ4_CLOBB Osmosensitive K+ channel histidine kinase KdpD OS=Clostridium botulinum (strain Eklund 17B / Type B) GN=CLL_A0981 PE=4 SV=1MIDERPDPDEILKKISSDENNKQGKLKIFFGYAAGVGKTYAMLEAAHIAKNSGIDVVAGYIEPHTRVETLALLDGLKMLPNLKVKYKGITLNEFDLDSAINRKPKLILVDELAHSNAYGCRHMKRYQDIQELLNNGIDVYTTINVQHIESLNDIVASITGIVVRERIPDSVFDNANQVELVDIEPDDLITRLDNGKVYKTDQARRALINFFTKEKLVALREIALRRTADAVNKKIENKRDEIKSTYYTEEHILICLSSSPSNTKVIRTAARMAFAFHGLFTALFVETSNSKDLSLENKKILETNLKLAEQLGAKIATVYGDDVANQISQYAKISGVSKIVIGRSNNKKSWFNNKKTLVDKLTEFAPNIDIYIIPDNLKAYKRNSSEKLKKITLPHFTVMDLIKTTAILGAVTATGVIFYNLGYSEANIINIYILGVLLTSITTTGKSCGLLVSILGVLVFNFLFTNPRFTFQAYDKSYPITFFVMLVSSIISSKLATRVKIEAKQSAEKAYRTEVLLETSQKLQMAKNKEEIFNKILIQIEKLLDKSVILYPADNEVLLEPIVFKKKNRTINIKEFITEDERAVAQWVFKNKKHAGSTTNTLPGAKCLYMAIRNHEKSFAVVAIPIDKDETLDSFKKKNLLIAILAESALSLEKEYINETKNEIYMKAEQEKLRSNLLRAISHDLRTPLTSISGNAGILMGNSRVLDESRKQRLYTDIYDDSMWLINLVENLLSVTRIENGTMDIELQPELIDEVIQESLQHINRESSNYNIEVEVEDELLMAKMDSGLIIQVIINIVNNAVKYTPKGSNIKIFGKKQGKSVVIEISDDGCGIEDSMKGKLFDMFFTLNSTSADGRRGLGLGLGLSCKSIINAHGGEVYVRDNEPKGTIFGFTLQCEEVIYSE	22~~KdpD (1.88212E-121)~~231;X;251~~Usp(1.92787E-35)~~374;X;401~~DUF4118 (2.63203E-14)~~500;X;528~~GAF (0.00000177102)~~652;X;669~~HisKA (0.000000000239218)~~735;X;799~~HATPase_c (1.99991E-19)~~891	KdpD protein
	4E-08	42.7	15.1	6.9E-08	42	10.5	1.3	1	A0A098G9H5_9GAMM	Histidine kinase (EC 2.7.13.3)	LFA_2760	Legionella fallonii LLAP-10	891	1212491	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella fallonii, Legionella fallonii LLAP-10	>tr|A0A098G9H5|A0A098G9H5_9GAMM Histidine kinase OS=Legionella fallonii LLAP-10 GN=LFA_2760 PE=4 SV=1MGESRPDPEKILRKVHDEERRERQGKLKIYLGAAPGVGKTYEMLRDAFAERNKGLDVVIGVVESHGREEIKHMMMDFEVLPRQVIYYHENKLEDFDIDAALKRNPGLILIDEMAHTNAPGQRHSKRWQDIKELLDRGVNVYTTLNVQHIESLNDDVAQIIQAPIKETVPDFMIDRADTIELVDIPPEDLLKRLHEGKVYFAQQAEIAAENFFRIGNLIALRALALRVTAERVGAEVISYRHDKHITKIWPTKEKILVCVGPGNESLKLIRAARRMATNLHATWMAVYVDIPRLRSSEEIKNKAIQNLRFAQQLGAETRFLSGTDIVKEIMNFAHEQNVTQIMVWKTIRTPRPDLFFRHLADEIVRYSGEIDVFIMTGTREQTKLAKEFRTEPEVFWSTYVSAISIVAVATLINSLLSPYVPMLNLIMVYLLSIIIVSLYGQQGPSLVASLLSVLAFDFFFVSPTYSFAVSDLAYIFTFVIMFFMAQVVSSLTIMIQRQAEAARFSEQQASALYKLTRDLASTRGTDKLLETGLHFISQQFFANKVVIFFAENGHLVFRDKAHNYEPPSLKEQSIAQWVYDLGQPAGLGTNTLSSAEALYLPLTGAENSIGVLRLGPIKQKRLLTPEQMHLLEACTSHLALAIEAERTHEQKGKSALSRDKNFMDNALLRSIAHQLRAPLAAIMVAANNQIELANKLSTNKIRSLGKDIYFESEQLSRLINNFLQITYLESRAARVNKQLNSLNDTLNTVLELSRLKLGGRTININIPDDFPVLYYDNALIQDVLINLIDNVVQLTPKDYPLDITAVQKDALVEISVEDNGAGIMPDEMHKVFEKFYRGRMITSERGLGLGLTICHRIIKAHGGTIWAENRKQGGAAFRFTLPLKINHDLPEV	22~~KdpD (1.59127E-102)~~232;X;254~~Usp(3.8197E-34)~~376;X;399~~DUF4118 (1.894E-16)~~498;X;525~~GAF (0.000000000000207981)~~642;X;664~~HisKA (0.0000872407)~~725;X;779~~HATPase_c (3.25887E-26)~~880	KdpD protein
	4E-08	42.7	7.9	9E-08	41.7	5.5	1.6	1	X2GN40_9BACI	Histidine kinase (EC 2.7.13.3)	T479_15025	Lysinibacillus varians	901	1145276	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus varians	>tr|X2GN40|X2GN40_9BACI Histidine kinase OS=Lysinibacillus varians GN=T479_15025 PE=4 SV=1MEKMRPTPEELLTRFHQEQTTVGRLKIFIGYAAGVGKTYAMLDAAHLAKKLGKDVVIGYIEPHPRPETLALLDGLEQIPTRTIHYKGRTFQELDIDAVLERKPEIVLIDELAHSNVPVMRHTKRFGDVEELLAKGIHVYTTVNIQHIESLHDVVEEITGVKVRERIPDYLIDQAALIKIVDIEPDELIQRLIEGKIYSKQQAEKALASFFRKQNLVALREIALRRTADTINYKQINDSESIRQTTQIEEHILVGISSSPTNAKVIRTAARLAQALHGKFTALYVQKVKEGDDNDANSERLQQHIKLTEQLGGHVVIVQENDVAAALANYAQMSGVTKLVLGRTVMKKKWWQPNAKIIDRLNDYVPNLAIHIVPDQENEQFYFPDLRNRLTFEWLDLLKMSVVFSLASCLALFFFTMGVSESNIITIYILSVLILAIWSSGWLMTIISSAVAVLLFNFLFTEPRFSLEAYHRDYPMTFMIMFFSGIITSSLTKKIKEQAIVAVRKSYRMEVLLETNRKLQHAKSIEDIITEGMSQIVKLVEKPVQFFEIENNMIAKSVFFPTPTLSNTENTKVATLFKNTNELGVVHWVINNNHFAGVSTDIFPEVNGYYLPVLSSGSVKGVVGIALSKQTPLPAFERHILNAIMNDFSFALDKWYLQNLNEKVAREAELEQMRANLLRAISHDLRTPLTTISGNADILLTNTVQIPDIEKTRLYEDIYKNSRWLVQMVENLLAVSMLEDGQFALEMQLELVEDIIQEALLHVIPRNNTHHISYHVEPELVMALMDARLIIQVLINIINNALTYTPAGSDISFIAKEEGEYVHFSIADNGPGIDDSLKEKLFEPFITGKVQRSDSRRGLGLGLALCQTILTLHDSKLVVEDNYPNGTIFRFTLKKGVVSIDE	23~~KdpD (4.31217E-115)~~230;X;250~~Usp(1.73757E-34)~~373;X;396~~DUF4118 (0.000000000000930365)~~497;X(173);670~~HisKA (0.000000000597273)~~735;X;789~~HATPase_c (9.41947E-25)~~892	KdpD protein
	5E-08	42.6	8.2	7.6E-08	41.9	5.7	1.3	1	B1HTG2_LYSSC	Histidine kinase (EC 2.7.13.3)	kdpD Bsph_3682	Lysinibacillus sphaericus (strain C3-41)	895	444177	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Lysinibacillus, Lysinibacillus sphaericus (Bacillus sphaericus), Lysinibacillus sphaericus (strain C3-41)	>tr|B1HTG2|B1HTG2_LYSSC Histidine kinase OS=Lysinibacillus sphaericus (strain C3-41) GN=kdpD PE=4 SV=1MENTRPTPEMFLARLQQEEHSIGKLKIFLGYAAGVGKTYAMLDAAHQAKKLGKDVVVGYVEPHPRPETLALLEGLEQIPTKKITYKGKIFQELDIDAVLQRKPEIVLIDELAHSNVPSMRHKKRFGDVEELLAKGIHVFTTVNIQHIESLHDLVEEITEIKVRERIPDYLIDQAAQIKVVDIEPDELIQRLQDGKVYVKQQAEKALDSFFRKQNLVSLREIALRRTADTINYQQLNSNESVRNYVQIEEHLLVGISSSPTNAKVIRTTARLAQALHGKFTALYVQNMQAHERNHADSERLQQYIKLVEQLGGHVVIVQEDDIAAALANYAQISGVTKLVIGRSSMRKKWWQPNAKISDRLNEYVPNLSIHIVPDQENEQFYFPRIKNKLAFEWLDLFKMFIVFSVISIVIGLYLYSIGISEPNIITIYILGVLILAIWSSGWLMSIISSIVAVLLFNYFFTEPRFSFDAYHRDYPMTFFIMFLSGVITSSLTKKIKEQTIIAIRKSYRMEVLLETNRRLQHAKSIEEIITEGMSQIVKLVEKPVQFFEIDNRVIGKSTFFRNDKISTIENQKIATLFNNPNEHGVVNWVTNNKHVAGVSTDIFPEVHAYYIPVISNGNVRGVIGIALSKLLPLPAFERNILHAIINDFSFAMDKWYLQKLHEEVAREAEMEQMRANLLRAISHDLRTPLTAISGNADILLNNAPLIPDIEKNKLYEDIFNNSKWLVQMVENLLAVSRLEDGQFALEIQLELVEDIIQEALSHVVHQNSSHKISYQIEPEFLLSLMDARLMIQVFINIIDNALTYTPPGSDITILVKECDGLVNFSISDNGPGIDDSLKSSLFEPFTTGKVQRSDSRRGLGLGLALCQTILKLHGSQITVSDNKPQGTIFNFSLKKE	23~~KdpD (1.58174E-117)~~230;X;250~~Usp(1.65349E-33)~~373;X;396~~DUF4118 (1.96245E-14)~~497;X(173);670~~HisKA (0.000000000061336 8)~~736;X;791~~HATPase_c (4.90627E-24)~~892	KdpD protein
	5E-08	42.6	7.9	7.8E-08	41.9	5.5	1.3	1	A0A0F2NK40_9DELT	Uncharacterized protein	VR65_08735	Desulfobulbaceae bacterium BRH_c16a	277	1629713	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, unclassified Desulfobulbaceae, Desulfobulbaceae bacterium BRH_c16a	>tr|A0A0F2NK40|A0A0F2NK40_9DELT Uncharacterized protein OS=Desulfobulbaceae bacterium BRH_c16a GN=VR65_08735 PE=4 SV=1MIRKQTAIIILVTLTVALIHLFIPQRFLTLHIVLRLLYFIPIILAALSSGRKGGLIAAGAISLVFSPHFFFHHASREFMVENAVTIILFLLSGFFIGSFRESSEIQLNKRLAEERMVVPVRDAERQRVLFYNDGSSLSLGTAKWFVGKHNLSKMSIVLLMVATQDREEMLADTMADKQQRERREQARKQSFIDIRQVLIEGGIPEKNIETVVTTVNEKVPISDKIIEYLSEHEFDFLLLCKHNKRKSEEFLFGDTAIQVLRKTTTPLLIVKGTGEAIA	7~~DUF4118 (0.000000000776548)~~100;X;115~~Usp(0.00000271496)~~269	non-KdpD DUF4118 protein

	5E-08	42.6	4.6	7.9E-08	41.9	3.2	1.3	1	H8GLT9_METAL	Histidine kinase (EC 2.7.13.3)	Metal_2935	Methylomicrobium album BG8	500	686340	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Methylococcales, Methylococcaceae, Methylomicrobium, Methylomicrobium album (Methylobacter albus), Methylomicrobium album BG8	>tr|H8GLT9|H8GLT9_METAL Histidine kinase OS=Methylomicrobium album BG8 GN=Metal_2935 PE=4 SV=1MQQIRSYAWGVAAPFLCTLIDWPLRHWVGQAGILMTYLLGVFLVASRCGRGPSLIASLLTAPLFAFYFARPIFSFAIHDLENMIGLTVMIVVANVTGSLLEKSKLQAELAWQREIRASALYRLSGDLLAAQDYESVGRIAVEHIHDEFGAASVLLSVDADNRLQRPSSLPLPMSLTGIDLAEAQRVFEARQFKQDNTIAYYPLKGSRAWQGVLMMQAAEPLAEQSSERAAFLDTFCHLIAQTLERLQLAAQAKEATLQAETEAMRNALLSSISHDLRTPLTRIIGAANTLIENDAEFEPSERQDFNHIVLEEAQRMSELTGKLLDMARLSRGEIILHRDWNAIEEIVGSALNRLDKHLQDRPVRTVLPDNLPLLWIDAVLIEQVLANLIENALKYSPAGSPIDICGQVQDGYCRLTVADYGPGIAKGQEMKIFEKFYRGAVESGQSGVGLGLALCKAIVEAHGGRINAGNRAGKGAEFVIALPLREPPSFVESEVHGNLS	7~~DUF4118 (0.00000000003854)~~99;X;132~~GAF (0.000505465)~~245;X;262~~HisKA (0.000000000000997387)~~328;X;381~~HATPase_c (5.54327E-29)~~482	non-KdpD DUF4118 protein
	5E-08	42.5	10.9	7.8E-08	41.9	7.5	1.3	1	G8QI81_DECSP	Histidine kinase (EC 2.7.13.3)	Dsui_3152	Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	499	640081	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Azospira, Azospira oryzae, Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) (Azospira oryzae)	>tr|G8QI81|G8QI81_DECSP Histidine kinase OS=Dechlorosoma suillum (strain ATCC BAA-33 / DSM 13638 / PS) GN=Dsui_3152 PE=4 SV=1MGHLLQRFSGYLMGMLFVLLGTALAAPFRAEIDLSNLALLYVLAVVAVGGHFGRGPAVACALAGSLAFAYVFVPPHFSLAITEIQYVMAAVIMVVVALVVGHLTAALRTQVELARDRARRARALYELAKHLAGSQTAEEVTQTCRRFLADALGARRIRLLEPATWDQPPPFITKALVRACLERRQLVAIPSPAPGISRALLPLAGTRDLQGLLGFEVDSGTLDDGEYREALDTMASVVAVALERTQYAAAVRESELRVAAETLRGTILASLSHDLRTPLTALVGMADGLALGKVVGAEKQKSMLLRLRDQALAINQLLGNLLEMARLRSGNVELQKEWQPIEEVIGATMGLMEPHAGGREIVINIAPELPPVHIDGVLIEIAVEALANLVKYSPAEQSIELRVAQSEGWLELSVCDRGEGLAPGQEEDLFGLFRRGRSESNVPGAGLGLAIARTIAEAHGGSVSAANRSGGGACFCLRLPLETPPDLADLADLESETP	16~~DUF4118 (0.00000796969)~~110;X;138~~GAF (0.000146194)~~244;X;261~~HisKA (0.00000000481429)~~326;X;379~~HATPase_c (6.04859E-30)~~480	non-KdpD DUF4118 protein
	5E-08	42.5	13.4	9E-08	41.7	9.3	1.4	1	I0XR10_9LEPT	Histidine kinase (EC 2.7.13.3)	LEP1GSC185_3490	Leptospira licerasiae serovar Varillal str. VAR 010	891	1049972	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira licerasiae, Leptospira licerasiae serovar Varillal, Leptospira licerasiae serovar Varillal str. VAR 010	>tr|I0XR10|I0XR10_9LEPT Histidine kinase OS=Leptospira licerasiae serovar Varillal str. VAR 010 GN=LEP1GSC185_3490 PE=4 SV=1MRPAEENRPDPDELLSRIGGEETNTRGKLKIFFGMAAGVGKTFEMLRDAQKAKSEGIDVWIGYLETHNRKETEAQAEGLPVIPRKRFKYKSVDLEEMDLDTILEKKPDLVLVDELAHTNVPGSRHPKRYQDVLEILDQGINVYSTLNVQHLESRAGIVEEISGAPVSERVPDSILEIADEVELVDLVPDDLIKRLKEGKVYPSDKVPQALHSFFKVPNLTALRELSLNFTSKLVDRELSRLEPTKDSKLSDKILVAVSSSPQAANLIRYAKRIAFGLKCPWVAVYVDDGNILAPDQKRLLRENLGLARELGAEILNFSDRDPVLGILRAINRSKATHVVIGRSGKSKFSRILRGGSFVDKLSEQSGDFQILLAPTEVSKEKPKIRFGFFTKGTRSKPIQYFISFLALLGVTSFNLLLNIITGYWSIGLVYLFFIMFVSLFAGRGPVLITASLSAIFWNFLFIPPKFTFYIEKVEDWMMFGTYFVLALVLGALTTRLRDREEALQAGEEALSGLYRLSVALSKTHSLDEIASVAVETIGDTFQSSVLILLADQDSLLSRTPHPKSGFKPDMKESALAAWTFQNRKPSGKDTDTVPMSKGLYLPLLTPGGCFGVVGLDREYKESLELEEETLLFSMLNQIALALERIHLLGIRANAKLVEESEKFYSALFNSVSHDFRTPLTVIRASLDLLESGCVKNEKEKSGLFSEIRIAYKKLDRLVGDLLDMSRLESGRLMLDLQWEDPVDLVNETIRIAEYEKGEHTLTVQTDESMPLVRMDRRLMIQVLIHLLQNAFLHTEKDSTVIVRASVPKDHLLLTVEDNGPGIPYGQEKRIFEKFTKVSGSMQGTGLGLSICKGLVEAQGGKIWAENRQEGGARFLIRIPVLTFPPLEDAIV	26~~KdpD (2.15472E-112)~~234;X;252~~Usp(5.44807E-29)~~374;X;399~~DUF4118 (1.65456E-15)~~499;X;525~~GAF (0.00000000756192)~~644;X;661~~HisKA (0.00000000240015)~~726;X;781~~HATPase_c (7.48417E-28)~~878	KdpD protein
	6E-08	42.4	10.4	8.4E-08	41.8	7.2	1.3	1	D9R3K9_CLOSW	Histidine kinase (EC 2.7.13.3)	Closa_4229	Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	363	610130	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1)	>tr|D9R3K9|D9R3K9_CLOSW Histidine kinase OS=Clostridium saccharolyticum (strain ATCC 35040 / DSM 2544 / NRCC 2533 / WM1) GN=Closa_4229 PE=4 SV=1MKMHQILSKRDLLRNFLITFHSLLVATILSYMMHILGGYTNNVGIIYMMAVVLVSRYSTGYVPGVIASFISVICVNFVFTYPYMAFNFTMEGYPVTFIALLVISTITSATTTHLKEQSRILNEREKRLMEAEKEALRANLLRAISHDLRTPLTGIIGASSTYLENFGNMPESEKTSLVTNIREDANWLLNMVENLLSVTRIRDTGAHVLKRPEPLEEVASESIERFRKRLPDSIVRVTVPDEFVMVPMDATLIEQVIINLLENAVYHSNSTEPIRLSISVEDGYARFEVRDHGVGISPERLDTLFDGFTSSPNSSYDSHKGMGIGLSICKAIVTAHGGNIKAANEEHGAVFTFTLPLGENAYE	15~~DUF4118 (0.00000000050077)~~102;X;134~~HisKA (0.000000000071083)~~200;X;253~~HATPase_c (5.62829E-27)~~355	non-KdpD DUF4118 protein
	6E-08	42.3	10.1	9.3E-08	41.6	7	1.4	1	R5AJG8_9FIRM	Histidine kinase (EC 2.7.13.3)	BN453_01898	Firmicutes bacterium CAG:102	665	1262998	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:102	>tr|R5AJG8|R5AJG8_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:102 GN=BN453_01898 PE=4 SV=1MNKLNNINSKQDHILACLSSAPSNAKIIRSAARMAKAFDSQFTALFVETPDFAVATDENKKRLEENRKLAEQLGATIETVYGDDIPYQIAEFARISGITRIVLGQSSAIQKHLFGKPTLTQLLLSYVPELDIHIIPDKAADTTYHPKKARKYHHEQIIKNTVKSALILFAATLLSLLFHEIGFTDANMIMVYILGVLLTSIATSHQIYSLISSIVSVFIFNYLFTAPRFSLAAYDTGYPVTFVVMFLTAYITGTLAIRYKEQARQSEKIAKRTKVLFDTDQLLSKAENKLAILQTAGQQINKLLGRSIVIFDHEGGRLSEPIRFISDGQRFYDEETELAIVEWVLQNNHNAGATTKNFPDAQYLYFAVRVNERIYGVVGIDAMAGALDASEQSILLSILGETALALENEKNIREKEAAAILAESEQLRANLLRAISHDLRTPLTTISGNAGNLLHNSHSFDDETKQQIYADIYDDSMWLTNLVENLLYSTRIEEGRMMLKTSPELVSEIIEEAMQHIRPNAKKHSITVNYGDDLLMVRVDAKLIVQVIINLVDNALKYTPLDTLISISAECKNGMAEIKIADTGKGISDVEKGKIFDKFYSGEHKIADNRRSLGLGLYLCKAIVEAHGGSIHVTDNLPHGSVFRFTLPLEEVIIHEEISNPRCGG	36)~~136;X;162~~DUF4118 (4.36231E-14)~~262;X;292~~GAF (0.0000168795)~~408;X;425~~HisKA (0.00000000177752)~~491;X;544~~HATPase_c (4.29446E-26)~~647	non-KdpD DUF4118 protein
	6E-08	42.3	9.1	9.9E-08	41.5	6.3	1.4	1	Q5GW24_XANOR	Histidine kinase (EC 2.7.13.3)	kdpD XOO3843	Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85)	886	291331	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas oryzae, Xanthomonas oryzae pv. oryzae, Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85)	>tr|Q5GW24|Q5GW24_XANOR Histidine kinase OS=Xanthomonas oryzae pv. oryzae (strain KACC10331 / KXO85) GN=kdpD PE=4 SV=1MNDARTQQADALIGELQREHGGRLTVFLGAAPGVGKTYAMLSRARERLRQGMDVVAGVVETHGRSETAALLEGLPLLPRARVSYQGRMLEELDLDALLARKPRLALIDELAHRNVPGSRHERRWQDIVELLDAGIDVYTTVNIQHLESLNDIVLRITGVRVSETVPDAVFDRLRDIVLVDLPPRELIERLQQGKVYLPEQATQALQAFFSPSNLTALRELAMQTAADRVDSDLRDTQAARGLPGTAALRRRVVVAIDGRGSSDYLVRVARRLSERRDAPWTVVTVQTRTVTDAAWRLEIDRAFALTRRLGGDTSLLHGTNVADALLDFAAQNGISTLVLGRTRERPLARMFNRTLTQQLLQRGAHYELVIVSSADARARARQRWRHPRQWLQRYDLVFAAIAAAGAVGVAWLLQRWTDINDLSMVFIVAVVLVASRTRMAAAVVAALLSFVAYNFFFIEPRFTLQISARQGVVTVCMFLIAALVAGRLASRLRSQVLALRAANAHANVLQALARQLSTAADLGQVLEAGRRALATALDADVWLRLEQRESDAPTSFGALDRSAADWTQRHGQPAGRFTDTLAGAQWWCLPVRHERGTLGVAALRFRQGVQRPGLEQRRLAEAMVEDIGQAALRTRLVADLEGARVSGETERLRSALLSSVSHDLRSPLASMIGSASSLASYGDAMDAHDRHSLLDTIQLEGERLDRYIQNLLDMTRLGHTGLTVNRDWIGVDELIGSATRRLQRYQPDVRLQLDLAADLPAIWVHPALVEQAIFNVLENAAKFSPPGIAVTVQATLRSGALQIDIGDQGPGIPEDERARIFDMFYSVERGDRGRNGTGLGLAICQGMIGAHGGSVEALAGAHGHGTTIRITLPLLVPAAPPRPDAD	19~~KdpD (1.39335E-114)~~229;X;251~~Usp(1.74718E-26)~~372;X;411~~DUF4118 (0.00000977775)~~495;X(155);650~~HisKA (0.000000000206875)~~716;X;770~~HATPase_c (3.8803E-23)~~872	KdpD protein

	6E-08	42.3	12.6	1E-07	41.5	8.8	1.4	1	F4CT89_PSEUX	Histidine kinase (EC 2.7.13.3)	Psed_4144	Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	857	675635	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Pseudonocardia, Pseudonocardia dioxanivorans, Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	>tr|F4CT89|F4CT89_PSEUX Histidine kinase OS=Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190) GN=Psed_4144 PE=4 SV=1MMAVGQGVERVGRAGELRIYLGAAPGVGKTFAMLGEARRRCERGTDVVVGLVETHGRPRTAELLEGLEVLPRREVVRGGNVLTELDVEAVLARRPDVVLVDELAHTNAPGSRHAKRWQDVEEILAAGIDVLSTVNVQHLESLNDVVQRITGVRQRETVPDGFVRRAEQIELVDITPEALRRRLAHGNVYAAEKVDAALANYFQPGNLIALRELALLWVADEVDVALQRYRSDKHIRETWETRERVVVALTGGPESETVLRRAARIAKRAGQADLLAVHVLRGDGLAGAPVGAAARLRTLADDVGASFHTVVGDSGASGVTDSLLEFARGVNATQLVLGTSRRSRLARLFDPGIGARVVQESGSIDVHMVTHDAAGSALRLPTLRSNVPGGRRMLGWVLCVLAPVAATALGVALRGIVGLSTDVVLFFLATVVAALVGGLGPALVAAVLGVLMLNFFLTPPLYSLTIGETENVVTLVAMLLVAVLVALVVDRAARRAEQAARARTEAALLASFARTVLTRADPLPRLLEKVREAFGLRCVALLERGDGAAGWARIAVSGPAECGRPEDAEVDVAVEAGLHLVGTGRSLPAHDRRLLEVVGGGQALVALRSQRAAADAVAAQRRAEANETRSGLLSAVGHDLRTPLTSIKASAGSLRDPSLPLSDADRAELAATIEESADRLTGLVDNLLDSSRLAAGAVTPLLEPLGYAEVVARALLGLPGAERIDLDVAEDLPDVCADAGLLERVVANLLDNALRHGDGAAVAVRGSAYADRVELRVVDAGPGVPPRQRDRLFTPFQRLGDRGTGTGLGLSVARGLTEVMGGTLTAEDTPGGGLTVVVSLPAVALRSSGSTAPGSTAH	12~~KdpD (5.88155E121)~~222;X;244~~Usp(5.29401E-20)~~370;X;396~~DUF4118 (0.00000000100383)~~474;X(151);625~~HisKA (0.000000000000943728)~~691;X;741~~HATPase_c (2.01265E-24)~~839	KdpD protein
	6E-08	42.2	3.7	1.2E-07	41.3	2.5	1.5	1	R7JU44_9FIRM	Uncharacterized protein	BN630_00105	Blautia sp. CAG:37	726	1262757	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:37	>tr|R7JU44|R7JU44_9FIRM Uncharacterized protein OS=Blautia sp. CAG:37 GN=BN630_00105 PE=4 SV=1MIVFLVGGESRLMDALITKMEKDGHKTYLLTGKRDGRGKYRRVFERYNFPYDSESVREIFTNVNPDLVIFLGAYDTNYDWSDARRESVRYTADLTNLLSAYAFKQNGRFVYLSSEVVYGRSYSSDIHETEPASSKSFQAMAILQGENICKSYRDTREMDTRVLRFDHMYDIPRKGKADNNPCFQMMLEMLKTNQIAANSRNVFSMIYQSDAVEFAYRVMMAEHPKYPLYHISSGEVISQMKLAELIQQNAGDGTTIRDDTVGEGYRLVLDGRRYRKEFDGKIFVPYEEGVKAVVEYMKKYSSSFLQREDTGAGWGNRVWRLLVRIFRMLAPYLENLICFIPFFMIHNRAVGSQYFAKLDAYLLYVLLFAIVYGQQQAIFSALLATAGYCFRQMYNQSGLEVLMDYSTYIWMAQLFILGMVVGYMRDQIIHHIKKDDQEEIGYLHGQLGDMTEINDSNVRMKQIFELQLVNQKDSLGKIYEITSSLDQYGAYEVLFYAAQTISKLMNTEDVAVYTVANQSYARLFSFTSPTARKLGNSIRYPEMEAMYTDLKERRVFINKTMDERYPLMAQAIYAEDEMQIILMLWGLPWDRMNLAESNRLTVISYLIQNAVVRANRYLEALREHRYLGNSSILEKEAFTQLVSAFFEAKRNGLTECSLVKITCGEEKYLEAAEVLGKKLRQTDYVGMLDGGLYVLLSDTEEKNALGVITRFAEAGYESTIANGEVAA	1~~NADB_Rossmann (0.00000000256636)~~300;X;331~~DUF4118 (0.000000000000135518)~~426;X;491~~GAF (0.00000000876753)~~612	non-KdpD DUF4118 protein
	6E-08	42.2	7.6	1.2E-07	41.3	5.3	1.4	1	S0PGB6_9ENTE	Sensor histidine kinase KdpD	I573_00527	Enterococcus sulfureus ATCC 49903	858	1140003	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sulfureus, Enterococcus sulfureus ATCC 49903	>tr|S0PGB6|S0PGB6_9ENTE Sensor histidine kinase KdpD OS=Enterococcus sulfureus ATCC 49903 GN=I573_00527 PE=4 SV=1MEENEYIHIDKGEGKFGKLRIFFGFAAGVGKTYAMLVEAHELQEIGKNIVIGYIEPHDRPETNRLIAGLPNIPTKKIHYKTLELNEPDVDQIIKQKPDIVLIDELAHTNAYGSRNKKRYQDVEEILKAGIDVFTTMNVQHIESLHDIVAQVTGIDVQETVPDTCLQQALIKVVDVEPEELIDRLEQGKIYADHAIKQALANFFIPEKLEKLRGLAIQRASDHINRINSKTLGIQSNLLTIVYDDFPKMSEKCIRWTARLAQGFHAEWTVITIKTQEEIEPSSTLAEKLGAKVIVIEEENSFETIIEFSKMTGVTDIIMGKNIKQHWYENVFAESFENRLLKRLQDTELHLIPFHESKKVWRFNYQEMLTDSGRNASIAVGGVICATLITEGMKFLHVGDQNLMLVYILFVLLIARATSGYVWSAISSIISVLAFNWFFVEPLYSLTVYKQGYPITLLIMFAVALMVSNLMVRLKKQAQTAIAKEKQMEILYELSKKFILTENRAQILAISTTYLSRLLDREIAIFDAKGQVEHVHCVEEQTSVLSEKAEAAVAYWTAKNQKEAGHKTDTLIGAKGYYLPILTRGNTLAVLGIKTIDEPPLTNDQFNYIKLVLAQIAIVLEQNELKQEKNAIQIENAQEKVRSNLLRAVSHDLRTPLTVISGIAQMLEQGNKLDPEMQKRFLQDIQVEAQWLIRMVENLLSITRIDSTTMDVEKTAEPVEEIMEAVYQHIKKVYPKAQLNIDLPEEMLFVQVDPILIEQALFNLVENALRHGQPQELIRISIYQDLDQTVFEIENKGEVPFKQFQKLQANLTQTYEVPVDSKNGLGIGLSIVKTIVHAHHGRINMTVNNGKTCVQIFLK	14~~KdpD (2.25389E106)~~223;X;246~~Usp(1.89935E-28)~~352;X;377~~DUF4118 (0.000000000000410087)~~476;X;505~~GAF (0.000000391001)~~620;X;638~~HisKA (2.68369E-14)~~703;X;756~~HATPase_c (6.72213E-14)~~857	KdpD protein
	7E-08	42.1	14.2	1.1E-07	41.4	9.9	1.4	1	A0A059MKD5_9NOCA	Histidine kinase (EC 2.7.13.3)	N505_01024930	Rhodococcus sp. BCP1	848	931223	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. BCP1	>tr|A0A059MKD5|A0A059MKD5_9NOCA Histidine kinase OS=Rhodococcus sp. BCP1 GN=N505_0124930 PE=4 SV=1MTGTARTAAPEASRRGRLRIYLGAAPGAGKTFAMLGEAHRRIARGGDVVVAIVNTHGRARTAEQLAGLETVPPRRIGYRDAVFEELDLDAVLARRPAVALVDELAHTNVPGSRHAKRWQDVEELLDAGIDVLSTVNIQHLESLNDVVEQITGVVQRETVPDDVVRRADQVELVDITPQALQRRLAHGNVYAPEKVDAALRNYFREGNLTALREIALLWLADQVDLALAKYRGEHAITDTWEARERVVVAVTGGPESETLVRRASRIAAKASAELMVVHVVRGDGLTGVSAPQMGKVRTLAASLGASLHSVVGDDVPTTLLDFAREVNATQLVLGTSRRPRWARILDEGIGAAVVRDSGKIDVHMVTHEHTARGPRMALLGRHERRLQSWIAAFVIPVVATGVMALIDHFTGFEGQHTLYFVVVLAVALFGGIGPAIVAALLSALLLNFFFTEPRYSFTIAEPANFVTTVVLLVVAVAVAALVDAAAARARAERLASQEAELLALFAGAVLRGADLPRLLEKVRETYAQHGVSLVRTDREPAQVLGTAGSAPPTSMQAADTVCEVDDSAYALLLGGPQLRARDRRILTAVAGQAAGLVRQQELAAEAARASALAETDRLRRLLLSAVSHDLRTPLAAVKAAVSSLRSTDVEFSPEDTAELLATIEESTDQLTGLVSNLLDSSRLAAGVITPVLQPVYLDEVVHRAMVTLSSGGSDTARNVRERIEVDVDDTVVAADSGLLERVLANLLDNALRYAPTGPIRVGAGTSGDRTTVTIADCGPGLAPGDTGNVFAAFPRAGDHRSSRGAGLGLTVARGFAEAMGGTVTATETPGGGTTMVVELAAAPARVPR	13~~KdpD (2.54674E121)~~223;X;245~~Usp(9.77689E-34)~~366;X;389~~DUF4118 (0.000210512)~~467;X(149);616~~HisKA (0.000000000000461332)~~682;X;739~~HATPase_c (7.91696E-25)~~839	KdpD protein
	7E-08	42.1	5.2	1.1E-07	41.4	3.6	1.3	1	R6CHZ4_9FIRM	NAD dependent epimerase/dehydratase family protein	BN708_00156	Firmicutes bacterium CAG:56	720	1263031	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:56	>tr|R6CHZ4|R6CHZ4_9FIRM NAD dependent epimerase/dehydratase family protein OS=Firmicutes bacterium CAG:56 GN=BN708_00156 PE=4 SV=1MNILLVGGTCSLMNNIILKLRKEGHRVFLLTGDKYKHSKYEKVFERYDFPYDSENLNEIIESVNPDVTILLGAFDTNYLWNGEERETVHFISHMVNILVAYSVVNRGKLIYLSSDEVFSGDYPDDITEGEKFSGYGIRPAALSQAEELCENFRVNRGLDITVLRLDHLYSIPKDKNDINNICAGMCLEYLRDGYIKADENHTFSMLYEKDAVEYIYKVVKSKKRAHSIYHLSSNDVVNEVELASWILQAMQSEANIVTTPGKNGRCVLSGRKFEEEFDVYTFCDCKKTIEKMALYMQKHKDVFVNEDKEGSILKNLWEKWKWLVRALVPFIENLICFIPFFMLNNRTVGSQYFANLDPFLLYVLLFAIVYGQQQATFSAICAVAGYMFRQMYTRTGFEVLLDYNTYVWIAQLFILGLVVGYMRDQIRTMRAESAELEEHLSRQIVDIRDINESNVRVREVMEQQLVGQKDSLGKIYSITRQLDQSMPDKVVFHAVEMLTKLMETKDVAFYSVVNDDYARLFSASSEKARSLGNSIRYREMTEIYDELLEEKVYINKTMDERYPLMVRGIYEDGKLQMVIMLWGLNWEKMTLGRANFLTVVSYLIQNAVLRAQRYIQALEEKRYSHGSRILEKDAFESLVQAYVKAEEKNLVECTLLKVCVQSEQYQEVGRKMVEKMRDSDYIGIMEDDQLYVLLANTGQENAVIVQKRFEENGYRTEIVE	3~~NADB_Rossmann (0.0000000802396)~~232;X;329~~DUF4118 (3.77757E-16)~~427;X;487~~GAF (0.000000000359385)~~610	non-KdpD DUF4118 protein

	7E-08	42	5.2	1.3E-07	41.2	3.6	1.3	1	R5WPC9_9FIRM	Uncharacterized protein	BN568_01735	Blautia sp. CAG:257	666	1262756	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	>tr|R5WPC9|R5WPC9_9FIRM Uncharacterized protein OS=Blautia sp. CAG:257 GN=BN568_01735 PE=4 SV=1MEDTRPDSEYLLKKLQYEEEQKLKKNKGKLKIFLGYAAGSGKTYTMLEAAHEAKKHNTDVVAGYIEPHDRPDTRRQAEGLETIPPLVVEYKGVKLREFDLDRALERKPQLILVDELAHTNAPGCRNEKRYQDVKELLRAGIDVYTTINIQHLESLNDLVGSITHIEVRERIPDSVFDHADQVEVIDIEPEDLLARMKEGKIYKPVQAERAMNNFFKREKLAALREITLRRTADRVNRIAEEERNITGDMDYHTGEHILACISAAESSAKVIRSAARLAYAFRGQFTGLYVETPAMQEADEKTKQGVRRNMELARALGAKIVTVYGSDIGSQVAEYAMVSNVSKVVLGRTNHRFFMRKPMAEVLEKLNSMAPNIDVYIIPDMKNRKAAGKYGHREGRRKAENAGMQALWEFGLINIILVLTTIAAWILQKFHLPESNIIMVYILGVLLSSYISDKKIYAVYSSLFSVLAFNFLFTEPYFSLKAYDKGYPTTFAMLFIVGLFTASQTRKLKLQNKESVKKAYRTEILLENSQKLRRCKSEKEVWQQAAAQVEKLLDLSLVIYPVNKDGLLGEAMLFPRQGTEKASLEPLLTSQEKAVAKWVAANHHRAGACTHTLPTARGMYLPVQDEEQVKGVVGIFLEERRQIQEFKYGLLIAMLNETGVKLKDRF	32~~KdpD (1.56142E-119)~~235;X;256~~Usp(3.21524E-31)~~379;X;415~~DUF4118 (7.52405E-15)~~507;X;537~~GAF (0.00000373654)~~662	KdpD protein
	7E-08	42	6.3	1.1E-07	41.3	4.4	1.3	1	U5RTD5_9CLOT	Histidine kinase (EC 2.7.13.3)	CAETHG_1797	Clostridium autoethanogenum DSM 10061	911	1341692	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium autoethanogenum, Clostridium autoethanogenum DSM 10061	>tr|U5RTD5|U5RTD5_9CLOT Histidine kinase OS=Clostridium autoethanogenum DSM 10061 GN=CAETHG_1797 PE=4 SV=1MEVIIIDYNERPDPYRILNKVEKEDSESERGKLKIFFGYAAGVGKTYSMLREAHDIKNLGKDIVIGYIESHERLETMDLTKGIESINTKVIDYRGVILKEFDLDAALLRKPEIILVDELAHTNAKGKRHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDVVESITHISVRETIPDKVFDNADKVEIIDIEPDELLKRFSDGKVYARDQVKSAFHNFFTKSNLYALREIALRKTADRVNYEIETARLSKGQITVVPASDQILACISSSPSSLRVIRTAARMAEVYHSKWIVVYVETTKSQKLSKEDRKRLNSYFNLGEQLGGEVVTIYGDDIADQVIQYAKFRNITKIIIGKNNKKTSKVFHFYAKDVVDKLMDSNSYIDVYYVIPNSLYDRKSNKITKKFSKEFNLSLKEAIKAALILSIVTCAAIIFDYVGFSEANVIMIFILGVIIVYMQTTGYLMGIISSLVGVSIFNYLFVPPKRSFHFYDKNYLITFIMILIEAFVIGNLTNKIQQDADESYTREKRTQTLYRVTSKLLSAVGNSDVVSIAIKYLSRLVDRTVVCYLSIDNKLSTPFVYYLDELKKDDLILNKDEAAVAYWSFLKGREAGSGTDTFYGARGYYIPVKVQNKILGVIGVSCEKDFLSHDQKFIVETVTGQMAIALDREILVGQQEKSKVEIERERLRSNLLRSISHDLRSPLAGIKGAVSTIIENGKFIPEKTKEDLLNGIYDDTEWLISLVENLLSMTKFDEGNMKINKNLELVEEVVSEAVQRSSKYFKDHKIKVEVPKKLIMVPMDGNLIEQVLINLIQNAAKFSKKQSFIQIKVYESVDDVFFEVIDDGIGISDKILPHIFDRFFTNGSSIADSRRGVGLGLTICKSIVEAHCGTIEAENKKEGGAIFRFNIPKGESTSNELM	28~~KdpD (9.15649E-123)~~238;X;261~~Usp(6.68043E-43)~~385;X;412~~DUF4118 (0.000000000000279045)~~512;X(166);678~~HisKA (0.000000000163033)~~744;X;797~~HATPase_c (3.12919E-26)~~900	KdpD protein
	8E-08	41.9	13	1.6E-07	40.9	9	1.5	1	R7RTY1_CARML	Histidine kinase (EC 2.7.13.3)	kdpD BN424_665	Carnobacterium maltaromaticum LMA28	897	1234679	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium maltaromaticum (Carnobacterium piscicola), Carnobacterium maltaromaticum LMA28	>tr|R7RTY1|R7RTY1_CARML Histidine kinase OS=Carnobacterium maltaromaticum LMA28 GN=kdpD PE=4 SV=1MQEEDIRPDPDQLLLQVGQDEETTMGKLRVFFGYAAGVGKTYGMLKEAIEQQETGKVVLAGYVEPHARPETMALLDHLNQLPSKKIPYKNMMLEEFDLDEALRLQPEIILVDELAHTNALGSRNKKRYQDIEELLQAGIDVYTTVNVQHIESLNDIVEDITHVRVHETVPDSFFDEALIKLIDVEPDELLGRLKEGKIYRPEHAKKAMNHFFTKENLKLLREIAIRRAADHIGMDNRIEEAYTEKRAHVKLLTCIDSEHQTGAEKCIRWTARLANAFRAEWVVLHVDESGDNEKSEAELALLKRNNELAERLGAEVVTLSGHNPVTTIAQYAKLTGVTDIIIGKHRRKLDYQRLLKDDIEDRLIKHLSNVELHIVPFIEKYPRIKNRFFSKERLIPKNLTIADSLKTMVLLLMATLLSEIFSFLGIGDQNVIVVYLLFILIISQVTTGYFYGVLSSIISVIFFNWFFVDPLFSLTVYKAGYPITLLIMLMVALFTSNMMIRVKSQARESIKKEHQMGVLYDFNKKLLATRNLNGIINLTNDYLVSTMNHSVIFYTEQGKNLLNHKALAFENKQDIEVLTGSDEEAVANWVFNNQKVAGYGTDTLMGAKGFYLPVLSQGRVLAVIGVLLSKENPLTHENLNFLKLIASQLSLALERQYLVTEQQQIMLETEKEKMRSNLLRAISHDLRTPLTGILGASSAILENKDKFDEELKLSLIKDIKEDSEWLIRMVENLLSVTRIDEGTMKVKKMPEAVEEIVAGAVRRIRKRFKEQELIVKVPDEFLLVPMDGTLIEQVLINLMENAIKHSGSKGAISVIVKRNRNKAIFEVTDNGIGIPEKKLASLFDQFGKESDTPIDATRGMGIGLSICKTIVAAHSGTIEVTNKQQGGAVFRFTLPID	26~~KdpD (2.88189E-111)~~232;X;250~~Usp(2.98447E-36)~~376;X;405~~DUF4118 (7.18311E-15)~~505;X;551~~GAF (0.00000000280051)~~655;X;672~~HisKA (0.0000000000518188)~~738;X;791~~HATPase_c (1.95015E-29)~~894	KdpD protein
	8E-08	41.9	11.1	1.3E-07	41.2	7.7	1.3	1	R5SZN3_9CLOT	Histidine kinase (EC 2.7.13.3)	BN771_00813	Clostridium sp. CAG:75	657	1262836	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:75	>tr|R5SZN3|R5SZN3_9CLOT Histidine kinase OS=Clostridium sp. CAG:75 GN=BN771_00813 PE=4 SV=1MNQKIEDDTQKADDHILVCLSAAPSNLKIIDTAAKMANALQARFTALYVQTGTKAEAMDKEKLGEHIRYAETLGAEIVMTHGENVPVQIAEYARLSGVTIIVIGQSNARRNHFFSKSTLTEKLIEIIPDIDIHIVQDAVKNRTYSKRSFTELAEKPSVKDYVLTAFIFVVCTLIGLLFQKLDFTDTNIVTIYIFGVLITSIVTDGYFCSIAGSFLSVFLFCFFLTEPRMSFQTYAVGYPVTFLIMLISSVLTGTLAAKLKTHAKLSAQLAFRTQILFDTDRLLQREKGETEILGVTCTQLIRLLNRNITAYIVKNGTLSEGKLFSGEKENSDDFLTQEEQDVARWTYENRQRAGVSTHHFPQAKCLYLAIRSGNNVYGVIGIPMQKETLDSYEYSILLSVINGCALAMENAQNAMEKEKNAILAKNEQLRADLLRAISHDLRTPLCSISGNADMLLGNSERLDEATRHQIYTDIYDDSEWLIGVVENLLSITRLNDGRLKFKFTDQLLDEVIAESLRHISRKHDDYKIMTDCEELVLVRMDVQLIQVLVNLIDNAIKYTPPGSVICIRGIKTEGKAQISVEDNGPGIPEEMKSHIFEMFYTGKTTVADSHRSLGLGLALCHSIIEAHNGTLILTDHAPHGCNFIFTLPLSEVTLNE	non-KdpD DUF4118 protein
	8E-08	41.9	11.8	1.3E-07	41.2	8.2	1.3	1	K0K8R8_SACES	Histidine kinase (EC 2.7.13.3)	kdpD BN6_59730	Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	897	1179773	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix espanaensis, Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	>tr|K0K8R8|K0K8R8_SACES Histidine kinase OS=Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764) GN=kdpD PE=4 SV=1MPLARSVEPGARGGGQAPDAVVYAFLARLDGHAEVRRHGEHTVRVDGKRKRGELRIYLGSAPGVGKTFAMLGEAHRRRERGTDVVVGLVETHGREKTARLLDGLEQLPRTAFGHRGVEFGEMDIDALLARAPEVAVVDELAHTNVPGSRNVKRWEDVEELLDAGIDVLSTVNVQHLESLNDVVQRITGVAQRETVPDEVVRRAEQVELVDITPEALRRRLAHGNVYAAHKIDAALGNYFRLGNLTALRELALLWVADQVDVALQRYRTEQHITDTWETRERVVAAITGGNESETLIRRARRIAVRAGADLMVVHIMRGDGLTGASPQVVGKLRKITEDVGATFHTVVGDDVPTALLDFARGVNATQLVLGTSRRSRLARVFDEGIGAAVIQSSGPIDVHMVTHAESRRGPRWTVGRNPLTRGRVLLGWALAVLLPLAVTGLGVLSRDDLTFSTDLIGFFLVTVVVALVGGLGPAVGAALFGAGLLNFFFTPPYYYSLAVATPENLITLLAMLTVAVLVALVVDRAARLAEQGARARTEAALLASYARTVLTSPYPLARLLEKVRENFGLESVALLERRGGEWERVACVGPRPCDEPDEADADVPVTSDVHLALRGRTLPAGDQRALEAAAGQALMALRQQRMAAETADAQRRAETTELRTALLSAVGHDLRTPLTSIKAAIGSLRDDTLPLSPEDTEELLETVEVSADRLAGLIDNLLDSSRLATGAVRPVLRAVTFDEVVARALAGIDDRRLVSVDVGEQLPQVRADVGLLERVVANVIDNALRHGRLSPRRLVDVDGDGAITADEPEVAVRASAYGDRVELRVVDHGRGLPKNTADAVFAPFQRLGDRDSTPGVGLGLSVAKGFVDAMGGTIVAEDTPGGGLTIVISLPVAEVAVA	50~~KdpD (3.3736E-118)~~259;X;281~~Usp(3.48495E-22)~~402;X;428~~DUF4118 (0.0000000000104288)~~511;X(145);656~~HisKA (0.000000000000873546)~~721;X;771~~HATPase_c (1.38623E-23)~~889	KdpD protein

	8E-08	41.8	11.1	1.2E-07	41.2	7.7	1.3	1	R6WIR0_9FIRM	Histidine kinase (EC 2.7.13.3)	BN546_00018	Firmicutes bacterium CAG:227	657	1263010	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:227	>tr|R6WIR0|R6WIR0_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:227 GN=BN546_00018 PE=4 SV=1MSFKAEENNKELSEHILVCLSAAPSNKKIIDTAAKMVKVLQARFTALYVRTGTKSEVLDKEKLEEHIQYAEKLGAEIVMTHGENIPVQIAEYARLSNVTKIVIGQSNARRNHFFSKATLTERLIEIVPDIDIHIIPDALKTRTHQKRSFARYVEKPSAKDYFLTVIIFAVCTLIGLLLFQRLNFTDTNIVTIYILGVLLTSILTDGYLCSVVGSVISVFLFCFFLTEPRMSFQTYAVGYPVTFLIMLISSVLTGALAAKLKTHAKLSAQLAFRTQVLFDTDCLLQKAKGGTEILDITCTQLLRLLNRNITAYVVENGNLSDGKLFSVEKESAKNILTPEEQGVARWVYENRQRAGASTHHFPQAKCLYLAIRGGDNVYGVIGIPMQKETLDYFEYSILLSVINECALAMENAQNAMEKEKNAVLAKNEQMRADLLRAISHDLRTPLCSISGNADMLVNNGDRLDEATKDQIYTDIYDDSEWLIGVVENLLSITRLNDGRLKIKFTDQLLDEVIAESLRHINKKHDEYKIVTDCEELVLARMDVRLIIQVLVNLIDNAIKYTPPGSIICIRGIKADGKAQISVEDNGPGIPDEMKPHIFEMFYTGKTTIADSHRSLGLGLALCRSIIEEHNGTLVLTDHAPHGCNFIFTLPLSEVTLNE	30)~~136;X;161~~DUF4118 (2.64611E-14)~~262;X;291~~GAF (0.000306853)~~410;X;427~~HisKA (0.000000000334408)~~493;X;545~~HATPase_c (1.34321E-27)~~648	non-KdpD DUF4118 protein
	8E-08	41.8	7.7	1.4E-07	41	5.3	1.4	1	B4RHL5_PHEZH	Histidine kinase (EC 2.7.13.3)	PHZ_c2647	Phenylobacterium zucineum (strain HLK1)	485	450851	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Phenylobacterium, Phenylobacterium zucineum, Phenylobacterium zucineum (strain HLK1)	>tr|B4RHL5|B4RHL5_PHEZH Histidine kinase OS=Phenylobacterium zucineum (strain HLK1) GN=PHZ_c2647 PE=4 SV=1MQRSMGRVRREWRDQLSRYGAALALVAASTAVAEALYRLTATTRLSMVFLAGVLLAAFLLGSGPAYFAAAVAFLVYNFYLVEPRFTIELTTPEELLTLLVFLAVAMLTGNLTGRVRDEAARAEARARATTALFDATREFSASSDEGLIRQRLAEHLAATAGGEGFVRDAGRLQMAPAGLRREDIPGGLPGAAEPAGGWTLRRLEVEGQALGTAGWRAPPDRRLSRDEHDLLELMCDAGAAAIARARLAAGKAEAEARARTEDLRNALLSSISHDLRTPLAAILASATSLREFGDSFDPGVRRDLAATIQEETERLDAVVANLLSMTRLQAGALAIQKAPFNVPEVVRRTVERRDRAHRRFTLTSITPRLPEGLGDPILFEQALGNVVENALRHTPEDTLVLVSMRLEDDRIVVDVCDRGPGVGEADLERIFDRFYRAGGARQTPGTGLGLSIARGLMEAMDGAIEARNDPAAGGLVVSLSLESAA	18~~DUF4118 (0.000000000002618 84)~~117;X(144);261~~HisKA (0.000000000053158 6)~~327;X;379~~HATPase_c (1.40485E-26)~~481	non-KdpD DUF4118 protein
	8E-08	41.8	5.6	1.4E-07	41	3.9	1.4	1	R7ISI7_9FIRM	NAD dependent epimerase/dehydratase family protein	BN596_02091	Roseburia sp. CAG:303	725	1262944	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:303	>tr|R7ISI7|R7ISI7_9FIRM NAD dependent epimerase/dehydratase family protein OS=Roseburia sp. CAG:303 GN=BN596_02091 PE=4 SV=1MNILLIGGEGSLINSMIVKLKKEGHRIYLLTGVQNKKVTYEKVFEKYNFTYDSENLNDIFESVNPDVTIFMGAYDTNFQWKQQEREAVRYSSSLMNILVAYSMTKRGKFIYLSSEEVYSGSYPAEIREDEPVSAVGFRGMTLAQGEKICENYQENWKLDIIILRLDHLYHIPRTSADVDNICARMCISAMEKGYIIADNQNICSLLYESDAVEFIYRVVKCKTHQHVLYHLTSDRRFREVTLARLVAEYMGGNVSVVENEEQGGRRILSGRRFEEEFGITAFRETEVVLKKMVQYMKKNEAVFLDKEEPRLSLWKRVLQKWGWFFRAIVPFLENLLCFVPFFMLNNRVVGSQYFSQLDFYLLYVLLFAIVYGQQQATFSALLATAGYLFRQTYTRSGFEVMLDYNTYVWIAQLFILGLVVGYMHDQIRRIRKESEELEAHLSRQLSDIRDINGSNVRVKDVLERQVIDQKDSIGKIYNITSRLDQYMPDEVLFYAVEMLTELLGSRDVAIYSIANKDYARMFSAGSVKAREMGNSIRYREMGEVYQEISAQRVYINRRMDEHYPLMANAIFEEDQMKMIIMIWGISWERMTLGQANLLKVISYLIQNAVLRANRYMMALEEKRYLEDTRILEPEAFTSLAGAYQKARKRNLTECSFLKIETDPSHYLEAGKVLKGNLRQSDYMGNLKDGGLYVLLANTNREEAGIVVERVEEKGYKSQIVERVEL	3~~NADB_Rossman (0.000000291241)~~231;X;330~~DUF4118 (2.78011E-15)~~429;X;488~~GAF (0.00000000309066)~~611	non-KdpD DUF4118 protein
	9E-08	41.7	10.7	1.4E-07	41	7.4	1.4	1	R7JW51_9CLOT	Histidine kinase (EC 2.7.13.3)	BN584_02244	Clostridium sp. CAG:277	657	1262790	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:277	>tr|R7JW51|R7JW51_9CLOT Histidine kinase OS=Clostridium sp. CAG:277 GN=BN584_02244 PE=4 SV=1MNQKIEDDIQKADDHILVCLSAAPSNLKIVNTAAKLANTLQARFTALYVQTGTKAEARDKEKLEEHIRYAEKLGAEIVMTHGENVPVQIAEYARLSSVTIIVIGQSNARRNHFFSKSTLTEKLIEIVPDIDIHIVQDAVKNRTYSKWSFTGPAGKPSAKDYVLTAFIFAICTLIGLLFQKLNFTDTNIVTIYILGVLLTSIVTDGYFCSIAGSILSVFLFCFFLTEPRMSFQTYAVGYPVTFLIMLISSVLTGTLAAKLKTHAKLSAQLAFRTQVLFDTDRLLQREKGETEILGVTCTQLVRLLNCNITAYIVKNGTLSEGKLFSGEKENTEDFLTQEEQNAARWIYENSQRVGVTAHYFSQVKCLYLAIRSGNNVYGVIGIPMKKETLDSFEYSILLSVINECALAMENAQNAMEKEKNAVLAKNEQLRADLLRAISHDLRTPLCSISGNADMLLSNSDRLDKATRHQIYTDIYDDSEWLIGVVENLLSITRLNDGRLKFKFTDQLLDEVIAESLRHISRKHDDYKIMADCEELVLVRMDVRLIIQVLVNLIDNAIKYTLPGSVICIRGIKTEGKAQISVEDNGPGIPEEMKPHIFEMFYTGKTTVADSHRSLGLGLALCHSIIEAHNGTLILTDHAPHGCNFIFTLPLSEVTLNE	15~~Usp(1.22593E-28)~~135;X;161~~DUF4118 (3.08362E-14)~~262;X(165);427~~HisKA (0.000000000565747)~~493;X;545~~HATPase_c (9.42526E-28)~~648	non-KdpD DUF4118 protein
	9E-08	41.7	10	1.3E-07	41.1	6.9	1.3	1	R6QGF3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN583_01050	Anaerostipes sp. CAG:276	902	1262699	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, environmental samples, Anaerostipes sp. CAG:276	>tr|R6QGF3|R6QGF3_9FIRM Histidine kinase OS=Anaerostipes sp. CAG:276 GN=BN583_01050 PE=4 SV=1MEEEMRRNPDRILKQIHREETEQARASGKLKIFFGYAAGVGKTYSMLKAAHDALEQGRDTVIGYIEPHTRPETMALVKGLETVPVKEIEYYNGMNLRELDLDGVIKRHPQLVLVDELAHTNGMGCRHKKRYQDVEEILKAGIDVYTTVNVQHIESLNDIVASITGVIVRERIPDSVFDNADSVELADIEPEDLLKRLKAGKIYREAQAGKAMQNFFIESNLVALREIALRRTADRVNHISEQQKEQEGKEGYYTDEHILICLSPSPSNQKVIRTASRMSRAFHGKFTAVFVKTEAADKISLDDEQRLVENVRLAEQLGAKITTIFGEDIPEQIAGYAKAAGVSKIVIGRSVNRSVFAARHNFADRLSALAPNLDIYIIPDQQAAPDSGRRTFWNKEKIRVRSEDVIRTASIFVFVTALGLWFQSIGFSESNIITIYILGTLITALVTEYYRFYSLLFSVCSVLCFNFLFIQPLFTLNVYGSGYPVTFAIMLLSALISGNLMTRVKQQARAASIQAYRTGILLETNRRLQNAADREEIIELSSKQMTRLLDRAIIFYDAEDDRLLEPRTYGNKTQTDFSRYLTHEERAVAEWVRKNNKHAGATTDTLPGAKGLYLAVRSADHVHGVIGICLEKTKLDTFEKELMISMLDEIGLALEKDKIAASQKEAELKAQREEFRANLLRSISHDLRTPLTSISGNAGVLRQSSDQISEEKKQELYTDIYDDAMWLINLVENLLSVTRIENGTMKIEKEPEIVEEVILEAVKHIDRRKNEHHIHIRIDDDMMADMDAKLMIQVIINLVDNAIKYTGKGSHIDISAEKKNGKVLIEVADDGEGISDEAKTRLFDMFYTGSKTVADSRRSMGMGLALCKSIVQAHGGTITVRDRKPRGTVFSFELQAEEVIVHG	28~~KdpD (4.19832E119)~~235;X;256~~Usp(5.00128E-32)~~378;X;410~~DUF4118 (1.43606E-16)~~505;X;531~~GAF (0.0000242252)~~654;X;671~~HisKA (0.000000000301534)~~737;X;792~~HATPase_c (2.44051E-27)~~893	KdpD protein
	9E-08	41.7	8.2	1.5E-07	40.9	5.7	1.4	1	F8A3G7_CELGA	Histidine kinase (EC 2.7.13.3)	Celgi_0204	Cellvibrio gilvus (strain ATCC 13127 / NRRL B-14078)	369	593907	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Cellulomonadaceae, Cellulomonas, [Cellvibrio] gilvus, Cellvibrio gilvus (strain ATCC 13127 / NRRL B-14078)	>tr|F8A3G7|F8A3G7_CELGA Histidine kinase OS=Cellvibrio gilvus (strain ATCC 13127 / NRRL B-14078) GN=Celgi_0204 PE=4 SV=1MSNRRNARGPALVVHGAIARRRRVAGFVLAGAGLPVISVLLVATRDDVALGSILLVYLLGVVAVSAVGGMLPGLIAAVLSFGLANWFFTPPLHTLAVEGGDTLIELAVFAVAAVVVAATVELAARDRLRYQQDLDAQVARTRELAAEDRARTALLASVGHDLRTPLASTKAAVSSLRQTDVAWPDDARAQLLATIEDSTDRLARLVANLLDMTRLRSDAVTARVRPIALDEVLARTTLGEHRASVDTVIADDLPLVLVDPGLLERVVDNLVENAVRFSPAGTRVRIRAATGRSGVDLSIVDHGPGIPPERRDEVFAAFQRLDDRDAGSHVGLGLAIARGFTEAMGVDLSPSTTPGGGLTMTLRPPVAPQ	34~~DUF4118 (0.0000000299431)~~106;X;148~~HisKA (0.000000000039029 7)~~214;X;263~~HATPase_c (3.718E-24)~~364	non-KdpD DUF4118 protein

	9E-08	41.7	11.5	1.3E-07	41.2	8	1.2	1	R6PMC4_9CLOT	Histidine kinase (EC 2.7.13.3)	BN618_00203	Clostridium nexile CAG:348	468	1263069	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	>tr|R6PMC4|R6PMC4_9CLOT Histidine kinase OS=Clostridium nexile CAG:348 GN=BN618_00203 PE=4 SV=1MKEKLEKAGSFMITLLLLSVATVIGWTFRVLHFPETNIVIVYILSVVLTARFTKGHVYGIMASLIATCAFNIFFTSPYFTLFVSNPTYLITFAVMTITSVATSTLTAKVKQKVREAQEKEVSARSLYHLTNRLTNAENLNETMEIATKAIGKVVGVEVSCICFDEELEEKEERKNPAFEEWQICGKKSILGVVRIPKENSETLSESEKKILRSMIESTAFAMDRFRSEAERIKVGEEIAQERYRGNLLRAISHDLRTPLSGIMGTSEILMGMTEKQDERYMLAENIYKDAAWLHALVENILNLTRMQDGKLVLKKQMEAVEEVIEMAVKVIGKRAPERDILIDIPEEMLLVPMDARLIGQVLVNLLDNAVKHTKVEEEIRLTVSVDEKEKKAVFSVADKGTGIAKEDIPNVFKMFYTTNRRGADTSRGIGLGLAICESIITAHGGEICVQSRKDTKGAEFIFTLPMGE	11~~DUF4118 (1.20382E-14)~~112;X(129);241~~HisKA (0.000000000114064)~~305;X;358~~HATPase_c (9.27282E-25)~~464	non-KdpD DUF4118 protein
	9E-08	41.6	2.1	1.4E-07	41	1.4	1.2	1	K0B4M4_CLOA9	Uncharacterized protein	Curi_c25110	Clostridium acidurici (strain ATCC 7906 / DSM 604 / KCTC 5404 / 9a)	424	1128398	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, unclassified Clostridiales, Gottschalkia, Clostridium acidurici (Gottschalkia acidurici), Clostridium acidurici (strain ATCC 7906 / DSM 604 / KCTC 5404 / 9a)	>tr|K0B4M4|K0B4M4_CLOA9 Uncharacterized protein OS=Clostridium acidurici (strain ATCC 7906 / DSM 604 / KCTC 5404 / 9a) GN=Curi_c25110 PE=4 SV=1MNTKKTIYCVSETILINVIIYFIFFTKQYNQDVYLSLNPHPLLLLCALMGLRYGNQLGLISAVISSIFYTYVFIQIHGDILTLFRYIDNCKYILLFFGSSMVFGSFKDNYDTRLEKALNENKLIKNRYKKLDESYKLTKKIQEELKKQIINSEESILNLYEIASRLETFELEAIYTETIGILSKYLKANTVSVYTYNEKSGYLRLKIRMGDHVEEKSSKQVQESPGLSKVVLEKIPVRWSDVKEEGFALMAAPLVKDGKVIAIVNVENMDFDKLSEYAYQLFRVIIDWVNKSLQKAMYVGELRESPYIDGTEIMEYRSFEERLEEEKRRKRDFGMEYGLLKYRVEDLQLEDVNEKMKKILRDVDIIGYDKLKKVIYILLPATPEDKLKIVEERILSKVSYGLEKIYDKHYEESESSKKALGAEI	12~~DUF4118 (0.0000908574)~~113;X;170~~GAF (0.0000000033663)~~289	non-KdpD DUF4118 protein
	1E-07	41.6	7.4	1.7E-07	40.8	5.1	1.4	1	R6RPX4_9CLOT	Histidine kinase (EC 2.7.13.3)	BN719_02218	Clostridium sp. CAG:58	876	1262824	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	>tr|R6RPX4|R6RPX4_9CLOT Histidine kinase OS=Clostridium sp. CAG:58 GN=BN719_02218 PE=4 SV=1MTEERQNAGEGGKSGQLKIFFGYAAGVGKTYAMLQAALTAEERGMDVVIGSIAPYRSLEDTALAERLRAMERLEEFDLDQAIRRKPDLILMDDLACENPKGSRHSRRYQDIRELLKAGISVYTTVSAQNIESLNDIVTAITRVPVKDRIPDSVFDHADQVELVDLEPRELLERLRNGALAEKEGEHSPGTAYFTVANLTALREVALRRCADRINMLTRGDGAAHGDEHVLVCLSASPSNAKIVRTAARMANAFRGAFTALFVKTPDLAYMDEEDRKRLQSHMRLAEQLGARIEILYSDDIPFQIAEFARISGVSKIVIGRSAATRDHIFSKPALTEKLISNAPDLDVYIIPDADPGSSFYRKRHFGTRRHLVFSAGDILKSIGILLAASCIGFFFYNLGVNEANIITIYVLGVLVTALVTKNQIYSLISSAVSVLVFNFLFTEPRYTLQAYAPGYPLTFSVMFLSAFITGSLVMRLKSHAKQSAEVAFRTRILFDTNRLLQQARGQEEITSVSAGQLVKLLKKDIVVYPAENGVLGEPQIFQAGETEPDAGCISARAREVEAAWTLKNNKHAGATTDTFSDAGCLYLAIRVGENVYGVGIVMEGGELDAMENSILLSVLGEWAFALENEKSTREKEEAAVLAKNEQLRANLLRAISHDLRTPLTSISGNASNLLAMGQDFDEETRKQLYTDIYENSMWLINLVENLLSITRLVEGRLNLNITEDLVDDVVAEALRHVNKKSAEHTIVTESGEEFLLARMDPRLIVQVIINIVNNAIEYTPAGSHITIRSEKKDGTIILSIADDGPGIPDQEKPRVFDMFYSGGNPIADSRRNCGIGLSLCRSIIDAHGGELTVSDNAPHGAVFTFTLPAGEVQLHE	12~~KdpD (5.33455E78)~~213;X;228~~Usp(3.8871E-38)~~351;X;378~~DUF4118 (0.000000000001945 06)~~477;X(168);645~~HisKA (0.000000000076293 8)~~711;X;764~~HATPase_c (4.38387E-27)~~867	KdpD protein
	1E-07	41.5	11	1.5E-07	40.9	7.7	1.3	1	D4LNL3_9FIRM	Uncharacterized protein	CK1_37150	Ruminococcus sp. SR1/5	292	657323	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, Ruminococcus sp. SR1/5	>tr|D4LNL3|D4LNL3_9FIRM Uncharacterized protein OS=Ruminococcus sp. SR1/5 GN=CK1_37150 PE=4 SV=1MSLKMEDTVKNRTYPKRPFAWYVEKPSAKDYLLTVFIFAVCTLIGLLFQKLDLTDTNIVTIYILGVLITSIVTDGYLCSVAGSFLSVFLFCFFLMEPRMSFETYAVGYPVTFFIMLISSVLTGTLAAKLKMHAKLSSQIAFRTQVLFDTDRLLQKAKSETEILGVTCTQLIRLLNRSITAYVVENGTLSEGKLFSGEKESTEDFLTQEEQQAARWTYENRQRAGASTQYFSQAKCLYLAIRSGNNVYGVIGIPLQKETLDSYEYSILLSVINECALAMENVQNAIEKEKMRF	31~~DUF4118 (0.000000000000727222)~~130	non-KdpD DUF4118 protein
	1E-07	41.4	13.1	1.8E-07	40.7	9.1	1.4	1	C6WFG8_ACTMD	Histidine kinase (EC 2.7.13.3)	Amir_1955	Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	902	446462	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Actinosynnema, Actinosynnema mirum, Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971)	>tr|C6WFG8|C6WFG8_ACTMD Histidine kinase OS=Actinosynnema mirum (strain ATCC 29888 / DSM 43827 / NBRC 14064 / IMRU 3971) GN=Amir_1955 PE=4 SV=1MSVLPSPPVVGTGTRSPPADPTAPTAHTDPVVDTKRKRGELRIYLGAAPGVGKTFALLNEAHRRRERGADVVVGLVEAHDRARTAELLDGLEQIPRRTTHHDGEPRSELDLEAVLRRAPAVVVVDELAHTNPPGAGNPKRWQDVEDLLDAGIDVLTTLNVHHLESLSDVVRRITGVDQRETVPDEVVRRAEQVELVDLTPEALRRRLAHGNVYPAHKVDAALADYFRPGNLAALRELALLWVADQVDVALQRYRADQRITDTWETRERVVVAITGGPESEPLIRRARRIALSAAAELLVVTVLPVAPRATGPDAPDAPSRFRRLTEDLGATYHTVVGDDVPTALLEFARGVNATQLVLGASRRSRLARAFDGGVGAAVIARSDSIDVHMVPHDESPEPPRRHPDRNPLTPSRQALGWLLSVLLPLVVTGIGTALAEDITFSTDLVGFFLATVVVALVGGLGPAVFAALIGAGMLNFFFTQPYYSLTVSAQENLLTLLVMVTVAVLVVDRAARLASQAARARTEAALLASYARTVLAGPDPLARLLEQVRENFAQESATLLERVDHDWTPVASAGPNPCADPDEADVDVPVNPDVHLALRGRPLAAGDRRALEGAAGQALLALRHQRMSAQAEDARRLAETTQLRTALLSAVGHDLRTPLTSIKASVGSLRDVELSLSAEDTAELLEAVELSADRLTGLVDNLLDSSRLATGAVTPVFKAIGYDEAVAAALAGVDERDRVLVEVREDLPPVRADLGLLERVVANVVDNALRHGSRRPAPRASGGPDAAGPGAAGPRVAGPEATTPEVGFPEVAVRASAHGDRVELRVVDHGPGVPRHTTEAVFAPFQRLGDRDAAPGIGLGLSVAKGFTEAMGGAITAEDTPGGGLTIVVSLPAAGPQTP	37~~KdpD (2.53535E100)~~246;X;268~~Usp(2.20991E-29)~~391;X;447~~DUF4118 (0.000000163056)~~499;X(146);645~~HisKA (0.000000000024334 6)~~710;X;760~~HATPase_c (1.92264E-21)~~894	KdpD protein
Disagreement between HMM and CDD prediction	1E-07	41.4	11	2E-07	40.6	7.6	1.4	1	Q92XJ2_RHIME	Histidine kinase (EC 2.7.13.3)	SMa2327	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	896	266834	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Rhizobium meliloti (Ensifer meliloti) (Sinorhizobium meliloti), Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	>tr|Q92XJ2|Q92XJ2_RHIME Histidine kinase OS=Rhizobium meliloti (strain 1021) GN=SMa2327 PE=4 SV=1MPHNDRDLKSRPDPDALLALAEQGRRGKLTVFLGAAPGVGKTFAMLTRARRLKEEGGDIVIGLVETHGRGETAALLEGLEVLPRRQVLHNGRTLHEFDLDAALARRPRVILVDELAHTNFGESRHPKRYQDIEELVDAGIDVWTALNIQHLESLSDVVAHIAGVPVRERVPDTVLNRADDVLLVDLPPAELIERLKEGKVYLPDNAKRAADRFFRLGNLTALRELALRRTADRVDDQMVDYLRQNAIEGPWGAAERLLVCIGPDPLSEKVVRTASRLASSLNADWMVVSVERAEAESSGAMRQLDETFRLAEQLGAETRRIIGNDFVEEILKLARREHATQIVIGTRRHYFPLRLFRRSLPDALAARAAGIAIHLVTDGSAPAVKPAARRRSTLPDGWGRGVAIATGTAAAATALGLLIEQFVVLQNISLLFLLAVLVSATYAGYVAAIAAALISILAYNFCFIEPVGTFTVAEPHEVFALFVFLAAAMLAGGLASRVREQAKTARRRAAATQALYDFSRKLSGTANAEDVLWAAVTQIHATLRRNAALLLPEDGDVRLMAAWPPDTELGLTDTMAGRWAFEKKEAAGNGTGTLPNSPFQFRPLMSPHGVVGVFGFLQEDKPLEINEERALAAILDQTAIAVDRARLSRESLDQAAQLEGEKFLAALLSSISHDLRTPLATITGAVTSLRQLGERMSEESRDDLLKSIEEESGRLTRFVANLLDMTRIEAGTVNAKRDWVDVADVVHSAVERARKYFPGRVFETSIAPDLPLIRGDSVLLGQVIFNLLDNANRFGDEPVSIYGRREEDEIVLSVTDLGKGIAPADLDRVFDKFFRKGKPDGRSLGTGLGLSISKGFVEAMDGRIKAESPAMKRRGTRISMRFPVAETGITEKERG	24~~KdpD (8.07348E127)~~234;X;256~~Usp(5.78793E-34)~~377;X(150);527~~GAF (0.000000387749)~~644;X;661~~HisKA (0.000000000269098)~~727;X;780~~HATPase_c (1.03139E-22)~~883	KdpD protein

	1E-07	41.4	12.4	1.9E-07	40.6	8.6	1.3	1	T0VE02_9ENTE	Osmosensitive K+ channel histidine kinase Kdp (EC 2.7.3.-)	HSIEG1_1767	Enterococcus sp. HSIEG1	492	1316414	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	>tr|T0VE02|T0VE02_9ENTE Osmosensitive K+ channel histidine kinase Kdp OS=Enterococcus sp. HSIEG1 GN=HSIEG1_1767 PE=4 SV=1MDRPTSVDTLKAENRKKGRLRVYFGFAAGVGKTYAMLLEAQELKALGKDVVIGYIEPHDRPDTNSLLAGLPQIPLKEIQYKGITLTEPDIDAIIQQQPAIVLIDELAHTNAEGSRNRKRYQDIEELLNAGIDVHTTVNVQHIESLNDIVEEVTGIEVKETVPDTFFQQATLKVIDVEPDELIDRLAQGKIYANENAKRALQNFFIPKKLEQLRGLAIQRASDHINRISGRTNGIQSKLITIVQDAFPKMAEKSIRWTARLAQGLGAEWTVLYIRSEEKNEATTLAEKLGAEVVVIEEDNYFETIIEYAKLVGATDIIMGKNLAKPWYEKLFVEELDVRLLKRLPDTEIHLIPYKEERASIFSLSKKVIEGGGKDLAIALISVFLATVTTEVMQYLHFGDQNLMLVYIFFILLVARLTSGYFWSALSSILSVLAFNWFFVEPLYSLTVYKQGYPITLVIMLLVALMISNLMVRLKNKLFIQWKKNSRWKYFMS	16~~KdpD (9.28329E-124)~~224;X;247~~Usp(2.57026E-27)~~352;X;375~~DUF4118 (6.33329E-14)~~476	KdpD protein
	1E-07	41.3	12.6	1.6E-07	40.8	8.7	1.2	1	R6LRZ4_9FIRM	Histidine kinase (EC 2.7.13.3)	BN524_01743	Coprococcus comes CAG:19	363	1263070	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus comes CAG:19	>tr|R6LRZ4|R6LRZ4_9FIRM Histidine kinase OS=Coprococcus comes CAG:19 GN=BN524_01743 PE=4 SV=1MMNDGGKKMTKERVKYMVQSIAIMAIATFLSFFLQSYGIRKENILMIYIVGVLVITVTTTGYLYGMMASVCSVLLFNYFFTVPVHTFAMTDQNDVVLLVFFLIAGFISASIMVRFHNQVRIAEETRAQMEREKLKSNMLRSISHDFRTPLTGIMGAAGLLKEADELDAGVRKELAGEIQEQSVWLMRLMENILNMTKLESEEFEIRKNQEVVDDLIYEAVSHIIGLREKRRFEIKLPSELIVVNVDGKLMVQVLVNLLDNAMKHTGENGWICIEARYDAGKVWISVEDDGDGIQEDLKENIFDEFVTRSDEKGDRQRGIGLGLAICKAVVNAHGGNICAENRKEGGARFMFWLEARQVSTDGR	(4.04303E-14)~~107;X;132~~HisKA (0.000000000003347 69)~~197;X;252~~HATPase_c (1.77947E-26)~~353	non-KdpD DUF4118 protein
	1E-07	41.3	7.3	2E-07	40.6	5	1.4	1	Q0RF14_FRAAA	Histidine kinase (EC 2.7.13.3)	kdpD FRAAL5304	Frankia alni (strain ACN14a)	880	326424	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia alni, Frankia alni (strain ACN14a)	>tr|Q0RF14|Q0RF14_FRAAA Histidine kinase OS=Frankia alni (strain ACN14a) GN=kdpD PE=4 SV=1MKKRPVRTFRCFPPRPDGRTMGGVPRGTLRIYLGAAPGVGKTYAALDEARRRRDRGTDVVVGLVETHARHHTAAMLDGLEVIPRRFAEHRGATFTEMDLDAVLARRPAVAVVDELAHTNVPGSRHAKRWQDVQELLDAGIDVISTVNVQHLESLNDVVETITGVAQRETVPDAVVRAASQVELVDMAPEALRRRMAHGNIYAADKVDAALANYFRPGNLTALRELALLWLAGKVDDQLDRYRAEHHIGGTWETRERVVVALTGGPEGETLIRRAARIASRTKGAELLAVHVARSDGLTGADPAALAGQRVLVDSLGGSFHQVIGDDVPTALLDFARAENATQLVLGASRRGRLARILTPGIGVTTTNQSGPIDVHMVTHAEAGTGWRLPRVRSGLTPRRRLVATALTLALVPALTAALVQGRGTLNLATEMLGYLIVVVSVALIGGFWPALLCALASSLLLNYYFTPPLHHWSVAEGNNALALAGFVLVATMVSRVVDLSARRYGQAARAAAEATTLSMLAGSVLRGEDALPALLDRARETFAMTSATLLERDGDGWRAVLSVGPDPCSRPEDGAVDVPVGDTLALTLTGRPLPAADRRILAAFAAQAAVALDQRRLAEAAARAVPIAQADRVRAALLTAVSHDLRTPLAAAKAAVTGLHSTEAVLSRDERDELLATAEESLDRLTRLVENLLDMSRLQAGALSVFPRPIGLDDVVPHALDELGPPARAIAIRIPDDLPTIDADPALLERVLVNLVGNALRHAPAGRPPVITASSLADRVELRVVDHGPGIPADHRDQVFRPFQRLGDRDNTTGVGLGLALSRGLTEAMNGTLTPEDTPGGGLTMVVSLPAAEPPPSLTALDDAELGPATRSPASVDDLA	26~~KdpD (2.81445E-120)~~234;X;256~~Usp(5.7719E-31)~~378;X;400~~DUF4118 (0.000413138)~~503;X(128);631~~HisKA (0.000000000002951 31)~~697;X;748~~HATPase_c (3.94163E-27)~~849	KdpD protein
	1E-07	41.3	8.5	1.8E-07	40.7	5.9	1.3	1	E4U0U0_SULKY	Integral membrane sensor signal transduction histidine kinase	Sulku_0650	Sulfuricurvum kujiense (strain ATCC BAA-921 / DSM 16994 / JCM 11577 / YK-1)	329	709032	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Sulfuricurvum, Sulfuricurvum kujiense, Sulfuricurvum kujiense (strain ATCC BAA-921 / DSM 16994 / JCM 11577 / YK-1)	>tr|E4U0U0|E4U0U0_SULKY Integral membrane sensor signal transduction histidine kinase OS=Sulfuricurvum kujiense (strain ATCC BAA-921 / DSM 16994 / JCM 11577 / YK-1) GN=Sulku_0650 PE=4 SV=1MHPIIPPFLLLIALALISKLFSQELELVNIGMIHLIPILYAAMRLGRRDTLIVSLGSVLSFNFFFIPPTFTFTVHDLRYLFSFVIMIVVGQIVSWLSARAAVAKELETSERLQETLLGSLSHELRTPLSAIMGASSGLLTEELDLNSEQKKELYHTIDNGAFRMRRLIDNLLDTARLQSGMLKLKIQECDIPELLGSTLSKTEHTFPATLTIKDTIGSVQGDAVLIEQALFNLLENAFKYGDAVNVTVENEPIGIKIRICNTGSIPPVHEASMAWKAFSRLSNVQGKEGIGLGLYVAYRIAQMHDGNVETMSDGVQFCATMRLPYRGEG	110~~HisKA (0.000000000000249 168)~~176;X;226~~HATPase_c (3.27041E-14)~~309	No DUF4118 detected by NCBI CDD
	1E-07	41.3	9.5	1.7E-07	40.8	6.6	1.2	1	C4Z7N4_EUBE2	Histidine kinase (EC 2.7.13.3)	EUBELI_20166	Eubacterium eligens (strain ATCC 27750 / VPI C15-48)	362	515620	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, [Eubacterium] eligens, Eubacterium eligens (strain ATCC 27750 / VPI C15-48)	>tr|C4Z7N4|C4Z7N4_EUBE2 Histidine kinase OS=Eubacterium eligens (strain ATCC 27750 / VPI C15-48) GN=EUBELI_20166 PE=4 SV=1MVIITEKTLKKLVKEFLITIGLLSIATVIGMLLIYIGFTESNVIMVYLLCVLLISIFTNGYIWSVAGSLVSVVLMNFFLTEPRFFTLHTYDTGYPLTCVIMLAASMLTGTLASKLKKHVRMSEQAAYREKTLQLRANLLRTISHDLRTPLTSISGNANNLMYNYDKLDNDTREQIFTDIYDDSEWLISLVENILFVTFREDGTVTLNMSDQLIDEVIAEALKHINRKSCEHKIHVDCGKELLLVRMDVRLIIQVIINIVDNAIKYTQEGSDIYIKARKEGRYVIISIEDNGEGIPDDMKENVFDTFFTCNNEIADNRRSLGLGLSLCKTIINAHGSELELRDNTPHGCIFEFKLQLSEVHLNE	(0.000000000000850 57)~~117;X;131~~HisKA (0.000000000073429 5)~~197;X;250~~HATPase_c (9.77795E-26)~~353	non-KdpD DUF4118 protein
	1E-07	41.2	7.8	1.9E-07	40.6	5.4	1.3	1	R5TPN1_9FIRM	Universal stress family protein	BN481_00424	Ruminococcus gnavus CAG:126	550	1263106	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	>tr|R5TPN1|R5TPN1_9FIRM Universal stress family protein OS=Ruminococcus gnavus CAG:126 GN=BN481_00424 PE=4 SV=1MTEENRPDPGLLLKKLQYEEKEKEKQTKGKLKIFLGYAAGSGKTYAMLEAAHEAKKHQVDVVAGYIEPHARPDTQAMAEGLEEIPPLMVDYKGIQLREFNLDAALERKPKLILVDELAHTNVRGSRNEKRYQDVRELLRAGINVYTTMNIQHLESLNDLVGNITNIEVKERVPDSVFDQADQVEVIDIEPEDLIERMKEGKIYGPVQAERALENFFRREKLVALREIALRRSADRVNRIAEEERNILGNTGYHTGEHILACISAAPSSAKVIRTAARLSYAFHAQFTALYVETPAMQEAGEKTKQTLKSHLELAKALGAKIVTVYGEDAAYQIAEYAIVSNVSKVVMGRTNHRGIWRRPRIEVMEKLTHMAPNIDVYIIPDIRKATHKREVQIQRRRKTSWKNVLLDLAEITGVMAAATLAAYVLWLFRLPESNIIMIYILGILLSSYIANKKIYALYSSLISVFAFNFFFTEPYFSLKAYDKGYPTTFVMLFLVGLFTATLTRSLKQQSRESAKKAYRMEILLENSQKLRRCKSKQEVWTQVAGRQESF	31~~KdpD (8.17056E-121)~~236;X;257~~Usp(1.82744E-35)~~380;X;408~~DUF4118 (4.16815E-15)~~509	KdpD protein
	1E-07	41.2	1.8	2.4E-07	40.3	1.2	1.5	1	R7CQR0_9FIRM	Nucleoside-diphosphate-sugar epimerase	BN806_00906	Ruminococcus sp. CAG:9	702	1262967	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:9	>tr|R7CQR0|R7CQR0_9FIRM Nucleoside-diphosphate-sugar epimerase OS=Ruminococcus sp. CAG:9 GN=BN806_00906 PE=4 SV=1MEVLLAGNTGYVTETFIEESFPECDVVVLGNEMLKSNRKKNILSRPFIKDEKELKEIFETYEFERIVYFSNYLTMHGRMTGELEQLRQILQLCKKNKEIRMLYLTGQESIYNITSGKTLLVSAAENVVMEYGNMYQINTKILRIPHLYSAVYTQDFFYKLFTEAEESGKIVFEESPEQNIYFVCMDDLAELLYKVYDNWGKERCLNVPDCFRQSFSDLEKEIRKTIPGKLDIRYQNSGQIYKVQPDDQIIRHEYGWFPKISVFEDILGMYQEYKKLSDSDSGHFANIRNWISKNTLLIHILELISGFILFEFLNKYTGTYAQFKMIDLRLVFIVFMGSLYGINYGISAAALETCSLIAAYRQENVNIYTLFYEASNWIPFIFYFAAGAVCGYIRLKNKEDIEFVTKENRLIKEKFFFMQEMYQETLQDKRQYKKQILGSRDSFGKIFDITRKLDVIQPQKLFMETIRVMEDVLENHTIVLYSLDSWKRFGRMEVSSPEIRRKMPNSIRIEEYQNAVETLEKGEVWRNRELLAGYPAYIAGIKRNGELVMLVFIQDAASSQMTLYYLNLIKILCGLVEVSLLRALEYQEAVRDREYLEGTHILKTEYFMERLKLFHSIKEQKIGSYALLQIENPEMTLEETERILKNKIRENDILGISEDGQLYLILSQVDDAMLPIVIERLEKNGLHCRVIDTRNESRVAEE	(0.000000000002997 21)~~400;X;458~~GAF (0.000000000143415)~~582	non-KdpD DUF4118 protein

	1E-07	41.2	10.9	2.7E-07	40.2	7.6	1.5	1	N0B533_9RHIZ	Histidine kinase (EC 2.7.13.3)	HYPDE_28238	Hyphomicrobium denitrificans 1NES1	906	670307	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium denitrificans, Hyphomicrobium denitrificans 1NES1	>tr|N0B533|N0B533_9RHIZ Histidine kinase OS=Hyphomicrobium denitrificans 1NES1 GN=HYPDE_28238 PE=4 SV=1MANTSRPEDTRRTSAKALLELAANERRGKLKVFLGMAPGVGKTYAMLSAARALKNEGLDVVVGVVETHGR SETAALLEGLEVLPRRTVPYRNRTLMEFDIDAAIARRPALLLVDEFAHTNAPGLVHPKRYQDVEGVLQAGIDVWTT LNIQHLESLTDVVERIAGITVRETIPDKVLERADEIVVVDLPPEELIRRLREGKVYLPDNARRAMDQFFQMGNLTALR ELALRRTADRVDEQMLSQLRRQGIEGPWPTAERLLVCVGNNELAETVVRAAARMAAALKSDWIAIHIVQSEREQT DRGSIRKMEKAMRLADRLGATTVRLHAKDLTSEVLAYAKRNNITQIIVGRSRPRFFDRWIGRSFSTSLVAEAAGPS VTVVAPDTPSTPLHLASVLPEISEFWSGGLAAVVAVAGGVAAGKMLAQITRLPNLSMVFLFAVLICALRFGIFSAIAA AVLSFLAFNFFFIEPRYTLTVASPYELFGLLIFLVVAAATGSLAGRLREQANATRERAEATQALYEFSGKLSAATKID DVLWLLAAQSAAVVKGKSIILLEQSHELSVVGSWPPEDTLGTADWAAARWAHRNGEPAGHLTETMPSAVYQFRP LVASTGSVGVLGVAPGDEEDALPSATASALQSFADQAAIAIERTRLVEQAAEAATAAESERLRGALLSSISHDLRTP LASILGSATSLRQLGDRMRKQDRADLLATIEEEESTRLSTFVSNLLDMTKLETGVLDIRRDWVDVADAVRGAVARAK KTFPTRRVETFIPAKLPLIRGDAALLEQVMFNLLDNAHKYSPPESVTRVSITLATGGAVHIVVADEGIGIPSEALNKVF DKFYRAHIGDGRKPGTGLGLSICAGIIAAMGGTILAQSPIANGKGTEISILLPAAEDSATEQNAPKDVA	25~~KdpD (1.7473E-126)~~235;X;257~~Usp(3.17615E-24)~~380;X;432~~DUF4118 (0.000000000000316046)~~503;X;530~~GAF (0.0000000565585)~~648;X;666~~HisKA (0.000000000007003 51)~~731;X;784~~HATPase_c (1.13356E-24)~~889	KdpD protein
	1E-07	41.1	11	2E-07	40.6	7.6	1.3	1	R6T030_9FIRM	Histidine kinase (EC 2.7.13.3)	BN714_02176	Ruminococcus sp. CAG:57	372	1262962	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:57	>tr|R6T030|R6T030_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:57 GN=BN714_02176 PE=4 SV=1MTANSIKSSKAFSVFKDSAICIVVLTAATLAGYAFKAFQLADADIIMLYIIAVLVISIFTSKMYFCLISSLVGVMLF NCFFTYPEFSLSVHDAGYLVTFVTMFITAFIAGTLANKLKRNILIAEQNAREKEEAALLAQNEQLRADMLRSISHDLR TPLTSISGNASTLISGGDTLDESARQQIYTDIYSESMWLIEMVENLLYATRIEDGRMQLNISVEILDDIVQEAVRHTKR THPKRNIIVDMYDEIIPVMADANLIVQVIVNLLDNAVKYSDEDSDVTVSVRRENAHTVVISVSDHGSGISDEEKEKVF DMFYTGGSRSSDSRRSLGLGLALCRSIITSHGGTISVSDNIPNGTVVSFTLPIGEVDLNE	22~~DUF4118 (0.000000000158338)~~119;X;140~~HisKA (0.0000000000266664)~~206;X;259~~HATPase_c (6.94219E-25)~~363	non-KdpD DUF4118 protein
	1E-07	41.1	11.1	2.1E-07	40.5	7.7	1.3	1	R5NN58_9FIRM	Histidine kinase (EC 2.7.13.3)	BN514_00302	Ruminococcus sp. CAG:17	525	1262951	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:17	>tr|R5NN58|R5NN58_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:17 GN=BN514_00302 PE=4 SV=1MKMEDTVKNRTCSKRPFAWYVEKPSAKDYLLTVFIFAVCTLIGLLFQKLDFTDTNIVTIYILGVLITSIVTDGYLC SVAGSFLSVFLFCFFLTEPRMSFETYAVGYPVTFFIMLISSVLTGTLAAKLKMHAKLSSQIAFRTQVLFDTDRLLQKA KSETEILGVTCTQLIRLLNRSITAYVVENGTLSEGKLFSGEKESTEDFLTQEEQQAARWTYENRQRAGASTQYFSQ AKCLYLAIRSGNNVYGVIGIPLQKETLDSYEYSILLSVINECALAMENVQNAIEKEKNAVLAKNEQLRGDLLRAISHDLR RTPLCSISGNADMLLSNSDRLDEATRYQIYTDIHEDSEWLIGVVENLLSITRLNDGRLKFKFTDQLLDEVIAESLRHV SRKHDAYKIVADCEELVLTRMDVHLIIQVLVNLIDNAIKYTPSGSVISIRGFKKAGKAQVSVEDNGPGIPDEMKPHIFE MFYTGKTTVADSQRSLGLGLALCRSIIEAHDGTLVLSNHAPHGCNFTFTLPLSEVTLNE	23~~DUF4118 (0.000000000000020738)~~128;X(167);295~~HisKA (0.000000000006025 55)~~361;X;413~~HATPase_c (8.57599E-30)~~516	non-KdpD DUF4118 protein
	1E-07	41.1	10.3	2.6E-07	40.2	7.1	1.5	1	A0A0F5FWK2_9RHIZ	Histidine kinase	VE25_03050	Devosia geojensis	894	443610	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia geojensis	>tr|A0A0F5FWK2|A0A0F5FWK2_9RHIZ Histidine kinase OS=Devosia geojensis GN=VE25_03050 PE=4 SV=1MSDTNADIRPDPRAFLKLAAGEGRGKLTVFLGAAPGVGKTYAMLARAQQRKVEGTDIVIGLVETHGRPETA RLMEGLEVLPRRKGERSGTTYDEFDLDAALQRKPAIIIVDELAHSNDAAARHPKRYQDIAELIAAGIDVWTALNVQH LESQSDLVSRIAGVPVRETVPDVVLKNADEVVLVDLPPAELIQRLKEGKVYLPDNAGRAVEGFFRPENLTALRELAL RRTADRVDDQMADIWRQQAVEGPWITSERLLVCVGPDPLSEKVVRTASRMALGLNARWMVLSLSRSADPIPDAD KAARLEATLVLAERLGAEVRRVVADDFVAEILKIARRENITQIVVGRMRAGLLTRLTRRSLPDALIASAEGIGIHLVPE AERPSASSLTPRRRSLPEWLATFGLPAATVGAITLLGLGISQLLALQNLSILYLLSVLVCAILVGRAAALLAAVFSFLT YNFFFIEPTGTFTIAKPHEVLTLVIFACVALVTGTLASRLRDQVERARQAVRNTQALYDFSRRLSAAYGLENVLTATA AQLHAMLGKGAVLLTPGETGTLELQVAWPPDQALDDTAMTAARWAHDKREPAGFMTGTLPAVPYLFLPIRSDQR IAGVVGLSRDMAQGPLSPDEDRQVSAVLEQAALAIDRARLVRENAKVAVAKEGEKLQTALLSSLSHDLRTPLASIT GAVTSLRQLGEKMSVETRADLLTSIEEETGRLTRFVGNLFDMTRIESGMIKPRREPVELEPLIGEVIARAGKLDPAL KVETSIAEAMPPALADAQLLEQVLFNLLDNARKYAGTAEPVAVYVRREEDMAVISVTDQGRGIPEDEIEAVFEKFH RRARGDGRPAGTGLGLSIARGFVTAMGGTIKAESPAVRKRGTRFVVRLPLALEGTA	22~~KdpD (3.89033E-113)~~232;X;254~~Usp(2.29708E-30)~~377;X;397~~DUF4118 (4.52085E-14)~~500;X;527~~GAF (0.00000000175669)~~646;X;663~~HisKA (0.00000000250424)~~729;X;782~~HATPase_c (2.85564E-28)~~886	KdpD protein
	1E-07	41.1	3.8	2.4E-07	40.3	2.6	1.4	1	R6C3E5_9CLOT	Uncharacterized protein	BN687_02044	Clostridium sp. CAG:510	726	1262816	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:510	>tr|R6C3E5|R6C3E5_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:510 GN=BN687_02044 PE=4 SV=1MNVLLIGGCSNVINNLIIKLNKEGHRIYLLTGSRYEKQPYQRVFEKYHFPYDAGCLNEIFESINPDLTIFMGAYD TNFHWDNEESEAVRYSACVMNILMAYAMKNKGRFIYLSSDEVYQGDFPEDISEETPAAPQGFKSMVLSQTEEMC ESYGKNCGRDIIVLRLDHLYSMPDTMADVTDICTKMCLESLDKYIITVDDNDTFSLLYVTDAVEYLYRLAVCETHKYH LYNLSSETPVTERQLAELVRKNMWFNVEIVSVGTNTKRKILSSARFAEEFKPSFLCDTPHVVARIVARMKKYRHIFL YGEKRKKTIRERILERAGWLMKTAIPYIENGICFVIFFMLNNRAVGSKYFHSLDFYLLYVLLFAIVYGQQQATLSATL AVAGYCFRQMYDRSGFELMLDSNTYVWIAQLFILGLAVGYMRDYITKLKREHGEEKEFLSQQLEDIKEINDSNVRV KDALETQIVNQNDSVGKIYSITSSLDQYSQEEVLFYAAEMIARLMKSRDVAIYTVSGGEYARLFSATSPKARSMGN SIRYRQLGEMYEVLGEKKVFINRSLNDKYPLMANAIFEENEIQMIIMIWGIPWESMTLGQANQLVVISALIHNAVVRA NKYLEALEEERYIDGTKILDDEAFTTLINAYLAAEKKGLTECIVLKVEAAPDITYKDLAMRISVRLRHQDYVGLLSDNR LYVLLSNARRQDAVPVMERLSAIGCRSEIMEEYEQ	3~~NADB_Rossmann (0.000000000170119)~~232;X;330~~DUF4118 (6.84769E-15)~~426;X;487~~GAF (0.000000000820527)~~611	non-KdpD DUF4118 protein
	1E-07	41	10.6	2.2E-07	40.4	7.4	1.3	1	Q0PAK0_CAMJE	Truncated KdpD protein (EC 2.7.3.-)	kdpD Cj0679	Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	606	192222	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Campylobacter, Campylobacter jejuni, Campylobacter jejuni subsp. jejuni, Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	>tr|Q0PAK0|Q0PAK0_CAMJE Truncated KdpD protein OS=Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168) GN=kdpD PE=4 SV=1MQRQSPEQILKKLEVKAKEEEKNKLVKLKIFLGYAAGSGKTYAMLSEARTLRDNGVDVVLGYIEPHDRPETM ALAQGFESIANLEIPYKNIVLKEFDLDATLKRKPALVLVDELAHTNAKGLRNEKRFQDIEELLKAGIDVYTTLNIQHLE SLNDLVANISKIEVKERIPDRIFDEADQVELVDIEPNKLLKRMQDGKIYKEKQAKLALENFFRQERLIALREIALRRLAS RVNLRASEQRLINDDLAYHTGEHILVCINASNAKVIRAAARLALAFHAKLSALYIKNPNIKEAKALEENIELAKSFDAKII SVYDDIARQIAEYSSLSNVSKIVLGKNKDKKSLKKRFLKLSLKKHPILIYILSMKIKFLLLKYEVKKSFDFLGFLKITGVL LLATFIAFVFHKFNTQPSNIVMIFILAVFASSFISDNKIFAFYSSLVSVLIYNFFFLEPIFSLKVHDSGNIITFTTMFIVGFL TAVFTRRLKLQSKELTKRAYRTAILLENSENLARVKSKQELWEQLGNQALKLLNLPIIIYPINKNNILSKPLLFFNDDK QMLKNCFSADEIAIAQWVATNKERAGVCTNTLPNANAMYLPIEDGKKLKGL	27~~KdpD (4.48022E-117)~~233;X;254~~Usp(7.10705E-18)~~337;X;386~~DUF4118 (0.000000000000051276)~~485	KdpD protein

	1E-07	41	12.4	2.2E-07	40.4	8.6	1.2	1	R5H0L2_9FIRM	Histidine kinase (EC 2.7.13.3)	BN555_00447	Firmicutes bacterium CAG:24	370	1263012	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:24	>tr|R5H0L2|R5H0L2_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:24 GN=BN555_00447 PE=4 SV=1MQRKNMIERKQSPEQKGRTILRNILITVGIMGAATIVCLALQHFSEADTHVPLLFVLAVVIVARFTEGYVYGILSAMAAVVLVNYVFTYPYFELNFSITGYPLTFVVMLATAVMVSALTTQIKWQEQIRLEVEKEKTRANLLRAVSHDIRTPLTSIQASASGILDNYDALGRQEKVELLEGIRDESRWLIRMVENLLSITRINGDRAQLQTTWEVVEEVVGGAVGKFQKQFAQIEVETSMPEEVVMAPMDGILVEQVLVNLMENSAIHGKTTTKIRISIQKLPERVLFCVEDNGKGIDPAILPIIFEGQLPTGDHAASDGKRSMGIGLSVCMSIIQAHQGDMKAENMAAHRGARIQFWLPCQEENWMEEA	23~~DUF4118 (4.68112E-14)~~127;X;135~~HisKA (0.000000000001224 2)~~201;X;255~~HATPase_c (3.20734E-21)~~359	non-KdpD DUF4118 protein
	2E-07	41	11.6	2.5E-07	40.2	8	1.4	1	R5QSP1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN521_00560	Coprobacillus sp. CAG:183	639	1262853	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, Coprobacillus, environmental samples, Coprobacillus sp. CAG:183	>tr|R5QSP1|R5QSP1_9FIRM Histidine kinase OS=Coprobacillus sp. CAG:183 GN=BN521_00560 PE=4 SV=1MINQQEHILLCLSSSTSNPDVIKMAAAVAHENKAIFTALYVETPDNSKISKDDRERLQYNTNLARKLGANIETAFGLDIAYQINEFCKNAKVTKVFFGHSQKDRKHLFSSRLDKKLLNLLKDLDINIVYHQNTGKDKSKQRDFNFVVKGKDLAISIFILLIATLIGILFHHLGFSEANTITVYILSVLITAITTSNRIYSLVSSILSVLIFNFMFTNPRFTLAAYGSGYPVTFAIMLIAAFITSTLAIRIKQQAKQSAQHAYRTKVLLETNRLLQKEKSIAGIKETAAKQIVKLLNKSVMIYQITENDTILHEVFHHNNMTVHDCDEIETNVHWVYQNNKTYQAKNYYLPLASTNDIYGVVVIILEDVILDAFENNLVLSIVGECALALEKEFFNQKKEEAAIEAKNERLRANLLRSISHDLRTPLTSISGNASVLINNSGSLDENKKMQLYEVIYDDSLWLINLVENLLSVTRIEDGKMNLHLETELIEEVINEALNHISHKKDEHRIEVKANDEFILAKIDAGLIIQVIINIVDNAIKYTPKGSMISIETFKHKDFVEIQIADDGAGISDKDKEKLFEMFYTVKHEVIDGRRGLGLGLALCKAIIVAHGGNIAVKDNIPHGTIFSFTLPIKEVEIHE	7~~Usp(8.27017E-20)~~108;X;152~~DUF4118 (1.28548E-14)~~253;X(155);408~~HisKA (0.000000000084533 4)~~474;X;527~~HATPase_c (3.93898E-25)~~630	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	2E-07	40.9	6.4	1.5E-07	40.9	4.5	1.7	1	Q47DQ1_DECAR	GGDEF protein	Daro_2293	Dechloromonas aromatica (strain RCB)	269	159087	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Rhodocyclales, Rhodocyclaceae, Dechloromonas, Dechloromonas aromatica, Dechloromonas aromatica (strain RCB)	>tr|Q47DQ1|Q47DQ1_DECAR GGDEF protein OS=Dechloromonas aromatica (strain RCB) GN=Daro_2293 PE=4 SV=1MRAMLLAGILLLAIATLDVLTRVQLRIPQFYLIPVVLIAWRVGLRASIATAILAAIIVFFSSIQAGNHNARAFLFYAEQLATLTFFIAAGVLAARLREIQDQTAEFVRRDQLTGIANRMALMERLKLELARHRRTSQSFALVFIDCDNFKEINDRRGHLEGDHFLQIVAATLQGAMRMTDLVSRLSGDEFIVLLPDTDPCGAQCVADTLEVRLREETIRTGWSMTFSIGVAVFPTPPANPDIAIQHADNLMYMAKQAGKGRSILEVFEV	108~~Nucleotidyl_cyc_III (2.21098E-54)~~261	No DUF4118 detected by NCBI CDD
	2E-07	40.9	12.5	2.6E-07	40.2	8.6	1.4	1	R6VWM4_9FIRM	Uncharacterized protein	BN746_00939	Erysipelotrichaceae bacterium CAG:64	635	1262981	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, environmental samples, Erysipelotrichaceae bacterium CAG:64	>tr|R6VWM4|R6VWM4_9FIRM Uncharacterized protein OS=Erysipelotrichaceae bacterium CAG:64 GN=BN746_00939 PE=4 SV=1MKQGKLKIFFGYCAGVGKTYAMLEAAHERRREGMDVVIGYIEKHDRLDTIALMQGLECIALKAIMYHGITLEEFDLDQALQRHPQLILVDELAHTNVQGARHPKRYSDIQELLHAGIDVYTTVNVQHLESLQDVVAGITRVQVQERIPDAVFDEADQVELVDIEPDELLERLKRGKIYHKTAAQKAMHNFFVRDNLIALREIALRRCADRVNKRVSLKDRKSTREHILLCLSPSRSNALVIRTAARMASAFFAEFTALYVENVNEEPLCREDLEQLEQNRRLAQHFHANIVSVAGENIAQQISEYAKISGVSKIVIGRSSPRPHSRARTLIDQLTLLAPDLEIYIIPDANVEPVKRKRHRLTHAHVFRHRDFMLTVLLFLGATGINLLMYHFQLPEANIIMVYLLAIVLISYNTSSRVYGLGVSLLIVAVFNFFFTAPRFSMEAYDPAYAMTFAVLFIVSFIISTLTRTMRMQLKVNAMQAHRMELLETSQQLQLAENMAQLGEEAVRQLYKLLNRTIIIYSVRNKTLQEPIIYHEHLNEEEQKYLTENERAVAQWVLKNNRKAGVSTSTLPYAKALYYSIRKKDRIYAVVGIALQQKEVLSPFERSMLATMLNEIALAMDSMRKQNHRRVNR	1~~KdpD (1.9228E-116)~~211;X;226~~Usp(1.31271E-26)~~347;X;372~~DUF4118 (1.24609E-14)~~471;X;499~~GAF (0.0000250014)~~623	KdpD protein
	2E-07	40.9	9.5	2.6E-07	40.2	6.6	1.3	1	A9KJX5_CLOPH	Histidine kinase (EC 2.7.13.3)	Cphy_0743	Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) (Lachnoclostridium phytofermentans)	342	357809	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Lachnoclostridium phytofermentans, Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) (Lachnoclostridium phytofermentans)	>tr|A9KJX5|A9KJX5_CLOPH Histidine kinase OS=Clostridium phytofermentans (strain ATCC 700394 / DSM 18823 / ISDg) GN=Cphy_0743 PE=4 SV=1MKHLPDWLKTIVFLAIATLCSLLFHLITNNTANIAIVYMLSIVLITKYTEGYRYGVIGSAVGVIGVNYFFTFPYLELDFTRTGYPITFLGMLAISFITSTTVVNLQAHQRLNADAEKEKMRANLLRAISHDLRTPLTGMIGASATYIEMKDNLTEEEKDELILHIHEDSNWLLHMVENLLSVTRIHSNNTTVTKVSEPVEEVVSEAVMRLKKRYPNAKILVKTPDEFLMVPMDATLIEQVMINLLENAYKYSKSKKPIELTVTKEPNFVRFSIMDYGVGINKDTIYNFFEGNTATKNTSSDSTKGMGIGLSICKTIIRAHGGVIEASNHSNGASFTFTLPLD	7~~DUF4118 (0.000000000093704)~~99;X;118~~HisKA (0.000000000028772 9)~~184;X;237~~HATPase_c (5.39387E-23)~~339	non-KdpD DUF4118 protein
	2E-07	40.8	3.9	4E-07	39.6	2.7	1.6	1	R6DFP6_9CLOT	NAD dependent epimerase/dehydratase family protein	BN547_01749	Clostridium sp. CAG:230	725	1262782	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:230	>tr|R6DFP6|R6DFP6_9CLOT NAD dependent epimerase/dehydratase family protein OS=Clostridium sp. CAG:230 GN=BN547_01749 PE=4 SV=1MKVFIAGSYNAFTNELIKKFHKENDKVYVLTGEQYHGNKPHNVFEQYTFPYTGDSIIEVLDSVQPDIILFTGAYDTNFKWQNMRSESMHYMSGLINILMSANVQHTKQFIYLSSSEVFSDPQEEFIKADTPTSAMDYKGIAITQGEELCRHFRATTGLNVSVLRIDHMYKEPLDIEDCTDPLSHVCKEALNTGSVTVNDNIHFSMIHVSDVVFGIYQFVQEKKHKKDLYHISSQKLLSDFDIAKLIHSVDDSIIIEDNTTGTPVSLALDNSEFCEEYHFSVFNSYEKTIPAIYKKMRKRRKDFLDQKNKNTSKNQIVQRIKTLFTAMLPFIENLVIFIPVFMINNRAVGSGYFDKLDFFLLYVLLFAGIYGTKQAVFSAALSVIGYCFRQLYFRTGIELLIDYNTYLWIAQLFIVAMAVGRLRDSTKNITYEKDEEISFLSSQLQDLVHINDSNNRIKNIYQNRIIDYDDSLVKIYSITSQLDSVEEGAILFYAADIISRILKTPDVAIYQVANADYCRLFSATSDQAKVLGKSVKYSEMTDMTDMLHNKQVYINKTMNEDYPLMASAIYRNDKPLEIIMIWGLSFEKMTQYQANLLTVLGFMIYNSVDRAERYLDALANTRFIKDTRLLTADAFMELCHIYQDAMDKHLTEYTVLQVASQKEMSYTEWSTLLSSKLRFSDYIGLDNQNRICILLTNSNTGDAQFIITRMQELGLSCVPKKEVVS	67~~NADB_Rossmann (0.000000000007653 01)~~232;X;329~~DUF4118 (4.40042E-15)~~424;X;486~~GAF (0.0000000487782)~~610	non-KdpD DUF4118 protein

	2E-07	40.8	9	3.1E-07	39.9	6.2	1.4	1	A0A0F5L0B4_9RHIZ	Histidine kinase	VW35_18790	Devosia soli	892	361041	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia soli	>tr|A0A0F5L0B4|A0A0F5L0B4_9RHIZ Histidine kinase OS=Devosia soli GN=VW35_18790 PE=4 SV=1MEEPRRPDPEALLAETQKAHRGRLKVFLGMAPGVGKTYEMLRQARRRKVEGLDVVVGLVETHGRKETESLLRGLEVLPRAPIDYKGRTLLEFDIDGSLKRRPELLIVDEYAHTNAAGSRHPKRWQDVEEILAAGIDVWTTLNVQHLESLVDVVLKITGVRQRETVPDSALSRADDIEVVDITPAELRERMAAGKVYVPETARLAIDNFFKPENLTALRELALRRAAQTVDDQLNAAMRVKGLEGPWAAGDRILVLVSDDPMASNLVRQGRRLSDTMGDAPWIAAHVARGRRDDGEAGTTSRLTDALKLAEQLGATTVVLTGDDLVKAVLAYAGKNNVTQIVIGKGPDRRIREILGLSLAAELLRAARGVAIHVVTEPGESQPRQRWRMARSLRQGWTQHLIGLVYVVAAAGLAYLLDVRFERADLGMIFLAAILAAAVIHGLGPGLVAGGFAFLLYNFLFLSPRYSFAIGSPTDLLTLFVFLAVALATGLLAGRSRDRANEAQRRAGDVSSLLVATRAFSRAPTKADAAQALAEQVTAATGARSVVLLPKGDDIAPATGAPELTALNEGAMAAARWAWERGDAAGHGTGTLPQTSWTFRPLDGVRNRTGVIGVEAHSSLPGSDEEKLLTALADGGAIAIERAELALQAVEGETLRRSDRFRSALLNSVSHDLRTPLSTVLGASSTLIELGDKLDPAVKDDLVVSIREEAERLNHYIGNLLDMTRLEGGGVTLRLQSCDVEEVLRAAAARLSRRLGEHSVAYDFPAALPRVIVDPGLLEQAIVNILENAIAYSPDNTEISIAAYEDRAKVIISIEDEGKGIPTDELERVFDKFRRLEEPTDRGKGVGLGLSITKGFIEAMGGTIVAASPIHGDKGTRMLIGLNKSPEDVWKEK	19~~KdpD (3.10383E-122)~~229;X;251~~Usp(3.92144E-32)~~375;X;438~~DUF4118 (0.00000000202972)~~498;X;527~~GAF (0.000164765)~~641;X;658~~HisKA (0.0000000000454198)~~724;X;777~~HATPase_c (5.26586E-24)~~879	KdpD protein
	2E-07	40.7	3.2	3E-07	40	2.2	1.4	1	A0A0C9MUP3_SPHPI	DNA, contig: SP637	SP6_37_00030	Sphingomonas paucimobilis NBRC 13935	324	1219050	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas paucimobilis (Pseudomonas paucimobilis), Sphingomonas paucimobilis NBRC 13935	>tr|A0A0C9MUP3|A0A0C9MUP3_SPHPI DNA, contig: SP637 OS=Sphingomonas paucimobilis NBRC 13935 GN=SP6_37_00030 PE=4 SV=1MTPELLNERQPKTRWRRNVRIALEIAIVFALLAALDEWLTGGVGFAGVRPSPYWIPVLVMALVYGTGPGIAAAVIASLLWLLAAHRDGSERDYLDWLLHLSIPPLLWCVVAVAVGEVTLSRKRHLAKALRRGAQAVRDVGRMTDAHERLRTRTNRDLQRRIATDPRTTGHIIATAARLSSVDPAARRGALAQLIGLAAQSDDFTCYRLGPDGARAWLRGGAVTGASMGRPDMLPPAMIETLAASGERRVRHVARRSDREWLAGLGVAAVPLADGDARLHGLLLFHDLPIEQFNAHRVAELAEIGHWLSPMILDQGQAPLRVMRSA	23~~DUF4118 (0.0000000000229125)~~124	non-KdpD DUF4118 protein
	2E-07	40.6	4	4.1E-07	39.6	2.8	1.5	1	I0IMJ4_LEPFC	Uncharacterized protein	LFE_0778	Leptospirillum ferrooxidans (strain C2-3)	616	1162668	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Leptospirillum, Leptospirillum sp. Group I, Leptospirillum ferrooxidans, Leptospirillum ferrooxidans (strain C2-3)	>tr|I0IMJ4|I0IMJ4_LEPFC Uncharacterized protein OS=Leptospirillum ferrooxidans (strain C2-3) GN=LFE_0778 PE=4 SV=1MNFWTREKKLWWLPYLEALGGILILTGFFLEFYGISSLILPRFHPFLPLVLLIAARYGFLPGVVSALLGCLDYYLLLLWQDHWDSLMPGHFSFLWPSAFLFSGMIVGELRDAESRRYSDLESQFIKEKDAARTATLQVEILIKAKKELEKRVFLDPNLATELFDVFRSLEKDEIDSIPSTLLSLCVSFVGADSVALYRRDRDHFFLEGSAGSFQCPDRVDRSYPPFFKVYDSRQAMTIRENGIFPEGVFASGKKHRPLCIYPVLSEEYRVEFLLVIWHAPFEKLTPDFFQMMRMIVDRASSRLEFLESHKKTRESVSIDETTGFLRPVFFARRAAEELSKSYRYQASFSLLEVSFRSSAGSKTDFRSALLSVREIVKRLLRDVDFSGLTGDGDGVCLCLPHTSLSGAEVVQKKFLVLWDELLSSFPLLQEVTPVLQVHSFFPSDGRGENDNKLYHSLMIRLDSVFLQDPSTGFYSGQGFWLELQKEKQLIEKEAEKIGLIAVCFETPSWEDVVLFGKALRGMRNLEGKPLLTERTLIGIPLDGNSLWLLLPKPDLNALEFIEGEVLSTWSGTDIPRLKRGSLSIKARLLDPSDAFLEAENLNQLLHLTGWSKYFGA	14~~DUF4118 (6.11572E-15)~~116;X;173~~GAF (0.000000000260362)~~304	non-KdpD DUF4118 protein
	2E-07	40.5	8.3	3.1E-07	40	5.8	1.3	1	R6DQR6_9FIRM	His Kinase A (Phosphoacceptor) domain./Histidine kinase-DNA gyrase B-and HSP90-like ATPase	BN553_01732	Firmicutes bacterium CAG:238	383	1263011	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:238	>tr|R6DQR6|R6DQR6_9FIRM His Kinase A (Phosphoacceptor) domain./Histidine kinase-DNA gyrase B-and HSP90-like ATPase OS=Firmicutes bacterium CAG:238 GN=BN553_01732 PE=4 SV=1MGSDMKKKRKQTEEQINTQRLLSERKQLVASHKRDMLLCVGVFAIATLASFFFKNMASDPSLNIAMLYTLGVFVITRYTNGYVYGMLFAIMSVLSVNFFFTYPYQDFNFSIEGYQVTFLGMFAIAIITSAMSSNMKEQAEQLAEQEKELMEAQKEKMRANLLRAVSHDLRTPLTGIIGNSSSYLEMGDRLTDEEKRALVTYINNDANWLLNMVENLLSVTRINNETASVAKSLEPVDEVASAAVIHFRKRFPDAEVHVTVPDNVVMVMMDAMLIQQVIINILQNAQMHAKSTKPLELTIDEDEEKVFFHIRDYGVGIDEHRLETIFDGEGYRSEKAKTDGYKGMGIGLSICKTIVTAHGGRIIAVNHRDGAEFCFSLPKEKED	36~~DUF4118 (9.27564E-14)~~138;X;155~~HisKA (0.0000000000841073)~~221;X;274~~HATPase_c (7.59254E-22)~~377	non-KdpD DUF4118 protein
	2E-07	40.5	12.1	3.5E-07	39.8	8.4	1.4	1	A0A0F0HCB2_NOCAE	Histidine kinase	UK23_07235	Lechevalieria aerocolonigenes (Nocardia aerocolonigenes) (Saccharothrix aerocolonigenes)	829	68170	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Lechevalieria, Lechevalieria aerocolonigenes (Nocardia aerocolonigenes) (Saccharothrix aerocolonigenes)	>tr|A0A0F0HCB2|A0A0F0HCB2_NOCAE Histidine kinase OS=Lechevalieria aerocolonigenes GN=UK23_07235 PE=4 SV=1MSAKPRRGELRIFLGAAPGVGKTFSMLGEAHRRRERGTDVVIGFVETHGRAKTAQLVEGLEIVQRRHCTHRGVELTEMDVDAVLARAPEVAVVDELAHTNVPGSRNAKRWQDVEELLEAGIDVLSTVNVQHLESLNDVVQRITGVPQQETVPDEVVRKADQMQLVDLTPEALRRRLAHGDVYAANKIDAALGNYFRVGNLTALRELALLWVADQVDVALLRYRAEQQITDTWETRERVVVAITGGKESETLIRRARRIATRAGGDLLVVHVLRGDGLAGADPHSLQKYRKLTEDLGATFHTVVGDDVPTALLEFSRGVNATQLVVGTSRRSRFARVFSAGIGSTVVQESGAIDVHMVTHPATTSGWRGRFASSPLRPSRLALGWFLAVVGPALVTAAGASMRGSLNFSTNVIVYLLVTLVVAIVGGLGPAITAALLNALLLNFFFTEPFYTFTIDAQQNVLTFFAMIIVGVSTALVVNYAARRATQAARARTEATLLASYARTVLTNPFPLARLLEKVKENFGLQSVALLERVDGEWERVACVGVSPCDEPDEADVDVAVTPDVHLALRGRSLPASDRRVLEAAAGQALLALRQQRMAEQALETQRQASRTELRTALLSAVGHDLRTPLTSIKASVGSLRDPELKLSGSDTAELLEAVEESADRLTGLVDNLLDSSRLATGAVEPQFRAVGYYEAVARALSGLSGDIEVDVPESLPPVRADVGLLERVIANVVGNALRYAGAVALRASAHGSEVELRVVDHGRGLPRGTADQVFAPFQRLGDRTPGGVGLGLSVAKGFTEAMGGTISMEDTPGGGLTVVISLPVEEKVS	5~~KdpD (4.47596E-123)~~215;X;237~~Usp(7.80667E-26)~~358;X;384~~DUF4118 (0.00000051048)~~479;X(133);612~~HisKA (0.0000000000436772)~~677;X;725~~HATPase_c (1.32946E-22)~~822	KdpD protein
	2E-07	40.4	12.4	4.2E-07	39.5	8.6	1.5	1	I1XJM2_METNJ	Histidine kinase (EC 2.7.13.3)	Q7A_1771	Methylophaga nitratireducenticrescens (strain ATCC BAA-2433 / DSM 25689 / JAM1)	516	754476	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Thiotrichales, Piscirickettsiaceae, Methylophaga, Methylophaga nitratireducenticrescens (strain ATCC BAA-2433 / DSM 25689 / JAM1)	>tr|I1XJM2|I1XJM2_METNJ Histidine kinase OS=Methylophaga nitratireducenticrescens (strain ATCC BAA-2433 / DSM 25689 / JAM1) GN=Q7A_1771 PE=4 SV=1MRFIVKTALTIFQKKRAAMRFRPTNTPLKHYLLAIGLILVIVVFAQVLNRYLPYTSLLLLFLAGVLLISAKTSFGPALLSSLLSFLTFNYFFTEPYYTFNMLHKADVATLIIFLMVALMTAHLATQMREAIAKQETALNRLSHFYEFSQMLSSATNTEATIEILWEALRRVLSNDGRVVIAIEQQSNLILHPEGISSGHPGEEVFKLMLSKHLDGETWHKGWLFFPLSWDGRQLGLVAINERINDRQIAAIETFCQLTAVVLHRTMLVAELSQTKLLAETEQLRATLLSSVSHDLRTPLSSIIGASSSLREYAQHLSTDDQQLLIQTIEDEAHRLDRHIQNLLDMTRLSQGKLNLNREWMDIDDLINGAISRLGHPLENVQFKLELAEETPMLFIQGLLIEQAIFNLLDNAIRHNTAELAITLIVQHDDNWITLDIIDNGPGIADAEKEKVFNMFYSLAQGDRHESSLPGTGMGLAICRGMIEAHGGEVMALDNPYGRGTMMRVKLPNNSNNANFN	88~~DUF4118 (0.00072767)~~130;X(151);281~~HisKA (0.0000000000014086 5)~~347;X;400~~HATPase_c (2.05732E-25)~~506	non-KdpD DUF4118 protein

	2E-07	40.4	8.4	3.6E-07	39.7	5.8	1.3	1	G7M3P4_9CLOT	Histidine kinase (EC 2.7.13.3)	CDLVIII_3973	Clostridium sp. DL-VIII	905	641107	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. DL-VIII	>tr|G7M3P4|G7M3P4_9CLOT Histidine kinase OS=Clostridium sp. DL-VIII GN=CDLVIII_3973 PE=4 SV=1MDINERPDPQYLLNQIRKEENESSRGKLKIFFGYAAGVGKSYAMLVEAHDVKRLGKDVVIGYIEPHARAETMALVNGIENIGVKVINYRGITLKEFDLDKALVRKPEIILVDELAHTNAATERHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDIVESITHIAVRETIPDKVFDDADKVELIDIEPDELLNRFSEGKVYSREQTRKAFNNFFTKNNLFALREIALRTADRVNYEVESVRLSKSQITVMPTSDVVLACISPSPSSARVIRTATRMAEAHHSKWIALYVEGTKSKNLGKEDRERLNSHFNLAEQLGGEVVTAYGDNAVEQIIQYAKFRNVTKIIIGKNHKKPNNLFHFYAKDIVDKLMESNSYIDVYVIPNSTFDKKREKTIKKNKYSSKISKKETLIAVVIMLITTIVALCIDYLGFSAANVIMIFILGVIIVNIKTRGYILGFISSIVSILLFNYLFTEPRYSLEVYDKSYIATFPIMLIVTFTIGTLTSKIQREALNSSKRENITQILYRVSRKLLSATGTADVVGIGIKYLSRLLERTVICYLGQENKLSTPFIYTATKGEKDRTLLSKDEEAVAYWTFLNDKECGAGTNTFHGAKGYYMPLKSHGKVLGVLGVSCINGPLKPEQKFIFETVASQIYIALDREILAEIQKKSNLEIESERLRSNLLRSISHDLRSPLAGIKGSVSTIIETGNLISEKTRGELLQSVYDDTEWLIRLVENLLSMTRFDGGDMKVKKDTELVEEVVYEAVQRISKRSTAHEIKVTVPEDVIMAPMDGSLIEQVLINLIDNAIKFTPKNSLIEVKVYENEKDIIFEVIDNGTGIAEDILPHIFDRFFTNGDKISDSRRGVGLGLAICKSIVEGHGGTITADNRESQEGAIFKFNIPKEGNSDGQ	23~~KdpD (3.2864E-123)~~233;X;256~~Usp(1.0762E-40)~~380;X;407~~DUF4118 (8.47856E-15)~~507;X;534~~GAF (0.00000374643)~~656;X;673~~HisKA (0.000000000100332)~~739;X;792~~HATPase_c (4.15009E-27)~~896	KdpD protein
	2E-07	40.4	6.9	3.5E-07	39.8	4.8	1.3	1	D4JZB0_9FIRM	Histidine kinase (EC 2.7.13.3)	FP2_19500	Faecalibacterium prausnitzii L2-6	627	718252	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii L2-6	>tr|D4JZB0|D4JZB0_9FIRM Histidine kinase OS=Faecalibacterium prausnitzii L2-6 GN=FP2_19500 PE=4 SV=1MAKAFGGTFTALYVRTPDSDQMGKEDRRRLQQHIRMAEQAGADISTIYGDDIPQQIAEFARISGITKIVLGRSSVHRRHFWSGPSLTEKLTLTAPNLDIYIIPDASAETGYGSGRKLFTRPLLPSVCDLLITAGILSCITLIGFFFLQLDFARYNIIMLYMLGVLFTALCTSGYTCGVLGSIASVALYNFFLTEPRLTFHAYDPGYQVTFALMLTSAIITCTLTTRLKDHAKMSAQAAFRTKILFDTNQLLQRAKSEEEILSQTASQLMKLLNRSLIVYPEQNGVLGSEQFFGVDGETAQNIFSAPEERDAANWTFANKKRSGAGTDSCPDAKGLYLALRTGGGVFGVIGIDLSEKPLDAFENSVLLSILGEGALAIENRRNALEKEQATVQAKNEELRANLLRTISHDLRTPLTSISGNASNLLSNGETLDTETRNKICTDIFDDAQWLIGLVENLLSITRIEDGRMNLQISPQLMDEMIEEALHHVNRKSCEHTITTQYGDEILLVNVDARLIMQVVVNLVDNAIKYTPVGSIIQISAYRKDHQVVVDVADNGPGIPDRAKAQVFEMFYTGQSRIADSHRSLGLGLPLCRAILTAHGGTLTLRDNIPNGSVFSFALPQSEVNIHE	1~~Usp(2.45424E-27)~~103;X;129~~DUF4118 (0.000000000000196897)~~230;X(166);396~~HisKA (0.000000000222158)~~462;X;515~~HATPase_c (8.40502E-25)~~618	non-KdpD DUF4118 protein
	2E-07	40.4	13.4	2.3E-07	40.4	9.3	1.9	1	F6ICE8_9SPHN	Histidine kinase (EC 2.7.13.3)	PP1Y_Lpl1705	Novosphingobium sp. PP1Y	481	702113	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Novosphingobium, Novosphingobium sp. PP1Y	>tr|F6ICE8|F6ICE8_9SPHN Histidine kinase OS=Novosphingobium sp. PP1Y GN=PP1Y_Lpl1705 PE=4 SV=1MQRSIASYAIALFGVAAIAWLTATLLPQIGIASAALLFLLPVLYAAVRGGLLPGLLAAFAGAIAYNFFLLPPRFTLRIHGFDNVISVLVFVVVAVVTSRLATLLKAREEEALARAACSEELAALSALLASKDAASALGEAISWLERRHDRILLIDEDFLSGNDAGLSALDLAAASWALHNADMTGHATQVMPAADWTFIPLGPRLGTDPDVLAVARPATGVTRGASELSHLGQIAALLGQARDRAALEQQTRERERLAQGDRLRRTFLASLAHDFHTPLTVITGRLVSLSQTVPDADEALEAARRLERMLEDLLGAARIEDGSVAPRMESVDLVDVVGAAVEAVRLPGRIALVRDIPPDLPFVHADPVLLRHCLINLLDNAGRHASGTVTLSARCAGSRMALAVCDDGGGIAEADRARIFERFIRLEGDDRGQGSGLGLSIVKGFAEAMAIPITVSDSASGGACFRLSLAQVSPRQPEPEE	3~~DUF4118 (0.0000000232957)~~74;X(187);261~~HisKA (0.000000136967)~~318;X;370~~HATPase_c (5.25682E-25)~~469	non-KdpD DUF4118 protein
	2E-07	40.3	11.1	4.3E-07	39.5	7.7	1.4	1	D0L4M9_GORB4	Histidine kinase (EC 2.7.13.3)	Gbro_4089	Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	845	526226	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia bronchialis, Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) (Rhodococcus bronchialis)	>tr|D0L4M9|D0L4M9_GORB4 Histidine kinase OS=Gordonia bronchialis (strain ATCC 25592 / DSM 43247 / JCM 3198 / NCTC 10667) GN=Gbro_4089 PE=4 SV=1MADSGDGRAGDGRGRLEVFLGCAPGVGKTYEMLATARGLIDEGSDVVVAVVESHGRSATAALVEGLEVVERTSVAYRDATLEEMDLEAVLERHPQVALVDEMAHTNAPGLRNTKRWQDIEVLRDAGIDVLTTINIQHLESLNDVVAQITGVTQRETVPDEAVRAADQIELVDIDPQALRQRLTAGKVYPGRRIDGALTNYFRQGNLTALRELALLWLADRVDDTLADYRAANAITATWEARERVVVAITGGPESAALIRRASRIASSSAELVVVHVVRGDGLAQRTPIDMTALRDLAAGFGAKIHTVVGDDVPATLLEFARGVNATQLVLGTSRRPRWQRILDEGVGATVVRESGRIDVMVTHEETRRRHRLDIRETRFHRPLSWAAAVLVPLAVTGILMLLDPWLGFSSESALFFVAVLAVSMLGGIAPAVLSAVVSGLLLNYFLTNPRYTFTIDEPDNLITIMVMLMIAIAVAVLVDSATVRRAQAQRAGRDAELLSLFSTTVLGGADVPALLEKVRETYDQRGVTLIRRPKRGAPVIESKVGTEPPADEQAATTVCPVPGGEFEMWLTGPELGGRDRRVLTSVATQAAGAVQRRQLESEAAEAAALAQTDELRRALLSAVSHDLRTPLAAAKAAVSSLRSTDVTFSPEDTEELLATIEESTDQLSALVGNLLDSSRLAAGVVRPELRRTYLAEVIHRALYAVDRRSVDTPDVTVDLQQEWAYTDAGLLERALANLVDNAVRHGGDEVRVQARPDGTRCVIRVIDHGRGIPPEQRERVFTAFQQYGDRNGSSTGVGLGLSVAQGFVRAVGGSISVSGTPGGGTTMEVSLPMFASPAEAGEL	16~~KdpD (6.80052E-107)~~221;X;243~~Usp(1.02814E-32)~~364;X;387~~DUF4118 (3.52315E-15)~~481;X(134);615~~HisKA (0.000000000000389831)~~681;X;733~~HATPase_c (2.29785E-27)~~833	KdpD protein
	2E-07	40.3	4.5	3.9E-07	39.6	3.1	1.3	1	KDPD_CLOAB	Sensor protein KdpD (EC 2.7.13.3)	kdpD CA_C3678	Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	900	272562	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium acetobutylicum, Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787)	>sp|P94608|KDPD_CLOAB Sensor protein KdpD OS=Clostridium acetobutylicum (strain ATCC 824 / DSM 792 / JCM 1419 / LMG 5710 / VKM B-1787) GN=kdpD PE=3 SV=2MDINYERPDPYYLLNKIDKEEKNKNRGKLKIFFGYAAGVGKTYAMLRAAHYMKELGKDIVIGYIEPHARMDTMSLTKGLPQIPVKNIDYKGVILREFDVDKALLRKPEIILVDELAHTNAKSQRNKKRWKDIEELLDAGIDVYTTLNVQHIESLNDIVANITHVSVRETIPDKVFDDADKVELIDIEPDELLKRFTDGKIYRKEQVKRAFNNFFTKNNLYALREIALRRTADRVNFEIEIARLSKGQITVMATSDQILACIGTSPSSARIIRTAARMAESYHSKWIALYVDTGRSLGKADKETLNANFNLVELLGGELVTVHGENVADQIIRYAELRNTTKIVIGKNHKRTGTLLHFYAKDVVDKLMDSNSYIDVYMIPNSSYYRDHKNSILSKISIQHKGSVKDVLKAIIIMAITTDIAELFSYMGFKDVNVIMIFILGVIIVYMATKGQIMGIISSIAAVLVFNYRFTEPKNSFIVYDKSYLVTFPIMMIVAFIIGSLTNKVQKEAQDSNMREKRTQTLYIVSGKLLSAVGTSEVVSIGIKYISRLVNRNVICYLADTSNKLSTPFVYKKDKGAKEEIIMSKDENAAAYWTFLNGKESGCGTSTFYRAKGYYIPIKIKNKVLGVIGVSCPSGPLRPQKKAVVDTVTGQIAIALDREILSKEQEKSKVEIERERLRSNLLRSISHDLRSPLAGIKGAASTILENGELIDEKRKQELINGIYEDTEWLIRLIENLLSMTKFDEGNTKIKKDVELVEEVVSEAVQRSSKYFKNHKIKVSVPEDVIMVSMDGSLIEQVIINLLDNASKFSPKGSTIEIKVYEKKKDVVFEIIDEGQGISEDILPNIFDRFFTNGSKISDSRRGVGLGLAICKSIVEAHGGKIEAVNKGSGGAIFKFNIPKEL	24~~KdpD (8.17085E-132)~~234;X;257~~Usp(3.22953E-40)~~379;X;407~~DUF4118 (7.48065E-14)~~507;X;534~~GAF (0.0000330086)~~657;X;674~~HisKA (0.000000000000820826)~~740;X;793~~HATPase_c (7.3625E-28)~~896	KdpD protein

Disagreement between HMM and CDD prediction	3E-07	40.2	10	4.1E-07	39.6	6.9	1.3	1	D5UDG8_CELFN	Histidine kinase (EC 2.7.13.3)	Cfla_3552	Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134)	402	446466	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Cellulomonadaceae, Cellulomonas, Cellulomonas flavigena, Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134)	>tr|D5UDG8|D5UDG8_CELFN Histidine kinase OS=Cellulomonas flavigena (strain ATCC 482 / DSM 20109 / NCIB 8073 / NRS 134) GN=Cfla_3552 PE=4 SV=1MPRCSAVAPGAGRSEECASLVGVPSWSVPRAVARSIVRGDVTRARRVTGFCLAVAGLPLVTVLLLTASEQLALGSVLLVYLLGVVVVSAVGGLLPGLVSAAVSFALANWFFTPPFHTLTVDGRDALVELVVFAGVALVVAATVEIAARDRLRYQRDLDEHEARARELAGEDRARAALRASVGHDLRTPLASTKAAVSSLRQSDVAWPEPVRAQLLATIEDSTDRLTRVVANLLDMTRLRSDAVTARLTPVALDEVVSRAVLTEHRASVAVLVADDLPLVLVDPGLLERVVENLVENAVRFTPAGERVELHAASVPAPDDAPEDAASWVELRVVDRGPGIAPERWAQVFTAFQRLDDRDSGSHVGLGLAIAQGFTEAMGAEITPSRTPGGGLTMTLRLPAAGR	171~~HisKA (0.00000000159726)~~237;X;286~~HATPase_c (9.58349E-24)~~397	No DUF4118 detected by NCBI CDD
	3E-07	40.2	7.2	4.2E-07	39.5	5	1.3	1	R5QKC3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN526_00096	Firmicutes bacterium CAG:194	654	1263008	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:194	>tr|R5QKC3|R5QKC3_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:194 GN=BN526_00096 PE=4 SV=1MSGQAEHVMVCLSPSPTNRKNIDEAAKLATAFHAAQFTALYVSKSPENSLPVEEQKRLQNNIRYAEDLGAAITTVIGENISFQIAEFARISGVTKIVIGRSNTRRYHFWDKQTVTEQLISIAPNIDIYIIPDSKANIKENQRKRFAQQIIPTGKDILITAGMLFAMTLLSLAFSRLGFTESNIITVYILGVLLNAILTRSHFCSLISSFCSVLFFNYYFTEPRFTFHAYEPGYSVTFVIMLIASLLTGSLAYRLKDNARESARGAYRTKVLFDTNQLLQKSRSYNDVLQVMANQAILLLDKDIIIYPVENNKVGKGYVYAKDSEENSSLFMEDSEEEVVKWVFENKKRAGATTKVFPNAKCLYLAVRINETVYGIMGIYVEKKTVSSFEYSILLSILGECALALENLNNEKAKEEAANMAQNEKLRANLLRTISHDLRTPLTAISGNASNLYSHYKMLDDATREQMFSDIYDDSEWLIQLVENLLSVTRIENGEMQLNKSPEVVGDVVEEALKHVDRNKSAHDIRVIQPEDIIVANMDAKLIIQVMINLVNNAIKYTQKDSMIRISYGDGGEMIYVSIADNGPGMDENAKEHAFDMFYTGQNMAADGKRSMGLGLALCKSVVEAHGGKIDITDNTPHGCIFTFCLKKGDVEINE	7~~Usp(6.70577E-35)~~131;X;156~~DUF4118 (0.000000000027948 7)~~257;X;285~~GAF (0.0000589178)~~406;X;423~~HisKA (0.000000000012997)~~489;X;542~~HATPase_c (5.48472E-26)~~645	non-KdpD DUF4118 protein
	3E-07	40.1	5	5.2E-07	39.2	3.5	1.5	1	R5I900_9FIRM	NAD dependent epimerase/dehydratase family protein	BN729_02399	Ruminococcus sp. CAG:60	729	1262964	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:60	>tr|R5I900|R5I900_9FIRM NAD dependent epimerase/dehydratase family protein OS=Ruminococcus sp. CAG:60 GN=BN729_02399 PE=4 SV=1MNILLAGGSCSLVDSLILKFRKEGHRVYILTGDKYRHNKYKKVFEKYEFPYDSENLGEIVQSVNPDVTILMGAFDTNYSWNEAEQETVRFTSHLMNILVALSAAKKGKVIFLSSDEVYSGDCRDEIIEETPTSSAGLRADTIAQAEEICDNFRRKRNLDIVVLRLDHLYSIPRDKKDINNICARMCLDCMRNGYIEANEKHTFSLLYEDDAVEFIYQVVKNKLHEKFLYQLSSDHVVSELKLASMVQKAMNSTANVIATSGDISRCVLSGKCFEKEYGVHAFAKPDEIIEKMAAYMLKHKAVFVEEDQLQLSWWQKLWNKWKWLLSVLFPFAENLICFIPFFMLNNRTVGSRYFANLDPFLLYVLLFAIIYGQQQATFSAILAVAGYMFRQMYTRSGLEILLDYNTYVWVAQLFILGLVVGYMRDQIRTMRMESQELEEHLSRQIADIKDINESNVRVKGVMEQQLIDHKDSIGKIYSITSKLDQYMPDEVIFYAVEMLTKLMQTKDAAIYNVVNKDYARIFSASSKKARSLGNSIRYKDMTEVYQALSEKRVYINKRMNDQYPQMACAIFEEDEIQMIVMLWGLSWEKMTLGQANFLTVVSYMIQNAVLRAQRYVQALEAQRYKEGSRILSPEAFEPLVQAYMNAETRNLAECVLLKICISPDRQMEIDEKMISHLRDSDYLGMMTDGNLYVLLANTTRANAVFVQERFDRNGYNTEVVENIAVCHKE	non-KdpD DUF4118 protein
	3E-07	40	12.8	4.6E-07	39.4	8.9	1.3	1	T2LC93_9GAMM	Histidine kinase (EC 2.7.13.3)	HALA3H3_800094	Halomonas sp. A3H3	381	1346287	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Halomonadaceae, Halomonas, Halomonas sp. A3H3	>tr|T2LC93|T2LC93_9GAMM Histidine kinase OS=Halomonas sp. A3H3 GN=HALA3H3_800094 PE=4 SV=1MTFRKPMFKPFGQIANQLRLPMPSEILIALASTLIALLIAWGLYTWLALANLSLIFLTAVLASAVLAGSYAALLCAVLGFLTFNFCFTVPHFSLAVEEQEQLLTLLFFLLVALVVGKLAGDSRQRLLELSAARLAEEQERLRSALLSSVSHDLRTPLASIIGAASSLRTLDAQLSQQDRFALLDGVLSESERLNRYIQNLLDMTRLGHGDMKIERDWVAFDDLVASARKRLGSALEGFQVEQHWSKELPLLYVHPALIEQALVNVLENAARFSPPNGHITIEAQCRDDKRAGDPSILLFSVTDQGPGIPEALRERVFDMFVTGNDGDRSLHGSGLGLAICRGMLGAHAGQIHASPGPDNVGTRITMTLPLSAPSKDAENEH	139~~HisKA (0.0000000000089360 9)~~205;X;258~~HATPase_c (2.24748E-24)~~368	No DUF4118 detected by NCBI CDD
	3E-07	40	5.6	4.9E-07	39.3	3.9	1.3	1	A8MET0_ALKOO	Histidine kinase (EC 2.7.13.3)	Clos_0860	Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	446	350688	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus oremlandii, Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	>tr|A8MET0|A8MET0_ALKOO Histidine kinase OS=Alkaliphilus oremlandii (strain OhILAs) GN=Clos_0860 PE=4 SV=1MGKFGIGKESIIMVFIVGVLVVTVSTNGYIYGILASVISVFIFNYYFTVPLHTFITYHTNDIVLMVSFLVVSLISGTMTKRFQKQLLIAKKNEHTARLLYKVTESFLNITGKKNIIMQGIDYIYQNTSYSSKVFLSDAKEAYTDDSRAFVVDEMDIMEIPIKGLTKQLGIMQVAYSKKNFSLEHELLIKTVVTQMGISLDREFIYNERENIRIAMEREKMRSNLLRAISHDLKTPLTGIVGASGVILENLTKLDNCNIKKLVCDINEEATWLSNLVENILNMTRISEGKLMIEKNYEVVDDIVYEAIRHVKNFSNTKNISVSMPEEVVMVFIDGKLMVQVLINLLDNAMKHTGDDCKIQITVYVHNDSAVFEVSDNGSGIDNNIEDSLFDSFVTSSVKTIDGKRGMGLGLSICKSIIEAHQGTITAGRSKEGGALFRFTLPLMEEK	11~~DUF4118 (0.0000000000698153)~~85;X(133);218~~HisKA (0.000000000330039)~~284;X;339~~HATPase_c (1.23934E-26)~~440	non-KdpD DUF4118 protein
	3E-07	40	4.9	4.8E-07	39.3	3.4	1.4	1	U2RI88_9FIRM	Histidine kinase (EC 2.7.13.3)	HMPREF1546_00027	Oscillibacter sp. KLE 1745	893	1226323	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	>tr|U2RI88|U2RI88_9FIRM Histidine kinase OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_00027 PE=4 SV=1MEKTENSTPYSPRYGEAETGGTGRLKIFFGYAAGVGKTYAMLEAAHQAQKEGVDVVVGYVEPHARPDTLALLEGLEVLSCREVDYRGIRLREFDLDGALARRPQLILVDELAHSNAPGCRHTKRYQDVEELLQAGINVYTTVNVQHLESLNDLVTSITGIVVNERIPDHVFDRANQVELVDIAPADLEKLREEGKIYQRQRQAKQALENFFTAENLTALREIAMRRTADQLNRTAVQEKKGKAARAGDHILICLSSAPSNAKVIRTAARMAEAFHSGFTALFVQTPETKELSGENIKRLRSNLRLAEQLGAQIATVYGADPAEQIAEYARVSGITKIVMGRVNHRQHPWIGQKSLADRLIERTDLDVYIIPDRQPLYKKPLGKLRKSRVRFSWRDAVVTLLCLAISTAVGFAFDWAGFSESNIITIYILGVLVTAVSTSGHLYGAANSLLSVLAFNFFTFEPRFTLQADGPSYPVTFLIMLSSSIIASSLASRVKEQARMAAEKSYYTELLLGSSQKLQTIRTEWDCLRLTAEQLSRMFDRPVIYALNDADKELDFRIEPADEHTLLEKLSTEEIGVAKWVQKNNKHAGATTNTLPDSKWLFLSVRGTRGVMGIVGVPIAGYVVPDAFEKNLMVALLGECGLSQERIRLEEERNQIALQTQRESLQANLLRAVSHDLRTPLTNINGSVGILMGKDQTLKPEVREQLYTAIDDDTNWLINMTENLLAATQLETDRTKLKTAPELLEDLFQSAVRQLDRRARDHHISVDLEDQTLMASMNAGMIQRVIINMMNNAIQYTPKDSHIILSGTRRKDWVEISVSDDGPGIPDEAKKHLFDLFYTAEQGKPDSKRGLGLGLHLCQSIVNAHGGTITVSDHAPSGTTFRFTLPAVRTDGVK	20~~KdpD (1.57525E122)~~230;X;248~~Usp(3.68646E-36)~~370;X;396~~DUF4118 (0.000000000914884)~~479;X(183);662~~HisKA (0.000000175677)~~724;X;781~~HATPase_c (1.42911E-28)~~884	KdpD protein

	3E-07	39.9	8.3	5E-07	39.3	5.7	1.3	1	R5D6Y3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN705_00817	Firmicutes bacterium CAG:555	649	1263030	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:555	>tr|R5D6Y3|R5D6Y3_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:555 GN=BN705_00817 PE=4 SV=1MEEILVCLSGAPSNVRVIKAAAKMAEAYGGNLTALYVEPPDFHEHDPGAKSRLEENFRLAHRLGAKVTRLYGEDAATQIAEYARVSGSTKIVIGKSPTHTSVFRKKTLIDRLNELAPDIDIFIIPDKATPSEKAHRLSFSDEKFSVADVLKTLGLLTAATLGGLVFTKLGFSTANVIILYTLAVLGIAVTTTGRSYSLASAVLSVFVFNFLFTVPEYSLSAEPNEIATFVVMFIAAIIISSLTTQVKRQARLKAQHSYRTEILLETSQRMQKAESEEQILSLAATQLGKLSGRGVMIFPVKDGTLGEPMLFPSVEGEDFAPYLAQSELAAAMQALATGHGTGCGTQSFPNAKGLYMSIRSAEGVLAVVCFAVNGKPERESYSKSLTVAILDECGIMLENERYKLAKREMEEKARVQELRANLLRSISHDLRTPLTGISGSASLLLTGKMSEDKRTELLKSIRDDSEWLITLVENLLCITRIEGRDKLTELEPELVGEVIADAMTHIDRSSAQHKVTTVIADDYLMAYMDARLIEQVLINLVNNAVKYTPAGSTICVSAESSGGSVLVSVSDNGPGIADESKGKIFDMFYTEAKTGDSRRGLGLGLALCKSIVTAHGGEISVSDAEPHGAVFTFSLPEVKTDEQGTDTGR	35)~~125;X;150~~DUF4118 (0.000000000008846 83)~~249;X(167);416~~HisKA (0.000000000000288 625)~~476;X;533~~HATPase_c (8.48101E-29)~~635	non-KdpD DUF4118 protein
	3E-07	39.8	10.9	6E-07	39	7.6	1.4	1	R2SE20_9ENTE	Sensor histidine kinase KdpD	UAU_02476	Enterococcus pallens ATCC BAA-351	863	1158607	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus pallens, Enterococcus pallens ATCC BAA-351	>tr|R2SE20|R2SE20_9ENTE Sensor histidine kinase KdpD OS=Enterococcus pallens ATCC BAA-351 GN=UAU_02476 PE=4 SV=1MAVTNSSEIQQPFTQRGKLRVFFGFAAGVGKTYAMLAEAHELLALGKDVVVGYVEPHDRPETNQLLEGLPQMPLKAVTYKQLTLYEPDIDRIIERQPDVVIIDELAHSNAAGSRNRKRYQDVDELLNAGISVMTTVNVQHIESLNDIVEVTGIEVKETVPDTFFQQALLKVIDVEPDELIERLEQGKIYSNENAKRALQNFFIPQKLEQLRGLAIQRASDHINRVGGKNTGVQVKLLTIIHDTLPKMAEKCIRWSSRLAQGLGAEWVVIQIRSLDTKSTGVPLAEKLGAQVISIEEDDSFETIVEYAKMIGVTDIIMGKNLSRRWYHALFSEEFEDRLLRRLSATEVHLIPYKEAQPSIFAYPKKVIEGGAKDFGIALSGVVAATLVTELMQYLHVGDQNLMLIYIFFILLVARLTSGYFWSALSSILSVLSFNWFFVEPLYSLTVYKQGYPITLVIMLIVALMISNLMVRLKAQAVRSKEKEHQMEILYELNKQYVLAENSQQIFEITTTYLSRLLNREVIFYDPAGEKKSVSVPENKTSKLSGAEEAAVAFWSAKNQKEAGNGTDTLVGSKGFYLPILSGGQSLGVLGIQRNRSQVLENSQLNYLRLVLTQIAVVLEQANLKSEKEKIEIENEREKVRSNLLRAVSHDLRTPLTAISGLAETMEKNPEIKPATREKLLADIQEESQWLIRMVENLLSITRINMDTMKVDKTEESLEEIVEAVYKHIKKVYPQRAIQVTLPEDFILLKVDPILMEQALFNLIENALRHGDGKLPVQLTAYQNEQRTIFEIENAGEIPLAQFQRIQNNLISDQEVPVDSKNGLGIGLSIVKTIVHAHGGQLEIETKPGRTIFRLALRRENHG	115)~~223;X;244~~Usp(1.04666E-25)~~352;X;382~~DUF4118 (9.17845E-15)~~476;X;504~~GAF (0.00000159629)~~620;X;638~~HisKA (0.000000000000701565)~~703;X;756~~HATPase_c (1.53396E-15)~~857	KdpD protein
	4E-07	39.8	10.3	6.9E-07	38.8	7.1	1.4	1	A0A0F5FJ97_9RHIZ	Histidine kinase	VE26_00560	Devosia chinhatensis	886	429727	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia chinhatensis	>tr|A0A0F5FJ97|A0A0F5FJ97_9RHIZ Histidine kinase OS=Devosia chinhatensis GN=VE26_00560 PE=4 SV=1MDRLDDERRPDPAALLQLAARERRGKLTIFLGMAPGVGKTYAMLERANALAANGTDVVVGLAETHGRNETAVLAEGLETLPRVEGARPYGEFDLDAALLRRPQLLIVDELAHTNSPSARHPKRYQDIAELIDAGIDVWTALNIQHVESLSELVGHITGIPVRETVPDVVLKKADEVVLVDLPPAELIERLKAGKVYLPDNAERALDGFFKPATLTALRELSLRRAADRVDDQMVDFLRQGAIEGPWATGERLLVCVGYDDMSERLIRDASRLASGLNARWTVLSLSHPHRLAPHQEAIDRLEATLRQAERFGAEIRRETASDYVKAILRLARRGNFTQIVIGQNRKNAFWRRSLPDALLRQAGEIGVHVVSGQGARAPVRAVRRRTLPEWTLTLGLPVLAVSATTLLGLGLSAIIALQNLSMMYLAAVLLSAMLAGRFSALLASLLSFLAYNFFFIDPTGRLTIAQPEEVLSLAIFVAVALVSGQLAARLRLSMDRTSQRARQAQALLDFARKMSAAFGQDQVLDTMASHLHGALGRPAVVLASDDGGELTLMTAWPPDQNLNDAAMTAARWALEKREAAGFLTGTLPQVSYLFLPVQSGQRVLGVVGLGMRHEDGPVSDAEQRTINALLEQSAIALDRARLTQDSTRASVTRESAKVQSALLSSLSHDLRTPLASITGAVTSLRELGDRMPAAARADLLASIEEEAGRLNRFVTNLFEMTRIEAGIVRAKRDPLDVAMVIKAAVNRALRLHPHLQVDVSVADRMPLATGDQVMLEQVLFNLLDNARKYAGDAPVTIYARREGSDVSIAVTDQGKGIPEGDLERIFEKFYRRAEGDGRQAGTGLGLAIARGLVAAMGGTIKAESPALRRRGTRFIIRLPRAGEESA	108)~~229;X;251~~Usp(2.57129E-29)~~371;X;398~~DUF4118 (0.00000266871)~~491;X;521~~GAF (0.000000000047010 6)~~639;X;659~~HisKA (0.000000014829)~~722;X;775~~HATPase_c (1.54661E-28)~~878	KdpD protein
	4E-07	39.7	10.7	5.6E-07	39.1	7.4	1.3	1	R6D8H7_9FIRM	Histidine kinase (EC 2.7.13.3)	BN718_00148	Ruminococcus sp. CAG:579	371	1262963	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:579	>tr|R6D8H7|R6D8H7_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:579 GN=BN718_00148 PE=4 SV=1MTVNSIKSSKAFSVFKDSAICLVVLTAATLAGYAFKAFQLADADIIMLYIIAVLVISIFTSKIYFCLISSLVGVMLFNCFFTYPEFSLLAHDAGYPVTFVMMFITAFIAGTLANKLKRNILIAEQNAREKEEAALLAQNEQLRADMLRSISHDLRTPLTSISGNASTLISGGDTLDESARQQIYTDIYSESMWLIEMVENLLYATRIEDGRMQLNISVEILDDIVQEAVRHTKRTHPKRNIIVDMYDEIIPVMADANLIVQVIVNLMDNAVKYSDEDSDVTVSVRRENAYAVISVSDHGTGISDEEKEKVFDMFYTGGSRSSDSRRSLGLGLALCRSIITSHGGTISVSDNIPNGTVVSFTLPIGEVDLNE	075)~~119;X;140~~HisKA (0.000000000025467 5)~~206;X;259~~HATPase_c (5.656E-25)~~362	non-KdpD DUF4118 protein
	4E-07	39.7	6	5.8E-07	39.1	4.2	1.3	1	H2FTB1_OCESG	Uncharacterized protein	GU3_07670	Oceanimonas sp. (strain GK1)	435	511062	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Oceanimonas, Oceanimonas sp. (strain GK1)	>tr|H2FTB1|H2FTB1_OCESG Uncharacterized protein OS=Oceanimonas sp. (strain GK1) GN=GU3_07670 PE=4 SV=1MLWDNPRLPPWLPSLGGPLLAVVLLLPLRGWLTTTDIAMALLLVVAIIAVRQGSRRASLATVLSVLLFDVLFVEPYYTLHVHNLDYLLTFAVMLAVGLLISRLSGQLRGRLERVRQLLRQLRGMFLLARGLPGHGRPEAMYAFVTQLLTRRLGSPVSIALKPPAAGEALPVFDKQQVVSYLCCASGPYRANRTLLRVAASLLGQALTRARLAGAEQQARLEAELASGRNALLRSLSHDLRTPLASIMGNASMLADPQVRLEEQEYREIAEAIYQQSRVLSSHFDKVMELNRVQRQDAVVAQALMPEEVVSAALRRRGNLFDTVHFDIDIDNKVPIHGDDTLLEIALANMLENAVRHGLPPYRLEGRWHGELYDFILTNGKPVRPAQPRGDGGAGLGLPICRAVADWHQGSFYLTEGDDGRVAVSHLVWPAWRTQP	(0.000000000637512)~~110;X(118);228~~HisKA (0.000000000549979)~~291;X;342~~HATPase_c (0.000000466683)~~414	non-KdpD DUF4118 protein
	4E-07	39.7	10.6	8.1E-07	38.6	7.4	1.5	1	A5FWF2_ACICJ	Histidine kinase (EC 2.7.13.3)	Acry_0713	Acidiphilium cryptum (strain JF-5)	867	349163	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acidiphilium, Acidiphilium cryptum, Acidiphilium cryptum (strain JF-5)	>tr|A5FWF2|A5FWF2_ACICJ Histidine kinase OS=Acidiphilium cryptum (strain JF-5) GN=Acry_0713 PE=4 SV=1MGSASPENRPDPDALLARANSDGRGQLKIFLGAAPGVGKTWEMLAAARRRFETGTDVVVGLVETHGRAETAEQLADLPVLPRRIVPYRGRLLEEFDLDAALKRRPALLLVDELAHANAPGLRHAKRWQDVAALLEAGINVWTTLNVQHLESLNDQVARITGIRVAETLPDTVLGLADDIELIDLPPEELRTRLKQGLVYRPDVARRALGGFFRPGNLAALREMALRRVAQHVDRDIAAYMRAQAIAGPWPAAERVMAVVEAGEAAEQVVRHASRLAEALRAPFFAFHAERAATGMAVQPALDLAIQLGGTVETTTNADVFAALLDAAARQNVAHIVIARGRGRWRWRRGLASRLARGARAYALHVVPDPAASRPAPPHRAPPPKLMPFGISLGIMILTTIGGFALRGVLPAEAMGYVFTAIVVGMASLYGRSVGIFAALTGFVLWNFFFLPPIYTLSVTNPRDVTALFAFLVVGVLTGSLAGRVRAEAETARTRIEALRRITLFGRALAQVSDEAGLAAVVEAEARALAGEAVLLLARDDGLPRAGGFDEAAVAAAEFAWRNRVATGMGTTTLPASAWRFQPLATEAGAIGVLGVRPETPPAEPVIQTLGALADQAALAAERLRLATSAAEARAHESTQRLRTALLSSLSHDLRTPLTAIRGAAETLAEADGELPEATRRDLLASIVEDVGRMTRFLANITGMARIETGEIVARHEKVDLAPVVEHAVARVKEAFHTAVNIPEDAATVRADPALLEQVLVNLLENAVKYGPEGGAISVFARRAGDSVVLSVADEGVGIPPEDLPHVFNSFFRVVRGDRVAPGTGLGLAIARAFVEAMGGTIAAESPRRDLPADGLPGTIIRVELPVP	114)~~232;X;254~~Usp(4.44242E-14)~~367;X;387~~DUF4118 (0.000000000011549 9)~~487;X(152);639~~HisKA (0.000000000069013 9)~~705;X;755~~HATPase_c (2.34419E-28)~~864	KdpD protein

	4E-07	39.7	11.3	5.9E-07	39.1	7.8	1.3	1	R7CM67_9FIRM	Histidine kinase (EC 2.7.13.3)	BN806_02467	Ruminococcus sp. CAG:9	521	1262967	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:9	>tr|R7CM67|R7CM67_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:9 GN=BN806_02467 PE=4 SV=1MSLKNVNHQKRSFTWSMEKPSAKDYFLTVFIFAVCTLIGLLFQKLNFTDTNIVTIYILGVLITSIVTDGYLCSVAGSFLSVFLFCFFLTEPRMSFKTYAVGYPVTFFIMLISSVLTGALAAKLKTHAKLSTQLAFRAQILFDTDRLLQNAKGETEILDVTCTQLLRLLNRNITAYVVENGTLSEGKLFSGEKEDTEDFLIPEEQQIARWVCENRQHAGASTHHFPQAKCLYLAIRSGDNVYGVIGIPLQKETLDTFEYSILLSVINECALAMENAKNALEKEKNAVMAKNEQLRADLLRAISHDLRTPLCSISGNADMLLGNSDRLDEATKHQIYSDIYDDSEWLIGVVENLLSITRLNDGRLKFKFTDQLLDEVIAESLRHISRKHDDYKIVTDCEELVLARMDVRLIMQVLVNLVDNAIKYTPPGSVIFIRGTKTDGKAQISVEDNGPGIPEEMKTHIFEMFYTGKTTVADSHRSLGLGLALCHSIIEAHEGTLVLTDHDPHGCNFTFTLPLSEVTLNE	>tr|R7CM67|R7CM67_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:9 GN=BN806_02467 PE=4 SV=1MSLKNVNHQKRSFTWSMEKPSAKDYFLTVFIFAVCTLIGLLFQKLNFTDTNIVTIYILGVLITSIVTDGYLCSVAGSFLSVFLFCFFLTEPRMSFKTYAVGYPVTFFIMLISSVLTGALAAKLKTHAKLSTQLAFRAQILFDTDRLLQNAKGETEILDVTCTQLLRLLNRNITAYVVENGTLSEGKLFSGEKEDTEDFLIPEEQQIARWVCENRQHAGASTHHFPQAKCLYLAIRSGDNVYGVIGIPLQKETLDTFEYSILLSVINECALAMENAKNALEKEKNAVMAKNEQLRADLLRAISHDLRTPLCSISGNADMLLGNSDRLDEATKHQIYSDIYDDSEWLIGVVENLLSITRLNDGRLKFKFTDQLLDEVIAESLRHISRKHDDYKIVTDCEELVLARMDVRLIMQVLVNLVDNAIKYTPPGSVIFIRGTKTDGKAQISVEDNGPGIPEEMKTHIFEMFYTGKTTVADSHRSLGLGLALCHSIIEAHEGTLVLTDHDPHGCNFTFTLPLSEVTLNE	(8.57461E-14)~~126;X;155~~GAF (0.000221026)~~274;X;291~~HisKA (0.000000000178108)~~357;X;409~~HATPase_c (1.09775E-28)~~512	non-KdpD DUF4118 protein
	4E-07	39.6	4.9	6.7E-07	38.9	3.4	1.4	1	E7GKF9_CLOSY	Histidine kinase (EC 2.7.13.3)	HMPREF9474_01404	[Clostridium] symbiosum WAL-14163	661	742740	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	>tr|E7GKF9|E7GKF9_CLOSY Histidine kinase OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_01404 PE=4 SV=1MSELTGGRSNRSFTEEHILVCLSGSPTNAKIIRTAARMAGAFKGSFTAVFVETPDFASDSDENKDRLRQNTRLAEQLGATIETVYGDDIAFQIAEFARLSGISKIVLGRSSTRRSFLGPPPLTERITRLSPNLDIYIIPDQNSRPYRAGARGSNRRILNTADLIKSVSVLAAATLICCIFDCLGLSEANIITIYILGVLVTAVITRHRIYSLTSSVICVLLFNFLFTEPRFTLNAYDPGYLATFPIMLIAAFLTSSLAVKIQRQARQAAETAYRTKVLFDTNQSLSNEKDMTGMITVTCNQLTKLLDRDILFYRIQDDGLAAPQLFAVNSGENVSDYADDNERAVASWVYHNNKRAGATTGTLGNAKCLYLSVRLAQEVFGVVGIAIDGRPLGAFENSIMLSILGECALALRNDKVSKESAAAALLAKNEQLRSNLLRSISHDLRTPLTSISGNAGILLSSEQSIGKEKRRKLYEDIYDDSLWLINLVENLLSVTRIEDGTMKLRLATELLDEVVGEALRHTDRRRCEHKIKIKQEEDFLLVKADARLIMQVIINLVDNAIKYTPPGSEVVIETKREGNLAVVTVADNGDGISDESKEHIFDMFYTAATKIADSRRSLGLGLALCKSIITAHGGTISVEDNVPHGAVFTFTLPMEEVTLHE	>tr|E7GKF9|E7GKF9_CLOSY Histidine kinase OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_01404 PE=4 SV=1MSELTGGRSNRSFTEEHILVCLSGSPTNAKIIRTAARMAGAFKGSFTAVFVETPDFASDSDENKDRLRQNTRLAEQLGATIETVYGDDIAFQIAEFARLSGISKIVLGRSSTRRSFLGPPPLTERITRLSPNLDIYIIPDQNSRPYRAGARGSNRRILNTADLIKSVSVLAAATLICCIFDCLGLSEANIITIYILGVLVTAVITRHRIYSLTSSVICVLLFNFLFTEPRFTLNAYDPGYLATFPIMLIAAFLTSSLAVKIQRQARQAAETAYRTKVLFDTNQSLSNEKDMTGMITVTCNQLTKLLDRDILFYRIQDDGLAAPQLFAVNSGENVSDYADDNERAVASWVYHNNKRAGATTGTLGNAKCLYLSVRLAQEVFGVVGIAIDGRPLGAFENSIMLSILGECALALRNDKVSKESAAAALLAKNEQLRSNLLRSISHDLRTPLTSISGNAGILLSSEQSIGKEKRRKLYEDIYDDSLWLINLVENLLSVTRIEDGTMKLRLATELLDEVVGEALRHTDRRRCEHKIKIKQEEDFLLVKADARLIMQVIINLVDNAIKYTPPGSEVVIETKREGNLAVVTVADNGDGISDESKEHIFDMFYTAATKIADSRRSLGLGLALCKSIITAHGGTISVEDNVPHGAVFTFTLPMEEVTLHE	17~~Usp(4.97691E-39)~~139;X;163~~DUF4118 (0.000000000100963)~~264;X(166);430~~HisKA (0.000000000029909)~~496;X;549~~HATPase_c (2.30652E-28)~~652	non-KdpD DUF4118 protein
	4E-07	39.6	9.7	8.3E-07	38.6	6.7	1.5	1	D9QFM8_BRESC	Histidine kinase (EC 2.7.13.3)	Bresu_3237	Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (Caulobacter subvibrioides)	902	633149	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Brevundimonas, Brevundimonas subvibrioides, Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) (Caulobacter subvibrioides)	>tr|D9QFM8|D9QFM8_BRESC Histidine kinase OS=Brevundimonas subvibrioides (strain ATCC 15264 / DSM 4735 / LMG 14903 / NBRC 16000 / CB 81) GN=Bresu_3237 PE=4 SV=1MSPDPPVEAGRLSRRPRRGRLKVFLGMSPGVGKTYEMLRAARRRKAEGGDVVVGVVETHGRKETESLLRGLEVMARRPIEHRDRTLLEFDIDGAIARRPELLLVDEYAHSNAPGSRHPKRWQDVEEILDAGIDVWTTLNVQHLESLSDVVLRITGVRQREAVPDSALSRADDIEVVDITPEELRKRLEEGKVYVPETARLASQNFFRIENLTALRELALRRAAQTVDDQLVATLRERGVQGPWAAGERVLVLIGGDGMAGMLVRTGRRMSDMMMDAPWTVATVDRPSSASGDVGRAQRLAEAFKLAEQLGGRTVLLTGDDVVRTVSDYAHRNNITQIVLGRSVVTGWRARFSEVFGRSLAAELLRAARGVAIHVVTDAATPDTPASRPAVPAGERLWDGRGYAIGAAFVAFATGLALLLDRSFERVDLGVLYLSAVLAAGVLYGLRPALAAATAAFLVYNFLFLEPRYSFAIGSPTDFLTLFVFWAVATVTGVLAGRVREQARRAQRRASAVSALLVASQSLSAAEDRGTAARVLAEQTAAAAGARAVVLLPEGEDIAVAALAPLKAGATEPPHTLSPADMAAARWAWERGEAAGHGTGTLPQTRWTFRPLNGVRKRSGVAGVEAAALAPGSDEERLALAVMDQGAVALERAELAGQALETETLRRTDRFRGALMNSVSHDLRTPLSTVLGSATTLIDYGETLKPEVRADLLTSIREEAERLNRYVGDLLDMTRLEGGGLNVKADWTDVRDVLNAAAERVSWRLGTRDLTRDFPADLSLVMLDQGLLEQAVVNILENAIAYSPDGSRIELAAYEDRGSVVISIEDEGRGIPTAELERVFDKFRRMDEPSDRSQGAGLGLAIAKGFVEAMNGRIAAASPIHGDLGTRVLISLPKAIATHHQLL	22~~KdpD (1.55093E110)~~226;X;248~~Usp(5.4013E-34)~~376;X;406~~DUF4118 (0.000000148723)~~500;X(168);668~~HisKA (0.000000000005224 14)~~734;X;787~~HATPase_c (1.77035E-24)~~891	KdpD protein
	4E-07	39.6	13.4	8E-07	38.6	9.3	1.5	1	H6R5W2_NOCCG	Histidine kinase (EC 2.7.13.3)	kdpD NOCYR_3889	Nocardia cyriacigeorgica (strain GUH-2)	865	1127134	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia cyriacigeorgica, Nocardia cyriacigeorgica (strain GUH-2)	>tr|H6R5W2|H6R5W2_NOCCG Histidine kinase OS=Nocardia cyriacigeorgica (strain GUH-2) GN=kdpD PE=4 SV=1MKRGHLRIYLGAAPGVGKTYAMLGEAHRRLERGRDVVAAVVETHGRAKTAALLDGIERIPPKVIEYRGTAFQELDVAAVLRREPAVVLVDELAHTNAPGSKNEKRWQDIEELLDAGIDVISTVNVQHLESLNDVVEQITGIQQRETVPDAVVRAAEQIELVDITPEALRRRMSHGNVYAADKVDAALRNYFRPGNLTALRELALLWLADQVDAALAKYRADHRITDLWEARERVVVAVTGGPESETIVRRARRIATKSSAELVVVHVVRGDGLAGVSTARLTRLRELAAGLDASLHTVTGEDVPAALLEFAREVNATQLVLGTSRRSRWARIFDEGIGSAVVQQSGKIDVHMVTHEEANRRRSWPSLRRPVWAWVAALVVPVLVCAIGAWFLDGALELGGLSAMFFVAVVLVSLLGGVLPAAISALLSGVLLNWFFAEPRYSLTVAEPDSIFTIAVLLIVAVAMAALVDRAAARSRQARKASRQAELLTVFAGAVLHGADLPKLLEQVRETYGMRAVALVAGEDVLAAVGAEPPCRPGDADTTIEAGDTVHRLLLAGHPLDPGDRPVLTAVANQAVGLVRQARLAEEAGAAAALLEADRLRRALLSAVSHDLRTPLAGAKAAVSSLRSDDVEFSPEDTAELLETVEESVDQLTALVGNLLDSSRLAVGVVSPQLRQVYLDEVVHRALVGVGMGARGLRRAAMDRVEVDVDALSVRADGGLLERVLANLIDNALRHSTPGTPIRITAERDGGKVAIAVVDIGPGIPAGAEEQLFEPFQRLGDRDNSTGVGLGLSVVRGFVEAMGGTVHAEPTPGGGLTMLVELPAGADAAPPRDSDESGEGPATMDSAGSSRGDDPAQGPDRAGVT	1~~KdpD (4.1814E-122)~~211;X;233~~Usp(1.47277E-33)~~354;X;389~~DUF4118 (0.000000000088230 6)~~469;X(129);598~~HisKA (0.000000000001013 32)~~664;X;721~~HATPase_c (3.03138E-28)~~822	KdpD protein
	4E-07	39.6	12.8	7E-07	38.8	8.9	1.3	1	G0FV52_AMYMS	Histidine kinase (EC 2.7.13.3)	RAM_09620	Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	845	713604	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis mediterranei (Nocardia mediterranei), Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	>tr|G0FV52|G0FV52_AMYMS Histidine kinase OS=Amycolatopsis mediterranei (strain S699) GN=RAM_09620 PE=4 SV=1MTTENGPAKPRRGELRIYLGAAPGVGKTFAMLGEARRRLDRGTDVVVGLVETHGREKTAVLLEGLEIVPRRHAEHRGRAFDEMDVDAILARAPEVAVIDELAHTNVPGSRNAKRWQDVEELLTAGIDVLSTVNVQHLQSLNDVVERITGVTQQETVPDEVVRRAEQLELVDITPEALRRRLAHGNVYPAERIDAALGNYFRPGNLTALRELALLWVADQVDVALQRYRAEQRITDTWEARERVVASITGGPESETLIRRASRIATRAGAELQVVHILRGDGLAGISPAAMARCRKLAEEVGATFHTVVGDDVPGALLDFARGVNATQLVLGTSRRSRVARLFDEGIGAAVVRRSGPIDVHMVTHSEAGGRLRTGLTASPLGLSRLVTGSVLGVVLPVLVTLVGVFVPTGLDFATDVIAYVLVTVVVALVGGLGPALVAAVLGAGLLNFFFTPPLYTLNVHTPQNLVTLIAMVVAVLVALVVDQAARRAAQAARARTEAALLASYARTVLTHANPIERLLAKVRENFALTSVTLLEKQDGVWQCVATAGEHPCADPDEADADIAVTADVHLTLRGRALPAADRRVLEAVAGQALLALRQQRTAAAAARAERKAEATELRTTLLSAVGHDLRTPLTSIKASIGSLRAADLELSEEDTAELMEAIELSADRLAGLIDNLLDSSRLATGAVRPHLRPVGYDEVVAHALSTVDGSDDVVVAVDDQLPSVLADPGLLERVVANVLDNALRHGGAPVSARASAHSGQVELRIVDHGKGLRKGAADSAFAPFQRLGGDRDTTPGVGLGLSVAKGFTEAMGGTIRAEDTPGGGLTVVVSLPAFSVEFEQEGVR	10~~KdpD (1.74823E122)~~220;X;242~~Usp(1.35597E-34)~~363;X;431~~DUF4118 (0.0000173857)~~471;X(146);617~~HisKA (0.000000000046309 3)~~682;X;732~~HATPase_c (9.85484E-21)~~832	KdpD protein

	4E-07	39.5	10.1	6.3E-07	39	7	1.3	1	R6GU74_9FIRM	Histidine kinase (EC 2.7.13.3)	BN476_01227	Eubacterium hallii CAG:12	524	1263078	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium hallii CAG:12	>tr|R6GU74|R6GU74_9FIRM Histidine kinase OS=Eubacterium hallii CAG:12 GN=BN476_01227 PE=4 SV=1MEENERREGVLKQHFALYAKKPSMKDCFVTVFIFMICTIIGLLFQKLHFTDTNIVTIYILGVLITSILTDGYLCSIAGSFLSVVLFCFFLTEPRMSFQTYAVGYPVTFAIMLVCSVLAGTLSAKLKMHARIYSQLAFRTQVLFDTDRLLQKARSSKEMLRVTCTQLVRLLNRDIVAYIVEEGKLSQGQVFYKNKEETDQQFLIPEEQKIARWVYENNKRAGVGTNYFKNAKCLYLAIRIGDHVYGVIGIPANKDVFDSVEYSILLSVVNECALAMENLRNAIEKEKNAVLAKNEQLRADLLRAISHDLRTPLCSISGNADMLLNNGACLDSKTKQQIYVDIYDDSEWLIGVVENLLSITRLNDGRLKFKFTDQLLDEVIAESLRHISRKHDEYTIVTKCEEELILVRMDVQLIIQVLVNLIDNAIKYTPKGSKICIRGMKCNGKAQICVEDNGPGIADEMKPYIFEMFYTGKSTIADSQRSLGLGLSLCQSIIEAHDGRLLLTDNTPRGCIFTFTLPLSEVTLNE	28~~DUF4118 (0.000000000001701 27)~~126;X;157~~GAF (0.0000000307759)~~277;X;294~~HisKA (0.000000000181729)~~360;X;412~~HATPase_c (2.21297E-27)~~515	non-KdpD DUF4118 protein
	4E-07	39.5	12.3	7.2E-07	38.8	8.5	1.4	1	V9XNV1_9NOCA	Histidine kinase (EC 2.7.13.3)	Y013_25420	Rhodococcus pyridinivorans SB3094	843	1435356	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus pyridinivorans, Rhodococcus pyridinivorans SB3094	>tr|V9XNV1|V9XNV1_9NOCA Histidine kinase OS=Rhodococcus pyridinivorans SB3094 GN=Y013_25420 PE=4 SV=1MTSTAPNTSRPLRRGRLRIYLGAAPGAGKTFAMLGEAHRRLVRGTDVVVAIVDTHGRARTAEQLAGLEIVPPRRRTYRGTEFEELDLDAVLARRPAVALVDELAHTNAPGSRHPKRWQDVEELLDAGIDVLSTVNIQHLESLNDVVEQITGVVQRETVPDDVVRRAEQVELVDITPQALQRRLAHGNVYAAEKIDAALRNYFREGNLTALREIALLWLADQVDVALAKYRGDHAITATWEARERVVAAVTGGPESETLVRRASRIAGRAGAELMVVHVVRGDGLTGVSAPQMTKVRTVAESVGASVHSVVGDDVPTTLLDFAREVNATQLVIGTSRRSRWARILDEGISSAVVRDSGRIDVHMVTHEHTSRAPKMALLGRHDHRLQSWIAAILIPFVATALMAGVDRLSGVAGQNALFFVVILVVALFGGVGPAIVAALLSGLLLNFFFTEPRYSFTIAEPDNFVTTIVLLVVAVAVAALVDAASARAREARLASQEAELLASFAGAVLRGADLPQLLEKVRETYSQDGVSLLRSDRNSPKLLGTAGTAPPMSQHAADTACEVDDSAYALLLAGPQLRARDRRILTAVAGQAAALVRQQELAAEASHASSLAETDRLRRLLLSAVSHDLRTPLAAIKASASSLRSTDIEFSPEDTAELLATIEESTDQLTALVSNLLDSSRLAAGVITPVVTPVYLDEVIHRALLTLTNGESELSRTIRERIHIDVGEATVAADGALLERVVANLLDNALRYAPTGPIRVESITSDGRTVLTIADTGPGLHHKDTDTFPRAGDHRATGGAGLGLTVARGFVEVMGGNLTTTDTPGGGTTMVVDLAAAPVEVRP	13~~KdpD (4.60305E120)~~222;X;244~~Usp(8.31841E-33)~~365;X;388~~DUF4118 (0.000000000610547)~~466;X(149);615~~HisKA (0.000000000000280297)~~681;X;738~~HATPase_c (3.18853E-17)~~818	KdpD protein
	4E-07	39.5	10.6	9.3E-07	38.4	7.3	1.5	1	A5FU13_ACICJ	Histidine kinase (EC 2.7.13.3)	Acry_3493	Acidiphilium cryptum (strain JF-5)	867	349163	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Acetobacteraceae, Acidiphilium, Acidiphilium cryptum, Acidiphilium cryptum (strain JF-5)	>tr|A5FU13|A5FU13_ACICJ Histidine kinase OS=Acidiphilium cryptum (strain JF-5) GN=Acry_3493 PE=4 SV=1MGSASPENRPDPDALLARANSDGRGQLKIFLGAAPGVGKTWEMLAAARRRFETGTDVVAGLVETHGRAETAEQLADLPVLPRRIVPYRGRLLEEFDLDSALKRRPALLLVDELAHANAPGLRHAKRWQDVAALLEAGINVWTTLNVQHLESLNDQVARITGIRVAETLPDTVLGLADDIELIDLPPEELRTRLKQGLVYRPDVARRALGGFFRPGNLAALREMALRRVAQHVDRDIAAYMRAQAIAGPWPAAERVMAVVEAGEAAEQVVRHASRLAEALRAPFFAFHAERAATGMAVQPALDLAIQLGGTVETTTNADVFAALLDAAARQNVAHIVIARGRGRWRWRRGLASRLARGARAYALHVVPDPAASRPAPPHRAPPPKLMPFGISLGIMIVTTIGGFALRGVLPAEAMGYVFTAIVVGMASLYGRSVGIFAALTGFVLWNFFFLPPIYTLSVTNPRDVTALFAFLVVGVLTGSLAGRVRAEAETARTRIEALRRITLFGRALAQVSDEAGLAAVVEAEARALAGEAVLLLARGDGLPRAGGFDEAAVAAAEFAWRNRVATGMGTTTLPASAWRFQPLATEAGAIGVLGVRPETPPAEPVIQTLSALADQAALAAERLRLATSAAEARAHESTQRLRTALLSSLSHDLRTPLTAIRGAAETLAEADGELPEATRRDLLASIVEDVGRMTRFLANITGMARIETGEIVARHEKVDLAPVVEHAVARVKEAFHTAVNIPEDAATVRADPALLEQVLVNLLENAVKYGPEGGAISVFARRAGDSVVLSVADEGVGIPPEDLPHVFDSFFRVVRGDRVAPGTGLGLAIARAFVEAMGGTIAAESPRRDLPADGLPGTIIRVELPVP	23~~KdpD (2.94869E113)~~232;X;254~~Usp(4.31871E-14)~~367;X;387~~DUF4118 (0.000000000017143 2)~~487;X(152);639~~HisKA (0.000000000063334 5)~~705;X;755~~HATPase_c (1.06629E-28)~~864	KdpD protein
	5E-07	39.4	9.9	8.3E-07	38.6	6.9	1.4	1	R3WCP8_9ENTE	Sensor histidine kinase KdpD	UC3_01132	Enterococcus phoeniculicola ATCC BAA-412	854	1158610	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus phoeniculicola, Enterococcus phoeniculicola ATCC BAA-412	>tr|R3WCP8|R3WCP8_9ENTE Sensor histidine kinase KdpD OS=Enterococcus phoeniculicola ATCC BAA-412 GN=UC3_01132 PE=4 SV=1MQGTEELGDERRGRLRVFFGFAAGVGKTYGMLAEAHELLLMGKHVAIGYIEPHDRPDTNRLLEGLPNIPPKIFTYKQLVLTEPDIDRIIQEKPEVILIDELAHTNATGSRNNRKRYQDVDELLNAGIDVFTTVNVQHIESLNDIVEEVTGIEVKETVPDTFLQQATIKVIDVEPDELIERLEQGKIYANENAKRALQNFFIPKKLDQLRGLAIQRASDHINRISGKTVGIQSKLLTVVTDVFPKMTEKCIRWTARLAQGLGAEWTVIQIRTQEETPTNIPLADKLGAEVISIEEDGSFETIVEFAKMTGVTDIIMGKNLRQPWYEKIFVEAYDDRLLRRLNDTELHLIPFKEEKQTLFSKTRKIIEGGGKDLSIALGGVFLATVITELMQYIHVGDQNLMLMYIFFILLVARTTSGYFWSALSSILSVLSFNWFFVEPLYSLTVYKQGYPITLLIMLVVALMISNLMVRLKKQADSSMEKEHQMEILYELNKKYMLAESRKQILEISVTYLSRLLEREVIIFDQQANMQSVHCVEDKSSVLNQKDEAAVAFWAAKNQKEAGNGTDTLIGAKGFYLPIIASGKTLAVLGVERNATLDLENDQLNYLKLVLTQIASILEQTELKTEKEQVELENEREKVRSNLLRAVSHDLRTPLTVISGIAETLGLGTDLKEETRQKLVKDIQEESQWLIRMVENLLSITRINMDTMKVTKTSEPVEEIIEAVYKHLKKVYPEGQVRIQLPETVIFIQADPILIEQALFNLIENAFRHGDKNQLVLNLIVYQENGQTVFEIENYGEIPLKQFQKIQSNLSSTNEVPVDSKNGLGIGLSIVKTIIHAHNGKMEMKVGEGKTVVKIYLK	10~~KdpD (3.30464E115)~~219;X;232~~Usp(7.90412E-30)~~348;X;378~~DUF4118 (2.33902E-14)~~472;X;501~~GAF (0.00000716288)~~616;X;634~~HisKA (0.000000000000548768)~~699;X;752~~HATPase_c (0.000000000001492 52)~~853	KdpD protein
	5E-07	39.4	1.9	7.5E-07	38.7	1.3	1.2	1	R7JVV9_9FIRM	ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein	BN630_00466	Blautia sp. CAG:37	331	1262757	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:37	>tr|R7JVV9|R7JVV9_9FIRM ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein OS=Blautia sp. CAG:37 GN=BN630_00466 PE=4 SV=1MEKEKQKTERKEHILVCLSFSPSNEKIIRTAAQMARAFGANFTALYVQTAEPAEKTPEDQARLQKHIRLAEQSGAEIVTTHSEDIALQIAEYARISEVTRIVIGKSMMDQGFFRKRRGWTERLTDLVPDLEIHIIPDSNIITIYLVGVMTTSILTSGYTCSVISSVISVVLFNYFLTEPRLTLYAYGSGYPVTFAIMLGISILTGTLASKLKENAKLSARDAFRTKIIFNTSQLLQKAEDASEIFDITATKLVKLLGRDLTAAPAGAQESRIVRGTLYSAQTGGKTEKIFDPREQEIIQWVLDSRKRGEKCLDRGGGQRPRDSKRVQRACV	13~~Usp(3.1477E-32)~~136;X;138~~DUF4118 (0.0000571528)~~214	non-KdpD DUF4118 protein
	5E-07	39.3	9.7	7.9E-07	38.6	6.8	1.3	1	C4ID05_CLOBU	Histidine kinase (EC 2.7.13.3)	CLP_3232	Clostridium butyricum E4 str. BoNT E BL5262	468	632245	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	>tr|C4ID05|C4ID05_CLOBU Histidine kinase OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_3232 PE=4 SV=1MNKSSIDYSIKLILVVLLSTIISMIMRKLGIEKDSIMMVFLVGVLLVTVITKGYFYGAVASILSVLIFNYIFTVPVHTFEIYSTSDITLLLFFFISSIISSSLTSRIQKQAEIAEKNECTARLLCEITDNFSNITGKKNIVIQGISYIYNHTGCKSKVTLSDTNETFYKDESINESKCNMNKLNLDIHGINKKLGEIEIFFSEDNLSLENELLIKMVATQIGISLDRELIYYERENIREMERERLRSNLIRGISHDLRTPLTAIVGASGVVIDNINKLPQETIKDLVKDINEEALWLNNLVENILNMTRIGEGKLVIKKQDEVVDDIVDESLRHISGLLSNRDVQVSLPREVISIPVDGKLIVQVLINLLDNAVKYTDEKCTIYLRVFQKDDFIVFEIADNGEGINESIIDKIFDSFVSYSGKIVDGKRGMGLGLAICKAIINAHGGEITAGKSPEGGALFSFTLPL	10~~DUF4118 (0.0000161817)~~94;X(150);244~~HisKA (0.000000000048496 4)~~310;X;363~~HATPase_c (1.69187E-26)~~466	non-KdpD DUF4118 protein

	5E-07	39.3	3.2	8.9E-07	38.5	2.2	1.4	1	E0RVB1_BUTPB	Uncharacterized protein	bpr_I1794	Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) (Clostridium proteoclasticum)	704	515622	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Butyrivibrio, Butyrivibrio proteoclasticus, Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) (Clostridium proteoclasticum)	>tr|E0RVB1|E0RVB1_BUTPB Uncharacterized protein OS=Butyrivibrio proteoclasticus (strain ATCC 51982 / DSM 14932 / B316) GN=bpr_I1794 PE=4 SV=1MDTLLVGNTSYFRKDEIVVACPQDMVVVCDSDQDAYKEDNITWFDQPVMSAKFRRLFNTYGFERVLFFSRS LTRDTNKVGEIEELRRVFSLSQKHHVKQFVYIVSDEALVDVDNSDSIIFDSTNNLCRYYAETYRIDVKIVYSPYLLSA YNRDDYWCRILRNIENKERVEIKSLEDEAAYFLKPADLADFLARLFADWEPEEDEKGEKTLFEKIYLKSGAKTTYGE IKNKILNVYPHADISLSKSGIKGKIIHGDNKAREIYGWFAHHDACWDFEEYISKYQELYHQKPTFSERIKKRFSFLGK ALMPIELIGGAAFVELYNYMSAGSVQFKMIDVRLLFVIVMALLYGTRIGTLSALIEITSLIVAYQLSGTNALLLFYDPGN WIAFILLLVAAAFCGYIKQKREEDILFVKEESETIKSENAFISKLYQEAMNYKNQYKADLIGSRDGFGRIFDVVKRLST TVPEEIFAESIPVMEDVLNNKAIAIYTINDPNARFARLNVCSEQLGQTLKKSINLDEYSEVLKTLTENDIWFNGNVIEG FPTYVAGIKSEGNVSVLIMIYRVEYMQISTYYSNLIRILAGLMENFILKAWDYQKAVVAETYVEGTGITKTAYFKQQF EIQKEMMDNRLTSFRLIRIQREGRSLEEIDEMFQSKIRNNDIIGIGDDQNIYLLAAQVDSSSEGIVLKRFRDMGLKCDI VHSVS	309~~DUF4118 (0.000000000318118)~~408;X;466~~GAF (0.0000000146942)~~589	non-KdpD DUF4118 protein
	5E-07	39.2	8.2	9.7E-07	38.4	5.7	1.4	1	D2B156_STRRD	Histidine kinase (EC 2.7.13.3)	Sros_0436	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	851	479432	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	>tr|D2B156|D2B156_STRRD Histidine kinase OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_0436 PE=4 SV=1MPRGRLRVYLGAAPGVGKTFAMLGEGHRRLARGRDVVVGLVETHGRPRTAELIDGMEVVPRRTVIHREAA FTELDVDAVIARAPRIALIDELAHTNVPGSRNAKRWQDVEEILDAGIDVVSTVNIQHLESLNDVVRQITGVPQRETVP DEVVRRADQVELVDMSPEALRRRLAHGNVYAPEKVDAALSNYFRVGNLTALRELALLWVAGKVDEQLDRYRAEH GIEGTWEARERVVVALTGGPEGDTLIRRAARIAARSKGADLLAVHVTRADGLAGGDPVNLARQRVLAESLGGTYH QVVGDDVPRALLDFARGVNATQLVLGASRRGRFAQILSRGVGVTTTALSGSIDVHMITHGEAQKGRRPPPSRAAL TRTRRLAGWAVAGAGLPTLTGVLLPFRETLTLPSEILFFLLVVVGVALIGGMWPAVTAAVGGSLLLNYFFTPPVHTL TIYDPENLFALVVFVLVAIMVSGIVDVAARRTREAARASADAEVLSTLAGHVLRGESALPSLLARLRETFALTSVTLL ERIDGPVPDDQSDPEAWRIVATAGATPCTCPGTADADVVIDEQLVLAVRGRLLEASDRRVLEAFAAEAAVALRQE RLRREADLAGPLAETDRMRTALLAAVSHDLRTPLASARLAVESLRGTEIEWSAEDREELLATADESLVKLDRLVAN LLDMSRLQAGVLGLALQPVALEEVIPRSIDDLGPLRDRVEGDVSVDLPEVVADPVLLERILVNVMSNAVRYSPAGR KALVAGSRHGDYVEIRVVDRGPGIPAEAHDRVFMPFQRLGDRDNHTGVGLGLALSRGLAEAMGGTLTPEETPGG GLTMILTLPVSSRADGLPAVERA	3~~KdpD (2.20801E-121)~~211;X;233~~Usp(4.93433E-20)~~355;X;381~~DUF4118 (0.000000000005049 74)~~476;X(142);618~~HisKA (0.000000000004284 7)~~684;X;735~~HATPase_c (3.30158E-25)~~836	KdpD protein
	5E-07	39.2	10.9	9E-07	38.5	7.5	1.4	1	G4KWP7_OSCVS	Histidine kinase (EC 2.7.13.3)	OBV_36690	Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	460	693746	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter valericigenes, Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	>tr|G4KWP7|G4KWP7_OSCVS Histidine kinase OS=Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20) GN=OBV_36690 PE=4 SV=1MEWGGVDAVAKNLLKTFVIVLATTSCSVLVSLFGVDNESVIMVFLLGVLFSAVLTSSRGWAAATAFLSVMLL NFLFTEPRFTFQVYNASDLMLLGFFLVTAIVAGTVTSRLQTQMELAGRNERTAQTLYQIASGFLSASGSKSVIKKGE DMVREYVGINGVVALGPEPATGVLEYPIMSTSGIHGKLVLQTQPGTQKILVIQAICAQLGIALEREDLVAEREKIRMD MERERQRSMLLRSIAHDLRSPLTALSGSGNLLADHYDRLSEAERKKLAGDVSEETVWLIDLVENILSMTRISEKQLV LHKQEEVVDDIVGEAIKHTERLLRGRQFTVRLPDEIITAPMDGKLISQVIINLLENSARHTPPDSAITLSVSTEGGRVA VSVADTGNGVSEKIRANLFERFVTQNEDIVDGRMGLGLGLAICKTIVEAHGGSISYADNPPHGALFAFTLPMEEQN E	12~~DUF4118 (0.000000000000062997)~~114;X(117);231~~HisKA (0.00000000854185)~~297;X;350~~HATPase_c (4.0848E-26)~~453	non-KdpD DUF4118 protein
	6E-07	39.2	9.4	9.8E-07	38.3	6.5	1.4	1	B0SYJ4_CAUSK	Histidine kinase (EC 2.7.13.3)	Caul_4239	Caulobacter sp. (strain K31)	894	366602	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter sp. (strain K31)	>tr|B0SYJ4|B0SYJ4_CAUSK Histidine kinase OS=Caulobacter sp. (strain K31) GN=Caul_4239 PE=4 SV=1MPAEEPKRPDPEALLAAANKAGRGRLKVFLGMAPGVGKTYEMLRAARRRKAEGQDVLIGLVETHGRRETE SLLRGMEVMPRRPLEHKGRTHLEFDIDAALARKPKLLLVDEYAHSNAPGSRHPKRWQDVEELLAAGIDIWTTLNV QHLESLVDVVQRITGVRQRETVPDSALSRADDIEVVDITPDELRERMGAGKVYVPETARLASENFFKVENLTALRE LALRRAAQTVDDQLVAAMREKGVEGPWAAGERILVLVGGDAMSSSLVRAGRRLSDMMMDAPWTVTHVERSDR SGPSPLAATRLRDALKLAEQLGGTTVVMTGVDIVATVMAYARRNNVTQIVIGKSAGNRWNELTGRSLAAALLREA RGEAIHVVTEAAHTHGDVPVERSRKRGPGWPAYVTGAAFVGLATLVAWGLDTAFDRVDLGMIYLAAVLAAGVMY GLRPALAAATAAFLVYNYLFLAPRYSLQIGSPTDFLTLIVFWAVALATGGLAGRVRDQARGSQRRAAAVSTLLAAA RTLSGATGRQLVAQAIADQVAATAGAKAVVFIPLNGDLTPAAGAPSLEPLGAAPMAAARWAWERGETAGFGTAT LPHAEWTFWPLEGVRGRAGVAGVEAGAMAQGSDDERLVLGLLDQGAIALERADLAADAVEAETLRRADRFRSAL LNSISHDLRTPLSTVLGASSTLTEYGDKMEPAVRADLMVSIREEAERLNRYVANLLDMTRLEGGALRLRNDWIDVR DVLGAAADRVTRRLGGRPLTRDFPSELSLVRADASLLEQVVVNILENAIAYSPPGAQIEMAAYEDRGNIVISIEDEG RGIPPAELERVFEKFRRMEEPTDRTGGVGLGLSIAKGFIDAMNGRIAAASPIHDGKGTRILISLPKAVHTPKDLL	21~~KdpD (2.33614E122)~~231;X;253~~Usp(5.90763E-33)~~377;X;405~~DUF4118 (0.00000000523292)~~500;X(160);660~~HisKA (0.000000000194074)~~726;X;779~~HATPase_c (7.09388E-27)~~883	KdpD protein
	6E-07	39.1	2.2	9.2E-07	38.4	1.5	1.2	1	B5EH12_GEOBB	Histidine kinase (EC 2.7.13.3)	Gbem_1094	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	364	404380	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	>tr|B5EH12|B5EH12_GEOBB Histidine kinase OS=Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622) GN=Gbem_1094 PE=4 SV=1MKRTDLARGTVLVACVIGISLLHYLTPLRLAMLHDIFQRLYYIPIILAAYWFGFRGGIGCALLVTFCYAPHILFQ WGGHIAMEMEKYLEVILYNVVGGITGMLSQQERSRREQLEETAKGLEDSYRQLRTQSELIIRIEEQLRRAERLSAL GELSAILAHEIRNPLASIRGTAEILREDGAAANRDEFLGILVKESDRLNHVVEDFLRMARSEPAIKKECDINYELANM VTLLSAQARGEEVELRFTPGEVPTLSADPEKLRQAFMNVLNGIQASAPGGRVLVTTSYDRQSRSIEIRFSDNGPGI AREAIGKIFEPFFTTKGSGTGLGLSITKKILEGHGGTLEVESTPGEGACFRARLPTET	11~~DUF4118 (0.000000261182)~~110;X;148~~HisKA (0.000000000000111326)~~211;X;261~~HATPase_c (2.03482E-27)~~360	non-KdpD DUF4118 protein

	6E-07	39.1	10.1	1E-06	38.2	7	1.4	1	D2Q286_KRIFD	Histidine kinase (EC 2.7.13.3)	Kfla_6791	Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	854	479435	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Kribbella, Kribbella flavida, Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	>tr|D2Q286|D2Q286_KRIFD Histidine kinase OS=Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399) GN=Kfla_6791 PE=4 SV=1MGGMAGRGRLRIYLGAAPGVGKTYKMLGEAQRRRERGTDVVVGFVETHGREHTAAMLDGLEVVPRRLVDHRGASFTELDLDALLARRPQVALVDELAHTNVPGSRNAKRWQDVDELLGAGIDVISTVNIQHLESINDVVEKITGVPQRETVPDRVVRAAHQIELVDMAPEALRRRMAHGNVYAADKVDAALGNYFRIGNLSALRELALLWLADRVDAGLQQYREQHQIDTTWEARERVVVALTGGPEGETLIRRAARIAARSAGGDLLAVHVTRSDGLTGADPGRLAQQRQLVESLGGSYHQVVGDDVPAALLTFARAENATQLVLGGSRRTFLSTLLTGPGIGATTIRESGDIDVHIVTHAEMGRGRLPQAQGSLSRRRLAYGFALAVLLPPVLALALGLGGDTLNLTSNVLAFLFAVVVVALVGGLWPALLTAVAGTVVLNFFFTPPTRAFTIAEPNNAFALLTFARAENATQLVLGGSRRTFLSTLLTGPGIGATTIRESGDIDVHIVTHAEMGRGRLPEPLLTGSVLGDVVEIRVVDRGPGLPAEDRDRVFAPFQRLGDTDNTTGVGLGLALARGLAEAMGGSLRPEDTPGGGLTMVVSMPSATMAEDAPVPGRLERGGTR	5~~KdpD (3.75779E-122)~~215;X;237~~Usp(6.41215E-23)~~360;X;421~~DUF4118 (0.000340319)~~479;X(138);617~~HisKA (0.000000000053732)~~683;X;732~~HATPase_c (7.88241E-25)~~832	KdpD protein
	6E-07	39	8.7	1.1E-06	38.2	6	1.5	1	C5C3W2_BEUC1	Histidine kinase (EC 2.7.13.3)	Bcav_3779	Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	857	471853	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Beutenbergiaceae, Beutenbergia, Beutenbergia cavernae, Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	>tr|C5C3W2|C5C3W2_BEUC1 Histidine kinase OS=Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432) GN=Bcav_3779 PE=4 SV=1MSDPAVDPGSAPSAGAEPGRRPGRLTVYLGAAPGVGKTYAMLDEAQRRRSRGTDVVVGLVETHGRAATLEKIGDLEIVPRRVVRHRGVELTELDTEAVIARGPEVALVDELAHTNAPGSPHPKRWEDVADLLAAGIDVVTTVNVQHLESLNEDVEAITGVRQKETVPDHVVRAADQIQLVDMSPQALRRRLAHGNVYRADQIDASLASYFREGNLTALRELALLWLADRVDDALTQYRTEHAIAGVWPARERIVVAVTGGPESATLLRRGARIAERAAGSELLAVHVLATDGLPTAPPAVIAADRALVESLGGTFHTVVGEDVPSAVVDFAQGANATMVVVGVSRHSRWREALLGSTSTEIARLAGAIDVHLVTHERARSGARPLASSALSPSRRLAGWVLAFVAPLALTGLLVLVQEDVSASTELMLFLAAAVGVALVGGRWPAVACAAASFLCLNWFFTEPTGRFTIADPENLLALVVFVLVAAAVASVVDLAARRASQAYRARAEASTLAALSRSVLSGEDTADAVVSRLAETFQLAHVALEERVAERAPWTTIAEAARSTASPGGGGSGSGSDSDDDRTIVRIDDTRRLVLTGRPLPAGDRQVLEAFGTQAGIVLEHRRLSARAEKARILEEADATRTALLAAVSHDLRTPLASIRAAVDGLRSDAVALDPDDEAALVDTAATSTARLEQLIDNLLDASRLESGALSPVLRDVSLDEIVPLAVDPFADHVSLEVPDDLPLVHTDPGLLERVVANIVANAVRHAPGGVPVRVLAARAGDSVELRVEDRGPGLDDARKARMFEPFQRLGDVSGTGLGLGLAVAAGLSRAVGATIAPEDTPGGGLTMVLTVPMAGG	19~~KdpD (9.68986E-111)~~230;X;252~~Usp(3.56346E-29)~~374;X;399~~DUF4118 (0.0000000649977)~~474;X(164);638~~HisKA (0.000000000000971262)~~704;X;752~~HATPase_c (5.40613E-21)~~852	KdpD protein
	6E-07	39	8.3	1.1E-06	38.2	5.8	1.4	1	F5XJC8_MICPN	Histidine kinase (EC 2.7.13.3)	kdpD MLP_28140	Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	868	1032480	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Microlunatus, Microlunatus phosphovorus, Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	>tr|F5XJC8|F5XJC8_MICPN Histidine kinase OS=Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1) GN=kdpD PE=4 SV=1MQVAAVGHTGGVERGILRVYLGAAPGVGKTFAMLQEGQRRAERGTDVVVAFVETHSRAKTAAALDGLEVLPRRQVDHGGLLVDELDLEAVLARRPKVALVDELAHTNAVDASSEQRRNPKRWQDVETILAAGIDVITTVNIQHLESLNDVVTSITGVRQRETVPDRVVRSADSIELVDMSPEALRRRLAHGNVYPADKIDAALSNYFREGNLTALRELALLWLADRVDAGLERYRGRHHITGTWPARERVVVGISGGPESIALMRRAARIASRSAGGEWLAVYVSRQDGLAAVSPAALERLRVAAEELGGEFQAVVAHDSATGLLDVARGVNATQVLIGASRRSRISALLQPGVGEEVIAGSGEIDVHVVTHDYARRAGRQRRRSRRTLSRRRQVAGYLLAVVGTVVVSLALLATSDLHGLPTESMLLLTLVVGTALLGGMWPSVIAAVLSSLALNFLFVPPTRTFTIADPENAFAIVLFLVGVAVASVVDRSARRTQEAQEARMEANTLAVLAHSLLQSGDDPEELLRQTGEALGMTGARLIRTAGDPLVGENAVEENAVEETVAVWGEPGSTVESSRVAAGPNLQLMLHGRPLNATDQRLLTAYAAHFAVLEERRRAEQESVRVRLLDEGNRTKTALLAAVSHDLRSPLAAIKAATSSLRNTAIAWSPHDREELLATVEESADRLDALVANLLDMSRLQTQLVTALTTEVDLLSAAEWTLANIAGADGIAVSGPDDLPPALADPGLLDRVIANVVENALKYGPASPITITGSSWTTPSGELRATLRIVDRGPGVPAEALDAIFEPFQRLGDVPAGGGVGLGLAVARGLAEAMGGTVTAEETPGGGLTVIIDLPSAGPNPPPAEDNL	13~~KdpD (2.52997E-114)~~227;X;249~~Usp(2.20585E-27)~~371;X;397~~DUF4118 (0.000000000001894)~~496;X(137);633~~HisKA (0.000000000000316147)~~699;X;749~~HATPase_c (0.000000000000002289)~~854	KdpD protein
	6E-07	39	9.8	1E-06	38.3	6.8	1.3	1	R7BVH8_9FIRM	Histidine kinase (EC 2.7.13.3)	BN674_00880	Firmicutes bacterium CAG:475	656	1263026	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:475	>tr|R7BVH8|R7BVH8_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:475 GN=BN674_00880 PE=4 SV=1MSDNRNKNTDKNAEHILVCISSSPSNTKIIQTASSMAKAFGAMFSALYIKTPSAASLESKDKERLLSNIHFAEECGASVTTVCGDDIPFQIAEYARLSGVTKIVIGRSVVNKKRLALQPTLTEKLISLAPNVDIHIIPDSDAVLPKGKAKVFEKPAFFKIVKGVIVSTIVLSIATLLGYIFSKFGFTDANIITVYMLGILITAILTESKICWVLSSVVSVLLFNFLFTEPRFSLLAYGNGYPVTFVIMLVASLVIGGTAEKLKTRERQATQTAYRTKILFDANQLIQQASDESKIFCVTANQLKKLLNRTVIVFDDKSQCRCSLPTEKDTIIMPQDCEQILLQVIKNNVKAGKGTSIFSENDYTFFPICKNGKNYGAIGVFVGNNPIDAFDESIVNSVIGECALAVDGIVNAKERERAAVLAKNEQLRANLLRSISHDLRTPLTSISGNASNLISNGNDIDDITKKQIYEDIYDDSLWLINLVENLLSVTRLEEGRMNINLTTELVGDVIDEALKHVHVKSEKQKITVIQPDDLLLAQMDARLIVQVLINLLDNAIKYTPSDSQITITAKRNGSMVCISVADNGLGIPDEQKSRVFDMFYTGANRISDCRRSIGLGLSLCKSIINAHGGEITIADNIPHGAIFAFTLPVGEVEIHE	non-KdpD DUF4118 protein
	6E-07	39	7.9	1.1E-06	38.1	5.5	1.4	1	F6FVZ1_ISOV2	Histidine kinase (EC 2.7.13.3)	Isova_1711	Isoptericola variabilis (strain 225)	493	743718	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Promicromonosporaceae, Isoptericola, Isoptericola variabilis, Isoptericola variabilis (strain 225)	>tr|F6FVZ1|F6FVZ1_ISOV2 Histidine kinase OS=Isoptericola variabilis (strain 225) GN=Isova_1711 PE=4 SV=1MSARRRTRPTLLAPARLALGWVLALLLPVALTAGFSVVDSDRVALAQEVMLFLAGVVAVALVGGLWPAVATAVVSNLCLNWFFTQPVGRLHVSEPENALALAVFVVVAVAVASVVDLAARRTAQAARARAEASALAALARSVLSGEDTAQAVVERVAETFPVAHARLEERDDEGAPWHAVAAADGPQEPPAGGGARRAGVDAETEVRIDPLRRLLLRGRPLSAADRQAVEAFGAQAGIVLEHRRLRERAEQAHALELAEATRTALLAAVSHDLRTPLAATRAAVDGLAAHDVDLHPDDREALVGTIAESTTRLERLIGNLLDISRLQTGAVHPVLRPTSLEEVVPLAVEPWLDAIALDVPEDLPLVHTDAGLLERVVANLVSNAVRHAPDGAPALVTASASADRVELRVVDTGPGVPRARRQTMFEPFQRLDDTGADGLGLGLAVAAGLSRAIGAELVARDTPGGGLTMALSVPRAAATEAPRAADGRDGIDL	50~~DUF4118 (0.00000964272)~~97;X(162);259~~HisKA (0.000000000000688153)~~325;X;373~~HATPase_c (3.08491E-22)~~473	non-KdpD DUF4118 protein

	7E-07	38.9	8.7	1.1E-06	38.2	6.1	1.4	1	Q8F1M3_LEPIN	Histidine kinase (EC 2.7.13.3)	kdpD LA_3109	Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	870	189518	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Leptospira, Leptospira interrogans, Leptospira interrogans serovar Lai, Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601)	>tr|Q8F1M3|Q8F1M3_LEPIN Histidine kinase OS=Leptospira interrogans serogroup Icterohaemorrhagiae serovar Lai (strain 56601) GN=kdpD PE=4 SV=1MIKDTRLDPDELLRKIQKEEQKEISGRLKVFFGMVAGVGKTYAMLNAARGLKKEGVDVVVGYIETHGRKETE ELLEGLEILPRKKIEHREIEFEEMDIDSILRRKPEVVLVDEFAHTNIPGSRHVKRYQDVIEILNHSINVFTTLNVQHLES QVESVEKNTSVKIRETIPDSILDMADEIVLIDLSPDDLRKRLQEGKVYVPEKANLAGDYFFKKENLTFLRETALNYTA RHVNVALDSEKFREKILVSIGSNPNSYSLLRYAKRLAYERNGELFAIYNQTRENLTKENLSQLEKNLSFARELGCEIL YAADEDTAEAILRISGQKSITRVVIEKSDTNWWWRWNSTASKLARIPSNFELCLVPYSFISGEESVLNRFLRTSSG GKQYLTSLTLILLATCISLFLEPIAGYWSISLLYLFFVSGIGSFFSKGPTVLAGLLSGIFWDFLFIPPRYTFFIEKLEDVL MFGAFLFISIIIGNVTSRLRQKEKVLVNRELRLTTLYELSKELGHARDVRRISEIGAEYLGKVFQTEIVILLENQGNIDF NSSRAGNFFPDPKETAVSNWVYKNKIPAGKFTDTLSLSLGTYFPMIAPGKVIGVIGVVLNERLNLDQENLLLTMGN QIALALERELLSEETRTRYLANQSERLYTIIFNSLSHELKTPLSSIRGAVTALLEPEIENSREARVELLNEINESSMILNL LLGNLLDMSRYESGFLKLRMDWHDPSDLIHVVVRRLRQTVKNSHCVIHLPENPVPTWMDFTLMEQALFNVVFNAV QISPEGTPVFIELICRKDKIQYIVEDEGPGIPKEDLEKIFEKFYRSKNRNHVGSGLGLSISKSIVETHGGTLTAENRTIV GARFCIEIPIKSS	26~~KdpD (1.28846E-103)~~233;X;245~~Usp(5.06249E-19)~~364;X;387~~DUF4118 (0.000000000000135552)~~487;X;513~~GAF (0.000000000005325 9)~~629;X;655~~HisKA (0.000176703)~~697;X;765~~HATPase_c (2.40073E-24)~~865	KdpD protein
	7E-07	38.9	11.7	9.3E-07	38.4	8.1	1.2	1	R7FRD7_9FIRM	Histidine kinase (EC 2.7.13.3)	BN651_01391	Dorea longicatena CAG:42	364	1263074	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea longicatena CAG:42	>tr|R7FRD7|R7FRD7_9FIRM Histidine kinase OS=Dorea longicatena CAG:42 GN=BN651_01391 PE=4 SV=1MKKTAKTDNSSDPKTLCHNILSTICILTLATVLAFSFFHITRSDPANIALIYILALIIIARITSGYVFGIISALFCVIFIN WCFTYPYFKVNFQISGYPVTFVFLLSISLIISTLTTQLKKQDKMILERERAINEADKERIRANLLRAISHDLRTPLTSIIG SSDSFIENYQNLTDPEKQSLVSSINEDSHWLLNMVENLLSVTRIQDDTGTVKKEDEVVEEVVSEAIIRLKRRLPDIEI HVSAPEDVLIIPMDSLLIEQVLMNLMENAFVHSESDRPIDLRITENPDTVTFHIIDYGKGIDEQTIPLILKGEYTAPRTS DTHRGMGIGLSICNTIVQAHGGKIAAHNHADGAEFLFTLPKGDT	(0.00000591655)~~122;X;139~~HisKA (0.000000000202364)~~205;X;258~~HATPase_c (2.02174E-21)~~359	non-KdpD DUF4118 protein
	7E-07	38.9	9.2	1.3E-06	38	6.4	1.5	1	D4LYW6_9FIRM	Histidine kinase (EC 2.7.13.3)	CK5_13790	Blautia obeum A2-162	590	657314	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, Blautia obeum, Blautia obeum A2-162	>tr|D4LYW6|D4LYW6_9FIRM Histidine kinase OS=Blautia obeum A2-162 GN=CK5_13790 PE=4 SV=1MIMEKGTLILSVCVIFGLGLFMASKLGSLIKESRKEIFDERSNRQLLKKVEMSSKGRKKNADMHVILGTAMPE TGQKQKFKLHIETPSVKDYILTVSIFIGCTLIGLIFQKLYFTDANIVTIYILGVLLTSILTDGYLCSLAGSFLSVVLFCFFL TEPRMSFQTYAVGYPVTFLIMLISSVLTGTLAAKLKEHARLSAQQAFCTQILFDTNRLLQQVKDRRDILCVTCKQLV RLLNCNIVAYIEENGELSGGSLFFHNDERERQGELLTSEEQYVARWAYENGQNAGATTNHFSSARCLYFVIKSGD NVYGVIGIPLQKKKLDSYESSILISVLNECALTMENSHNAIEKEKNAVFAKNEQLRADLLRAISHDLRTPLCSISGNAD MLLNNGSCLDEATKRQIYSDIYDDADWLIDVVENLLSITRLNDGRLKIKFTDQLLDEVITESLRHISRKHEDYQIDVEC EEFILVHMDVRLIIQVLVNLIDNAIKYTLPGSKICIRGIKKDGKAQISVADNGPGISDEVKPHIFEMFYTGNNTIADSHR SLGLGLSLCRSIIEAHGGTLVLTDNIPRGCMFTFTLPLSEVILNE	92~~DUF4118 (0.000000000000333247)~~193;X(167);360~~HisKA (0.000000000050903 1)~~426;X;478~~HATPase_c (7.8252E-27)~~581	non-KdpD DUF4118 protein
	7E-07	38.8	12	1.2E-06	38.1	8.3	1.4	1	R5KA75_9CLOT	Histidine kinase (EC 2.7.13.3)	BN743_01355	Clostridium sp. CAG:632	657	1262830	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:632	>tr|R5KA75|R5KA75_9CLOT Histidine kinase OS=Clostridium sp. CAG:632 GN=BN743_01355 PE=4 SV=1MILRTEGNTKKVDEHILVCLSAAPSNKKIVDTAGKMAKMLKARFTALYVRTGTKSEDLDKEKLEEHIRHAEKL GAEIVMTHGEDIPVQIAEYAKLSNVTKIVIGQSNARRNHFFSKPTLTEKLIELVPDIDIYIIPDALKNRNYQKRPFTWY MEKPSAKEYFLTVFIFMVCTLIGLLFQKLHFTDTNIVTIYILGVLITSIVTDGYLCSIAGAFLSVFLFCFFLTEPRMSFQT YAVGYPVTFLIMLISSILTGALAAKLKTHAKLSAQLAFRTQILFDTDRMLQKARGEAEILSVTCTQLLRLLNRNIIAYVV ENGDLSEGKLFSGEKVSTDNFLTPEEQQVARWVYENRQRAGASTHHFPQAKCLYLAIRGGNNVYGVIGIPLQKET LDSFEYSILLSVINECALAMENAKNAMEKEKNAILAKNEQLRADLLRAISHDLRTPLCSISGNADMLLSNSDRLDENV KHQIYTDIYDDSVWLIGVVENLLSITRLNDGRLKFKFTDQLLDEVIAESLRHISRKHDDYKIVTDCEELVLARMDVRLII QVLVNLIDNAIKYTPPGSVICIRGIRAGRKAQISVEDNGPGIPEEMKSHIFEMFYTGQTAVADSHRSLGLGLALCRSII EAHEGTLVLTNHDPHGCNFTFTLPLSEVTLNE	15~~Usp(3.15716E-31)~~136;X;161~~DUF4118 (7.94101E-14)~~262;X(165);427~~HisKA (0.00000000186572)~~493;X;545~~HATPase_c (3.19062E-28)~~648	non-KdpD DUF4118 protein
	7E-07	38.8	4.4	1.4E-06	37.9	3	1.4	1	R6YTN8_9FIRM	Uncharacterized protein	BN600_01071	Roseburia sp. CAG:309	727	1262945	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:309	>tr|R6YTN8|R6YTN8_9FIRM Uncharacterized protein OS=Roseburia sp. CAG:309 GN=BN600_01071 PE=4 SV=1MNVLLIGGPGSLTNRMIVKLKKEGHRVSLLTGESYARKGYEKVFETYSFTYDSDSLKEIFESVCPDCILFMGA YDTNFNWNESEREAGRFISAVMNILLSYSVQKNTRFFFLSSDEVFGQGNSEDIKEEDAVWGDSAKTTALIQAEEIC RDFSENWGKDVTVLRLDHLYQIPKTIAEAIQNPCASLCMSALKANYISADKENIYSLLYEDDAVEFIYEVMAAKHRE YSFYHLSSGDPVSEWQLAQEIKEVLGGHITVLEVKRADSRRRVLSNERFSEEFPSKIRHEREEGVKKIVKYMKKNR AVFVDETEEKLSLGKRMLRQFGWFLKAIFPFLENMVCFIPFFMLNNRTVGSQYFSRLDFYLFYVLLFAIVHGQHQA LFSAVLAVCGYLFRQMYTRSGFEVMLDYTTYVWMAQLFILGLVVGYMRDQIRDIRQESAEIQENLNHQLGDIKDIN NSNVRVKDVLEQQVVDQKDSIGKIYSITSSLERYMPEEVLFHAVEIVRDLLNCPDVAIYTVHHSGYARMFSATSEQA RKLGNSILYQDMTDMYEALKEQRVYINRNLDASYPLMANAIYDNEEIQMILMLWGLPWERMTLGEANRLVVVSYLI QNAVLRANRYLAALEERRYLADTKILEAEAFTSLVQAYYNAKKKNLTECTLLRIECDSATFKRSEEILLDNLRQTDYL GTMDDGKLYVLLSNTVKTEAQIVVNRFMKAGFNSRIIDRIAR	2~~NADB_Rossman (0.0000001011 09)~~288;X;332~~DUF4118 (0.000000000000351 47)~~431;X;490~~GAF (0.000000000570635)~~613	non-KdpD DUF4118 protein
	7E-07	38.7	6.7	1.3E-06	38	4.6	1.4	1	R7JV49_9FIRM	Histidine kinase (EC 2.7.13.3)	BN630_01601	Blautia sp. CAG:37	662	1262757	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:37	>tr|R7JV49|R7JV49_9FIRM Histidine kinase OS=Blautia sp. CAG:37 GN=BN630_01601 PE=4 SV=1MRQLEKEKQKKEHILVCLSSSPSNEKIIRTAAQMAQAFQAGFTALYVQTAEKTEKTPEDLARLQKHVRLAEQ SGAEIVTTHSEDIALQIAEYARISEVTRIVIGKSMMKQGYFHQRRVWTERLTDLVPDLEIHIIPDSDVYRRYQKRKKF PEWMELPSWKELMLTVLILAAATGIGEIFFRLGFTDANIITVYLFGVMLTSILTSGYTCSVVSSVASVVLFNYFMTEP RLSLHAYGSGYPVTFAIMLGTSILTSTLASKLKENAKLSARDAFRTKILFNTSQLLQKAEDASEIFDITATQLIKLLGRN LVVAPVEKKKNGIVQGTLYNAETGIKSEKVFNEKEQEILQWVLKNRKRAGAMTERFSEEPYLYLSIYAAQNRYGVI GIFIGQKPLDVFENSILLSILGECAMALDREQSAREKEEAAVMAKNEQLRVNLLRTISHDLRTPLTSILGNADSLISNF DALDEGMRKQIFSDIYEDAGWLIELVENLLALTKIEDGSVKLQLSDQVVEDVVREALRHVERRKNEHEITVDCGEDI LLARMDAKLIVQVLVNLINNAVKYTQAGSKIRITAGKEEKNVWIAVEDNGPGIPAECREHVFEMFYSGKNKVSDSR RSLGLGLALCRSIVNAHGGELVLRDCAPHGCHFRFTLPLSEVNLNE	13~~Usp(2.86695E-23)~~136;X;162~~DUF4118 (0.0000001211 22)~~263;X(168);431~~HisKA (0.000000000076003 8)~~497;X;550~~HATPase_c (6.91335E-28)~~653	non-KdpD DUF4118 protein

	7E-07	38.7	10.1	1.3E-06	37.9	7	1.4	1	F8AWU8_FRADG	Histidine kinase (EC 2.7.13.3)	FsymDg_3009	Frankia symbiont subsp. Datisca glomerata	889	656024	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia symbiont subsp. Datisca glomerata	>tr|F8AWU8|F8AWU8_FRADG Histidine kinase OS=Frankia symbiont subsp. Datisca glomerata GN=FsymDg_3009 PE=4 SV=1MDVVSRGTLRVYLGAAPGVGKTFAALDEAHRRRDRGTDVVVGFVETHGRPRTAALLDGLEVVPRQEISYR GSTFTEMDVDAVLARRPAVAVVDELAHTNVPGSRNAKRWQDVQELLDAGIDVISNVNIQHMESLNDVVETITGVA QRETVPDEVVRQADQVELVDMAPEALRRRMAHGNIYAPEKIDAALSNYFRVGNLTALREIALLWVADKVDEQLDR YRAEHGISGTWETRERVVVALTGGPEGDTLIRRAVRIADRGKGADLLAVHVARSDGLTGANPRALARQRALVEDL GGTYHHVIGDDVPAALLDFARAENATQLVLGASRRGRFAQVLSPGIGVTTTKLSGSIDVHMVTHEEAGRGWRLPR RAHGLRPRRRLIATAMAAIVLPLLTIGLANSRGSLNVTTDVLVYLLAVVITALVGGFWPALLAAVASSLLLNYYFFAA HHRWTIAERNNVFALVAFVLVGIMVSRVVDLAARRYTQAVRASAEAATLSVLAGSVLRGEDALPALLERVRETFG MTAATLLERTDDSRQSGPGTRNERNGQNARSGGGVGVARTATAADADRPLLPGGRGWRAVHSVGLDPCTRPE EGDVDVPVGDNLALVLRGRPLPAADRRILAAFAVQAALALEQRRLAEAAAEAGPLAEADRVRTALLAAVSHDLRSP LASARAAVTSLRSRDVTWTPDEQAELLATADESMDRLTRLVDNLLDMSRLQAGVLSVFPRQTGLDDVVPHALDEL GLPGRTVEIQVPDGLPDIYADPALLERIVVNLAANALRHSPAGTHPVITASALEDRVELRVIDRGPGIPVENRDRVFQ PFQRLGDRDNTTGVGLGLALSRGLAEAMGGSLVTDDTPGGGLTMVLTLPAAWSVQHPVPAAPPSG	6~~KdpD (3.36588E-122)~~214;X;236~~Usp(1.33975E-29)~~358;X;380~~DUF4118 (0.000000000021637)~~483;X(171);654~~HisKA (0.000000000000582112)~~720;X;771~~HATPase_c (1.71719E-25)~~872	KdpD protein
	8E-07	38.7	8.8	1.4E-06	37.9	6.1	1.5	1	W5TT91_9NOCA	Histidine kinase (EC 2.7.13.3)	kdpD NONO_c56360	Nocardia nova SH22a	836	1415166	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia nova, Nocardia nova SH22a	>tr|W5TT91|W5TT91_9NOCA Histidine kinase OS=Nocardia nova SH22a GN=kdpD PE=4 SV=1MKRGQLRIYLGAAPGVGKTYAMLGEAHRRLDRGRDVVAAVVETHGRSRTAELLEGIERIPPVMRSYRGATIA ELDLDAVLRRAPAVALVDELAHTNAPGSKNEKRWQDVHALLDAGIDVISTVNVQHLDSLNDVVEQITGVVQRETVP DWVVRGADQVELVDITPEALRRRLSHGNVYAADKVDAALRNYFRPGNLTALRELALLWLADQVDAALAKYRADH RITATWEARERVVVAVTGGPESETIVRRASRIATKSSAELMVVHVVRGDGLAGVSAQRLHRLRDLATGLGSSLHT VTGENVPAALLDFARGVNATQLVVGTSRRSRWARIIDQGIGATVVQRSGSIDVHMVTHEEAQHGPRWSALVRRQ RSAVSWAAALVVPTLITTLCYLWLDSRLDLAGESALYFIGVIAVALLGGVAPAALSAVLGGLLLNWFFTTPRHSLTIA EPDNFLTIVVMAAVAVAVAALVDISANRTREARTASREAELLTLFAGAVLHGADLPDLLERAREIYGQRAVSFTTDD EVIACVGDDPARTPGSADTAIGAGDEEHWLLLNGRALTPGDRRVLAAVAGQAAGLVRQRELAGQAQAAAAGVMAA DRLRRALLSAVSHDLRTPLAAAKAAVSSLRSEDVQFSPADTAELLETIEESTDQLTALVGNLLDSSRLAAGAVEPQL RQVYLEEVVNRAIVGVGMGTRGVRQAVLDRVKVEVGDISVHADSGLLERVLANLIDNALRYSASGPQAPDTPVRV GAERDGDRVSITVVDYGPGVPTGLEDQMFEPFQRLGDRDNSTGVGLGLSVVRGFVEAMGGTVHAEPTPGGGLT MVIELPAEEAR	1~~KdpD (1.60921E-119)~~211;X;233~~Usp(3.47738E-32)~~354;X;377~~DUF4118 (0.0000000100141)~~457;X(144);601~~HisKA (0.000000000000834469)~~667;X;724~~HATPase_c (4.47318E-29)~~830	KdpD protein
	8E-07	38.6	9.3	1.5E-06	37.8	6.4	1.3	1	H2JYA4_STRHJ	Histidine kinase (EC 2.7.13.3)	SHJG_2400	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	831	1133850	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	>tr|H2JYA4|H2JYA4_STRHJ Histidine kinase OS=Streptomyces hygroscopicus subsp. jinggangensis (strain 5008) GN=SHJG_2400 PE=4 SV=1MSDVRPGRLKVYLGAAPGVGKTYRMLDEGRRRAARGADVVVGFAECHGRPHTEAMLDGLESVPRASCAY RGGRFEEMDLAALLARRPQVAIVDEFAHGNVPGDGRNPNRRQDIEMLLDAGIDVITALNIQHLESLNDVVEKITGIP HHETVPDEVVRRARQIELVDMEPEGLRRRMAHGDIYAPEKIDAALANYFRPGNLTALRQLALLWVADRVDEALQE YRTRHGIGGVWETRERVVVALTGGPEGDTLVRRAARIADRSAGGDLLAVHVARSDGLASGVSHASLARQRRLVE DLGGSYHSVVGDDVPTTLVEFARGENATQLVLGTSRRGRLTRFLTGPGTGETVTELSGDIDVHRVTHERAGRGTL LPSRRRTLSPARLIAGPVTGLVLPVLLTVVLARTRGPLNLTSEALLFLLAVVGVACIGGVASAVIASVTASLLLNYWFI PPIGAFTLDDPNALLALAVFAVVAAVVAAVVDRSLRLSRRSARATAEAETMSSLAGSIVRGEATIPALLERTRETFG MESAELVDEAPEEAGVTAVPAGPGAWLALRGRTLSSSERRVLAAFAAHAGSAVERARLAEAAAEVEPVKAGDRL RTALLRAVGHDLRTPLAAGWAAVTSLRSRDIEFPPEDRDELLATADESMAKLNRLVENLFDLSRLEAGALTLDLRA TSLEEVLPTALADVPDVDVVDLEEIPAVLADPPLLERVIANLAGNAARHTPDGRKVLVTASVLADQVELRVVDRGPG LPAEGRDRLFEPFQRLGDTDNATGLGLGLALARGLTEAMNGTLSPEDTPGGGLTMVVSLPFAQRTSSAVPTKAS RRPE	5~~KdpD (5.45443E-106)~~215;X;237~~Usp(1.07918E-28)~~361;X;415~~DUF4118 (0.0000607328)~~461;X(137);598~~HisKA (0.0000000611921)~~664;X;711~~HATPase_c (5.37033E-24)~~812	KdpD protein
	8E-07	38.6	1.7	1.3E-06	38	1.2	1.3	1	A0A0G0PRK0_9BACT	Sensor histidine kinase	UT63_C0096G0002	Microgenomates (Gottesmanbacteria) bacterium GW2011_GWC2_39_8	401	1618450	cellular organisms, Bacteria, unclassified Bacteria, Microgenomates, unclassified Microgenomates, Microgenomates (Gottesmanbacteria) bacterium GW2011_GWC2_39_8	>tr|A0A0G0PRK0|A0A0G0PRK0_9BACT Sensor histidine kinase OS=Microgenomates (Gottesmanbacteria) bacterium GW2011_GWC2_39_8 GN=UT63_C0096G0002 PE=4 SV=1MNKMKSETTKTDFEKEYRDKKRILIIFLLLSLITVLHYFTPIRDKQFHDMFRRFYYIPIILGSFWFGIRGGIVIPILA GFLFAPHVLFQWREFPTKEIDQYLEIIVYFAVGVVTGVVAEKEKKQRKKYQQAARNLEVSYKKLQAQTAELLEKDQ QLIRADRLATMGELAAGLTHEIKNPLGSILGAAEIIKDDYSPGEKKYEFLEIMIKEVNRLNKSISNFLSFAKLKAPQFKL SNVNDILNSVKDLVEFRLQKEKIKIDIGLDRNLKEMRVDAEQLEQAFLNVILNSLQAMKNGGTLKIYTRVMNPEGLN GSKGEGENIQSQRDNKLLMYVEIGIDDTGCGIPEERLNHIFNPFFTTREEGTGLGLAITKRIIEAHGGNISVESRQGE GTKFRIRLPLRN	162~~HisKA (0.000000000000203139)~~226;X;277~~HATPase_c (3.43715E-24)~~397	No DUF4118 detected by NCBI CDD
	8E-07	38.6	10.5	8.1E-07	38.6	7.3	1.7	1	E8T6I8_THEA1	Uncharacterized protein	Theam_0805	Thermovibrio ammonificans (strain DSM 15698 / JCM 12110 / HB-1)	413	648996	cellular organisms, Bacteria, Aquificae, Aquificae, Desulfurobacteriales, Desulfurobacteriaceae, Thermovibrio, Thermovibrio ammonificans, Thermovibrio ammonificans (strain DSM 15698 / JCM 12110 / HB-1)	>tr|E8T6I8|E8T6I8_THEA1 Uncharacterized protein OS=Thermovibrio ammonificans (strain DSM 15698 / JCM 12110 / HB-1) GN=Theam_0805 PE=4 SV=1MLFRDLGVKFVLVEVVFFVVLFTLVGHYFNPSDPLYLTGPISPVFLLLLVITLYYGLAYGIVAFIVEVLLAKLLYP NFPLRTILWHLLNVVVVGEFHYFWSKKIEILQEKNDYFQDKLRRFASDSMILKLSHDQLEKHYLVKPVSIRSLVAQV KEALMGRSQGDKGPFQVLRDILDAAFYVQSGELYRYSNDSFHSILAVGPSEPLNLEDPLVRKALDSRESVFLSEIN GNSSYLAVIPVYSYVNDDRLLGLFVLRKIPFNYLNSDTVLSLSVILYWFLNEVERLSNLNPVELATLPLSYDFLREVVI LKKLYSRLKADSTVVVFKLPHPSEDFGFFLKERLRAVDFMDSFRGNGSDYYFVLLPLSDASSAKGFLDRIARDYER TFGSDELPPYRVLKVDDAIEEKIRSVVGV	26~~DUF4118 (0.00149419)~~103	non-KdpD DUF4118 protein

	8E-07	38.6	13.5	1.4E-06	37.8	9.4	1.4	1	D5WU13_KYRT2	Histidine kinase (EC 2.7.13.3)	Btus_0568	Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	905	562970	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Kyrpidia, Kyrpidia tusciae, Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	>tr|D5WU13|D5WU13_KYRT2 Histidine kinase OS=Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) GN=Btus_0568 PE=4 SV=1MTKDERIPPRRDPDALLADLREEARRGKLTVFLGATAGVGKTYAMLESAHERLRQGVDVVVGWVETHGRPETEALLQGLPVVPPKTLTYKNRTFQEMDLEGILARRPSLVLVDELAHTNIPGSRHAKRYLDVEELLAAGFDVFTTVNIQHLESLNDVVARITGVTVKETVPDRVLETAYQVQLVDVPPDELLQRLREGKVYVPEVARQAARSFFRPGNVQALRELALRYTAQKVDRQVEDYMRAHAIDGPWPAGERVMVCISPSPFSAQLIRVGRRMAAGLKAPWLVAYVESPSKPPGDAERIRVSKYLRLAEELGAETAVMTADRVAEELVKLAKRRNVTQIIIGKPLHSRLEDWLRGSLVDQVIRGSEGVRIHVIPGKPGKTAMVATRRWPRRRTAAKSRPWGQYGIALGMVIVWTVVLYLVEPVLGLVNVALLYLFPVLFSAVRWSLGPAAVAAVAGVLAFDYFFVPPTFSFTVADLRYALTFAVFLSVAVLTGRLATGLRQQIRTIQRRETQTAALYALSRQMTAVSDLNAIAESIVVHVAESVDGEVALFLPDETGHLAVRRSTGSGAWLTGAQELATAQWVFHRGEPAGRGTQTLAEAEALYLPLRFERRVLGVLAVRPGNPGDIGEIPSEQRELLHAFAGLAAAAIARVRLAEQAKVAEVAAESERLRTALLNSITHDLRTPLASVIGSVTSLLEGDEIFDPKDRRELLMTIYQGALRMNRLIANLLDMARIESGMMQLHKKWCDLEDVVGVALAQSEEWLHNREVHLNIPREMPMVLADDVLLERVMANLLGNAVKFSPPGSPIEVAAEVEDGAVEVSVTNRGAPIPEEELEKVFEKFYRAPGAHVQPGTGLGLAISKAIVEAHGGSIWAENIPGGVRVAFRLPADRPPELARREET	24~~KdpD (4.01008E-118)~~234;X;256~~Usp(2.19892E-38)~~378;X;415~~DUF4118 (0.0000000030535)~~506;X;532~~GAF (0.000000115237)~~633;X;672~~HisKA (0.000000000001261 11)~~738;X;791~~HATPase_c (6.63396E-28)~~891	KdpD protein
	9E-07	38.5	9.2	1.3E-06	37.9	6.4	1.3	1	D4K5J9_9FIRM	Histidine kinase (EC 2.7.13.3)	FPR_27450	Faecalibacterium prausnitzii SL3/3	592	657322	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Faecalibacterium, Faecalibacterium prausnitzii, Faecalibacterium prausnitzii SL3/3	>tr|D4K5J9|D4K5J9_9FIRM Histidine kinase OS=Faecalibacterium prausnitzii SL3/3 GN=FPR_27450 PE=4 SV=1MAEQAGADISTIYGDDIPQQIAEFARISGITKIVLGRSSVHRRHFWSGPSLTEKLTLTAPNLDIYIIPDASAENGYGSGRKLFTRPLLPSVRDLLITAGILSCITLIGFFFLQLDFARYNIIMLYMLGVLFTAWFTSGYTCGVLGSVASVALYNFFMTEPYLTFHAYDPGYQVTFALMLTSAIITCTLTTRLKDHAKMSAQAAFRTKILFDTNQLLQRAKSEEEILSQTASQLMKLLNRSLIVYPEQNGDLGSEQVFEIDGEVPCNIFSAPKERDAANWTFANKKRSGAGTDSYPDAKGLYLALRTGGGVFGVIGIDLSEKPLDAFENSVLLSILGEGALAIENRRNALEKEQAALQARNEELRANLLRTISHDLRTPLTSISGNASNLLSNGETLDTETRNKICTDIFDDAQWLIGLVENLLSITRIEDGRMNLQISPQLMDEMIEEALHHVNRKSCEHTITTQYGDEILLVNVDARLIMQVVVNLVDNAIKYTPVGSVIQISAYRKDHQVVVDVADNGPGIPDRAKAQVFEMFYTGQSRIADSHRSLGLGLPLCRAILTAHGGTLTLRDNIPNGSVFSFALPQSEVNIHE	1~~Usp(1.65692E-14)~~68;X;94~~DUF4118 (0.000000000000316714)~~195;X(166);361~~HisKA (0.000000000181952)~~427;X;480~~HATPase_c (3.62189E-25)~~583	non-KdpD DUF4118 protein
	9E-07	38.4	9.2	1.3E-06	38	6.4	1.2	1	R5Q9K8_9FIRM	Histidine kinase (EC 2.7.13.3)	BN734_01249	Ruminococcus torques CAG:61	345	1263108	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus torques CAG:61	>tr|R5Q9K8|R5Q9K8_9FIRM Histidine kinase OS=Ruminococcus torques CAG:61 GN=BN734_01249 PE=4 SV=1MLFTATAVSFCFFHLGNKNSANITVIYTLALILTALKTSGYVYGIVASLFCVIAVNFLFSYPFFKFNFSLDGYPVTFIGMLAITLITSATTTSLKQHQKAAAEREKALAEADKEKLRANLLRAVSHDLRTPLTSIIGSSSSYLENGSDMTEYERTELVSNIKEDSEWLLNMVENLLTITRIDNNSQDKVKKSPEVVEEVVSEAIQRLRKRLSDVRIKVHMPNDFLMIPMDATLIEQVLINLLLENASVHSESTEEIDLIITQTKECVSFSVRDYGKGIDPEQLPYIFEGQRSSEKNSDHHKGIGIGLSICKTIIEAHGGKLTAVNHKHGAEFIFTLPKEKEVEANA	3~~DUF4118 (0.0000000000431908)~~97;X;114~~HisKA (0.000000000011731 2)~~180;X;234~~HATPase_c (5.01587E-26)~~335	non-KdpD DUF4118 protein
	1E-06	38.4	12.2	1.4E-06	37.9	8.5	1.2	1	R6LNY2_9FIRM	Histidine kinase (EC 2.7.13.3)	BN515_01711	Firmicutes bacterium CAG:170	372	1263006	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:170	>tr|R6LNY2|R6LNY2_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:170 GN=BN515_01711 PE=4 SV=1MKKAVPAREVSGFRLRLRTLFPFCWRDLGVCIVILVLATLLCHFLRLFDKSDVFVALIFELAVVFVSRFTSGYLFGLLASVIGVFGINYIFTYPYYAFNFTLSGYPLTFVVMLAVSVTVGTLTSQIKQQEKLRAEVEKEKMRGNLLRAVSHDIRTPLTSIVGGIDTILDSGAELSPELQRELLQNIREESHWLIGVVENLLSVTRVSGGASIQKELEAGEEVLSSAAMKLGRRYPDVQISVRAPEELLIPMDAILIEQVLINLMENAIQHGQTTTRLELHLRREDGLAVFEVADNGKGIAREAFPHLFEGYLSHTHEGHSDAKRNMGIGLSVCLSIVEAHGGTMEAENRAHGGAIFRFTIPLEEDNHDDQG	32~~DUF4118 (0.000000000016114)~~129;X;139~~HisKA (0.000000000003508 04)~~205;X;257~~HATPase_c (6.91963E-24)~~361	non-KdpD DUF4118 protein
	1E-06	38.3	10	1.6E-06	37.6	6.9	1.2	1	R6SD47_9FIRM	Histidine kinase (EC 2.7.13.3)	BN586_00554	Dorea formicigenerans CAG:28	351	1263073	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Dorea, environmental samples, Dorea formicigenerans CAG:28	>tr|R6SD47|R6SD47_9FIRM Histidine kinase OS=Dorea formicigenerans CAG:28 GN=BN586_00554 PE=4 SV=1MKILKNIIITAAMLAAATAICFILRPLVPTDTHVPLIYVLSVLCVSRLTEGYFYGVLASMVAVVGVNYIFTYPYFQVDFTVTGYPLTFIVMLTVSISVSALMTQIKMQEHVRLKAEKERMRANLLRAVSHDIRTPLTSIEGAAAGIIDNKDVLTEEQKEELLLNIKEEAQWMVRMVENLLSITRMNDEGTRLTTHEELAEEIVSSAVVKFSKRFPDIKVEVDIPEEVVIVPMDPILIRQVIVNIMENAVIHGGSTTQVKVTVSANETEAIFSIEDNGKGIDGKILPMLFTGQISHREGETYDNKRSMGIGLSVCKSIIDAHRGKVWAENKIDGGAKISFTLPLEEEEQNGD	21~~DUF4118 (0.0000000693289)~~106;X;118~~HisKA (0.000000000000438834)~~184;X;237~~HATPase_c (1.79132E-22)~~341	non-KdpD DUF4118 protein
	1E-06	38.2	5.3	1.9E-06	37.4	3.6	1.4	1	A6LV16_CLOB8	Histidine kinase (EC 2.7.13.3)	Cbei_2027	Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) (Clostridium acetobutylicum)	861	290402	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium beijerinckii (Clostridium MP), Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) (Clostridium acetobutylicum)	>tr|A6LV16|A6LV16_CLOB8 Histidine kinase OS=Clostridium beijerinckii (strain ATCC 51743 / NCIMB 8052) GN=Cbei_2027 PE=4 SV=1MLMEAHDMKKLGHDIVIGYIEPYARQETMALVNGLENLDNKIVEYKGINLKEFDLDKALIRKPEIILVDELAHTNVITQRHRKRWQDIEELLEAGIDVYTTLNVQHIESLNDIVESITHISVRETIPDKIFDEANKVELIDIEPDELLKRFSDGKVYSKGQARNDVNNFFTKNNLYALREIALRRTADRVNYEVESVRLSKGQITVMPTSDAILACISPSPSSSRVIRTATRMAEAHHSKWIAFYVETTKSQNLSKEDRKRLSEHFNLAEQLGGEVITVYSDNIVEQIIEYAKFRNVTKIIVGKNRKKPNVFFRFYARDIVDKIMESNSYIDVYVIPNSTAIKRNENHIKKNKTKFIISFKEILISSLIMLISALATLFIDKLGYGEANVIMIFILGVIIVNIKTRGYILGFICSTISVILFNYLFTKPRYSLQFYDKSYLVTFPIMLIVAFTIGTLTNKIRREAENSLARENTTQILYRVSRKLLSATGTSDVIGIGIKYLSRLLERTVICYLAQENKLSTPFIYTVIKGGKDRSLLNKDEEAAAYWTFVNDKESGAGTNTFYGAKGYYIPLKSHGKILGVLGISCINGTLKPKQKFIFETVASQIYIALDREILAETQKKSNLEIESERLRSNLLRSISHDLRSPLAGIKGAVSTIIETGNLISEETKGELLQGIYDDTEWLIRLVENLLSMTRFDGGNLKVRKSIEIVEEVVYEAVQRTAKRFRDYKMEVTVPEEVIMVPMDGSLIEQVLINLFDNAVKFTPKGSLIEVKIYENNKNVIFEVIDNGMGISEEILPHIFERFFTNGDKISDSRRGVGLGLAICKSIVEAHGGTISAHNKDEGGAVFRFNIPKEEMSDGQ	1~~KdpD (1.04655E-102)~~190;X;213~~Usp(3.40546E-44)~~337;X;363~~DUF4118 (0.000000000001836 72)~~464;X(166);630~~HisKA (0.000000000037100 5)~~696;X;749~~HATPase_c (4.45353E-29)~~852	KdpD protein

	1E-06	38.2	10.2	2E-06	37.4	7.1	1.4	1	Q3IYD7_RHOS4	Histidine kinase (EC 2.7.13.3)	kdpD RSP_1268	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	887	272943	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides), Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	>tr|Q3IYD7|Q3IYD7_RHOS4 Histidine kinase OS=Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158) GN=kdpD PE=4 SV=1MADEDLRPEPEALLAEAAREGRGRLKIFLGAAPGVGKTFAMLEAARQRLREGTDVVAGVIETHGRAETEALVHDLPVVPRRPGYYRGRILSEMDLDALLARRPRLALIDELAHTNLEGSRHEKRWQDVEEVLAAGIDVWTTLNVQHVETLNDAVARITGIRVRETVPDRILDTADEIELIDLSPEDLIARLRAGKVYVPEQAARAVQNFFAKGNLTALRELAMRAAADRVDAQLREHMAANAIPGPWPAQERLLVCVSDSPAARNAIRAAKRSADRARVEWIALSVTSPRIETLPEGARDDLALALRLAERLGATVASLQAGGDVAREILDFARRNNVRRIIVGRPRPRSTLHALAHPFRERVAERLLRLGTEFEVTLVSAEPGRARPQARRLPALSFPATGWALLATALASGAAWVVDRMLPVASLALLFMTAVIVVATRFGRWASALTAVSGFFAYNFFFTEPRLTFTVHYRDQILTLGLFLAASLLTGGLAAELRARVDAQRAAADRMGKLYDFSRRVAAAAAFDDVVWAAVSHVSMTLACRTVLLVPEGERLAVAGGFPPEDRLELRDMSAARYAWQRGEEAGRGSATLPAADWLFLPIRAGERRLGVVGVAYEGGRSFSPVDRRLLDALIDQVALAMERVRLAEDLEGARLAAETDRLRTALLSSVSHDLRTPLVTIIGAAGSLAEPGALPPEAQQALAETIREEGERLDRYVQNLLDMTRLGHGALKPAVQPSDLAELVGAARTRLAAVLRGHRLGTDLPPDLPAVLVDPVLTEQVLVNILDNAAKYAPPGSPITLAARLDAGRVVLSVADEGPGIPPADREKVFDMFYRVAGTDRRRAGTGLGLAICRGLLEAQGGTIRAEAARPDGQGTRILLTLPVAP	20~~KdpD (6.09076E-121)~~230;X;252~~Usp(1.48771E-32)~~380;X;403~~DUF4118 (0.000000000023606 61)~~500;X;528~~GAF (0.000000000019985 4)~~644;X;661~~HisKA (0.000000000000517 158)~~726;X;780~~HATPase_c (7.12646E-28)~~883	KdpD protein
	1E-06	38.2	13.8	1.9E-06	37.4	9.6	1.3	1	A4FMI4_SACEN	Histidine kinase (EC 2.7.13.3)	kdpD SACE_6086	Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	879	405948	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharopolyspora, Saccharopolyspora erythraea (Streptomyces erythraeus), Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338)	>tr|A4FMI4|A4FMI4_SACEN Histidine kinase OS=Saccharopolyspora erythraea (strain ATCC 11635 / DSM 40517 / JCM 4748 / NBRC 13426 / NCIMB 8594 / NRRL 2338) GN=kdpD PE=4 SV=1MAGKSARRGELRIYLGAAPGVGKTYAMLGEAHRRAARGTDVVVGLVETHAREKTAALLDGLEVVPRRRIAHRGVEVTEMDLDAVLARRPEVAVVDELAHTNAPGSRNEKRWQDIDELLDAGINVLSTVNVQHLESLNDVVEAITGVRQQETVPDEVVRRAGQIELADITPEALRRRMAHGNVYSADRVDAALGNYFRTGNLTALRELALLWLADQVDVALRRYRAERKITDTWEARERVVVSITGGPESETLIRRARRIAARAGAELQVVHVLRGDGLAGASPGNLARARRLADGVGASFHTVVGDDVPEALLEFARGADATQLVVGTSRRSRWARLLDEGIGAAVVQKSGSIDVHMVTHPEAGGRRLFKNIARNPLSSARQLWGWVLALALPSAVTALAYFSGAMALSADVVGYFLATVVVALVGGMAPAITAALLSGGLLNFFLTPPLYSLTIAEPQNVVTLLAMLFVGLLVAILVDRAARLAERAAHARTEAALLASYARTVLTHPDPLPRLLEKVVENFGLTSAALLERQEGDWHVAASTGPRPCTRPGESDVDIEVNPDVHLVLKGPGDRALPAADRTVLEGAAGQALVALRQQRMAAEAREAQRRADATELRTALLSAVGHDLRTPLASIKASVSSLRAPDLRRLSEEDTTELLTGVEESADRLTALVDNLLDSSRLATGAIVPRLDPVGYDEIVFRALAGLDGRQHVDIDTDESLPDVLADAGLLERVVANVVQNALKYGRPEGGRIGVRASAHASWVELRVVDHGPGLPEGAAETVFAPFERLGDRGGRGDQGETGVGLGLSVAKGFMEAMQGSIRAEDTPGGGLTIVLSLPAASPAVGDGVGSAGDGAVVHGGGAAPGAVVPADVDEQGRR	6~~KdpD (1.27886E-121)~~216;X;238~~Usp(5.84955E-25)~~359;X;386~~DUF4118 (0.000000000000405 423)~~479;X(137);616~~HisKA (0.000000000022162 6)~~681;X;731~~HATPase_c (8.05383E-25)~~838	KdpD protein
Disagreement between HMM and CDD prediction	1E-06	38.1	11.9	2.5E-06	37	8.3	1.6	1	C3MF86_RHISN	Histidine kinase (EC 2.7.13.3)	NGR_c01200	Rhizobium sp. (strain NGR234)	894	394	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Sinorhizobium fredii group, Rhizobium fredii (Sinorhizobium fredii), Rhizobium sp. (strain NGR234)	>tr|C3MF86|C3MF86_RHISN Histidine kinase OS=Rhizobium sp. (strain NGR234) GN=NGR_c01200 PE=4 SV=1MPEIDRDPASRPDPDALLALAEKGGRGKLTVFLGAAPGVGKTYAMLMRAQRLKEEGADIVIGLVETHGRSETAALLEGLEVLPRREVAHGGRTLHEFDLDAALARHPRIIVVDELAHTNFGESRHPKRYQDIEELVDAGIDVVTALNIQHLESLSDIVAQIAGVPVRERIPDTVLNRADEVLLVDLPPAELIDRLKEGKVYLPDSAKRAVDNFFRLGNLTALRELALRRTADRVDDQMVDYLKQNAIEGPWPASERLLVCIGPDPLSEKVVRTASRLASGLNADWIVVSVERADREAADGEAMRQLDETFRLAEQLGAETRRIIGSDFVEEILKLARRENATQIVIGARRHRFPLNLFRASLPDALAKRVSGIGIHLVTGKIEPVARTRRRSKQLLPEGLERALAIAGGTVGLATVLGLLIEQFIILQNISLLYLLAVLASAVYAGYFAALAAALFSVVAYNFFFIEPVNTFTVAEPHEVFALFVFLAAAALAGGLASRIREQAKTARNRATATQALYDFSRKLSGTANADDVLWAAVTQMQSTLRRNAVMLLPEDGDIALRAAWPPDTELTVSDMIAARWAFEKKEAAGNDTGTLPNSPFQFRPLMSPQGVVGVCGFLQEDSPLEINEERALAAILDQTAIAVDRARLSRESLDQAAQLEGEKFRAALLSSLSHDLTTPLATIGSAVISLRQLGEGTPKDAREDLLKSIEEESGRLTRFVTNLLDMNRIEAGTINARRDRVDVAEVVHDAVERARKYFPGRVFETSIALGLPAMRGDGVLLGQVLFNLLDNANRFGGDEPVSIYARREGDEVVLSVTDLGKGIAPADLEHVFDKFFRKGKPDGRSLGTGLGLTISRSFVEAMGGRIKAESPALRRRGTRISMRFPAAEAELSN	24~~KdpD (2.31693E125)~~234;X;256~~Usp(1.17225E-37)~~379;X(150);529~~GAF (0.0000507582)~~646;X;663~~HisKA (0.000000673496)~~729;X;782~~HATPase_c (1.20416E-24)~~885	KdpD protein
	1E-06	38	3.3	1.9E-06	37.5	2.3	1.2	1	H6NPL6_9BACL	Uncharacterized protein	PM3016_5971	Paenibacillus mucilaginosus 3016	412	1116391	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus mucilaginosus, Paenibacillus mucilaginosus 3016	>tr|H6NPL6|H6NPL6_9BACL Uncharacterized protein OS=Paenibacillus mucilaginosus 3016 GN=PM3016_5971 PE=4 SV=1MIYTQERRWIPWTELVILFLLLAAASHFGSVRFSEWTPNPLFFVVLYFALRYGTRLGLPAAAGAALLYGWDYYRGGGDGYTLLHEWADYQPLAVYAGLALFVGHYSSTQRYRYRSLAEEHEDLQSRLALVEKSYSDLSMVKDALEKRIVGAQESLFTLYKMAKALGSDDPEIIFTDAVRLFRELIHAESIVIYRMDASGRVLRLKVSFGSKPEGYPGSVFLEQPSLYRRVCDSRQIQLRDAGDPPRDPLMAGPIIGEEGELIGIIGLDGLDFKTMNKATADLFKLILGWMGESCVRAFREAAKLRGERYFMDTLIMKPEPFYKRLSEETLRATDFSQKFTLFQLPIEFEGLDTDSALQEMDALLRQTLRADDVVGYDAFRGELLFLLPATAPELRERIESRIRGRFGEGDSP	11~~DUF4118 (0.00000631124)~~112;X;169~~GAF (0.000000000018870 1)~~291	non-KdpD DUF4118 protein
	1E-06	38	11.5	2.2E-06	37.2	7.9	1.4	1	R5WGP1_9CLOT	Histidine kinase (EC 2.7.13.3)	BN512_00488	Clostridium sp. CAG:167	662	1262777	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:167	>tr|R5WGP1|R5WGP1_9CLOT Histidine kinase OS=Clostridium sp. CAG:167 GN=BN512_00488 PE=4 SV=1MKKGQIHSDINGAEHIMVCLSASPSNVKIIKTAAKMASAFGGSFTALYVKSANTDKMNEFDKKRLQSNIQLAEQLGAEIAITHGEDVSFLIAEYARISGVTQIIIGRSNIKRHHFWSKPTLTEKLTEIAPNLDIHIIPDGSLGTTYKNREASVLYRLAISHPKDIFTMLLLLTGVTLLGQVFYHFGFTEATIIAIYIWGVLLISLFTRGYACGIVGSLMSVTLFNFFFTKPRLTLHAYDSRYIVTFGIMMAVSIMTGTLASKVKLHAKMSAQNAFRTKVLLDTNQLLQKAKSDEDIINITATQLMKLLNRSVVVYTVKEEKLSKGLLFPVKPEANSGELFSDLEYNAAHWVYQNRHRGGATTDAYTNAKCLYLAILIYDKVYGVIGIHVEKKLDSFENGMLLSIIGECALAMDNNRNAKEKEMAAVLAKNEQLRANLLRAISHDLRTPLTAICGNAENVLTNYETLDADMREQIFKEIFDDSQWLIGIVENLLSVTRIEEGRMNFNMSIQLMDEVISEALAHIRQKRNRHDIKVYCEDELLAKMDAKLIVQVIINLVDNAIKYTPYGTSIRIVAKKESKAVAVSVIDNGPGIPKEIKPRVFDMFYTGENKVADSRRSLGLGLALCKSIINAHGGEITLTDNQPQGCNFTFMLPLEEVRIDE	31)~~138;X;182~~DUF4118 (0.000000000336319)~~264;X(167);431~~HisKA (0.00000000513114) ~~497;X;550~~HATPase_c (1.28361E-28)~~653	non-KdpD DUF4118 protein

	1E-06	38	10.4	2.3E-06	37.2	7.2	1.4	1	G8NW44_GRAMM	Histidine kinase (EC 2.7.13.3)	AciX8_1119	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	481	682795	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	>tr|G8NW44|G8NW44_GRAMM Histidine kinase OS=Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8) GN=AciX8_1119 PE=4 SV=1MSVRFRSVIATLAACVLVVAFGAINVRHTLGLATTIPLYMLLTLLVAWRVGFRAAMVVSICATVSLDLFFAQPLFTLRVAAPENITALATFICVSLLVSYLSHTVKRTDQALQRHDEQQLALYELLQRMLLLDWRESVGIHLSMLVQQCFHLDGVGLWEAHEERFSWTGDAEGAAAALRAALLADRDVDSESRKEAIRVLRSGTRPVGAVLLRGDLIDPLMASAVGTLMASALERARALKAEVVAESEKLSEQLRSAVLDGLAHAVKTPLTTIAISSAGLSEIGGLTPVQIELVDLIEGQASRLSSLTNKLLRTSRLDVGEMRLQRKPLELRALLQATIEELGSEFDTERLHTHFEEGLAIEGDRELLSMALAQILENALKYSPAASAIELSAKADGGSVILSIHNDGSYIPVEERALIFRRFYRSQDVEHRAPGTGIGLSVALRAVEAHGGELWVESERDTGTTFSISLPAKGLSISLSA	9~~DUF4118 (0.00000000988258)~~107;X(145);252~~HisKA (0.00000109368)~~316;X;368~~HATPase_c (1.84255E-24)~~470	non-KdpD DUF4118 protein
	1E-06	38	15.1	2.2E-06	37.2	10.5	1.4	1	M4V6P6_9DELT	Histidine kinase (EC 2.7.13.3)	A11Q_658	Bdellovibrio exovorus JSS	896	1184267	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio, Bdellovibrio exovorus, Bdellovibrio exovorus JSS	>tr|M4V6P6|M4V6P6_9DELT Histidine kinase OS=Bdellovibrio exovorus JSS GN=A11Q_658 PE=4 SV=1MTDESRLDPDALLKVIDDEAKLRSQGKLRVFLGMSAGVGKTYAMLKAAHRAQSEGHSVLVGVVETHGRSETAELLTGLEILPRKIIQHRGIDLEELDLDAILIKKPDIVIVDELPHSNVPGSRHEKRYQDVLEILRAGIDVFTALNVQHLESRKDAVESITGIRIRETVPDSILDQATLVEVVDIAPSELLKRLADGKVYLKDKATEAAAKFFKEDKLTALREIALRMTAERVDQDLQRFSVKRNDSPWQTNERLLVAVSHSPYSEKLLRATRRLAYNLESPWIAVHIDTGIKLSDEDQAQLVKNLHLARELSAEVITTTDTSIASAIKRIARQKNVTQVVVGRPTRRWFRDVIEGGSLLSRLVNESHDVDVHVIRMENLKHRRPSFWAELALYRTKTGIIKYWNTLCFLVGVTFFSALFQDYIGYRAIGFIFLLAVLIVGMFGSIGAVLFAAAFSALFWDFLFIAPRFTFTIASPEDIILCISYFAVALITGFLTNRIRFQEKLMREREERMEVLYRILKDISESYDKKEFIQKVRARVGQLFDGECGVLLKAKESVLDFSNSDEYPLPLNDKERAVALWTFQNQKAAGWSTETLSQAQALYLPLNGMNETVGVFVFRPEKKIRKFGLDQETLLYTIVGQLGFSIERHFLRKRIIEAQRVEDSEKLQQTILASISHELRTPLTAILGSAAALDSDLISNPLAKDIVKDIEFNSERLNRVIENLLDMSRLSSGSLALNLEWQDISDLIGVVLKKHAKPLQSHRVEVGLQSELPLVRMDFRLFEHALANLILNAAQYSQPDTKIIIRAYTHEKQLVLEVKDHGAGIPVEFIGQIFEKFYRVPGTLPGGTGLGLSIVKNIVELHRGTILYHKNEPQGSRFIIYLPLEPQPTLPIEENA	26~~KdpD (8.39929E106)~~233;X;254~~Usp(4.81031E-35)~~375;X;406~~DUF4118 (1.87136E-15)~~502;X;528~~GAF (0.00000821033)~~648;X;665~~HisKA (0.000000000000306781)~~729;X;782~~HATPase_c (7.12197E-18)~~882	KdpD protein
	1E-06	37.9	7.1	2.2E-06	37.2	4.9	1.3	1	R5AWI6_9FIRM	Histidine kinase (EC 2.7.13.3)	BN455_00082	Firmicutes bacterium CAG:103	357	1262999	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:103	>tr|R5AWI6|R5AWI6_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:103 GN=BN455_00082 PE=4 SV=1MQKASKRLPQWLRDTLMFILIMGCAVAVCELLSVCYDDNNPFATSVFILAVVLVSRFTTGYWPGILASAVGVVSVNYLFTYPFHEFNLTIDGYPLTFAVMLVVSVLVSTLTTQIKRQEQLRYEAERDRMRANLLRSVSHDIRTPLTAIMGLSATVEESETLTDEGRGMVEEIHQNAQWLLHLSENILSVTRFCDEGVVIEKSDEVVEEIVGSAIRRFRKNCDTDIPITVSKPEEILLAPMDATLIEQVLLNLLENVAKHSPSATEIFIEIRAEGRRVWLTVADNGDGIPPQLLGVLFDGYLPLGAVEASDRSRHMGIGLSVCRAIVRAHGGEIYARNKIDGGAEFRFWLPAEEESNT	19~~DUF4118 (0.000139012)~~98;X;127~~HisKA (0.000000000001531 88)~~191;X;245~~HATPase_c (3.50357E-26)~~349	non-KdpD DUF4118 protein
	2E-06	37.8	11.1	2.4E-06	37.1	7.7	1.3	1	C1AAN1_GEMAT	Histidine kinase (EC 2.7.13.3)	GAU_2787	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	378	379066	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	>tr|C1AAN1|C1AAN1_GEMAT Histidine kinase OS=Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505) GN=GAU_2787 PE=4 SV=1MWARHRRSLILWLLWVVALAALVAILVPSREQVEQTHAALMMLLIVLGASATVGFTAGVSIALLAFALLSYYFESPLDTIDLPTGVDLIELTSFLIVAVVAARLLTIARTRATLAELRAREIERLAAERTALATQAAQAEGLAEANRMKDALLATVSHDLHTPLTTIRALAGRRSVADDADWLLVQQETDRLAHLVRELLDYSRIRGGALPVRIESYPAEDLVGAVARECAHRLGAHTLHTHVPMSGPVLAGMFDLVLSTRVLVNLVENAAKYGTADSRIDLHVERIGSTLRFAVSNQGPTIADADRERIFEPFTRGGSTVAQSRVPGVGLGLAIARALTEAQAGSLALAVTQGANDSGTTTFVLTLPATDWTEMAPE	10~~DUF4118 (0.000000562515)~~111;X;146~~HisKA (0.000000015819)~~204;X;261~~HATPase_c (2.02682E-19)~~367	non-KdpD DUF4118 protein
	2E-06	37.8	12.1	2.6E-06	37	8.4	1.4	1	J9SQL2_9ACTN	Histidine kinase (EC 2.7.13.3)	KTR9_4019	Gordonia sp. KTR9	849	337191	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia sp. KTR9	>tr|J9SQL2|J9SQL2_9ACTN Histidine kinase OS=Gordonia sp. KTR9 GN=KTR9_4019 PE=4 SV=1MSSAAGHPEGRGKLRVFLGCAPGVGKTYEMLAQARTLVDEGTDVVIGVVESHGRVATAALVEGLETIPRISRSYRGTPLEDMDLDAVLARRPEVALVDELAHTNIPGSRNRKRWEDIEELLGAGIDVYSTINIQHLASLNDVVAQITGVVQRETVPDDIVRGADEIELVDIDPQALRQRLSAGKVYPGGRVDGALANYFRQGNLTALRELALLWLADQVDDKLADYRAAHSITETWEARERVVVAVTGGAESPTLLRRASRIASRSSAELLAVHVVRGDGLTGVGVDLAALKELAAGFGARIHTVVGDDIPDTLLEFARGVNATQLVLGTSRRPRWQRIFDEGVGAAVVSDSGRIDVHMVTHDETSRRSRLDIRDTRFRRPLSWLFAVLVPAGVTGVLQLLDPWLGFASQSALYFVAVLAVSMLGGILPAALSAVISGLLLNFFFTDPRFTFTISQPDNLITILVMLMIAIAVAALVDSATVRRAQADAAREAELLALFSSVVLGGADVPVLLERFRETYDQSAVSVVRRTSRAGRVVEAAVGESPPVSPEDADTVCVVPGEKFELLLRGPKLGARDRRVLAAVAGQAAGAVQRHALEAEAATAEALARTDELRRALLSAVGHDLRTPLAAAKAAVSSLRSDDVTFSPEDTAELLATVDESVDHLTSLVGNLLDSSRLAAGAVRPHRQRTFLPEVVHRAAAAVARTDREPALTFDLGHAWAYTDPGLLERALANLIDNARRHGGGHVEVTARLTPADPPRCEIRIIDHGPGLPVVDRDQIFAAFHQGGDTSGASSGVGLGLSVAQGFVTAIGGVLGVEDTPGGGATMVVDLPATDDLDVPVETAGPVR	12~~DUF4118 (0.000000000023958 3)~~113;X;123~~HisKA (0.000000000004832 88)~~189;X;242~~HATPase_c (1.31145E-25)~~345	KdpD protein
	2E-06	37.7	11.9	2.7E-06	36.9	8.3	1.4	1	R5EML3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN466_00606	Firmicutes bacterium CAG:110	353	1263000	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:110	>tr|R5EML3|R5EML3_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:110 GN=BN466_00606 PE=4 SV=1MMKQHKRVFLDFAYAAVILVTAFALNLALLQWFRIPSVTPMVFVLGVFLIAWRTQGYFWGIASSLVSVMAVNYAFTYPYWAFNLIRPECLASAVVMLMVSIMTSTMTTQIKRQEQMKAEAEKERMRGNLLRAVSHDLRTPLTSIYGACSAMLENYDALPRQTHMKLLSDVCADAQWLVRMVENLLSVTRVDTSTVRLSKNDTVLEELIDAVLVKFHKHYPDTEVHVEIPEEFVSIPMDAMLISQVLMNLLENAVFHAKGMKDLWLRVEVKGLWAYFYVEDDGCGIPEEKLPKLFTGMLGSEAPMDQSRSSMGIGLSVCSAIIKAHGGEIWANKRAGGGTEVGFRLEMEDENGE	12~~DUF4118 (0.000000000023958 3)~~113;X;123~~HisKA (0.000000000004832 88)~~189;X;242~~HATPase_c (1.31145E-25)~~345	non-KdpD DUF4118 protein

	2E-06	37.6	4.5	3.1E-06	36.7	3.1	1.4	1	R5E0M4_9FIRM	Uncharacterized protein	BN798_00739	Eubacterium sp. CAG:86	739	1262895	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:86	>tr|R5E0M4|R5E0M4_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:86 GN=BN798_00739 PE=4 SV=1MRVLIVGAFGTVTSAIIRKFGKEGARIYALTGGKNSENRYKKVYEQYDFSYDNNCIKEVFESVNPDVTIFTGAFDSNFEWSSGYSEMVKFGAGLYNCLNAFSFLNHGRFIFLSSNEVNGFDESTYKEILHSQRPLESGAIRTYARVYKASALKNGEDICSNYRKTTGSDVIALRIEELSFETKKPEEAVDTCTRMCSELLRENSITKESEKYSPIYITDVVEALYKLVNKDLLKYSLYRIHSDSSITQNELAELINTSFDTQVSIKENISDISSNDDIHDMSEEIEVKIFKDAKSCAQQIIKNIKNNRSVFASGSTVTEKFSKRIAQYFKGMLVALIPFIENMVIFIPFFMINNRTTGSTYFARLDCYLIYVLIFAMVYGQQQALFSSILAVCGYFFRQMYSRTGFEIMLDYNTYVWIAQLVILGLSVGYLRDQLNSLKADKEDEVGYLDSRLKDIEDINIINAKLKDELETQVINQSDSLGKIFEITSTLDKDEPEEVFFHAAEVVSKLMDCKEVAIYNVSNRNFARLMAFTSHNAKKLGNSIEYTKYTEMYETLKRGDVYINRKLEKDYPLMAAAIMAEESISSIVMLWDISWEQMNLAQSNRLRVVSYMIQNAVLKANRYIEMIENERYVEGTRLLETQAFKKLLDAFTNARKRGLADCSIIKINPGTKDVKEASIDLQKNFRNSDYLGSLDDGYLYVLLANTNNADAGFVTGRIKDAGYSYEMIDGDVDGGAYGD	93~~NADB_Rossmann (0.00000203207)~~238;X;338~~DUF4118 (0.000000000000070331)~~436;X;495~~GAF (0.00000000028111)~~617	non-KdpD DUF4118 protein
	2E-06	37.4	12.4	2.9E-06	36.8	8.6	1.3	1	R5R6L9_9FIRM	Histidine kinase (EC 2.7.13.3)	BN526_01011	Firmicutes bacterium CAG:194	353	1263008	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:194	>tr|R5R6L9|R5R6L9_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:194 GN=BN526_01011 PE=4 SV=1MNKNIRRNILKTVLIPSVCLLVCIIIEHYLAIDMVAPAIMALAVFLVSRVTEGYVYGIVASILSVLALNFVFAFPYFAFNFSIPENIISALIMLIITIMTSTVMTQLKWQEKVRAESAKEKMRGNLLRAVSHDFRTPLTTIYGSSTTIIENYDHLKKEQILQLITGIREDTQWLMNMVENILSITRIDNGGVRLKKNSVVLEELINSVLVKFKKRYPNQKVTVSIPDEFISIPMDAVLIEQVIINILENAVQHAQGMTELSLTVHTEGGKVVFEITDNGCGIPRERLKSIFKDYFEIKDAPVDHNKKSMGIGLAVCASIIKAHDGEISVENREEGGCIFRFTLDEEDSLSEQL	8~~DUF4118 (0.000000000049123)~~108;X;120~~HisKA (0.0000000017853)~~186;X;239~~HATPase_c (6.58947E-26)~~343	non-KdpD DUF4118 protein
	2E-06	37.4	12	3.3E-06	36.6	8.3	1.4	1	A0A0F3L059_9GAMM	Histidine kinase	VI08_04320	Luteibacter yeojuensis	888	345309	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Luteibacter, Luteibacter yeojuensis	>tr|A0A0F3L059|A0A0F3L059_9GAMM Histidine kinase OS=Luteibacter yeojuensis GN=VI08_04320 PE=4 SV=1MTDTRDARADALLNTVNGDVGQRLKIFLGAAPGVGKTYAMLSAARDLRRQGVDVVVGFVETHGRAETSALLEGIEVLPTRTVPYAGRDFQEFDLDAALARKPAVLIVDELPHTNLPGGRHARRWQDIADLLDAGIEVYTALNVQHLESLNDQVRRITNVAVRETVPDAFLDRARDIVLIDLPPRELITRLKQGKVYVPETAAVALDAFFSPTNLAALRELAVETVAHHVDSDLREHMLARGGAMPVRRRTMAAIDGHAQSEYLVRMTRRIAERRGGPWSVLFVDTGHVDGERRERVDAAMRLARRLGGEPVILRGHAIADELLAWADREGVGQIVVGRTRERPIARRMGFSLTQQLLRRGAHLELTIVATPAERARARRKLRSGVGAAGGTRRDYAFATAATAVAMGLSFVADRFLSVANLSLIFLTAVLVVAVRTRMAVAVYTAILCFFGYNFFFAPPRYTLAIANADDVLAVVLFLVAALVCSRLATRLAGQVQSLRAAQVRGRALVTLGQQLATSADAEGIRTAGARALARALEAEVAMLARNAGGELALAVSSPDAFALSTQDRAAADWCDKHAEPAGRYTDTLHGASCWMLPLGTEHHRAGVVALRFPLGAREPDADRRGLAQAMAEDIAQALERARLAVELESARVQGETERLRSALLSSVSHDLRSPLASMIGSAGTLLSYDAQLPNDERHALLQAILGEGQRLDRYIQNLLDMTRLGHGTLQLHRDWVDAGEIVAAAVARLRKLMPDTHVDVHLPRDTVLLHVHPALIEQALFNILENAASFSPAGEPVRVLVRTEAGRLLFDVSDRGPGIPEEERARIFDMFYSVSRGDRGKQGTGLGLAICRGMVGAHGGTVEALPHAGQGTTIRVSLPLPPPPDEPA	23~~KdpD (1.23155E111)~~229;X;249~~Usp(1.34507E-28)~~369;X;407~~DUF4118 (0.000000000116719)~~494;X;557~~GAF (0.000959609)~~651;X;657~~HisKA (0.000000000015939)~~723;X;776~~HATPase_c (1.94307E-25)~~877	KdpD protein
	2E-06	37.4	9.4	3.2E-06	36.7	6.5	1.3	1	B8J1F2_DESDA	Histidine kinase (EC 2.7.13.3)	Ddes_1680	Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	961	525146	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio desulfuricans, Desulfovibrio desulfuricans subsp. desulfuricans, Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949)	>tr|B8J1F2|B8J1F2_DESDA Histidine kinase OS=Desulfovibrio desulfuricans (strain ATCC 27774 / DSM 6949) GN=Ddes_1680 PE=4 SV=1MTDKHTRPDPDALLAQLRQTGTPQGIQADELSGGHLPVRGTLKIFFGYAAGVGKTYAMLRAAHTAAEQGQDIVVGYVEPHPRPETAALLQGLESLAPLRLEYRGIPLHELDVDAVLDRKPEIALVDELAHSNAIGCRNRKRYQDVEELLQGGISVWTTVNVQHLESLNDVVAAMTGVAVRERVPDSVFDGADHVELVDLEPDELMARLREGKIYAQAQAQHALGHFFLPANLIALRETALRRMADRINRRAIPAEPGSREAARQVKEHILICLSGAPSNARVIRTAARMAEAFHADFTALFVRNNTSGHNDTQSLGTLRKNTRLAEDLGAAIVTAQGEDIPVQIAEYARMSGVSKIVIGRSPASGWLRRGKTLVERLAELAPEMETYIIPDAEPISRNASRPGTLYRMVRAFRGTAPRSWRQWGATAALLAICTMTGLIMSSMGMPNAVITGLYMLGVLGVSILTTGPWYGVTASILGVALFDFLFVAPRFSLTVYDDGYLSLFAAMLIVSAAASAITGRARSQARQSAARALHTELLLGNSRRLQKAENENAILAEAARQFGTLLGCDAVLYPVYNGHLETRRIFPYYTAAQASREPGRPHTLPRQLAKGQTECTHRTEKDELAVAQWVAKNGRPAGAGTDSLPGARLCYIPISSRTTVLAVAGLDVSPGSASPLNAADSKNIVLALAGECAMAVEKERLARANADIAVRAQQEKLRADVLRSVSHDLRTPLTAICGNAAMLAAGGDIEMQRRKSLARAIEEDARYLVEMVENLLALTRLEQYGFTLRLAPELMEDIIREALAVTRRRAAAHNIRVDMADALLMARMDARLMVQVLVNLLDNAVKYTPAGTTIRISAQADGARARLEVADNGPGISAEEKTRIFDMFHSAVIKKGDSRRGMGVGLALCRSIVQAHGGDLRVHDNTPRGAVFSLDLQREIEEGPVPESLRETPPTGTGARE	39~~KdpD (2.38321E113)~~247;X;268~~Usp(5.42718E-29)~~390;X;422~~DUF4118 (0.000000000000214371)~~524;X(191);715~~HisKA (0.00000000039714)~~780;X;835~~HATPase_c (4.53607E-29)~~936	KdpD protein
	2E-06	37.3	13.3	3.4E-06	36.6	9.2	1.4	1	Q24QZ1_DESHY	Histidine kinase (EC 2.7.13.3)	DSY3762	Desulfitobacterium hafniense (strain Y51)	473	138119	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium hafniense (Desulfitobacterium frappieri), Desulfitobacterium hafniense (strain Y51)	>tr|Q24QZ1|Q24QZ1_DESHY Histidine kinase OS=Desulfitobacterium hafniense (strain Y51) GN=DSY3762 PE=4 SV=1MTINRKNREIARSVMKVLVVLTLSLLGSLLIAGLGAGRESILMMFLLGVLFVTILTNGYIYGLAASVAGVVLFDFFFTEPRYAFLIYSAVDVMLLLFFLVTAVVSGTITSRLQKQISISHQSELTARLLYKVAEDFLHITGKGNIILRGIKYIYDHTGYASRVILDGDDQEYFSEQYVQSDMEGLTIPIQGVAKQMGSLTLYCGRDELTFQQELVVKTVATQLGAALDREYSYRETEEIRVAMERERLRSTLLRSVAHDLRTPLTALTGASSLLTDKFEQLSLEEQKKLAADISEEMIWLANFVENILNMTRIGEGQLFLHKEDEVVDDVVNEATSHMSRILQNRHLEVSLPNEVISLPMDGKLVVQVLVNLLDNAVKHTPLESCIDLKVGILGNDVVFEVCDNGNGIAEDIMNRLFDGFTTPKNNIIDGKRGMGLGLAICKAIVEAHGGAIRAENQPAGGARFVFSLPNGGE	41~~DUF4118 (0.000000000043057)~~115;X(131);246~~HisKA (0.000000000161588)~~312;X;374~~HATPase_c (1.07231E-23)~~468	non-KdpD DUF4118 protein

	2E-06	37.3	6.2	3.8E-06	36.4	4.3	1.4	1	B1VXM4_STRGG	Histidine kinase (EC 2.7.13.3)	SGR_1661	Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	847	455632	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces griseus group, Streptomyces griseus subgroup, Streptomyces griseus, Streptomyces griseus subsp. griseus, Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	>tr|B1VXM4|B1VXM4_STRGG Histidine kinase OS=Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350) GN=SGR_1661 PE=4 SV=1MGRGTLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLHGLELLPRRELEYRGTVF TEMDVDAVLERAPAVALVDELAHTNVPGSRNAKRWQDVEELLKAGIDVISTVNIQHLESLGDVVESITGVRQRETV PDEVVRRADQIELVDMSPQALRRRMAHGNIYRPDKMDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRGE HNIRTTWQARERIVVGLTGGPEGRTLIRRASRMAAKGSGSEILAVYIARSDGLTSASPKELAVQRTLVEDLGGTFH HVIGDDIPAALLEFARGVNATQIVLGSSRRKTWQYIYGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPMARGA RLGRARILWGWLVGVVGPVLLAVVLRSMEDAPGLANDVLLFLFLTVAAALLGGVRPALASAAVGSMLLNYWFTPP THTLTVQDPENLVAIVIFFAVAVAVSSVVDLAARRTHQAARLRAESEILSFLAGSVLRGETALDALLDRVRETFAME SVALLERSSDVEPWTCAGYVGPAPVTRPEDADVDMPVGDNMALALSGRVLPAEDRRVLGAFAAQAAVVLDRQR LVGEAEQARRLAEGNRIRTALLAAVSHDLRTPLASIKAAVSSLRSDDVAWSEEDEAELLEGIEDGADRLDHLVGNLL DMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVDLDIPETLPMVAVDPGLLERVVANIVENAVKYNPGQEPVAV AASALGGRVELRVVDRGRGVPDEAKERIFEPFQRYGDAPRGAGVGLGLAVSRGFAEAMGGTLDAEDTPGGGLT MVLTLTAAPGGVRTETELPARATS	1~~KdpD (2.29705E-123)~~211;X;233~~Usp(4.50791E-31)~~356;X;381~~DUF4118 (0.000000030185)~~466;X(146);612~~HisKA (3.18897E-14)~~678;X;727~~HATPase_c (4.74353E-27)~~828	KdpD protein
	2E-06	37.3	8.9	3.3E-06	36.6	6.2	1.3	1	R6I2S1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN556_01891	Firmicutes bacterium CAG:240	491	1263013	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:240	>tr|R6I2S1|R6I2S1_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:240 GN=BN556_01891 PE=4 SV=1MLAFCTGIGYLFSDLGFSTANVIVIYIIGVLGIAMLTAGRSYSLAASILSVLICNFFFTEPYFSLFSDPSHIMTFIV MFAAAFFISSITARIKRQTHQTALRVYRTEILLETSQKLQQAIGTEQILTVTAGQLVKLLERSVLIYPVENGALSEPML FPVNENAGFDDYLTQYDRDSARWVLENDRRAGNGTDTRQKSNGIYMAIHANGRVFAVAGVAMKASPMLESFEK TLTVAILDECGLVLENEYNRIEKRRIEEKARAEELRSNLLRAISHDLRTPLTNISGTAALLMENELPEEKRRQMYVSV YDDAHWLIDLVENLLSITRMEGGSRIEDLQPELLDDIFREAVSHSDRLLSEHELEIRLDDELLMAHMDARLIVQVVIN LINNAVKYTPRGSHICLEASARDDRVLISVADDGNGISDEAKEKIFDMFYTGNKASSDARRGLGLGLALCKSIVQAH GGSIAVSDNTPHGAVFTFDLKRAEVQPDE	6~~DUF4118 (0.000000000002219 83)~~95;X(167);262~~HisKA (0.000000000002258 81)~~326;X;379~~HATPase_c (3.46513E-27)~~482	non-KdpD DUF4118 protein
	2E-06	37.3	4.2	3.4E-06	36.6	2.9	1.2	1	A5G7X6_GEOUR	Histidine kinase (EC 2.7.13.3)	Gura_3741	Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	367	351605	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter uraniireducens, Geobacter uraniireducens (strain Rf4) (Geobacter uraniumreducens)	>tr|A5G7X6|A5G7X6_GEOUR Histidine kinase OS=Geobacter uraniireducens (strain Rf4) GN=Gura_3741 PE=4 SV=1MKRANIVRLVVPAVFILGISLLHYLTPLHLPMLHDIFQRLYYLPIILAAFWFGLRGGLVSSIVVSIMYAPHVLFQ WGVHPSLELEKYLEILLYNIVGGVTGLLSQREVARREELHKTARGLEDSYKKLQSQADLVIEIEEQLRRAERLSVLG ELSAVLAHEIRNPLGSIKGTAEILKDSFRPGESNYEFLEILLKETDRLNRVVEDFLGLARPLQVERATCDIMAELNEIV TLISTEAAARGVSIELNPAELPAVHGDREKLRQAFLNLLMNGLQATGRGGKLTVSASCPGPAEESPAVVELSFADT GEGIEPDRLNRIFEPFFTTKPDGTGLGLAITQKIVESHGGSIQVASEKGKGTTFTVRLPV	9~~DUF4118 (0.000000407142)~~110;X;148~~HisKA (2.08282E-14)~~212;X;262~~HATPase_c (3.67776E-27)~~365	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	2E-06	37.3	10.8	3.6E-06	36.5	7.5	1.4	1	Q2J7V2_FRASC	Histidine kinase (EC 2.7.13.3)	Francci3_3283	Frankia sp. (strain CcI3)	854	106370	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain CcI3)	>tr|Q2J7V2|Q2J7V2_FRASC Histidine kinase OS=Frankia sp. (strain CcI3) GN=Francci3_3283 PE=4 SV=1MASGRLRIYLGAAPGVGKTYDMLCEAQRRKARGTDVVVGLVETHGRPRTAALLDGLEIMPRRTVSYRGATF TEMDVDAILARAPAVVLVDELAHTTVPGCRNAKRWQDVHELLNAGIDVLSTLNIQHLESLNDVVERITGVPQRETV PDAVVRAAEQVELVDMTPEALRRRMVHGNIYGPDKVDAALGNYFRVGNLTALRELALLWLADKVDEQLDHYRTE HQISGIWETRERVVVALTGGPEGDTLIRRAARIADRAKGADLLAVHVTRSDGLAGASPAHLARQRVLVESLGGSYH QVVGDDIPIALLEFARAENATQLVLGASRRGRLAHMIDPGIGVTTTKLSGPIDVHLVTHEEVGKGRLLPRRARGLTL RRRLAGVLAAVVLLPLLTLALTHQRTGLNLTSNVLGFLIVVVAVALVGGLLPALLAAVGGLLLLNYYFIQPVHRFIVAE SNNVLALLAFLAVAVMVSSVVDLAARRTSQAVRATAEAEMLSTLAGSVLRGEQALPALLTQVRETFGLTSVALLER AAEGGQNGARKADRHGWRVVDSAGPDPCLRPDEADTEVPVSENLTLVLRGRPLPAADRRVLTAFAAQAAVALE QRRLAQVAAEAGPLAEADRTRRALLTAVSHDLRSPLATASAAVANLRGNEVEWSAEEQAELLATAEEALDHLARL VENLLDMSRLQAGRLSVFPAPVGLDDVIPGVLRDLGPAARDVAVTVPDDLPLVYADPALLERVIANLLSNAARYSP PGQPPLITASALHDRIQLRVIDRGPGLPAEDRDQAFTPFQRLGDTDNASGIGLGLALSRGLTEAMGGTLTPEDTPG GGLTMVVALPVATVGDSTQPADGAA	4~~KdpD (2.67594E-120)~~211;X;233~~Usp(3.04034E-21)~~355;X(265);620~~HisKA (0.000000000030881 2)~~686;X;737~~HATPase_c (1.27374E-25)~~838	KdpD protein
	2E-06	37.3	11.4	3.5E-06	36.5	7.9	1.3	1	D4MY64_ANAHA	Histidine kinase (EC 2.7.13.3)	CL2_04910	Anaerostipes hadrus	658	649756	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, Anaerostipes hadrus	>tr|D4MY64|D4MY64_ANAHA Histidine kinase OS=Anaerostipes hadrus GN=CL2_04910 PE=4 SV=1MSTGEFVELNKENEHILVCLSSSPSNEKIIRTAAKMARDMRARFTALYVQTGKRERESDKRRLEAHVQFAKE SGAEIVMTHGENVPVQIAEYAHLSNVTKIVIGQSSAKRNHFFSKQTLTEKLIEAVPDIDIHIIPDAMNLDNYRKPHGAV YVGKPTMKDSLLTLFIFAVCTLIGLFIQKLQFTDTNIVTIYILGVLLTSILTDGYLYSIGGSVLSVFLFCFFLTEPRMSFQ TYAVGYPVTFVIMLISSVITGTLAAKLKTHARLSAQSAFRTQILFDTDRLLQKAKNDTDILSITCTQLIKLLDRSIVAYV VEGDELSAPHIFSNKKKEQIEDLLTSREQEIAKWVYENKQRAGATTERFKDAQCLYLAICIEDNVYGVIAIPVDEYTL DSFEYSILLSVINECALAMENKKNIMEKEKISVLAKNEQLRADLLRAISHDLRTPLCSISGNADMLLNSGERLDDITKH QIYTDIYDDSEWLINIVENLLSITRLNDGRLKLKFTDQLLDEVIAESLRHISRKHEEYQIVTECDELILAHMDVRLILQVL INLVDNAIKYTPKGSTIRICAMNENGKAKIQVEDNGPGICDEMKPHIFEMFYTGKNTIADSHRSLGLGLALCRSIIEVH NGKLVLEDNTPHGCIFSFTLPLSEVTLNE	33)~~136;X;162~~DUF4118 (0.000000000000110 152)~~262;X;291~~GAF (0.000000760206)~~411;X;428~~HisKA (0.00000000013634) ~~494;X;546~~HATPase_c (8.48385E-27)~~649	non-KdpD DUF4118 protein
	2E-06	37.3	5.9	3.3E-06	36.6	4.1	1.3	1	A0A0F0CBD6_9CLOT	Sensor protein KdpD (EC 2.7.13.3)	kdpD_4CLFS41_46290	Clostridium sp. FS41	663	1609975	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. FS41	>tr|A0A0F0CBD6|A0A0F0CBD6_9CLOT Sensor protein KdpD OS=Clostridium sp. FS41 GN=kdpD_4 PE=4 SV=1MEKEWDGRPDPELLLRQNFPDSNNKGRGKLKIFFGYAAGVGKTFAMLEAARQEKAGGRDVVVGYIEPHDR PDTLALLDGLELLTPKYVEYKGITLREFDLDGVLIRHPDLVLVDELAHTNAQGCRHKKRYQDVTELLDAGINVYTTV NVQHLESLHDIVASITHVRVNERIPDRVFDNAAQVELVDIGPEELRQRLEEGKIYHREQADRASISFFTAQNLSALR EIALRRTADRVNREVIRERDAAGKDYFTGEHVLVCLSPSPTNAKVIRTAARMASAFHADFTAVLVETEHLKKEHVRI SRSMEANINLAKQFRANVITLYGDDIVEQVASYARQNGISKIVIGRTVRTRHSIFAKPTLIDRLIKAVPNMDIYVIPDAS ARERKRNGGTEQKRRVGSDLLKTALVMAFCTAMSLILDHYQLGIINAAMIYMMGTMLSAYLTRAGWCGLLASVAS VLLFNFFFTEPRYTLQADASIYPFTFAAMLVCALVTSSMASRLKREAAKGEAESRYMQILFDINRNLRKGSTGEEIL DICGTLVRNLLKRNIVIYDTREGRTDRMKIYPASENEDSARLTSLFKQQSEAAVAFWVYKNRHKAGATTDTLPGAQ ARYTPVYKDDRVYAVIGVEMKGGDTIQPNDKNVLNIIAEETSYRLGDMKEGCPR	25~~KdpD (2.54532E113)~~235;X;255~~Usp(3.67268E-34)~~378;X;401~~DUF4118 (0.000000000046028 1)~~502;X;530~~GAF (0.0000679823)~~651	KdpD protein

	2E-06	37.3	7.8	3.7E-06	36.5	5.4	1.3	1	R6UQ33_9FIRM	Histidine kinase (EC 2.7.13.3)	BN746_00932	Erysipelotrichaceae bacterium CAG:64	515	1262981	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, environmental samples, Erysipelotrichaceae bacterium CAG:64	>tr|R6UQ33|R6UQ33_9FIRM Histidine kinase OS=Erysipelotrichaceae bacterium CAG:64 GN=BN746_00932 PE=4 SV=1MKSAIIGTEKRGLMKNSHIWKNLCITTVILFLCTLVSFVFDDIEIRTENIMLIYLIGVLLIVVETGSFLWGITSSLLS ILTFNYLFTNPTFSLQIDDFNYIITIIVFLIVSFVTGSLVNKLQQHAHKARSSARQTSALYEITRAYLTLSGVDTILQHTIR SLYTAQQTICTVYYTDGEALKKIQEPMDTAAEPDDGMAAWCMEKDCDCGRGTSFYEEQAWTYHPMHCNNQLLG VYALYEETSLREEQRLFVHTLISQMMMAVEREMLYAEQEQSRVEIEKEKLRNNLLRSISHDLRTPLTGIAGSSTLIC ENYQDLDDDTIYHLVKSISSDALWLNQLVENLLNMTRIQDGKLLLKQQEEVVDDIICEAVSRCESRKREHTLKVTLP DEVLLVEMDGRLIIQVLVNMIDNAIKHTPDATMIDIRCYKDHGWAVFEVIDQGEGIDESIREHLFESFVTTKSECSDS RRGVGLGLTICKSIVEAHHGEIFAYNRKDVQGAVFGFQLKLATERKEYHA	26~~DUF4118 (0.000000000006081 94)~~124;X(157);281 ~~HisKA (0.0000000021257)~ ~347;X;400~~HATPase_c (2.62268E-25)~~504	non-KdpD DUF4118 protein
	2E-06	37.2	11.2	3.4E-06	36.6	7.8	1.3	1	Q5QZN2_IDILO	Histidine kinase (EC 2.7.13.3)	kdpD IL1659	Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	343	283942	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Idiomarinaceae, Idiomarina, Idiomarina loihiensis, Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR)	>tr|Q5QZN2|Q5QZN2_IDILO Histidine kinase OS=Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) GN=kdpD PE=4 SV=1MSKQPWLGYLASVAITCTAAGLAYLLDHWLLPTSGTVLILQLAVLLIAFLTLNFRAALLAVVLALLLFNFLFTEPR YSLHMTDIDEMVTAIVFIAVGVITSHLVTLFRNQKESLRQAQLRSNILLSVSHDLRTPLASVIGNLSTLQAYQERLPE QERAELLQGALDESDRLHRYIENLLQATRLQHGEIRLTHAVQDIRPVISKTLSRFASQERLLVKDNLQHAMVEVQSS LLEQALFNVIDNAMRFSGETAPVTLSLSETDKFIVIDIKDEGPGIETSKRSLVFNVFYSSREKDSGTGGTGLGLSVAK GIIDIHNGHIGIEESPDGCLVRIKLPRANITEEVS	117~~HisKA (0.000000000230284)~~182;X;232~~HATPase_c (0.0000000001774 76)~~333	No DUF4118 detected by NCBI CDD
Disagreement between HMM and CDD prediction	2E-06	37.1	5.4	5.3E-06	36	3.8	1.6	1	E3JB50_FRASU	Histidine kinase (EC 2.7.13.3)	FraEul1c_6701	Frankia sp. (strain Eul1c)	913	298654	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain Eul1c)	>tr|E3JB50|E3JB50_FRASU Histidine kinase OS=Frankia sp. (strain Eul1c) GN=FraEul1c_6701 PE=4 SV=1MTSDAVDGPRRGRLRIYLGAAPGVGKTYAMLSEGHRRAGRGTDTVIGLVETHGRHLTAEMIGEFEIVPRRT VYHRGARFTEMDVDAVLARKPALALVDEYAHSNVPGSRNAKRWQDVEDLLGAGIDVVTTLNIQHLESLNDVVSTIT GVPQRETIPDAVVRAADQVELVDMAPEALRRRMAHGNVYAADKVDAALANYFRVGNLTALRELALLWVAGKVEE QLDDYRVDHGITDTWEARERVVVAITGGPEGDTLIRRAARIAARSTGGSDLLAVHVSRPDGLVTGADPAALARQR ALVESLGGSYHLVLGDNVPKALLDFARAENATQLVLGASRRGRFAHLVSRGVGVTTTARSGSIDVHLVTHEESSA GGRGTRIPGEDGSKSGGAWVLGAGRARRRASSLTLSASRQLAGFTLAGGALALLTVLATSSRQEVNLTSDTLLYL LVVVASAFIGGIWPALAAAVAASLLLNFYFTPPLHTWTIDDRNNAFALAAFVAVAIAVSRVVDLARRRSVQAARASA EAETLATLAGTVLRSEHPLPAILERVREGFGMTSVTLLAARSGDDASNPPPPGSGRDLWEIVANVGPRPAEHPSD GDVEVPAGRFTLVLRGRPLPAADRRLLAGFAAQAATAAERLRLAQEAASVKPLAEADRVRSALLTAVSHDLRTPLA AAKAAVTGLRAEDVVWSPEERAELVATADESLDRLTTLVENLLDMSRLQAGVLSVFPRAVHVEDVVALALDCLGP DAVGVRIQVSADPEVPAMRADPVLLERVIANVVANAIRFSPAGSPPLVSASTLGDRVQIRVVDRGPGVPKTDRDAI FQPFQRLGDRDNTVGTGLGLALSRGLTEAMNGTLTPEDTPGGGLTMVVELPAASGTTEEAVDPATSGGPATSGG PEPSGGPATSGGPR	9~~KdpD (7.59854E-117)~~219;X;241~~Usp(4.37116E-21)~~365;X(290);655~~HisKA (0.000000000000195196)~~721;X;774~~HATPase_c (9.30371E-25)~~875	KdpD protein
	2E-06	37.1	12.4	3.8E-06	36.5	8.6	1.3	1	R6R2L2_9FIRM	Histidine kinase (EC 2.7.13.3)	BN668_00598	Firmicutes bacterium CAG:466	526	1263025	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:466	>tr|R6R2L2|R6R2L2_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:466 GN=BN668_00598 PE=4 SV=1MKRRSKSFEFHFTMILYDLFKTILVFLIATTFALCLQEADVMNDNIFGVYMLAVAITSSITSGYFWGIVASFCGV VGVNFFFTFPYFALNFTLAGYPVTFGILLLMSILTSALTAKVKQAAILSSIREKRAESLNSMSKALLSANNIDEIMQITI DSVYAANQCSAVLYIGSPVSPEKKVTKYVNEKDELILESILEQQVAEQAFQKGEMTGLGTEKTSQNCLGTYIPFSN KDRIYGVLGLLFSKNGYIENDALQFANFMTSQTILAIDRQEIVDESQKILLEKEKENMRSNLLRAISHDLRTPLTCILG STATLMENRSMLQEDVCDRLLSDIHHDAEWLIQMVENLLSVTKISGEGTKLKKQEEVVEEIVAESVAKIQKRFPSS QIRVRVPDELLLVPMDAMLIEQVLINLMENAIRHSGTAKPIYLTVKHLWHHVYFSVLDQGIGIEEERLPHIFDGTTSS KSSDSSRGLGIGLPICKTIISAHGGEIYAKNNENGGANFTFVLPMKGEVEHVQQTEDTGCRR	19~~DUF4118 (0.000000000001543 28)~~120;X(167);287 ~~HisKA (0.000000000580652)~~353;X;406~~HATPase_c (4.26819E-25)~~507	non-KdpD DUF4118 protein
	3E-06	37.1	5.8	4.2E-06	36.3	4	1.4	1	D6Z0C9_DESAT	Histidine kinase (EC 2.7.13.3)	DaAHT2_2498	Desulfurivibrio alkaliphilus (strain DSM 19089 / UNIQEM U267 / AHT2)	400	589865	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfurivibrio, Desulfurivibrio alkaliphilus, Desulfurivibrio alkaliphilus (strain DSM 19089 / UNIQEM U267 / AHT2)	>tr|D6Z0C9|D6Z0C9_DESAT Histidine kinase OS=Desulfurivibrio alkaliphilus (strain DSM 19089 / UNIQEM U267 / AHT2) GN=DaAHT2_2498 PE=4 SV=1MNGRFLALVLIVAAIGLLHYFTPGHLHFYHDTFRRLSYFPIVLGALWFGMRGGLILAGLSSLAFIPHLFHFFGQ GLETYLGELTEITLYLATGLVVGVIADREHRLREQYRRLSEKLEKSHRRLQRETGQLLAAEKQLAAAQRLSALGRLS ASLAHEIKNPLSSIRGTAEIFLDEFPPGHPRREFVEILLKETSRLNATVDKVLGYSRGQRADNPEPGSTGEPTTYAD PAEPLEPLDRLLTRIAALAANPMGKKNIQYRVHGLEQAADLAVPANPVSQVLLNLLLNAIDAVSPGGEISLAVERRAL EVQVTVADNGPGIAEADKEKIFTAFYTAKPEGTGLGLLISRKIVESLGGTITAGDRPGGGALFTLRLPAENFSAVTE PGDDGISDQPGPNRCPT	7~~DUF4118 (0.0000000196376)~ ~103;X;144~~HisKA (0.000000000002017 89)~~208;X;278~~HATPase_c (3.97891E-29)~~373	non-KdpD DUF4118 protein
	3E-06	37	11.8	4.5E-06	36.2	8.2	1.4	1	A0A099GBC0_9RHOB	Histidine kinase (EC 2.7.13.3)	IX56_15165	Paracoccus sp. 5503	921	1525717	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Paracoccus, Paracoccus sp. 5503	>tr|A0A099GBC0|A0A099GBC0_9RHOB Histidine kinase OS=Paracoccus sp. 5503 GN=IX56_15165 PE=4 SV=1MTDAPRPDPERFLAEANAEAGVTTAAGRGRLKIFLGASPGVGKTYAMLEEAGARARAGTDVTVALAETHGR AETAALLARLDQMPRRVVTYRDRQLTEMDLDALLARRPGLALIDELAHSNVPGSRHPKRWQDVEEVLAAGIDVYT TLNIQHIESLNDLVARITGVRVQETVPDAVLQMADEIKLIDLPPEDLIQRMREGKVYMPAEAGRALGNFFSKPNLTAL RELALRTAASRVDAEMLALTRGTGRAAAQDRLMVCLDDPATAKGLVRAGRRMTDRARIPWVVATVVTPAVEAQG PQAAGAMTDALQLAERLGAQARTLRSEGDVAAAFLDAARQLNVTRLIVGRATRAGWRDRIAALIRPPLAQTLLAQA EGFEVTVLDPAPDRPSPPQPPTSPAPATEPAARWRETDWRAGPGRDWGRIAVAALGAAVAGTLAAWPFWSILP VASLAVIYLVGVLAVGMRLGTAGAVAAAVLSFLAYNYFFTEPYYSLQVSAEESVVALLVFTISAVFTGTLAGRLKRQ VEFMRVTQARTETLYDFARKIASATTTDDVLWAAAAHIARTLECHSLILMPDATGALQQVQGFPSIEEGLDAHALAA ARWAYEKDQPAGRDTDTLPTAGWMFIPLATQGAPLGVIGLRFTDPARRMDPETRRLLVAVEDQVAVAVERMAVE DDLERARLTSETEKLRAALLNSVSHDLRTPLVTVIGALSAVEAGGLSPAQERGLVVEALDEARRLDRFVGNLLGMT RLGHGALVPRRAAVAVAEVIGRARADLSRVLARFRVAVEIDPATPPLAVDPVLIGQALVNLLENASKYAPEGSTIRL TAAPVPEGVALTVIDEGPGIPVAERSRVFDLFHRAVQGDGQPAGTGLGLAIVKGMVEANGGTVAAIAPPDGRGAAI RLLLPAAAAAAAEDADA	26~~KdpD (8.59928E-115)~~236;X;255~~Usp(3.17786E-17)~~382;X;436~~DUF4118 (0.0000661526)~~524;X;550~~GAF (0.000000000868009)~~671;X;688~~HisKA (0.0000000288298)~ ~752;X;805~~HATPase_c (8.79346E-21)~~899	KdpD protein

	3E-06	36.9	11.4	4.4E-06	36.2	7.9	1.3	1	R7A3J8_9BACE	Histidine kinase (EC 2.7.13.3)	BN656_00234	Bacteroides pectinophilus CAG:437	350	1263051	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides pectinophilus CAG:437	>tr|R7A3J8|R7A3J8_9BACE Histidine kinase OS=Bacteroides pectinophilus CAG:437 GN=BN656_00234 PE=4 SV=1MSRMQKCIKNILITAFVLAGAFIISLVFQHVFEIEERITTLFVFAVFLISMLTEGYIYGIVSAIAGVLAVNYAFTFPFFEFDFATPVNVMSAIVMIVLAILTSTLTTKVKQHEAFKAESEKERMRANLLRAVSHDLRTPLTTIYSSASALADNRENLSVQQQDEILNAIKEDSEWLVSMVENLLSITKLGTGNVKINKKPVVLEELIDSVIFKFKKRYPSHDVIIDIPGDIVMIPMDAMLIEQVIINLLENAVQHATGMKHLWLSVFVIGNNAVFEIKDDGCGVSDEAMKSMFSGAYVSKASVPDGNRNNAGIGLSVCETIIKAHGGDISASNSMNKGAVFRFTLGMEEN	10~~DUF4118 (0.0000136951)~~112;X;122~~HisKA (0.000000000002897 1)~~188;X;241~~HATPase_c (1.85868E-20)~~345	non-KdpD DUF4118 protein
	3E-06	36.9	8.8	5.4E-06	36	6.1	1.4	1	R5PV40_9FIRM	Histidine kinase (EC 2.7.13.3)	BN766_01056	Ruminococcus sp. CAG:724	651	1262966	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:724	>tr|R5PV40|R5PV40_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:724 GN=BN766_01056 PE=4 SV=1MGERFANNNDHILVCLSSAPSNTKIIQTAAAMARAFHASFSALYVKTPASEYMEAEDKNRLLANIHFAEKCGATIVTACGDDVPFQIAEYARLSGITKIVIGRSVVGKRRFFGRPTLTEKLISLAPNVDIHIIPDSDAAIAKGKKTLFEKPHFAKLLKGLAISTFVLLLSSLLGCLFSRLGFTDANIITVYILGVLLIAIFTESKICWVISSVASVLVFNFLFTEPRFTFRAYGSGYPVTFIIMLAASLIIGGTTEKLKTRERQATQTSYRTKILFDANQLIQKASDEQEVFQVTADHLRKLLSRNVIIFNESAEKICDSFTDTKDSPSKDYRQIVRWVINNNQKAGKGTGIYSDSSYVFLPICKNEKNYGAVGIFVGNNPIDSFDESIVVSAIGECAIAVDGIVNAKERERTAVLAKNEQLRANLLRSISHDLRTPLTSISGNASNLISNGNAFDDATKMQIYEDIYSDSLWLINLVENLLAVTRLEEGRMNINLTTELVGDVIAEALKHIHKKSEMQKITVIQQDELLAKMDARLIVQVLINLLDNAIKYTPDSDQITITAKKDGNMISVSVSDNGNGIADEQKSRVFDMFYTGTNKIADSRRSIGLGLSLCKSIINAHGGEITITDNNPHGAVFTFTLPIGEVEIHE	11~~Usp(1.05376E-24)~~134;X;174~~DUF4118 (0.0000000019514 3)~~261;X(159);420~~HisKA (0.000000000573988)~~486;X;539~~HATPase_c (1.02288E-29)~~642	non-KdpD DUF4118 protein
	3E-06	36.9	10.8	5E-06	36.1	7.5	1.4	1	Q87G84_VIBPA	Histidine kinase (EC 2.7.13.3)	VPA1433	Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	348	223926	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio harveyi group, Vibrio parahaemolyticus, Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633)	>tr|Q87G84|Q87G84_VIBPA Histidine kinase OS=Vibrio parahaemolyticus serotype O3:K6 (strain RIMD 2210633) GN=VPA1433 PE=4 SV=1MMYFMFAHWRDNTFLFSAIVIVGAVVASWLLDQLFDSTAAVLLILQLAVVVVAFQCNSRFAYAAAVIEALSFNFFFTTPRYSLQMFRPEDIFNLVVFMVVAFITSTFADLYRRQQGELKQTKLQNSILLSVSHDLRTPLATIIGTLTTLNEYMPKLNDLERKELLDSATSESHRLHQYIENLLQATKLQHGTLKITKKDEPIANIVRDAVSRLPNYTEKVSMNMDDSVGYLSVSRSLIEQAIFNVLDNAMRFSPENESVEVSLSKQGLSCVIDVRDMGIGITAEDAEKIFSLFYSGANNKSADSGTGMGLAVAKGIITAHQGEIQSMPVSEGTLIRIRLPLNQGAEQA	14~~DUF4118 (0.0000000021204 9)~~114;X;130~~HisKA (0.0000000037351 5)~~187;X;238~~HATPase_c (4.67054E-24)~~339	non-KdpD DUF4118 protein
	3E-06	36.8	6.3	5.9E-06	35.8	4.4	1.5	1	D4M4P0_9FIRM	Histidine kinase (EC 2.7.13.3)	RTO_16100	Ruminococcus torques L2-14	899	657313	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, [Ruminococcus] torques, Ruminococcus torques L2-14	>tr|D4M4P0|D4M4P0_9FIRM Histidine kinase OS=Ruminococcus torques L2-14 GN=RTO_16100 PE=4 SV=1MSESRHNPDQLLKEIQADEEKRNKGHLKIFFGYAAGVGKTYAMLEAAHMEKQQGIDVVAGYVEPHAHPKTAALLNGLEVLPTREVFYNGMILDEFDIGMALKRKPQLILVDELAHTNAEGCRHAKRYQDIKELLNAGIDVYTTVNVQHIESLCDTVASITEIVVRERIPDSIFDNADQVELIDIEPQDLINRLNTGNVYRQTQEKQAVENFFTIENLTALREISLRRCADRVNILTENTRIKNHGDYHTGEHILVCLSSSPSNAKIIRTAAKMASAFKGEFTALFVETPDFSVMSEENVKRLRSNICLAEQLGAKIETVYGEDVPFQIAEFTRLSGVSKIVIGRSSATKRHLLSKPTLTEKLIDYAPNLDVHIIPDTVSNAAVYQLREGRKKNHIVFSVTDTLKSTAILILSSLVGMIFQKFGFDEANIITVFVLGVLVTAVITKHQIYSLISSIVSVLVFNFLFTEPQFTLQAYDQGYPVTFIIMLLAAFLTGSLAIRIKNQAKQAAQSAYRTKVLFDTNQLLQQAKDKNEIVSATSNQLIKLLRKDIVFYLADGEVLDTPHIFSVTEENLESCISENEKAVAGWVLKNNKRAGATTGTLSNAKCLYLAVRSSSMVYGVIGIVMGEIPLDPFENSILLSILGECALALENEKNAREKQEAAILAKNEQLRANLLRAISHDLRTPLTSISGNASNLLSNGDFFDNDTKKQLYMDIYDDSMWLINLVENLLAVTRIEEGRLNLRITEDLMDDVITEALHHINRKSEEHHISVESKEEFLLAKMDAKLIVQVIINIVDNAIKYTPKNSHIVIRTEKRGKQAIVSISDDGNGIADEIKPRIFDMFYSGANQIADSRRSLGLGLSLCKSIINAHGGELTVSDNLPHGTVFTFTLPAGEVKVYE	23~~KdpD (1.40208E118)~~232;X;252~~Usp(4.78401E-37)~~375;X;403~~DUF4118 (0.0000000000067861 3)~~503;X(165);668~~HisKA (0.000000000327017)~~734;X;787~~HATPase_c (6.92882E-28)~~890	KdpD protein
	3E-06	36.8	8.8	5.4E-06	36	6.1	1.4	1	R7FX73_9FIRM	Histidine kinase (EC 2.7.13.3)	BN797_00298	Eubacterium sp. CAG:841	651	1262894	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:841	>tr|R7FX73|R7FX73_9FIRM Histidine kinase OS=Eubacterium sp. CAG:841 GN=BN797_00298 PE=4 SV=1MGERFANNNEHILVCLSSAPSNTKIIQTAVAMARAFHASFSALYVKTPASEYMEAEDKNRLLANIHFAEKCGATIVTACGDDVPFQIAEYARLLGVTKIVIGRSVVGKRRFIGKPTLTEKLISLAPNVDIHIIPDSDAAIAKGKKTLFEKPHFAKLLKGLAISTFVLLLSSLLGCLFSRLGFTDANIITVYILGVLLIAIFTESKICWVISSVASVLVFNFLFTEPRFTFRAYGSGYPVTFIIMLAASLIIGGTTEKLKTRERQATQTSYRTKILFDANQLIQKASDEQEVFQVTADHLRKLLSRNVIIFNESAEKICASFTDTKDSPSKDYRQIVRWVINNNRKAGKGTGIYSDSSYVFLPICKNEKNYGAVGIFVGNNPIDSFDESIVVSVIGECAIAVDGIVNAKERERTAVLAKNEQLRANLLRSISHDLRTPLTSISGNASNLISNGNAFDDVTKMQIYEDIYSDSLWLINLVENLLAVTRLEEGRMNINLTTELVGDVIAEALKHIHKKSEMQKITVIQQDELLAKMDARLIVQVLINLLDNAIKYTPSDSQITITAKKDGNMVSISVSDNGNGIADEQKSRVFDMFYTGTNKIADSRRSIGLGLSLCKSIINAHGGEITITDNNPHGAVFTFTLPIGEVEIHE	11~~Usp(4.00499E-30)~~134;X;174~~DUF4118 (0.0000000027283 1)~~261;X(159);420~~HisKA (0.000000000625542)~~486;X;539~~HATPase_c (4.81685E-30)~~642	non-KdpD DUF4118 protein
	3E-06	36.8	4.6	5.5E-06	35.9	3.2	1.4	1	G2NR18_STREK	Histidine kinase (EC 2.7.13.3)	SACTE_5033	Streptomyces sp. (strain SirexAA-E / ActE)	847	862751	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. (strain SirexAA-E / ActE)	>tr|G2NR18|G2NR18_STREK Histidine kinase OS=Streptomyces sp. (strain SirexAA-E / ActE) GN=SACTE_5033 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVLLHGLEQIRRRDIEHRSAVFSEMDVDAVLERAPAVALVDELAHTNVPGSRNAKRWQDVEELLRAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVARRADQIELVDMSPQALRRRMAHGNVYQSDQVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRGEHDISTPWQARERIVVGLTGGPEGRTLIRRASRMAAKGSGSEIMAVYIARSDGLTSASPKELAGQRTLVEDLGGTFHHVIGDDIPSALLAFARGVNATQVVLGSSRRKAWQYVYGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPIARGARLGRTRILWGWAVGVGGPAVLALLLRGMENGPGLANDVLLFLFMTVAAALLGGLAPALASAAVGSLLLNYWFTPPTHTLTVQDPENFVAIVIFFAVAVAVASVVDLAARRTHQAARLRAESEILSALAGSVLRGETALDALLDRVRETFGMESVALLERQSEVEPWTRAGSVGPAPVARPDDADVDMPVGDHMALALSGRVLPAEDRRVLGAFAAQAAVVLDRQRLVDEAEAARRLAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSDEDEAEFLAGIEDGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVELDIPETLPMVAVDPGLLERAVANIVENAVKYSPDEARVTVAASALGARVELRVADRGRGVPDEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAESMGGTLGAEDTPGGGLTMVLTLKAVPGRVRDGPGAPEPAAR	1~~KdpD (7.2878E-121)~~211;X;233~~Usp(1.03601E-29)~~356;X;392~~DUF4118 (0.0000300039)~~458;X(154);612~~HisKA (2.48358E-14)~~678;X;727~~HATPase_c (6.27793E-28)~~828	KdpD protein

Disagreement between HMM and CDD prediction	3E-06	36.8	10.4	5.5E-06	35.9	7.2	1.4	1	B5GUP4_STRC2	Sensor protein (EC 2.7.13.3) (Turgor pressure sensor)	SCLAV_4779 SSCG_03029	Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	847	443255	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces clavuligerus, Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	>tr|B5GUP4|B5GUP4_STRC2 Sensor protein OS=Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602) GN=SCLAV_4779 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLHGLEQIHRRELEYRDAVFTEMDVDAVLERRPAVALVDELAHTNVPGSRNAKRWQDVEELLAAGIDVISTVNIQHFESLGDVVESITGVRQRETVPDEVVRRADQIELVDMTPQALRRRMAHGNIYKSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRGEHNIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGLTSASPKELNLQRTLVEDLGGTFHHVIGDDIPASLLEFARGVNGTQIVLGSSRRKAWQYIFGPGVGATVARDSGPDLDVHIVTHDEAGKGRGLPVARGARRLGRSRIIAGWLVGVAAPVLLSLLLTGLDDSLGLANDVLLFLFLTVLAALLGGLLPALASAAVGSLLLNFYFTPPVRTLTVVDPKNIVAIVIFFAVAVAVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLQRVRETFGMESVALLERRSDVDPWTTAGSVGPRSVVRPEDADVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLVGQAEEARTLAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSEEDEAELLEGIEAGADRLDHLVGNLLDMSRLQTGTVTPLIRVTDLDEVVPMALVSVPDESVELDIPESLPMVAVDRGLLERAVANIVENAVKYSPAGTPVSVSASALGDRVEVRVADRGPGVPDDEKERIFEPFQRYGDAPRGAGVGLGLAVARGFTEAMGGTLSAEDTPGGGMTMVLTLKAAPGVEPVSADLPARITS	1~~KdpD (2.15483E-123)~~211;X;233~~Usp(1.7517E-29)~~356;X(256);612~~HisKA (2.81428E-14)~~678;X;727~~HATPase_c (8.96409E-29)~~828	KdpD protein
	3E-06	36.8	5.3	5.9E-06	35.8	3.7	1.4	1	A0A0F0CR15_9BACT	GAF sensor-containing diguanylate cyclase	OMAG_002260	Candidatus Omnitrophus sp. SKK-01	489	1609969	cellular organisms, Bacteria, unclassified Bacteria, Omnitrophica, Candidatus Omnitrophus, Candidatus Omnitrophus sp. SKK-01	>tr|A0A0F0CR15|A0A0F0CR15_9BACT GAF sensor-containing diguanylate cyclase OS=Candidatus Omnitrophus sp. SKK-01 GN=OMAG_002260 PE=4 SV=1MREDFNFFLTDRTGRFMKKNNFIIFLEMLLAFFACNCVNYVFFSDDPGFLKSEFNPYWLIIFVITTSYGLLPGILSGLLASAHILLFTFGSIPTKTGIEQFLETGGGTLFLQFILASTLLGAFRQNNLNKEILLRENVNSLIRHNENLEKQCSALNKTRESLEKRIVDETSTFKILYNAAIKLEGHDAEKIYNGCLEILKEHFNVEKASIYFKENEYYVLKASLGWDKTNTIEGKVPVEESIMTIAFEKSSVINIDDILSTHNALKYSSQHGDILWIFPIKNNNNNTVGVVNIEQINFLSFTTPVREMISLVIEWVEKALNRKKINDIFFDSMINDIELDIYSFSYFKDTLGHEIKKAKRYGSCFTLALIMLNEYGCYTENQQKILIKSLSALIKKFSDNTDMIFKYTVDGFLVCLSPYQETERISEKINTINKALEEIFTADNNSFYGIKSNIITCDGNTPDVSTAIAALENTERAINALTPITSGAN	25~~DUF4118 (0.0000000918668)~~124;X;187~~GAF (0.0000005458)~~322;X;346~~Nucleotidyl_cyc_III (0.000122736)~~448	non-KdpD DUF4118 protein
	3E-06	36.6	6.2	5.3E-06	36	4.3	1.3	1	R5FAQ5_9CLOT	Uncharacterized protein	BN723_02738	Clostridium bolteae CAG:59	664	1263064	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	>tr|R5FAQ5|R5FAQ5_9CLOT Uncharacterized protein OS=Clostridium bolteae CAG:59 GN=BN723_02738 PE=4 SV=1MDGQRDERPDPELLLKQNFPRESDKARGRLKIFFGYAAGVGKTYAMLEAARQEKAAGRDVVAGYIEPHDRPDTMELLAGMELLTPMAVTYKGIILKEFDLDAALMRRPDLILVDELAHTNAQGCRHKKRYQDVIELLDAGINVYTTVNVQHLESLHDIVASITHVRVYERIPDDIFDDAGQVELVDIAPEELRQRLEDGKIYHKDQADKASVRFFTVENLSALREIALRRTADRVNREVVRERDAAGKDYYTGEHVLVCLSPSPTNARVIRTAARMAGAFHADFTAVLVETADMKREHAKISRSMEANINLAKQFRANVITLYGDDIVQQIAGYARRNGISKIVIGRTVRKRSFLHLKSTIIDRLIKAVPNMDVYVIPDAAARENGKIKKPENGRKYSMDILKTGLIMAGCTFLSMVLDHYKLGIINVAMIYMMGTMLAAYVTRAGTYGFLASVASVLLFNFFFTPPRYTFQADGSIYPFTFAAMLVCALITSSMAARLKREAEKSEAESGYMQILFGINRNLRKGTTREEILDICGRLVQSLLKRNIVIYDMLDGKMNRMKIYPASEREDASSLTSLFKNPDEMAVAAWVYKNHHKAGATTDTLPGARARYTPVYKDDTVYAVIGVEMKGGDIIKPNDKNVLNIIAEETSYRLKDMSGPRICR	25~~KdpD (1.4993E-117)~~235;X;255~~Usp(4.43648E-38)~~378;X;401~~DUF4118 (0.000000000009016 18)~~502;X;530~~GAF (0.000170915)~~651	KdpD protein
	3E-06	36.6	11	5.5E-06	35.9	7.6	1.3	1	W5WJG4_9PSEU	Histidine kinase (EC 2.7.13.3)	KALB_7344	Kutzneria albida DSM 43870	850	1449976	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Kutzneria, Kutzneria albida, Kutzneria albida DSM 43870	>tr|W5WJG4|W5WJG4_9PSEU Histidine kinase OS=Kutzneria albida DSM 43870 GN=KALB_7344 PE=4 SV=1MRPDRRRRGELRIYLGAAPGVGKTFAMLGEARRRAERGTDVVVGLVETHDRAKTAELLDGLEVLPRKHISHRGLDFQEMDLDAVLARAPEVVLVDELAHTNVPGSRNDKRWQDIEELLDAGIEVLSTVNVQHLESLNDVVERITGVTQRETVPDQVVRNAEQIELVDITPEALRRRLAHGNVYPARKIDAALGNYFRVGNLTALRELALLWVADQVDVALQRYRSEQQITETWETRERVVVSVTGGPESETLVRRARRIATRAGAELLVLHVLRGDGLAGVPADTVARYRRLAEDVGATFHTVVGDDVPTALLDFARGVNATQLVLGTSRRSRVARLFEEGIGATVVQESGPIDVHMVTHGEARRALRWRLSRSPLTPSRQVLGWLLALLVPSLATLLGVLLRGTVTVSTDLVDYFLATVVVALIGGVGPAVAAAVLSAGLLNFFFTPPLYSLTVAEGENIVTLVAMVVVAVMVALVVDRAARRAEQAARARTEAALLASYARTVLTSPYPLVRLLEKVRENFGLTSVALLEKRHGTWDRVACVGPRPCDEPDEADIDVPVTPEVHLALRGRALAAADQRALEAAAGQALALRQQRMAAQTADAQRRAETTELRTALLSAVGHDLRTPLTSIKAAASSLRDPELRLSTEDTGELLATVEESADRLAGLVDNLLDSSRLATGAVQPLLRPVGYYEVVAKALSGIDDRRSVQVDVDERLPQVLADVGLLERVVANVIDNALRHGRAGTRVNGDEPPVAVRASAHAAQVELRVVDHGRGLPKGAGEALFAPFQRLGDRDATSGVGLGLSVAKGFTEAMGGSISAEDTPGGGLTLVISLPVSTGAVPEEAQGS	7~~KdpD (8.24272E-121)~~216;X;238~~Usp(9.2784E-26)~~359;X;385~~DUF4118 (0.0000000020105 2)~~463;X(150);613~~HisKA (0.000000000001056 14)~~678;X;728~~HATPase_c (7.17314E-23)~~836	KdpD protein
	3E-06	36.6	11.3	6.7E-06	35.7	7.8	1.5	1	D2UFZ5_XANAP	Histidine kinase (EC 2.7.13.3)	KdpD XALc_2829	Xanthomonas albilineans (strain GPE PC73 / CFBP 7063)	892	380358	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas albilineans, Xanthomonas albilineans (strain GPE PC73 / CFBP 7063)	>tr|D2UFZ5|D2UFZ5_XANAP Histidine kinase OS=Xanthomonas albilineans (strain GPE PC73 / CFBP 7063) GN=KdpD PE=4 SV=1MSDLRTQQADALIGELKRERGGRLTVFLGAAPGVGKTYAMLSRARQLQQQGSVLVIGVVETHGRVETAALLEGLTVQPRRRVEYRGRTLDEMDLDALLALRPPLVLVDELAHRNAPGSRHERRWQDVEELLDAGIDVYSTVNIQHLESLNDVVHRITGVRVVSETVPDAMFDRLRDIVLVDLPPRELIERLQQGKVYLPEQAGQALQAFFSPSNLAALRELAMQTAADRVDNDLRDVQAAQGRPGLALRRRVMVAIDGRGQSDYLVRVARRVAERRGSPWTVVTVQTQAQPEEAWQLEIDRAFALARRLGGDAALLRGSSVADALLDHAARNGVSTLLLGRTRERPLARMINRTLTQQLLQRGAHYELVIISSPEARARSRRRWRSPGHWLSRDDLAFAMVASALAVVVAWIAERWVGIDDLSMVFIVAVVMVAAKTRMAAAVLAALLSFFGYNFFFIEPRFTFQIGTRQGVVTVLLFLVAALVAGRLASRLRSQVLALRAANAQTTALQRLGRELTSAADLGQVLDAGRHALSTTLDAEAWVRLQPLEAAHAGADDYAPSMAAVDRSAADWAQRHGQATGRFTDTLAGASWWFLPVRHERGAIGVVGLRFAAGVQRPGLEQQRLAEAMVEDIGQAALRTRLVADLESARVSGETEHLRSALLSSVSHDLRSPLAAMIGAASSLSSYGQAMSAEDRRSLLDTIQMEGERLDRYIQNLLDMTRLGHNGLTLNRDWIGVDELIGSAARRLQRYQPEVLLDIVLAADLPTLWVHPALVEQAVFNVLENAAKFSPPDTAIRVAAMMVEGRLRIDIADRGPGIPEDERARIFDMFYSVERGDRGRHGTGLGLTICQGMIGAHGGSVEALPGPDGRGTTIRITLPLIEPAAPPRRPDAD	19~~KdpD (2.7046E-120)~~229;X;250~~Usp(1.57413E-21)~~371;X;423~~DUF4118 (0.00532811)~~494;X;520~~GAF (0.000354159)~~635;X;655~~HisKA (0.000000000084437 1)~~721;X;775~~HATPase_c (2.42511E-23)~~877	KdpD protein

Disagreement between HMM and CDD prediction	4E-06	36.6	8.2	6E-06	35.8	5.7	1.4	1	C1A1E6_RHOE4	Histidine kinase (EC 2.7.13.3)	kdpD RER_37230	Rhodococcus erythropolis (strain PR4 / NBRC 100887)	846	234621	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus erythropolis (Arthrobacter picolinophilus), Rhodococcus erythropolis (strain PR4 / NBRC 100887)	>tr|C1A1E6|C1A1E6_RHOE4 Histidine kinase OS=Rhodococcus erythropolis (strain PR4 / NBRC 100887) GN=kdpD PE=4 SV=1MSSSEKVGQSFGRARKRGELRIYLGAAPGVGKTFAMLGEAHRRRDRGCDVVAAVVETHGRARTAAQIGDLEIIPPKLVDYRGTRMPELDVEAVLARRPALVLVDELAHTNTPGSKNHKRWQDVQELLEAGIDVLSTVNVQHLESLNDVVAHITGVVQQETVPDAIVRSAAQVELVDITPEALRRRLSHGNVYSPERVDAALGNYFRRGNLTALRELALLWVADQVDAALAKYRAENKITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVVRGDGLTGVSAPEMGKVRALAVGVGATLHTVVGDDVPSTLLEFAREENATQLVLGTSRRSRLARILDEGIGAAVVQQSGGIDVHMVTHEETTVRRRISLFGRSEYRLLSWIAAVVVPTAAAGLMGLIDRISGVQGENALFFVVVVLVALLGGVGPAMLSALLSGLLLNYFFTDPRYSFTIAEPDNFITTVVLLIVAVAVAVLVDAAAKKAREAKRASEEAELLTLFAGSVLRGADLSTLLEKAREIYRQRGVQASVVHHEDGVVAAVGAEPPAREADADSVCEVNDGEYALMLSGPELSARDRRVLTVVAHQAVGMIRQDKLTVEASKAAALTEADQLRRALLSAVSHDLRTPLAGVKAAVSSLRSDDIEFSPEDTAELLATIEESADQLTALVGNLLDSSRLAAGVVKPTLRAVYLDEVVHRALLGLGIGGRSDSRSHSVIVDVGTVAVQADQGLLERVIANLVDNALRYGGTTPVRVGAARVGDRTVITVADTGPGVPRGEAESMFEPFQRMGDRDNTGGVGLGLSVVRGFVDAMGGTVSATDTPGGGLTMMVELAGAGTNGSES	16~~KdpD (6.16064E118)~~225;X;247~~Usp(2.93088E-32)~~368;X(247);615~~HisKA (0.000000000000080864)~~681;X;736~~HATPase_c (3.97134E-27)~~836	KdpD protein
	4E-06	36.5	11.3	6.7E-06	35.7	7.8	1.4	1	E8RMG3_ASTEC	Histidine kinase (EC 2.7.13.3)	Astex_1107	Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	506	573065	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Asticcacaulis, Asticcacaulis excentricus, Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	>tr|E8RMG3|E8RMG3_ASTEC Histidine kinase OS=Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48) GN=Astex_1107 PE=4 SV=1MRLPPFLDHPPLPVPRGQRALWQEAVLSLVMVFAAACVSYVLMQSGFPSPEALSILFVLPVLAAAIFLDLRLALVTVALSVITYNLVLLPPFWTFDLTNPQALAKIVVLLIVTLVVSALTTRLRRITGESQARENVLRGLYQLNQDLVGKTTVAQVQAASEACLSALTTVPCQIWYKDVPVDDPLLSEAAQEGASAGAGQELAPHDPRLILPLIDGEKTLGVLVFTPQDRVPFPVELYPPSLLPTLAAQVANALSRAALAEAHEQQARQADRERFMSAMLSSLSHDFKTPLVGIVGALEALEGRVDSEARDIVADGLAEALRLNRYVVNLVEISRLEAGVRPRSEPLHIRDAISGVLRTLRPLIGRQKFRITVEAGFPLLNLNASLFDLVLLNLIENALKYGPAEGEITIDARVTSDSVEIDVDDEGAGIPPPLREPVFTKFYRAVEGDRKIAGTGLGLYICREIVASYGGRIEAIDPPDGTGACMRVWLPEAATLRLATFEEETE	26~~DUF4118 (0.0000356429)~~125;X;177~~GAF (0.0000502722)~~256;X;273~~HisKA (0.000000195647)~~335;X;390~~HATPase_c (6.7164E-27)~~490	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	4E-06	36.5	4.7	6.6E-06	35.7	3.2	1.3	1	E6SA85_INTC7	Histidine kinase (EC 2.7.13.3)	Intca_2832	Intrasporangium calvum (strain ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP)	383	710696	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Intrasporangiaceae, Intrasporangium, Intrasporangium calvum, Intrasporangium calvum (strain ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP)	>tr|E6SA85|E6SA85_INTC7 Histidine kinase OS=Intrasporangium calvum (strain ATCC 23552 / DSM 43043 / JCM 3097 / NBRC 12989 / 7 KIP) GN=Intca_2832 PE=4 SV=1MWQPDRVERWAGGVDVRTRGESGSATALPRRRQLMGFGLCLVGLPLLTVATLAAGLPDRGESILLVYLLAVVVIAVVGGLLPGVLAGVGGFLSANWFHTPPYKTLTVERPEALVDLVVFVLVAVIVSVVVEIGARDRARAEHNRLATAREAARAERLVETDRVRSALLTAVSHDLRTPIAAIKAASSGLRQEDVDWEPAQQSELLAAIEGGADRLADLVDDLLAMSRIQAGALSVQLTAIPVDEVIDRALAGWVDPVTVVVSDPVPVVLADSPLLERALANVLDNARRFTPDGHAPEIRAGRAGGSQRRRVEIRVVDHGPGAPPARWESMFAPFQRLDDRTPGGLGLGLAVARGLVAAMSGTIRPEATPGGGLTMCIDLPEAR	161~~HisKA (3.17477E-14)~~227;X;275~~HATPase_c (4.23431E-19)~~379	No DUF4118 detected by NCBI CDD
	4E-06	36.5	10.7	6.7E-06	35.7	7.4	1.3	1	V6KD61_STRRC	Histidine kinase (EC 2.7.13.3)	M878_19690	Streptomyces roseochromogenus subsp. oscitans DS 12.976	1000	1352936	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	>tr|V6KD61|V6KD61_STRRC Histidine kinase OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_19690 PE=4 SV=1MSDVRPGRLKVYLGAAPGVGKTYRMLDEGRRRAARGADVVVGFAECHGRPHTEAMLDGLDTVPRASCSYRGGQFQEMDLAAVLTRRPQVAIVDEIAHSNVPGEGRNPKRWQDIEALLDAGIEVITALNIQHLESLNDVVEKITGVPQHETVPDEVVRRAWQIELVDMPPEGLRRRMAHGNIYAPEKIDAALANYFRPGNLQALRQLALLWTADRVDEALQEYRSQHGIGRVWETRERVVVALTGGPEGDTLVRRAARIADRSAGGDLLAVHVARSDGLAAGVSHASLARQRRLVEDLGGSYHSVVGDDVATALVEFARAENATQLVLGTSRRGRLTRFLTGPGTGETVTELSGDIDVHRVTHERAGRGTLLPSRRRTLSTARLIAGPVAGLVLPVLLTALLAQLRGTLNLTSEALLFLLAVVGVACIGGVASAVIASVTASLLLNYWFIPPIGAFTLNDPNALVGLTVFAVVAAIVAAVVDRSLRLSRRSARATAEAETMSSLAGSIVRGEATIPALLERTRETFGMESADLVDEPPDAAGPDAGRLDPGRLDAGGLDAGGAQVFGSHVVRSHASGSHVGGADMGGSCVGGGDGAGSHVGGVDGAGPHVAGADTGGSYVVGVDGAGSHVGGADMGGSYVAGADAAGSHTVGSHEAGPHAAGSEAGGPRAAGFHSASSGAVFVSAGLHVAGADACGSPTVVPHVAGSHAAGATAVPAGPGAWLVLRGRTLSSSERRVLAAFAAHVGSAVERARLAEAAAEVEPVKAADRLRTALLRAVGHDLRTPLAAGWAAVTSLRSRDVAFSDEDRDELLATADESMAKLNRLVENLLDLSRLEAGALTLNLRATTLEEVLPLALADVPGVRVTDMEGIPAVLADPPLLERVIANLVGNAARHTPPGKQVLVTASVLAGRVELRVVDRGPGLPADGRDRLFEPFQRLGDTDNTTGLGLGLALARGLTEAMNGTLSPEDTPGGGLTMVVSLPFAGRRVGAEASEQSVGGP	5~~KdpD (9.0558E-101)~~215;X;237~~Usp(1.05563E-29)~~361;X;391~~DUF4118 (0.0000000143939)~~469;X(298);767~~HisKA (0.00000000177203)~~833;X;880~~HATPase_c (6.82399E-25)~~981	KdpD protein
	4E-06	36.5	9.9	8E-06	35.4	6.8	1.5	1	A0A0F0HJ10_9PSEU	Histidine kinase	UK12_27900	Saccharothrix sp. ST-888	853	1427391	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix sp. ST-888	>tr|A0A0F0HJ10|A0A0F0HJ10_9PSEU Histidine kinase OS=Saccharothrix sp. ST-888 GN=UK12_27900 PE=4 SV=1MSRDLTPGTLTRRGKLRVYLGSAPGVGKTYRMLDEARRQERGADVVVGYIECHGRRHTENMLAGLDIVPRLRTRTYRDTEFQEMDLEGVLARRPTVVLVDELAHTNIPGGRNAKRWQDIDELLDAGIDVITTVNIQHLESLNDVVQKITGIPQRETVPDEVVRRADQIELVDMAPQALRRRMAHGNVYKAEKVDAALSNYFRVGNLTALRELALLWVAGRVDEGLRDYRASHNIDRVWETRERVVVALTGGPEGETLIRRAARIADRTAGGELLAVHVTKSDGLAGASPGALAQQRQLVETLGGSYHVVVGDDIPTALLAFARGRDATQLVLGTSRRGRITRLLTGPGIGETTVDASEDIDVHMVTHEFTGRGRLPSLGRRHSRNRTIAGYVAGLVVPSLLTAVLSQFHTQVNLTTDALIFQLGVVAVALLGGAVSALLASLVASLLLNYFFIPPTHTFTIGETNNVIALLVFAMVALTVSTVVDHATRLTSRAARATAEAETLSTLAGSVLRGADAVPALLEKSRTAFAMATVALLDRSSGEVLARSDADAEGTSGEAVTEIAVGADAVMILTGRRLPAADQRVLTAFAAHVAAALERDRLASVAAEVEPIKAADRMRTALLAAVSHDLRTPLAAALASIGSLRSPDVEFSPEDEAELLTMADESLVKLTRLVDNLLDMSRLQAGALTLHLVPTHLEEVLPRALDSLSDPDAPVQPLGLDSAPPVLADPPLLERVLANVITNALRHNAPGAPVLVAASSLPQPPAGGTPLPNRVEIRVIDRGPGIAPEDRDRVFLPFQRLGDTDNTTGVGLGLALSRGLAEAMGGTLEVEDTPGGGTTMLLTLPAAGTGEPTP	12~~KdpD (1.84018E117)~~221;X;243~~Usp(7.95736E-30)~~366;X;391~~DUF4118 (0.000823939)~~489;X(127);616~~HisKA (0.000000000072113)~~682;X;733~~HATPase_c (7.9752E-26)~~843	KdpD protein

	4E-06	36.4	10.4	9.2E-06	35.2	7.2	1.6	1	A0A0E9MQ63_9SPHN	Uncharacterized protein	SCH01S_39_01720	Sphingomonas changbaiensis NBRC 104936	433	1219043	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas changbaiensis, Sphingomonas changbaiensis NBRC 104936	>tr|A0A0E9MQ63|A0A0E9MQ63_9SPHN Uncharacterized protein OS=Sphingomonas changbaiensis NBRC 104936 GN=SCH01S_39_01720 PE=4 SV=1MFDRNGHAKGAIVAPDSRTTPGYARSILAAVGRGSTSLTVVRRAAELAAAFRCSWEAVHVVTPDAFDKNSDFDAAEALTHAAELGATVARIPAASVADGLSSHLEDALVTDIVIGAHRRTGLSARVRPRLPTELIDRGITAAIHLIPSAAQPLPKRGKKPVKSPGSGGAYAKAAGLTVVTAAVAGALSPWLSTGALSLLFLFPVIGAAALFGTRPGLLSAALAVLLTNFLFVTPHFAFRLSAPQSWVLAVVLGLAAAHTGFVTSELRRRVGLSDRNARENASLASFALQLTRVSDWDGTAAIVCSEVSNLMGGLQTVVVRDVDGALKCVAAVPAEPVFSPVDTTALEWAWQQGEEAGSGTKLLADANWQFQPLRTSLGTLAVLGLAAEDGRDPVRADQKVLLATLLAQAALAHERLRLEDDMRASGAAVTSAG	27~~Usp(1.24953E-15)~~147;X;169~~DUF4118 (0.0000144961)~~269	non-KdpD DUF4118 protein
	4E-06	36.4	5.9	3.9E-06	36.4	4.1	1.9	1	C8W6P0_DESAS	Histidine kinase (EC 2.7.13.3)	Dtox_3426	Desulfotomaculum acetoxidans (strain ATCC 49208 / DSM 771 / VKM B-1644)	556	485916	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfotomaculum, Desulfotomaculum acetoxidans, Desulfotomaculum acetoxidans (strain ATCC 49208 / DSM 771 / VKM B-1644)	>tr|C8W6P0|C8W6P0_DESAS Histidine kinase OS=Desulfotomaculum acetoxidans (strain ATCC 49208 / DSM 771 / VKM B-1644) GN=Dtox_3426 PE=4 SV=1MGKDNRQAEINEYLISMHIYCNMLLLFGLIFSYKIHPFIGCYTTFNIFIFLLLGLSNIGIIVFYNKYCNDQENDNRFNWVNIPCIVLPTIISSIAIFTISNNVLFKETILFIPVLIAASIMGKNTGIFMAFICSLILVFHDLLTKDNIYIIKVIESNIIFISVLFIVGWFTGRITGIEAQHRKSLNKSLLSLQKEIHLRNIAEEEMRKLTRAVELSPSIMIITDLSGNIEYVNSKFKQITGFTSVEIFNKNIADPLVNHNMDYSRIWETVKSGNEWSGELFSKKKNGEIYIEYVSMIPFKDNEGVITHFLRASENITERKQMEKEIARLDKLNLVGEMAAGIGHEIRNPMTTVRGFLQLLASKEECVKYKEYYDLMIEELDRANSIITEYLSLAKNKPVSLRMVNLNSILATIFPLIQADVLKRNNDVKMEIKDVPDLILDENEIRQLILNLVRNSLEAMPLGGNLTIKTFQDKDFVVLEVQDEGSGIPLELLDKIGTPFFTTKDEGTGLGLAVCFSIAARHNASIEVNTDSSGTVFSVKFCCHPTPKLLLKEKNN	78~~DUF4118 (0.000000000431909)~~181;X;216~~PAS (0.0000607389)~~316;X;332~~HisKA (0.000000000015728 6)~~395;X;445~~HATPase_c (2.4005E-21)~~541	non-KdpD DUF4118 protein
	4E-06	36.3	13.1	7E-06	35.6	9.1	1.4	1	K0F3U7_9NOCA	Histidine kinase (EC 2.7.13.3)	O3I_031400	Nocardia brasiliensis ATCC 700358	848	1133849	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia brasiliensis, Nocardia brasiliensis ATCC 700358	>tr|K0F3U7|K0F3U7_9NOCA Histidine kinase OS=Nocardia brasiliensis ATCC 700358 GN=O3I_031400 PE=4 SV=1MKRGQLRIYLGAAPGVGKTYAMLGEAHRRLERGRDVVAAVVETHGRAKTAALLEGIERIPARTVRYRGAELPELDVEAVLRRRPTVALVDELAHTNAPGSKHEKRWQDVEELLDAGIDVISTVNVQHLESLNDVVEQITGIQQKETVPDAVVRGADQVELVDLTPEALRRRLSHGNVYAADKVDAALRNYFRPGNLTALRELALLWLADQVDAALAKYRADHKITELWEARERVVVAVTGGPESETVVRRASRIASKASAELVLVHVVRGDGLAGVSTARLARLRELAASLDASLHTVTGDDVPTALLEFAREVNATQLVLGTSRRSRWARMLDEGIGSTVVQQSGKIDVHMVTHEEAHRGLRRSSFMPRQPIRAWLAAVLVPMAVCGIGIVFLDGYLQLGGLSAVFFIGVVAVALLGGVVPAAFSALLSGLLLNWFFADPRYSLTISEPDNFVTVVVLLFVAVAVAALVDVAAKQTLQARRASQEAELLTMFAGAVLHGADLPNLLEQVRETYGQRAVSMLCGEQVVAEVGADPPQRATDADTTIQAGDATSLLLLAGRPLAAGDRPVLNAVANQAAGLVRQSRLAEEASAAAALLEADRLRRALLSAVSHDLRTPLAGAKAAVSSLRSDDIEFSAEDTSELLETIEESVDQLTALVGNLLDSSRLAVGVVKPQLRQVYMDEVVHRALVSVGMGARGLRRAAMDRVKVEVGDVSVRADSGLLERVVANLIDNALRHATRDMAFTQPAGSGDYHPPPVRVTAEREGDRVSIAVVDTGPGVPPGAEEQLFEPFQRLGDRDNTTGVGLGLSVVRGFVEAMGGTVHAEPTPGGGLTMIVDLPAAANGASSS	1~~KdpD (2.28119E-124)~~211;X;233~~Usp(1.58734E-34)~~354;X;375~~DUF4118 (0.0000000340636)~~453;X(147);600~~HisKA (0.000000000001500 51)~~666;X;723~~HATPase_c (4.35012E-28)~~838	KdpD protein
	4E-06	36.3	11.5	4.2E-06	36.3	8	2.2	2	A5HYM7_CLOBH	Putative signaling protein	CBO0333	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	567	441771	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum A, Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	>tr|A5HYM7|A5HYM7_CLOBH Putative signaling protein OS=Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A) GN=CBO0333 PE=4 SV=1MNDVGNNKRNQINNIVSVVKLCSLLFSAIAIFKCFFSGNNKALDYKNNMSAIHIISTTILIFSLIYCIWVFLTTNKFRGRYNKRIYFIENIVLILLFFVVVLGTGTYASQYKFLFLFMIIITTIQSGMKYGIIIACLASFIILIMDIVCAPNLVVNEYFEQDLILAGVFILTAWPLGFYVKVENEHIEKLESLVNKDGLTDVYNHRFFHDALSKEVIECEEKNEALSMIFIDIDYFKHYNDLYGHQKGDQVLKTIGEILKNNTRKEDIVARYGGEEFAVLLPNTSEQDAINIAEKIRKKIEYTYFEGEENQPNGNLTVSMGISVYPYKAKSDMELIKSADDALYRAKFFNKNRVEAYTSILDELKNDIDEEHIDLVTSIKTLISVINAKDRYTYGHVERVVLYSRLLADKLKLSEEDKKNFIYGAYMHDIGKINISREILNKKMPLAKEEWEILKQHPVNGVEIIKPVSSLQNISDLILHHHERYDGKGYPDKLKGDNIPFLARALTVVDSFDAMTSNRPYNRRKTYEEAIEELKRCSGTQFDSYIAEKFIEVIIENKDSFDDLSLL	87~~DUF4118 (2.45047E-15)~~186;X;195~~Nucleotidyl_cyc_III (1.53706E-61)~~354;X;391~~HDc (3.44218E-24)~~534	non-KdpD DUF4118 protein
	4E-06	36.3	8.4	7.5E-06	35.5	5.8	1.4	1	R5C281_9FIRM	Histidine kinase (EC 2.7.13.3)	BN499_02256	Blautia hydrogenotrophica CAG:147	895	1263061	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	>tr|R5C281|R5C281_9FIRM Histidine kinase OS=Blautia hydrogenotrophica CAG:147 GN=BN499_02256 PE=4 SV=1MERCPDTDVSVSDMKPQQTRSRGSLKIFFGYASGVGKTYSMLRAAHEAKSRGIDVVAGFVDTHGRAQTTQLLHGLESLRTRKMDFESGLKREFDLDAALRRSPRLILVDELAHTNVPGCRHTNRYQDVEELLRAGIDVYSTVNVENIESLNDMVAAITGEAAKDRILDSVFDEAAQVELVDVEPEELIERLQAGEIYQDEKEKEEAAELFTLDKLTALREIALRRCADRINKMTELVQAKSRRGYFTDEHILVCLSSAPSNAKIIRTAARMAKAFHGEFTALFVETSDFSVMEEEDKERIRVHMRLAQQMGAKIETVFGEDVAFQISEFARLFGVSKIVVGRAGAKRNRLFGKPTLTEKLISYASGIDIYIIPDKYAAVYRARRAKRESEAFSLADMSKGAAALVAATLAGMVIEKLGFSEANIITVYILSVLATSVIVSKRMYSLIFSAINVVVFNFFFVTPKYSLTAYDSGYPITFLVMFLAAFITSSLAVRLKNHVKQSAQTAFRTQILFDTNQLLQQEKEKEGIVNITANQLIKLLSRDIVYYPVEKEQLREPKVFLTLNGKTDEKCVTQGKEREVAAWVLKNNKHAGATTDTLSEAKCLYLAVRVNHVVYGIIGILLGEKPLDAFENSIVLSILGECALALENERTARERREEAAVLAKNEQLRADLLRAISHDLRTPLTSISGNASNLLFNSEDFDKETKKGLYKDIYEDSLWLINLVENLLSVSRIEEGRMNLRLSAELMDEVISEALQHVNRRSIEHVIVVENSDDILLARIDARLIVQVVINIVDNAIKYTPRGSHITISTVQTGQIITVKISDDGPGMDDEVKSHVFDMFYTGSNKVADSRRSLGLGLSLCRSIIHAHGGEITVKDNQPQGTVFSFTLPAGEVQLHE	22~~KdpD (5.64643E97)~~230;X;250~~Usp(4.53375E-32)~~373;X;411~~DUF4118 (0.000142)~~498;X(166);664~~HisKA (0.000000000367847)~~730;X;783~~HATPase_c (3.18567E-28)~~886	KdpD protein
	4E-06	36.3	4.2	6.7E-06	35.6	2.9	1.3	1	Q39SU5_GEOMG	Histidine kinase (EC 2.7.13.3)	Gmet_2454	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	367	269799	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter metallireducens, Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	>tr|Q39SU5|Q39SU5_GEOMG Histidine kinase OS=Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210) GN=Gmet_2454 PE=4 SV=1MTLTGPLRILFLAAAIIGISLFHYLTPLHLPALHDIFQRLYYLPIILAALWFGLRGGLAASIIVSILYVPHVLFQWGVHPSLELEKFLEILLYNVVGGVTGFLCQKEGERREELERAARRLEESYRALRSQADLIIGIEEQLRRAERLSALGELSALMAHEIRNPLGSIRGTAEILRDDFQPGHPKHEFLEILLKETDRLNRVVEDFLRLSRPGDGERKTCDLAAELRELVTLLGSDAAARGVRIGLEADEVPPVTGDPEKLRQAFLNLMLNGIQATGAGGTVTVRVKMFPRSGDDRPLVELAFADTGAGIPRESLERIFTPFFTTKEGGTGLGLAITQRIVEGHGGTVTVESEPGQGTTFRVRLPL	9~~DUF4118 (0.000000744696)~~103;X;148~~HisKA (2.78883E-16)~~212;X;262~~HATPase_c (9.361E-29)~~365	non-KdpD DUF4118 protein

	4E-06	36.3	8.1	7.2E-06	35.6	5.6	1.3	1	F8DYL4_CORRG	Histidine kinase (EC 2.7.13.3)	kdpD CRES_1323	Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	972	662755	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium resistens, Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026)	>tr|F8DYL4|F8DYL4_CORRG Histidine kinase OS=Corynebacterium resistens (strain DSM 45100 / JCM 12819 / GTC 2026) GN=kdpD PE=4 SV=1MATMTKRGTLKVYLGFAPGVGKTCAMLSEAHDLVDRGYDVLVGIVEDHGRARTKKLTEGLPILPRKSVAHRGGSYDELDLEAALEAHPQIILVDELAHTVVGTQETDGDRPVEGAKRWHDVYALLDAGIDVISTMNIQHLESLNDVVSAVTGTRQRETVPDQVLRDADEIELVDLSPDALRIRLARGEVYRQQQAETALNSYFRVGNLTALRELSLLWLADKVDEVLEKYREDEKIQENWPARERVVVAVQGDEVSEALIRRGARITERVAGREMLVVYVFSADAALEGDLPQRLQRLQELTESLDGQWRVLEGDDVANTLLEFARTVNASQLVIGLGTRMSRLFSSTAHKIIDGSGRIDVHIVSTTNASLSAKGSKDSEQGGAGSGSRVQRSGFSNIPALLRRAVAYALGGSRRRASALDTSKQLSPGRKLAGWALALLGPIALTMLMMPLDHEEGALGSILLGYLTIAVFSALAGGFGPAIVAVLFGSILANWFFTHPYRTLTVTEPTNLVQILLFFVISVAMAAVVDIAERRRAVSNRRLGQAVVLSDLARGALDEGDDDIRSLLERLRETFNLRRVDLQQYSKERKKWVTMETTDPGGIGVPWPGKKAPAHVGAGDGMRFVLGGRDLSPAESAMIEAHGARITAIIDREQIDAMRRATAALEAGNRVGTALLTAVSHDLRTPLAGIKAAISGLTMDDVELDDDSRALLMETIESSTDRLETVIGNLLDMGRVNSNTVTVRNMPVQYADVIDAVCAELPEAAQHIDNLVEETTQPVIGDAGLVQRIVANIVINARIYAPHSRIEIRAQVMPDSKAIQLRVIDHGPGFPPEKFNDVFVPFQRLGDHSANTNGLGLGLAVARGFAEAMGGTLEAENTPGGGATLVLTLPAADTEPMAAHSAPHALGSAESRPADSAPEPHPDTSAPAPHPQGTSAPEPHPQGTSAPEPHPDTSTHNPQDTHANTPPAHEETR	6~~KdpD (3.00783E-101)~~223;X;245~~Usp(7.37738E-22)~~365;X;435~~DUF4118 (0.000000000006510175)~~535;X(137);672~~HisKA (0.000000000311886)~~734;X;786~~HATPase_c (1.52912E-24)~~888	KdpD protein
	4E-06	36.3	7	6.8E-06	35.6	4.8	1.3	1	R5B3J9_9CLOT	Histidine kinase (EC 2.7.13.3)	BN545_01302	Clostridium sp. CAG:226	378	1262781	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:226	>tr|R5B3J9|R5B3J9_9CLOT Histidine kinase OS=Clostridium sp. CAG:226 GN=BN545_01302 PE=4 SV=1MVKGIHMDSSAKKKNAKLTWRDVGITIGTLAATTLLCYALRPFAGEEKFEAILFVVAVLIISRFTNGYVYGVAASILGVLIVNCIFTYPYYQLNFTLTGYPIAILSMLSAAMITGTLTTRIKEQEQLKIDAERERTRSNLLRAVSHDLRTPLTAISGACSVLKEGGDTLSEQEKNKLLNQIEEDSQWLIRLVENLLIVTRIDAPDGGANIAKESEVVEEVAASALTQFRKHFPNVKVETHMPDELLLVPMDGMLIRQVIMNLFENAAIHADGMTKITLDISREGENAVFRVTDDGRGIDPNLLPHILEGDFKRSVGSSEDKKRNMGIGLSVCSTIISAHEGKMRAYNGQNGGAVFEFTLPLDMAEMELYDCDDRQEDE	26~~DUF4118 (0.000000000053905 7)~~124;X;134~~HisKA (0.000000000000269132)~~200;X;255~~HATPase_c (2.58268E-23)~~359	non-KdpD DUF4118 protein
	4E-06	36.3	11.9	6.5E-06	35.7	8.3	1.3	1	R5C094_9FIRM	Histidine kinase (EC 2.7.13.3)	BN499_00277	Blautia hydrogenotrophica CAG:147	512	1263061	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	>tr|R5C094|R5C094_9FIRM Histidine kinase OS=Blautia hydrogenotrophica CAG:147 GN=BN499_00277 PE=4 SV=1MSDKRTVVLKMIQVLKSVAVMIGCLAGATLIGMVFHWMKFPDTNVVIIYIFSVLLTARFVPGYGYGVAVSVAATLTFNYFFTAPYFTLNVYDLSYLVTFVIMTVTAIMTSALTSRARKSERQAWEKEKIANALYGLTHRLTNAADLDEIVSAVIEQVSKVLGCDAACLCFNQEGCPMETYQQQRGSERMIQKTGEEDFARYSEGNVFGKNTVCVGEKFCDWPIYGKDRILGVLRLPKDTAVGTMRGYLPLMQAMLENTALAMERVWNVQESNRSKAEMTQERYRGNLLRAISHDLRTPLAGIMGSSELLMDMLKEDKEGRELASGVYKDADWLLSLVENILNLTRLQDGRLILNKQPEAVEEILGSAIAHVTKRYPGREITVDIPEELLMVPMDGRLMEQVLVNLMDNAVKHTSEEKEIRVVVKTQEEQGEVLFQVLDEGSGIAPADLPHIFQLFYTTSTKSADAKRGVGLGLAICESIVKMHGGTITAGNRKDCKGAEFSIRLPMEVSHEK	15~~DUF4118 (0.000000000000598368)~~118;X;145~~GAF (0.0000391539)~~264;X;281~~HisKA (1.24368E-14)~~345;X;398~~HATPase_c (1.72825E-26)~~504	non-KdpD DUF4118 protein
	4E-06	36.2	10.3	6.9E-06	35.6	7.2	1.3	1	I0JQM7_HALH3	Uncharacterized protein	HBHAL_4105	Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	411	866895	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Halobacillus, Halobacillus halophilus (Sporosarcina halophila), Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) (Sporosarcina halophila)	>tr|I0JQM7|I0JQM7_HALH3 Uncharacterized protein OS=Halobacillus halophilus (strain ATCC 35676 / DSM 2266 / JCM 20832 / NBRC 102448/ NCIMB 2269) GN=HBHAL_4105 PE=4 SV=1MIYTQTSTWRKFIELFVIMLIAALLDQYLEMNMTQWTLSPFIMIVLFFSLRYGLTLGLSAFLLTVSYLIVSVELNNGDLFLLFYESDTYLVMLFTLLIAVISGTYSTSFKERYESLTYSYGEIMDERNELKKTIELMKESQRVMQEKVLDSEYTLSRIYQVGIALDQPTPDLIRNEATTIISNLFKAEEVGIYHLDSSRKALRLHVRNGESKRLPQTLFIDEHSFFYKRIFQNKTVTIRTVDDDENTPLVAGPIVSNNEVEEVLIIDQLDFSRLTKYEIQIMSLVLDWMSNRMERAKEAKREEDKENMYPGTRVVYYADVFEDLVDVQRMRKEHYHVPFSVVSVDLSSHKNLSVIETEIILRAYLRELDVIGFNQETHTFYFLLPGTEEAKAWMVEKRIKQALRTKGVMPVG	11~~DUF4118 (0.000000000084771)~~112;X;169~~GAF (0.000000000018589 6)~~295	non-KdpD DUF4118 protein
	4E-06	36.2	12.9	7.6E-06	35.5	9	1.3	1	C9A6Y8_ENTCA	Sensor histidine kinase	ECBG_00518	Enterococcus casseliflavus EC20	866	565655	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus casseliflavus (Enterococcus flavescens), Enterococcus casseliflavus EC20	>tr|C9A6Y8|C9A6Y8_ENTCA Sensor histidine kinase OS=Enterococcus casseliflavus EC20 GN=ECBG_00518 PE=4 SV=1MSENNQQTIPEEMLLQAGFGPKRGKLRVFFGFAAGVGKTYTMLTEAHECLLMGKNVVIGYIEPHKRPDTNRLLEGLPQVPLKQYQHKQLTLYEPDIDRLIQLKPDIVLIDELAHTNPIGARNKKRYQDVDELLNAGITVYTTINVQHIESLNDIVEKVTEVEVRETVPDTFFQHASLRVVDVEPDELIDRLEQGKIYADENAKRALKNFFTPEKLDHLRGLAIQKASNHINQMNGGRKRVQSKLLTIIDDRLPKMAEKCIRWTARLAQGVGAEWTVIQVRSLDDTPTEVPLAERLGAEVINIEADDSFETIVEYAKMTGASDIIMGKQVSQKWFQKLFVEDLEDRLIRRLDDIEIHLIPFKEKMQRPRLTFSQLFEGGGRDFTLTFGLIMLATLVTEGMQYLHFGEQNLMLVYIFFVLLVARYTSGYLWSAMASIISVLSYNWFFVEPLYSLTVVYKAGYPITLVIMLIVALMISNLMVRLKTQAENAKEKEHQMEILYELNKQYMETRNEQEIYESTTTYLARLLQREVALYDREGHLRSLHSSRETLSQLTGKDEKAVAFWVVKNQKEAGRGTDTLIGANGFYLPIVLNGKPLGALGVERNEEHQLANSQLNYLRLVITQIATVLEQVSLASEKEQIQLENEREKVRSNLLRAVSHDLRTPLTTISGIAETLSETEGVIKKETKQKLLGDIQSESQWLIRMVENLLSVTRINLTNMAVKRSEEPIEEIIEAVLTHLKKVYPQQKIIVKMPDQLIFVQVDPILIEQALFNLIENGVRHGTADTPIFLRVSQEQEVVIEIENQGEIPLGQYQKIQANLTNDTEVPVDSKNGLGIGLSIVKTIIHAHEGKLAIETKSGSTIFRIYLKQ	21~~KdpD (7.75715E-108)~~230;X;243~~Usp(3.56898E-26)~~359;X;385~~DUF4118 (4.26578E-15)~~483;X;509~~GAF (0.00000000350628)~~627;X;645~~HisKA (0.000000000243371)~~711;X;764~~HATPase_c (0.000000000000756934)~~864	KdpD protein
	4E-06	36.2	13	7.7E-06	35.5	9	1.4	1	R6ERZ3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN497_00928	Firmicutes bacterium CAG:145	377	1263005	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:145	>tr|R6ERZ3|R6ERZ3_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:145 GN=BN497_00928 PE=4 SV=1MKIWKKSGSTPYEYSFNKDELKKIHQRDCMTFFLVLMGITFIALIFQGIVANPDVNITMFYILGIVLVARYTYGYVWGFLFSLLSVISINYFFTFPYHKLNLTLEGYPITFAAMFIIYIMTSAMTTNMKEQAKILAAQEKELMEVQKEKMRANLLRAISHDLRTPLTGIIGNSSSYLKMENELSDRDKHEIVENIKSDAGWLLNMVENLLSVTRINNETAKVNKSMESVDEVISSAVDRFKKRFPDAQLRVFPSDDVIMIMMDPLLIEQVISNILQNAQVHANSTKPLELSVSEENDKVWFRIRDYGVGIDEDKIETIFDGVGYREDRQTTADGYKGMGIGLSICKTIVTAHGGKINARNHGSGSEFYFYLPKGTEE	33~~DUF4118 (0.000000000007756 41)~~131;X;148~~HisKA (0.000000000006562 15)~~214;X;267~~HATPase_c (1.02051E-25)~~371	non-KdpD DUF4118 protein

	5E-06	36.2	11.1	4.6E-06	36.2	7.7	1.7	1	F7QKF0_9BRAD	Histidine kinase (EC 2.7.13.3)	kdpD CSIRO_2045	Bradyrhizobiaceae bacterium SG-6C	896	709797	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, unclassified Bradyrhizobiaceae, Bradyrhizobiaceae bacterium SG-6C	>tr|F7QKF0|F7QKF0_9BRAD Histidine kinase OS=Bradyrhizobiaceae bacterium SG-6C GN=kdpD PE=4 SV=1MPHEETKRASPDALLARAGREGRGRLKIFLGAAPGVGKTYAMLTAARSEKAGGKDVAAGLIETHGRRETEQLVEDFEVLPRKPIVYRNQVMREFDLDAALARRPEILLVDEYAHTNVPGSRHPKRWQDIDELLRAGINVWTTLNIQHLESLNDVVQKISKVRVRETVPDKVFDNADEVILVDFPPDELLRRLAEGKVYVQDTAARAVDNFFKPQNLTALRELALRRAAERVDAALVESMQAQAIEGPWAAGERILACVGPDQISPSVVRAAKRLADLMDAPWMAVTVERPGAYADSATRRRLDDIMKLAESLGAETQTLTGTDLPAELLRFAKFENVTQIVVGRAPGGFFSELLRRSLPHELVRRTRDIAIHLVTREADGTVKPVPSSRRWISETFNWQHFIYAALTVGGAVGAGEILTRLTPIPNLSIVFLLAVLFIAMNFGIWPAVFASLLSFLAYNFFFISPVHTLTVAEPYELLALLIFLVVAIASAAMAARVREQARVSADRVRATRRLYEFTRRLSGLASPEDVAEGAASEIHISLRRPVVVLLARNDDIVLTAAWPPEDDLDAAAMTAARWAYNHGEAAGTNTGTLPIIPWLFTPLKIGDKVLGTIGVATAKDTPSLDSEERALLDTLCEQAAAALERASLAGEMVDAKTATEAERVRNTLLASISHDFRTPLSSILGAATSLLDYDDKLDAASKNDLLGQIKEEAEGLDEMVRNLLAMTRIDAGALELRSDWIDLREVAARVVNAARRRGALQTFAIELPAELPLVRADAILIEQAIGNIVTNAVLHTPHQARIVIDAETGASEVRLRFTDDGPGIAPDILPRIFGRFVKGEALKSASADGGQGTGLGLAIAKGIMEAHHGTIVAESPVAHGHGTRFTMVFPQKELAA	21~~KdpD (6.06062E119)~~231;X;253~~Usp(1.59614E-35)~~375;X;400~~DUF4118 (0.000000000001452 39)~~486;X;526~~GAF (0.0000000025086)~~645;X;662~~HisKA (0.000000000046141 3)~~728;X;781~~HATPase_c (4.43182E-27)~~889	KdpD protein
	5E-06	36.2	12.7	8.1E-06	35.4	8.8	1.4	1	F8L2N8_PARAV	Histidine kinase (EC 2.7.13.3)	kdpD PUV_26190	Parachlamydia acanthamoebae (strain UV7)	876	765952	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydiia, Chlamydiales, Parachlamydiaceae, Parachlamydia, Parachlamydia acanthamoebae, Parachlamydia acanthamoebae (strain UV7)	>tr|F8L2N8|F8L2N8_PARAV Histidine kinase OS=Parachlamydia acanthamoebae (strain UV7) GN=kdpD PE=4 SV=1MSEQERPAPEDFLRMTEIQESEEKGQLKIFLGMAAGVGKTYAMLEEAQALQKEGVNVVIGIVDTHGRSETSALVSGLKKIPEKVITYRDREFQELDLDAIILLKPDVVLVDELAHTNIPGKRHNKRWQDVLEILDHGIDVYTTLNVQHIESLKDVVHGITGVVVQETVPDLIIEKAASIQLVDLTTDELLQRLKEGKVYLPEQSKIATQNFFKKDKLTALREIVLRYAADKVDRDLRQMEPTGERSTLWRAREKFLVAVSQSPYSQKLIRRACRMAVNFDAPWIALYVNNERILNEQDSQQLTKNLQLARNLGAEVVTIKNPTIAEGIQSIVRQKGVTQILLGRSLEKTVFGTSTYFSLPDLLAAECPEVDIHILRQDKDASYTKKMLFLPFSHIPFINYIYVFLFAGLFTLANFFLAPFVGYETIGVIYLLGILLLSLFFTKGPIIFAAFLFALCWDFFFIPPIWGFEVSKKEDIALLVLYIMTAASTGILVDRARGHKEMFQKSEETTRLLYDVVKKIASGPSTQEIFKSVKEELDRFFKGKFEIIVKQLGNGLKFDDSNSLLTNDMEKNTAIWAFENGKEAGWSTDTLPSANNLYIPLKGFHEIVGILVFKPDTAKNLSPEEKNFIYTIGGQLTGHIERKFSEEETKQNEQLKLMERVHKTILDRISHEFSDPIVSIQTSVQILKDQNKDSLEVQKIDNAAETLSKILTNVLAMAQLSEGLVPLNLSLQDVKELIHECCFNVKRAQNGHRLNIHIDEKIPLIPIDFYLIEILLYNLLFNAFEYSPSDSTIEVEAKKLDKYVVISVADEGKGIPEDQLETIFEKFFRLPEETGPGMGLGLAIAKTIAEVHKGKLKVENLPVKGAKFSLYLPIKI	22~~KdpD (1.92465E111)~~232;X;254~~Usp(1.31238E-26)~~375;X;399~~DUF4118 (0.00000000120007)~~497;X;525~~GAF (0.00000963079)~~642;X(130);772~~HATPase_c (5.78851E-26)~~872	KdpD protein
	5E-06	36.1	3.7	7.6E-06	35.5	2.5	1.3	1	G2LD97_CHLTF	Histidine kinase (EC 2.7.13.3)	Cabther_A1203	Chloracidobacterium thermophilum (strain B)	463	981222	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, unclassified Acidobacteria, Acidobacteria subdivision 4, Chloracidobacterium, Chloracidobacterium thermophilum, Chloracidobacterium thermophilum (strain B)	>tr|G2LD97|G2LD97_CHLTF Histidine kinase OS=Chloracidobacterium thermophilum (strain B) GN=Cabther_A1203 PE=4 SV=1MSVCALTAAGFYLKVHSTTAALLYLIVIVLVALRTGAAPSAVTALLAYIGLDSFFTAPLFRPAMNQPLDVVAPIVFLTTAFTINRLAAKNRQSFQEIQSLQDQLRLVMDTIPGLVWSESPNGSVEFLNQRWRDFLGASSAPVTDLRRNLPVHPAEADALAEQWQQARERGRAFETEVRVRRADGVYRRLRLHVVPAGEPGQVVKWYGLGTDIEDWRQAEETLARVESELALVARRTLLGELAASIAHEINQPLAAIVTNGNACLRWLGATPPNLPEARTTVTAIIRDGNRAAEIIARIRAMLSRTELKKATFDLGAALVEVLSLIRNDLVRKGITIHTRLASDLPAVFGDRVQCQQVVLNLLVNAVEALLPVTERWREIWLSAEPYGDGQVLVTVEDNGVGLGEAHEADIFDAFYTTKPDGMGLGLAISRSIIENHGGRLWCVAGDGFGAKFQFTLLTEGHAG	20~~DUF4118 (0.0000000629139)~~92;X;111~~PAS (0.0000000667898)~~212;X;237~~HisKA (0.0000084226)~~304;X;355~~HATPase_c (7.24358E-23)~~456	non-KdpD DUF4118 protein
	5E-06	36	11.6	9.9E-06	35.1	8	1.5	1	H2J5Y3_MARPK	Uncharacterized protein	Marpi_1821	Marinitoga piezophila (strain DSM 14283 / JCM 11233 / KA3)	404	443254	cellular organisms, Bacteria, Thermotogae, Thermotogae, Petrotogales, Petrotogaceae, Marinitoga, Marinitoga piezophila, Marinitoga piezophila (strain DSM 14283 / JCM 11233 / KA3)	>tr|H2J5Y3|H2J5Y3_MARPK Uncharacterized protein OS=Marinitoga piezophila (strain DSM 14283 / JCM 11233 / KA3) GN=Marpi_1821 PE=4 SV=1MAKKKGYYGYIELFIIYTLILIVDIYGKYFGYAFIDPNPYFIFSLFIAIRYGINLALVSGFLSTAYLFFSLYIQAKENFTGLIVSWQILKIPLFTFSLSFIIGFFRDMYIQEIENRDERIKVLNEKVKDLENEIRKYKNVTVDLEKKLVLERKGVSLLVERLKEIDYESAEDIFNESIDLIFDFIEATTVSIYTLSKNNFLRMRVRKGPQYLPNSFDIEKSVVISMAKEFGAANVNVLYLTEMEYNFEFEPAMAVSISAGKNILGFVIIELIDPEKVNKNTETYLKILSDWLSTLLMASKELAESDEEMFIKPYEEFEITLKYIEERRKRFEIPYSIIYFTVTQNVEIEKYRKIIRDTDFVFYDPEDKKGAIILTSCGKTGLKRVLENIEKIKSIKVLEAYSKE	10~~DUF4118 (0.000000000035741 2)~~112;X;171~~GAF (0.00000219331)~~296	non-KdpD DUF4118 protein
	5E-06	36	2.8	8E-06	35.4	1.9	1.3	1	Q74DJ7_GEOSL	Histidine kinase (EC 2.7.13.3)	GSU1319	Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	367	243231	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter sulfurreducens, Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA)	>tr|Q74DJ7|Q74DJ7_GEOSL Histidine kinase OS=Geobacter sulfurreducens (strain ATCC 51573 / DSM 12127 / PCA) GN=GSU1319 PE=4 SV=1MRLPGSARISLLAVFIIGISLFHYLTPLHLPALHDLFQRLYYLPIILAAFWFGLRGGLGTAVVVSILYVPHVLFQWGARPSLELEKFLEILLYNVVGGITGYLSQKEEERRNELERAARRLEDSYRTLRGQADLIIGIEEQLRRAERLSALGEMSAMLAHEIRNPLGSIRGTAEILRDDFSPGDRKFEFLEILIKETDRLNRVVEDFLRLARPLDGEKKRCDLAAELRELVTLQESEATARGIGLSLEAGEAPTVAGDRERLRQAFLNLILNALQATGEGGRVAVRLAMRGASGDMPAGVEITVSDTGRGIDPAQREKIFTPFFTTKEGGTGLGLVITQRIVEAHGGTIGLESEPGRGTTFRVWLPV	9~~DUF4118 (0.00000761691)~~106;X;148~~HisKA (1.05816E-15)~~212;X;262~~HATPase_c (1.75133E-29)~~365	non-KdpD DUF4118 protein

	5E-06	36	7	9.1E-06	35.2	4.8	1.4	1	G2P2E4_STRVO	Histidine kinase (EC 2.7.13.3)	Strvi_2184	Streptomyces violaceusniger Tu 4113	870	653045	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces violaceusniger, Streptomyces violaceusniger Tu 4113	>tr|G2P2E4|G2P2E4_STRVO Histidine kinase OS=Streptomyces violaceusniger Tu 4113 GN=Strvi_2184 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEGHRRVERGADLVVGFVEHHGRRRTQVMMHGLEEVPRRELEYRGSTFTEMEVDAVLARRPAIALVDELAHTNVPGSRNEKRWQDVEELLRAGIDVVSTVNIQHLESLGDVVESITGVRQRETLPDEVVRRADQIELIDMSPQALRRRMAHGNIYAPDKVDAALSNYFRPGNLTALRELALLWTADRVDEYLQQYRDEHSIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGLTSASPKELAVQRTLVEDLGGTFHHVIGEDIPGALLEFARGVNATQIVLGSSRRKTWQYVFGPGVGTMVARDSGPDLDVHIVTHDEVAKGRGLPVARGARLGRSRLIAGWVVGVAGPALLTLLLTGTGATLASEAGPGFANQVLLFLFLNVLAALLGGMVPALASAAVGSLLLNYYFTPPTHTLTIADPENIVAIAIFVAVAVCVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETSLEALLERVRETFAMDSVALLERESDVAPWTCAGSVGSHDGTPAPERPEDAEVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLAQQAGQARELAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSEEDEAELLEGIEDGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALVGVPMAKVTLDIPEELPMVAVDPGLLERGVANIVENAVKYSPPDHPVLVSASALGDRVELRVADGGPGVPDSEKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMDGRLTAEDTPGGGMTMVLTLRVAAGRPPADPGLPVQVGSTSGTTTRKGRPAT	1~~KdpD (2.12538E-123)~~211;X;233~~Usp(3.9968E-30)~~356;X;426~~DUF4118 (0.00000758081)~~471;X(151);622~~HisKA (1.63107E-14)~~688;X;737~~HATPase_c (6.92415E-26)~~838	KdpD protein
	5E-06	36	5.2	9.2E-06	35.2	3.6	1.3	1	R5C8F7_9FIRM	Histidine kinase (EC 2.7.13.3)	BN499_00279	Blautia hydrogenotrophica CAG:147	662	1263061	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	>tr|R5C8F7|R5C8F7_9FIRM Histidine kinase OS=Blautia hydrogenotrophica CAG:147 GN=BN499_00279 PE=4 SV=1MSAHIQSAADENEHIMVCLSASASNPEVIRQAARISSSFHGKFTAFYVEMSGMDDMPVQERNNLQANIRMAEQCGANIIVSYGNDVAEQIAEYVKVAKVTQIIMGKTYKGRRWLFKRDSISDKLLKIAPNLKVMLIPDPLEEEHKVHWVRRRRNQDFYRNSLRLSIDILTIFLFLLLSTGICVLFEENEFQTDNLLMIYMMGGLLQALFARCRISSILYALGSVIVFNYFFTEPRLTLHVNDTSYITTFFVMFATSMTVSTLVQQMKRVAKQAAEKAYRTEILLETSQKLQQAEDVSQIALQSIQQLEKLLNCTVYCIPGKPSSDMKLQDYFASNKEANGLSRDEIAVASWAYKNNKHAGATTGTLPGARCLYLTVRNGDKIFAIIGIELNGKVPTAFEKSVMLALLNESALAFEKEELRRRERETALRLQQEQLRGNLLRAISHDLRTPLTSISGNADMLMKSYQMMADSERTRIFHDIYEDAVWLINLVENLLSVTRIENGTMDIVLQPEMVEDVLDASMKHLNRHVKNHKLKVSQADDMLMAKMDAKLIIQVLTNLVDNAFKHTPEGSEIEINVYEKRHKVVFEVADNGDGVPDDQKEKIFTMFYSGDHTTSDGRRCMGMGLTLCKSIIEAHGGRIWVEDNHPHGAVFRFEIEAEEVNF	14~~Usp(9.14449E-31)~~137;X;179~~DUF4118 (0.0000000162804)~~268;X(165);433~~HisKA (0.000000000014735 4)~~499;X;552~~HATPase_c (8.05998E-31)~~655	non-KdpD DUF4118 protein
	6E-06	35.9	1.7	9.9E-06	35.1	1.2	1.3	1	B9M5D4_GEODF	Histidine kinase (EC 2.7.13.3)	Geob_1530	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter daltonii, Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	367	316067	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter daltonii, Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32)	>tr|B9M5D4|B9M5D4_GEODF Histidine kinase OS=Geobacter daltonii (strain DSM 22248 / JCM 15807 / FRC-32) GN=Geob_1530 PE=4 SV=1MQQIKNIRLLIAASSILGISLLHYLTPLHLPMLHDVFQRLYYLPIILSGLWFGLRGGLTASLVVSIMYVPHILFQWGIHPSLELEKYLEILLYNVVGGVTGLLSQREETRREELERTAKGLEESYRKLHEQADLLIKTEEQLRRSERLSALGELSATLAHEIRNPLGSIKGTTEILKDSFAPGEKKYEFLEILLKEADRLNRVVENFLGLASPVRVEQNRCDIMLELRELVAFTTAEALSMEVKVRLEPAEIPPIKGDTEKLRQVFLNLLMNALQATGTGGEVVISAVGPLHTSENQPVIELSFADNGQGIDQEMLERIFQPFFTTKKGGTGLGLAITQKIVESHGGTIRVTSTKGKGTTFTVILPA	9~~DUF4118 (0.0000378196)~~104;X;148~~HisKA (0.000000000000186421)~~211;X;262~~HATPase_c (5.80439E-30)~~365	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	6E-06	35.9	7.7	1.2E-05	34.9	5.3	1.6	1	I4ETM6_MODMB	Histidine kinase (EC 2.7.13.3)	kdpD MODMU_1289	Modestobacter marinus (strain BC501)	841	1144889	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Geodermatophilales, Geodermatophilaceae, Modestobacter, Modestobacter multiseptatus, Modestobacter marinus (strain BC501)	>tr|I4ETM6|I4ETM6_MODMB Histidine kinase OS=Modestobacter marinus (strain BC501) GN=kdpD PE=4 SV=1MGGMARGSLRIYLGAAPGVGKTFAVLGEAHRRLARGQDVVVGLVETHGRRRTLEQLEGLEVLPRLEVTHRGVTLTELDVDAVLARHPDLVVIDELAHTNAPGSRHAKRWQDVEELLAAGISVLTTVNVQHLASLTDVVEQITGIAQQETVPDEVVRRADQVELVDMSPEALRRRMAHGNVYPAERVDSAMGNFFRVGNLTALRELALLWLADRVDEGLRRYRSEHDIDHVWETRERVVVALTGGPEGETLVRRAARVARRNGNGVLMAVHVLHSDGLAGASPEALRAQRALVESLGGSYHQVVGDDVATALLQFARGADATQLVIGTSRRRSRWARAVRGGIGGEVIARSGEIDVHIVTHAAAGSPGWRLPVLTTAVTWRRRWAGLALALGGVPLVTVLCLTAGSVLSLASVLLVFLLLVVAVALVGGLGPAVVAAVVGGLAENWFFTQPTGRLTVNQVDDVVALLGYLVVGVAVATVVDRSARRAVAARSAAETEMLASLSRSVLAGDRALPSMLEQIREAFGLDEVTMVERTADGERTVGSCGQAHGRTGDDVPITDTIALRLCGRPLDAGDRRVLVAFAEQAAVALQQGRLTAQAAEADRLAAGNSMRTALLAAVSHDLRTPLAGIKAASSALRSTDLALTDDDRTELVATVDESADRLTGLVDNLLDMSRLQSGAVAPTLDPTDLVAVLGTALTWLDGPQRARVVVHSPDGLPAALADPGLLERVVANLVGNATQHAPSGVVDVRAGVAAGRVELRVADRGPGVPEADRERVFAPFQRLGDAPGGQGVGLGLAVARGLTEAMGGTLTAEDTPGGGLTMVLSLAPAELPARRDAVGAA	4~~KdpD (5.18334E-119)~~214;X;236~~Usp(1.05745E-24)~~358;X(250);608~~HisKA (1.82313E-14)~~674;X;726~~HATPase_c (9.11505E-26)~~826	KdpD protein
	7E-06	35.7	4.3	1.9E-05	34.2	2.7	2	1	R7HCN4_9FIRM	Uncharacterized protein	BN634_01546	Eubacterium sp. CAG:38	735	1262889	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:38	>tr|R7HCN4|R7HCN4_9FIRM Uncharacterized protein OS=Eubacterium sp. CAG:38 GN=BN634_01546 PE=4 SV=1MKVFIIGGCNTVVNALLQKFNKEGLKLYVLTGSHQYHNKYKHVYEQYHFSYENNCIKEVFESVRPDVTIFTGAFDSNYHWENGFREITSYCSGLYNILTAYSLLQYGRFIYLSSDEISRITEDEYAAITKQMAEPENSFHENYAAACKANALKNGEEICCNYKETTGLDILTLRINELCYLPKSADEADFCLSELCMEALTEKKITLSKDLYMPFYLSDMTEFLYRLVKADDLKHHFYYMGAANGISANELCLQIDSCLALSTHREQNTGDEMLWIDSRLPYNLADEVSCTCFYDAKTCIQMLCKHIQKHKKQLIINKETTGTKHNVKKWLAHIFQAALPFIENMICFIPFFMINNRVTESAYFARLDCYLLYVLLFAIVYGQQQASFSAILSIGGYFFRQMYHRTGFEVALDYNTYVWIAQLMILGLSVGYLRDQLSTMKADKADEITYLNNRLKDIEEINAINTRLKNDLETQVVNQSDSIGKIFEITSSLDSDEPESVFFHAAEVVSQLMDCRDVAIYNVSNRNYARLMSSTSESARRLGNSIAYTEYTQMVEAFKNRTVFVNRQLTENVPLMAAAILSNDEIQSIIMLWDISWDRLNLSFMNRFQVIGYLIQNAVLRANRYIDVLEHERYINGTKILEPAAFRTLLKAFLHAQQKGLTDCSLIQITPKAEGIAHASRALERLFRNSDYLGSINDGFLYVLLANTSPKDAGYVTQRIAEAGYSYRLVTDIKD	340~~DUF4118 (0.000000000003164 88)~~435;X;497~~GAF (0.000000000001220 35)~~621	non-KdpD DUF4118 protein

	7E-06	35.7	6.6	1.1E-05	35	4.6	1.4	1	V6KFS0_STRNV	Histidine kinase (EC 2.7.13.3)	M877_08465	Streptomyces niveus NCIMB 11891	848	1352941	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces niveus (Streptomyces spheroides), Streptomyces niveus NCIMB 11891	>tr|V6KFS0|V6KFS0_STRNV Histidine kinase OS=Streptomyces niveus NCIMB 11891 GN=M877_08465 PE=4 SV=1MRRGKLRIYLGAAPGVGKTYAMLAEAQRRVERGTDCVVGFVEHHHRPRTEVMLHGLEQIGRLEIPYRGTVFTEMDVDAVLARRPAVALVDELAHTNVPGSRNSKRWRDVEELLQAGIDVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMDPQALRRRMAHGNIYQPDKLDAALSNYFRPGNLTALRELALLWTADRVDEYLQQYRGEHNIRSTWQARERIVVGLTGGPEGRTLVRRAVRLAEKGAGGEVLAVYIARSDGLTSASPKELTAQRILVEDLGGTFHHVIGDDVPSSLLEFARGVNATQVVLGSSRRKTWQYVFGPGVGQTVTRDSGPDLDVHIVTHGEVARGRGLPVARGARLGRARIVGGWLTGVVGPVLLTLLLDGLAPDVGLANDMLLFLTLTVAAALLGGLVPALASAAFGSLLLNYYFTPPLHEFTISDPKNIVAIVIFFGVAVSVASVVDIAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFAMESVALLERESDIAPWTCAGSVGPAERVERPEDADVDLPIGDHMALALAGRVLPAEDRRVLSAFAAQAAVVLDRQRLLGEAGQARELAEGNRIRTALLAAVSHDLRTPLAGIKAAVTSLRSHDVEWSEDDHRELLAGIEEGADRLDNLIGNLLDMSRLQTGTVSTLIRETELDEVVPMALGGVPEGSVVLDIPESLPMVAVDPGLLERAVANIVENAVKYSPDNAPVFVSASAIADRVEVRVVDRGPGVPDDAKDRIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLTAEDTPGGGFTTVLTLRTAAGHPPTRPDLPPTVTS	1~~KdpD (1.7925E-121)~~211;X;233~~Usp(2.30761E-28)~~356;X;403~~DUF4118 (0.000000430472)~~466;X(147);613~~HisKA (1.90074E-14)~~679;X;728~~HATPase_c (2.49735E-25)~~829	KdpD protein
	7E-06	35.6	15.2	1.1E-05	35	10.6	1.3	1	R5L6U1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN508_01625	Eubacterium sp. CAG:161	354	1262881	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:161	>tr|R5L6U1|R5L6U1_9FIRM Histidine kinase OS=Eubacterium sp. CAG:161 GN=BN508_01625 PE=4 SV=1MVKDKSYLKNILVTAGILLISFVISLLLQHVFKVHEHITAVFIFAVFLISLLTNGYVYGIVAAFISMIAVNYAFTFPFFSINFMIPVNMISAIIMIVIAILTSTLTTQIKRHEAMKAEGEKERMRANLLRAVSHDLRTPLTTIYGSAATLLENRDTLEEEQQTKILQGIKEDSEWLVRMVENLLSITRIDSGNVKIIKTPIVLEELIDSVIVKFRKRYPDFDITLDLPEDIVVIPMDAMLIEQVIVNILENAIQHAEGMTELILRVFVLGKQAIFEIKDNGCGISKEKLPYIFSGYYENKEEPSDGQKRNTGIGLSVCKTIIKAHGGDISAENIKGGGAVFRFTLDTEEEIDAQ	10~~DUF4118 (0.0000000000539907)~~112;X;122~~HisKA (0.0000000000007814 64)~~188;X;241~~HATPase_c (1.61861E-24)~~345	non-KdpD DUF4118 protein
	7E-06	35.6	13.7	1.1E-05	35	9.5	1.3	1	B9K2I0_AGRVS	Histidine kinase (EC 2.7.13.3)	kdpD Avi_6071	Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	902	311402	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium vitis (Rhizobium vitis), Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	>tr|B9K2I0|B9K2I0_AGRVS Histidine kinase OS=Agrobacterium vitis (strain S4 / ATCC BAA-846) GN=kdpD PE=4 SV=1MSDAQRDTNRRPDPDALLGLANRDGRGKLTIFLGAAPGVGKTYAMLSRARGQKTAGIDIVIGLVETHGRSETELLTDGLETLPRKQIAYKDRVLEEFDIDAALARRPAVIIVDELAHSNVPESRHPKRHQDIEELLAAGIDVWTALNIQHLESLSEIVTQITGVQVRETVPDRVLKQADVVVLIDLPPEELIVRLREGKIYLPDNARRATDSFFRLGNLTALRELALRRTADRVDDQMVDYLKQNAIEGPWRTGERLLVCIGPDALSEKVVRTASNLASGMNARWLVVSLEQADQADENPGDQTRIEELFRLAERFGAETRRVQGRDFVHEILRLAKKEHVTQIVIGAPKRSRWQRLFRRSLPDALLDVRSGMGIHLVTGEAAPEKTKRVGLTKTFSLKSLPVRPRDIITALITTTVAVIGARGIIHFVALPNVSMLFLLAVLVSALREGYVAAVLTSVLSALAYNFFFISPVFTLTIAAPHEVFAFVMFIAAALIAGGIAARIRAQGQIAARRATQTQILYDVSSKLAGTVDADGVVWTAVSQLNGIIKRPVALLSPQNGTLALRSCWPPDTELGVAEMAAARFALEKGETAGAGTGTLPNSKLQFRPLRSPAGTLAVCGHEMTGEPLDPMEERALSAILDQVTIALDRANLTIRSVEDQARLERERFQSTLLSSISHDLRTPLATITGAVTSLKEFGERMPVESRRDLLQSIEEEGERLSRFVGNLLDMTRIEAGALEAKHDWVDLNDVISDSIARARRVAPATEISASIAKDLPLLRADSLLLGQVLFNLIDNACKHGGGEPVTVYARADDTVLSLSVTDMGKGISEKDIDRIFEKFYRRGKGADGRKPGTGLGLAIAKGFVEAMGGTITVESPAVKRIGTRFTLRFPLENMEKDRAEA	25~~KdpD (4.08072E-120)~~234;X;256~~Usp(1.07901E-33)~~379;X;408~~DUF4118 (0.00000000079178)~~490;X;533~~GAF (0.000159446)~~650;X;667~~HisKA (0.000000000005076 37)~~733;X;786~~HATPase_c (2.21488E-27)~~890	KdpD protein
	7E-06	35.6	6.2	1.3E-05	34.7	4.3	1.4	1	F3ZIK4_9ACTN	Histidine kinase (EC 2.7.13.3)	STTU_1469	Streptomyces sp. Tu6071	885	355249	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. Tu6071	>tr|F3ZIK4|F3ZIK4_9ACTN Histidine kinase OS=Streptomyces sp. Tu6071 GN=STTU_1469 PE=4 SV=1MARGKLRIYLGSAPGVGKTYAMLAEAHRRLERGTDVVVGYVEHHARPRTEVLLTGLEELPRAHHTHRDAAFTEMDVDAVLRRAPAVVLVDELAHTNVPGARNAKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVESITGVTQRETVPDEVVRRADQIELVDMSPQALRRRLAHGNVYAPDKVDAALANYFRPGNLTALRELALLWTADRVDEYLQQYRGEHNIESTWQARERIVVGITGGPEGRTLIRRAARMAAKGSGSEILAVYIARSDGLTAASPKELAVQRTLVEDLGGTFHHVIGDDIPAALLDFAKGVNATQIVLGSSRRRSWQYALGPGVGMTVARESGPDLDVHIVTHEAAAKGRGLPVARGARLGRSRILTGWLVGVGGPVLLALVLRSLDEGPGLANDVLLFLFLTVGAALLGGLVPALASAAVGSLLLNFWFTPPTHTFTISDPSNIVAIVIFFSVAVAVASVVDLAARRTHQAARLRAESEILSFLAGDVLRGETTLDALLDRVRETFAMHSVALLEREGDREPWTPAGSVGPQPAARPEDADVDMPVGDHMALALSGRVLPAADRRVLAAFAAQSAVVLDRERLQRQARQARTLAEGNRIRTALLAAVSHDLRTPLAAIKAAVTSLRAEDVAWSEEDRDALQEAIENGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGLPPDALVDLDVPETLPMVAVDAGLLERAVGNVVENAVKYSPSRTPVLVAASTLGERVELRVVDRGPGVPDEAKDRIFEPFQRYGDAPRGSGVGLGLAVARGFTEALGGTLSAEDTPGGGLTMVLTLPVARRRPKENSAEAADEGSGPPEDRPGPVPPEDDPPRAARPQPSSPDRPDRKAARS	1~~KdpD (1.23715E-119)~~211;X;233~~Usp(3.20446E-31)~~356;X;391~~DUF4118 (0.000000000409708)~~466;X(146);612~~HisKA (0.000000000000491331)~~678;X;728~~HATPase_c (1.88454E-26)~~829	KdpD protein
	7E-06	35.6	9.2	1.1E-05	35	6.4	1.3	1	A6TTB9_ALKMQ	Histidine kinase (EC 2.7.13.3)	Amet_3308	Alkaliphilus metalliredigens (strain QYMF)	461	293826	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus metalliredigens, Alkaliphilus metalliredigens (strain QYMF)	>tr|A6TTB9|A6TTB9_ALKMQ Histidine kinase OS=Alkaliphilus metalliredigens (strain QYMF) GN=Amet_3308 PE=4 SV=1MIKLALIIAISTILSLFLGSVGIGKESIIMVFLVGALIVTVTTKGYFYGIFAAIGSVLIFNYYFTVPIHTLITYDSNDVILMVSFLCVSLVSGTMTKRFQKQLQISQQNEHTARLLYRITESFVNITGQKNIIMKGINYIYENTGYNSRVLLSEPGEVYVDESKEFTTDKMMEIPIRGLTKQLGVMQVAYSKERFTFEHELLIKTVGTQMGLSLDRELIYNERENIRIAMEREKMHSNLLRAISHDLRTPLTGIVGASGVILENLNQLEKSSIESLVSDINEEAIWLNSLVENILNLMTRIYEGKLVIEKKYEVVDDVVSEAINHANSFAKTRSIFVSMPDEIVTVLIDGKLIVQVLINLLDNAIKHTEDHCSIFVNVYIEDDMAVFEVADNGDGIDESIHNSLFDSFVTISSKIIDNKRGMGLGLSICKAIVEAHGGTITGGKSTEGGALFSFRLPLTGGE	1~~DUF4118 (0.000000000092277 3)~~102;X(131);233~~HisKA (0.000000000918406)~~299;X;352~~HATPase_c (1.19064E-24)~~455	non-KdpD DUF4118 protein
	7E-06	35.5	8	1.1E-05	35	5.6	1.2	1	A0A0F2J7Q4_9FIRM	Sensor protein of zinc sigma-54-dependent two-component system	UF75_5224	Desulfosporosinus sp. I2	211	1617025	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	>tr|A0A0F2J7Q4|A0A0F2J7Q4_9FIRM Sensor protein of zinc sigma-54-dependent two-component system OS=Desulfosporosinus sp. I2 GN=UF75_5224 PE=4 SV=1MLNHEPPAQNRARTLFDLIAIGLVVVILTAIHYTNYHYEMNYHILLQFAYYLPVIYAAMRFGPAGGIISSLVITVLILPLMMYFQAMAPSAMYTQWVEIGLINVIGWLTGFLTEQERKASRNYQLALTVQKELVEKLKREGQERERLEGEIRQTERLTALGHMSAGLAHEIRNPLGIMKVSIQLMALEKSDDGVVSDYCRVLIEECERLNR	15~~DUF4118 (0.0000015162)~~119;X;157~~HisKA (0.0000000209787)~~211	non-KdpD DUF4118 protein

	8E-06	35.5	8	1.5E-05	34.5	5.6	1.5	1	B0SY75_CAUSK	Histidine kinase (EC 2.7.13.3)	Caul_2695	Caulobacter sp. (strain K31)	897	366602	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter sp. (strain K31)	>tr|B0SY75|B0SY75_CAUSK Histidine kinase OS=Caulobacter sp. (strain K31) GN=Caul_2695 PE=4 SV=1MAADDSRHAEKTRPDPEALLAAANRASRGRLKVFLGMAPGVGKTYEMLRAARRRKADGQDVLIGLVETHG RRETESLLRGMEVLPRKPIDHRGHVMMEFDLDTALARKPALLLVDEYAHSNAPGSRHPKRWQDVEELLAAGIDV WTTLNVQHLESLVDVVQRITGVRQRETVPDSALSRADAIELIDITPDELRERLTEGKVYVPETARLASENFFKVENL TALRELALRRAAQTVDDQLVAAMREKGVEGPWAAGERILVLVGGDAMASGLVRAGRRLSDMMMDAPWTVTHVD RLDQPVGGPAAAARLRDALKLAEQLGGTTVVLSGADIVATVMAYARRNNVTQIVIGKSADSRWRELLGRSLAAALL REARGAAIHVVTEATHEPIVEPPRRRPAVGWTAYLISAACVAVATVAAWGLDVAFDRVDLGMIFLAAVLAAGVLRG LRPALAAATVAFLVYNYLFLDPRHSFAIGSPTDFLTLVVFWAVALAAGGLAGRVRDQGRDARRRASAVSALLAASR TFSAAAGREAAAKALAEQTAAAVGAKAVVLLPIHGELRPAAGAPTLDDLDAAPMAAARWAWEKGEAAGFGTGTL PQTRWTFWPLEGVRSRAGVAGVEAGAMVAGSEDERLLLALLEQGAVALERAELATEAVETETLRRADRFRSALL NSISHDLRTPLSTVLGASTTLIDYGKGMTAAVRDDLLLSIREEAERLNRYVGNLLDMTRLEGGALRLRTDWTDVRD VLGAAAERVSRRLGDRALVRDFPGELSLVRADSSLLEQAVVNILENAIAYSPAATRIEMAAYEDRSNVVISIEDEGR GIPTAELEQVFEKFRRMEEPTDRNQGAGLGLSISKGFIDAMGGRIAAASPIHDGRGTRILISLPKAVATPHHLL	26~~KdpD (9.6172E-122)~~236;X;258~~Usp(1.47451E-32)~~382;X;431~~DUF4118 (0.00000405774)~~487;X(176);663~~HisKA (0.000000000797189)~~729;X;782~~HATPase_c (3.75907E-24)~~886	KdpD protein
	8E-06	35.5	13.4	1.1E-05	34.9	9.3	1.3	1	Q9A3K5_CAUCR	Sensor histidine kinase	CC_3198	Caulobacter crescentus (strain ATCC 19089 / CB15)	327	190650	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter vibrioides (Caulobacter crescentus), Caulobacter crescentus (strain ATCC 19089 / CB15)	>tr|Q9A3K5|Q9A3K5_CAUCR Sensor histidine kinase OS=Caulobacter crescentus (strain ATCC 19089 / CB15) GN=CC_3198 PE=4 SV=1MPISARIRGKVGGYLFAILATLVAWALRYALDDWFPPGFPYLTFFPAVVVTAYFAGLRPSILCAVLSGLMAWY FFIPPFHSLSLNFPTAVALVFYAFVVAVDVFFIDGMRKALRQLEEERTRYAALAESRDLLYRELHHRVSNNLHVVGA LLRLQGAGVQDEDARHALAEAGGRIELIAKIQRELHNAVGQPAPFRSFAEVVLAGAAAAAGAKVSLAIHGGGQPLH PDQAMPVTLVMLESFNNALEHGFGEGGSGRVEVHLDQSGLTHVLTVRDDGAGPPADFDPAQSKSLGLRIVRAMA QQLGGQFEMSSEGGWTICRLSYAPKQD	17~~DUF4118 (0.000000000335453)~~112;X;136~~HWE_HK (7.85485E-16)~~186;X;236~~HATPase_c (0.000000000084612 5)~~314	non-KdpD DUF4118 protein
	8E-06	35.5	13	1.2E-05	34.8	9	1.3	1	R6BEC1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN708_00395	Firmicutes bacterium CAG:56	580	1263031	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:56	>tr|R6BEC1|R6BEC1_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:56 GN=BN708_00395 PE=4 SV=1MYEMLKKFDAFCDANRQNLWLEEDAVPEEKEESAEQVMDDCLSSSVSAERNGRLEKLLAAFQREKKIQNF RDLYTSILILLAASVMGYFFNSLGFANANIMTVFVFAVQLIAVLTNHRTYSMIAAVLSVLIFNFLFTTPRYTFHAYGEG YPVTFLIMFGIAFLTGTLALKLKNQAKQSEMVAFRTKILFDTNQILQCARGREEIISKTGQQLRKLLGRNVIFYSVKDH ELEKSKVFMMQDREWSEQQKLKKEKYVAEWVLKHRKRAGAGTGNFPGAECLYLTVGVNETVYGVLGISIEKKQL ESFEKSILQAIIGECALALENEQITIEKEKAAILAKNEQLRSNLLRAISHDLRTPLTSISGNASNLLSNADYFDKETKKQ LYLDIYDDSMWLINLIENMLSVTRLEEGRMNLNISVELVDDVIQEALRHVDRKKDEHTITVEHEDELLLARMDSRLIV QMVINLVDNAIKYTQKGSHIDIRTGREGKNAVISVADDGPGISDEMKEHIFETFYTGTNKIADSRRSLGLGLALCKSI VNVHGGEIKVSDAHPHGAVFQFTLPAGEVYLYEQTTDTGCGR	76~~DUF4118 (0.000000000000169867)~~174;X;202~~GAF (0.0000351412)~~323;X;340~~HisKA (0.000000000169162)~~406;X;459~~HATPase_c (6.65616E-29)~~562	non-KdpD DUF4118 protein
	8E-06	35.5	10.2	1.3E-05	34.7	7.1	1.4	1	A0A075JHN9_9MICO	Histidine kinase (EC 2.7.13.3)	HX89_12865	Dermacoccus nishinomiyaensis	879	1274	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Dermacoccaceae, Dermacoccus, Dermacoccus nishinomiyaensis	>tr|A0A075JHN9|A0A075JHN9_9MICO Histidine kinase OS=Dermacoccus nishinomiyaensis GN=HX89_12865 PE=4 SV=1MTRGTLRIYLGAAPGVGKTMAMLAEGRRRAERGTDVVVGFCETHGRTATAAALEGLEVMPRLRREYRGAT LEEMDLDAVLRRAPQVALVDELAHTNVPGGRHEKRWQDVEDLLAAGIDVVSTVNIQHLESLNDAAFAITGVLQRET VPDVVVRRAEQVELIDMAPEALRRRMAHGNVYKPEKVDAALANYFRQGNLTALRELALLWLADRVEESLTAYRSD HDIVGTWPTRHRVVVALSGGREGATLLRRAARIAARGSGGEMHAVFVVRDDGLRTAEADVVSGLRRLTEELGGT FHTVSGPDAAEAVLHYARGVNADQIVVGLSRRSRAQAMLRPGTGERIIAGSGEDIDVHVVTHELAHVGSSPTERE GLSTRRVRLGFLTSVTAPALLSALLVPLRSGVGLPLIVQLYLLLTVVVALIGGMAPAITAGVLSSLLINWFFTPPIGTLT ISDPQNVVALVLFVVIGAAVSLVVHASARRAADVSASHQEATALAELSHTMLSSADQLALLLTRSLEMFDQDAAAV VRTRGPGRSVIASTDGYSDVAAQALPREKTTVERIDDEHDLVLVGRPVPAERQRLLGAYAMHAAAVLHRRALLDL AESADTLARDNKARTALLSAVSHDLRTPLAGIKAAVGSLRSDEVTFSPEDEAELLEAVETSADRLDALIGNLLDASR LQTGALVANPREIDLAEVVTPAVRALETPDRVTWHLDDAARHVVADPGLLDRVLANVLENALRHGGSDGVVVTTS TLGPRVELRVADHGPGIPDEAREEIFRPFQRYGDAPAGDGIGLGLAVARGLTEAMGGMLEAETTPGGGVTMVIVL PAVANAAGATSEAEPGAESEPESAPEARPQDAEADQPVDTRFADATTRGDS	3~~KdpD (1.65358E-113)~~211;X;233~~Usp(4.75387E-20)~~356;X;381~~DUF4118 (0.000000000003034 31)~~474;X(138);612~~HisKA (0.000000000000535419)~~678;X;728~~HATPase_c (6.12064E-26)~~828	KdpD protein
	9E-06	35.3	9.8	1.4E-05	34.7	6.8	1.3	1	D4MY81_ANAHA	Histidine kinase (EC 2.7.13.3)	CL2_05080	Anaerostipes hadrus	383	649756	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Anaerostipes, Anaerostipes hadrus	>tr|D4MY81|D4MY81_ANAHA Histidine kinase OS=Anaerostipes hadrus GN=CL2_05080 PE=4 SV=1MEQNEKGLMQWEKDFLISITILIIATIIAHIFFYQTAHNINVPMIYTLATFFISRYTKGYGWGIVSSLLSVIFINWR FTFPYFKINFMIDGYPMTFLGILVIAIITNMTTTSLNREKEAAVKREKELAKLNEYNKQINELQIEKEKEKMRSNLLRAI SHDLRTPLTGMIGASSTYLEAKDQLDEEAKDQLVMGIKEDANWLLNMVENLLSITRIQSNGSDTQPHVKKVPEPLE EVVAEAIQRYQKRYPDSELKVKIPEDFLMVPMDPTLIEQVIMNLLENAWVHSGSDAPIELDIKEEGNKVVFYIRDHG NGIAPERLDQLFDGCAGALDHESRKGMGIGLSICKSIVMAHQGDVYARNYEDGAEFSFSLPMDEKELTEEKEL	32~~DUF4118 (0.00000010212)~~106;X;147~~HisKA (0.000000000010734 1)~~213;X;270~~HATPase_c (4.99049E-24)~~370	non-KdpD DUF4118 protein

	9E-06	35.3	11.4	1.4E-05	34.7	7.9	1.3	1	A0A023NTT4_9GAMM	Histidine kinase (EC 2.7.13.3)	CH75_16325	Dyella jiangningensis	888	1379159	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Dyella, Dyella jiangningensis	>tr|A0A023NTT4|A0A023NTT4_9GAMM Histidine kinase OS=Dyella jiangningensis GN=CH75_16325 PE=4 SV=1MSEPSREARADALLDSVQEENGRRLKIFLGAAPGVGKTYAMLSAARELKRQGIDVVVGLVETHGRAETQALLEGLEMLPRRKVNYRGRDFTEFDLDAALQRRPAVILVDELAHSNLPGGRHERRWQDIAELLDAGIEVYSALNVQHLESLNDQVRRITNVTVRETVPDAFLDRARDIVLVDLPPREIIQRLKQGKVYVPETAVAALDAFFSPTNLVALRELAVDTVAGHVDSDLREQMLARGGAMPVRRRVMAAIDGHSQSEYLVRIARRIAERRGAPWSVAFVDTGATLDKGRRERLDAAMRLARRLGGDTVVLRGHAIADELIAHADREGIGQIILGRTRERPLARMLGRSLTQLLLRRGAHLELTIIATPAERAKSRLRLRMPGGKGRRDEYVFATGATLAAFGLSFIADRYLSVANLALIFLMAVMVVAARTRMTVAVYTAILCFLGYNFFFAPPRYTLAIANFDDVLAVCLFLVAALVCSRLATRLASQVESLRAAHANARALLSLGQRLSTSTDAAGIRKVGVDALSHVLHCDAAILARDASQVLRVVATAPRDFSLTTQDLGAASWSEQHMEQAGRYTDTLNAAPCWVLPLGSADNPLGVAALRFPPEQGEPPVDERSLALAMVQDIGQALQRARLADELEGARVQGETERLRNALLSSVSHDLRSPLASMIGSAGTLASYGDQLPAGERRELLEAILGEGQRLDRYIQNLLDMTRLGHGTLKLNRDWTDVAEIVAASSNRLRKLFPDLRLDIALPSKTILLYVHPALIEQALFNILENAARFSPPGEAVRIVVRPNGEKVQIDVIDRGPGIPEDERARIFDMFYSVSRGDRAPQGTGLGLAICRGMIGAHGGSVEALPGDGVGTTIRITLPLPAPPENNA	24~~KdpD (2.79196E-117)~~230;X;250~~Usp(1.82502E-26)~~371;X;395~~DUF4118 (0.000000000001921)~~494;X;529~~GAF (0.00427211)~~640;X;657~~HisKA (0.000000000056223)~~723;X;776~~HATPase_c (2.09886E-27)~~878	KdpD protein
Disagreement between HMM and CDD prediction	9E-06	35.3	7	1.5E-05	34.5	4.8	1.4	1	D7C8J1_STRBB	Histidine kinase (EC 2.7.13.3)	kdpD SBI_03259	Streptomyces bingchenggensis (strain BCW-1)	857	749414	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	>tr|D7C8J1|D7C8J1_STRBB Histidine kinase OS=Streptomyces bingchenggensis (strain BCW-1) GN=kdpD PE=4 SV=1MGRGKLRIYLGAAPGVGKTYGMLSEGHRRVERGTDLVVGFVEHHGRPRTQVMLRGLEEVPRREMEYREARFTEMDVDAVLARRPAVVLVDELAHTNVPGSRNAKRWQDVEELLRAGIDVVTNLNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWTADRVDEYLQQYRSEHSIRSTWQARERIVVGITGGPEGRTLIRRAARMAAKGSGSEVLAVYVARSDGLTSASPKELAVQRTLVEDLGGTFHHVIGEDVPRALLDFARGVNATQIVLGSSRRKTWQYIFGPGVGVTVARDSGPDLDVHIVTHDEVAKGRGLPVARGARLGRTRLIAGWLTGVAGPVLLTLLLTHSGGALATDGGPGFANEVLLFLFLTVVAALLGGLLPALASAAVGSLLLNYYFTPPTHTLTIADPQNILAIAVFVAVAVCVASVVDLAARRTHQAARLRAESEVLSFLAGSVLRGETSLEALLERVRETFGMDSVALLERESDVAPWTCAGSVGGNGGAPLPERPEDADVDMPVGDHMALALSGRVLPAEDRRRVLAAFAAQAAVVLDRQRLALEAERARDLAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSPEDEAELLEGIEQGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALVGVPETCVSLEIPEELPMVAVDPGLLERSVANIVENAVKYSPDGLPVLVSASALGDRVELRVADRGPGVPDSAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFVEAMGGRLAAEDTPGGGMTMVLTLRAAGGREPVGSPLPAQVTS	1~~KdpD (7.91125E-123)~~211;X;233~~Usp(9.6955E-32)~~356;X(266);622~~HisKA (8.94945E-15)~~688;X;737~~HATPase_c (2.16676E-25)~~838	KdpD protein
	9E-06	35.3	12.1	1.4E-05	34.6	8.4	1.3	1	A0A0A8UNS1_LEGHA	Sensor protein KdpD	kdpD LHA_1369	Legionella hackeliae	648	449	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella hackeliae	>tr|A0A0A8UNS1|A0A0A8UNS1_LEGHA Sensor protein KdpD OS=Legionella hackeliae GN=kdpD PE=4 SV=1MVERRPNPDALLHSVQEEERQQKHGKLKIYLGAAPGVGKTHEMLHDALELLNKGLDVVVGIAESHGRQEINSLLTHFNVLPKKTIDYHGKQLSEFDLDGALKRYPGLILVDEMAHTNVPGSRHKKRWQDIKELLDRGIDVYTTLNVQHIESLNDDVSQIVHAPIKETIPDSIIEIADTIELVDLPPEELLKRLQDGKVYFPAQAKLATESFFRKGNLSALRELALRTAAKCVSAQVLLYRQGLGIRKIWPTKEKILVCVGPGISSLTLIRAAKRTARNLQAPWIAIYVDIPYGSQSEEKRQKAVENLRLAKQLGAETRILTGFNVVKTVLDFAHDQNITQIMIWKHIRTRWRDLFLRSLADEILRYSEEIDVYIMTGDRQVKKQEKKYKKRSPWVIYLASLVIVTLTTMINYLLYPVLSASNLIMVYLLGVTGIALFGRVGPSILGSVLSIFAYDYFFSPPLYTFSIPNLNYSFTLLVMLIVTQVISQLIIITRRQMAAARLHARQTSALYELSKQLSNTRGKNKLLNIGINYISKIFNSEVAVFLPQNKRLIAHAKKGLRPILDAEESEIIQWVYELGQRAGLGTDTFPTAEALYLPLPGIRKVVGVLRLQSPKGEDLDSPEKIQLLEACASQFALALEIENLNSIV	23~~KdpD (4.24452E-107)~~229;X;254~~Usp(1.82225E-36)~~376;X;397~~DUF4118 (5.92764E-14)~~496;X;524~~GAF (0.000000000012863)~~640	KdpD protein
	9E-06	35.3	12.5	1.3E-05	34.7	8.6	1.3	1	E7GIA9_CLOSY	Histidine kinase (EC 2.7.13.3)	HMPREF9474_00652	[Clostridium] symbiosum WAL-14163	374	742740	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	>tr|E7GIA9|E7GIA9_CLOSY Histidine kinase OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_00652 PE=4 SV=1MCSQDNGDMKKQHALFKQYGTINDWIVTGALLAVATCLSYIFFHIMDNPTANIALCYILALFLTARFTSGYFYGLFASLFGVVCVNFLFTYPYFALDFTLTGYPITFIAMFSISIATSALTTNMKEQAKVLSEREKLLMEAEKEKMRANLLRAISHDLRTPLTSIIGSSTVYLENGKYLTETEKSDLVSHILEDSNWLLNMVENLLSVTRINNETTKVNKSLESVEEVLAEAVLRLKKRLPDARVNVCVPDEVLMIPMDAVLIEQVLINLMENAFVHSKTTEPVECYVDTGDDYITFHVQDHGIGIPPEKLSTIFDGSSSTTSTSNDGRKGMGIGLSICKTIIVAHGGDIKAANHNNGAEFYFTLPKEGSKIDS	25~~DUF4118 (0.000000000042093)~~127;X;144~~HisKA (0.0000000000686261)~~210;X;263~~HATPase_c (8.42858E-24)~~365	non-KdpD DUF4118 protein
	9E-06	35.3	16.3	1.4E-05	34.6	11.3	1.3	1	F2NHJ4_DESAR	Histidine kinase (EC 2.7.13.3)	Desac_1324	Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	677	880072	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfobacca, Desulfobacca acetoxidans, Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	>tr|F2NHJ4|F2NHJ4_DESAR Histidine kinase OS=Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2) GN=Desac_1324 PE=4 SV=1MPPNHRDPVEGITSPDSASHPAGQRFLVCLGPDSNALELVQTARRMAEGVKAEWYALFVDTPSHTDGTRSDREHAVHSLQAAESWGAKTFKVSGLVVAAEIINFARQNGITTIFLGRSKQKKWYSRLTTSLATKLLRGLEGVDIYLVAPESTAPQPGKRRTLQLPRRLKGYFLAVAGVILCTVLAFGVFYYLPLSNLVMFYLLTMVIIATVSERGPTILASLLSIGLFAFFFVTRYFSFWVENVEYTVTLVMMLVVATLISGLTARARYQAKVARQQEWQTTALYDMNQGLLGKSGLEELLAAAVEQISRLFDSRVSILLPHMDDLEVRAGEPLPQDDVREGMVAQWVFKNNCLAGAGTQTLPQVKGLYMPLKTANRQVLGVLRLERRSPSTGKYVEVEYLRLLEALGHQIALALERESLSQQTRRAQLQVEAERFRNTLLSSVSHDLRTPLTVIAGSASSLLEAQENLDDKIRLELIQTIYEEAKRLDLVVQNLLEISRLQSGEIRINKEWHVLEEVIGCALSQLEGQLKQHSVTINLPQDLPLVQMDALLIERVFINLLENASKYTPPGTKIEISGALEPEALHLVVADQGPGLPPGQEERIFEKFYQARPGAIRGAGLGLAICRCIIEAHDGQINAINRPEGGAAFHFTLPFTGDQPDWQEPMLDLEQETRNEA	25~~Usp(1.71782E-28)~~148;X;171~~DUF4118 (0.000000000000260)~~270;X;297~~GAF (0.000000000000229244)~~417;X;434~~HisKA (0.000000000000290222)~~500;X;553~~HATPase_c (2.84956E-27)~~653	non-KdpD DUF4118 protein

	9E-06	35.2	10.1	1.5E-05	34.6	7	1.3	1	A6W6R8_KINRD	Histidine kinase (EC 2.7.13.3)	Krad_1019	Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	858	266940	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Kineosporiales, Kineosporiaceae, Kineococcus, Kineococcus radiotolerans, Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	>tr|A6W6R8|A6W6R8_KINRD Histidine kinase OS=Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216) GN=Krad_1019 PE=4 SV=1MPQTGRVEPRRDEKRRGRLRVFLGAAPGVGKTFAALDEAHRRRRRGTDVVVGLVECHGRERTEALLAGLEVLPRRTVEHRGLAVAELDVEAVLRRRPEVVVVDELAHTNAPGSKHPKRWQDVEEILAAGVDVVSTVNIQHLESLNDVVEHITGIEQRETVPDAVLRSADQVQLVDMTPEALQRRISHGNVYAGDRVDAALSNYFRTGNLTALRELALLWLADRVDEGLERYRAQQGIDATWPARERVVVALTGGAEGATLVRRAARLAGRGAGGELHAVHVARGDGLLRTSPVRLAEQRELVETLGGTYHQVVGDDVATSLLEFARGVNASQIVVGASRHRRLASLFRRSVGDGVVRGAGAVDVLVVTHEEQARRSGLPRPARAALSGTRRVLGWLVALLGPLLVTGVLLAIPHQDLSTDLMVFLVVVVGAALAGGVLPALAAALVAGLAVNWFFTEPLHRFTIAQPANAVALAVFLLVALAVSSTVDTAARRTRDAARSRAESEALSVLTRTALLAADPLAEALRHTRETFAVDSVTLLERSDVRAPWAVAAATGAPVCTRPADADAEVVLDDLTCLVLRGRLLGAGDRRVLEVFATQIAAVRQKQRLRAEAAQVRRLEEGEAVRGALLTAVSHDLRTPLATLKASLDSLRAKDIDLPEEIRDELLAEVGNSADRLQGLIDDLLDLTRVRSGTVEPLLVVVDLEDVVAGAVRDVGPGRVVVDLPPGLPPVSTDPGLLQRVVANLVQNAVRHGGTRVEVVASSSTDDARRVVRLLVVDHGPGLPDAAKERAFTPFQRLGDRSTAGLGLGLAVARGLAEAVGGRLEAQDTPGGGLTMVLDLPPAGHAQALVPAPGGSPA	14~~KdpD (1.66616E-117)~~224;X;246~~Usp(1.40852E-31)~~368;X;395~~DUF4118 (0.0000229276)~~484;X(139);623~~HisKA (0.0000000000103566)~~689;X;738~~HATPase_c (1.56429E-20)~~840	KdpD protein
	9E-06	35.2	11.1	1.5E-05	34.6	7.7	1.3	1	R7AQX9_9CLOT	Histidine kinase (EC 2.7.13.3)	BN593_00333	Clostridium sp. CAG:299	370	1262792	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:299	>tr|R7AQX9|R7AQX9_9CLOT Histidine kinase OS=Clostridium sp. CAG:299 GN=BN593_00333 PE=4 SV=1MNKHEDRLRHFPAPKTRAANMAVTLAFLFTATAVSFFFFTKMEEPSSSISLCYILALFLTARYTTGYFYGVLSALISVGCVNFLFTYPYFELNFTLTGYPMSFIAMFTISIITSALTTNIKEQARIISEREKLLMDAEKEKMRANLLRAISHDLRTPLTSIIGSSTVYLENEAHLTDIEKKSLVSHILEDSNWLLNMVENLLSVTRINNETARVNTSMEPVEEVMGEAVSRLKKRIPDAPIHVRVPDEILIIPMDAILIEQVLINLMENAVVHSKSTKPIECFADSSPDFVTFHVRDYGVGIPAEKLNTIFDGSSSTASSSTDGRKGMGIGLSICKTIINAHGGTLAAFNHPDGAEFYFKLPKEDSSIVS	20~~DUF4118 (0.00000000125956)~~123;X;140~~HisKA (0.000000000210361)~~206;X;259~~HATPase_c (6.92163E-22)~~361	non-KdpD DUF4118 protein
	1E-05	35.2	9	0.00002	34.2	6.3	1.5	1	A0A0F4JR63_9ACTN	Histidine kinase	VR45_11645	Streptomyces sp. NRRL S-495	890	1609133	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-495	>tr|A0A0F4JR63|A0A0F4JR63_9ACTN Histidine kinase OS=Streptomyces sp. NRRL S-495 GN=VR45_11645 PE=4 SV=1MARDLTPGTGHRRGRLRVYLGSAPGVGKTYRMLDEARRRQDRGADVVVGWIECHGRRHTEAMLDGLEVVPGVHRAYRETDFEEMDLDGVLRRKPTVVLVDELAHTNIPGGRHGKRWQDVDELLDAGIDVITTVNIQHLESLNDVVQKITGIPQRETVPDEVVRRADQIELVDMAPQALRRRMAHGNVYKAEKVDAALSNYFRVGNLTALRELALLWVAGRVDEGLRDYRASHNIDRVWETRERVVVALTGGPEGETLVRRAARIADRTAGGDLLAVHVTRSDGLAGASSGALAQQRQLVESLGGSYHVVVGDDIPTSLLAFARAHDATQLVLGTSRRGRTARFLTGPGIGETTVDASEDIDVHMVTHEFTGRGRLPALGRRHSRRRTVAGFLAGPIVPSLLTLVLSQFHDTVNLTTDALIFQLGVVVVALLGGATSALLASLVASVLLNYFFIPPVHAFTIGETNNIIALVVFAAVALTVSTVVDHATRLTARAARATAEAETLSTLAGSVLRGADALPALLEKSRTAFGMSSVALLGRTGGEVLASCDTAAEVKDAADGDRADNGGAAPDHTLVTTEVPVGADAVLVLTGRRLPAADQRVLTAFAAHVAAALERDRLAVVAAEVEPIKAADRMRTALLAAVSHDLRTPLAAALASVGSLRSPDVEFSPEDQAELLATADESLVKLTRLVDNLLDMSRLQAGALTLHLAETHLDEILPRALDSLADPYAPVQPLDLETVPPVLADPPLLERVLANVITNALRHNAPGAPVLVAASHHAGRVELRVIDRGPGIAPEDRDRVFLPFQRLGDTDNTTGVGLGLALSRGLAEAMDGSLEVEDTPGGGTTMLLTLPAAPARPLPAGPVPVPADPLPADPLPAGPMPAQHPGEAPV	11~~KdpD (9.09957E-116)~~221;X;243~~Usp(1.09605E-30)~~366;X;392~~DUF4118 (0.000000000861322)~~485;X(147);632~~HisKA (0.000000000002383)~~698;X;749~~HATPase_c (2.43989E-27)~~849	KdpD protein
	1E-05	35.2	6.9	1.5E-05	34.5	4.8	1.3	1	R6R2Y2_9FIRM	Uncharacterized protein	BN652_02355	Firmicutes bacterium CAG:424	675	1263022	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	>tr|R6R2Y2|R6R2Y2_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:424 GN=BN652_02355 PE=4 SV=1MEKEEYERPDSSQLLRRLQFEEEEKLKKSRGKLKIFLGYAAGSGKTYAMLKAAHEAKKHHIDVVAGYVEPHARPDTQALVKGLETIAPMEIAYKGVKLREFDLDAALKRNPRLILVDELAHTNVKGCRNEKRYQDVKELLRAGIDVYTTMNIQHLESLNDIVGNVTHIEVRERVPDKVFDHADQVEVIDIEPEELIERMKEGKIYGTLQAERALENFFRREKLVALREITLRRTADRVNRIAEEERNALGEMDYHTGEHVLVCISPSPSNAKVIRTASRLAYAFHASFTGIYVETPKMQEADEKNKAAVKNHMDLARALGADIVTVYGTDIAYQIVEYAIVGNISKIVMGRSRKQWMFGKSRSEVLEQLTYRAPNIDVYIIPDMKHTKEYREKGKSSEKKEESGKMVLLELGEITAIMALSTMAAYIFQWFRLSEANLIMVYMVGVLLSSYVADKKIYALYSALISVLSFNFFFTEPYFSLKAYDKGSPVTFAMLFAVGFFMASMTRQLKAQTRESAKKAYRTEILLENSRKLRRCRTREEVWKQVAAQVGKLLNLSIIIYPVDKKGNLEEPMLFPRKGMGLPELKENVNGKERAVAQWAASNRHRAGTCTHTLPDANAMYLPVQSTEEVKGVMGILLEERRPVKDFEYGLLIAMLNETGVKLQDTFLEKEIKIN	28~~KdpD (9.08415E-122)~~238;X;259~~Usp(3.40886E-37)~~382;X;411~~DUF4118 (0.000000000000780)~~512;X;540~~GAF (0.000000440509)~~664	KdpD protein
Disagreement between HMM and CDD prediction	1E-05	35.1	7.9	1.7E-05	34.3	5.5	1.4	1	A0A0A1DR30_NOCSI	Histidine kinase (EC 2.7.13.3)	KR76_23675	Nocardioides simplex (Arthrobacter simplex)	833	2045	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Pimelobacter, Nocardioides simplex (Arthrobacter simplex)	>tr|A0A0A1DR30|A0A0A1DR30_NOCSI Histidine kinase OS=Nocardioides simplex GN=KR76_23675 PE=4 SV=1MDRGRLRVYLGAAPGVGKTFAMLDEGHRRAERGTDVVVGYVETHGRPKTEQALGDLEQVPRRRLGYKGAELEEMDLQAVLDRRPAVVLVDELAHTNVPGSVNEKRWQDVEALRDAGIEVVTTVNIQHLESLNDVTEAITGVRQRETVPDHVVRSADQIELVDVSPQALRRRMAHGNIYAADKIDAALSRYFREGNLTALRELALLWLADRVDEGLERYRAQHEIDSTWATRERVIVPVSGGPESLTLMRRAARIASRSAGGEWQALYVTRRDGLSGIAPDRLAQLRAKAEGLGGSFHTVVGDDPAEGILDFARAENATQVLIGASRRGRVSALLRPGVGERVVAASGDIDVHIVTHEHARRGGPSPLRPPASLGRRRRVAGLVFAVLGPVGFSLVLWASNDLHGLPTEAMTLMVVVVVTALIGGLLPAVLAALLSGVLLNLLFTPPFYTLTIDEPENAIAILLFVVVGIAVATVVDNAARRTAQAAKARAEADALTVLSHSLLNASDDLAGLLTSACELFSARGAAVFRRRDDGTEEVLGACGTPPESVAAADMSADIDERTVLVLVGSRLPASERGLLNAYAAYAGVMAERRRATRAEVERLRLAEADRTRTALLAAVSHDLRSPLAAVKVAVSSLRSTDVQWSAQDEADLLETIEEATDRLTALVTNLLDMSRIHTGSVRVALTETGLVRALDQAVAPLAGGARIEVRVDPDLEVLADPGLLDRVLANICENALKYTPDSARIRIDAVTDGDRVTLRIADTGPGVAAGDHARLFVPFQRLGDVPDQDGVGLGLAVAAGLTEAMGGTIATEETPGGGLTFVLELPAAEEVQG	3~~KdpD (7.91414E-116)~~211;X;233~~Usp(1.46767E-28)~~355;X(254);609~~HisKA (0.000000000025237)~~675;X;724~~HATPase_c (6.86415E-26)~~825	KdpD protein

	1E-05	35.1	3.1	2.6E-05	33.8	2.2	1.7	1	F4A196_MAHA5	Diguanylate cyclase and metal dependent phosphohydrolase	Mahau_1838	Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	561	697281	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family IV. Incertae Sedis, Mahella, Mahella australiensis, Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON)	>tr|F4A196|F4A196_MAHA5 Diguanylate cyclase and metal dependent phosphohydrolase OS=Mahella australiensis (strain DSM 15567 / CIP 107919 / 50-1 BON) GN=Mahau_1838 PE=4 SV=1MNNTKDAQKAKLSIIIALMKVMCTVFIGIAVTSILSNIIALDIRCVQVRIMLVLGTMAISWWQWLSTNNQPRLWEQPRLADCAESLFYIVAVTWILCASQPETSIFKLTYIFIIMVNAFRFDMKYGFMSAGVSSASVIFCDVAKLEQLRRFAYLEQDMLLIVSFFVLAFIMGYISMSQKQDFDNMARMATTDELTGLYNNRIFHESLLRYIEETNDNKRYENVWVALLDIAEFRRYNELYGYTMGNAVLTQVGVIISEGARGAQLVSRYGDDKFGLIFTDCSLRHVKDIVSRIKRNIENYPFYGKDNMPGGVISVYAGIAGYPMNGLTKEEMIKSAVDDINFAKLIYNNIDPIHMVHMEGMSVMQVFINMLNSRDHFTYEHTQRVIAYADMLARALNMHQRFIDDVKFGAYLHDIGKIDLPTPILVKTQPLSVVEDDIFKNHVIWGADIVGSVESLAHIVPIIRHHHERWDGLGYPDGLQGTDIPLEARIVALANGFDMMMLMGRWPDEPDCRGVAGAVQCLMRNAGTYFDPDLVDIFIKTIRSYNLQHLFPNDAFSVTIDA	89~~DUF4118 (0.000117605)~~181;X;190~~Nucleotidyl_cyc_III (9.95716E-29)~~336;X;376~~HDc (4.82799E-23)~~507	non-KdpD DUF4118 protein
	1E-05	35.1	13.5	1.6E-05	34.4	9.4	1.4	1	R5ACP1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN453_01920	Firmicutes bacterium CAG:102	519	1262998	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:102	>tr|R5ACP1|R5ACP1_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:102 GN=BN453_01920 PE=4 SV=1MKKRIKRTLNNFNAAALFQDFIRTAAVYLVATCLALCLNGAEVLNENIFGVYMLAVALISYMTSGYFWGVIASIGGVIGVNFFFTFPYFALNFSITGYPITFSIMLLMSILTSFVTAKVKMAALLSAAGKKRAETLTEMSKAILSASDVDTIIDISAKYFSETNQCSVILYVDQPLKPLKQSICTLRDEDERILYSFLEKQVAQRAYDTQNPVGAEIEDGTQNCKGTYFPIITEDKIYGVVGFLFDETKLLIDDTFSFINVMISQTILALQRQQARKKAQEILLETEKEKMRSNLLRAVSHDLRTPLTGIIGAATTLLENGTQIASEDSRRMLMDIQHDAEWLIHMVENLLSVTKITGGTTNLKKQDEIIEEIVGEAVGRIRKRFPDSVVNVSVPEEMLIVPMDATLIEQVLINLMENAIRHSGSTAPIGVKVSRKKSGAVFTISDNGKGIDPSRIPDIFDGKTQHGSSDSSRGIGIGLSICKSIILAHDGKIFAKNNLNGGASFTFVLPMKGESDYAQ		non-KdpD DUF4118 protein
	1E-05	35.1	11	1.8E-05	34.3	7.6	1.3	1	E8N3E5_ANATU	Histidine kinase (EC 2.7.13.3)	ANT_09250	Anaerolinea thermophila (strain DSM 14523 / JCM 11388 / NBRC 100420 / UNI-1)	853	926569	cellular organisms, Bacteria, Chloroflexi, Anaerolineae, Anaerolineales, Anaerolineaceae, Anaerolinea, Anaerolinea thermophila, Anaerolinea thermophila (strain DSM 14523 / JCM 11388 / NBRC 100420 / UNI-1)	>tr|E8N3E5|E8N3E5_ANATU Histidine kinase OS=Anaerolinea thermophila (strain DSM 14523 / JCM 11388 / NBRC 100420 / UNI-1) GN=ANT_09250 PE=4 SV=1MSNSRLKIFLSYADGAGKTSAMLSDAFQQKARGVDVLVAWVKLPENSETRQLLEELEVLPPSSHGVDLDEVLRRRPQLVLVDELEGVNPAGSRHLYRWQDVEELLNAGISVYTTLNILHVESLKDTVEEITGLPVEQTVPDRLLDRADELEVVDLPPEELLERLHPHSPAPPAGTLRQKSNLLALRQLTMRRAAMRVEDQARALLGTARAPLGTERVCVGISNRPEAERLVREGRMLADALNAEWFVLYVETPTAAGERAEERANLLKAMRIAEENGANTLLIPAETIAEGIESFCRQQGITRLVLGKPRDPLWRMRLGVSPVEHLLRSGLPVDVILVDTPHKPLVRAGTPPRWWVYLRNGGAVFLAVLLVTLLGWSLRQRPGAMGMEGIYLLLVIALSFWLGRSAGVLAAGLSTLAFAWFFFGASMGLDGADLPLLLTFLGWATAGWVTASLARAVRRQTRAMRWRQVQSAVLNTLSRELAGALDMPAVLSIIVRHIVGVFNRAVMVLLLEEGQLKVAHSEGNVSLSERDWKISRWVLEHRRPAGLDTDTFADSPMREIPLMAHDLPVGVLVVVPDPASHTLLPEQREIRDGIAGLASLAIERVRLNQQAQQAAVLQMTEKLQTALLNSISHDLRTPLSAVEGSLSSLLEAETNGLQMDRETRLDLLENATEEAERLNRLVGNLLDMTRIEAGALRIRRRPCDVQDLIGTALTQFQRRLQDRKVSTHIASDIPEVEMDFVLIEQVLERLLDNAVKYSPPGSEINVEAKVRDGALYISVADRGEGIPPEDLERIFGKFYRVQRPDGVSGTGLGLSICKGIVEIHGGRIWAENRPDGGAKFTFTIPIKASGESK	5~~KdpD (1.29568E-68)~~197;X;216~~Usp(6.87714E-30)~~338;X;363~~DUF4118 (0.000000000006413 11)~~460;X(161);621~~HisKA (0.000000000160683)~~690;X;743~~HATPase_c (7.0547E-34)~~844	KdpD protein
	1E-05	35.1	13.7	1.7E-05	34.4	9.5	1.3	1	R6ENZ5_9FIRM	Histidine kinase (EC 2.7.13.3)	BN538_00483	Lachnospiraceae bacterium CAG:215	517	1262985	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	>tr|R6ENZ5|R6ENZ5_9FIRM Histidine kinase OS=Lachnospiraceae bacterium CAG:215 GN=BN538_00483 PE=4 SV=1MALKRLKVKHEFLHSGLITAGILAVATGIGFLFQSLGFTEENIIIVYVLGVLVIAAITANRGWSIFASVFSVLLFNFLFTVPRFSFAAYASGYPVTFVIAFLAALIASNLAIQLKRQAEISAKMAARTQMLLETNQILQKAEDVDEILEKTANQIVKLFGRTAIFYRNTKEGLKAPVLYPVNPKIDENRYLSEQEYKAAAEVLKQNGEVRSDQNCMYFPVGNTHKTYGVIGIVSEKQRMTEVEENFLQAILGECALALEKEYFNRKREEAVTKAKNEQLRANLLRSISHDLRTPLTSISGNADILLSEEIRLEQAKRRQLYTDIYEASMWLISLVENLLSITRIEDGTMNLNLQVELVDEVVEEALKHLTRKSTEHIITFQPSDEILAKMDSRLIMQVVINLVDNAVKYTPPGSRIEVTTEKKGEWVCVSVSDNGNGITDEMKEKIFDMFYTGTGQASDSRRGLGLGLFLVKAIIQAHGGTIRVKDGKTDGTIFTFRLKAEEVTLDEQTTDSCSGR	17~~DUF4118 (0.000000000014753 2)~~117;X;143~~GAF (0.00000123686)~~260;X;277~~HisKA (0.000000000006630 42)~~343;X;396~~HATPase_c (9.80572E-31)~~499	non-KdpD DUF4118 protein
	1E-05	35	10.7	1.7E-05	34.4	7.4	1.3	1	A1SHT9_NOCSJ	Histidine kinase (EC 2.7.13.3)	Noca_1864	Nocardioides sp. (strain BAA-499 / JS614)	371	196162	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Nocardioides, Nocardioides sp. (strain BAA-499 / JS614)	>tr|A1SHT9|A1SHT9_NOCSJ Histidine kinase OS=Nocardioides sp. (strain BAA-499 / JS614) GN=Noca_1864 PE=4 SV=1MVRRASTGVEMAGGTMVRGSLSLERRVVGYVLAAVGSAGLLALLVPLRVHLDLASEALLFLLLVVTTAIVGGLGPALLACVLCSAILNFFFTAPFHTFRIHEASDIVAVLVFAMVAVMVSWVVDLAARRASAVREAAELEAGNRLRTALLAAVGHDLRTPLATAKAVVSGLRSREVTLAEDDRHELLETADDALDRLADLIDDLLDLSRLQAGALPVRTRAVPVEDIVARALDDLGVVPRAVVLDLPEQVPEVLVDPALLERVIVNVVANAQRYAPGPPLITAAAVGDRLELRVIDRGPGIPTADRDRVFVPFQRLGDTGPAGLGLGLALSRGLVEAMGGRLVLEETAGGGLTLVISLPTASTAPPVQVTP	30~~DUF4118 (0.000000110507)~~129;X(131);260~~HATPase_c (8.04222E-24)~~358	non-KdpD DUF4118 protein
	1E-05	35	7.1	1.8E-05	34.3	4.9	1.3	1	F2R822_STRVP	Histidine kinase (EC 2.7.13.3)	SVEN_5545	Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	847	953739	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces venezuelae, Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	>tr|F2R822|F2R822_STRVP Histidine kinase OS=Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745) GN=SVEN_5545 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEGHRRVERGTDCVVAFVEHHGRPRTEVMLHGLEQVPRRTLEYRATTFTEMDIDAVLARRPAVALVDELAHTNVPGSRNPKRWQDVAELLAAGIDVISTVNIQHLESLGDVVEAITGVRQRETVPDEVVRRADQIELVDMSPEALRRRMAHGNVYTSDKVDAALSNYFRPGNLTALRELALLWTADRVDEYLQQYRGEHNIRSTWQARERIVVGLTGGPEGRTLIRRATRLAEKGAGGEVLAVYIARSDGLTAASPKELAVQRTLVEDLGGTFHHVIGDDIPSALLEFARGVNATQIVLGSSRRRTWQYVFGPGVGQTVARDSGPDLDVHIVTHGEVAKGRGLPVSRGARLGRSRIIGGWLAGVAGPLLLALLLTHVDADLGLANDMLLFLALTVAAALLGGFLPALASAAVGSLLLNWFFTPPIHRLTVADPKNIVAIAVFLGVAMSVASVVDLAARRTHQAARLRAESEVLSYLAGSVLRGETSLDALLERVRETFSMESVALLERQDEVEPWTRAASVGPHPAVRPEDADVDMPVGDHLALALSGRVLPAEDRRVLGAFAAQAAVVLDRQRLVGEAEEARKLAEGNKIRTSLLAAVSHDLRTPLAGIKASVSSLRSDDVEWSEQDRAELLEGIEAGADRLDHLVGNLLDMSRLQTGTVMPLIRTVDLDEVVPMALGGVPDGSAELDIPETLPMVEVDKGLLERAVANIVENAVKYSPDGVPVAVAASTLGDRVELRVVDRGPGVPDEAKDGIFEPFQRFGDAPRGSGVGLGLAVARGFVEAMGGTLGAEDTPGGGLTMVLTLKASRTGAPAPPDLPAHAVT	KdpD protein

	1E-05	35	5.4	2.1E-05	34.1	3.7	1.4	1	A0A059W4G8_STRA9	Histidine kinase (EC 2.7.13.3)	DC74_5947	Streptomyces albulus	851	68570	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	>tr|A0A059W4G8|A0A059W4G8_STRA9 Histidine kinase OS=Streptomyces albulus GN=DC74_5947 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDVVVAFVEHHGRPRTEVMLHGLEQVQRRELEYRGSTFTEMDVDAVLERKPAVALVDELAHTNVPGSRNGKRWQDVEELLEAGITVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQAIRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYRAEHSIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEVLAVYIARSDGLTSASPKELADQRTLVEDLGGTFHHVIGDDIPGALLEFARGVNATQIVLGSSRRKTWQYVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRSRIIAGWLVGVAGPVSLSLFLTKLSNGPGLANDVLLFLFLTVLAALLGGQLPALASAAVGSLLLNFYFTPPTHTLTVSDPKNIVAIAIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFGMDTVALLERRSDVDPWTCAGRAGGGDNTPPLARPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRQRLVGEAERARELAEGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVAWSEEDEAELLEGIEAGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVTLDIPEELPMVAVDPGLLERSVANLVENAVKYSPDGEVVLVSASALGDRVELRVADRGPGVPDSAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAVGGTLAAEDTPGGGMTMVLTMPAAAGLPPVRPDLPAQATT	1~~KdpD (1.31877E-123)~~211;X;233~~Usp(8.22103E-33)~~356;X;420~~DUF4118 (0.00000851277)~~466;X(150);616~~HisKA (0.000000000000167677)~~682;X;731~~HATPase_c (3.83192E-24)~~831	KdpD protein
	1E-05	34.9	14.5	1.9E-05	34.2	10	1.4	1	B8DIW1_DESVM	Multi-sensor hybrid histidine kinase (EC 2.7.13.3)	DvMF_2683	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	1358	883	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	>tr|B8DIW1|B8DIW1_DESVM Multi-sensor hybrid histidine kinase OS=Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637) GN=DvMF_2683 PE=4 SV=1MSAEPRPESSHPGSSPSPSPMVSDTPPGFASDVFSSAPPASLAFVASARGMLLALVLPLGTLALQWMLWDYIRPYVWFLFYPAVFLASLAGGLAGGLIATLLSALLVLYFFIPPVLSFMVVKPVDVVAVAMFLGIGLMISLAHQRVRDAVRRVVETQERQQAERVEADEATSRLRATNAELAARCARAEELDVLKTRFFANISHELRTPLTLLLGPLERLLAETSEDDEHRHSLFTMLRNARLLHQHVDDMLDLSRVDAGAMQPRHAEADLSALTRTTCAYFDTLAAQRGMHYGVQAPLRLDAQVDTDKYRRILLNLLSNSFKFTPDGGSVSVTLERQGDEALLSVSDDGPGVPAHLRGAVFERYRQSGEGARGLHGGSGLGLAIVKEFAELHGGTTSVGQGAEGGALFQVRLPLAAPPGVEVAPAESVAGSGSFAGDPGWLASGHVPQYAPAAGRDGGLVLVVEDNRDMIAYIVDILRPHHQVAVAFDGEEGLRKALDLRPDLIVCDVMMPRVDGQRMVEQLRRYPGMADVPVLMLTAKADDELRVHLLHGAVQGYIQKPFTAAGLLASVHAELRDRARHKAELDESETRFRATFEQAAMGLALVAPDGSWLRVNGKLCAIVGYSAEELTKLRFQDITHPEYLDSDLALMHRLLAGTIDNYSLEKQYLRKGGEPVWVNLTVALVRKADGTPDYFISVVEDIQQRKTFERRLAESEERFRQVVEHAPEAIFLQKEGRFAYANPAARVLFGVDDPKEIMGRGVLEFFHPDDRSMVVERIRQLNEERRTVPRGHVRIQRRDGTVVDAETSAVPFRLGGRHGALVFVRDISDRLWAERERIDLARFPGENPNPVMRVSPALVLLHANRSSGTFLECYGARVGSPFPAPFAEVVAESLRTWAPRTFEAQCLDRIYAMTVNPIADGGYANIYGMDITERKNAELELINAREVAETATKAKSAFLANMSHELRTPMNGVLGMLQLLDATPLDPEQRGYVQVAHAAGSNLTRLLGDLLDLARVESGRLTIREEPFDFNGLTQEVLAVLRPEADRKGIVLEAATDGMPGALLGDPQRIRQMLLNIVGNAVKFTDRGHVRLLARFEPSAGPSATAEPGGQGEPGGQGTLYLAVEDTGIGIPSDMLGNIFEPFTQVEDAVSRRHGGAGLGLSIVRRIVDLMEGEVSMTSEEGRGTTVTLRLPVAAMDRLPAQEPTRNGLADPPVRQGRLLLVEDDHVNRLTVLWMLEKLGYDALAVGDGAAALQALRQGRFDAVLMDVQMPVMDGLQATAAIRNATDLPGGAEVPVIALTAYAMEGDRERLLAAGMDDYVEKPVDVQALRRVLSRFVGEPDAPALSDASRLADVPDNP	51~~DUF4118 (0.000000000060729 4)~~141;X(170);311~~HATPase_c (9.37364E-19)~~413;X;462~~REC (2.12769E-24)~~573;X;599~~PAS (0.000000000126452)~~702;X;730~~PAS (0.000000000000325176)~~827;X(126);953~~HisKA (4.54998E-15)~~1015;X;1070~~HATPase_c (1.95747E-27)~~1191;X;1220~~REC (8.90351E-31)~~1335	non-KdpD DUF4118 protein
	1E-05	34.9	7.8	2.1E-05	34.1	5.4	1.4	1	A0A0A1CX93_9MICC	Histidine kinase (EC 2.7.13.3)	ART_2196	Arthrobacter sp. PAMC25486	845	1494608	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. PAMC25486	>tr|A0A0A1CX93|A0A0A1CX93_9MICC Histidine kinase OS=Arthrobacter sp. PAMC25486 GN=ART_2196 PE=4 SV=1MTRGILRIFLGSAPGVGKTYSMLEEGHAQAAAGVDVVAGVILDHGRAQTRAQLAGLESVPTQHLSYRGSDFQELDVAALLARRPALALVDEYAHSNIPGAGNAKRWQDVEELLAAGIDVYSTVNVQHLASLRDVVESITGVRQQETIPDDVVRRAEQIELVDIPPELLRQRLSTGHVYAADKVDAALANYFRLGNLTALRELALLWLADRVEEGVAAYRHSHGIAENWPTRERVVVGLSGGAEGEVLLRRAARILSRVSGGELLAVHVPRSDGVSGDAPSALEGQRQLVTDLGGSYHSVVGGEDPARALLDFARNAGATQIVIGSSRRKPRLGFLLGAGVGARVVRDAGDMDVHMVPHPHSAAGGVVRNRGELNRKRVVAGFALAVVLPVLVQLGTGPLSLQTTMVIQLAAAIGVALVGGLWPAILAAVWGSLLLNYFSAPPVGNLTINDPENLLALLVFLVVAVAVALAVDQSARRSREAVQAGAEAATLSELARGILASQDTVQVFLEQVRDHFGMRSVALFATAAPPGTWHLAASVGEEPPQNPAAADTVEEVSDHWVLGLSGRILPARDRRLLSAFGAHLLALEQREALSETQREQVQLSQDNNIRTSVLRAVSHDLRTPLAGIKLAVSSLRQTEVTFSPEDEAELLATIEHVYSDRMDALVGNLLDMSRLSAQMVRPVAGPVTWQEVLPGALHGVPSERVRRELPPNMPPIEADPGLLERVIANIVENAVKYAPDSDILVVGSVGGSGSATINGRPASELRVIDHGRGVPAAEVMAMFRPFQRLDDVSYGPHGGSGVGLGLAVAKGFTEIMGGVLEAEQTPGGGLTMTIRMPLSTGIVRTLP	3~~KdpD (8.21449E-106)~~211;X;233~~Usp(2.12514E-25)~~356;X;377~~DUF4118 (0.00026007 1)~~452;X(154);606~~HisKA (0.000000000007678)~~672;X;721~~HATPase_c (2.7726E-17)~~833	KdpD protein
	1E-05	34.8	6.4	2.2E-05	34	4.4	1.4	1	B0RCI0_CLAMS	Histidine kinase (EC 2.7.13.3)	CMS0459	Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	798	31964	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Clavibacter, Clavibacter michiganensis, Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) (Corynebacterium sepedonicum)	>tr|B0RCI0|B0RCI0_CLAMS Histidine kinase OS=Clavibacter michiganensis subsp. sepedonicus (strain ATCC 33113 / DSM 20744 / JCM 9667 / LMG 2889 / C-1) GN=CMS0459 PE=4 SV=1MLEGLEILPRREVSHRGVEITDLDVDAVIARRPTIALVDELAHTNAPGGRYKKRWQDVDLIRDAGIDVISTVNIQHIASLNDVVEKITGVPQRETIPDRVLREAHQIEVIDLAPKALRDRLAGGRVYPAERIDAALSHYFRLGNLTALRELALLWLADEVDTALAAYRDEKGIDARWEARERVVVALTGGPEGETLLRRGARIAARSAGGELMAVHVSSQDGLRSGSPEALASQRALVDSLGGSYHQVVGDDIPRALVEFARASNATQLVLGVSRRSRLAAAATGPGIGATVIRESGDIDVHIVTHAAAGGRFRLPRVRGGALSMRRRILGGVLALGGGPLLTWLLSATRSDDSITSDVLSYQLLVVLVALVGGIWPALFAAVLSGFTLDYFFIDPLYTITVDEPLHLLALVLYVVIALLVSWIVDQATRRTRLARLAVAEAELLATVSGSVLRGEGAVHALVSRTREAFGLQGVKLVDRDETIAWDGVVTGAAATDVPVGSRGVLTLYGDDLEASGRRLLRVIAAQLDAALEHRDLSDTAREVGPLAQTDRVRTALLSAVSHDLRRPLSAATAAVSALRSPGMTWADGDREELLATAEESLGTLADLVTDLLDVSRVQAGVLGVRLMDVDLDDVVLAALDELDLGPADAVLDLAPDLPGAVADPGLLERVVVNLLSNAVRHAPDGVPVRLSTSAFADAVEIRVVDHGPGVAPERRDDMFVPFQRLGDTDNASGLGLGLALSKGFTEGMGGTLTAEDTPGGGLTMVVALPACRADAPVPEPAEPALADPDTDSEQVSA	1~~KdpD (2.75422E-83)~~160;X;182~~Usp(1.10163E-31)~~305;X;374~~DUF4118 (0.00000238363)~~431;X(120);551~~HisKA (0.00000000304836)~~617;X;668~~HATPase_c (4.29213E-26)~~769	KdpD protein

	1E-05	34.7	10.4	2.8E-05	33.7	7.2	1.5	1	D2ATK3_STRRD	Histidine kinase (EC 2.7.13.3)	Sros_3803	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	846	479432	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	>tr|D2ATK3|D2ATK3_STRRD Histidine kinase OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_3803 PE=4 SV=1MSRARGRLRVYLGAAPGVGKTFAMLDEGHRRLARGTDVVVGLVEAHGRPRTAELADGMEVVPRRTVIYRETAFTELDVDAVIARGPKVALIDELAHTNVPGSRNAKRWQDIEEILDAGIDVVSTVNIQHLESLNDVVRQITEVPQRETVPDEVVRRADAVQLVDMPPDGLRRRMAHGNIYAPEKVDAALSNYFRVGNLTALRELALLWVAGEVDEQLDQYRAEHGIEGTWEARERVVVALTGGPEGDTLIRRAARIAARTKGADLLAVHVTLSDGLGGADPARLARQRALVENLGGTYHQVVGENVPRALLDFAGGVNATQLVLGASRRGRLAHLFSRGVGLTATALSGSIDVHMIPHAEAGKGARRIRPGAALTRTRRLAGWAMALLGIPVLTAALVPFRADLTLPNGILLFLLMVVGVALAGGMWPAVTAAVAGFLLLNYFFTPPFDRFTVSDPHNLLALSVYVLVAVMVSAVVDLAARRTREAARASADAEVLSTLAGHVLRGESALPSLLARLRETFALTSVTLLERVGEPAPDDQSEPGAWRIVATSGGPPCGCPGAADTDVVIDGSLVLAACGRLLEASDRRVLEAFAAEAAVALRQERLRREADLAGPLAEADRMRTALLAAVSHDLRTPLASARLAVESLRGTEIEWSAEDRAELLATADESLIKLDRLVANLLDMSRLQAGVLGLTLQPVALEEVIPRSIDDLGPLRDRVEGDVSVDLPEILADSALLERILVNVMSNAVRYSPAGKKVLITASRHGDHVEIRVVDRGPGIPAEAHDRVFMPFQRLGDRDNHTGVGLGLALSRGLAEAMGGTLTPEETPGGGLTMVLTLPTSSGARP	4~~KdpD (3.66E-118)~~213;X;235~~Usp(1.70276E-18)~~357;X;383~~DUF4118 (0.000000000370931)~~477;X(143);620~~HisKA (0.000000000005770 82)~~686;X;737~~HATPase_c (3.35861E-28)~~838	KdpD protein
	1E-05	34.7	14.2	5.1E-05	32.8	9	2.1	1	R2QA65_9ENTE	Histidine kinase (EC 2.7.13.3)	UAW_02560	Enterococcus haemoperoxidus ATCC BAA-382	890	1158608	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus haemoperoxidus, Enterococcus haemoperoxidus ATCC BAA-382	>tr|R2QA65|R2QA65_9ENTE Histidine kinase OS=Enterococcus haemoperoxidus ATCC BAA-382 GN=UAW_02560 PE=4 SV=1MERQVEEERLDPEQLLAKWKKNEQSLRSGRLKVFFGYAAGVGKTYAMLKEAHEQQAEGKNVLIGYVEPHARPETQTLVNGLPTLSTKTYEYKGIQINEFDVDAALKEKPDIILVDELAHTNAIGARNRKRYQDIEELLKAGIDVYTTVNVQHIESLNDVVEQVTGIHISETVPDTFFETSSLKVVDIETDELLDRLKQGKIYHSENARKAMANFFTSDNLTLLRGLAIRKASDHINTTNQQETQKSTGIHSKLLTIIDEKNPDMTKKCLRWTARLAQALGAEWIALEILEDTSEHTESENSKLATKLGGEVVTLESDNQRETIIQYVKMRGVTDLVMGKIIKRSRFLRLYRPDLEDELVAFIPDVDIHLVPYQSSKYLLNKYATKKKNLKSIFTWQDFYMTCGLLTVATILSEFGSYFHIGDQNLILIYILFVLLVARLTTGYLWAALASIASVLMFNWFFVEPLYSLTVYKQGYPVTLIFMLLVALLVSNLMMQIKKQAFYAMKREHQLEILYELNKKYLVTHDQKEILATTAEYLSNMLDREVVLYGEEELKNPTGAPIKGPLRSLEELAVANWVFVNQKEAGYGTDTLMGAKALYLPVLSNGVTLAVIGIEKSKEDPITDEIITFIELISTQLSLAIEQNNLTLERQQILFENEKERMRGNLLRAISHDLRTPLTGISGSVETVLDDHEATKLPEETKRKLLVGIKEDADWLIRMVENLLSITRINEETMKVAKSKEAAEEVVSSAIQRIKKSYPSESISVTLPDEFILVPMDSILIEQVLFNLMENAIRHSNCHSPIFVSVTATAKEVTFEVADQGKGLTGEQIKLLFDGMSKQNTPVDSKSGMGIGLSIVKTIIMAHDGTLNAGNRPQGGAVFTFTLPLERKEQK	27~~KdpD (3.87747E-108)~~235;X;262~~Usp(3.96288E-25)~~371;X;405~~DUF4118 (0.000000000000453902)~~499;X;525~~GAF (0.000000000123694)~~641;X;659~~HisKA (0.000000000011554)~~727;X;780~~HATPase_c (5.70492E-23)~~882	KdpD protein
	1E-05	34.7	14	2.8E-05	33.7	9.7	1.5	1	R5C547_9FIRM	Uncharacterized protein	BN499_00280	Blautia hydrogenotrophica CAG:147	516	1263061	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	>tr|R5C547|R5C547_9FIRM Uncharacterized protein OS=Blautia hydrogenotrophica CAG:147 GN=BN499_00280 PE=4 SV=1MKERVPDTVFDSADQVKIIDIEPETLIQRLQEGKIYKSIQAERALNNFFAKEKLISLREIALRRTADRVNRIAIEESKMYRDKKYYTGEHVLTCISPSPTCAKVIRSASRLAYAFHANFTALYVETPDLQNADRKVKKMVEENMHLAEALGAKIATVFGEDIPFQIAEYAKICSASKLVLGRTNHKIWLGQKKGTLTDQITQYIPNMDIYIIPDTSNRAERWAVPKDVAKHKKEEKNGSLFLDLIRGVATLGIATVVSLGVEQVGFMSANIIIIYLFAILMLSLYSRRRWVSAVAALLSVFLFNFFFVPPIYSFAVHAPAYYTTFVFMFLFAFIISTIITSERKQAKESAKFAYRTELLLENSKRMRRVHTVRALLKELSNQVLKLMNLSVIFFVKKDNKMTGPWLFPRVGMDKAQLRDMLDDQERAVVQWVLENKKRAGCCTHTLPGAQAMYLPIKSGDEIYAVMGIVLEEKREIPPFEYGLLTAMLNEAALVFARIYMTNNNVEEQKGDQKTVR	2~~KdpD (3.14383E-30)~~69;X;90~~Usp(6.57176E-34)~~213;X;248~~DUF4118 (0.000000000000663217)~~345;X;371~~GAF (0.000000184807)~~497	KdpD protein
	1E-05	34.7	11.5	2.4E-05	33.9	8	1.4	1	B5ECD6_GEOBB	Histidine kinase (EC 2.7.13.3)	Gbem_0535	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	554	404380	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	>tr|B5ECD6|B5ECD6_GEOBB Histidine kinase OS=Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622) GN=Gbem_0535 PE=4 SV=1MWVLASFFPLAALALQWLLWERLRPYVWLFFYPAVFLSSWAGGRVAGLLATAFSATVVWYFFIPPEQSFSLEHPSTAIALLIFAGMGILFSLFHERLRRADRQIRLTLAEATSGREQLERRMEERTKELVDLVDELRRKETDLRRSQELLKLFIEYAPVPLAMFDSEMRYLYASRRWRSDYGLGNRPLVKVSHYEIFPEIPQHWKELHQRGLAGEILREEAEEFRRADGTVQWLRWELRPWYDAGGMVGGIVIFSEDITNRKCAEDALQKLNEELELRVVQRTETLDQILGEREAQNAELQRAYHELEAETAQRIRMVEELRQKEQLLIHQSRLAAMGEMLGYIAHQWRQPLNVLGLHLQVLGLSYQHGTFTRELLEQSVEKAMGIIRHLSRTIDDFRDFLVLNKEKTLFQVDEVVVKTVGLIEENLKKAGINIEVACTNPPEVNGFPNEYSHVILNLLTNAKDAFSERQTEHPVIRVHSGFEQGKTVVTIGDNAGGIPEEIIGKIFDAYFTTKGLGKGSGVGLFMSKMIIEKNMGGSLTVRNVNGGAEFKIEV	23~~DUF4118 (0.000000000323715)~~100;X;157~~PAS (0.00000019611)~~258;X;334~~HisKA (0.0000491647)~~400;X;453~~HATPase_c (6.87208E-17)~~554	non-KdpD DUF4118 protein
	1E-05	34.6	8	2.1E-05	34.1	5.5	1.2	1	R6R887_9CLOT	Histidine kinase (EC 2.7.13.3)	BN719_00963	Clostridium sp. CAG:58	356	1262824	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	>tr|R6R887|R6R887_9CLOT Histidine kinase OS=Clostridium sp. CAG:58 GN=BN719_00963 PE=4 SV=1MKQHTVIKNSLITAGILGAATGFCFLIQEAAESDTHVPLLFVLAVLFISRFTDGYIYGIVASMIAVVGVNYVFTYPYFAIDFTITGYPVTFIAMLAVACSVSALTTQIKKQEQIRLEAEKEKMRGNLLRAVSHDIRTPLTSIMGAASVVLENYGELSDEKRMDFLKDIREESQWLIQIVENLLSITRIGDNGGSASIDKQEEMVEEIVGSAVLKFRKRYPDVEVAVRLPEDPLLVPMDGILIEQVLVNLMENSVLHGKHTSKVEVSAEEEKDRVVFYVDDDGAGIRPSALPKLFEGTFRQGDEESCDSRRNMGIGLSVCMSIIRAHQGDMKAENRKEGGARLSFWLPMERGTDQWR	11~~DUF4118 (0.000000000460564)~~111;X;121~~HisKA (4.52825E-14)~~187;X;242~~HATPase_c (2.25184E-21)~~346	non-KdpD DUF4118 protein
	1E-05	34.6	7.1	2.3E-05	33.9	4.9	1.3	1	I4DAD7_DESAJ	Histidine kinase (EC 2.7.13.3)	Desaci_3883	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	390	646529	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	>tr|I4DAD7|I4DAD7_DESAJ Histidine kinase OS=Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4) GN=Desaci_3883 PE=4 SV=1MLNHEFPNQNQARTLFDLIAIGLIVAILTAIHYTNYHYETNYHILLQFAYYLPVIYAAMRFGPTGGILSGLLITLLILPFMTHFHAMNPSAIYTQWVEICLINVIGWLTGFLTGQERRAKRKYHIALTVQKELVEKLKQEGSERERLEGEIRQTERLTALGHMSAGLAHEIRNPLGIMKVSIQLLAQEKSDDGVVSEYCRVMLEECERLNRLVSEFLTFARPREPVRELVTLGKLLDEGVTLIQPALRQHNIELMQARSQVNDQEVEVDPDQMKQVILNILLNAIDAQREGGVIRLEGVQQKGFVGFVVSDEGPGILPDAMPYIYDPFFTTKEKGTGLGLSVVHRILDQHGGKISAENRRERGVQLEILLPLSSERGMHEAITISGLRSR	15~~DUF4118 (0.0000026322)~~119;X;157~~HisKA (0.000000000000285269)~~221;X;273~~HATPase_c (1.08239E-22)~~370	non-KdpD DUF4118 protein

	2E-05	34.5	12.5	0.00003	33.5	8.7	1.4	1	Q0SHD3_RHOJR	Histidine kinase (EC 2.7.13.3)	kdpD RHA1_ro01229	Rhodococcus jostii (strain RHA1)	845	101510	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus jostii, Rhodococcus jostii (strain RHA1)	>tr|Q0SHD3|Q0SHD3_RHOJR Histidine kinase OS=Rhodococcus jostii (strain RHA1) GN=kdpD PE=4 SV=1MSGTGTDGERRDAEHRRGELRIYLGAAPGVGKTFAMLGEAHRRRERGCDVVAAVVETHGRDRTAAQLGDLELVPPKLIAYRGTLGRELDVEAVLARRPALVLVDELAHTNTPGSVHEKRWQDVEILLAAGIDVLSTLNVQHLESLNDVVQRITGVVQQETVPDEVVRAATQVELVDITPEALRRRLSHGNIYAADKVDAALSNYFRKGNLTALRELALLWVADQVDAALAKYRAENKITDTWEARERVVVAVTGGLESETLVRRAGRIASRSSAELIVVHVVRGDGLAGVSAPEMGKVRTLAASIGASLHSVVGDDVPTTLLDFARTANATQLVLGTSRRSRWARIFDEGIGASVLHQSGSIDVHMVTHGESHRPRRRLSPVGSRSRTAIAWIAAVLVPSVATLVMSAVDRWLGLVGEGALFFIVVLLVSLLGGVAPAAFSALISGLFLNYFFTPPVRSFTIAEPDNFITTVVLLVVAVAVAVLVDAAAKRSREARRASQEAELLALFAGSVLRGADLGTLLEKVRETYGQDSVSVLHRDRGPVGSVGPHPPVSVDDADTVCEVGEGEYALALRGSELHARDRRVLLAVANQAVGMIRQTELAQEAGQAQALAEADRLRRSLLSAVSHDLRTPLAAVKAAASSLRSDDVDFSPEDTAELLATIEESADVLTSLVGNLLDSSRLAAGVVTPTLRPVYLDEVVHRALVGLGIGGRTGTRARERVEVDVGTVAAMADSGLLERVLANLIDNALRYGEDSVIRVGAAAVGDRAVVTVADTGPGIPRGRADEMFAPFQRLGDRDTTTGVGLGLSVVRGFVDAMGGTISATDTPGGGLTMVVELAGAGGAHP	15~~KdpD (7.87507E-117)~~225;X;247~~Usp(2.05392E-31)~~368;X;390~~DUF4118 (0.000000022426)~~469;X(146);615~~HisKA (0.000000000000566735)~~681;X;737~~HATPase_c (6.37608E-27)~~837	KdpD protein
	2E-05	34.4	6.8	1.7E-05	34.4	4.7	2.3	1	A5HYN4_CLOBH	Histidine kinase (EC 2.7.13.3)	CBO0340	Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	617	441771	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium botulinum, Clostridium botulinum A, Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A)	>tr|A5HYN4|A5HYN4_CLOBH Histidine kinase OS=Clostridium botulinum (strain Hall / ATCC 3502 / NCTC 13319 / Type A) GN=CBO0340 PE=4 SV=1MSEINKSREKNIYSITCTVKLASLLFSSIILYNYVSQNNCASKNSYYNVLLPMILSLITSLIYLIWSFFTVKTRMFKNILFIQRIENIFFILIFTILIIMSGKYNSHYKYLFLFIIITTTIQRGLKSGMIISSVIILTIDLSMANYNCINTYFENDLILSGVFILTAVSLGYYVKLGNESIKEKNIQLEDLNKKLNEKDSQRKYIEELLFKNDTCYNLLIENARDAIIIHRKDKIVFANESAAELLICSNNNELQNLNINSFILKEEQKKIRNKLELVYRNKRDIVCVEQVIQNNKRKKINVESISTYIIYNNKPAILSILRDITSQKQVEKLQKDVEKNIELLNESREYNKLITDFLANISHELKTPLNVIFTAVQILDLYKKDAESYDKKEQYIKVIKQNCYRLMRLINNLLDTTKLDSGYLKLNLVNCNIVNLVEEITLSVVYYAESKNINIIFDTDVEEKIMAVDPDKIERIVLNLLSNAIKFTGSGGNIYVTVKDFEDNIIISVKDTGIGIPRDKIENIFDRFVQVDKTLRRNKEGSGIGLYLVKSFVNMHEGTIDIQSEIGKGSEFIINIPVKLVKEDLEKENNVFYSPSKEYVDMEFADIYSEVSSK	100~~DUF4118 (0.000578579)~~177;X(177);354~~HisKA (0.000000000000124008)~~421;X;476~~HATPase_c (5.04225E-31)~~579	non-KdpD DUF4118 protein
	2E-05	34.4	12	2.7E-05	33.7	8.3	1.3	1	R6I910_9FIRM	Histidine kinase (EC 2.7.13.3)	BN556_00506	Firmicutes bacterium CAG:240	359	1263013	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:240	>tr|R6I910|R6I910_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:240 GN=BN556_00506 PE=4 SV=1MEKKLTQNKVFRTIRNWLILAAALTAAWVLCSSLSTVGTSDTFVPMIFILAVLIVSLTTDGYFYGIVTSLASVIGVNYAFTFPYMKLNFSIYGYPVTFVTMLAVSLVISTLTTRAREQEKLRHEAAQAKLRADLLRAISHDLRTPLTSIIGSIDTVLNEGDHLSSDERNVLLSDAKQDAEWLVRMVENLLSITRISGTEQTHIEKSPELVEEILGECLANFKKRNPETNLKVTIPDEPVLVNVDAMLIAQVIMNLLDNAAKHASGMTELRLDVTLDGKWVHFTVSDNGSGIDPKILPVLFRGQIDPEKGKPYDSNRFRGIGLAACQAIVSAHGGKISASNRPEGGAVFDFSLPAEEEEE	42~~DUF4118 (0.000000000050799 6)~~118;X;129~~HisKA (0.000000000008993 56)~~194;X;248~~HATPase_c (3.43937E-25)~~352	non-KdpD DUF4118 protein
	2E-05	34.3	12	3.4E-05	33.4	8.3	1.5	1	A0A0A8DVX1_9XANT	Histidine kinase (EC 2.7.13.3)	SB85_09135	Xanthomonas sacchari	892	56458	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas sacchari	>tr|A0A0A8DVX1|A0A0A8DVX1_9XANT Histidine kinase OS=Xanthomonas sacchari GN=SB85_09135 PE=4 SV=1MPDPRTQQADALIGELQRERGGRLTVFLGAAPGVGKTYAMLSRARQLQQQGSNLVVGVVETHGRAETAALLEGLTVQPRRRLEYRGRTLDEMDLDALLALRPPLVLVDELAHRNAPGSRHERRWQDVQELLDAGIDVYSTVNIQHLESLNDVVHRITGVRVSETVPDAIFDRLRDIVLVDLPPRELIERLQQGKVYLPEQAGQALQAFFSPSNLAALRELAMQTAADRVDNDLRDVQAAQGRTSVALRRTVMVAIDGRGQSDYLVRVARRLAERRGAPWTVVTVQTQAQPDADWQLEIDRAFALARRLGGEAALLHGANVADALLDHAARSGVSTLVLGRTRERPLARMINRTLTQQLLQRGAHYELVIISSPEARARARRRWRSPAHWLSRDDLLFATVASALAVVVAWIAESWVGIDDLSMVFIVAVVMVASKTRMTAAVLAALLSFFSYNFFFIEPRFTFQIGARQGVVTVLLFLVAALVAGRLASRLRMQVLALRAVNAQTTALQRLGRELTSAADLGQVLEAGRRALAGTLDAEAWLRLQPLERAHDGADDYAPTMAAVDRSAADWAQRHGQATGRFTDTLAGASWWFLPVRHERGTIGVVGLRFGAGVQRPGLEQQQRLAEAMVEDIGQAALRTRLVADLESARVSGETERLRSALLSSVSHDLRSPLAAMIGAASSLSSYGKAMDAEDRRSLLDTIQMEGERLDRYIQNLLDMTRLGHTGLTLNRDWIGVDELIGSAARRLQRYQPQVRLDIALAAELPTLWVHPALVEQAIFNVLENAAKFSPADAAIRVAAGMVEGRLRIDISDRGPGPIEDERARIFDMFYSVERGDRGRHGTGLGLTICQGMIGAHGGSVEALPGPDGRGTTIRITLPLIEPAAPPSRPDAD	19~~KdpD (8.97406E-121)~~229;X;251~~Usp(1.44693E-30)~~371;X;423~~DUF4118 (0.00000000360435)~~492;X;520~~GAF (0.000113705)~~635;X;655~~HisKA (0.000000000039361 6)~~721;X;775~~HATPase_c (2.05774E-23)~~877	KdpD protein
	2E-05	34.3	9.9	0.00003	33.6	6.9	1.3	1	C1ABQ3_GEMAT	Histidine kinase (EC 2.7.13.3)	GAU_2888	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	378	379066	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	>tr|C1ABQ3|C1ABQ3_GEMAT Histidine kinase OS=Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505) GN=GAU_2888 PE=4 SV=1MHARETRELNDHRRSGRAAWLVSILALLLATLALHQVRDALDKAHVALVLLLVVLGGSAAGGRVLGVVLALAGFVVFDLFFLPPFNTLVVADPLDWLVLVVFLATGVVAAQLLTRAQREADEARRRSEEVAALTAQAQTDAAHAAALREADQLKDALLATVSHDLRTPLTTIRGLAHDIVRDGDDRALAIEEEVERLNRLVTDLLDLSRLKAGGVPLALALNTADELMGATLQRVSGAATGRDIRASLDPNEPLLVGTFDLTHSVRILGNLLENALKYAPDNAPIDFTVVREGPMLAFRVADRGPGIADEERERIFTPFHRATSARPDVGSVGLGLAIARGLADAQGGSLQVTPRDGGGSVFTLHLPAADLIDTFETR	58~~DUF4118 (0.0000115839)~~119;X;151~~HisKA (0.000000000000571495)~~209;X;266~~HATPase_c (7.135E-27)~~366	non-KdpD DUF4118 protein
	2E-05	34.2	12.2	3.1E-05	33.5	8.5	1.3	1	I2EQY1_EMTOG	Histidine kinase (EC 2.7.13.3)	Emtol_0933	Emticicia oligotrophica (strain DSM 17448 / GPTSA100-15)	364	929562	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Emticicia, Emticicia oligotrophica, Emticicia oligotrophica (strain DSM 17448 / GPTSA100-15)	>tr|I2EQY1|I2EQY1_EMTOG Histidine kinase OS=Emticicia oligotrophica (strain DSM 17448 / GPTSA100-15) GN=Emtol_0933 PE=4 SV=1MKDILTKKYTQGNSAYLISIIIVCLISAICYPFSDLIGYRTVALILLFTVSVLAMKLSLYPVLLSAVLSAFIWDFFFIPPHFTFHVSKSEDVLMLAMYFIIVMLNGVLTARIKHFESLAIQREERVNALKLYDTLFNSISHEFRTPIATILGATDNLLTDNSKFSETNKINLYQEINTAADRLNRLVGNLLNVSRLESGSIRPKLDWYDLTELIHTAINQLETELKFHEVKVEMPPNLPFLKLDFGLLEQAIYNILYNCSIYTPEKTLIHISADYVNEKCIIKIQDNGKGFPKGDLSQVFTKFYRSKNTQTGGLGLGLSITKGFIEAHGGTIKVGNRAGSGALFTIEIPTKANWGDDFSGGFLQ	15~~DUF4118 (0.00000000109339)~~113;X;129~~HisKA (0.00000000031132)~~195;X;248~~HATPase_c (5.6513E-25)~~348	non-KdpD DUF4118 protein

	2E-05	34.2	8.3	3.4E-05	33.4	5.7	1.4	1	L8EQ10_STRRM	Histidine kinase (EC 2.7.13.3)	SRIM_19057	Streptomyces rimosus subsp. rimosus ATCC 10970	855	1265868	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rimosus, Streptomyces rimosus subsp. rimosus, Streptomyces rimosus subsp. rimosus ATCC 10970	>tr|L8EQ10|L8EQ10_STRRM Histidine kinase OS=Streptomyces rimosus subsp. rimosus ATCC 10970 GN=SRIM_19057 PE=4 SV=1MARGKLRIYLGAAPGVGKTYSMLSEAHRRVERGTDVVVAFVEHHDRPRTEVMLHGLEQIERVELEYRGSVFTEMDVDAVLRRDPAVALVDELAHTNVPGSRNAKRWQDVEELLEAGIDVISTVNVQHLESLGDVVESITGVRQRETVPDEIVRRADQIELVDMSPEAIRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRAEHSVSKIWAGRERIVVGLTGGPEGRTLIRRASRMAAKGSGSEVLAVYIARSDGLTSASPKELAVQRTLVEDLGGTFHHVIGDDIPNALLEFARGVNATQIVLGSSRRKAWQYVFGPGVGATVARDSGPDLDVHIVTHDEVAKGRGLPVARGARLGRARIIAGWLLGVAGPVLLSLLLAALDNGPGLANDVLLFLFLTVAAALIGGLLPALAAAAVGSLLLNFYFTPPTHSITIADPKNIVAIVIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFGMESVALLERTGDVAPWTCAGRVGGTAEGDPKAKPLMRPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRQRLVGEAERARELAEGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVAWSEDDEAELLAGIEAGADRLDHLVGNLLDMSRLQTGTVTPLIRDIDLDEVVPMALGGVPEGSVTLDIPEELPIVAVDPGLLERCVANLVENGVKYSPDGERVLVSASALGDRVELRIADRGPGVPDSAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLAAEDTPGGGMTMVLTLRAAAGRPPVRPDLPAQATT	1~~KdpD (1.49188E-122)~~211;X;233~~Usp(1.08924E-30)~~356;X(264);620~~HisKA (0.000000000000363911)~~686;X;735~~HATPase_c (5.41491E-25)~~836	KdpD protein
	2E-05	34.2	9.3	2.9E-05	33.6	6.4	1.3	1	U2SY24_9FIRM	Histidine kinase (EC 2.7.13.3)	HMPREF1546_00512	Oscillibacter sp. KLE 1745	360	1226323	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	>tr|U2SY24|U2SY24_9FIRM Histidine kinase OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_00512 PE=4 SV=1MKITRSSLKRTFSFSWRDLLVSAAILLCATGACALLHQTADTIDGFASPVYVLAVLLISRFTSGYLFGLIAAVLGVIGVNYVFTYPYMAFNFTISGYPLTMFTFLVVSLVTSTLTTKTKEQDRLRMENEKVKMRADLLRSVSHDIRTPLTSIMGATSAILENPALSPAEQQSLLVDVRDDAQWLIRVVENLLSITRIGNESAKITKEPEAAEEVLDEAVRKFRKRFPAVSVEVHVPDELLLVPMDAILIMQVLSNLMENAVFHGGTTTHIALSAQRDGPWARFYVQDNGQGIPPQKLHTLFSGALRCEDSSPGDGKRNMGLGLSVCMAIIRAHGGTLEAKNLESGAEFSFCLPLTKEEVS	19~~DUF4118 (0.000000000969236)~~121;X;132~~HisKA (0.000000000001224 8)~~196;X;249~~HATPase_c (5.88944E-23)~~352	non-KdpD DUF4118 protein
	2E-05	34.2	10.1	3.9E-05	33.2	7	1.5	1	K9QKL1_9NOSO	Multi-sensor hybrid histidine kinase	Nos7107_5425	Nostoc sp. PCC 7107	1170	317936	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	>tr|K9QKL1|K9QKL1_9NOSO Multi-sensor hybrid histidine kinase OS=Nostoc sp. PCC 7107 GN=Nos7107_5425 PE=4 SV=1MSKIQRSYLQRYYVSVLSVLIALLLGLMLDSLLKLEVSPLFFAAVVLSSWYGGLAPGLLATVLAVLVNNYFFIPPIYSLIPDTWTDALQLIVFSLISLLISSLNSELHIAKQKSEAKLAKLTVSYRSLLETAYEGIWIFDQDGQTEYVNSQLAQMLGYSAEQMRDRTIFDFMEHETQIEIQQWLEQNQQHHQESKQQLEVGLRRQDAAELWVIVSLSSILNEQGKFAGMVAMLTDITERKHSETILAEEQANRDRESQLLRAMLDILPVGVVISDAKGKFIEINPAIKAIWGENAPFLDNTSQYHEYKGWRADTGQPIAAEEWTLARVLATGETIIGEEIDIESFDGQRKTILNSVVPIRDETGVIIHAVAVNVDITERKQAEEKLRQSEALAKARAEELETIMETVPAAVWIAHDPQCNQMTVNRSAYKLMRLQPGSIMTATPVSGDYTFPFKIQKNGQDVPPNELPMQQAGLTGQEVEGEFEFVFGEDDVQFLYGKAVPLRDYSGTVRGVIGAFIDITERKQAEEVLRQKEEWLDLAQTVGKIGSFEWNILTNVNIWSKELEAIYGLQPSEFGGTYEDWKNLVHPDDVAIADTYIANSLKTGEFFTDFRVVWPNGSIHWLHARAKVYYDREGKPLRMVGVNVDISDRKQAEAALRQSESRLRQLLESSIIGIIEAEPDKITFANDAFLQMLGYTQADILAGNLGWQKMTPPEYNQLDQAKVEEVFVSGVCTPFEKEYIRKDGSRVPILLGATLLTRSPFRWVCFILDLTELKQAERERAQALERERAARIELERANRMKDDFLAIVSHELRSPLNPILGWAKLLKSRRLDAAKTTQALETIERNAKLQARLIEDLLDVSRILRGKLSLNICAVDLVTTIESALETVRLAAETKSIHLHTEFAIGKVKVEGDPNRLQQIIWNLLTNAVKFTPEGGRVELRLEKVGNFAQIQVTDTGKGISAEFLPFVFDRFRQADEVTTRKFGGLGLGLAIVRHLVELHGGSVQVTSPGENLGATFTVHLPLMAATTEILIEYPLIENAPNLQGVQIVIVDDDVDTLNLLTFILEQYGATVQAVNSAQDALKAIAQTQPDLLLSDIGMPTMDGYMLIEQVRSTTSASILPAIALTAFAGEANSQKIISAGFQRHLTKPIEPAELAAVIANLMRMSKNDK	40~~DUF4118 (0.00000130359)~~93;X;132~~PAS (2.08522E-14)~~236;X(310);546~~PAS (0.000000648087)~~646;X;670~~PAS (0.000000000165799)~~770;X;798~~HisKA (6.2638E-15)~~862;X;917~~HATPase_c (1.10778E-32)~~1021;X;1050~~REC (4.79921E-26)~~1163	non-KdpD DUF4118 protein
	2E-05	34.2	8.7	3.4E-05	33.4	6	1.4	1	A1TED5_MYCVP	Histidine kinase (EC 2.7.13.3)	Mvan_4762	Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	850	350058	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium vanbaalenii, Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	>tr|A1TED5|A1TED5_MYCVP Histidine kinase OS=Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1) GN=Mvan_4762 PE=4 SV=1MDDESVAASPHKAKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDVVAAVVETHGRKKTAELFEGIEIVPPKLIAYRGSDFAELDVEAVLRRNPQVVLVDELAHTNTPGSKNTKRWQDIEELLDAGITVITTVNVQHLESLNDVVTQITGIEQQEKVPDEVVRAADQVELVDITPEALRRRLAHGNVYAPERVDAALSNYFRRGNLTALRELALLWLADQVDSALEKYRADNKITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVVQGDGLSGVSGPQMGKVRELAASIGATLHTVVGDGAGGVPAALLDFAREMNATQLVLGTSRRSRWARIFDEGIGATVVQKSGRIDVHMVTHEQAGGESLWARVSPRQRHAVSWLAALAVPGAICAATVLLLDRFLGIGGESAMFFIGVLVVALLGGVAPAALSAVLSGVLLNFFLVEPRHTFTISEPDSAITIVVLLVVAVAVAALVDGAANRTRESRRAAREAELLALFAGAVLRGADLNTLLERVREAYSQQSVTLVRGEAHGGGVVGCAGSEPCVTVETADTAIEVGSKDDPEEFWLLLAGRRLDARDRRVLGAVANQAAGLARQRELAEEAGRAEAIARADELRRSLLSAVSHDLRTPLAAAKAAVSSLRSEDVGFSPEDTAELLATVEESIDQLSSGLVGNLLDSSRLAAGVVRPELQPVYLEEAVPRALLGISRGSTGLRAGLDRVKVEVGDTVVMADSGLLERVLANVIDNALRYAPDGPVRVTAGRVADRVLIAVADEGPGVARGAETELFAPFQRLGDQDTSSGVGLGLSVARGFVEAMGGTISATDTPGGGMTVEIDLAAPR	13~~KdpD (1.49548E120)~~223;X;245~~Usp(7.55268E-31)~~369;X;392~~DUF4118 (0.0000000384976)~~472;X(152);624~~HisKA (0.000000000027794)~~690;X;746~~HATPase_c (5.63078E-24)~~846	KdpD protein
	2E-05	34.1	6.9	4.3E-05	33	4.8	1.6	1	A0A089KU75_9BACL	Histidine kinase (EC 2.7.13.3)	R70331_15305	Paenibacillus sp. FSL R7-0331	893	1536773	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. FSL R7-0331	>tr|A0A089KU75|A0A089KU75_9BACL Histidine kinase OS=Paenibacillus sp. FSL R7-0331 GN=R70331_15305 PE=4 SV=1MAQHSIQTKKRGRLKIFFGYAEGVGKTSAMLNAAHDELRDGTDVVAGFIESHGRPETGVLLNGLEQLPVLELRSNPSSRQELEFNLDQALRRRPELILVDELAHYNAAGCRHKKRYQDIEELLRAGINVYTTINVQHIESLHDVVTAITGITVHERIPDSVFDGADQIELVDLPPDDLLERLNKGKLASEGLAEPGGPAAYLPVFVRTKLIALREIALRYTADQQERITRESGSRSGKDTYSTADHILVCLSSAASSKKVIRTAARMAEAFRGSFTALYVETPKSKELTAKSKAELRDNLRLAEQLGAQPATVYGDDVAGQIAEYAVSSRVTKIVIGRSRSGKKRWIAKGNLIDKLTELAPNIDIHIIPDNQPARHKRPFLFVRPQRFSLPDTLKTLGILAVCTLIGLWFQYLGFREANMIIVYILGVLLNAIVTSGRLYSAANSVLSVLVFNYLFTEPYYSLWAADSGYPVTFLVMLTASFISSTLTTRIKEQARQNAQKAYRTEVLLETSRILQQAEDAEAIINETAVQMVKLVDRTVIFYPAGQEGLADPLVYPKPEADLDPSKYTGMNEWAVADWVYKNNKRAGATTDTFSAASCLYHAVRAGETVFAVAAVVMDQEEPLGIFEKSLLIAMLGECALALEKEQLSNTQKEISIQIRQEQLRANLLRGISHDLRTPLTSISGNAGILMANSNVLSDAQLRGLYTDIYDDSMWLINLVENLLSITRIDNGSLNLNFQAELLDEVIAEALLHVNRSSVEHNIQVKLEDELLMARMDSRLIIQVLINLVDNAIKYTQTRSTITITAGQEQQTVRVSVADDGPGISEEAKAKLFEMFYTADNLRGDGRRGLGLGLSLCKSIVHAHGGTIEVMDNNPQGAVFTFTLQAEEVNVLE	9~~KdpD (1.94657E-96)~~224;X;246~~Usp(2.57694E-42)~~369;X;394~~DUF4118 (0.000000000020388 7)~~494;X(168);662~~HisKA (0.000000000648977)~~728;X;781~~HATPase_c (2.54355E-20)~~884	KdpD protein

	2E-05	34.1	8.2	3.9E-05	33.2	5.7	1.4	1	A0A0F5VG60_9GAMM	Histidine kinase	KY46_04840	Photobacterium halotolerans	889	265726	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	>tr|A0A0F5VG60|A0A0F5VG60_9GAMM Histidine kinase OS=Photobacterium halotolerans GN=KY46_04840 PE=4 SV=1MTDNTARSQQADALLSKLKQEEKGKLTVFLGAAPGVGKTYAMLSAAKERLQQGADVVVGLVETHGREETEAMLVELEVMPRKEIGYHNTYLTEFDLDSALERRPELILVDELAHTNVPGSRHKRRYQDVDELLSAGIDVYTTVNIQHLVSLNDLVMQITGVRVRETVPDSFIDDAYDIRFIDLPPVNLVERLQQGKVYLPEYARLAMDTFFSISNLTALRELAMKRVIEQVDAHLINELEAKSEKADFILKDKLLVLISTNSDHSYLIRIGRQIADRRQIPWTVVWVDTGKTQDLQRRKRLNDAMVMAKELGASAEVLRGSSTYRSILPFLNEHRHNTVLVGAGTRRQFLWQRKRLYQQLIESGLPVEVSVYRAPEQLKMPKEPELRLSPLGDKKGHIFGIVSTAVATVFALLLQQVLSSGNLVLLYVIAILAVGLKFGARPALATAIWSFLSFNFFLTAPTFTFKVHSQDDVATLIFLVCIGLISGPAASRIRNQFILLKESNQYAETLRELAQELSVADDENALWKSVNRHIERAVHVKCYSVMAGKDDHKQFVPLLLTPLKHIDHSAIDWVFQHGRTAGRFTDTLSASQMTVIPVLQEKKVIAVVALCWDKSQTQFNPFEQELVHAMLQQASSTWQRIHLVSDLESARVKTEVEQIRSALLSSVSHDLKSPLSAMMGAAESLRVFDKQLNEQDRFDLLDTILQESRRLDSYIQNLLDMTKLGHGTLKIERDWVSVDDIIGSALSRLKRYFPSVKVDYIRHNEPPLLYVHAALIEQALFNILENAVRYSPEEEPITIVMDTTQNQCRVSIEDQGPGIPKAAQKEIFNMFYVVSDGDQKKONTGMGLAICKGMISAHGGKVRAVDGAGGRGTRIEVELPLDYPNMKOE	21~~KdpD (2.00234E-116)~~231;X;253~~Usp(7.69666E-15)~~369;X;401~~DUF4118 (0.000000000036597 4)~~496;X(161);657~~HisKA (0.000000000001405 56)~~723;X;776~~HATPase_c (7.70108E-24)~~879	KdpD protein
	2E-05	34.1	7.2	2.1E-05	34.1	5	1.6	1	R5JHY9_9FIRM	Histidine kinase (EC 2.7.13.3)	BN781_00700	Coprococcus sp. CAG:782	899	1262863	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, environmental samples, Coprococcus sp. CAG:782	>tr|R5JHY9|R5JHY9_9FIRM Histidine kinase OS=Coprococcus sp. CAG:782 GN=BN781_00700 PE=4 SV=1MSESRHNPDQLLKEIQADEEKRNKGHLKIFFGYAAGVGKTYAMLEAAHMEKQQGIDVVVGYVEPHACPKTAALLNGLEVLPTREVFYNGMILDEFDIGMALKRKPQLILVDELAHTNAEGCRHAKRYQDIEELLNAGIDVYTTVNVQHIESLCDTVASITEIVVRERIPDSIFDNADQVELIDIEPQDLINRLNTGNVYRQTQEKQAVENFFTIENLTALREISLRRCADRVNILTENTRIKNHGDYHTGEHILVCLSSSPSNAKIIRTAAKMASAFKGEFTALFVETPDFSVMSEENVKRLRSNICLAEQLGAKIETVYGEDVPFQIAEFTRLSGVSKIVIGRSSATKRHLLSKPTLTEKLIDYAPNLDVHIIPDAVSNAAVYQLRGGRKKTHIVFSVTDTLKSTAILILSSLVGMIFQKFGFDEANIITVFVLAVLVTAVITKHQIYSLISSIVSVLVFSFLFTEPQFTLQAYDQGYPVTFIIMLLAAFLTSSLAIRIKNQAKQAAQSAYRTKVLFDTNQLLQQAKDKNEIVSATSNQLIKLLRRDIVFYLADGEVLDTPHIFSVTEENLESCISENEKAVAGWVLKNNKRAGATTGTLSNAKCLYLAVHSSSMVYGVIGIVMGEIPLDPFENSILLSILGECALALENEKNAREKQEAAILAKNEQLRANLLRAISHDLRTPLTSISGNASNLLSNGDYFDNDTKKQLYMDIYDDSMWLINLVENLLAVTRIEEGRLNLRITEDLMDDVITEALHHINRKSEEHHISVESKEEFLLAKMDAKLIVQVIINIVDNAIKYTPKNSHIVIRTEKRGKQAIVSISDDGNGIADEIKPRIFDMFYSGANQIADSRRSLGLGLSLCKSIINAHGGELTVSDNLPHGTVFTFTLPAGEVKIYE	23~~KdpD (1.54788E-119)~~232;X;252~~Usp(5.64904E-37)~~375;X;403~~DUF4118 (0.000000000028856 3)~~503;X(165);668~~HisKA (0.000000000346235)~~734;X;787~~HATPase_c (6.60057E-28)~~890	KdpD protein
	2E-05	34.1	11.2	3.3E-05	33.4	7.7	1.3	1	R5GWY6_9FIRM	Histidine kinase (EC 2.7.13.3)	BN555_01598	Firmicutes bacterium CAG:24	353	1263012	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:24	>tr|R5GWY6|R5GWY6_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:24 GN=BN555_01598 PE=4 SV=1MKNRQRQKDILFSILIFCSAFAVNLLIQKLFTTQTLVPMIFVFGVFLISLKTHGYCYGIISAIVSVFAVNFAFTYPYYAFDFFVEESILSAVIMLVVAISTSTLNIRIRDQEKLRSENEKERMRGNLLRAISHDLRTPLTSIYGSSSTLISKYDALPKEQQLKLLGEIQEDSEWLIRMVENLLSVTRIDGAKVEVVKTPTVLDELIDSVLMKFSKKHPSQKVITQIPDEFVDIPMDSLLIEQVLLNLLENAVFHAKGMTKLMLSVSLAGDKAVFEVADNGCGIPEDALQKIFTGSYEKNAAPVDGTRSNMGIGLSVCAAIVKAHGSDITAKNKSGGGAVFSFALEREGEDDGQ	10~~DUF4118 (0.000000000059047 3)~~111;X;121~~HisKA (0.000000000000268 294)~~187;X;240~~HATPase_c (5.83383E-24)~~344	non-KdpD DUF4118 protein
	2E-05	34	9.4	3.8E-05	33.3	6.5	1.4	1	Q24N66_DESHY	Histidine kinase (EC 2.7.13.3)	DSY4737	Desulfitobacterium hafniense (strain Y51)	505	138119	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfitobacterium, Desulfitobacterium hafniense (Desulfitobacterium frappieri), Desulfitobacterium hafniense (strain Y51)	>tr|Q24N66|Q24N66_DESHY Histidine kinase OS=Desulfitobacterium hafniense (strain Y51) GN=DSY4737 PE=4 SV=1MKSSWTDTFKTIGLLTAATLFSMGLRALAIGEQNVIMVYILSVFIISRTTNGYIYGSVGSALSVLLFNFFFTTPYYTFHVIQADYPVTLLIMLLVASLTSALTIRAGSQAQLALEREHRTELLYEISKQLLVTRGLDKIIHLINHYMIKLFERSAIFYAQDPGTSQGVLRQSPAEADASFMLAEDERAAAQWAFLHKAQAGLGSDTPMDSQGFYVPVIAQGKVLGVIGLSCAQGELNTAGRSLLQVITSQVALALERQRHLSDEQRRLFVESEKEKMRSNLLRAISHDLRTPLTAILGASSALLENRQTLDEPTQQQLLANIKEDSQWLIRMVENLLSVTRIREGTMNVAKTAEAAEEIVAAAVSRIRKRFPQQRIKVEVPEELLLVPMDGTLIEQVLINLIENAIKHSPENAAIEVNVKKLEKEALFEVIDYGTGIPEQNFPYLFESYVPNGKRSADSARGMGIGLSICMSIVKAHHGKMEAANKKAGGATFRFTLPLEGTDLEQ	9~~DUF4118 (0.000000000951333)~~103;X;136~~GAF (0.00000002488)~~257;X;274~~HisKA (9.55181E-14)~~340;X;393~~HATPase_c (1.17567E-26)~~496	non-KdpD DUF4118 protein
	2E-05	34	10.3	3.6E-05	33.3	7.2	1.3	1	R7KU16_9FIRM	Histidine kinase (EC 2.7.13.3)	BN622_01191	Ruminococcus sp. CAG:353	357	1262955	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:353	>tr|R7KU16|R7KU16_9FIRM Histidine kinase OS=Ruminococcus sp. CAG:353 GN=BN622_01191 PE=4 SV=1MQKFGLKKQLGALPERKDYILTLAVLAVACVLSGLLVNFDGSSYVQLIFVLAVAVISRFTNGYLCGLISSLLGMFAVNYAFTYPYFKLNFSITGYPVTFATMLLVTVIIGMLTSQLKEQSRVWAEMEKEKTRGNLLRAVSHDIRTPLTSISGAASAILENKDKLDEQGMMSLVTDIKEDAEWLIRMVENILTVTRISEETGTISKTPEAAEEIISEAVMKFRRRYDVPVEITIPDELMLIPMDAILIEQVIVNLLENSVLHGKTTTLIKLTLSSDGENAVFSVADNGSGINEKKLPMLFSGYFIHAEEQSGDVKRNMGIGLSVCLTIIKAHGGTMTAGNLPEGGAEFTFTLPLERAL	20~~DUF4118 (0.000000000344302)~~119;X;129~~HisKA (0.000000000000637 829)~~195;X;247~~HATPase_c (2.10126E-21)~~351	non-KdpD DUF4118 protein
	2E-05	34	5.5	3.5E-05	33.4	3.8	1.3	1	A0A0F2S5R2_9FIRM	Kinase	VR66_26655	Peptococcaceae bacterium BRH_c23	374	1629714	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c23	>tr|A0A0F2S5R2|A0A0F2S5R2_9FIRM Kinase OS=Peptococcaceae bacterium BRH_c23 GN=VR66_26655 PE=4 SV=1MLNNEPPAQNRARTLFDLIAIGLVVAILTIIHYTNYHYEVDYHILLQFAYYLPVIYAAMRFGPAGGIISSFVITLLFLPLMTHFQHTMTPAAKYTQWVEVGLINVIGWLTGFLTEEERKAKRKYQRALTVQKELVEKLKREGQERERLEGEIRQTERVIALGHMSAGLAHEIRNPLGIMKVSIQMLAQEKSDDGVVTEYCRVLLEECERLNRLMSEFLTFARPKELVRERIPVGKLLDEEVSLIQPTLWQKNIELEQARNSIDRQEVEVDPDQMKQVILNILLNAIDAQGEGGVIHLEGVQQDGLVGFAVSDEGPGISPDAMPYIYDPFFTTKEKGTGLGLSVVHRILDQHGGKISATNRSKRGVRVEILLPSV	18~~DUF4118 (0.000000902038)~~120;X;160~~HisKA (0.000000000001098 24)~~222;X;274~~HATPase_c (2.26797E-24)~~371	non-KdpD DUF4118 protein

	2E-05	34	7.2	3.7E-05	33.3	5	1.3	1	A0A0F2JC11_9FIRM	Two-component sensor PilS	UF75_3099	Desulfosporosinus sp. I2	374	1617025	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	>tr|A0A0F2JC11|A0A0F2JC11_9FIRM Two-component sensor PilS OS=Desulfosporosinus sp. I2 GN=UF75_3099 PE=4 SV=1MLNHEPSAQNRARTLFDLIAIGIVVVILTVIHYTNYHYEMNYHILLQFAYYLPVIYAAMRFGPAGGIISGLVITILILPLMMSFQAMSPSAMYTQWVEIGLINVIGWLTGFLTEQERKASRKHQLALLVQTQLVEKLKQEGQERERLEGEIRQTERLTALGHMSAGLAHEIRNPLGIMKVSIQLLAQEKVDDRVVSEYCRVLLEECERLNRLVSEFLSFARPKEPVRGGIALGKLLDEGVSLIQPALGQHHIELKQARSQVDEQVVEVDPDQIKQVILNILLNAIDAQGEGGVIKLEGVRQVGFVGFAVSDDGSGISPDDMPYIYDPFFTTKERGTGLGLSVVHSILDQHGGKISTTNRTDGGVRVEILLPSFK	15~~DUF4118 (0.0000235718)~~119;X;157~~HisKA (0.000000000002436)~~221;X;273~~HATPase_c (3.09079E-23)~~370	non-KdpD DUF4118 protein
	3E-05	33.8	9.9	3.9E-05	33.2	6.9	1.3	1	R6TTT2_9FIRM	Histidine kinase (EC 2.7.13.3)	BN503_00594	Oscillibacter sp. CAG:155	363	1262910	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, environmental samples, Oscillibacter sp. CAG:155	>tr|R6TTT2|R6TTT2_9FIRM Histidine kinase OS=Oscillibacter sp. CAG:155 GN=BN503_00594 PE=4 SV=1MSASPNRPSRLFTFSWKNFLISAGILACAVVLCMLLSMADSRDGFASPIFVLAVLLISRFTDGYLFGLIASVLGVIGVNFIFTYPYWAFNFKITGYPLTFLTLLMVSVITSTLTTQAKQQEQLRVENEKEKMRANLLRSVSHDIRTPLTSIMGATSTILENPGLTQDEQRELLEDAHDEAQWLIRVVENLLSITRISDTQTAQITKEPEAAEEVLGEAVRKFRKRFQQIKVTVEAPDTLLLVPMDPILIEQVLSNLMENAAIHGETTTQVRVSVQKEGAFACFSVWNDGQHIPARELPTLFDGTIKHSDTAPGDGKRNMGLGLSVCMAIVGAHGGTMEAKNLDVGVEFTFRLPLSEEEFDEHP	10~~DUF4118 (0.00000000013966)~~120;X;130~~HisKA (9.98991E-15)~~195;X;249~~HATPase_c (3.66796E-20)~~352	non-KdpD DUF4118 protein
	3E-05	33.8	5.4	4.6E-05	33	3.7	1.4	1	A0A0A8EGX6_9ACTN	Histidine kinase (EC 2.7.13.3)	GZL_02853	Streptomyces sp. 769	851	1262452	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	>tr|A0A0A8EGX6|A0A0A8EGX6_9ACTN Histidine kinase OS=Streptomyces sp. 769 GN=GZL_02853 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDVVVAFVEHHGRPRTEVMLHGLEQVQRRELEYRGSTFTEMDVDAVLERKPAVALVDELAHTNVPGSRNGKRWQDVEELLEAGITVISTVNIQHLESLGDVVESITGVRQRETVPDEIVRRADQIELVDMSPQAIRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRAEHSIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEVLAVYIARSDGLTSASPKELAVQRTLVEDLGGTFHHVIGDDIPGALLEFARGVNATQIVLGSSSRRKTWQYMFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRSRIIAGWLIGVGGPVLLSLLLTRLSNGPGLANDVLLFLFLTVVAALLGGQLPALASAAVGSLLLNFYFTPPTHTLTVNDPKNIVAIAIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFGMDAVVLLERRSEVEPWTCAGRAGGEGGVSPLARPEDADVDVPVGDHMALALTGRVLPAEDRRVLSAFAAQAAVVLDRQRLVGEAERARELAEGNRIRTALLAAVSHDLRTPLAGIKASVTSLRSDDVAWSEEDEAELLEGIEAGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVTLDIPEELPMVAVDPGLLERSVANLVENAVKYSPDGEAVLVAASALGDRVELRIADRGPGVPDSAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAIGGTLAAEDTPGGGMTMVLTLPTAAGVPPVRPDLPAQATT	1~~KdpD (6.9447E-123)~~211;X;233~~Usp(1.35226E-32)~~356;X;402~~DUF4118 (0.000000264815)~~466;X(150);616~~HisKA (0.000000000001629916)~~682;X;731~~HATPase_c (7.47401E-24)~~832	KdpD protein
	3E-05	33.8	2.1	4.2E-05	33.1	1.5	1.3	1	R7BMC1_9FIRM	Uncharacterized protein	BN803_00847	Firmicutes bacterium CAG:882	696	1262991	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:882	>tr|R7BMC1|R7BMC1_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:882 GN=BN803_00847 PE=4 SV=1MEVDILFAGNTMAVSDEFYEYVGKEYRMVVLKNESAKEKQRKKNLLFFRNTCEEDTERIFRTFDFETVVFFSQVLDGEKKIFDELEKLEYILYLCRKKKVKSFMYITGNRGAVDEENGEASRVILLNACEQLCRKAADNDGINVQLIRVPYLYHCVIKSSHVGRWLGAAISQGKVELPGYQDTMTDFVREDDLAELIGRIFDDPWNGSYLETRISGRNKLTFRQLADMLKAFAAPGGNVEVIYTGKDECTPTYQEDSWARNEYGWIPKGNIEADLKEAAGRYIKERERKHRGIIKRLYSNRLVRIATEQTALCAAVEALNYVTRGNVMFNFLDFRLVYIAIMACMNGLGAGAAAALISCAGYIASNVSAVSWEVIFFNIENWFPFACYMLLGCVLGYTTDKAQDEIKSKTNELELLKEKYEFLHGLYMEAAEGKERFNNQIIGYKDSFGKMYSVAKKLNTTLPEKVFFEAIDTMEEILGNSYAAVYSVTPGSAYARLYVCSKRCTGKATRSLKITDYPEVYEALKNKVTFINRQAKEGYPAYASPICRGGELVGMILILEADYSQMNMEFYNKLRMMSDMIQDSLVRAMEFYEMNDNVMENTRILEPDSFEKVLGVKRQMRKRQYLDYVMLKIDSCGQNLSEQNDRLSGLVRENDVLGVRKDGNLYLLLTQTGVKDIKTVADRLKKNNIVFEEVRE	88~~NADB_Rossmann (0.000666579)~~197;X(111);308~~DUF4118 (0.000502521)~~405;X;463~~GAF (0.00000000108121)~~587	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	3E-05	33.8	7	5.1E-05	32.8	4.8	1.5	1	E4NDZ4_KITSK	Histidine kinase (EC 2.7.13.3)	kdpD2KSE_36210	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM 6054) (Streptomyces setae)	857	452652	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Kitasatospora, Kitasatospora setae, Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	>tr|E4NDZ4|E4NDZ4_KITSK Histidine kinase OS=Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) GN=kdpD2 PE=4 SV=1MPADPRPRPHPEDRRPGRLRVYLGAAPGVGKTYRMLDEAHRRRERGTDVVVGWLDTHDRPRTARLLDGLEQLPRATREYRGAEFAELDLDGLLARRPELALVDELAHTNVPGGRHAKRWQDVEELLAAGIDVVTTVNIQHLESLNDVVQKITGVPQRETVPDEVVRRADQIELVDMAPQALRRRLAHGNVYRAEQVDAALAHYFRIGNLTALRELALLWLAGRVDEGLRDYRAAHRIDRVWETRERVVVALTGGPEGVTLIRRAARISDRAAGGELLAVHVSRSDGLAGASPGRLAEQRRLVESLGGSYHSVVGDDIPEALLAFARARDATQLVLGTSRRGRLNRFLTGPGIGETTVDRSEDIDVHMVTHAFTGRGRLPPLGRRHSRRRTRSGYAAGLAVPVMLTAALSQAHHALNLTTDALILQLGVVAVALLGGAVSALLASLAASLLLNYYFIPPVHTFTIGEANNFIALAVFAAVALCVSTVVDHAGRQTARAARATAEAETLSTLAGSVLRGADAVPALLERTRTSFGLDTVTLLDRATGRALDAVESPVESPAESPAESPDTTATADPVHTTDLPVGPDALLRLTGRRLPDTDQRVLAAFGAHLAAALERDRLATAAAEVEPIRAADRMRTALLAAVSHDLRTPLAAALASVGSLRSPDVDFSAEDRAELLTLADESLHRLTRLVDNLLDLSRLQAGALTPHLRPTHLDEVLPAALDALATPDAPVRSAVTEAVPPVLADPPLLERVLANVLANALRHNPPGAPVLVTASAHADRVEIRVVDRGPGIPPEDRDRVFLPFQRLGDTDNTTGTGLGLALSRGLAEAMGGTLTAEDTPGGGTTMLLTLRAAETP	15~~KdpD (1.40408E-115)~~224;X;246~~Usp(3.29128E-30)~~369;X(264);633~~HisKA (0.000000000032169999)~~699;X;750~~HATPase_c (2.30218E-31)~~851	KdpD protein
	3E-05	33.7	4.4	3.9E-05	33.2	3.1	1.2	1	D2YRA7_VIBMI	Histidine kinase (EC 2.7.13.3)	VMD_22630	Vibrio mimicus VM573	339	671076	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio mimicus, Vibrio mimicus VM573	>tr|D2YRA7|D2YRA7_VIBMI Histidine kinase OS=Vibrio mimicus VM573 GN=VMD_22630 PE=4 SV=1MRWLHRRHLLPVLVFFTAMFVSLGIDQSLGSTIAVLLILQLSIVIIALQCHSRMAYFAAVAEALSFNFLFTDPRYSLRMFHQDDMINLVVFVAVAFTTSQLAERYRRQQNALKQMRLRHQILLSVSHDLRTPLAGIIGNLTTIKEYSAQLNEAEKNELLDSAITESHRLHQYIENLLQATKLQHGVVRINKAQESILHILKNVIERFSSSSERVSVDVKGSVKLLEVSRALLEQALFNVLDNALRYSPKDKAVRVTVEQNHDQVVIDIYNQGQPLKPDEAENMFELFYSGGEKKSADSGSGLGLSVAKGVISAHQGTIECIDVEQQGCLIRITLPSGQQG	12~~DUF4118 (0.0000000101034)~~108;X;115~~HisKA (0.000000000985407)~~181;X;232~~HATPase_c (1.93857E-20)~~333	non-KdpD DUF4118 protein

	3E-05	33.7	9.4	4.7E-05	32.9	6.5	1.4	1	B2HPR8_MYCMM	Histidine kinase (EC 2.7.13.3)	kdpD MMAR_0634	Mycobacterium marinum (strain ATCC BAA-535 / M)	839	216594	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium marinum, Mycobacterium marinum (strain ATCC BAA-535 / M)	>tr|B2HPR8|B2HPR8_MYCMM Histidine kinase OS=Mycobacterium marinum (strain ATCC BAA-535 / M) GN=kdpD PE=4 SV=1MTPDYPRKRGELRIYLGAAPGVGKTFAMLGEAQRRLERGTDVVAAVVETHGRKRTAELLEGIERIPPKFIEY RGSRFAELDVEAVLRRQPQVVLVDELAHTNTPGSKNPKRWQDVEELLDAGITVISTVNVQHLESLNDVVAQITGIE QQEKVPDEIVRAAEQVELVDITPEALRRRLAHGNVYAAERVDAALANYFRTGNLTALRELALLWLADQVDAALEKY RADKKITATWEARERVVVAVTGGPESETLVRRAFRIASKASAELMVVHLARGDGLSGVAAPQMGKVRELAASLGA TVHTVVGDDVPTALLDFAREMNATQLVLGTSRRSRWARVLDEGIGATVVQQSGPIDVHMVTHQEAGRPARWSW LWPREHHLVSWLAAVVVPSLICALTVAWLDRFLAVGGESALFVIGVLVVALLGGVAPAALSAVLSGLLLNYFLIEPR YTFTIADPDNAVTTLVLLVVAVAVAALVDNAAKRSREAGRASREAELLALFAGSVLRGADLEALLEKVRETYSQRAV SILRIEAGTSQGAIVSCVGEDPCVDVDTADTAIDVGDDEFWMLMAGRKLLARDRRVLTAVAKQAAGLIKQRELADE AGKAQAIEQADQLRRALLSAVSHDLRTPLAAAKAAVSSLRSDDVDFSADDMGELLATIEESVDQLTALVGNLLDSS RLAAGVVRPQLRRVVLEETVQRALLGISRGATGYGRSGLDRVKVEVGGAVAIADAGLLERVLANLIDNGLRYAPDS PVRVYAGRVGDRVLINVADEGPGIPRGAEEQMFAPFQRLGDRDNRIGVGLGLSVAKGFVEAMGGTISATDTPGG GLTVVVDLAAA	8~~KdpD (1.47146E-119)~~217;X;239~~Usp(1.04886E-34)~~360;X;383~~DUF4118 (0.000000326348)~~459;X(154);613~~HisKA (0.000000000001097 33)~~679;X;736~~HATPase_c (1.48738E-25)~~836	KdpD protein
	3E-05	33.7	4.4	5.2E-05	32.8	3	1.4	1	R7AJL4_9BACE	Uncharacterized protein	BN656_02123	Bacteroides pectinophilus CAG:437	720	1263051	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides pectinophilus CAG:437	>tr|R7AJL4|R7AJL4_9BACE Uncharacterized protein OS=Bacteroides pectinophilus CAG:437 GN=BN656_02123 PE=4 SV=1MKVLLIGDANRITGAIADKLNKEGHRVFALMSSKRTHYRHVYEKYIFEYDNTCMKDVFESIMPDLTIFSGAYD DSFDWNGLEDAQVAYTAALGNMLAAYSRLGRGRFVYLSSEEVYRADMTQASQENAAVIKARSVRQGETTCANY RIATGMDIIVARAENICFVPKNAQEVRDVCSRACVEMLEDGQIHCPGTDVSLLALPDAVWFLYNIFTAEKCRYPVYT VTTNSHISYSDMIDMINAAFGRRVHVVYDDSENVIWVEELEVHDYAEEFTFAIFSGTKECAEAVIKAVNKNPGRYIT KKAEQLGRSQQIAASLKSILKTFVPFIENMICFIPFFMINNRAVGSQFFGKLDSYLLYVLLFAIIYGQQQATFSAILAVA GYCFRQMYTKSGLEVIVDYNTYVWIAQLVILGLAVGYLRDRLVVLKRDKDDEIEYLKHRLRDIEEINRTNVKLKNEM ERQIVNQSDSMGKIYEITSSLDKYEPEEVLFYAAEVVSRLMESRDVAIYTVSNENFARLISFTSKTARQLGNSIEFRS YKNMYEDFAADRVFVNRRLEEGLPMMALAIRSEGVMKLIVMLWDIPFERMNLSMANRLKIIGSLTQNSVVRADRY MSILAGQRYISGTHILEKDAFTSLAGAFVNARRRGLAECSFIKVDAGDGGIAKAGESLERIIRNTDYMGDAGDGCLY IMLASTDADGMRYVEHRIDEAGYQYEIPEEMGA	1~~NADB_Rossmann (0.000000718036)~~205;X(120);325~~DUF4118 (0.000000000002786 55)~~422;X;482~~GAF (0.000000000000661 328)~~606	non-KdpD DUF4118 protein
	3E-05	33.7	9.3	5.1E-05	32.8	6.4	1.4	1	D9T8N8_MICAI	Histidine kinase (EC 2.7.13.3)	Micau_0598	Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	848	644283	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Micromonospora, Micromonospora aurantiaca, Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	>tr|D9T8N8|D9T8N8_MICAI Histidine kinase OS=Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442) GN=Micau_0598 PE=4 SV=1MGRGELRIYLGAAPGVGKTYAVLEEAQRRAERGTDVVIGLVETHGRRHTAEMVGDLEVVPRRSMTYRGVE FTEMDLDAVLARRPEVVVVDELAHTNVPGSRHEKRWQDVQELLDAGISVLSTVNVQHLESLNDVVAQITGTTQRE TVPDQVVRAAEQVELVDMTPEALRRRMAHGNIYRPDKIDAALGNYFRVGNLTALRELALLWLADKVDEQLDAYRA QQGISDTWEARERVVVALTGGPEGETLIRRAARIAARSKGADLLAVHVARSDGLAGADPAQLARQRVLVESLGGT YHQVLGTDIPAALLDFARGVNATQLVLGASRRGRFAQVFSRGVGVTTTALSGPIDVHLVTHPEAGRGRRGTSVPA ALSRRRRLIGYALAVLGMPLLTLVLRTLPDLTLNTDILLFLAGVVGVALVGGLWPALVAALGGSLLLNWFFTPPYRTL TIAEADNLLALGVFVGVAIAVSWVVDVAARRTREAARASADAQTLATVAGSVLRGERPLPALLDRLRETFGLRAVS VLELTDEAGGRPARARGADAWRVVASVGERPPGSPGAGETVVPVDDRLSVVLAGRRLEAADRRVVEAFAAQAA VALRQERLAEEAATARPLAAADRMRTALLAAVSHDLRTPLASAKAAVSSLRSHDVEFDADDREELLATADESLDRL GRLVANLLDMSRLQAGALGVSATAIGLEDAVPLALDELGPAAAEVTTDIPADLPAALADPGLLERVLVNIVANALRH SPPGRPPAITGSAHAGQVELRVIDTGPGIPEDQWEHVFLPFQRLGDRDNQTGVGLGLALSRGLAEAMGGSITPET TPGGGLTMVLRLPAATQPEGPQE	1~~KdpD (3.08596E-119)~~211;X;233~~Usp(2.1901E-20)~~355;X;424~~DUF4118 (0.000117754)~~475;X(144);619~~HisKA (0.000000000000745 247)~~685;X;736~~HATPase_c (6.74021E-26)~~837	KdpD protein
	3E-05	33.5	16.1	5.7E-05	32.7	11.1	1.4	1	B2IXP2_NOSP7	Multi-sensor hybrid histidine kinase	Npun_R3083	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	701	63737	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	>tr|B2IXP2|B2IXP2_NOSP7 Multi-sensor hybrid histidine kinase OS=Nostoc punctiforme (strain ATCC 29133 / PCC 73102) GN=Npun_R3083 PE=4 SV=1MWGLTRRSQLQGYGIAFLTVLLALLLTLLLWQLHRLNSIYPLFLAAVMVSSWYGGLNPGLLATFLSAIVCAYF LLPPFYSLAITGFSVVGLLQFVLVALLISLLNTALRQARSQAQMNAVAALQNYERLRESQDSLRQSEERYRLLVEGV TNYAIFMLDPNGNVTTWNIGAERILGYQEAEIIGQPFERVFSPEAIKQGLPKQVLRKAVAEGFSRENRWHIRKDGT FFWAHCLITPLLDDDGNLRGFSKIMQDITERKQAEEEKEQLLLREQAARAVSEAAQSAAEAANRSKDEFLAIVSHE LRTPMTAIIGWAGMLQTGVLDEAKATLALEIIERNANLQMQLIEDLLDISRIVRGELSLSIDLVDLVEVITAAIEVVQSL ANAKDIQLETILDTSIEKIWGDSDRLQQVVLNLLTNAIKFTPNGGRVEVRLSKEMGSREEFSQPAIPNYLQIEVTDTG KGISPDFLPHVFERFWQADSTHTRSNKGLGLGLAIALHLVELHGGTIDAQSQGIGQGATFTVKLPILEESRGAALRL RSVTEEQGSRGAGDNNLHFFSQSPAPNPQSPVPNPLSGLRVLVVDDEADVRQWITAVLEECGAEVSAFSSTGQA LEALEKLHPDVLISDIGMPGEDGYALMRKIRKLEPELGGRIPAIALTGYARVEDYKEALAAGFQLHVAKPVRAAELIA VVASLGKMSGKL	36~~DUF4118 (0.000000193868)~~111;X;151~~PAS (2.68309E-14)~~254;X;289~~HisKA (9.37979E-16)~~353;X;408~~HATPase_c (1.07693E-29)~~524;X;579~~REC (4.90494E-27)~~694	non-KdpD DUF4118 protein
	3E-05	33.5	7.5	5.2E-05	32.8	5.2	1.3	1	E4RK43_HALHG	Diguanylate phosphodiesterase	Halsa_1164	Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	557	656519	cellular organisms, Bacteria, Firmicutes, Clostridia, Halanaerobiales, Halanaerobiaceae, Halanaerobium, Halanaerobium hydrogeniformans (Halanaerobium sp. (strain sapolanicus))	>tr|E4RK43|E4RK43_HALHG Diguanylate phosphodiesterase OS=Halanaerobium hydrogeniformans GN=Halsa_1164 PE=4 SV=1MIIIKTDFFAYNKLKTFKNHSKALQGFLLIFILLIGALVYYTGGTRNSYAHLIYLPIVLSGYFYGLKGGITAAVISGL VLGPFMPIDTETMLMQQPQNWLFRMVFLIIIGSFVGYLFANLERQVIKNRKIAYFNQETGLPNKSTLKNVIDNKIDNK KEFHLFILTINNLLNIYKLTGFSNFTDYMDLLIEHIKQYPALGKQIYYINENHYGIILDKDKVDDLVEFSNDFLKYLDKPV NFGNISIYNNFTMGITTYPDYAKKTDKIINQAFLSIKKAKNKKLPFWHYENINFKEKNINLDLLAEINNSIENNNFEIYY QPKINLKNNKVQTFEALLRWNHPGKGYISPGDFIPLVEKSSLIEPLTEWVINEVLKDISNFKAKNNSFKYDIAINISAR NLQQPNFVELLIDYLKQYNVNPERFSIELTETDLMVEIDKNIKKLNQLKEKGINIYLDDFGKGYSSLKYLKEIPIDFIKID QYFIKNLTKEKKSLDIVRSIIELAHALNIEVVAEGVETEAQLEVLKDINCNYAQGYLFAKPDKKEKIIEFLKELEAESYA	28~~DUF4118 (0.0000000327993)~~123;X(190);313~~EAL (1.00397E-103)~~538	non-KdpD DUF4118 protein

	3E-05	33.4	9.9	5.7E-05	32.7	6.8	1.4	1	S0LFX1_ENTAV	Sensor histidine kinase KdpD	OMU_00613	Enterococcus avium ATCC 14025	853	1140002	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus avium (Streptococcus avium), Enterococcus avium ATCC 14025	>tr|S0LFX1|S0LFX1_ENTAV Sensor histidine kinase KdpD OS=Enterococcus avium ATCC 14025 GN=OMU_00613 PE=4 SV=1MEKKQMGDGRRGRLRVFFGFAAGVGKTYSMLSEAHELLLMGKDIIVGYIEPHDRPDTNRLLEGLPQIPPKKILYKQMLLTEPDIDQIIQQKPEIVLIDELAHTNAEGSRNRKRYQDVDELLNAGIDVFTTVNVQHIESLNDIVEEVTGVEVKETVPDTFLQQATIKVVDVEPEELIDRLEQGKIYASESAKRALQNFFIPQKLDQLRGLAIQRASDHINRISAKTIRIQSKLLTVVNDAFPKMTEKSIRWTARLAQGLGAEWTVIQVRTQENTLTNIPLAEKLGAEVISIEEDNSFETIVEFAKMTGVTDIIMGKNLRQPWYEKIFIEAFDDRLLKRLNDTELHLIPFKEEKQSLFLRTRKIIEGGGKDLVIALGGVFLATIVTELMQYIHIGDQNLMLIYIFFILLVARTTSGYFWSSLASILSVLSFNWFFVEPLYSLTVYKQGYPITLLIMCLVAILISNLMVRLKKQAESSMEKEHQMELLYELNKQYVLADNRNQILDISATYLSRLLEREVILFDSQAKVESIHCISGKPSILSTKDEAAVAFWTAKNQKEAGNGTDTLIGAKGFYLPIIASGKTLAVLGIERNAGLDLENNQLNYLKLVLTQLAVILEQTELKSEKERVEMENEREKVRSNLLRAVSHDLRTPLTVISGIAETLGNSSDLKENTRQKLLADIQDESQWLIRMVENLLSITRINMDTMKVNKTAEPIEEIIEAVYQHLKKVYPEGQVEISLPSEVTFIQADPILIEQALFNIVENAFRHGEEKQPVKLTVYQKNDQTVFEIENDGEIPLKQFEKIQTNLSSTSEVPVDSKNGLGIGLSIVKTIIHAHNGKMEMMVGEGKTLVRIYLK	9~~KdpD (4.64306E-120)~~218;X;231~~Usp(1.85692E-31)~~347;X;370~~DUF4118 (0.000000000001711 88)~~471;X;499~~GAF (0.0000310285)~~615;X;633~~HisKA (0.000000000005896 29)~~698;X;751~~HATPase_c (7.82971E-14)~~852	KdpD protein
	3E-05	33.4	6	6.8E-05	32.4	4.1	1.5	1	B8HP08_CYAP4	PAS/PAC sensor hybrid histidine kinase (EC 2.7.13.3)	Cyan7425_3270	Cyanothece sp. (strain PCC 7425 / ATCC 29141)	796	395961	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7425 / ATCC 29141)	>tr|B8HP08|B8HP08_CYAP4 PAS/PAC sensor hybrid histidine kinase OS=Cyanothece sp. (strain PCC 7425 / ATCC 29141) GN=Cyan7425_3270 PE=4 SV=1MTSRNIGLKLDRTVLTGERLLPYGIALGSVALSLGISLQLGSLIKPMPASLFFLAVMVSAWYGGLKPGLVATVVSTFAISYYFIPPYGSLRITDLHTLFRLGVFVLVALLTSSLNESRRIALRHAEIMRRRSEAAQEEVQATKQHLERVLCSIHDGFYVLDRHWRYTYVNDRYCEMAGMQREAILGENLWQLFPDGVDTLFDHHLQRAIDKQIPLQFEYFYGAWQRWYEHRVYPSPDGITVFVNEITDHKQVQVALRQSQERFRISQELSLDAFTILNSVRDQTGTIVDFVWIYANPKAAEILQYSVDQLIGQRLLDLLPGNQTNSDLFDRYVRVVETGEPHDIELAYNSEGISGWFRNMAVKLEDGVAIFFSDITDRKQAEAERERLLKEAQAARAEAEAANRIKDEFLAVLSHELRSPLNPILGWTQLMQSQRFDAAKTTEALAAIERNAKLQTQLIDDLLDVAKILRGKMSLNRVPVNLMFVIKAAIDIVMTAAVAKSIQLHSELAQIGAVYGDAGRLQQVIWNLLSNAIKFTPAGGRVEIRLKRVEQQLYQPQPNSLPSIHPLPTTPYAHITVSDTGKGINPNFLPYIFESFHQEDASITRKYGGLGLGLAIVRYLVEAHGGTVTAESPGEGQGATFTVCLPLLDAEPDIHQTDSPSEPELDLSGIRVLTVDDQPDTGELLNVVLTQYGANVLTVTSAAEVLPALASFQPDVFVSDIGMPEVDGYTLLQQIRLLPPEQGGQVPAIALTAYAGELNYQRAMAVGFQRHLSKPVEPKVIARELASLIVKRTAAQ	30~~DUF4118 (0.00000000624029)~~119;X;153~~PAS (0.000000831809)~~257;X(146);403~~HisKA (0.000000000000142889)~~467;X;521~~HATPase_c (7.92453E-30)~~645;X;673~~REC (3.46855E-23)~~789	non-KdpD DUF4118 protein
	3E-05	33.4	9.8	5.2E-05	32.8	6.8	1.3	1	D7GVM7_9FIRM	Histidine kinase (EC 2.7.13.3)	CK3_22900	butyrate-producing bacterium SS3/4	356	245014	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, unclassified Clostridiales, unclassified Clostridiales (miscellaneous), butyrate-producing bacterium SS3/4	>tr|D7GVM7|D7GVM7_9FIRM Histidine kinase OS=butyrate-producing bacterium SS3/4 GN=CK3_22900 PE=4 SV=1MSTKVRSVLKNSGIAFGILGIATAFCFLVQRISESDTHVPLLFVLAVLFVSRFTDGYVYGIVASIIAVFGVNYVFTFPYFKLNFAITGYPLTFVAMLAVACSVSALTTQIKKQEQMRLEVEREKMRANLLRAVSHDIRTPLTSIVGSASGIIDNYDALSKENILELLEDMKSEGQWLVRMVENLLSITRIGDGTARINKEDELVEDVISGAITKFRKRFPDIEVVPKVPEDVLFVPMDAILIEQVIVNLLENCVLHADGMTKIWLIVTEDGDQVKFSVEDDGAGIKESVLPRMFDGSFESEDGKESDSRRNMGIGLSVCMTIVRAHDGIMKAENRKEGGARVMFWLPKGVDTEYGD	15~~DUF4118 (0.000000000142492)~~113;X;123~~HisKA (0.000000000002047 02)~~189;X;242~~HATPase_c (2.07746E-21)~~346	non-KdpD DUF4118 protein
	3E-05	33.4	12.1	5.3E-05	32.8	8.4	1.3	1	A6LLQ7_THEM4	Uncharacterized protein	Tmel_0997	Thermosipho melanesiensis (strain DSM 12029 / CIP 104789 / BI429)	398	391009	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Fervidobacteriaceae, Thermosipho, Thermosipho melanesiensis, Thermosipho melanesiensis (strain DSM 12029 / CIP 104789 / BI429)	>tr|A6LLQ7|A6LLQ7_THEM4 Uncharacterized protein OS=Thermosipho melanesiensis (strain DSM 12029 / CIP 104789 / BI429) GN=Tmel_0997 PE=4 SV=1MQKYFNYIEIIVLNTIIFFIDILFKYYGYVLSYPNPYFVLNIYISIRHGINLFFFSTSLSLFYYFTSLYIHYKINIFSVIFSWSVMRIPLIILSIGFLIGFFFRDMYIQKINEQANQIKILNEKIKRLKENIKKYSSLTKDLQNKLLLENKGVSLFVDKLKEIEFNNPEDIFNEAVELISDFVNAITVSIYTISKNNFLRLKVRKGSQILPNSFPIEKSKIISTANELGFSSASVLYLSDENVDFSMEPVMAAKISQKNKTVGFVVIENIDPEKINKNTETYLKLLSDWLSNLLYVSLELEKQTITTDVEKFNLIFEKIDERFRRFKIPYSFIKISVSKEFEVNEIKKYIRETDFVFFNKEKNELNIILTSCNSKGLERVLEKIRLEKNIKVLEAYTKE	6~~DUF4118 (0.000000000011629 4)~~109;X;166~~GAF (0.0000000135673)~~293	non-KdpD DUF4118 protein
	4E-05	33.3	13.5	5.9E-05	32.6	9.3	1.3	1	D6DLI7_CLOSC	Histidine kinase (EC 2.7.13.3)	CLS_33610	[Clostridium] cf. saccharolyticum K10	370	717608	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium saccharolyticum, [Clostridium] cf. saccharolyticum K10	>tr|D6DLI7|D6DLI7_CLOSC Histidine kinase OS=[Clostridium] cf. saccharolyticum K10 GN=CLS_33610 PE=4 SV=1MKKCKNKLLRFLESQTRVSNTVIMLVLLFTATAVSFFFAKMEAPSSSISLCYILALFLTARYTSGYFYGILSALVGVVCVNFLFTYPYFELNFTLSGYPITFIAMFTISIITSALTTNIKEQSRIISEREKMLMEAEKEKMRANLLRAISHDIRTPLTSIIGSSTVYLENETSLSDSDKRALVSHILEDSNWLLNMVENLLSVTRINNETAKVSTSLEPVEEVLGESISRLKKRLPDAQVKVSVPDEFLMIPMDAILIEQVLINLMENAIVHSKSTKPIECFVEAGVSCVTFHVRDYGIGIPPEKLETIFDGSSSTTSTSTDGRKGMGIGLSICKTIITAHGGTLAAVNHADGAEFYFTLPKGEQNIGT	25~~DUF4118 (0.0000000036912)~~123;X;140~~HisKA (0.000000000088568)~~206;X;259~~HATPase_c (1.39108E-22)~~361	non-KdpD DUF4118 protein
	4E-05	33.3	1.2	5.7E-05	32.7	0.8	1.3	1	A0LLQ1_SYNFM	Histidine kinase (EC 2.7.13.3)	Sfum_2675	Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	339	335543	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophobacteraceae, Syntrophobacter, Syntrophobacter fumaroxidans, Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	>tr|A0LLQ1|A0LLQ1_SYNFM Histidine kinase OS=Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB) GN=Sfum_2675 PE=4 SV=1MALNSNKTRIALISLVVLAITVAHSFGIRSRGGYLHHLYHACFFLPLMLAGFWFGLKGALATSLSITLLNLPEVITHFEKFSPIEFDYMLQMGIYNVVAVCLGMLRDRERREQKRALEAGRLAAIGKAISCVAHDMKTPLIAIGGFGQLLMKHFETGDPRLEKLEIIVKETRRLEMMVREMLDFSRPLELHRSEEDMCLLVRESLEVVNEAATAKRVIVFSTPANPPRISVDPLRIKQVLINLMINAVEASPEGEIVTVATYKQGRNLVIDVSDKGDGIPDGKAEEIFSPFYTTKKDGTGLGLTIARKIVEAHEGRLELLQNSGKGLIVRVILPIGRRS	12~~DUF4118 (0.0000210689)~~112;X;122~~HisKA (0.000000000074786 1)~~186;X;236~~HATPase_c (6.69686E-24)~~333	non-KdpD DUF4118 protein

	4E-05	33.3	11.5	8.1E-05	32.2	8	1.6	1	F2JRN7_CELLD	Histidine kinase (EC 2.7.13.3)	Clole_2249	Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	512	642492	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Cellulosilyticum, Cellulosilyticum lentocellum, Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) (Clostridium lentocellum)	>tr|F2JRN7|F2JRN7_CELLD Histidine kinase OS=Cellulosilyticum lentocellum (strain ATCC 49066 / DSM 5427 / NCIMB 11756 / RHM5) GN=Clole_2249 PE=4 SV=1MSVLRNSIKTFSLLVGATLLAYLYTKVTANHTNVAIIYILAIFLTARFTSGYFWGILASIIGVVGVNYFFTYPFLQIDFTINGYPITFLGLLTIAFITSGMTAHVTERNKIISEREEMTHKLNDINNQLLISDHVDQIIELTLNTVIDFTKSSVIFHKTDPLKKINYIEKLYSDEDREMLTTPHELERAHWAFSKVQNSDFSSSDIAYGSGLYLPLISHEHIWGVIGIYHFPTTLYKNNTLTLLKLMLTQVAMAIERQHLVDEHHQLALETEKEKMRANLLRAVSHDLRTPLTSIIGAGATYLENDEEQDDLVKHILEDANWLLHMVENLLSITRIKEGQVKVNKTPEPLEEVVSEAILRLKKRYPKSNVNVKVPDTFLMIPMDATLIEQVILNLLENALKYAHSKEPIELIVTDDTTYVTFRIIDHGIGLAEEQLEGIFDGNALNPKAQSDSSKGMGIGLSICKTIVCAHGGKISAQNHIAGGAEFIFTLPSQGGNIHEQNIYTHC	8~~DUF4118 (0.000000000626688)~~108;X(166);274~~HisKA (0.000000000001546 61)~~340;X;393~~HATPase_c (2.32138E-26)~~496	non-KdpD DUF4118 protein
	4E-05	33.3	9	6.2E-05	32.5	6.2	1.3	1	L0J3C9_MYCSM	Histidine kinase (EC 2.7.13.3)	Mycsm_05135	Mycobacterium smegmatis JS623	885	710686	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis JS623	>tr|L0J3C9|L0J3C9_MYCSM Histidine kinase OS=Mycobacterium smegmatis JS623 GN=Mycsm_05135 PE=4 SV=1MTSHDQPLAPGPSDADDPPTLPASGSDLLPVRASSDADALTHRTDYKKKRGELRIYLGAAPGVGKTFAMLGEAHRRLERGTDLVAAVVETHGRKKTADMLAGIEAIPPKYIEYRGTKFPELDVEAVLKRQPEVVLVDELAHTNTPGSKNPKRWQDVEELLDAGITVISTVNVQHLESLNDVVAQITGIEQQEKVPDEIVRAADQVELVDITPEALRRRLAHGNVYAPERIDAALSNYFRRGNLTALRELALLWLADQVDAALEKYREENKITQTWEARERVVVAVTGGSESETLVRRASRIASKSSAELMVVHVVRGDGLSGVSAPQMGKVRELVLSLGATLHTVVGDDVPSALLDFAREINATQLVLGTSRRSRRWARIFDEGIGATVVQDSGTIDVHMVTHPEASRGSWWSRVSPRQQHLASWVAALVVPSAICALIVALLDPYLKISGESALFFVGVLVVALLGGVAPAALSAVLSGLLLNYFLIEPRYTLTIAEPDNAITSFVLLVVAVAVAALVDSAAKRTREARHASQEAELLALFSGSVLRGADLETLLERVRETYSQRAVSMLRVLDGDSEGEIVACVGDDPCVDVDSADTAIEVGDDEFWMLMAGRKLPARDRRVLTAVAKQAAGLVKQRELTEEASKAEAIAQADELRRSLLSAVSHDLRTPLAAAKAAVSSLRSSDIDFSAEDTAELLATIEESIDQLTALVGNLLDSSRLAAGVLRPELQRVYLEETVQRALLAISKGITGFRRQGLDRVKVDVDDAVVMADSGLLERVLANLIDNALRYAPDSPIRVTAGQVGERVLIAVIDEGPGIPRGTEEQLFAPFQRLGDHDTSIGVGLGLSVARGFVEAMGGTISATDTPGGGLTIEIDLAAPQDGVA	48~~KdpD (2.04736E123)~~258;X;280~~Usp(1.85505E-33)~~401;X;424~~DUF4118 (0.0000000641491)~~503;X(151);654~~HisKA (0.000000000031212 7)~~720;X;777~~HATPase_c (4.75317E-27)~~877	KdpD protein
	4E-05	33.3	6.2	7.3E-05	32.3	4.3	1.5	1	E8X5C3_GRATM	Histidine kinase (EC 2.7.13.3)	AciX9_2434	Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9)	478	1198114	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella tundricola, Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9)	>tr|E8X5C3|E8X5C3_GRATM Histidine kinase OS=Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9) GN=AciX9_2434 PE=4 SV=1MHSKLIISVTRWFSAAIGLGGIVFFFHVVLQVNPTTVALTLLLFIHSLASRWGLRYAVVISFAAGACYNYFFLPPVGHFIISDPQNIVALLVFLITSIFASRMSERIREESKEARASKAELEILYRLSRALLQTDEFVQLTKTVPNAVAVATGAQAVLFFLLDGNRIYRFGSDWTPHLSEDALKELSHAPGIISSAGAQAEAMIPLRSGVPRPGILIIRGLTLSHQSLDALGGLVSIALDRSNAIDEVSRTEAAKENERLRALMLDSITHELGAPLAFIDRSLDSLLAQGLEPAESRALLGSVQGESNRLSRLVAQAVEMAKFDTQELRMTFVPQSMEEMINDAIQTAEDVLKGHPVQVTLAPRLPSVQADSIWVGRLLTKLLQNAAKYSPDDAPIFITAEQDGRFVTCSIADRGIGIEPIEQSFIFDKFLRSGNREQRSSGTGLGLAICRTIVEAHGGKIEVSSQPGRGSVFSFTLRV	11~~DUF4118 (0.00000000398036)~~110;X(147);257~~HisKA (0.00000706178)~~321;X;376~~HATPase_c (1.7247E-28)~~476	non-KdpD DUF4118 protein
	4E-05	33.3	8.5	5.7E-05	32.7	5.9	1.3	1	R5IUX8_9FIRM	Histidine kinase (EC 2.7.13.3)	BN480_01720	Firmicutes bacterium CAG:124	369	1263002	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:124	>tr|R5IUX8|R5IUX8_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:124 GN=BN480_01720 PE=4 SV=1MTRNTKDQILRGRLRQIFLFSWRDCAVCVGILAAAALLCALLRMIDSSDVYVALIFECAVVLVSRFTDGYLFGLLASVIGVVGVNWIFTYPYMQLNFTISGYPLTFLVMLAVSVVVGTLTTQIKQQEKLRAEAEREKMRGNLLRAVSHDIRTPLTAIVGGIDAILENGSQISPETSRDLLENMRDESNWLIGVVENLLSVTRMSGASNIKKELEAGEEVLGAASMKFKRHYPAVEVSITAPDTLLMIPMDIILIEQVLINLMENAVQHGKTTTRIELRLSSAGGLAVFEVADNGCGIEKELLPHLFEGYLTRDQEEISDQRRNMGIGLSVCMSIVQAHGGTMRAENRKKGGALLQFSLPLEENRHEHQR	45~~DUF4118 (0.000000253444)~~126;X;136~~HisKA (0.000000000069084 7)~~202;X;254~~HATPase_c (2.9426E-23)~~358	non-KdpD DUF4118 protein
	4E-05	33.2	6.7	6.8E-05	32.4	4.6	1.4	1	S5VP11_STRC3	Histidine kinase (EC 2.7.13.3)	B446_27470	Streptomyces collinus (strain DSM 40733 / Tu 365)	858	1214242	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces collinus, Streptomyces collinus (strain DSM 40733 / Tu 365)	>tr|S5VP11|S5VP11_STRC3 Histidine kinase OS=Streptomyces collinus (strain DSM 40733 / Tu 365) GN=B446_27470 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVGHVEHHDRPRTEVMLHGLEQVPRRRLEHRGAAFAEMDVDAVLHRAPAVALVDELAHTNVPGSRNAKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNAYRSEHQVSRIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYISRSDGLTSASPKELAVQRTLVEDLGGTFHHVVGDDIPASLLDFARGVNATQIVLGSSRRKAWQYVFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVARGGRLGRTRIVSGWLVGLAGPAIFAVLLNTVDLGLANDMLLFLAVTVAAALLGGLLPALASAAFGSLLLNYFYTPPLHRLTVADPKNIVAIAIFFGVGMSVASVVDLAARRTHQAARLRAESEILSFLAGNVLRGETGLDELLERVRETFAMESAALLERAGDVEPWTCAGRAGFGPPLGRPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVALDRRRLQEEADQAKELAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSEDVAWSEEDRAELLEGIEEGADRLDRLHLVGNLLDMSRLHTGTVTPLIREIDVDEVVPMALFGVPEDSVELDVPETLPMVAVDPGLLERSVANLVENAVKYSPARHRVLVSASALVDRVEVRVVDRGPGVPDEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGSLNAEDTPGGGLTMVLSLRAAGTRPEHLPAGEPGTSAGEPGTEPEROAS	1~~KdpD (2.36248E-124)~~211;X;233~~Usp(1.85027E-31)~~356;X;430~~DUF4118 (0.00129294)~~480;X(131);611~~HisKA (7.53991E-15)~~677;X;726~~HATPase_c (7.3468E-19)~~827	KdpD protein
	4E-05	33.2	13.3	6.7E-05	32.4	9.2	1.4	1	I0H1T2_ACTM4	Histidine kinase (EC 2.7.13.3)	AMIS_17490	Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	475	512565	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes missouriensis, Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	>tr|I0H1T2|I0H1T2_ACTM4 Histidine kinase OS=Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431) GN=AMIS_17490 PE=4 SV=1MAGGEFWEWIGRGAWRTPTPALSRRRRAAGFLVVMLGLPSLTAILLAVPEQQLVTAILLFLVVVVGVALIGGLWPALLAAVGGSLLLNWYFIPPYGRFLIAQEQNLLALAIFVLVAVAVSWVVDVAARTTRQAAQASAEARTLATVAGSVLRGERPLMALLSQLRETFVLESVALCEGGETVAAVGRPVLRPELADDTVKADGDLVILLKGHPLAAADRRIVEAFAAQAAVALRQERLAAEAATAKPLAEANKLRTALLAAVSHDLRTPLASAKAAVASLRSSEVEFDDDDRAELLATADESLDKLGRLVANLLDMSRLQAGALGVVPIEVGAEEVVPQALDDLGVEGRAVTVRVPDDLPLLRADPGLLERVLVNLVANALRYSPPDAPPMITGSARGDTVELRVIDHGPGIPADRWDDVFLPFQRLGDRDNHTGVGLGLALSRGLTEAMGGTLTPDETPGGGLTMIISLPAVAS	73~~DUF4118 (0.000111136)~~128;X(124);252~~HisKA (0.00000000003291 54)~~318;X;369~~HATPase_c (9.99914E-25)~~470	non-KdpD DUF4118 protein

	4E-05	33.2	4.5	6.3E-05	32.5	3.1	1.3	1	G7WCE8_DESOD	Histidine kinase (EC 2.7.13.3)	Desor_0569	Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	381	768706	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus orientis, Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) (Desulfotomaculum orientis)	>tr|G7WCE8|G7WCE8_DESOD Histidine kinase OS=Desulfosporosinus orientis (strain ATCC 19365 / DSM 765 / NCIMB 8382 / VKM B-1628) GN=Desor_0569 PE=4 SV=1MENQGYEGKKHQPARALFDLIGIGLVIGILTIIHYTNYHYEVDYHILLQFAYYLPVIYAAMRFGSVGGIISSFLITILFVPLMLHFQKDLTAAAKYTQWVEVGLINVFGWLTGFLTEEERKAKNKYRLALKVQQDLVEQLKQEEQERQRLEAEIRQTERIAALGHLSAGLAHEIRNPLGIMKVSIQMLAQEKQGDEVVAEYCQVLREECERLNRMVSEFLSFARPKELVRKRILLGKLVEESLALIQPALGKNHIQLEQILDSGLDQEVEVDPDQIKQVILNILLNAVDAQEQGGVIELEEIEEEGFIGFAVSDEGTGISPEDMPFIYDPFFTTKEKGTGLGLSVVHRILDQHGGKIRTFNRPDRGVTVKILLPKVPVKDK	20~~DUF4118 (0.000000906825)~~122;X;160~~HisKA (2.71603E-14)~~224;X;276~~HATPase_c (3.09055E-19)~~373	non-KdpD DUF4118 protein
	4E-05	33.2	8	6.8E-05	32.4	5.5	1.4	1	H2K2C9_STRHJ	Histidine kinase (EC 2.7.13.3)	SHJG_6969	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	852	1133850	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	>tr|H2K2C9|H2K2C9_STRHJ Histidine kinase OS=Streptomyces hygroscopicus subsp. jinggangensis (strain 5008) GN=SHJG_6969 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVALVESHGRPRTEVMLHGLEQVPRRQLEYRGAVFGEMDVEAVLRRAPAVALVDELAHTNIPGSRNTKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADDIELVDMSPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDAYLNAYRSEHRVSTIWGSRERIVVGLTGGPEGRTLIRRATRLAEKGAGGEVMAVYIARSDGLSSASPKELAIQRTLVEDLGGTFHQVVGDDVPAALLDFARGVNATQIVLGSSRRKAWQYVFGPGVGATVARDSGPDLDVHIVTHEEVAKGRGLPVARGGRLGRARIIWGWAVGLAGPAVLAVLLNTVDLGLANDMLLFLAVTVAAALLGGLLPALASAAFGSLLLNYFYTPPLHRLTVADPKNIVAIAIFFGVGMAVASVVDLAARRTHQAARLRAESEILSFLAGNVLRGETSLEELLERVRETFAMESAALLERASDVAPWTCAGRAGFGPPLERPEDADVDVPVGDHMALALSGRVLPAADRRVLAAFAAQAAVVLDRRRLKEEADRARTLAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDQAELLEGIEEGADRLDHLVGNLLDMSRLQTGTVTPLIREIDVDEVVPMALGGVPEDSVELDVPETLPMVAVDPGLLERSVANLVENAVKYSPHGRRVLVAASAIADRVEVRVVDRGPGVPDEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLTAEDTPGGGLTMVLSLRAAGPRPEPLPAGESRTEPERQATW	1~~KdpD (2.8211E-124)~~211;X;233~~Usp(5.14819E-31)~~356;X;430~~DUF4118 (0.00025917)~~480;X(131);611~~HisKA (2.90354E-15)~~677;X;726~~HATPase_c (3.28916E-26)~~827	KdpD protein
	4E-05	33.2	10.2	6.8E-05	32.4	7.1	1.3	1	A0A075K9I1_9FIRM	Histidine kinase (EC 2.7.13.3)	UFO1_0782	Pelosinus sp. UFO1	895	484770	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Pelosinus, Pelosinus sp. UFO1	>tr|A0A075K9I1|A0A075K9I1_9FIRM Histidine kinase OS=Pelosinus sp. UFO1 GN=UFO1_0782 PE=4 SV=1MPEESKEKKRPDPDVLLTKLNKENRGKLTVFLGAAAGVGKTYTMLEIAHEMLASGVDVVIGWVETHKRVETEKMVEGLPRLPAREIEHRGRTLHEMDIDAILARKPKVVLVDELAHTNVAGSRHVRRFQDVEEILNAGIDVSTTLNIQHIESLNDIVAQITGVTVRETVPDSIVEQADQVQLIDIPPNELIKRLKEGKIYMPHQAELALNKFFRPGNINALRELSLRFTAYRVDKELNEYMQEHDIPGPWPAGERVMVCVSSSPFSAQLIRAARRLARGLQAELLAVHIDTPRRLELSEKERDRIFRNMRLAEELGAKTISVVGKDLTEEILSMTREYNVTHLVVGKPLRGRIWEWLNGGAVVNKLIRYSGGVNIHVIQGNTEVKDEPKFKTLATKATIPLWNYMAGVLMIFLITAGNWLWREYIESIHMMLYLVPVLLSAVWWGKGPSYVVALASVLLFDFFFIPPFFSFSVADLRYLWSLPLFLLVSFTIGGQTEKLRLEAMLARQREKTTRALYSFSREIAAVVEVNAIVGILVEQAWQTLERPVAVFLPQDNGTLLLAAEAGTKKSGIDTSEQAVAIWAYEHSEIAGRCTETLPGARYMYLPLTTSDNTVGVLGIRIQEKMLTPVQRRLMEAWAGLAAIAVERVNLADQARRAALLVESDQLRTALFNSISHELRTPLASIIGAVSGLLDVEGIYSGEDRKELLETVKEGANRMDRLVANLLDTARLESGMMQLKIDWCDIEDITGIALRRVEESLNDRALLVRIPADLPLVKADCVLVELVLVNLLDNACKYSAPGSEIVITASQDEKVVRVSVADRGPGIPSEYLTRVFDKFYRVEQPKSVSGTGLGLSICKGIIEAHGGTIHAENRPGGGTVMTFALPCDEQPPSNMV	23~~KdpD (9.1558E-119)~~233;X;255~~Usp(9.99609E-42)~~378;X;403~~DUF4118 (0.00134662)~~493;X;528~~GAF (0.000000000004545555)~~647;X;664~~HisKA (6.47151E-14)~~730;X;792~~HATPase_c (1.61176E-27)~~884	KdpD protein
	4E-05	33.2	5.5	3.9E-05	33.2	3.8	2.4	1	D9SLR6_CLOC7	Histidine kinase (EC 2.7.13.3)	Clocel_4040	Clostridium cellulovorans (strain ATCC 35296 / DSM 3052 / OCM 3 / 743B)	612	573061	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium cellulovorans, Clostridium cellulovorans (strain ATCC 35296 / DSM 3052 / OCM 3 / 743B)	>tr|D9SLR6|D9SLR6_CLOC7 Histidine kinase OS=Clostridium cellulovorans (strain ATCC 35296 / DSM 3052 / OCM 3 / 743B) GN=Clocel_4040 PE=4 SV=1MQITENENKNGINEIIYTVKLASLILAAIIIIRYNFSGDGSIYLNDNYRFNMNYVVMLITILVLILAVWYLTYLATVKSKYKKLTIITENIILISFFSVLIIISDNSVEQYKFLFLLIIISSTLQMGMNFGMANAMVVSLIMLSIDIFYDPKAVVNMRFENDLILAGIFLLTAWPLGYFTKINSEALKKKDVELNVLNKELIKNHIHRRNIEELLINNQDCYNLLINNSLDAIVVHRELTCLFANDSAVNLFGMKNGKRIYKQKLIELIEEGERDRVAQFFRDAIKDKCQSLKFESVIKSKDKNLEVESTSIFITYEGEPTTLTIFRDISHKKQVEKLKIDVQRNVELLTESLEFNNSIMQLFSNISHELKTPLNIIFAAVQVLSISMRDKAREEYLPMSEKYFNIMKQNCYRLTRLINNFLDITKIDSGFVNITLKKCNIVNIVEDITLSVAPYVESKELKITFDTEVEEIIINCDVDKIERCLLNLISNAIKFTNPGGDIFININQCDDKVAISVRDTGVGIPEDKLELIFERFGQVDKTLRRNREGTGIGLTLVKSLVEIQGGQIEVHSLLGVGSEFVMKFTIEEEEFIGEDTEYFTNKETINTEFSDI	91~~DUF4118 (0.000000000361499)~~186;X(170);356~~HisKA (0.000000000054680)~~426;X;481~~HATPase_c (4.82929E-28)~~584	non-KdpD DUF4118 protein
	4E-05	33.1	7.2	7.3E-05	32.3	5	1.4	1	A0A0F5MTF9_9MYCO	Histidine kinase	WR43_16135	Mycobacterium arupense	842	342002	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium terrae complex, Mycobacterium arupense	>tr|A0A0F5MTF9|A0A0F5MTF9_9MYCO Histidine kinase OS=Mycobacterium arupense GN=WR43_16135 PE=4 SV=1MNSGDAPSRRGELRIYLGAAPGVGKTYAMLGEAHRRMERGTDVVAAVVETHGRKKTAELLAGIEILPPRWIDYRGKSFPELDVAAVLARRPQVVLVDELAHTNTPGSANPKRWQDVEQLLAAGITVISTLNVQHLDSLNDVVAQITGVEQQETVPDSFVRQASQIELVDIDPEALRRRLAHGNVYAPEKVDAALSNYFRSGNLTALRELALLWVADQVDAALAKYRADKKIATAWEARERVVVAVTGGPESETLVRRASRIASKSSAELLTLHVLRGDGLAQLPTARIGKIRELATSLGGSLHVVVGDDVPSALLDFAREVNATQLVIGTSRRSRWARLVDEGIGARVVRLSGTIDVHIVTHEESRQGFRRSAIAPRQRLVLRWLAALLVPSVVCLVTALWMDPFLHTGGESALFFVSVLVVALLGGVAPAVLSAVVSGLLLNYFLTDPRHSFTIAETDSAITEIVLLLVAVAVAVLVDRAAERSREAGRASQEAELLALFAGSVLRGADLATLLERVRETYALRSVSILRERPDGAGPTLVASAGLDPCTTVESADTAIDVGDDEFWMLAAGRQLAGRDRRVLSAVAKQAAGLVRQGELTTEANRAEAVMRADELRRSLLSAVSHDLRTPLAAAKAAVSSLRAEDVGFSPQDTAELLATVEESVDQLTALVGNLLDSSRLAAGAVQPELRRVYLEEAVERALVSIGRGETGFRRSGIDRVNVEVGDAVVLADAGLLDRVLANLLDNALRYAPDSPVRVSACRAADRVLIDVADQGRGLPPGGERLFEPFQRVGDQDNTTGMGLGLSVARGFVEAMGGTIRATETPGGGLTMVVDLAAPPPT	8~~KdpD (2.40109E-118)~~218;X;240~~Usp(1.0658E-33)~~361;X;383~~DUF4118 (0.0000292653)~~463;X(151);614~~HisKA (0.000000000023608)~~680;X;737~~HATPase_c (1.27119E-25)~~836	KdpD protein

	4E-05	33	8.6	7.5E-05	32.3	6	1.4	1	A8KYG2_FRASN	Histidine kinase (EC 2.7.13.3)	Franean1_0599	Frankia sp. (strain EAN1pec)	938	298653	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain EAN1pec)	>tr|A8KYG2|A8KYG2_FRASN Histidine kinase OS=Frankia sp. (strain EAN1pec) GN=Franean1_0599 PE=4 SV=1MRNAGRGRAGAFRRPPRRPHHGWVPRGTLRIYLGAAPGVGKTYAALDEAHRRSERGTDVVIGFVETHGRPRTAAMLHDLEIVPRRTLTYRGGSFTEMDLDAVLARRPKVAFVDELAHTNVPGSRHAKRWHDVQELLAAGIDVISTVNVQHLESLNDVVGTITGVPQRETVPDDVVRRADQVELVDMAPEALRRRMAHGNVYGPEKVDAALANYFRVGNLTALRELALLWLAGKVDDQLDRYRADHGIGGTWETRERVVVALTGGPEGDTLIRRACRIAARGKGADLLAVHVARSDGLTGADPSALARQRALVESLGGSYHQVIGDDVPTALLEFARAENATQLVLGASRRGRLARILSPGIGATTTTRSGSIDVHMVTHPEAWGHRPAPAGGVDAAAHRPARPGWPGWRLPRGRTALEPRRRIIAAGLTLVLVPALTAGLAASRGTFNLTTEMLAYLLIVVTVALVGGFGPALLCAIASSLLLNYYFTAPVRAWTIADGDNALALLGFVLVASLVSRVVSTSARRYEQAVRASAEAATLSVLAGSVLRGEDALPALLARARETFGMTSVTLLERTDDDQVGVEWSPVATIAGTGPDGASVDGASGAGPGTSQAGAGGPTGGRADPDGDGDGSEIVDIPVREDLRLVLTGRSLPAADRRILTAFAAQAAVALDQHRLREAAAEAAPIAAADKVRTALLTAVSHDLRTPLAAAKAAVSCLRGYDITLTDDEEAELLATADESLDKLTRLVENLLDMSRLQAGALSVFPRAVGLDDIVPPALDEIGPAANRIGVRVPDDLPDVRADPVLLERVIVNLVTNALRYAPADTPPVITASALGDRVELRVVDSGPGIPVRQRDNVFQPFQPRLGDRDNTTGVGLGLALSRGLAEAMGGALTDPETPGGGLTMVLSLPAALNPTAVTNPITAPLDVPTGPAADDRAG	26~~KdpD (2.43516E-117)~~234;X;256~~Usp(4.85796E-31)~~378;X;422~~DUF4118 (0.00000000251662)~~525;X(165);690~~HisKA (0.000000000010570 1)~~756;X;807~~HATPase_c (5.71126E-26)~~908	KdpD protein
	5E-05	33	1.6	7.4E-05	32.3	1.1	1.4	1	E8UXA3_TERSS	Histidine kinase (EC 2.7.13.3)	AciPR4_2265	Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	479	401053	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus saanensis, Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	>tr|E8UXA3|E8UXA3_TERSS Histidine kinase OS=Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4) GN=AciPR4_2265 PE=4 SV=1MKRAFRIRPFLWGCGGCVGILALGALTFRYERGAAASVPLYIFLTLIVAWRGGFRASIPVAICATLGLDFLFTEPRFNLRVASPQDVFSLASFAGVSLLVSHLSNRIRNHSERLKEAEQQQRALYEISRSTLLIDWNSSGGEQFCALIQEKLRLYGVGIWDDRERSFSYSGDASDSFDSLQASFRAMKDFNLPSKDQRIRLLRFGVRTVGTIYFHGELELLMADTVATLLATHLERIRALKAEVTAASQMVSEQLRTAVLDGLAHAVKTPLTTILVSSSGLKELGNLSPLQIELAEVIENQASKYLATLTDKLLRTSKLESRELFVQKHKTSLRDIFESAVEELRIEFDISRIVPCFPESRIECDMDQDLVRMALVQLLENALKYSLGGSKVLMSVRVFLEEIEIAIHNEGSYIPAEERELVFERYFRSPSVEHGAPGTGIGLSVARRAVEAHNGRIWIESDPEKGTTFHVSIPLEGVRR	9~~DUF4118 (0.000000108715)~~110;X(143);253~~HisKA (0.000000554771)~~317;X;373~~HATPase_c (2.67821E-21)~~472	non-KdpD DUF4118 protein
	5E-05	33	11.6	4.5E-05	33	8	1.8	1	G8NY99_GRAMM	Histidine kinase (EC 2.7.13.3)	AciX8_2456	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	1048	682795	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	>tr|G8NY99|G8NY99_GRAMM Histidine kinase OS=Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8) GN=AciX8_2456 PE=4 SV=1MGSQGDRSSDRMHARAVENPILRLLICIAAVGVLTAVLYTVPLHDRTLSAALTFLFLVWTVSYFWGFRYALFVSLLAALAFSWLLPPVGVFFQLSDSRDIFALAAFLFIGITTSYLSDRVRREALNARRAEAAARRSEEGLREVIETMPAMAWSALPDGSNAFINKQWAEYTGLSAEQTAGWLSTVHPEDASGHTEKWRQSLATGQPLEHEVRLRRIADGQYRWFLVRGMPLRDEHGEVLKWYGIATDIEDHKRADEALRASERELNLIINTIPALSWSARTDGTADFFNQHYLDFVGLSAEQAQDWGWTVAVHPDDLGGLAGSWQSIMATGKVGEAEARLRRFDGEYRWFLFRANPLRDESGNIVKWFGINTDITARKRAEDLLTGEKRILEMVAKGDPLNQILDGVCRFVEEQASGFLASVLLVDGGRLRHGGAPSLPRTYTDAIDGLTFGPSTGSCGTAAYRGEQVIVADIATDPLWENYREAALPHSLRACWSTPVFSSQGKVIATFAMYYREPRSPSSHDLETIEQITHLVGVAIERKLIQEALQRSESYLAEAQRLTHTGSWAWNVRTGAYFWSQEIFRIYDCDPRMVPTWDFLIEKTHPEDRAKIERRVKIESLKKEWKDFESDFRIVLTDGTIKHLHALAHPVVDESGEITEVVGTIMDVTERKRAEEKLRRSEESLLEAQRLSHMGSWRHDVASGAVIVSPEILRIFGVQPDEDSSSAEFWFSRNHPEDQQRIRELFEKSERLKTDYEGDYRIVLTDGTIKHLHAVAHPVLSLSGELVEMIGTTIDVTERKRAEEERERLRQLETDLAHMNRVTMLGELASSLAHELNQPIAAAITSANACSRWLAHNPPDLERARAAATRIEHDGSRAAEIIQRLRAFYKTGAPPERELVDMNEVAGEMLALLRDEADRHSISLRTELATQLPQIMADRVQLQQVLLNLLLNGMEAMTGRPAGRLMIRSQSTEDGLLLISVSDTGVGLPCEKLDQLFRAFYTTKPQGTGMGLAISRSIIEAHGGRLWATANAERGATFHFTLPAELQP	20~~DUF4118 (0.000000000031224 6)~~123;X;163~~PAS (0.000000000271321)~~249;X;273~~PAS (0.000000178795)~~375;X;389~~GAF (6.93617E-15)~~553;X;563~~PAS (0.00000115932)~~668;X;692~~PAS (0.0000000521804)~~796;X;824~~HisKA (0.0000154001)~~890;X;958~~HATPase_c (3.28974E-19)~~1042	non-KdpD DUF4118 protein
	5E-05	32.9	10.2	9.1E-05	32	7.1	1.5	1	V5XI24_MYCNE	Histidine kinase (EC 2.7.13.3)	D174_21895	Mycobacterium neoaurum VKM Ac-1815D	838	700508	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	>tr|V5XI24|V5XI24_MYCNE Histidine kinase OS=Mycobacterium neoaurum VKM Ac-1815D GN=D174_21895 PE=4 SV=1MTDRPKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDLVAAVVETHGRSKTAELLEGIEIIPPRLVEYRGATFGELDVDAVLARRPQVVLVDELAHTNTPGSANPKRWQDIEQLLAAGITVITTVNVQHLESLNDVVAQITGIEQQEKVPDEVVRAADQIELVDITPEALRRRLSHGNVYAPDRIDAALSNYFRRGNLTALRELALLWLADQVDAALAKYRSDNKITATWEARERVVVAVTGDKESETLVRRASRIASKSSAELMIVHVVRGDGLAGVSAPMMGTVRDLAASLGASVHTVVGDDVPAALLDFAREMNATQLVVGTSRRTRWARILDEGIGAAVVQNSGTIDVHMVTHEQTGRATARSGNRNWRQHAASWLAAVVVPTALAAVAVLWLDRYLGVSGESALFFVGVLAVALLGGVAPAALSAVLSGLLINYFLAEPRYTFTISEPDSAITIAVLLMVAVAVAALVDSAAKRARAERARRASQEAELLAHFAGSVLRGADPTALLERVREVYSQTAVSLLRERDGETHVVACAGKQPCVDVDSADTAIEVGDDEFWLLMSGRKLPAKDRRVLGAVAKQAAGLVRQRELISEAGRAEAVARADELRRSLLSAVSHDLRTPLAAAKASVSSLRSSDIDFSPEDTAELLATVEESVDQLTALVGNLLDSSRLAAGVVKPELRRVYLEEAVQRALLGISRSSKDSGWDRVKVDVGDAVALADPGLLERVLVNVIDNALRYGGDNPVRVNAGRVGERVLITVADEGPGIPRGAEEQLFAPFQRLGDQDNSTGVGLGLSVASGFVTAMGGTISATDTPGGGLTVVIELAAPQEGPQP	5~~KdpD (1.15881E-122)~~215;X;237~~Usp(1.29367E-32)~~358;X;381~~DUF4118 (0.000000390734)~~464;X(145);609~~HisKA (0.000000000003143 37)~~675;X;729~~HATPase_c (1.44929E-24)~~829	KdpD protein

	5E-05	32.9	8.3	9.1E-05	32	5.7	1.4	1	E8N7S7_MICTS	Histidine kinase (EC 2.7.13.3)	MTES_1369	Microbacterium testaceum (strain StLB037)	852	979556	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium testaceum (Aureobacterium testaceum) (Brevibacterium testaceum), Microbacterium testaceum (strain StLB037)	>tr|E8N7S7|E8N7S7_MICTS Histidine kinase OS=Microbacterium testaceum (strain StLB037) GN=MTES_1369 PE=4 SV=1MLAGIHRRRVVRRGTLRVLLGMAPGVGKTYEMLEEGRRLAAEGRDVVIAVVETHGRAATAAQAEGLEVVPRRPVAHRGVALDEMDLAAVIARHPDLALVDELAHTNAPGSANDKRWTDVEELLDAGIDVITTVNVQHIASLNDVVEKITGVTQRETVPDAVVRAADQIEVVDLAPQSLRDRLSAGFVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALQRYRTEHGIEGSWQARERVVVALTGGSEGETLLRRGARIAARSAGGELLAVHVSTQDGLRTSNPAALETQRALVEQLGGTYHQVVGDDVATALVDFARSVNASQLVIGVSRRGRLGAALTGPGIGNTVIRESGDIDVHIVNHARAGGRFALPRLTGPALSMKRRILGFVTALVGGPIISLLLLATGSDDSITTDVLSYQLLVVIVALIGGIWPAVFAAVLSGLTLDFLFIAPLHTVTISDPVHAIALVLYVVIAMLVSVVVDQAARRARAARRASAEAELLATVAGSVLRGEVAVPALVSRAREAFGLAGVRLIAADGRVLATDGEPVRDDRRTTVPVGDGRATLELHGGDLDAGARRLLDVVVAQLAAALERADLAETAAEAGLRAAGLRRAAGDHLSEDDRRELIETADESLATLSVLVTDLLDVSRVVQAGVLAVSLAPVDAADVVIAALDELDLGPDEVELALDPDLPSLRADAVLLQRVLVNVLANAQRYTPEGVRVRIATSRLGGIAEIRVIDHGPGIAVERRDDMFSPFQRLGDTDNTAGLGLGLALSRGFAEGMGGTLVPEDTPGGGLTMVVTLPVAEGGAEAVASGIREDAP	12~~KdpD (4.43074E-114)~~221;X;243~~Usp(1.57747E-30)~~366;X;402~~DUF4118 (0.00000000504511)~~487;X(128);615~~HisKA (0.00000000303265)~~681;X;732~~HATPase_c (1.05131E-23)~~833	KdpD protein
	5E-05	32.9	8.3	8.3E-05	32.1	5.8	1.4	1	A0R398_MYCS2	Histidine kinase (EC 2.7.13.3)	MSMEG_5395	Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	839	246196	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	>tr|A0R398|A0R398_MYCS2 Histidine kinase OS=Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155) GN=MSMEG_5395 PE=4 SV=1MTTRASNASKRGELRIYLGAAPGVGKTYAMLGEAHRRLDRGTDLVAAVVETHGRKNTAELLAGIEVIPPRYIEYRGGRFPELDVPAVLDRKPQVVLVDELAHTNTPGSKNAKRWQDVDELLNAGITVISTVNVQHLDSLNDVVAAITGIEQQETVPDEVVRSADQIELVDITPEALRRRLSHGNVYAPERIDAALSNYFRRGNLTALRELALLWLADQVDAALAKYRADNKITALWETRERVVVAVTGGTESETLVRRAFRIASKSSAELMVVHVVHGDGLTGISAAQMGKVRELAVSLGATVHTVVGDDVPTALLDFARDINATQLVLGTSRRSRWARMFDEGIGATVVQQSQKIDVHMVTHEAAKRGFRWSSTSPRQRHAASWAAALMVPSLICAFSVAILDPFLDVGGKSALFFVGVLVVALLGGVAPAALSAVLSGLLLNYFLTSPRHTFTMSDPDSALTIVVLLAVAVAVAALVDGAAKRAREARHASREAELLALFAGSVLRGADLTALLERVRETYAQRAVSLLRETSDGATIVDCVGQDPCDRVAAADTAVEAGDEFWLLLSGRELPARDRRVLGAVANQAAGLVRQRELTEEAAKANAIAKADELSRSLLSAVSHDLRTPLAAAKAAASSLRSCDIDFSAEDTAELLATIEESVDALTALVGNLLDSSRLAAGVIHPELRPVYLEETVQRALLGIRRGPTGYGRSAVDRVKVEVGDSVALADGGLLERVLANLIDNALRYAPDGLIRVAAGVIHPELRPVYLEETVQRALLGIRRGPTGYGRSAVDRVKVEVGDSVALADGGLLERVLANLIDNALRYAPDGLIRVVTAGRVANKVLIAVVDEGPGIPRGAEDALFAPFQRLGDTNTTTGVGLGLSVAKGFVEAMGGTISAGDTPGGGLTVEIELAVPA	9~~KdpD (5.7279E-121)~~219;X;241~~Usp(1.37285E-33)~~362;X;385~~DUF4118 (0.000000190821)~~465;X(151);616~~HisKA (0.000000524543)~~678;X;735~~HATPase_c (1.32538E-26)~~835	KdpD protein
	5E-05	32.9	10	8.6E-05	32.1	6.9	1.4	1	K9W2P3_9CYAN	Multi-sensor hybrid histidine kinase	Cri9333_3808	Crinalium epipsammum PCC 9333	1600	1173022	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Crinalium, Crinalium epipsammum, Crinalium epipsammum PCC 9333	>tr|K9W2P3|K9W2P3_9CYAN Multi-sensor hybrid histidine kinase OS=Crinalium epipsammum PCC 9333 GN=Cri9333_3808 PE=4 SV=1MLRVIRDRTKPYIVTLGIVASALSLTLLLKPLLGTTNLPLFYAAVSVSAWYGGMNAGLLATLLSTIAIQYFFIIPLHNFAINDLTHIVRLGVFVLVTLLISSLNSELRAAKQRIEKSLIKLKASEEQYRLIVDTAYEGIWKYNSDAETEFVNQRLAEMLGYTSEEMLGRKVFDFIDKDKREQVEQILQRRKQGIKEQYDFCFRCKDNSELWAIVTSSPIIDQNGESIGGIAMLTDVTERKQAEFALKESEARFRSIVESDMIGIAFWESDGSIKDPNAAFLNIIGYREADFIDKKIRWQDLTPAEYFHLDAIALTEIKNNRFCTPFEKEYIRKDGSRVPILIGGCSFNGYTDKGAFFVLDITKRRLAEQALRQSESRLKHLVDSNLIGIIFADFNGNIIEANDAWLNILGYTRSEVLSGKINFLEITPPEYRHLDLQAIEEMKRTQKHTPFEKEYIRKDGSRIPVLVGTAYIPGDEGVGIGFLIDLSERKQIEKAINESENRFRTLIEQSPLSIQILASDGRTIKVNRAWEKLWGISIDKIPEYNMLEDQQLVEKGIMPYIKQAFAGEAVEIPAIKYDPNESIPDRTINQDPIRWVSAVAYPVKNEDGSIREIVLIHEDMTARKRAEDALQEREAELTLITNAVPVLISYIDTEQRYRFNNQKYEEWWGNSPTEIYGKHIQEVLGVAAYERVFPYIKTVLSGQQVSFESEIYYHKMGKRYVSITYVPQFGHNKEVKGFVALISDLTERKQAEDAIRESEERFRIMADTAPVLIWMSGLDKLCYYFNQRWLDFTGRTLEEELGNGWAEIVHPEDLQRYLDIYTNSFDAHQEFQMEYRLKRFDGEYRWVLNKGIPRFLPDGTFIGYIGSCADISDVYNELRLRKLAEAELQATNQTLQALIKACPLAITVFDFNGIVKLWNPAAETIFGWSEQEAIGQFIPPVPEHKQQEFIANLDAIKQGQQFIGLEARRQTKSGVMIDVALWAALLQDHQGNLNCISIIADITKRKQLEAERTKLLELEQAARIVAVNEAARSAAAQQRVAFLAEASRVLSSSLDYKTILSSIADLVVPGIADFCFFDAVTPENKIERVVWRHADPNKKEWFNQVQYYVPTHDVKAHPVTSVLLTGKAQFIPEVSDEWFQKIAINSEHLQFLRGLNSRSLITVPIIAHDRILGTLTFCVTPGFERSYTHDDLLLADDLAHRAALALDNASLYTEAQQANRMKDEFLATLSHELRTPLNAMVGWIQLLRTRTFDPQTSARALETIDRNTKSLAQLIEDVLDVSRIITGKLQLKTHPIEIVPVIEAAIETVQAAANAKYIKIECLLNSTEKVLGDPNRLQQVAWNLLSNAVKFTPQNGRVEVRLEQINNHVHIKVIDTGRGIKSEFLPYVFERFRQADNSITRSYGGLGLGLAIVRHLVELHGGTVHVESEGEGKGATFVVILPAIAHNHNQVKPETSTYNQNIDLSPPPDSVSSSLLSGLHILVVDDEPDARELLIAILGDYGAEVTAVSSAREAFELLQKLQPNVLVSDIGMPGEDGYTLIRKIRALHPEQGGKIPAIALTAYARTEDRNQAILAGFQLHISKPVNPTELATMVANLLIN	40~~DUF4118 (0.000000343171)~~110;X;135~~PAS (0.000000000039883)~~236;X(152);388~~PAS (0.000000000082086)~~484;X(161);645~~PAS (0.000425571)~~745;X;769~~PAS (0.000000000034018)~~871;X;903~~PAS (0.000000412014)~~1002;X;1051~~GAF (0.0000273497)~~1178;X;1219~~HisKA (1.19302E-16)~~1283;X;1337~~HATPase_c (3.9045E-33)~~1441;X;1482~~REC (9.1663E-31)~~1598	non-KdpD DUF4118 protein
	5E-05	32.8	10.2	0.00008	32.2	7	1.3	1	R6PMH6_9CLOT	Histidine kinase (EC 2.7.13.3)	BN618_00211	Clostridium nexile CAG:348	514	1263069	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	>tr|R6PMH6|R6PMH6_9CLOT Histidine kinase OS=Clostridium nexile CAG:348 GN=BN618_00211 PE=4 SV=1MGEQGAKRHNDSWKGIGVTIVILAIATGIGAMFRYLRFTEANILIVYVLGVMITAVITASRMWSVLSSLCSVLLFNFLYTEPRFSLTAYDSGYPITFVIAFLAAIIASNLAIQLRKQAEQSALMAYRTKILLETNQILQKAENAEEIIREAAGQIVKLIGKSVVYYECTDGILCEPSVCLAQGEQEKEIYISAKERETARYAFESKKRAGAGTEVKKDAVCMYLTIRNCDNVYGVIGIALKGVQLNTFESNLLLSILGECALALEKEIYNRKREEAVTKAKNEQLRANLLRSISHDLRTPLTSISGNAAILLNNEEAFDKEKRRQLYTGIYDDSMWLINLVENLLSVTRLEESSMQLNMQVELVDEVIEEALKHISRKREEHQLVYEPSEELLLAKMDSRLIVQVLINLVENAIKYTQEGSRIEVSAVQKADMIEISVADNGKGIKEEAKEKIFDMFYTAENKPADSRRGLGLGLFLAKSIIHAHGGTIWVADNVPSGTIFSFTLQAEEVTISE	19~~DUF4118 (0.000000000154723)~~117;X(166);283~~HisKA (0.000000000114749)~~349;X;402~~HATPase_c (6.43618E-29)~~505	non-KdpD DUF4118 protein
	5E-05	32.8	8.1	7.9E-05	32.2	5.6	1.3	1	R5TC08_9CLOT	Histidine kinase (EC 2.7.13.3)	BN544_00316	Clostridium hathewayi CAG:224	358	1263067	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	>tr|R5TC08|R5TC08_9CLOT Histidine kinase OS=Clostridium hathewayi CAG:224 GN=BN544_00316 PE=4 SV=1MKIKRQGKMPKEDLMRNIVVTSVFLLLATICSTLFLFIGGNRTNVGIVFMLAVMLTARYTDGYVPGIIASVIGVICVNYVFTYPFMELDFTLDGYPVTFIAMLLISGITSTTTTHLKEQNHILMEAEKETMRANLLRAVSHDLRTPLTGIIGASSAYLENRDHMSETEKTAMVSNINEDANWLLNMVENLLSVTRIRDSETQVTKSSEPLEEVASEAVQRFHKRLPDTVVHVTVPDEFIMVPMDATLIEQVIINLLENAVYHSHTDEPIDLTVTVHDGLAWFDITDHGIGIPPERLDTLFDGYTPSPNSSGDSHKGMGIGLSICKTIITAHGGTITAANGKHGARFTFTLPLGEDTYE	17~~DUF4118 (0.0000000074877)~~106;X;129~~HisKA (0.000000000169489)~~195;X;248~~HATPase_c (1.76835E-25)~~350	non-KdpD DUF4118 protein

	5E-05	32.8	10.5	0.0001	31.9	7.3	1.4	1	K8GLY6_9CYAN	Histidine kinase (EC 2.7.13.3)	OsccyDRAFT_0254	Oscillatoriales cyanobacterium JSC-12	767	864702	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, unclassified Oscillatoriales, Oscillatoriales cyanobacterium JSC-12	>tr|K8GLY6|K8GLY6_9CYAN Histidine kinase OS=Oscillatoriales cyanobacterium JSC-12 GN=OsccyDRAFT_0254 PE=4 SV=1MTRHRLFRLNAYLVAGFSVFVATVFTLLFQLSLANTILPFYFVAVAISSWHGGLKPGMVAVVCSVICVNYFFIP PINTFTVTTLGDLIRLGTFFTVATIISLLNENLRNAKQQLQQLSDSQLQTYAMQLQQALKAAHMGMWSWNLVTGEV TWSPEHEQLFGLAPGTFDGRIETFEAFLHPEDRESLNQAIQTAVQGQCNYQHEYRVVWQDGSIHWVEGRGQVF YNATNQPVYMAGTIMNIDQRKQAELALMQSEERFRSVFEQSPLAMMRFAPDGRLLCVNPAWETMWGTPPQMLA DYNILQDQQIAAIGDQPAVQRAFAGEVVDLPARFYDPALMGHSGQAHWVEPFLYPIQDCTGQVLEIILVSRDVTAR KQAEQSLQQLNNELEQRVATRTAELKVLNERLLQSLSELQSSKQEVEDLYNQAPCGYHSLDAEGRFIRINQTELN WLGYEADEILGKQFTDFLTPEGIRQFQKNFPILKQQGWIHDLEYDLRCKDGSLLPISLSATAVKDANGNLVMTRTN VFDRRERKRIDQIKSEFISIVSHELRTPLTSINGALELLSTGLLKPESERGQQTIQIAAQEADRLTRLVNDILDLERLES GKVRLEIKPCNLADLMFRAADFMQLAADQAAITLTVVPLSLSLNIDSDRILQVLTNLLSNAIKFSPPGSTVWLTAEFS SPPYSAPSILFSVKDQGRGIPPTMLESIFERFHQVDTSDSRKKGGTGLGLAICRNIIEQHGGKIWAESVVGQGSCF KFILPLENSQ	>tr|K8GLY6|K8GLY6_9CYAN Histidine kinase OS=Oscillatoriales cyanobacterium JSC-12 GN=OsccyDRAFT_0254 PE=4 SV=1MTRHRLFRLNAYLVAGFSVFVATVFTLLFQLSLANTILPFYFVAVAISSWHGGLKPGMVAVVCSVICVNYFFIP PINTFTVTTLGDLIRLGTFFTVATIISLLNENLRNAKQQLQQLSDSQLQTYAMQLQQALKAAHMGMWSWNLVTGEV TWSPEHEQLFGLAPGTFDGRIETFEAFLHPEDRESLNQAIQTAVQGQCNYQHEYRVVWQDGSIHWVEGRGQVF YNATNQPVYMAGTIMNIDQRKQAELALMQSEERFRSVFEQSPLAMMRFAPDGRLLCVNPAWETMWGTPPQMLA DYNILQDQQIAAIGDQPAVQRAFAGEVVDLPARFYDPALMGHSGQAHWVEPFLYPIQDCTGQVLEIILVSRDVTAR KQAEQSLQQLNNELEQRVATRTAELKVLNERLLQSLSELQSSKQEVEDLYNQAPCGYHSLDAEGRFIRINQTELN WLGYEADEILGKQFTDFLTPEGIRQFQKNFPILKQQGWIHDLEYDLRCKDGSLLPISLSATAVKDANGNLVMTRTN VFDRRERKRIDQIKSEFISIVSHELRTPLTSINGALELLSTGLLKPESERGQQTIQIAAQEADRLTRLVNDILDLERLES GKVRLEIKPCNLADLMFRAADFMQLAADQAAITLTVVPLSLSLNIDSDRILQVLTNLLSNAIKFSPPGSTVWLTAEFS SPPYSAPSILFSVKDQGRGIPPTMLESIFERFHQVDTSDSRKKGGTGLGLAICRNIIEQHGGKIWAESVVGQGSCF KFILPLENSQ	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, unclassified Oscillatoriales, Oscillatoriales cyanobacterium JSC-12	(0.000000000077057 2)~~110;X;136~~PA S (0.000000000022274 7)~~240;X;264~~PA S (0.000177965)~~369; X;425~~PAS (0.000000000031538 7)~~526;X;534~~His KA (3.16405E-17)~~600;X;653~~H ATPase_c (2.63179E-33)~~761	non-KdpD DUF4118 protein
	6E-05	32.7	7.5	0.0001	31.8	5.2	1.4	1	A0A0D4DJP8_9ACTN	Histidine kinase (EC 2.7.13.3)	T261_2153	Streptomyces lydicus A02	851	1403539	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	>tr|A0A0D4DJP8|A0A0D4DJP8_9ACTN Histidine kinase OS=Streptomyces lydicus A02 GN=T261_2153 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDLVVGFVEHHGRPRTEVMLHGLEHIARRDLEYRGTSF TEMDVDAVLERRPAVALVDELAHTNVPGSRNGKRWQDIEELLEAGIDVISTVNIQHLESLGDVVESITGVRQQETV PDEVVRRADQIELVDMSPQALRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYRAEH SIRSTWQARERIVVGLTGGPEGRTLIRRAARMAAKGSGSEVLAVYIARSDGLTSASPKELAVQRTLVEDLGGTFHH VIGDDIPVALLEFARGVNATQIVLGSSRRKAWQYVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGAR LGRARIVAGWLVGVAGPVLLSLLLTSVVNGPGLANDVLLFLFLTVVAALLGGQLPALASAAVGSLLLNFYFTPPTHT LTISDPKNIVAIVIFFAVAVSVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFGMETVVLL ERAGDVDPWTCAGRAGGTGTGAPPARPEDADVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQR LVGEAERARELAEGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVAWSEEDEKELLAGIEAGADRLDHLVGNLL DMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVTLDIPEELPIVAVDPGLLERSVANLVENAVKYSPDGETVLVS ASALGDRVEVRIADRGPGVPDSAKDRIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLAAEDTPGGGMTM VLTLRAAPGGPPVRPDVPAEAVT	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	1~~KdpD (2.5183E-122)~~211;X;233~~Usp(2.17746E-31)~~356;X;402~~DUF4118 (0.000000054122)~~466;X(150);616~~HisKA (0.000000000000201231)~~682;X;731~~HATPase_c (5.96416E-25)~~832	KdpD protein
	6E-05	32.7	7.9	9.9E-05	31.9	5.5	1.4	1	G8RR39_MYCRN	Histidine kinase (EC 2.7.13.3)	MycrhN_3443	Mycobacterium rhodesiae (strain NBB3)	840	710685	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium rhodesiae, Mycobacterium rhodesiae (strain NBB3)	>tr|G8RR39|G8RR39_MYCRN Histidine kinase OS=Mycobacterium rhodesiae (strain NBB3) GN=MycrhN_3443 PE=4 SV=1MTDRPGSQRKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDVVAAVVETHGRKKTADLIEGIETVPPKL VEYRGKQFPELDVEAVLRRAPQVVLVDELAHTNTPGSTNPKRWQDVEELLAAGITVISTVNVQHLESLNDVVTQIT GIEQQEKVPDEIVRAADQIELVDITPEALRRRLAHGNVYAPERVDAALSNYFRRGNLTALRELALLWLADQVDAALE RYREENQITATWEARERVVVAVTGGAESETLVRRASRIASKSSAELLVVHVVRGDGLSGVSAPQMGRVRELAVSL GATLHTVVGDSVGGVPAALLDFARDENATQLVIGTSRRSRWARIFDEGIGASVVQQSGPIDVHMVTHPEARKESL WSRISPRQRHLTSWLAAAVVPSAVCALLVLLLDPFLGVGGESALFFIGVLVVALLGGVAPATLSAVLSGVLLNYFLI EPRHTFTIAEPDNAITTVVLLAVAAAVSVLVDNAAKRAREARRASQEAELLALFAGSVLRGADLETLLERVRETYAQ RAVSMLRVNAGIVACVGDNPCVDVDSADTAIEVGDDEFWMLMAGRKLPARDRRVLTAVAKQAAGLVTQRELAEE AGKAEAISQADELRRSLLSAVSHDLRTPLAAAKAAVSSLRSDDIDFSAEDTSELLATIEESIDQLTALVGNLLDSSRL AAGVLRPELGPVYLEETVQRALLGISKGTTGFRRHGLDRVKVEVGDTVAKADSGLLERVLANLVDNALRYAPDSPI RVTAGQVGNRVLIAVVDEGPGIPRDNEDRLFAPFQRLGDQDTSIGVGLGLSVARGFVEAMGGTISATDTPGGGLT VEIDLAAAS	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium rhodesiae, Mycobacterium rhodesiae (strain NBB3)	10~~KdpD (2.17877E-121)~~219;X;241~~Usp(2.02045E-31)~~365;X;388~~DUF4118 (0.0000022622)~~467;X(146);613~~HisKA (0.000000000001935 14)~~679;X;736~~HATPase_c (3.72045E-27)~~836	KdpD protein
	6E-05	32.6	9.9	0.0001	31.8	6.8	1.4	1	A0A0F7NCT0_9ACTN	Histidine kinase	AA958_26985	Streptomyces sp. CNQ-509	853	444103	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. CNQ-509	>tr|A0A0F7NCT0|A0A0F7NCT0_9ACTN Histidine kinase OS=Streptomyces sp. CNQ-509 GN=AA958_26985 PE=4 SV=1MTRGKLRIYLGAAPGVGKTYAMLSEAHRRLERGTDVVVGFVEHHDRPRAEVLLHGLEQIPRRELDYRGTRF TEMDVDAVLARRPTVVLVDEMAHTNVPGSRNEKRWQDIKELLSAGIDVISTVNIQHLESLGDVVENITGVRQRETV PDAVVRKAGQIELVDMSPEALRRRMAHGNIYDPGKIDAALSNYFRPGNLTALRELALLWVADRVDDYLREYRSEH DIRDTWQARERIVVGITGGPEGRTLIRRGARLATKGAGGEIMAVYISRSDGLTPLNTAPPEELAVQRTLVEDLGGT FHHVIGDDVPDALLEFARGVNATQIVLGSSRRKAWQYAFGPGVGATVARESGPDLDVHIVTHGEVAKGRGLPLAR GARLGRGRIAAGWLVGLAGPVLLTAVMLRLDSTLGLANEVLLFLFATVLAALLGGTLPALASAGAGSLLLNYYFTPP VETFTIADARNIVALVVFFAVAVAVASVVDLAARRTSQAARLRAESEVMSLLAGSVLRGEGSLESLLDRVRETFGM ESVSLFERQRGEDGWTCVGRVGASAGAPAGPDDADADMPVGDDMTLALTGRKLPAADRRVLGAFAAQAAVVLE RQRLAAEAVEARKLAEGNRIRTALLAAVSHDLRTPLAAIKAAVTSLRSDDVAWSEEDEAELLTAIEEGADRLDALVG NLLDMSRLQTGTVTPLLREVDLDEVVPKALAGVPEGSVTLGIPETLPMVTVDAGLLERSVANVVENAVKYSPPGTP VLVQASALGDRVELRVVDRGPGVPDSGKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEALGGTLVAEDTPGG GLTMVLTLRAAPGRGTPAPAELPAQATT	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. CNQ-509	3~~KdpD (6.52155E-122)~~211;X;233~~Usp(2.46324E-31)~~359;X;386~~DUF4118 (0.0000190536)~~467;X(150);617~~HisKA (6.95436E-14)~~683;X;732~~HATPase_c (4.90523E-24)~~833	KdpD protein
	6E-05	32.6	8.6	0.00006	32.6	6	2.2	1	A6TMR5_ALKMQ	Histidine kinase (EC 2.7.13.3)	Amet_1278	Alkaliphilus metalliredigens (strain QYMF)	471	293826	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus metalliredigens, Alkaliphilus metalliredigens (strain QYMF)	>tr|A6TMR5|A6TMR5_ALKMQ Histidine kinase OS=Alkaliphilus metalliredigens (strain QYMF) GN=Amet_1278 PE=4 SV=1MYNLEKMRRKKIYEIISTVKILSILCCCMVIFSIYDDGKEIGIVSKVYELDLIILGLIGIIILILVYPIWVLLSKETEDRS IVGFKGNLEMGGFFLLLAILTLLSGGHTSNYKFLFLFIIIISTLQYGKKYGVNIALLSSLFILVVDLLSMSSLESNTYFQI DIVLSAVFLLTAWLLGDYVHIEKDYAQKMILYFNEREVAEKELVATLELDKIKNEFFGNISHELKTPVNVIFGTVQLLD VQAKEGNVCNDKYLKIMKQNCYRLIRLVNNLVDTTKLDSGFYDLNLQNVNVVNVVESITLSVAQYVEGKGLTLEFD TDVEEKVLACDSEKIERIMLNLLSNAVKFTDIGGKIIVNMTDKGSHIIISVKDTGIGISPKDLKVIFQRFKQVDKSLTRN SEGSGIGLSLVKSLVEMHGGRVYTESQLGKGSNFIIELPVKMVDTEENNYKGIFERGESSEIERIKVEFSDIYL	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus metalliredigens, Alkaliphilus metalliredigens (strain QYMF)	109~~DUF4118 (0.0000000100702)~~186;X;212~~HisKA (0.000000000012743)~~277;X;332~~HATPase_c (1.93885E-29)~~435	non-KdpD DUF4118 protein

	6E-05	32.6	8.9	0.00006	32.6	6.1	2.1	1	Q9A7X5_CAUCR	Histidine kinase (EC 2.7.13.3)	CC_1594	Caulobacter crescentus (strain ATCC 19089 / CB15)	892	190650	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter vibrioides (Caulobacter crescentus), Caulobacter crescentus (strain ATCC 19089 / CB15)	>tr|Q9A7X5|Q9A7X5_CAUCR Histidine kinase OS=Caulobacter crescentus (strain ATCC 19089 / CB15) GN=CC_1594 PE=4 SV=1MPVDDPKRPDPEALLAAANKARRGRLKVFLGMAPGVGKTYEMLRAARRRKAEGADVLIGVVETHGRRETESLLRGMDVLPRRPIEHRGRVQMEFDIDAALERKPKILLVDEYAHSNAIGSRHPKRWQDVEELLAAGIDVWTTLNVQHLESLVDVVQRITGVRQRETVDPDSALSRADDIELVDITPDELRERMAAGKVYVPETARLAADNFFKVENLTALRELALRRAAQTVDDQLIATMREKGVEGPWAAGERILVLVSGDAMAATLVRAGRRLSDMMMDAPWIVTHVERTDRPLARDGDAARLREAYRLAEQLGGATVALSGGDIVDTVMAYARRHNVTQIVIGKSVESRWRELLERSLAGALLREARGVAVHVVTEAAPEREPRPPAPLRPDRWRGYAVGALFIAAATLAAWGLDVAFNRVDLGMIFLTAVLAAGVLHLGLRPALAAATVAFLVYNCLFLEPRYSFVVGSPTDFITLVVFWAVALASGGLAGRVREQALGSQRRAAAVTTLLAASRTFSAASGRDAVAKALAEQVSAAAGGLAVVLLPQGDEIALAHGSPELAPLDAAQMAAARWAWDKGEVAGFGTGTLPQSRWTFWPLDGVRARTGVAGLAAGAAPLGADQERLVLALLEQGAVALERSQLAAEAVETETLRRADRFRSALMNSVSHDLRTPLSTVLGASTTLIDYGDKLAKPVREDLVVSIREEAERLNRYVANLLDMTRIEGGALRLRTDWIDVRDVLNAAADRVSRRLGGRELARDFPRELSLIQADASLLEQVVVNVLENAIAYSPPEARIEMAAYEDRANVVISIEDEGRGIPTSELERVFDKFRRMEEPSDRTQGAGLGLSIAKGFIDALGGRIAAASPIHDGRGTRILISLPKTVTTPHHLL	21~~KdpD (3.51939E-123)~~231;X;253~~Usp(1.22407E-39)~~377;X;399~~DUF4118 (0.000000000114198)~~498;X(160);658~~HisKA (0.0000000011793)~~724;X;777~~HATPase_c (7.0379E-24)~~881	KdpD protein
	6E-05	32.6	13.2	0.00011	31.8	9.2	1.4	1	A0A023Y7L0_9GAMM	Histidine kinase (EC 2.7.13.3)	DX03_18410	Stenotrophomonas rhizophila	886	216778	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Stenotrophomonas, Stenotrophomonas rhizophila	>tr|A0A023Y7L0|A0A023Y7L0_9GAMM Histidine kinase OS=Stenotrophomonas rhizophila GN=DX03_18410 PE=4 SV=1MSDPRTRQADALVERLQREAGGKLTVFLGAAPGVGKTFSMLSRAHEQLRRGVDVVVGLVETHGRAETSALLEGLPQVPLLQRDYQQHVLGEMDLDAVLARHPALVLVDELAHRNVPGSRHERRWQDVMELLEAGIDVWTTVNIQHLESLNDVVMRITGVRVSETVPDAVLDRLHDIVLVDIPPRELIERLQQGKVYVPEQAAQALQAFFSPANLTALRELAMQEAADRVDSSLRETRAARGEGNLPLRRRVLVAIDGGGQSEYLVRVGRRIAERRDAPWTVVTVQGRRNDEATRREIDAAFALARRLGGEAELLHGSSIADALLDHAAHNSVSTLILGRTRERPVARMLNRTLTQQLIQRGAHYEITIIGTPQARARARRTGLSVPSRSTGQDTLLALGATAIACLVALVAERWVGLYDLSMVFIVAVVMVAARSRTSAAVIAAALCFLAYNFFFIAPRFTFAISARQGVITVFLFLAAALVAGRLASRLRMQVLALRAANRHANARQALGRQLTRAASNEEVAQAGREALEQAMDAPAWLRIGQDTSTSGSAAPGDTDLAAADWARRHGQPSGRFTDTLAGAEWWFLPLLDGDDRAIGVAGMRFARNAPRLTPEQRQLAEAMVDDIAQAALRTQLVADLEKAHVSNETERLRSALLSSVSHDLRSPLAAMIGSADSLGSYADAMDAQDRRALLDTILVEGERLDRYIQNLLDMTRLGHEGLQINRDWIGVDELVGSAARRLQRYQPEVQLKLDIPATLAPIWVHPALVEQAVFNVMENAAKFSPPGAAVEVQARLVEGELRIDVLDAGPGIPDDERARIFDMFYSVERGDRGRHGTGLGLTICQGMIGAHGGSVQALPGRDGRGTLIRITLPLLQPHPADDHDDP	19~~KdpD (2.08221E-121)~~229;X;250~~Usp(2.62423E-30)~~370;X;397~~DUF4118 (0.000000000002026 48)~~491;X(159);650~~HisKA (0.000000000075320 8)~~716;X;770~~HATPase_c (1.70618E-21)~~872	KdpD protein
	7E-05	32.4	7	0.00013	31.5	4.8	1.5	1	V6KLU9_STRRC	Histidine kinase (EC 2.7.13.3)	M878_19640	Streptomyces roseochromogenus subsp. oscitans DS 12.976	845	1352936	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	>tr|V6KLU9|V6KLU9_STRRC Histidine kinase OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_19640 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRIERGTDCVVAFVEHHHRPRTEVMLHGLEQVPRRELEYRGTVFTEMDVDAVLARRPQVALVDELPHTNIPGSRNAKRWQDVEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNEYRREHRVSTIWGSRERIVVGLTGGPEGRTLIRRASRLAEKGAGGEVLAVYISRSDGLTSASPKELAVQRTLVEDLGGTFHHVVGDDIPVALLDFARGVNATQIVLGVSRRRSWQYAFGPGVGATVARDSGPDLDVHLITHDEVGKGRGLPVARGARLGRPRVIWGWVVGVLGPVPLTWLLTGAAPDVGLANDMLLYLTLTVAAALLGGLFPALASAVVGSLLLNWYFTPPVHTWTIADPKNIVAIAVFFGVAASVASVVDQAARRTHQAARLRAESEILSFLAGHVLRGETTLEALLERVRETFGMESVALLERTGETAPWTCAGSVGPEPARIPEDADVDVPVGDHMALSLRGRVLPAADRRVLAAFAAQAAVVLDRQRLQREADRAGELAEGNRIRTALLAAVSHDLRTPLAGIKAAVTSLRSDDVEWSERDQADLLEAIEEGADRLDHLVGNLLDMSRLQTGTVTPIIRESDLDEVVPMALGGVPEDSVELDIPETLPMVYVDRGLLERAVANVVENAVKYSPPGEPVLVSASALADREVRVVDRGPGVPDEAKDRIFEPFQRYGDAPRGVGVGLGLAVARGFAEAVGGTLLAEDTPGGGLTMVLAVPTAPERERPGGLVVSGG	1~~KdpD (5.19781E-124)~~211;X;233~~Usp(5.11039E-30)~~356;X;381~~DUF4118 (0.00000000268333)~~482;X(130);612~~HisKA (9.45605E-15)~~678;X;727~~HATPase_c (2.63844E-24)~~826	KdpD protein
	7E-05	32.4	11.2	0.00014	31.4	7.7	1.5	1	A1UKX9_MYCSK	Histidine kinase (EC 2.7.13.3)	Mkms_4295	Mycobacterium sp. (strain KMS)	836	189918	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. (strain KMS)	>tr|A1UKX9|A1UKX9_MYCSK Histidine kinase OS=Mycobacterium sp. (strain KMS) GN=Mkms_4295 PE=4 SV=1MTVANGPKRGELRIYLGAAPGVGKTYAMLGEAHRRLARGTDVVAAVVETHGRAKTAELLDGIEVLPPRHVTYRGGRFPELDVDAVLARRPEVVLVDELAHTNTPGSRNAKRWQDVEALLAAGITVISTVNVQHLESLNDVVTQITGIEQRETVPDEVVRSADQVELVDITPEALRRRLSHGNVYAPERIDAALSNYFRRGNLTALRELALLWLADQVDAALAKYRADNRITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVVRGDGLTGVSAPEMGRVRELAASLGATLHTVTGDDVPTALLDFARERNATQLVLGTSRRSRWARILDEGIGAAVVQRSGKIDVHMVTHDEAHRSPTASPRTRRAASWLAALAVPAAICALTVLLLDPLLGVAGESAVFFVGVLLVALLGGVAPAALSAVLSGLLLNYFLINPRHTFTIAEPDSALTIVVMLAVAVAVAALVDGAASRRREARHAAREAELLALFAGAVLRGADLTVLLERVRETYGQRAVSLLRIEKAGVVVACVGADPCVDVNTADTAIEVGDDEFWLLLAGRKLAARDRRVLSAVAGQAAGLVRQRELTEEAGRAEAIARADELRRSLLSAVSHDLRTPLAAAKAAVSSLRSDEVDFSADDRAELLATVEESVDQLTALVANLLDSSRLAAGVVRPQLSAVYLEEAVQRALLGISRGATGSGDIGIDRVEVDVDGCVVAADSGLLERVLANLIDNALRYAPDGPVRVTAGRVGERVLIAVTDTGPGIPPGGQDRVFGAFQRLGDQDTTSGVGLGLSVARGFVEAMGGTVTANDTPGGGLTVEIDLAAPQEAHA	7~~KdpD (1.03504E-121)~~217;X;239~~Usp(7.29206E-35)~~360;X;410~~DUF4118 (0.0000035244)~~460;X(145);605~~HisKA (0.000000000097867 73)~~671;X;728~~HATPase_c (1.57177E-28)~~828	KdpD protein
	7E-05	32.4	13.2	0.00012	31.6	9.1	1.4	1	H6MWK3_GORPV	Histidine kinase (EC 2.7.13.3)	kdpD GPOL_c44110	Gordonia polyisoprenivorans (strain DSM 44266 / VH2)	848	1112204	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Gordoniaceae, Gordonia, Gordonia polyisoprenivorans, Gordonia polyisoprenivorans (strain DSM 44266 / VH2)	>tr|H6MWK3|H6MWK3_GORPV Histidine kinase OS=Gordonia polyisoprenivorans (strain DSM 44266 / VH2) GN=kdpD PE=4 SV=1MVSTADARGTLEVFLGCAPGVGKTYEMLAHAHDLIGEGADVVIAVVESHGRSATAGLIEGIEVIPRRRIVYRGTELEEMDLDAVLARHPQVALVDELAHSNVPGSANAKRWQDIDVLRDAGIDVLTTVNIQHLESLNDVVAQITGVTQRETVPDAVVRAADQIELVDIAPQALRQRLSAGKVYPSGRIDGALANYFRQGNLTALRELALLWLADRVDDNLADYRAAHAITDTWEARERVVVAITGGAESSTLIRRASRIASRSSAELIVVHVVRGDGLAGRSGVELSELTELAAGFGARVHSIVGDDIPTTLLEFARGVNATQLVLGTSRRPRWKRIFDEGVGATVVASSGRIDVHMVTHEETAKRNRLDIRETRFHRPLSWVLAVVVPLVMTGILAILDRWLGFASETALFFVTVLAISMLGGVAPAALSAVVSGVLLNYFFTAPRFTLTINEPDNLITILVMLVIAIAVAALVDSATVRRVQAQRAAREAELLAVFSDAVLGGADVAGLLLERVRETYDQRAVSVVRRRADGTVEVSAAVGEDPPHRDSEADTVLPARGDEYELLLCGASPEAQDRRVLTAVATQATAALERADLEAGAAAARALAQTDELRRALLSAVSHDLRTPLAGAKAAVSSLRSEEVTFSPEDTAELLATIEESVDQLSALVANLLDSSRLEAGAIRPNMARTYLVEVVHRAANRSGPAAAGIAFRFGHVWAWTDGGLLERVLANLIDNAVRHGGGQVEVATSLDESDPQSPRTIIEVVDHGPGIPVERREQIFDDFRQGFDRNGSDGGVGLGLSVAQGFTSTMGGNLAVVDTPGGGTTMVVDLPAIEQSEQSAPAEGVAHG	7~~KdpD (6.00293E-114)~~216;X;238~~Usp(2.57E-31)~~359;X;382~~DUF4118 (0.000000000051728 4)~~476;X(134);610~~HisKA (0.000000000001169 52)~~676;X;725~~HATPase_c (2.41333E-22)~~830	KdpD protein

	7E-05	32.3	10	0.00013	31.5	7	1.4	1	F7YUX7_9THEM	Uncharacterized protein	Theth_1482	Pseudothermotoga thermarum DSM 5069	391	688269	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Thermotogaceae, Pseudothermotoga, Pseudothermotoga thermarum, Pseudothermotoga thermarum DSM 5069	>tr|F7YUX7|F7YUX7_9THEM Uncharacterized protein OS=Pseudothermotoga thermarum DSM 5069 GN=Theth_1482 PE=4 SV=1MRVYEIFIFSGLIFLVDIVFKYYGYLTADINPYVLFAVYVAARYGLMSSLILTFLSTLLTILSVYMHYGKAATQIVLSWATLRVPLLILMISIVAGILTDLRERKIRDLENELVITRNTIKEYKQNLEKYETITNTLQKRIVLEEGVSAFVEKLRQIELYNREDIFNQAIDLISKFIEATTISIYLLSSNNFLRLRVRKGPGFLPNSFPMNRSLVVSKSAELGVFSVADLYFTSENVDFSIEPAISVAIRSQEKVFGFILVEVISPEHLNRSTQTYLQVLADWLASLLEISSDLTNLVVTDDEMKFYSFLLKISERYEKYKIPYSVIHAKLGNSKEFDELKRLLRETDFVLHKEGELRIILTVCGEDGLKRVLERLQKVPSLTIEEAYSRS	5~~DUF4118 (0.00000125168)~~105;X;163~~GAF (0.00000000156861)~~289	non-KdpD DUF4118 protein
	8E-05	32.3	11.9	0.00015	31.3	8.3	1.5	1	U5VTG1_9ACTN	Histidine kinase (EC 2.7.13.3)	AFR_03310	Actinoplanes friuliensis DSM 7358	816	1246995	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	>tr|U5VTG1|U5VTG1_9ACTN Histidine kinase OS=Actinoplanes friuliensis DSM 7358 GN=AFR_03310 PE=4 SV=1MPRGRLRIYLGAAPGVGKTYTMLGEAHRRAQRGTDVVVALVETHDRTHTTAMIDGLEVLAPTPRGELDLDAVLARKPELAVVDELAHTNGPGSRHAQRWEDVDELLDAGIDVLSTVNVQHLESLNDVVAQITGVAQRETVPDAVVRAAEQVELVDMTPEALRRRVAHGNVYGPDEIDAALGNYFRAGNLTALRELALLWLADTVEDQLGRYRAEQDISATWETRERVVVALTGGPEGDTLVRRAARIANRTRGADLQAVHVMRNDGLTGADPAVLARQRVLVENLGGSYHQVAGPDIARALLDFARAVNATQIVLGASSRGRFAQLLTAGVGVTTTALAGAIDVHLVPHERAGKGTRAQRMPAALSRGRRLAGLALTLAGLPALTGLLLTLAPSLTTDILLFLMVVVAVALIGGLWPALLAAVAGSLLLNWFFTPPYGRFLIAEGDNLLALVIFVVVAVAVSWVVDQAARKTRLAAEAGADAQTLATVAGSVLRGTRPLPALLERLRETFQLTSVTLLERGEVVANVGDSACTDVAGADGAVQVDDELVMLLCGRSPAASDRRIVEAFAAQAAVALRQERLAAEAATARPLAETDRMRTALLAAVSHDLRTPLASAKAAVASLRSTEVHFDEDDRSELLETADESLERLDRLVTNLLDMSRLQAGALGVTIIGVGAEEVVPRVLDDLGPDGRAVITRIPDDLPALLTDPGLLERVLVNLVGNALRYSPADRPPVITASALGDRIELRVIDHGPGIPPDRHDDVFLPFQRLGDRDNHSGVGLGLALSRGLAEAMGGTVTPEETPGGGLTMVVTLPAG	3~~KdpD (2.05407E-106)~~204;X;226~~Usp(2.37689E-28)~~348;X;399~~DUF4118 (0.000000578277)~~449;X(146);595~~HisKA (0.000000000000355887)~~661;X;712~~HATPase_c (3.38517E-28)~~813	KdpD protein
	8E-05	32.3	8.4	0.00012	31.6	5.8	1.3	1	A0A0F2JBX0_9FIRM	Two-component sensor PilS	UF75_3161	Desulfosporosinus sp. I2	375	1617025	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus sp. I2	>tr|A0A0F2JBX0|A0A0F2JBX0_9FIRM Two-component sensor PilS OS=Desulfosporosinus sp. I2 GN=UF75_3161 PE=4 SV=1MLNHIPEPPARNRARALFDLIAIGLVVTILTIIHYTNYHYEMNFHILLQFAYYLPVIYAAMRFGPAGGILSGLVITLLILPFMTHFHALDPSAIYTQWVEIALINIIIGWLTGFLTGQERRAKRKYQIALTVQKELVEKLKKEGQERERLLGEIRQTERITALGHMSAGLAHEIRNPLGIMKVSIQMLAQEKNDDEVVSEYCRVLLEECERLNRLVSEFLSFARPKEPIRERITLGTLLDEGVSLIQPALRQNHIELERTQNLIDEHEVEVDPDQIKQVILNILLNAIHAQGEGGVILLEWVQQDGFVGFAVSDEGPGIPAEAMPYIYDPFFTTKEKGTGLGLSVVHRILDQHGGKISAANRSEGGVRVEILLPFI	16~~DUF4118 (0.000000106667)~~121;X;161~~HisKA (0.000000000000155929)~~223;X;275~~HATPase_c (2.30983E-24)~~372	non-KdpD DUF4118 protein
	8E-05	32.2	7	0.00021	30.8	4.8	1.7	1	K9Q5D0_9NOSO	Multi-sensor hybrid histidine kinase (EC 2.7.13.3)	Nos7107_0214	Nostoc sp. PCC 7107	1685	317936	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	>tr|K9Q5D0|K9Q5D0_9NOSO Multi-sensor hybrid histidine kinase OS=Nostoc sp. PCC 7107 GN=Nos7107_0214 PE=4 SV=1MPYIPYSQLLRYGFVVVIVATALVIMLLLDPLLDMKGTPFLLFFSAVMMSAWYGGLKAGLLATFLSVIVSDYFFLSEHYALSLSLSNGVKILLFAVQGLLFSFLCEELRHAKRKAEINLQKFKISEERFRVALSNSDIVVFQQDRNFRYQWVHNLQGIDKAEALLGKTDDELFPVAIAQQLTAIKRRAIEQDISAREEVCVILRGKVLYYDLLVEPLTGIDGGVTCVGVNITERKQTELEKAKLQSQLQQALQQKDESLALLNAWLMSSPMALAFLDTELRYVYANEALAAINGVPQNQHIGRTLPEVLPEWASQLEPIFQELMITKQPLLNQEISGETYPSGVYRYGLVSYYPVSLPDGQLLGVGITGVDITPVKKAEQALRESEAKFRSVVESNMIGIGFWEGDGRITDANEALLKMLGYSRQELVEKKLDWRNLTPVEYRRLDEQALTQFQENSFCTPYEKEYIRKDGSRFQVLVGGSCVEGTLERGAFFVIDITERKQAEDKLRYIAEISSLLSTSLDYEETLQQIAKISVPQLADWCIVDILEEDGSIRRLPVVYTDPFQAKLAQKLQEYVPNAQGTHLIARVLQTAIPKLIAEVSDSVLIAATQNEEHLEIVRQMGLKSVIVVPLIAHQRVLGCISFAIAHRCYDQADLNLAIDIAYRAALAVENAQLYRDNHQALINYAESLLLLDALLAGAPVAVCFLDRELRYVRINQVLADINGFPIEAHLGRKFGDIFSSMATQFEAQLQQVLETGEPLLNVEISGEMPGKPGVYGYWLGNYYPVRNALDETVGIGIMLSDVTATKVAEVALRESESRFRAMFNQAAVGIALVALNGKFLQVNPALCDITGYSQEELIQMSFQDITHPDDLAIDWEQAGRVLTKEISGYSLEKRYIRKDGSVVWVNLTSSAVWDIHGQAKYAVGIIEDISERQAALRDRQQAELAQTFLVEASSLLAASLDCQVTLNNVASLLVPTLADWCVVDVLGENDVIEQIAMISANLVQKERLTELRRRYPPRYENNSPFRETLLNKQSVFYPELPDQILAQMAEDEEHLKLLQSLGMNSLMIIPLHLRGKVFGVISLVRTASSSAYNSADLALAEDLAHRAATAIDNARLYQKTQQAKQAAELAVSRTVRLQKITAALSEAITPQQVADVVVNQGIAALGASAGSVSLLAEKGSCLKVVQATGYPSSVLDAWKSFSVTAAVPLAAAVRTGTPIFIESPAAFAANYPHLAELPSVTGNSAFACIPLILEKQVIGALGLSFSHTQIFSEADQGFMLTLGQQCAQAIARAQLYEAERHARSEAETANRIKDEFLAVLSHELRTPLNPILGWAKLLRTRKNDEATIVRALETIERNAKLQAQLIEDLLDVSRILRGKLSLHIRTVDLNSTMTAALETVRLAAEAKSIQLQTVLPQHKVEVMGDGDRLQQIVWNLVSNAVKFTPAEGRVEVRLAQVGMEAQIQVIDNGKGITPEFLPYVFEYFRQADGKTTRVFGGLGLGLAIVRHLVELHGGTVFADSPGEEQGAIFTVRLPLHKSTESVSTANSVQMDLATQDSLLAGVRILFVDDQADVLEFFSFALEQYGAEVTAVASAAEALEALVKLQPDILLSDIGMPIMDGYMLLRQVRQLPPDKGGEIPAIALTAYAGEIDYKQAMAAGFQRHIPKPVDPLDLAMAIVQLISQK	14~~DUF4118 (0.0000842361)~~115;X(284);399~~PAS (0.00000000244903)~~481;X;522~~GAF (0.0000000596258)~~669;X(158);827~~PAS (7.20618E-17)~~930;X;963~~GAF (0.000000000832979)~~1122;X;1148~~GAF (0.000000000001634)~~1292;X;1311~~HisKA (5.12483E-15)~~1375;X;1430~~HATPase_c (6.33501E-32)~~1534;X;1566~~REC (3.96458E-19)~~1682	non-KdpD DUF4118 protein
	8E-05	32.2	13.2	0.00014	31.4	9.1	1.4	1	A0A0F0LD98_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpDRS83_00569	Microbacterium oxydans	847	82380	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium oxydans	>tr|A0A0F0LD98|A0A0F0LD98_9MICO Sensor protein KdpD OS=Microbacterium oxydans GN=kdpD PE=4 SV=1MTRERRGRLRVLLGAAPGVGKTFEMLVEGRRLLDEGRDVMIAVVETHDRAATRAQTVGLPEIPRRTDVHRGVPLTELDLDAVLARRPEIALVDELAHTNIPGSRHPKRWQDVDALLDAGIDVITTVNVQHIESLNAVVEKITGIAQQETIPDAVVRAADEIEVVDLAPQSLRDRLAAGVVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALRSYRADHGIEGAWQARERVVVALTGGPEGETLLRRGARIAARSAGGELLAVHISTQDGLRDETPGALAAQRALRVESLGGSYHQIIGDDIPGTLVEFAQGADATQLVIGVSSRRGRLMAALTGPGIGSEVIRRSGDIDVHIVTHAAAGGRVALPRITGGALGWRRQVLGFAVAVVFGPLLSWVMFTFRSPESITSEVLAYQLLVVVVALIGGIRPAVFAAVLSGITLDLLFVAPLFTITIAHPLHVLALVLYVVIAILVSLIVDQAARRARTAKRATAEAELLAAVAGNVLRGDNSVLALVSRTREAFGLSGVRLLSPTGEVLACDGEPLADGRATSVPVGSDGTPRAMLELHGDSLDAPARRLLDAIVAQLAAAIEHTDLRETAKEVAALAETDQVRSALLSALSHDLRRPLASAVAAIGGLRGAHELSADDRAELLATADESLATLSTLVTDLLDVSRVQAGVLAVSSAPMDATGPILAAVDELGLGPADVDLSLDPNLPLLQADAVLLQRVLVNVLANAHRYAPDGTRVLISTSALGERAEIRIADRGEGVPAERRDSIFQPFQRFGDTDNTTGLGLGLALSRGFAEGMGGSLTPEDTPGGGLTMVISLPLAEADPLRHAQESLEETE	4~~KdpD (1.13447E-114)~~214;X;236~~Usp(4.86183E-29)~~359;X;387~~DUF4118 (0.00000000642391)~~480;X(131);611~~HisKA (0.00000000783989)~~676;X;727~~HATPase_c (4.22505E-23)~~828	KdpD protein

	8E-05	32.2	8.7	0.00014	31.4	6.1	1.4	1	D5VJC0_CAUST	Histidine kinase (EC 2.7.13.3)	Cseg_1856	Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (Mycoplana segnis)	892	509190	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter segnis, Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) (Mycoplana segnis)	>tr|D5VJC0|D5VJC0_CAUST Histidine kinase OS=Caulobacter segnis (strain ATCC 21756 / DSM 7131 / JCM 7823 / NBRC 15250 / LMG 17158 / TK0059) GN=Cseg_1856 PE=4 SV=1MPADEPKRPDPEALLAAANKARRGRLKVFLGMAPGVGKTYEMLRAARRRKAEGADVLIGVVETHGRRETESLLRGMEVLPRKPIEHRGRVQMEFDIDAALARKPKILLVDEYAHSNAIGSRHPKRWQDVEELLAAGVDVWTTLNVQHLESLVDVVQRITGVRQRETVPDSALSRADDIELVDITPSELRERMAAGKVYVPETARLAADNFFKVENLTALRELALRRAAQTVDDQLVATMREKGVEGPWAAGERILVLVSGDTMAASLVRAGRRLSDMMMDAPWTVAHVERTDRPLAKDGDAARLREAYRLAEQLGGATVGLTGGDIVDTVMAYARRHNVTQIVIGKSVESRWRERLGRSLATALLREARGAAVHVVTEAAHEPQPKPTRPLGQGLWQGYAVGALFIGVATLAAWGLDVTFDRVDLGMIFLAAVLAAGVLVLHGLRPALAAATVAFVVYNYLFLEPRYSLAVGAPTDFITLVVFWAVALASGGLAGRVVRDQALGSQRRAAAVTTLLAASRTLSAATGRDAVARALAEQVSAAAGGRSLVLLPEGEEIAPAFGSPSLEMLDAAQMAAARWAWEKGEPAGFGTGTLPQARWTFWPLDGVRARTGVAGVEAGAAPPGSDHERLVLALLEQGAVALERSQLASEAVEAETLRRADRFRSALMNSAAAERVSRRLGGRELARDYPRELSLVQADASLLEQVVVNVLENAIAYSPPEARIEMAAYEDRSNVVISIEDEGRGIPTSELERVFDKFRRMEEPSDRSQGAGLGLSIAKGFIDALGGRIAAASPIHDGKGTRILISLPKGVATPHHLL	21~~KdpD (3.67214E-123)~~231;X;253~~Usp(6.8613E-38)~~377;X;399~~DUF4118 (0.000000000043531 2)~~498;X(160);658~~HisKA (0.000000000647993)~~724;X;777~~HATPase_c (5.06607E-24)~~881	KdpD protein
	8E-05	32.1	10.8	0.00011	31.8	7.5	1.1	1	R6EMS0_9FIRM	Uncharacterized protein	BN749_01672	Firmicutes bacterium CAG:65	122	1262994	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:65	>tr|R6EMS0|R6EMS0_9FIRM Uncharacterized protein OS=Firmicutes bacterium CAG:65 GN=BN749_01672 PE=4 SV=1MFRSLSDKKSPRKSFRLKPPFTRHAISILICAACMLCATLASFLYQHIVPDNHANVALFYILALVIIARWTVGYGYGIACTLFSVIAINYLFTYPYYTLNFTLTGYPITFLLMSGAALSPSC	28~~DUF4118 (0.0000693521)~~118	non-KdpD DUF4118 protein
	8E-05	32.1	6	0.00015	31.3	4.2	1.4	1	E4NB97_KITSK	Histidine kinase (EC 2.7.13.3)	kdpD1 KSE_26670	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM 6054) (Streptomyces setae)	877	452652	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Kitasatospora, Kitasatospora setae, Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	>tr|E4NB97|E4NB97_KITSK Histidine kinase OS=Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) GN=kdpD1 PE=4 SV=1MVHTARGRLRIYLGAAPGVGKTYAMLAEAHRRIERGADVAVGFVETHGRARTAELLTGLETVPRRTMTHRGAEFTELDLDAVLARDPAVALVDELAHTNVPGARNAKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVEGITGVRQRETVPDEVVRRADQIELVDMSPQALRRRLAHGNVYAPEKVDAALAHYFRPGNLTALRELALLWTADRVDEYLQRYRAEQGIQGTWQARERIVVGLTGGPEGATLVRRAARIAARNSAGELLAVHISRSDGLSGSSPQALIEQRALVESLGGSFHTVLGDDPAAGLLDFARGVNATQIVIGTSRRKVWQYVYGPGVGYTVTRDSGDIDVHMVNHEHAARGRGRIPIRRVTDLGRTRTVAGWVIGVAGPPLLALLLTRLGGPGLSTDMLLFLALTVCAALVGGLFPAIASALVSSSALNYYFAPPIHTFTIAQPENIVAVAIFAAVGIAVATVVDVAARRSHVAARAQAEAQTLSALAGTVLRGAPTGEGVLTALLEQVRETFQQEAVALLERTDAHGPWQAAAAVGPRPPAGPEQADADVPVGERLALVLRGRVLPAADRRMLGAFANQAAVLLERRRLAGEAAAARREAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRAEDVEWDEEDEAELLAGIESGADRLDHLINNLLDMSRLQTGTVTPLLRPTDLDEVVPFALGGVPPGSVRLDVPESLPMVRADAGLLERVLANLVENAVKYGPPGSPVLVKADLLERSGRVELRVVDRGPGVPEEARERIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGAVTAEDTPGGGLTMVVALPAAPSGPHPDERTERTERTEHAERAEQGGRTERDERKAGPA	5~~KdpD (3.0703E-122)~~214;X;236~~Usp(4.9536E-22)~~358;X;413~~DUF4118 (0.000000533705)~~472;X(146);618~~HisKA (0.000000000001606 49)~~684;X;733~~HATPase_c (2.80406E-26)~~836	KdpD protein
	9E-05	32.1	5.4	8.6E-05	32.1	3.8	1.8	1	E8V6Y2_TERSS	Histidine kinase (EC 2.7.13.3)	AciPR4_4263	Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	481	401053	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus saanensis, Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	>tr|E8V6Y2|E8V6Y2_TERSS Histidine kinase OS=Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4) GN=AciPR4_4263 PE=4 SV=1MNSQRAVAITRWTITSLALAGIVLVYSRWLHVNPTTVALTLVLLILVLAAKFSLRYAVGASIVAAGCFNFFFLPPVDTFTISDPQNWLALLTFLATGVIGSRLSQRARDEAEDARARQREIEILFTLSRELLQAENVAALVNTLPSVIAGVSSAESVALFLLQGDRLYQSGQRATSTIDAVHLRQIALTLNGPETVPGDEIRIPLRSGVRPRGLLMLRGVTLSEGSFQAMGGLVSIALDRVEALENVAKSEAAKESERLRTLLLDSITHELRTPLTSIKGAATTLLSNDNISEADRLELLTIVDEESDRLNRLVSQAVEMAQLEANEVHMTFAPMSMEEAIGRAREACAHVEQMHPLQVSLPPLPPVMADIEVVIKVLCNLLEAAKYSAEGSPIFVSAVHEGDEVLTSVADRGIGIPSDEQPLIFDRLYRARSQGGTIPGTGMGLAISRAIVEAHGGKITVTSQPGHGSVFTFSLPVVEI	52~~DUF4118 (0.000000340224)~~110;X(147);257~~HisKA (0.000000000040639)~~322;X;377~~HATPase_c (4.80637E-29)~~476	non-KdpD DUF4118 protein
	9E-05	32.1	7.9	0.00014	31.4	5.4	1.4	1	K9XRW2_STAC7	Putative PAS/PAC sensor protein	Sta7437_1701	Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	629	111780	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Stanieria, Stanieria cyanosphaera, Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	>tr|K9XRW2|K9XRW2_STAC7 Putative PAS/PAC sensor protein OS=Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437) GN=Sta7437_1701 PE=4 SV=1MFKSQSQLQSYGLAISATFLALVLMLGLDPWFETSQTPFLLFFGAVTVSALFGGTRSGFLATVLSALLINYFFLELKRAISFELVNNVRLLLFILQGFGISYLCGAFRTAEKKAQVSLKQLQRSQEALRESEEQYRQLAENLVEIGFWLSEPQKARLIYVSPAYERIWGCSRTNLYANFMAWSEAIHIDDRERVQKAFYEQALCGGYDQEYRIVRPDGSVRWIHDRGFPMKDESGEPYRVVGLVEDISERKETEISLQETLERLNLAQDSAHAGWWNWDMVNNHVIWSEEYRDLFGLDSTIVPSYENWLACIIEEDREQTDCKTRQALEKQTELNVEFRIQHPSKGMRWLMAIGRPFYSSEGKPVRMAGITLDITERKHSEEALHQSEAIALAWAKELETFMETVPAAIWVARDPQCYQMSANRTAYELMRVPFGSIATSTPASGGQYPFSFKTFKNGQEVPLEELPMQRAARTAQEVEEEIEFVFSETDIRYLYGKAVPLLDEFGKVRGAIAAFLDITERKQMQEALRRREEELRLVTNQVPVLISFVNSQQRYRFNNLTYQKWFGRSPAEVCGKHLREVLGESAYQKILPYIEQVLAGQQVSYSSQIPYQDGGTRYRDREQLLQFNCR	13~~DUF4118 (0.00000000386237)~~114;X;156~~PAS (0.000000000039534)~~247;X;271~~PAS (0.00000721135)~~374	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	9E-05	32	11.3	0.00017	31.2	7.8	1.5	1	B0SYJ2_CAUSK	Putative transmembrane protein	Caul_4237	Caulobacter sp. (strain K31)	190	366602	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Caulobacter, Caulobacter sp. (strain K31)	>tr|B0SYJ2|B0SYJ2_CAUSK Putative transmembrane protein OS=Caulobacter sp. (strain K31) GN=Caul_4237 PE=4 SV=1MATGALKTTDRPRWREAARGALGREPGALLGYGVALLGVAAAALAAFLAEHLITAPNLALIFVIPVLGVAFAYGWRASLLAAVAAVLTYDYLFVTPRFSLRVGSPSDMWALLLLAIVAAVASAVAAQSRRQAARASGEADRAEALRGLARSVTEGASSAAVIVSASQALGRIFQAPVVVLVERDTGPPPP	50~~KdpD(5.89E-09)~~190	KdpD protein

	9E-05	32	9.7	0.00015	31.3	6.7	1.4	1	E8SI99_STAPH	Histidine kinase (EC 2.7.13.3)	SPSINT_0108	Staphylococcus pseudintermedius (strain HKU10-03)	874	937773	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus pseudintermedius, Staphylococcus pseudintermedius (strain HKU10-03)	>tr|E8SI99|E8SI99_STAPH Histidine kinase OS=Staphylococcus pseudintermedius (strain HKU10-03) GN=SPSINT_0108 PE=4 SV=1MERHLTIKRGALTIYLGYSPGVGKTYEMLSNAIDAYHEGADIKIGYIEPHQRKETQALAEQLPVIQTKSKNHGSHTFHYLDVDQIIEDDPDVVLIDELAHTNISKERHEKRYMDIEEILSHGIDVHTTLNIQHIESLSEQVALLTGVKIKERVPDQFIMSSDAIEVIDISPKQLINRLKAGKVYKKERLDTAFSHFFTYENLTELRELTLRTAADMMSQKEHLYKKNTDITPHVAVAISGSISNETVIREARRIANREHAQFTAVYIDVFDHEGKQYANNSQVHQNLMLAQSLGASVKVIYDNQIASGLDDWCKSQKVTKLVIGQHMNDKWHTRLKRPLIDQLLDLKHHYKIEIVPIKHIQMKAKPERQHQHMQQKRWTVDIFKMIAIQAICVLLGLWIYSTGKGEQDTIILLLFLLGIVVLSMWTQSYLIGFFAAILNVLVFNFFFTVPRFTFEVYRFDYPITFTISIIVSIVTSGLLKQIKHQYIVTKHQLYRTDILLQFNDSIKQTYTIPDLLVNARHQIQHLLKQEVTIYLVEDEKISKTIPVEGPQTNDSRHQQALSWIIKNQKRAGATTDTFPGIHYLLIPIGTKPVKAIVSIHFSEAQIIDSYDNSILESMLNEMSLAVENLSLLRQTRESMLRAEREVARAHFLRSISHDIRTPLTSIIGNLDVLLLNGKEMPRAEQQQLVSRSFDEAQYLHMLVSNILSLTRLEHSNMKLNRQLYLIEELVEEIESVLERRRLNKQVKVSALHEICFVDIDSQLILQAVFNLIENALKHTPPETPITLRINKNEPHILFEVIDRGPGLSDEEQQTIFQPFEKHQLFKDNKKDSMGLGLYLVQAILQKHDSQLKYRQNEPHGSIFYFNLPFEKNTN	8~~KdpD (5.14653E-107)~~215;X;233~~Usp(4.46822E-32)~~356;X;432~~DUF4118 (0.0000067264 6)~~476;X(169);645~~HisKA (0.000000000102214)~~711;X;764~~HATPase_c (6.87918E-23)~~867	KdpD protein
	9E-05	32	9.7	0.00017	31.2	6.7	1.4	1	E7GNZ5_CLOSY	Histidine kinase (EC 2.7.13.3)	HMPREF9474_02640	[Clostridium] symbiosum WAL-14163	498	742740	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	>tr|E7GNZ5|E7GNZ5_CLOSY Histidine kinase OS=[Clostridium] symbiosum WAL-14163 GN=HMPREF9474_02640 PE=4 SV=1MASEQRGETDSLPKKIVKMTVIYILATLLALGLWTIRVRAENIIMVYLISVIILMIEIHQFLWGGIYTVICILSFNFFFTAPRYTLRVNDPNYIVTMVIFLIVSVITGLLVSKLREQVEVSQRNENRMKALFEISCGYLKLSGLDNIVYYVLKSLFQAAGERCVVYLAKSPGELGKPYFIKSHFDENMVDNNTPAVWCFINNTVCGAGTGFFSDSRWVYMPVKNRESCIGVIGIYTDGKEVDSNHMVFVNTVMSEMVMAVEKENIELERSRVELEGQRGKFLDALNHSLQCNFIRPFTSNMEEFKNVIAGCREEDRQRNRLSELYLRFRTLYNRTVNTIQMYNIEFGEVYAEREKTDFQKLVDEALACYEECAGERIVWLRRPDGELPVRVDAGQMKQVISNILNNALVYTPENTKIYISLTKEQGKGKLEISDSGSGITPQLLQKSMSDEEKQENILGCGLIAASEIVEANGGRMIIRSSQYGGTLFMISLEEAEPD	15~~DUF4118 (0.000000000022660 4)~~117;X(279);396~~HATPase_c (2.12179E-15)~~492	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	1E-04	32	11.9	0.00016	31.2	8.3	1.4	1	E9T4H6_RHOHA	Histidine kinase (EC 2.7.13.3)	HMPREF0724_13396	Rhodococcus equi ATCC 33707	857	525370	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus hoagii (Corynebacterium equi), Rhodococcus equi ATCC 33707	>tr|E9T4H6|E9T4H6_RHOHA Histidine kinase OS=Rhodococcus equi ATCC 33707 GN=HMPREF0724_13396 PE=4 SV=1MRSPRVNDGVVSSPEQHRAPRRGELRIYLGAAPGVGKTYAMLGEAHRRLERGGDVVAAVVETHGRARTAEQAAGLELIPPKFVEYRGTAMPELDVEAVLARRPAVVLVDELAHTNTPGSRNEKRWQDVYELLDAGIDVLSTLNVQHLESLNDVVQQITGVTQQETVPDAVVRAASQVELVDITPEALRRRLSHGNVYSAEKVDAALGNYFRRGNLTALRELALLWVADQVDAALAKYRAENKITDTWEARERVVVAVTGGPESETLVRRASRIAGKASAELMVVHVVRGDGIEGVSAAEMGKVRKLATSIGASLHSVVGDDVPTTLLEFAREVNATQLVIGTSRRSRWARILDEGIGAAIVQQSGSKIDVHMVTHDEAATRHRISFLGRGERRAVSWLAAVVVPSIAAALMGLIDRVAGVGGQNALFFVVVLVVSLLGGVGPAILSALISGLLLNYFFTAPLYSFTIAQPDNFITTVVLLVVAVAVAILVDAAAKRSREARRASQEAELLALFAGSVLRGADLPALLEKVRETYSQTGVSVVRRGEGVVSAAGASAPSTVDEAGTVCEVSDGEYALLLAGEELGARDRKVLYAVANQAVGLIRQRQLAEEASKAQALAEADRLRRSLLSAVSHDLRTPLAAVKAAVSSLRSDDVEFSPEDTAELLATVEESTDQLTALVGNLLDSSRLAAGVVKPTLRRVYLEEVVDRALVSGANLSDDVEFSPEDTAELLATVEESTDQLTALVGNLLDSSRLAAGVVKPTLRRVYLEEVVHRALVGAGFGGPGSARRVRDQVKVEVGDAAVMADAGLLERVIANLVDNALRYAPDEPVRIGAARAGDHMTITVADTGPGLARGTHEQVFDAFQRLGDRDNTVGVGLGLSVVKGFVEAMGGTVGVTDTPGGGLTMIVELDAAPAGAGEVEGAR	20~~KdpD (1.07133E119)~~230;X;252~~Usp(3.35176E-33)~~373;X(247);620~~HisKA (0.000000000013584)~~686;X;743~~HATPase_c (3.40198E-27)~~843	KdpD protein
Disagreement between HMM and CDD prediction	1E-04	31.9	10.8	0.00018	31.1	7.5	1.4	1	C8XB10_NAKMY	Osmosensitive K channel His kinase sensor	Namu_5030	Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	815	479431	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Nakamurellales, Nakamurellaceae, Nakamurella, Nakamurella multipartita, Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	>tr|C8XB10|C8XB10_NAKMY Osmosensitive K channel His kinase sensor OS=Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) GN=Namu_5030 PE=4 SV=1MGTRGQLRVYLGAAPGVGKTYKMLEEAHRRLERGTDVVVGVVEGHERPLTEALLVGLEVIPRQVRPYRGARFAEMDLDAVLARRPQVVLVDELAHTNVPGSRHGKRWQDVEELLDAGITVITTVNIQHLESLNDVVQEITGVVQRETVPDEIVRRADQIELVDMTPEALRRRMAHGNIYRPDKVDAALHNYFRVGNLTALRELGLLWLADKVDDQLDRYRADHHITDTWEARERVVVALSGGPEGDTLIRRAARIADRTKGTDLIAVTIIRSDGLAGPGPAHLARQRALVESLGGTYHQVVGADIPTALLDFARGVNATQLVLGASRRGRFAQLFARGVGVTTTAGSGAIDVHLVTHEKAQSGRRPPRPSWAGALTRRRRVLGFVLALVGMPLLSLALIGLRGQLSLPSDILALLLGVVGVALVGGLLPALVAAFLGFGLLNYYFVPPLHQFTVAEAENLLALLAFLLVAVAVSVVVDLAARRTGQASRAQAEAATLSTLAGSVLRGERPLPALLEQVRETFGQDSVTLLERHPDTVAGPDLRRDQRAWSVAAWVGESPSTAPAQGVEVAVNDEVSLVLRGPALAAADQRIVEAFGAEAAVALRQQRLSEQAAAVVRLTEVDRLRTALLTAVGHDFRTPLAAATAAVTSLRSSDVTFGPQDRDELLATAEESLARLSRLVENLLDMSRLQAGALAMHLQPIGVAELVPIAVDDLGEAGRAVQVRDADDVPDVTADAALLERVLANVIANAVRHSPRTGRRWSPSASTTGGSRCASSTATVPAASVWAWRCPAD	2~~KdpD (1.96103E-114)~~212;X;234~~Usp(1.76203E-29)~~356;X(266);622~~HisKA (0.000000000672718)~~688	KdpD protein
	1E-04	31.9	13.7	0.00016	31.2	9.5	1.3	1	Q8YLH1_NOSS1	Histidine kinase (EC 2.7.13.3)	all5327	Nostoc sp. (strain PCC 7120 / UTEX 2576)	559	103690	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	>tr|Q8YLH1|Q8YLH1_NOSS1 Histidine kinase OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=all5327 PE=4 SV=1MRKLTRWAFPNLWRRSLTDQRSSQPQSHSIAFFSVLLALILTLLLWQIQRLNSIYPPFLAAVMVSSWYGGFNSGLLATFLSAVVCSYFLLHPFYSLAVSGFSVVGLLQFVLVGLLISSLNSALRQARSQAQMNARVAQQNYERLLQSQYNLRRSEERYRLLVEGVTNYAIFMLDSNANFTTWNIGAERILGYQEAEIIGQPFELIFAPEAIERGQPQQVLKQALTEGFSRENRWHIRKDGTFFWAHCLITPLRDENGNLRGFSKIMQDITERKQAEEEKEQLLLREQAARAEAEAANRSKDDFLAIVSHELRTPMTAIIGWAGMLQTGALDEARASLALETIERNANLQMQLIEDLLDISRIVRGELSLSIDLVDLVEVITDAIEVVQSLADNKGIQIKSRPDTSIDKIWGDSDRLLQVVLNLLTNAIKFTPNGGRIEVCLSKELGTGDWGLGLNRGDETNVSCPIPHYAQIQVIDTGQGISADFLPHIFERFRQADSSHTRSNKGLGLGLAIARHLVELHGGTIQAQSQGIGQGATFTVKLPITEESRGVNTIQHNHHC	51~~DUF4118 (0.000000348641)~~126;X;166~~PAS (7.50221E-14)~~269;X;299~~HisKA (1.9898E-15)~~361;X;416~~HATPase_c (6.90629E-28)~~541	non-KdpD DUF4118 protein
	1E-04	31.9	11.8	0.00017	31.2	8.2	1.4	1	W0JK97_DESAE	Histidine kinase	DESACE_07650	Desulfurella acetivorans A63	652	694431	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfurellales, Desulfurellaceae, Desulfurella, Desulfurella acetivorans, Desulfurella acetivorans A63	>tr|W0JK97|W0JK97_DESAE Histidine kinase OS=Desulfurella acetivorans A63 GN=DESACE_07650 PE=4 SV=1MQENDIKRPSPEELLEVAKQQEASEQKKGKLTIYLGYAPGVGKTYTMLSDAHLRKKEGIDVVVGYAETHGRVETEKLLEGLEVIEPLIVDYKGLKLKEVNFEKIIQRKPQLVIIDELAHTNPPNFKNVKRYQDVEEILNAGIDVYTALNVQHIESLNDLVYQITNIAIKETVPDKFIEQASEIKLVDLTPEELLKRLHEGKVYVRDMAQAAIGKYFRSGNLLALRQIALRIVADSVDGKMRSYMKQHAIAGPWAVKEKVLVGIFASPYAEQLVRATYRFATEIDAQWIAVHVETQKNQYFTDQEKAWLNKAFDLVRSLGGQIVWIKGDDITTEIVNYAKSQNVTKIVIGKPRKFSMFSPTIPEKLIMQTEFIDVYLIAPKDKKPQEFLKKKKYGIKNIKDYLYSTINIGAVTLLSLILKNHLNHSSLMSIFLAALVLNALIFEIPAVIVSIVISLVFDFFFIPPQYTFYISNFNYLISFLVYVVVIVFISVLATKLKTKVNLLKESQLRELSLYELSNNLVMASTKEQVLSILINHIKKLFNVEAAIFIADENNKLKVGAKTKDFEINSETLGIANWSFINKKNAGFGTDTISNATALYIPMITTNGVFGVIAINLKQLNKPVTIDQTVAIDAIAHLGAIALERLKLMRCS	27~~KdpD (1.52678E113)~~236;X;258~~Usp(5.02857E-32)~~378;X;401~~DUF4118 (0.000000321014)~~500;X;528~~GAF (0.0000003715 51)~~645	KdpD protein

Disagreement between HMM and CDD prediction	0.0001	31.8	8.6	0.00016	31.2	5.9	1.3	1	Q838F4_ENTFA	Sensor histidine kinase KdpD	kdpD EF_0570	Enterococcus faecalis (strain ATCC 700802 / V583)	850	226185	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus faecalis (Streptococcus faecalis), Enterococcus faecalis (strain ATCC 700802 / V583)	>tr|Q838F4|Q838F4_ENTFA Sensor histidine kinase KdpD OS=Enterococcus faecalis (strain ATCC 700802 / V583) GN=kdpD PE=4 SV=1MQSGDGRRGRLRIFFGFAAGVGKTYGMLTEAHELLMMGKHVVVGYIEPHDRPDTNRLLEGLPQIPPKNIFYKQMVLTEPDIDQIIQQKPEIVLIDELAHSNAEGSRNRKRYQDIDELLNAGIDVFTTVNVQHIESLNDIVEEVTGIEVKETVPDTFLRQATIRVIDVEPDELIERLEQGKIYANENAKRALKNFFIPQKLDQLRGLAIQRASDHINRISGKTIGIQSKLLTVVNDAFPKMTEKCIRWTARLAQGLVVDWTVIQVRTQENTPTNIPLADKLGAEVISIEEDDSFETIVEFAKMTGVTDIIMGKNLRQPWYEKIFIEAFDDRLLKRLKDTELHLIPFNEEKRSLFFKTRKVIEGGGKDLVIAIGGVFLATVVTELMQYIHVGDQNLMLIYISFVLLVARTTSGYFWSSLSSILSVLSFNWFFVEPLYSLTVYKQGYPFTLLLMLVVALMSSNLMIRLKKQADTSMKKEHQMEILYELNKRYVLVESRKQILDISATYLSRLLEREVIIFDRQVKTESVHCINEKKSILNNEDEAAVAFWAAKNQKEAGNGTDTLNGAKGFYLPIAAGRKTLAVLGIERNADLDLENDQLNYLKLVLTQIAVILEQTELKDEKQVELENEREKVRSNLLRAVSHDLRTPLTVISGIAETLGIGNDLKEETQRKLLKDIQEESQWLIRMVENLLSITRINMDTMKVNKTAEPVEEVIEAVYKHLRKVYPDGQVDIHLPEEVIFIQADPILIEQALFNLIENAFRHGENDLPVKLNVYQEKEQTVFEIENHGEIPLKQFQKIQSNLSGTNEVPVDSKNGLGIGLSIVKTIVHAHNGKMEMTIGRGKTLVRIYLK	6~~KdpD (1.70682E-121)~~215;X;228~~Usp(6.15568E-31)~~344;X(153);497~~GAF (0.00000363306)~~612;X;630~~HisKA (0.000000000000197056)~~695;X;748~~HATPase_c (0.000000000004809 3)~~849	KdpD protein
	0.0001	31.8	12.7	0.00019	31	8.8	1.4	1	K9ZJM4_ANACC	PAS/PAC sensor hybrid histidine kinase (EC 2.7.13.3)	Anacy_3129	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	894	272123	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	>tr|K9ZJM4|K9ZJM4_ANACC PAS/PAC sensor hybrid histidine kinase OS=Anabaena cylindrica (strain ATCC 27899 / PCC 7122) GN=Anacy_3129 PE=4 SV=1MKVRVSLILEYIVAIVSVSIALLLTAVLHVTLQSDVFLMFYAAVAISTWYGGIKPGILATILSIIAVGYYFIDPKFSFYIGNQNSVIKLVLFLLVTIFLSWLNSELRTAKQNLKISNQQLAFSELKFRRLRNSNIIGVIISEINGSILEANDAFLNIIGYTREDLLSGRINWREITPPEYLEQSKNIIIELKKIGFHQPFEKEYIRKDGNRISILMGLALLEKNSEQVIGFAVDLSKRKQVEDNLRQKEEELRLITNTLPVNISYIDAQQRYRFNNKGYEEWFGVPTSEIYGQHLQEFLGESVYQSIYPYVETVLSGEQVSYESKLFHQDGKQHDVSITYIPQFNQQGKVEGFVALIRDITEQKQAQAALKQSEEKFRKLTEKVRVIPWEADAATGNFTYIGPQTEDILGYPLNDWYSDNFWTQHIHPEDQEWVIKYCLECSHSLNNYEFEYRMLAADGSVVWLYDIVSVVQGEDRPKQLHGLMIDMTERKQVEQEREQLLEREKAARAEAETANRIKDEFLATLSHELRTPLNAILGWIQLLRSRKFDENTTVIGLETIDRNSHALAQLIEDVLDVSRIIRGKLQLNLHAVELIPVVVETAIETLRPAADAKEIVIESEFDPAAGIVTGDANRLQQIVWNLLTNAVKFTPKGGRVKVQIERINSRVQIRVTDTGAGISADFLPHVFERFRQADSSTTRSHGGLGLGLAIVRHLVELHGGTVSATSPGIEQGATFIVNLPMKAVAISDKPEQFSPIKNSDYVNHQLSILEGLRVLIVDDEADARHLLTTILGQYGAKVMAVSSAPEAITALPEFHPDILVSDIGMPQEDGYTLIRKIRTLPSDEGGKIPAAALTAYAAEDRTQALLAGFQLHIPKPVNPTELAAVVANLAQRTR	11~~DUF4118 (0.000000000746764)~~107;X;137~~PAS (0.00000000125074)~~233;X;259~~PAS (0.00000866737)~~360;X;394~~PAS (0.000000178773)~~487;X;515~~HisKA (2.14979E-15)~~579;X;634~~HATPase_c (3.62433E-32)~~738;X;774~~REC (1.2445E-21)~~890	non-KdpD DUF4118 protein
	0.0001	31.8	12.1	0.00016	31.3	8.4	1.2	1	R6ZT57_9FIRM	Histidine kinase (EC 2.7.13.3)	BN699_01309	Firmicutes bacterium CAG:534	369	1263027	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:534	>tr|R6ZT57|R6ZT57_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:534 GN=BN699_01309 PE=4 SV=1MKQTKRTGSSLFSPQYMVRDILISLFLLAGATAISFGFFHVVPENSANIALIYISAVVLTARLTNGYLYGIVASLVSVVAINYLFTPFFAVNFTLTGYPVTFIVTLLISISVSTLTTRIKEQADTLIEREKFLMEAEKEKMRANLLRSISHDLRSPLTGIIGNSTAYIDNAESLSDTEKLELVKHIREDSNWLLNMVENLLSVTRISANSMKIATSMESVEEVVSEAISRLRKRLPDAAIKVQVPEEFLMLPMDAMLIEQVIINLLENAIVHSKSTLPAELTVTADPRQASFHVKDYGIGISPDKLDSIFDGSCYDPDSSSDGHRGMGIGLSICKTIITAHNGEINAINHENGCEFIFTLPRNEETKA	21~~DUF4118 (0.000000000915293)~~123;X;140~~HisKA (0.00000000199324)~~206;X;259~~HATPase_c (9.97952E-23)~~361	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0001	31.8	8	0.00024	30.7	5.6	1.5	1	A0A0A8F4C3_9ACTN	Histidine kinase (EC 2.7.13.3)	GZL_08788	Streptomyces sp. 769	865	1262452	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	>tr|A0A0A8F4C3|A0A0A8F4C3_9ACTN Histidine kinase OS=Streptomyces sp. 769 GN=GZL_08788 PE=4 SV=1MVREGLSVAPNRVAAEASDARPGKLKVFLGAAPGVGKTYRMLDEGRRRLRRGTDVVVAYAECHGRQYTEEMLDGLEMVPRLHRSYRGSTFTELDLDAVLARRPAVALVDELPHTNVPGGRNAKRWQDIDELLAAGIDVVTTVNVQHLESLNDVVEKITGVPQRETVPDDVVRRADQIELVDMPAEALRRRMAHGNIYQPEKVDAALAHYFRIGNLTALRELALLWVAGRVDETLQKYRSEHGIGTVWETRERVVVALTGGPEGETLIRRAERIADRPRALNSVRAGGTPISGGDLLAVHVARSDGLAYASPAALAKQRALVESLGGSYHSVVGDHVPTALLDFARAENATQLVLGTSRRSWFSRLVAPRGIGEDTVELSGDIDVHLVTHEGAGRGRRLPVPGRQLPHARRVVGPVAGLVLPLLLTTVLTHTRGALNLTSEALLFMVTVVGVACLGGVVSALLASLASLLLNYYFIPPSGEFTITEPNNALALAVFALVAVTVAALVDRSLRLSRRAASATAEAETLSSMAGTILRGEQGVSVLLERTRETFGMESAELVPRAGQETDADEERDDLVKVPAGPDRLLVLRGRRLPASEHRVLTAFAAHLAAALDHARLMEAAAQVEPVKAADRLRTALLAAVSHDLRTPLASGRAAISSLRSPDVVFSPAERNELLATAEESLIELNRLVDNLLDMSRLRAGALSLSLQPTAFADVLPLALATLPATPVRIAFQGLAEVRDVLADPPLLERVIANLVTNAVRHCAASQRVLITASSLGSRVELRVVDQGPGLPPEDRDRIFVPFQRLGDRDNTSGLGLGLALSRGLAEAMGGTLDPEDTPGGGLTMVLSLPAAPVAEPVEAVELG	20~~KdpD (4.13389E-113)~~230;X;252~~Usp(3.17719E-28)~~388;X(244);632~~HisKA (0.000000000018772 3)~~698;X;749~~HATPase_c (5.4852E-28)~~850	KdpD protein

	0.0001	31.7	9.4	0.00022	30.8	6.5	1.4	1	B7K937_CYAP7	Histidine kinase (EC 2.7.13.3)	PCC7424_4442	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	1267	65393	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	>tr|B7K937|B7K937_CYAP7 Histidine kinase OS=Cyanothece sp. (strain PCC 7424) GN=PCC7424_4442 PE=4 SV=1MLTHYRPQTQRYSIAVLSVIIALGLMLLLDPWMPMETSPFLVFFVAVTVSAWYGGIKPGLVATFLSAIASYYW FFIPKETWDISTADAFRLMIFILECILISILCEALHQAKRKVEINLHSLQQKESMLEKANTQVSRILESIGEGFFALDYQ WNFTYINNPGEIIFKQSRQTLEGKNIWQILPEIEGTVYEQFHRAIKEQIPICLEQNIFTESNQFYEIRAYPVSEGLAVY LLDVTERRLAALQLKESELRFRQLAENISKVFWISDLEKSEILYVSPAYERIWGKSCESLYQYPSSWLEAVHPEDRN RVNLAISQMKNGEQDFKEDYRIIRPDGQIRWIGARTFPIYDENGKRYRIAGFAEDITERKRAEQALQESERRFRRLV ESNLFGVAFANIAGRLHYANDYYLNMVGYSREDLENGLIQWNQMTPPEWLDLDFKALEEMKVKGVTTPFEKEYL RKDGSRVPILIGAAFLDEPYEIAQEMIGFFLDLTRLKETEKALQQREEELRLIADATPALIAYVDSHQRYRFNNRRYE EWFGVPIDQISGKTLQEFLGDSLYEKVRPRIEKVLKGEQVIYEEEITLPNSESRYIRANYMPRFDSQGKVEGFVALI NDFSDRKRMEDNLRESEERFRMMANSSPVMIWLTDETAGCIFVNQTWLNLTGRTLEQELGEGWTDNIHPEDLSY VLEDYLQAFNTRQPYEMQYRVKSANGDYRWILERGSPRFTPEGKFSGYIGSCTDVTERQQAIQALQQSEQALQQ HAQMLDLANDSIIIRDLNEAIAYWNHGAERLYGWTKTEAEGHQIHNLLKTIFPQPKTEIYSILTRQGYWQGELTQTK QDGSQIIVSSRWTLQYNSQGQAIAILEISDDITERKQVEAALRVSEERFRAIFEQAAVGMSLLNLDGRWLRVNQKL CEITGYTQEELLQKTFQDITYPEDLETDLNYVSKLLAGEIETYSLEKRYIRQDKSLIWVEITVSLMWDQTQSKSSSKV PKPQYFITVIEDISEAKRGEIERQQAQIALQERAKELTSLNTVLASTTTMLQKRNQELDQFAYVVSHDLKAPLRAIAN LSEWIEEDLEGQLPPENQEQLQLLRQRVHRMENLINGVLEYSRVGRKETKIETFSVDELLTEVIDSLSPPPTFTVEI GEGMPTLTTSKVFLAQIFSNLISNGINHYPGSDGHLWIRVKELDKFYEFAVADNGKGIAPEYHQRIFGIFQTLEKSE NLESTGIGLAIVKKIIEYQGGNIKVESELGQGTTFRFTWPK	15~~DUF4118 (0.000000000196318)~~95;X;143~~PAS (0.000842953)~~207;X;261~~PAS (0.000000000021708 1)~~365;X;392~~PAS (0.000000186913)~~493;X;517~~PAS (0.00000239666)~~617;X;642~~PAS (1.64882E-14)~~744;X;771~~PAS (0.0000000599571)~~872;X;896~~PAS (0.000000000013185 9)~~1007;X;1049~~HisKA (0.000000000022458)~~1115;X;1163~~HATPase_c (6.18654E-31)~~1264	non-KdpD DUF4118 protein
	0.0001	31.7	11.5	0.00018	31.1	8	1.2	1	I4D1F1_DESAJ	Histidine kinase (EC 2.7.13.3)	Desaci_0560	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	379	646529	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	>tr|I4D1F1|I4D1F1_DESAJ Histidine kinase OS=Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4) GN=Desaci_0560 PE=4 SV=1MPSYKLDLKNRHRVYFDLLIISIVIVILTVIHYTTYHYTMNYHIMLQFAYYLPVIYAAMRFGLAGGILSGLLITVLIL PFMTFFQTMTMTSSAMLTQWVEIGLTNGIGWLTGFLIEQERKATRKHQLALQIQKELVEKLKHESLERERLQSEIR QTERLIALGHLSAGLAHEIRNPLGIMKVSIQLLAQDKREDREVLEYCRVLQEECERLNRLVSEFLSFARPKELVRGR VKLGKLLAEGVSLIQPALRQHQIELSQTGGQVDDYEVEADSDQIKQVILNILLNAIDAQGEGGRILLEGIQPKDFVGF AVSDEGQGISPDVLPYIYDPFFTTKEKGTGLGLSVVHRILDQHGGKISVSNRNGRGTRVEILLPRCEEGP	37~~DUF4118 (0.00000706407)~~121;X;161~~HisKA (0.000000000000240766)~~223;X;275~~HATPase_c (3.33282E-26)~~372	non-KdpD DUF4118 protein
	0.0001	31.7	13.7	0.0002	30.9	9.5	1.4	1	A0A0F2C8J6_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpD RS85_01850	Microbacterium sp. SA39	854	1263625	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium sp. SA39	>tr|A0A0F2C8J6|A0A0F2C8J6_9MICO Sensor protein KdpD OS=Microbacterium sp. SA39 GN=kdpD PE=4 SV=1MSREHSRRGRLRVLLGAAPGVGKTFEMLAEGRRLRDEGHDVVIAIVETHERAATQAQTVGLEEVPRRIDDH RGVPLTELDLDAVLSRAPEIALVDELAHTNSPGSRHPKRWQDVDELLAAGIDVITTVNVQHVESLNAVVEKITGVAQ QETIPDAVVRAADEIEVVDLAPQSLRDRLSAGLVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALRTYRA EQGIEGTWQARERVVVALTGGPEGETLLRRGARIAARSAGGELLAVHVSAQDGLRDETPGALAAQRTLVESLGG SYHQVVGDDIPATLVEFAQGADATQLVIGVSRRGRLAAALTGPGIGSEVIRRSGDIDVHIVTHAAAGGRLALPRMT GGALGWRRQVLGFAVALVFGPLLSWVMFAFRSPESITAEVLAYQLLVVVVALIGGIRPAVFAAVLSGITLDFLFVAP LFTITVAHPLHVLALALYVVIAILVSIIVDQAARRARTAQRAAAEAELLAAVAGNVLRGDNAVLAMVSRTREAFGLSG VRLLSPDGDVLASDGEPVADGRSTTVPVGVGANGSPRATLELHGQPLAGPERRLLDAIVAQLSAAIEHTDLRATAL EAEALAETDQVRSALLSAVSHDIRRPLASAVAAIGGLRGAHELSASDRAELLATADESLATLSALVTDLLDVSRVQA GVLAVSATRLDATAPVLAAVDELGLGPSDVELALDSALPALHADPVLLQRVLVNVLANAHRHAPSGSRVLVSTSAL GERAEIRIIDRGAGVAPERRDSIFQPFQRFGDTDNTTGLGLGLALSRGFTEGMGGTLTPEDTPGGGLTMVISLPLA ATSPTLRQAQESHMTEDTE	6~~KdpD (1.73471E-112)~~216;X;238~~Usp(9.15303E-29)~~361;X;389~~DUF4118 (0.00000000603261)~~482;X(133);615~~HisKA (0.0000000143933)~~680;X;731~~HATPase_c (1.42434E-22)~~832	KdpD protein
	0.0001	31.7	11.4	0.00024	30.7	7.9	1.5	1	D3PV90_STANL	Histidine kinase (EC 2.7.13.3)	Snas_1437	Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	854	446470	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Glycomycetales, Glycomycetaceae, Stackebrandtia, Stackebrandtia nassauensis, Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21)	>tr|D3PV90|D3PV90_STANL Histidine kinase OS=Stackebrandtia nassauensis (strain DSM 44728 / NRRL B-16338 / NBRC 102104 / LLR-40K-21) GN=Snas_1437 PE=4 SV=1MKRGHLRIYLGAAPGVGKTYAALEEARRRVARGTDVVVGFVETHGRRSTAALLDGLEVLPRHSVGYRGTAF EEFDVDAVLRRRPEVAVVDELAHTNVPGSRNQKRWQDIDELLDAGINVISTVNIQHLESLNDVVTKITGVPQQETV PDEVVRRAEQVELADLTPEALRRRMTHGNVYPPEKIDAALSNYFRVGNLTALRELALLWLADKVEDQLSKYRSDK DIKDTWESKERVVVALSGDAEGDTLIRRAKRIAARSGGADLRAVYVASGDGLAGARNAKNLARQRLLVESMGGTF HQVIGDDIPTALLDFARGVNATQLVLGASRRGRFAQILSTGVGVTTTAKSGSIDVHLVTHDRVAKVKRPTSPAPLSR QRRITGFTATILGLPALVAALLPLRDDLNATSIMLIMLTAVMGIALTGGMWPAVLAAVGGFLLVNFFFLPPLYTFAIGD QEHLLALCVFFVFVGFVGATVVNILAARTRQAGRASAEAQTLSILAGSVLRGEDALPALMNQMLDTFGLTSVTLLER RRDGVGPDERHDPADWTMVACAGTPCASPGEAETDIPIDDKLSLALKGRTLDAADRRIVEAFAMQAAVALKQERL AAEAATARPLAAADKMRTALLAAVSHDLRTPLASAKAAVAGLRGNGDMFSAADRDELLLTADESLDRLDRLVSNLL DMSRLQAGALGAHTIPIGLEEVVPTALDELGEAGREVRLDVAGDLPEVAADPGLLERIIVNVVGNALRHSPPGTPPL VKAGAHDDIVELRVIDHGPGVPDVDQEQLFTPFQRLGDRDNASGVGLGLALSRGLAEAMSGTLTAENTPGGGLT MVLSLPQAGVNIDMESNPRQEES	1~~KdpD (1.4442E-120)~~211;X;233~~Usp(2.52908E-27)~~356;X;385~~DUF4118 (0.000000000134531)~~480;X(138);618~~HisKA (0.000000000032939 1)~~684;X;735~~HATPase_c (2.30145E-25)~~836	KdpD protein

	0.0001	31.6	9.5	0.0002	30.9	6.6	1.3	1	Q4JUR7_CORJK	Histidine kinase (EC 2.7.13.3)	kdpD jk1272	Corynebacterium jeikeium (strain K411)	898	306537	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium jeikeium, Corynebacterium jeikeium (strain K411)	>tr|Q4JUR7|Q4JUR7_CORJK Histidine kinase OS=Corynebacterium jeikeium (strain K411) GN=kdpD PE=4 SV=1MTKRGTLKVYLGFAPGVGKTYAMLSEAHDLYDRGRDVLIGIVEDHGRERTRKLTEGLPTLPRKSVPYRGGHYEELDLEAALEAHPEIVLVDELAHTVVGENNADSSRPAEAIKRWHDVYALLDAGIDVISTMNIQHLESLNDVVSAVTGTRQLETVPDQVLRDADEIELVDLSPDALRIRLARGEVYRQQQAETALNNYFRVGNLTALRELSLLWLADKVDEGLAKYREDKKIEENWPTRERVVVAVRGDEVSEALIRRGARITQRVAGREMLVVYVSGADEALGVDLPERLRRLQELTESLDGQWRVIEGDDIANTLLEFARTVNASQLVIGLGTRMSRLFSSTAHKIIDGSGRIDVHIVSTSSVSSDDGATKMSKRALRKASQLMGLTRDRGTGLDTSKQLSPTRRWIGWLLAVPGPILLTLLVLPFFRENGALGSILLGYLTIAVFAALAGGFGPAIVAVIIGSVMANWFFTHPYHTLTVTEPANLVQIILFFVISAAVAVVVDIAERRRAIANRRLGQAVVLSDLARGALDEGDDIRSLLARLRETFNLERVDLQQYSKERKKWVTMATTDPGGIGVPWPSKKAPSHVGAGDGMRFVLDGRDLTPAEDAMIEAHGARITAIYDREEIDAMRRATAALEAGNRVGTALLTAVSHDLRTPLAGIKAAVSALNMDDMELDEESRSLLMETIESSTDRLETVIGNLLDMSRVNSNTVAVHRAKVHYNTVVEAVLAELPEATQHVDSFIDATVPPVLGDAGLVQRIIANIVVNARTYAPNSRIELHAQQVPAGADDKTGAEASTVELAIVDHGPGFPSEHLNDVFTPFQRLGDQSANQNGLGLGLAVAHGFAEAMNGTLEARNTPGGGATLVLSLPTATGESEDGEERGVQKKVQGEAP	3~~KdpD (9.46941E-103)~~220;X;242~~Usp(1.93077E-20)~~360;X;412~~DUF4118 (0.00000000193721)~~499;X(150);649~~HisKA (0.000000000051406 1)~~711;X;763~~HATPase_c (1.13233E-17)~~874	KdpD protein
Disagreement between HMM and CDD prediction	0.0001	31.6	11.2	0.00024	30.7	7.7	1.5	1	F4F4Z0_VERMA	Histidine kinase (EC 2.7.13.3)	VAB18032_21895	Verrucosispora maris (strain AB-18-032)	850	263358	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Verrucosispora, Verrucosispora maris, Verrucosispora maris (strain AB-18-032)	>tr|F4F4Z0|F4F4Z0_VERMA Histidine kinase OS=Verrucosispora maris (strain AB-18-032) GN=VAB18032_21895 PE=4 SV=1MPRGELRIYLGAAPGVGKTYAMLEEAQRRAERGIDVVIALVETHGRPHTAAMIGDLEVIARRTATYRGGTFQEMDLDAVLARHPAVAVVDELAHTNVPGSRHAKRWQDIQELLDAGISVLSTVNIQHLESLNDVVAQITGTTQRETVPDQIVRAAAQVELVDMTPEALRRRMAHGNIYPPDKIDAALGNYFRVGNLTALRELALLWLAGTVDEQLDAYRAQQGISATWEARERVVVALTGGPEGATLIRRAARIAARSKGTDLLAVHVARNDGLAGADPAHLARQRVLVESLGGTYHQVLGSDIPAALLDFARGVNATQLVLGASRRGRFAQVLSRGVGVTTTALSGPIDVHLVTHPEAGRGRRTAGVPALSRRRRLLGFTLAVLGMPVLTASLKALPDLTLTSDILLFLAAVVGVALVGGLWPALLAALGGSLLLNWFFTPPFATLTIAGADNLLALAVFVGVAVAVSGVVDMAARRTRDAARASAEAQTLATVAGSVLRGQRPLTALLDRLRETFALRAVSVLELVDAADGRPDRAREEAAWRLVASVGDAPATSPGAGETAVPVDDRLTVVLCGRRLAASDRRVVEAFAAQAAVALRQQRLAAQAAAARPLAAADRMRTALLAAVSHDLRTPLASAKAAVSSLRSHDVEFDAADRDELLATADESLDRLGRLVANLLDMSRLQAGALGVHAVAIGVEDVVPRALDELGPPAAGVRTDIPADLPAATADPGLLERVLVNIVANALRHSPPHRPPLVTASAHAGLVELRIIDHGPGIPADQWEHVFQPFQRLGDRDNTAGVGLGLALSRGLAEAMGGSITPETTPGGGLTMVLRLPAAASVTAMEEPPA	3~~KdpD (4.06331E-117)~~211;X;233~~Usp(3.28198E-19)~~355;X(263);618~~HisKA (0.000000000018769 8)~~684;X;735~~HATPase_c (2.66848E-26)~~836	KdpD protein
	0.0001	31.6	12.4	0.00021	30.9	8.6	1.4	1	A9WQL7_RENSM	Histidine kinase (EC 2.7.13.3)	kdpD RSal33209_0916	Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	892	288705	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Renibacterium, Renibacterium salmoninarum, Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235)	>tr|A9WQL7|A9WQL7_RENSM Histidine kinase OS=Renibacterium salmoninarum (strain ATCC 33209 / DSM 20767 / JCM 11484 / NBRC 15589 / NCIMB 2235) GN=kdpD PE=4 SV=1MWLICTVQTSHNSTLDGGWRGITTAEKAGIGEDGIMARGTLRILLGAAPGVGKTFAMLEEAHLKIGQGVDTVVAIALHHGRKDTQALLAGLEVIPTKQVEYRGSHFEEMDVDAVLERAPQLALVDEYAHTVVSEHGTKASRKRWEDVELLLDAGIDVISTLNIQHLASLGDVVSQITETKQGETVPDDIVRRADQIELIDISPELLRQRLSAGNIYSADKVDAALASYFRMGNLSALRELALLWLADQVEDGLSAYRADHSIEASWPTRERVVVGLTGGPEGEVLIRRAARILARVSGGELLGVHVRASDGVLAESPRELETQRQLLKDLGGSYHSVTGEDQAQALLDFARRVNATQLVVGTSRRRPLARLVRGAGVGSKVVRGSGDIDVHMVSHPLGGRGVVFRKAGALGRRRLMLGFALAIVIPVILEWALVQWVPDSFTTETLIQLTGCVVVAVIGGLWPALLAAVFSSLLLNFFTAAPIGTLTIADPENLLALIIFLIVSAVVAVVVDLATRRTRDALRAGAEAATLSELARGAVAGEDSLQTFLDQGREAFRVDHGRGVAAKDVVAMFRPFQRLDDVPDGSGVGLGLAVAKGFTEAMGGVLTAEQTPGGGLTMVMRLPLSSGAAEAVRATQVERSVK	36~~KdpD (2.6879E-99)~~249;X;271~~Usp(7.74525E-29)~~394;X;416~~DUF4118 (0.0000000278921)~~502;X(148);650~~HisKA (0.000000000006657 36)~~716;X;765~~HATPase_c (3.37334E-19)~~872	KdpD protein
Disagreement between HMM and CDD prediction	0.0001	31.6	7.8	0.00022	30.8	5.4	1.4	1	B5H8P9_STRPR	Histidine kinase (EC 2.7.13.3)	SSDG_01621	Streptomyces pristinaespiralis ATCC 25486	847	457429	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pristinaespiralis, Streptomyces pristinaespiralis ATCC 25486	>tr|B5H8P9|B5H8P9_STRPR Histidine kinase OS=Streptomyces pristinaespiralis ATCC 25486 GN=SSDG_01621 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRAERGTDCVVALVETHERPRTARLLDGLEQIERREITHRGAVLTEMDIDAVLERRPAVALVDELAHTNVPGSRNSKRWQDVEELLAAGTDVISTVNIQHLESLGDVVETITGVRQLETVPDEVVRRADQIELVDMAPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWLADRVDEYLQQYRGEHNIRSTWQARERIVVGLTGGPEGGTLIRRAARLAEKGAGGEVLAVYIARSDGLTSASPKELAVQRTLVEDVGGTFHHVIGDDVPSALLEFARGVNATQIVLGSSRRKAWQYLFGPGVGATVARDSGPDLDVHIVTHDEAGKGRGLPGARGTRLGRSRIAGGWLVGVAGPALLTALLTSLENGPGLANNVLLFLFLTVIAALLGGLLPALASAAVGSLVLNYFFTSPTHTLDIAEPRNLVAIVIFFAVGVAVASVVDLAARRTHQAARLKAESEILSFLAGSVLRGQTALDALLERVRETFAMESVALLERESDVDPWTCTASVGPRPATRPDDADVDMPVGDRMAMALSGRVLPAEDRRVLAAFATQAAVVVDRQRLVGEAEQARELAEGNRIRTALLAAVSHDLRTPLAGIKAAVTSLRSDDVAWSEEDEAELLAGIEEGADRLDHLVGNLLDMSRLQTGTVTPLIRETSLDEVIPLALVGVPAESVELDIPESLPMVAVDRGLLERAVANIVENAVKYSPDAVCVTVAASSLGQRVELRIVDRGAGVPDEAKERIFEPFQRYGDAPRGAGVGLGLAVARGFMEAMGGTLTAEDTPGGGMTMVLTLTAVPGHGTTPAGLTAEATS	1~~KdpD (2.38412E-121)~~211;X;233~~Usp(7.40869E-31)~~356;X(256);612~~HisKA (0.000000000000152 707)~~678;X;727~~HATPase_c (1.24116E-26)~~828	KdpD protein
	0.0001	31.6	5.9	0.00018	31	4.1	1.2	1	Q1IMX6_KORVE	Uncharacterized protein	Acid345_2773	Koribacter versatilis (strain Ellin345)	192	204669	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Candidatus Koribacter, Candidatus Koribacter versatilis, Koribacter versatilis (strain Ellin345)	>tr|Q1IMX6|Q1IMX6_KORVE Uncharacterized protein OS=Koribacter versatilis (strain Ellin345) GN=Acid345_2773 PE=4 SV=1MSLATPAFTERRSSYRSYFVAIASVAIATLISFPLRDMFDHSRGLLLFVAIMFSAWYGGMRPGLLAGLLTGISFTVFFNDQHGLNVNLYGFTRVTVFSAAAFTVSYLMAKRNQALADALTANQELEKAIEEIHVLRGILPICMHCKQIRDGEGSWQEVESYIAAQTEAKFSHGVCPDCLDKFYPEVHNIAAR	18~~DUF4118 (0.0000000300008)~~114	non-KdpD DUF4118 protein

	0.0001	31.6	13.7	0.00026	30.5	9.5	1.5	1	E8RLR6_ASTEC	Signal transduction histidine kinase	Astex_1002	Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	338	573065	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Caulobacterales, Caulobacteraceae, Asticcacaulis, Asticcacaulis excentricus, Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48)	>tr|E8RLR6|E8RLR6_ASTEC Signal transduction histidine kinase OS=Asticcacaulis excentricus (strain ATCC 15261 / DSM 4724 / VKM B-1370 / CB 48) GN=Astex_1002 PE=4 SV=1MHRVEGFFREITRWFRKREDQTAFRYGVAVAFFGVALGVRFVSDKALPPGFPFLTFFPAVMLTAWLVGLWPGIVCAGLSALAAWFFFIPPAFSFDVSPPVLVALGFFLLVSAVDIAVIHGMRLAQEKLSAERNTNAALVVHQKTLYAELQHRIANNLAFVASMLTLQSKKLQGNREATDALTDARRRLETLSRIHRKLYDPDNVNVPLRTLLRDIAEDVLHTRDGRIQLEVEVPDITLPAEQVMTLSLFVVEVLTNSLKHAFSAGQGAVTIRLDDTKPDVFVLSIRDDGPGLPGGFDLAASKSLGMRILHSFARTLKGDVAFTSERGLKTCLTFARVA	25~~DUF4118 (0.0000000105267)~~113;X;148~~HWE_HK (3.36593E-16)~~222;X;246~~HATPase_c (0.000000000415572)~~334	non-KdpD DUF4118 protein
	0.0001	31.5	9.3	0.00028	30.4	6.4	1.5	1	A0A0F2TI26_9ACTN	Histidine kinase	VM95_06620	Streptomyces rubellomurinus	851	359131	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces rubellomurinus	>tr|A0A0F2TI26|A0A0F2TI26_9ACTN Histidine kinase OS=Streptomyces rubellomurinus GN=VM95_06620 PE=4 SV=1MARDLTPGTGTRRGRLRVYLGSAPGVGKTYRMLDEARRRQERGADVLVGYIECHGRRHTEAMIDGLEVQPRVHRSYRDAEFEEMDLDGVLARRPSVVLVDELAHTNIPGGRHAKRWQDVEEILAAGIDVITTVNIQHLESLNDVVQKITGIPQRETVPDEVVRRADQIELVDMAPQALRRRMAHGNVYKAEKVDAALSNYFRVGNLTALRELALLWVAGRVDEGLRDYRASHNIDRVWETRERVVVALTGGPEGETLIRRAARIADRTAGGDLLAVHVSRSDGLAGASSGALAQQRLLVETLGGSYHVVVGDDIPTALLAFARAHDATQLVLGTSRRGRITRFLTGPGIGETTVDASEDIDVHMVTHEFTGRGRLPSLGRRHSRRRTVVGYLAGLALPWLLTAVLSQAHATINLTTDALIFQLGVVIVALLGGATSALLAAFIASVLLNYYFIPPVHSLTIGETNNIVALVVFAAIALAVSTVVDHAGKLLTTRAARATAEAETLSTLAGSVLRGADALPALLEKSRTAFGMRTVTLLSRTGEVLAHSEADHPDDGSGEHETTEVPVGADALLVLTGRRLPAADQRVLTAFAAHVAAALERDRLAVVAAEVEPIKAADRMRTALLAAVSHDLRTPLAAALASVGSLRSPDVEFSPEDQAELLATADESLVKLTRLVDNLLDMSRLQAGALTLHLTETHLDEILPRALDSLPDPDAPVQPLDLDTTPPVLADPPLLERVLANVITNALRHNAPGAPVLVTASHHADLVEIRVIDRGPGIAPEDRDRVFLPFQRLGDTDNTTGVGLGLALSRGLAEAMGGSLEVEDTPGGGTTMLLTLPAATTTDFGEEPAHHE	12~~KdpD (9.10268E-118)~~221;X;243~~Usp(1.59309E-29)~~366;X;387~~DUF4118 (0.00000000126596)~~485;X(132);617~~HisKA (0.000000000089552)~~683;X;734~~HATPase_c (5.8517E-29)~~835	KdpD protein
	0.0001	31.5	9.6	0.00021	30.8	6.7	1.3	1	H1XVR1_9BACT	Histidine kinase (EC 2.7.13.3)	Calab_1004	Caldithrix abyssi DSM 13497	363	880073	cellular organisms, Bacteria, unclassified Bacteria, Caldithrix, Caldithrix abyssi, Caldithrix abyssi DSM 13497	>tr|H1XVR1|H1XVR1_9BACT Histidine kinase OS=Caldithrix abyssi DSM 13497 GN=Calab_1004 PE=4 SV=1MNKKYWLVIIVVLILTITYFHYHTPTSIWQFHLILMQLYFIPILLAAFQFGIKGGVISALAITVFYLPHVFLQWGGLVETNLLRFLQVLLFNVIGYLTGLKAEGERKETEKYRKLAEKLKELNEQQKQQSELLLEMERKLRMADRLAIIGELTASLAHEVRNPLASIRGSIQILKEQAPENLKASEFFTILEHETQRINTVVDNYLNFARRPAQSKSTINLYEVLDILIKMIESKARKQNVSIQTAFEENLPLFDSDPNALKQVLMNLLLNGLQAMPEGGRLIVQARQDNGQLIISIIDRGKGMTEEQLEKIFQPFYTTKKEGTGLGLSIVKRIADENNWQIKAESKLNEGSRFDLIIPLPSA	0~~DUF4118 (0.000000101057)~~100;X;146~~HisKA (0.000000000006180)~~210;X;261~~HATPase_c (3.24251E-27)~~358	non-KdpD DUF4118 protein
	0.0002	31.3	13.9	0.00023	30.7	9.6	1.3	1	R7I3K7_9CLOT	Histidine kinase (EC 2.7.13.3)	BN648_00155	Clostridium sp. CAG:411	353	1262802	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:411	>tr|R7I3K7|R7I3K7_9CLOT Histidine kinase OS=Clostridium sp. CAG:411 GN=BN648_00155 PE=4 SV=1MNKYYRCLRNSLKTIIILGISFFISLIIEEFLGASTLIPAIMALAIFLISRITDGFLYGIIASVLSVLLLNFAFMLPYFAFNFSISENIISAVIMLIITIMTSTLTTQLKWQEKVRMESEKEKMRGNLLRAVSHDLRTPLTAIYGSGSTIVENYKQLSEQQLLQLANGICTDSQWLMRMVENILSITRIDNEGVKITKTSTVLEEELIDSVLIRFKKTYPDQKIIVDIPQEFISIPMDAVLIEQVLVNILENAMQHATGMTEIKLSVYVMGDKVVFEIKDNGCGIEKERLKGIFKDYFEIKEGPIDNQKKSMGIGLAVCASIIKAHDGVITASNRKEGGCCFRFALDMEMDENE	12~~DUF4118 (0.000000000060787)~~110;X;122~~HisKA (0.000000059635)~~188;X;241~~HATPase_c (7.08118E-21)~~345	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0002	31.3	7.3	0.00026	30.5	5.1	1.4	1	U5WM98_MYCKA	Histidine kinase (EC 2.7.13.3)	MKAN_08405	Mycobacterium kansasii ATCC 12478	848	557599	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium kansasii, Mycobacterium kansasii ATCC 12478	>tr|U5WM98|U5WM98_MYCKA Histidine kinase OS=Mycobacterium kansasii ATCC 12478 GN=MKAN_08405 PE=4 SV=1MSAVDPPRKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDLVAAVVETHGRMKTAALLDGIEIIPPHYVEYRGTTFPELDVPAVLARHPQVVLVDELAHTNTPGSKNHKRWQDVEELLDAGITVISTVNIQHLESLNDVVAQITGIEQKETLPDSVVRQAAQVELIDITPEALRRRLSHGNVYASDKIDAALSNYFRRGNLTALRELALLWLADQVDTALAKYRAENQITDLWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVIRGDGLAGLSEARMSKIRELAGSLDASLHTVVGDDVADALLDFAREINATQLVIGTSRRTRWARLFEEGIGQAIVERSGKIDVHLVTHEESRRGLRTTPIAPRERRVASWLAAAVIVPSLICAITVAVLDRYLDTSGESALFFVGVLVVALLGGVAPAVLSAVLSSLLLNYYLTDPRHTFTIAEPSAAVTEAVLLLVAVAVAVLVDGAAKRAREARRASQEAELLTLFAGSVLRGADLETLLERVRETYSQRAVSMLREYADEDRTRSEVVASVGKEPCATVDSADTAIEVGDDEFWMLMAGKKLSARDRRVLNAVARQAAGLVRQREMAEEASRTEAIVRADELRRSLLSAVSHDLRTPLAAAKVAVSSLRAQDIAFSPADTAELLATIEESIDALTALVGNLLDSSRLAAGVLRPDLQRVYLEEEVQRALVSIGKGATGFYRSAIDRVKVDVGGAVVMADAGLLERVLANLIDNALRYAPDCVVRVNAGRVGDRVLINVIDEGPGVPPGSQGQIFEPFQRLGDNDNTTGVGLGMSVARGFVEAMGGTVAAGDTPGGGLTVVVDLAAPPEDGDL	9~~KdpD (7.82852E-120)~~218;X;240~~Usp(9.00212E-35)~~361;X(255);616~~HisKA (0.000000000053709)~~682;X;739~~HATPase_c (9.84087E-26)~~839	KdpD protein
	0.0002	31.2	7.1	0.00026	30.5	4.9	1.3	1	J7IU80_DESMD	Histidine kinase (EC 2.7.13.3)	Desmer_0645	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	374	768704	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	>tr|J7IU80|J7IU80_DESMD Histidine kinase OS=Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10) GN=Desmer_0645 PE=4 SV=1MQNHEAPEHNRSRALFDLIIIGLVIVILTTIHYTNYHYEVDYHILLQFAYYLPVIYAAMRFGPAGGIISSFIITLLFIPLMTHMQSSLTPAAKYTQWVEVGLINVIGWLTGFLTEEERIAKRKYQLALMVQKELVEKLKREGQERERLEGEIRQTERVTALGHMSAGLAHEIRNPLGIMKVSIQMLAQEKFGDGVVSEYCRILLEECERLNRLLSEFLSFARPKELLREKIALGELLDEGVCLIQPALQQNHIELERVRSELDQKEVEVDPDQIKQVILNILLNAIEAQGIGGMIHLQVVEEEGYVGFAVTDQGPGITQEVMPYLYDPFFTTKDKGTGLGLSVVHRIMDQHGGKVTISNHNERGARVGVLLPLV	37~~DUF4118 (0.0000248924)~~118;X;160~~HisKA (0.000000000014202 8)~~222;X;274~~HATPase_c (5.64353E-23)~~371	non-KdpD DUF4118 protein

	0.0002	31.2	9.9	0.00029	30.4	6.9	1.4	1	D7B4M1_NOCDD	Histidine kinase (EC 2.7.13.3)	Ndas_1632	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	844	446468	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	>tr|D7B4M1|D7B4M1_NOCDD Histidine kinase OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_1632 PE=4 SV=1MTRGHLRVYLGAAPGVGKTYRMLDEAHRRRDRGADVVIGFVESHGRAMTEAMVDDLETIPRAVLTHRGARLEEMDLDAVLARRPQVVLVDDLAHANAPGARNARRWQDIEALLEAGITVLSTLDVQHLESLNDVVERVTGTRQSETVPDAWVRGADQIELVDMTPEALRRRLAHGNVYGPDRIDAALGHRFRADTLTALRELALLWLAGRVDDELRRHRGEHRAASAWQTRERVVVGLSGGPGGEALIRRAARIAGRGRGVELLAVHVALGDGPVGADPALLARQRVLVEDLGGTYHQVLGEDVPAALTAFAQGVDATQLVLGASGRGRLARLLRPGVGAATAALSESIDVHLVTLEEAERGSGRARSGAVSRRRRLAGYALALTALALLVFGTGVPHSEEYLSGGILLVFATVTATALVGGLWPALAAAFSGFVVVLNLFFTEPYETLVVNQPGNLLTLVVFVFVAVAVSVVVDKAARRTREAARASAEAQTLATVAGSVLRGSRPLEALLERLRETFSLESVALLERRPQASSRPDHRNDPGAWEAVASVGELPHSAPGGADVDVPVDEGLTLVLHGHRPRAGERRIIEAFAAQAAVALRQERLAQEAAAAGTLAEADRMRTALLAAVSHDLRAPLASAKASVTSLRSREVRFSEEVQAELLATADESLDRLTRLVTDLLDMSRLQAGVLGVTVTGLSLRESVFAVLDDLGEQGRAVRVRVPEELPEVAADPGLLERVLANVVGNALRFSPHDRPPSVTASWTGDQVELLVADHGPGVPEHERERMFVPFQRLGDTDAATGLGLGLALARGLMEAMGGSLLPETTPGGGLTLRLVLPVAGAAG	3~~KdpD (5.09907E-105)~~211;X;233~~Usp(6.44538E-23)~~355;X(264);619~~HisKA (0.000000000016630 7)~~685;X;736~~HATPase_c (1.12498E-23)~~837	KdpD protein
Disagreement between HMM and CDD prediction	0.0002	31.2	5.7	0.00029	30.4	4	1.4	1	V6KSM8_STRRC	Histidine kinase (EC 2.7.13.3)	M878_10520	Streptomyces roseochromogenus subsp. oscitans DS 12.976	860	1352936	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	>tr|V6KSM8|V6KSM8_STRRC Histidine kinase OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_10520 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLAEAHRRVERGTDCVVAYVEHYDRPRTEVMLHGLELVPRKRLEYREAVFTEMDVDAVLRRAPAVALVDELAHTNVPGSRNAKRWQDVEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSPEALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNAYRSEHRVSKIWGSRERIVVGLTGGPEGRTLIRRASRLAEKGAGGEVLAVYISRSDGLTSASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGVNATQIVLGSSRRKAWQYVLGPGVGATVARESGPDLDVHIVTHEEAAKGRGLPVARGARLGRARIIGWLVGLGGPVALAVLLNAVDVGLANDMLLFLAVTVAAALLGGLLPALASVAFGSLLLNYYYTPPLHQWTIADPKNIVAIAIFLCVAVSVASVVDLAARRTHQAARLRAESEILSFLAGNVLRGETSLEELLERVRETFAMESAALLERAGDVEPWTCAGRAGFGRPLERPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAIALDRRRLQEEADQARALAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDRAELLEGIEEGADRLDHLVGNLLDMSRLQTGTVTPIIREIDVDEVVPMALGGVPEDSVELDIPETLPIVEVDPGLLERSVANLVENAVKYSPRGRPVLVSASAIADRVEVRVVDRGPGVPDEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLSVRTAPERRPEQPSLPAAATS	1~~KdpD (1.18718E-121)~~211;X;233~~Usp(7.00039E-31)~~356;X(255);611~~HisKA (1.46959E-14)~~677;X;726~~HATPase_c (1.33143E-25)~~827	KdpD protein
	0.0002	31.2	16.2	0.0003	30.4	11.2	1.3	1	A0A0F5FHW6_9RHIZ	Uncharacterized protein	VE26_16485	Devosia chinhatensis	335	429727	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia chinhatensis	>tr|A0A0F5FHW6|A0A0F5FHW6_9RHIZ Uncharacterized protein OS=Devosia chinhatensis GN=VE26_16485 PE=4 SV=1MLTTAENFRKRPVLAYLVAIAAVALALLVRFLVNDALPTGFPYLTFFPAVLLTAFFCGTGPGIVAAMLSVVAAWYWFIPPFNSFSLDYQSTIAVVFFVAILSADILIIHLMHSSLRRLKQEQARTAHLLERQHTLFEELQHRTANNMSFIGALLSMHKRRAAHSPEVKSVFEDAASRLESMARIHRRLYDPTNNDLPLGAYLEDLLRDVFESAGREDIAIDVRTNIGRLDVNRLITLSLLVSELATNSIKHAYMDRQGRFSILLEDQGDMICVTVRDDGPGFPAGFDPSASDRLGFRVLSSFVRNLDGKLDFRSENGALTIITFPSADPKAAATA	(0.00000821623)~~101;X;138~~HWE_HK (3.96014E-18)~~213;X;237~~HATPase_c (0.000000000012702 6)~~324	non-KdpD DUF4118 protein
	0.0002	31.2	6.7	0.00027	30.5	4.6	1.3	1	A0A0F2NGK7_9DELT	Uncharacterized protein	VR65_13665	Desulfobulbaceae bacterium BRH_c16a	326	1629713	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, unclassified Desulfobulbaceae, Desulfobulbaceae bacterium BRH_c16a	>tr|A0A0F2NGK7|A0A0F2NGK7_9DELT Uncharacterized protein OS=Desulfobulbaceae bacterium BRH_c16a GN=VR65_13665 PE=4 SV=1MAIKTLFVVFLVGSISAVHLLYTGTDLGFHVLHQQLFYIPLVLASFWFGTRAGLSTAVAVSILYGPAMLLRHHEGGMHLTVVTQIALYLFVAFLMGWLSDRQRRQQQQLLKNERITALGKAASTLGVEIRDIVTGVHSIYRQSGGLKNDDANDDFLSEIDRLKRMVDGLSHFAPTLDHTSLSTDLNDILRHSFKKYSRQAAGKGLNMTIEPTGTGCPSTISVEPLFRIFDELVNNAIDFSQRGQAVVLRSFSGENEWVLEVADSGPGVAKENEEKLFTAFFTTRPDGYGLSLSSGRKLLRDLGGDLIYRPGAHGGAIFRMLIPKEQ	225~~HATPase_c (1.00471E-16)~~322	No DUF4118 detected by NCBI CDD
	0.0002	31.1	7.9	0.0003	30.3	5.5	1.4	1	D7BWQ6_STRBB	Histidine kinase (EC 2.7.13.3)	SBI_00291	Streptomyces bingchenggensis (strain BCW-1)	849	749414	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	>tr|D7BWQ6|D7BWQ6_STRBB Histidine kinase OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_00291 PE=4 SV=1MARGKFRIYLGAAPGVGKTYSMLSEAHRRVERGTDCVVAFVEHHHRPRTEVMLHGLEQMPRKELEYRGGTFTEMDVDAVLARRPQVVLVDELAHTNVPGSRNAKRWQDVEELLAAGIDVISTVNIQHLESLGDVVESITGIRQQETVPDEVVRRADQVELVDMSPEALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLTEYRSEHKVRAIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVMAVYIARSDGLASTSNSPKELAVQRTLVEDLGGTFHHVVGDDVSAGLLDFARAVNATQIVLGVSRRKGWQYVFGPGVGATVARESGPDLDVHLITHDEAGKGRGLPVARGARLGRTRIIGGWLAGVLGPALLTLLLNGVVPEMGLANDMLLFLAMTVAAALLGGLLPALASAVVGSLLLNWFFTPPVHTLTIADPKNIVAIAVFIGVAVSVASVVDLAARRTHQASRLRAESEILSFLTGNVLRGETSLDALLERVRETFGMESVALLERHSDVDPWTCAGSVGADPAQCPEDADVDVPVSEHMALALSGRVLPAADRRVLAAFAAQAAVVLDRQRLQGEADQAKDLAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSEDVAWSEEDQAELLEAIEEGADRLDLLVGNLLDMSRLQTGTVTPVIREADLDEVVPMALGGVPEGSVELDIPETLPMVHVDKGLLERAVANVVENAVKHSPPDRRVLVSASAMADRVEVRVVDRGPGVPDEAKDRIFEPFQRYGDSPRGTGVGLGLAVARGFVEAQGGTLHAEDTPGGGLTMVLSVRTAPERRPEQPSLPAAATS	1~~KdpD (1.38596E-124)~~211;X;233~~Usp(2.31972E-32)~~358;X(256);614~~HisKA (2.85978E-15)~~680;X;729~~HATPase_c (1.56018E-26)~~830	KdpD protein
	0.0002	31.1	8.1	0.00029	30.4	5.6	1.3	1	Q6LKJ9_PHOPR	Histidine kinase (EC 2.7.13.3)	SO0060 PBPRB0328	Photobacterium profundum (Photobacterium sp. (strain SS9))	347	74109	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium profundum (Photobacterium sp. (strain SS9))	>tr|Q6LKJ9|Q6LKJ9_PHOPR Histidine kinase OS=Photobacterium profundum GN=SO0060 PE=4 SV=1MTLKSLIAKPFSITALVISFALLISGVLDLWLGSSIAVLMILQLAVVVIALQCSPGWAYLSAVFEAVCFNFFLTNPRFSLQMLNVDDIVNLCVFLIVAIITSKLAEYYRQQQNQLKQAQLRNSILLSVSHDLRTPLATIIGTLSTLEEYMDKLSKAEKAELFDSAIVESNRLYQYIENLLQATKLQHGAVVLKKDEHSLVHIIHLVIERFSKQTDRIILDAQSDLPSVQMSSSLIQQAIFNVIDNALRYSPYDKNVNINIYRSSEHLIVDIKDEGVGITKEQSEHIFDLFYSASSPKRNDSGTGLGLAVSKGIISAHQGTMQAVPVDSGSLIRIQLPMVNGGQHLVL	14~~DUF4118 (0.00000816204)~~109;X;120~~HisKA (0.0000000156765)~~184;X;235~~HATPase_c (2.44597E-21)~~336	non-KdpD DUF4118 protein

	0.0002	31.1	10.1	0.00025	30.6	7	1.2	1	R5AH56_9CLOT	Histidine kinase (EC 2.7.13.3)	BN454_01866	Clostridium sp. CAG:1024	367	1262770	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:1024	>tr|R5AH56|R5AH56_9CLOT Histidine kinase OS=Clostridium sp. CAG:1024 GN=BN454_01866 PE=4 SV=1MKPSRAVFQRIRRVSRNLFLTTILLFATMALCLLLTQIDGVEKSNDYVPMLFVLSVLLVSRFTDGYFYGVAASFAGVLLVNYVFTYPYFAFNFSLPGYPIAILCMLTVSVLTCTLTTTIKHQEQARREADREMIRSNLLRAISHDLRTPLTSILGANSVLMENGDSLSVEQKRKLHQEIDSDAQWLIRMVENLLTITRIRQDRDCAAKIEKTPEIVEEVLAEAVTKHCKRFPDSPVKVHVPEEMLICPMDAMLIEQVLINLLENAVTHAKHATEILVSAEKEGDAAVTFTVSDNGCGVEPEALAHLLEDHGRTSAQTSDSKRNMGIGLSVCNAIIRAHGGSMHAENRDGGGLSVHFRLPAKESEDGE	17~~DUF4118 (0.00000000267569) ~~122;X;135~~HisKA (0.000000000184493)~~198;X;254~~HATPase_c (7.60145E-26)~~358	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0002	31.1	8.6	0.00029	30.4	5.9	1.4	1	F5Y2B3_RAMTT	Candidate histidine kinase, hybrid	Rta_00270	Ramlibacter tataouinensis (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310)	680	365046	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Ramlibacter, Ramlibacter tataouinensis, Ramlibacter tataouinensis (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310)	>tr|F5Y2B3|F5Y2B3_RAMTT Candidate histidine kinase, hybrid OS=Ramlibacter tataouinensis (strain ATCC BAA-407 / DSM 14655 / LMG 21543 / TTB310) GN=Rta_00270 PE=4 SV=1MGRGCGASVLFGCMALQIFHPPARAPWRTAGLRPYGAAAAISAAFILLRLALEPVLQGQVPLLVLLAAPLLTCWYFGFAPALLATLLCALFGEWLFVAPRFDAVPQNPVEWVRLGVFLLYALVFSWLIDTRHRALHLLLREREDLIAARDELARREQQARERAARQAEADKALLLAARAAAGESDAMFRTLSDNIAQLAWMTDETGFIRWYNRRWFEYTGTTSEQMKASDWRQVHHPEHMDRVLAKFRRHMGTGEPWEDTFPLRRHDGEYRWFLSRAFPLRDRAGRIVSWFGTNTDIHAQHQAEEALRQADRRKDEFISVLAHELRNPLAPVRNAVEILKRVAQPEPRVERARDVIARQVAHMVRLIDDLLDVSRIARGKLTLRKERCDLAAIARQTAEDYRASLQAAGQQLELHQPPGPAWVEGDPVRLAQMLGNLLTNAARFTNGPGTVRVRTAVDEAGRSALLTVQDTGVGLPPELLGRLFDPFEQAAQDSARTQGGLGLGLALTKGLAELHGGSVSAESAGPGQGASFTLRIPLSPEQPPAVPRGEARPAEPQARRILVVEDNPDAAATLGELLQLGGHQVEVAHDGRSGVAAARALRPDVVISDLGLPGEVDGYALARALRQEPALAGTRLIALSGYADEQARRRCREAGYDTHLPKPPDLAALDRAIEAAGGQPA	199~~PAS (3.58712E-14)~~296;X;310~~HisKA (2.94623E-15)~~374;X;429~~HATPase_c (2.89742E-17)~~535;X;561~~REC (1.07237E-24)~~675	No DUF4118 detected by NCBI CDD
	0.0002	31.1	8.6	0.00018	31.1	6	2.2	1	A0A0F2Q5R4_9CLOT	Uncharacterized protein	VR72_12060	Clostridiaceae bacterium BRH_c20a	543	1629719	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, unclassified Clostridiaceae, Clostridiaceae bacterium BRH_c20a	>tr|A0A0F2Q5R4|A0A0F2Q5R4_9CLOT Uncharacterized protein OS=Clostridiaceae bacterium BRH_c20a GN=VR72_12060 PE=4 SV=1MNYKYKRKKIIDNYIFISQVVFFLLLGILILRVYNFSYETFYTDSLQVFIFIILLSLIPFIKILNYNSKFKPIYIDTIVIFLYLIIVCYFITIEKESIFKIILLMPVVVISIKYGLRPSFLAAFVSSLALITISLVNSNISFDADIMLSGVLFLLAWLLGNMTETEAKIREELERLATHDGLTDLLNHRSFQSILDEKITEAKRKKSSLSLLLLDIDYFKVYNDSLGHQKGDIVLKTVADIMKNATEGKGYCARYGGEEFVIILPETSIHEARKLADTIREQIEKTEFIGMQVLPKGKVTVSIGIAQLPLMADTKEKLIQKADEALYKAKFVSKNKVEVYYSVFDELSLILKDEEQELLNSIRTLTTVINAKDRYTYGHSERTMELCRNYSRLLKFDDFLTKNLIYGSLLHDIGKIEISREVLNKPKKLNQSEWEMFKQHPQWGADIIRPIKTLQDSLEIILYHHENYDGTGYPKGLKGKDIPIGARILRIVDSYDAITTKRPYKEAMSKEQAVEELAKYSGTHYDPIILEQFCEMILKKDDV	74~~DUF4118 (0.00000000934684) ~~163;X;178~~Nucleotidyl_cyc_III (1.39829E-52)~~337;X;374~~HDc (3.37572E-19)~~505	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0002	31.1	9.3	0.00032	30.3	6.5	1.4	1	C9Z0G1_STRSW	Histidine kinase (EC 2.7.13.3)	SCAB_24001	Streptomyces scabiei (strain 87.22)	880	680198	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces scabiei, Streptomyces scabiei (strain 87.22)	>tr|C9Z0G1|C9Z0G1_STRSW Histidine kinase OS=Streptomyces scabiei (strain 87.22) GN=SCAB_24001 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRIERGTDCVVAVVEHHGRPRTEVMLHGLEQIPRRELAHRDAVFTEMDVDAVLARRPRVALVDELAHTNVPGSRNDRRWQDVQELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNVYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNAYRSEHQVSRIWGSRERIVVGLTGGREGRTLIRRAARLAEKGAGGEVMAVYIARSDGLTSASPKELAAQRTLVEDLGGTFHHVVGDDIPAALLAFARGGNATQIVLGVSRRKSWQYVFGPGVGATVARNSGPDLDVHLITHDEAGKGRGLPVARGARLGRVRMIWGWLVGTAGPLLLALVLVASSTDLGLANDMLLFLSLTVAAALLGGLLPALAAAVLGSLLLNWFFTPPVHTLTVDDPTNIVAIVVFIGVAVAVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETSLEALLERVRETFGMESVALLERGSDVEPWTCAGSVGPRRVVDRPEAADVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAAVVLDRRRLQQEAGRARELAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRTEDVEWDEADEAELLAGIEAGADRLDHLINNLLDMSRLQTGTVTPLIHEIDLDEVVPFALGGVPLEAVKLDVPETLPMIHADAGLLERSLANLIENAVKYSPDGVKVLVKADALHPPGTPGRVELRVVDRGPGVPEAAKERIFAPFQRYGDAPRGAGVGLGLAVARGFVEAMGGTVAAEDTPGGGLTMVVTLPAVDLPDVNFPEQPPLPPNRKAEPE	1~~KdpD (4.09078E-121)~~211;X;233~~Usp(2.24079E-22)~~356;X;385~~DUF4118 (0.000000002399)~~482;X(134);616~~HisKA (1.65525E-14)~~682;X;731~~HATPase_c (5.2607E-24)~~837	KdpD protein
Disagreement between HMM and CDD prediction	0.0002	31.1	10.8	0.00031	30.3	7.5	1.4	1	A0A0A1FTM0_9MYCO	Histidine kinase (EC 2.7.13.3)	G155_23795	Mycobacterium sp. VKM Ac-1817D	845	1273687	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. VKM Ac-1817D	>tr|A0A0A1FTM0|A0A0A1FTM0_9MYCO Histidine kinase OS=Mycobacterium sp. VKM Ac-1817D GN=G155_23795 PE=4 SV=1MSTPSSSPAKRGELRIYLGAAPGVGKTYAMLGEAHRRLERGTDLVAAVVETHGRRKTAELLEGIETIPPRYVEYRGGRFPELDVAAVLARNPQVVLVDELAHTNTPGSKNPKRWQDVEELLAAGITVISTVNVQHLESLNDVVTQITGIEQQEKVPDEVVRAADQIELVDITPEALRRRLSHGNVYAPERVDAALSNYFRRGNLTALRELALLWLADQVDAALAKYRADNKITDTWEARERVVVAVTGGAESETLVRRASRIASKSSAELMVVHVVRGDGLSGVSAPQMGKVRELAASLGATVHTVVGDDVPAALLDFARERNATQLVLGTSRRSRWARIFEEGIGPAVVQQSGKIDVHMVTHDQARRGFGWATATPRQRHIASWLAAVVVPSAICLLIVGVLDPILGVSGESALFFIGVLVVALLGGVAPAALSALLSGLLLNYFLVAPRHTFTISEPDSAVTVVVLLLVAVAVAALVDGAASRAREARKASQEAELLTLFAGSVLRGADLTTLLERLRETYSQRAVSLLREQNGTAEIVACVGTKPCAEVDTADTAIEVGDDEFWLLMAGRKLAARDRRVLSAVAKQAAGLVKQRELTEEASKAAAIAQADELRRSLLSAVSHDLRTPLAAAKAAASSLRSEDIDFSAEDTAELLATIEESVDALTALVGNLLDSSRLSAGVVRPELRRVYLEETVQRALLGISKGTTGFTREGLDRVKVEVGDAVAMADAGLLERVLANLIDNALRYAPEGPIRVSAGQVADRVLIAVIDEGPGMPRGAEEQLFAPFQRLGDHNTTIGVGLGLSVARGFVEAMGGTISATDTPGGGLTVEIDLAAPPKDDAL	9~~KdpD (6.54684E-122)~~219;X;241~~Usp(1.75443E-35)~~362;X(251);613~~HisKA (0.00000000990324)~~679;X;736~~HATPase_c (2.18882E-27)~~836	KdpD protein

Disagreement between HMM and CDD prediction	0.0002	31	6.7	0.00033	30.2	4.6	1.4	1	K4R0W2_9ACTN	Histidine kinase (EC 2.7.13.3)	kdpD1 BN159_2584	Streptomyces davawensis JCM 4913	849	1214101	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces davawensis, Streptomyces davawensis JCM 4913	>tr|K4R0W2|K4R0W2_9ACTN Histidine kinase OS=Streptomyces davawensis JCM 4913 GN=kdpD1 PE=4 SV=1MGRGRLRIYLGAAPGVGKTYAMLSEAHRRAERGTDCVVALVEHHDRPRTEVMLHGLEQLPRKQLAYRGTA FTEMDVDAVLARRPEVALVDELAHTNVLGSRNAKRWKDVEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQET VPDEVVRRADQIELVDMSPQALRRRMAHGNVYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLRTYRG EHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTAASPKELAVQRTLVEDLGGTF HHVVGDDIPAALLAFARGVNATQIVLGSSRRKTWQYVFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVARG ARLGRSRIVWGWLAGIGGPALLTLLLTNVDADLGLTNNMLLFLTLTVAAALLGGLLPALASAAFGSLLLNWFFTPPV NRLTIADPKNILALVIFVGVAVSVASVVDLAARRTHQAARLRAESEILSFLAGDVLRGETSLEALLERVRETFGMESA ALLERASEVEPWTCAGRVGLGPTVERPEDADVDMPAGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLR EEADQARALAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDEAELLAGIEEGADRLDHLVGNLLD MSRLQTGTVSAIVREIDLDEVVPMALGGVPEDSVELDVPETLPMVAVDPGLLERSVANIVENAVKYSPPGMPVLVS ASSIADRVEVRVVDRGPGVPDDAKERIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLTAEDTPGGGLTMV LTLRAAAGPLFRPAFPEPERQAT	1~~KdpD (1.75849E-121)~~211;X;233~~Usp(4.77426E-32)~~356;X(257);613~~HisKA (7.03885E-14)~~679;X;728~~HATPase_c (6.25304E-26)~~829	KdpD protein
	0.0002	30.9	7.4	0.00035	30.1	5.2	1.4	1	Q9X1C7_THEMA	Uncharacterized protein	TM_1407 Tmari_1414	Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)	398	243274	cellular organisms, Bacteria, Thermotogae, Thermotogae, Thermotogales, Thermotogaceae, Thermotoga, Thermotoga maritima, Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099)	>tr|Q9X1C7|Q9X1C7_THEMA Uncharacterized protein OS=Thermotoga maritima (strain ATCC 43589 / MSB8 / DSM 3109 / JCM 10099) GN=TM_1407 PE=4 SV=1MKPRKKSWFVEVLISYGIVFLFDYLYKTDVFKESFLNFYWIPLLIFCVRYDLVVHVFSSILFFTFIVVSKFLSEE GLNFSSDFALANSIMLVISTVLSLINEVRVKNMERLSLELAYRNEDVSRLEEEVRKLKKQINSLEQKLFYESTGISSLL IELREIFTEDFEKFAQRFVEIVSEYFDVKRMYVYRYKDGFLRLAAGIGRPELGFSLKKGVSLVVDKALQEGVGRILD VVDQVKSSNEPWLAVRIGDGENILGVITVEETATDNLELVEEYLTALATWIHIVMRKLEFEKYEKYRLKDGTFPADF YETEKNRLKVLEAQHGIPFIEVCVRIKREELGKLLKILRRNDLATKMSEDGEYLLLKLLFPLCDEIGFNIIKKRLESEIS EVEIVDCESH	8~~DUF4118 (0.0000000155184)~~107;X;164~~GAF (0.0000000015238)~~282	non-KdpD DUF4118 protein
	0.0002	30.8	6.6	0.00035	30.1	4.6	1.3	1	A0A0F2NMH5_9DELT	Uncharacterized protein	VR65_08635	Desulfobulbaceae bacterium BRH_c16a	365	1629713	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, unclassified Desulfobulbaceae, Desulfobulbaceae bacterium BRH_c16a	>tr|A0A0F2NMH5|A0A0F2NMH5_9DELT Uncharacterized protein OS=Desulfobulbaceae bacterium BRH_c16a GN=VR65_08635 PE=4 SV=1MQSSLDKIWVAPTLINRAFSEFPCGTLFYSLLPRDNKGGKNMVVKTLFIVLLVGSISAVHLLYTGTDLGFHML HQQLFYIPLVLASFWFGTRAGLSTAVAVSILYGPAMLLRHHEGGMHLTVITQIALYLFVAFLMGWLSDRQRRQQQ QLLKNERITALGKAASTLGVEIRDIVTGVDSIYRQSGGLKNDDANDDFLSEIDRLKRMVDGLSHFAPTLDHTSLSTD LNDILRHSFKKYRPQAAGKGLNMTIEPTGTGCPSTISVEPLFRIFDELVSNAIDFSQRGQDVVLRSFSSENEWVLEV ADSGPGVAKENEEKLFSAFFTTRPDGYGLSLSSGRKLLRDLGGDLIYRPGDNGGAVFRMHIPR	266~~HATPase_c (2.2366E-18)~~363	No DUF4118 detected by NCBI CDD
Disagreement between HMM and CDD prediction	0.0002	30.8	11.4	0.00038	30	7.9	1.4	1	F6EL20_AMYSD	Histidine kinase (EC 2.7.13.3)	AS9A_4250	Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1)	449	443218	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Amycolicicoccus, Amycolicicoccus subflavus, Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1)	>tr|F6EL20|F6EL20_AMYSD Histidine kinase OS=Amycolicicoccus subflavus (strain DSM 45089 / DQS3-9A1) GN=AS9A_4250 PE=4 SV=1MLPALFTVAFLPLKNHVAFANIAMTFLLIVVVTAVVGGLLPALAAVVLSAALLNFFFTEPFHTPFIADAENIMTLT VMVAAAVLVAIVVNRSAVRAAEAERARREAALLFSFARIILFDDNPADRLLARITEDFELESAALEEFDGTHWHTTD HARCQPSKPVEVKIQVVQVSPDVRLVVAGNELARDDWAVLETAGFQAVLALRHQRMSATAAEAERQADAAALRN ALLSALGHDLRTPLTSLKTAIGSLQDEQLRFSPEDRRELLSVADESAAQLSGLVDNLLDSSRLVTGAVRPNLGNLAV EDAIARALRHVTESDSISLDIADNLPEILADGGLLERVIANLADNALRHGGKGVTITVRAISDDVVISVADHGPGLPLG PRDETFAPFRRRGDRNMTTGIGLGMSVAKGFTEAMAGTIEVAETPGGGLTVNCAFPAVEYAGAGEG	224~~HisKA (0.000000000045954 1)~~289;X;339~~HATPase_c (1.25084E-21)~~434	No DUF4118 detected by NCBI CDD
	0.0002	30.7	8.3	0.00042	29.9	5.7	1.4	1	D5UVQ0_TSUPD	Histidine kinase (EC 2.7.13.3)	Tpau_3247	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	853	521096	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Tsukamurellaceae, Tsukamurella, Tsukamurella paurometabola (Corynebacterium paurometabolum), Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	>tr|D5UVQ0|D5UVQ0_TSUPD Histidine kinase OS=Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) GN=Tpau_3247 PE=4 SV=1MPKGQLRVYLGAAPGVGKTYAMLTEGARRAARGTSVVVGYVETHGRPQTEAQVLGLDVIPRRRVDYRGAV LEEMDTDAVIAAHPTVALVDELAHTNAPGSRNDKRWQDIAQLLEAGITVITTVNIQHLESLGDVVESITGVRQRETIP DAVLRAADQVQLVDMTPEALRRRMAHGNIYAPDKVDAALSHFFRVGNLTALRELALLWLADRVDEKLEQYRSAQ GISTVWPTRDRTVVALTGGPEGATLLRRGARLAAKGAGGELKALYVARSDGLSGASPAALTQLRQLTESLGGTFQ IVTGDDVAAAILQYAQSINAARIVLGQSRHRPVASLLRRSVSDAVIDGSGDIDVNVVTHERAVSQRRRGLPRLDRSD SALLGTRRTIAGWVLALAGPPALTAVLANTRDYHSFATELMLYLMLTVAVALVGGIRPAVPAALLGSVLLNYYFAPP LYTFTVSSGENVFAVVMFVLTAIAVASVVSLAARQTARAARARAEADVLSGLADTLLAADREGQAVLPALLDQAVA TFSLRGASLLRREAPSDPWTVVAAEGDAPSTPEEATDSSLIGDTVALAVNGPPLSASEHGLLVAFAAHAAARLDRE ALSAAASRARALAEGNRARTALLSAVSHDLRTPLAGIKAAVTSLRSDDVEWSEEDEAELLETIEESADRLDSLVGNL LDMSRLESDSLTLLTREVGIEEVLPAIWTALPDADLSFEFADDAPTAYADPGLLERVLANLVENAVRHSDGKPVTV GVSGVHTPDTGDRLQVHVRDHGPGVPEAQREAMFAPFQRMGDAPAGNGVGLGLAVARGLTEAMGGTLTAEDT PGGGLTMIVDLPAAQPVSPEPKEMS	3~~KdpD (5.70516E-119)~~211;X;233~~Usp(1.03339E-27)~~355;X;383~~DUF4118 (0.0000000084761)~~477;X(142);619~~HisKA (3.5952E-15)~~685;X;734~~HATPase_c (7.82194E-26)~~839	KdpD protein

	0.0002	30.7	12.7	0.00044	29.8	8.8	1.5	1	A0A0F0KJB4_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpD RN50_02064	Microbacterium foliorum	845	104336	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium foliorum	>tr|A0A0F0KJB4|A0A0F0KJB4_9MICO Sensor protein KdpD OS=Microbacterium foliorum GN=kdpD PE=4 SV=1MTAERMPRRGRLRVLLGAAPGVGKTFEMLVEGRRLIDEGRDVVIAIVETHDRAATAAQTIGIPEVPRRTDLHRGVPLSEMDLEAVLARRPEIALVDELAHTNTPGSAHPKRWQDVDALLDAGIDVVTTVNVQHIESLNAVVEKITGIAQQETIPDAVVRAADEIEVVDLAPQSLRDRLSAGLVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALRSYRADHGIEGTWQARERVVVALTGGTEGETLLRRGARIAARSAGGELLAVHVATQDGLRDQTPGALAAQRALVESLGGSFHQIVGDDIPGTLVSFAQGADATQLVIGVSRRGRVAAALTGPGIGSEVIRRSGDIDVHIVTHAAAGGRVALPRITGGALGWRRQVLGLAVALVFGPLLSWLMFTFRSPESITSEVLAYQLLVVVVALIGGIRPAVFAAVLSGITLDLLFVAPLFTITIAHPLHVLALALYVVIAILVSIIVDQAARRARTAQRAVAEAELLAAVAGNVLRGDNAVLALVSRTREAFGLSGVRLLAPDGEVLASDGEPVPDGRATTVPVGSGGSAPALLELHGEPLDTPARRLLDAIVAQLAAAAIEHTDLRATAREVAALAETDQVRSALLSAVSHDLRRPLASAVAAIGGLRGAHGLSASDRDELLATADESLATLSSLVTDLLDVSRVQAGVLAVSSMPLDVAGPVLAAVDELGLGPADVELVLDGELPAVSADPVLLQRVLVNVIANAHRHAPTDTRVIVSTSSLADRVEIRIIDRGRGVPAEQRDRIFQPFQRMGDTDNTTGLGLGLALSRGFAEGMGGTLTPEDTPGGGLTMVVSLPRAEDPDPLQEETE	7~~KdpD (2.27054E-112)~~217;X;239~~Usp(3.47319E-28)~~362;X;389~~DUF4118 (0.0000000115587)~~483;X(131);614~~HisKA (0.00000000851059)~~679;X;730~~HATPase_c (2.53815E-24)~~831	KdpD protein
	0.0002	30.6	9	0.00039	30	6.3	1.3	1	R5JW15_9CLOT	Histidine kinase (EC 2.7.13.3)	BN743_01807	Clostridium sp. CAG:632	341	1262830	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:632	>tr|R5JW15|R5JW15_9CLOT Histidine kinase OS=Clostridium sp. CAG:632 GN=BN743_01807 PE=4 SV=1MKKQLIIIKNISVTIAILLAGFGLCLVMQNVFEEHVLIPSIFMLGVFLISVITDGFVYGVIASVVSVLAVNYAFTFPYFRINFTIPENLLSAIIMIAMTLITCCLTSKIKHQEQIRLEGEREKMRANLLRAVSHDLRTPLTTIYGASSALLENGQDFTEEQKNQMLEGIKEDSQWLHRMVENLLSITRLDGENVTIIKTPTALDELLDSVLVKFSKRYADQEVEVDIPDELVMIPMDALLIEQVIVNILENAVQHAEGMDKIWLRAFTISDKVIFEIRDNGKGIPEDKLKTIFAEGIGLSVCATIIKAHGGDITAENSNSGGAVFRFTLDVEERESDEESI	14~~DUF4118 (0.0000000233519)~~112;X;122~~HisKA (0.000000000052709)~~188;X;241~~HATPase_c (8.26392E-24)~~329	non-KdpD DUF4118 protein
	0.0003	30.6	8.5	0.00045	29.8	5.9	1.4	1	R5F6Y2_9CLOT	Histidine kinase (EC 2.7.13.3)	BN723_00815	Clostridium bolteae CAG:59	510	1263064	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	>tr|R5F6Y2|R5F6Y2_9CLOT Histidine kinase OS=Clostridium bolteae CAG:59 GN=BN723_00815 PE=4 SV=1MARSRILDTLKTMAVLAAATAIGFLLETLGLSQANIITVYILGVLVVAAVTASRWYSISASLASVLLFNYIFTEPMFVLKAEDAGTQLTLLITFLAAVFTSSFTVQMKEKARLSQQDAYRSGVILDTSQMLQKAAAPADILTCTAIQLNKLLKRDITCFEQDGAGLKSPLCFREYSSPATGRGPAPDTLEELTAARKCFQEGKETGAATGLFPAAAYHFLPLQSSGAVYGVMGIHVGTTPPGDFENSLAVAIIAQCSMALEKEYISRKREEEAAMARAEQLRSNLLRSISHDLRTPLTSISGNAGVLMSDGENLSAEHRSRIYRDIYDDSMWLINLVENLLSITRMEGQGVHLHMETELLEEVIDEAMRHINRRHEHHTIRVNQVGDYILADMDARLIIQVITNLVDNAVKYTPEGSTIMVNSRQEGASAVIDVSDNGPGIPDESKEKIFEMFYTTGHKSADGKRGMGLGLPLCRAILSAHKGTIEVLDNKPAGSIFRLTLPAKEVSLHE	10~~DUF4118 (0.0000000147243)~~110;X(170);280~~HisKA (0.000000000320385)~~345;X;398~~HATPase_c (2.75865E-28)~~501	non-KdpD DUF4118 protein
	0.0003	30.6	13.2	0.0016	28	3.5	2.5	2	C4II83_CLOBU	Ggdef/hd domain protein	CLP_2966	Clostridium butyricum E4 str. BoNT E BL5262	558	632245	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium butyricum, Clostridium butyricum E4 str. BoNT E BL5262	>tr|C4II83|C4II83_CLOBU Ggdef/hd domain protein OS=Clostridium butyricum E4 str. BoNT E BL5262 GN=CLP_2966 PE=4 SV=1MKDVRNDRRNQINDIVSIVKVSSLLFVGIILCKTFNTNISIFMFELKNYNEYVFFSIPLIIIILIYCIWSFSNKKRKYSNIFNNFEIVLFISMFSLITLICGINQSQYKVLYLFIIITTTIQFGMKSGIIVSIISSFIILVMDLIFIPSSEISAYFQDDLLLAGIFFLTALPLGFYVKIEKQHIEKLENMINIDGLTELYNHRYFCDSLAEEIKIGEKENSPVSMIFIDIDYFKNYNDIYGHQKGDYVLKKIGKIIKSSIGNQHISARYGGDEFAIILPDTTEDMAVNIAESLRKKIENTYFEGEENQPNGKLTVSMGVSVYPDKARSDIELIKSADDALYRAKFFYKNRVETYISILDEIKSNIDEEDAELVTSIKTLISVINAKDRYTYGHVERVVVYGRMLAESLGLNERDKNILIYGSYMHDIGKINISKDVLIKKMKLTDDEWEVLKQHPANGVEIIKSVKSLNMIIPLIISHHEKYDGTGYPNNLKGDEIPYLARVLTVIDSFDAMTSNRPYNKRKTYKEAIEELQRCRGTHFDPEIVKVFIKALKTNYNIN	192~~Nucleotidyl_cyc_III (4.17811E-57)~~351;X;388~~HDc (3.60432E-23)~~531	No DUF4118 detected by NCBI CDD
	0.0003	30.5	14.2	0.00049	29.7	9.9	1.4	1	K9TGF0_9CYAN	Histidine kinase (EC 2.7.13.3)	Oscil6304_1397	Oscillatoria acuminata PCC 6304	1145	56110	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria acuminata, Oscillatoria acuminata PCC 6304	>tr|K9TGF0|K9TGF0_9CYAN Histidine kinase OS=Oscillatoria acuminata PCC 6304 GN=Oscil6304_1397 PE=4 SV=1MVRPIPRSPVFSYSAAVFTVVIALLLTVTFKPILASTLFLFFFLAVTGMTWYGGIGPGLVTTILSVLALDYFFLVPTHSLTVLSGTNLLRMGLFVLVTLAIAKLNTKLQQTKRQLEISLSQLKQSEERYRRIVETASEGIWILDEAGRTRYVNQRMAQMLGCSPESMLDRPFFEWFDQGSRPEGYQTLTQPYPGYPEQWDGRFRRSDQSLLWAIVSMNSIFDDQGQFQGTHLMLTDVSDRQQTQERLQLSLEAGRMGFWDWNLSTNEIVRSDNLAEIYGVSPGQLEQTFESSLNLIHPEDRERVQEAIAQAVAENTPYSLEFRIQPSPENIRWILGKGRVFKDAQGTAVRMIGIAMDISDRKQTEEVLGQTQQRFETFMNYSPVAAYFKDEAGRYIYVNPIVERLWQRSQEKWVGQTDADLFPEAVAQELQAHDATVLETDQALEFLETVEHLDGKHYWISWKFPMHEPSGRRLLAGISLDITDRKRTQEERDLLLANLESQQELLSAVLQQMPAGAIVAEAPSGQLVLMNQQVREILGISLTPLITIPSYLHTSYQIFHPDGQPYHPDALPLARSISQGEVVVEEELQIQRADGTRVTVLANSGPIRNAEGEIVAAVVTFYDITAQKRAQAEIKRYADVVKNIQVGLSVWQLTPGEEPPSFELISANPAASQLAGRDLDRAVGMRIETLFPHLVKTSRIAELIEVLNSSSAREFPEVIYNDDAGEERCCSMKAFSLPNRCLGLAYEDITDRKQAQFALLESEQRFRTMADAAPVYIWLSGIDQLCYYFNKPWLEFTGRTLEEEIGNGWTEGVHPDDFKFCLDTYQKSFDLRQPFEMEYRLRRYDGEYRWVLDRAVPRFSPDGRFEGYVGSCIDISDRKLYEGEIKRLNASLERRVTDRTAQLEAANQELESFAYSVSHDLRAPLRHISGFVNLLRKRIEPSLDENSQRYLDIIVASTHQAEELIDNLLAFSRMARAQMRFIKVDMNQLVNEVRQTLEIHRGDRKILWKIASLPPVKGEPTMLRLVFQNLLDNAIKYSQRRETAEITVGFNESDLEFIFFVRDNGIGFDMRYAHKLFGVFQRLHSNPDYVGTGIGLANVRRIIHRHGGRTWAEGEVDLGATFYFSLPKQPEGDQVDAS	10~~DUF4118 (0.0000000156378)~~110;X;136~~PAS (0.000000000914478)~~237;X;256~~PAS (0.0000000027084)~~358;X;390~~PAS (0.000902728)~~482;X;513~~PAS (0.0000479375)~~624;X(149);773~~PAS (3.22151E-14)~~875;X;907~~HisKA (0.000000000049743)~~973;X;1023~~HATPase_c (3.11141E-25)~~1126	non-KdpD DUF4118 protein

	0.0003	30.4	7.2	0.00058	29.4	5	1.5	1	A0JW43_ARTS2	Histidine kinase (EC 2.7.13.3)	Arth_1878	Arthrobacter sp. (strain FB24)	883	290399	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. (strain FB24)	>tr|A0JW43|A0JW43_ARTS2 Histidine kinase OS=Arthrobacter sp. (strain FB24) GN=Arth_1878 PE=4 SV=1MARGTLRIFLGAAPGVGKTYEMLEEAHRLSKRGEDVVVAFAMDHGRSDTRALLDGLEVIPPRRLPYRGTEFEEMDLDAVLARAPETAIVDEYAHTNIPGSRHTKRWEDIDELLNAGINVLSTVNIQHLASLGDVVNAITDVRQAETVPDEIVRRADQIHLVDISPELLRQRLGDGKIYSADKIDAALSNYFRLGNLTALRELALLWLADRVDEGLARYREENDIQATWPARERIVVGLTGSPEGEVLIRRGARILNRVNGGDLLAVHVRAADGVAEESPRALEAQRRLIQDLGGSYHVVAGEDPASALLDFARSVNATQIVVGISRHKKLAGLLGALLGGGIGTRVVVRDSGDIDVHMVSHPLGGRGTGPVRQRDLGRVRVTAGFVLAAVLPALLQLMLSANSEPNIATAVLIQLSGSVLVALIGGLWPAIVAALWSSLLVNYYSTPPVGTLTISDPQNLLALLVFVGVSAAVAVVVDISARRSKEASRARAEATTLGDLTRSAARAEDTVKGLLEQALDVFQVSGAALYTSAGDTGTEAPGGTGWRSVAEAGAVPPAGPDTADNIEQIDPTTRLVLTGRTLPASDRRLLGAFGVHLAAQLERQQLAASRREVLRLAESNTMRTSILRAVSHDLRTPLAGIKLAVGGLLQHGVTYTPEEERDLLQTIDACADRLDLLVGNLLDMSRISADSVNPLLRPVRWSEVVPAALHGTPQGRVRVELPANMPEIDADPGMLERVIANIVENAVKYAPDSEIVLVGAVGGFRSATIAGRPASELRIIDHGQGVPAERVVEMFRPFQRLDDIPQTTGVGLGLAVAKGFTEAMGGTLRAEETPGGGLTMVIRLPLSTGLAIDDGDRQAPVQPQSLLARRTDSRPFQPSATENP	1~~KdpD (4.96228E-110)~~211;X;233~~Usp(3.03936E-26)~~359;X;385~~DUF4118 (0.000000399156)~~463;X(156);619~~HisKA (0.000000000001352 46)~~685;X;734~~HATPase_c (2.19973E-21)~~843	KdpD protein
	0.0003	30.4	17.3	0.00028	30.4	12	1.6	1	B9L636_NAUPA	Uncharacterized protein	NAMH_1432	Nautilia profundicola (strain ATCC BAA-1463 / DSM 18972 / AmH)	386	598659	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Nautiliales, Nautiliaceae, Nautilia, Nautilia profundicola, Nautilia profundicola (strain ATCC BAA-1463 / DSM 18972 / AmH)	>tr|B9L636|B9L636_NAUPA Uncharacterized protein OS=Nautilia profundicola (strain ATCC BAA-1463 / DSM 18972 / AmH) GN=NAMH_1432 PE=4 SV=1MKLYALIETFVIFIVLVLFNYFFSPKEMFYSEYLINIYLYALIIISLFYGFIYSLVFYILYFAAQYFFLGSVDIFMLSHYFIFLLIFSEFKYFWNRKLEKLNEENSFLKRRVEDLGNAYYLLKISHDELEKNYILKPFSIREILKEIKESIKKDKNKSIDIFLNLLKKLFKLEQASLFFKKEDGDYELKGNIGEKINLDMDDELVKQVLENKHLSYSINTDNSSKYIAVIPVVSLSDELKGLFVIKSMPFFSLSKDNLITISLFLTYFVNLLNIPEKYHKYVIDPLVAKEIESLRYLSKKYGIKNHIVIFNIKNPLQSVQISKMIRGVDIFFEYKDKLVVILPFTNEIGVNQFLNKVLRKIDVEYKVYDLMQMDLDNLNKALNEDS	5~~DUF4118 (0.00000000567866)~~97	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0003	30.4	12.8	0.00058	29.4	8.9	1.5	1	A0A0A8F065_9ACTN	Sensory histidine kinase in two-component regulatory system wtih KdpE	GZL_08794	Streptomyces sp. 769	837	1262452	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	>tr|A0A0A8F065|A0A0A8F065_9ACTN Sensory histidine kinase in two-component regulatory system wtih KdpE OS=Streptomyces sp. 769 GN=GZL_08794 PE=4 SV=1MARGRLRIFLGAAPGVGKTYAMLAEGQRLRALGTEVVVGFVEPHGRRPTAAMAEGLETIPRRALRHRGARFTEMDPDAVLARRPQVALVDELAHSNVPGTRNAKRWQDVEELLDAGIDVVTTLNVQHLESLNDVVRQITGVRQRETLPDEVARRADQIELVDLPPEVLRRRMVHGDIYPADRIESALTHYFRVGNLTALREIALLWLADRVEEGLQRYRAEHGIVAPWETRERILVALNGGPEGETLIRRAARISARTPGTELLALHVVPEDGLTHVDPSVLDAQRTLLESLGGSFHQTTGEDVVEALLQFAEAENVTQIVLGASRHGRVASLLRAGVGERTIKGSGPIDVHIVTHEEAAASAALRLPRPGNGMGPRRLGAAAAGAVVLLPLLTLLLTVVRGPMGLAGALVLYLLVVVVVALVGGVVPALLAAVAAALLADYSFIAPVHSFDIERPDEIVALVVFVVTAVLVGTAAGAAARHTRQAARAIAEARTLSRLAAGVLRGQDLPALVEMIRENFGLSAVSLLERDPRASPVPRWYVVASAGDHPPERPYEAEVESPVDDLLTLAARGPGLSSQDRRLLDACAAELGLAHARGRIAGPAGLGDPLAEAERTRASLLLAAGRDLRAPLRTAEDALGRLRRRGGERAPDERRLLETARAAVHRAAQLVTDLDDLSRLHAGALDLYLRPVDLNEAWGAALDDLGPGGHSIVLRLPEYLPDVIADAALLTRALTALAADALRHSPPGRPPVVTAETHDGRVAIRVADGSGGEGAAAAGRSGSRADSLALRLSRDLAEAMDGSLRTSGRGSAFTVTLSLPSSAPGRPRRGKRPKHST	1~~KdpD (3.10106E-115)~~211;X;233~~Usp(6.44063E-28)~~355	KdpD protein
	0.0003	30.4	9.5	0.0008	29	6.6	1.8	1	W0RGL1_9BACT	Histidine kinase (EC 2.7.13.3)	J421_1938	Gemmatirosa kalamazoonesis	557	861299	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, Gemmatirosa, Gemmatirosa kalamazoonesis	>tr|W0RGL1|W0RGL1_9BACT Histidine kinase OS=Gemmatirosa kalamazoonesis GN=J421_1938 PE=4 SV=1MRRGMSVPNAARWAVWLGVLAGMTAGMLAVRGYLDKAHVALVYLLVVLGASADVGRRLGLVVATLGFLLFNALFLPPYNTLVVANPLDWIVLFAFLATSIVAAQLLARERATAETATARAREIDRLAALGAETLSVPRADDALLAIASVIRSALGVDECEVYQRGLDGRVTPVARAGDVRDGADASARPAGVPAVDDASLVAFLVANRASAVELADGGVRLAHPPDDAHPSDGSGVLGDAIGEAEWLPGVAHVVDGASWAGARALLLSLTARGHTVGVLRLASRAGLRFTPEQARLLTALAYYAALGVERVRLVASAERAEAERRAEQLRSALLMAVSHDLRTPLTTIKGIAHEVADGADPMLARQIEREADHLNALVGDLLDLSRIQAGAVVPNVEVNTVDDLLGAALQRAAGALRERDVRVEQPEDALLAGRFDLSQTLRIVVNLLENAAKYAPRDTPIVVRAERESDRLRVTVLDRGPGVPEGEGERIFEPFYRPPGTPPDVRGTGLGLSIARGLAEAQGGSLRYAPRDDGGAAFVLELPAEVLPDDEQAGVEG	55~~DUF4118 (0.00064462)~~105;X;200~~GAF (0.0000259331)~~310;X;328~~HisKA (0.000000000030115 3)~~386;X;442~~HATPase_c (8.73668E-26)~~542	non-KdpD DUF4118 protein
	0.0003	30.4	11.1	0.00059	29.4	7.7	1.5	1	A0A0F0LTG6_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpD RR49_02066	Microbacterium ginsengisoli	845	400772	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium ginsengisoli	>tr|A0A0F0LTG6|A0A0F0LTG6_9MICO Sensor protein KdpD OS=Microbacterium ginsengisoli GN=kdpD PE=4 SV=1MRRGRLRVLLGAAPGVGKTYAMLEEGHRLSAEGADVVVGVVETHGRAATAALTRGLEVVPLRRRDRHRGVSLDELDVEAVITRHPSVALIDELAHTNAPGSAHAKRWEDVEQLRDAGIDVITTVNVQHIASLSDVIEQITGTVQRETVPDAVVRGADQIEVVDLAPQSLRDRLSAGLVYPAERVDAALSNYFRLGNLTALRELALLWLADEVDSALKQYRAEHDIDGTWTTRERVVVALTGGPEGETLIRRGARIAARSAGGELLAVHVLSQDGLRGATPGALATQRALVEQLGGTYHQLVGDDVAHTLVEFARSVNASQLVIGVSRRSRMSAALTGSGIGATVIRDSGDIDVHIVTHSAAGGKLRLPRVRGGALSRGRRLLGFAVALVGGPLLSWLLFSFRSDDSITSDVLAYQLLVVIVALVGGIWPALFAAVLSGFTLDYLFVQPLFTITIAHPLHALALGLYVVIAILVSYIVDQAARRARVAERATAEARLLATIAGSVLRGDSAVEALVSRAREAFGLHAVRLVGEGGTVLAEDVADGPAPANAACTRLPVGARVGGAPRATLELTGDEPDGASRRLLDVIVAQLAAAIDHLELTAAAREADALAETDQVRSALLSAVSHDLRRPLAAAVAAVGGLRAADVRLSPTDRAELLETADESLRTLSMLVTDLLDVSRVQAGVLAVSLAPVDAAGALLAALDELGYGPDEVEVALDPDLPPLVADPVLLQRVLVNLLANARRFAAPGTHVVVVTTSRLGELAQIRVIDRGPGVPADRRDDIFAPFQRQGDTDNTTGLGLGLAISRGFTEGMGGTLTPEDTPGGGLTMVVELPVQPAAETTTQGAR	1~~KdpD (3.85656E-112)~~211;X;233~~Usp(8.27437E-31)~~356;X;379~~DUF4118 (0.000000000077013 4)~~477;X(136);613~~HisKA (0.000445695)~~679;X;730~~HATPase_c (3.73936E-24)~~831	KdpD protein

Disagreement between HMM and CDD prediction	0.0003	30.3	8.7	0.00055	29.5	6	1.4	1	K4R5Q9_9ACTN	Histidine kinase (EC 2.7.13.3)	kdpD3 BN159_7227	Streptomyces davawensis JCM 4913	844	1214101	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces davawensis, Streptomyces davawensis JCM 4913	>tr|K4R5Q9|K4R5Q9_9ACTN Histidine kinase OS=Streptomyces davawensis JCM 4913 GN=kdpD3 PE=4 SV=1MGRGRLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLHGLEQLPRKELAYRGTTFTEMDVDAVLARRPQVVLVDELAHTNIPGSRNSKRWRDVEELLAAGIDVISTVNIQHLESLGDVVESITGVRQQETVPDEVVRRADQIELVDMSPQALRRRMAHGNVYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLREYRGEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTAASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLAFARGVNATQIVLGVSRRKSWQYVFGPGVGATVARESGPDLDVHLITHDEVGKGRGGLPVPRGARLGRLRILWGWAVGGLGPVLLTFLLTSVTPEVGLANDMLLFLTLTVAAALLGGLLPALASAVVGSLLLNWYFTPPVHTFTIADPTNIVAIAIFVGVAVSVASVVDLAARRTHQAARLRTESEILSFLAGNVLRGETSLEALLERVRETFGMESAALLERASEVDPWTCAGSVGPRPCTNPEGADVDVPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLREEADQARALAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDEAELLAGIEEGADRLDHLVGNLLDMSRLQTGTVSAIVREIDLDEVVPMALGGVPEDSVELDIPETLPMVNVDKGLLERAVANVVENAVKYSPTGTSVLVSASAIADRVEVRVVDRGPGVPDEAKERVFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLHAEDTPGGGLTMVLSLPRAQGSRPEARTPAA	1~~KdpD (5.4682E-124)~~211;X;233~~Usp(1.60443E-31)~~356;X(257);613~~HisKA (2.66755E-14)~~679;X;728~~HATPase_c (1.92467E-26)~~829	KdpD protein
	0.0003	30.3	5.8	0.0006	29.4	4	1.4	1	K9WGV2_9CYAN	Histidine kinase (EC 2.7.13.3)	Mic7113_3713	Microcoleus sp. PCC 7113	846	1173027	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	>tr|K9WGV2|K9WGV2_9CYAN Histidine kinase OS=Microcoleus sp. PCC 7113 GN=Mic7113_3713 PE=4 SV=1MREAKRLLLSSYGVPVLASLLALLLRSLLAPLLRENAPLLVFIIPVMISAWYGGLKPGLLATAISALIGCYFFVQPVFSLDITGVANGVRIGIFLVEGVLISWLSETRRGAMQRSEAIASSLRESEESYRLLVEGVEDYAIFRLDPKGNIVTWNNGAERIKGYKAADILGQNYSILFTVEDIERHKPEQALLMAVREGHFVEDSWRRRKDGSLFWASTTITALRNESGKLCGFSNVIRDITQRKQAEEELRKLVKDLSDVKFAIDRAAILATTDERGNITNVNDKFCELSQYSREELIGQNHRLINSGYHPQEFFANLWSTIKRGDVWHGEIKNRAKDGSYYWVDTTIVPFLDDAGQPFQYLAIRFDISDRKHAQEVLHRYAQRLEALHEIDRAILRAESTKQLARAALLRLHSVVPYEQAMVVLFRFQTQEAELLTREWNGELRRETIPISDLIPQVSLQQVSIRYIENLSTLAPCPPLLERQLAEGKRSFLSISLIAEGELIGELGVFARPVAAFTQEHQEIVTEVANQLAIATQQARLREQRQNYAAELEQRVIERTAELQEANEALEVFVYSASHDLRAPLRGIQGLAQVLLEDYGDLFDSEGQLYAQRLVLSAQEMSALLQDLLDYSRLSRAEINLQRIDLASIMTSALTQLQTELQAQKAQVRVEIPCFEVMGHRATLIQVVTNLITNAIKFVPPGVQPQVRIWAEERGVGDEEHQNVSADENMTQLQPRDENKTLLPDIRTPSRYAIPNNQVTPVAAVSANIRLWIEDNGIGIEPRHQENIFQAFERLHGVETYSGTGMGLAIVRKGVERMGGRVGVESQFGDGSRFWIELRQTTSTA	39~~DUF4118 (0.000000752558)~~109;X;138~~PAS (0.000000000014136 9)~~240;X;269~~PAS (0.000000000000288519)~~368;X;383~~GAF (0.000000000011019 4)~~550;X;568~~HisKA (0.000000000620166)~~634;X;685~~HATPase_c (2.59522E-22)~~839	non-KdpD DUF4118 protein
	0.0003	30.3	5	0.00055	29.5	3.5	1.3	1	A0A0F4JBV1_9ACTN	Histidine kinase	VR45_25750	Streptomyces sp. NRRL S-495	861	1609133	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. NRRL S-495	>tr|A0A0F4JBV1|A0A0F4JBV1_9ACTN Histidine kinase OS=Streptomyces sp. NRRL S-495 GN=VR45_25750 PE=4 SV=1MGRGRLRIYLGAAPGVGKTYAMLAEAHRRLERGTDVVVAFVEDHGRRHTAARVAGLELVPRRELTHRGAVFTELDLDALLARRPQVALVDELAHTNVPGCRNEKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVEGITGVRQRETVPDEVVRRADQIELVDMSPQALRRRLAHGNVYAPEKVDAALANYFRPGNLTALRELALLWTADRVDEYLQKYRAEQGIKGTWQARERIVVGLTGGPEGATLIRRAARIAARGSGGELLAVHISRSDGLAGSGSGSSSQTLIEQRALVEGLGGSYHAVLGDDPAAGLLEFARGVNATQIVLGTSRRPAWQYIYGPGVSGTVTRESGDIDVHIVTHEHEAKGRGRIPIRRVTDLGRTRTVAGWLIGVAGPPLLALLLINVDGLGLTTDMLLFLSLTVCAALVGGLYPAVASALVSSSALNYYFAPPIHTFTIDEPQNILAVAIFTAVGIAVASVVDLAARRTHQAARSQTEAQTLSALAGTVLRGAPSGDGVLTALLEQVRETFQQESAALLERPDPLGAWHPVATAGPRPPERPETADVDVPVGENLALALRGRVLPGEDRRLLGAFAAQAAVVLERRRLAGEAAAARREAEGNRIRTALLAAVSHDLRTPLAGIKASVSSLRSADVEWDEADEAELLAGIEAGADRLDHLINNLLDMSRLQTGTVTPLIQETDLDEVVPFALGGVPPGAVRLDVPETLPMILADGGLLERSLANLIENAVKYSPEGVKVLVKAGALRPPGEPGRVELRIVDRGPGVPEDAKERIFAPFQRYGDAPRGAGVGLGLAVARGFVEAMNGSVTAEDTPGGGLTMVVTLPAAERVPGPGDAPGPELPAAPA	1~~KdpD (4.76402E-125)~~211;X;233~~Usp(5.18766E-20)~~358;X;404~~DUF4118 (0.0000000672132)~~484;X(134);618~~HisKA (1.98352E-14)~~684;X;733~~HATPase_c (9.18432E-25)~~839	KdpD protein
Disagreement between HMM and CDD prediction	0.0003	30.3	7.3	0.00069	29.2	5.1	1.5	1	A0A059VV35_STRA9	Histidine kinase (EC 2.7.13.3)	DC74_380	Streptomyces albulus	845	68570	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	>tr|A0A059VV35|A0A059VV35_STRA9 Histidine kinase OS=Streptomyces albulus GN=DC74_380 PE=4 SV=1MAPRVTAEAAGERQGKLKVFLGAAPGVGKTYRMLDEGRRRLRRGTDVVVAYAECHGRQHTEEMLDGLEVVPRLHRAYRGSTFSELDLDAVLARGPAVALVDELPHTNVPGGRNAKRWQDIDELLAAGIDVVTTVNVQHLESLNDVVEKITGVPQRETVPDEVVRRAHQIELVDMPAEALRRRMAHGNIYQPEKVDAALAHYFRIGNLTALRELALLWVAGRVDETLQKYRSEHGIGTVWETRERVVVALTGGPEGETLIRRAERIADRSSGGDLLAVHVARSDGLAYASPAALAKQRALVESLGGSYHSVVGDHVPTALLDFARAENATQLVLGTSRRSWFSRLVAPRGIGEDTVELSGDIDVHMVTHERAGRGQRLSIPGRQLPHARRIAGPVAGLVLPFVLTAVLTHIRGPLNLTSEALLFLATVVGVACLGGVVSALLASLTASLLNYYFIPPSREFTITEANNALALAVFALVAVTVAALVDRSLRLSRRAASATAEAETLSSMAGTILRGDQGVSVLLERTRETFGMASAELVPRAEQEPGTEAEEEAEGLVKVPAGPDRLLVLRGRRLPASEHRVLTAFAAHLAAALDHARLMEAAAEVEPVKAADRLRTALLAAVSHDLRTPLASGRAAISSLRSTDVAFTAAERSELLATAEDSLIELNRLVDNLLDMSRLRAGALSLHLQPTAFADVLPLSLATLAAAPVRIASRGLAEVCDVLADPPLLERVIANLVTNAVRHSGAAESVLITASAMGPRVELRVIDRGPGLRPEDRDRIFVPFQRLGDRDNTSGLGLGLALSRGLAEAMGGTLSPEDTPGGGLTMVLSLRAATAGDAVEADTP	12~~KdpD (2.15338E112)~~222;X;244~~Usp(2.88691E-29)~~367;X(246);613~~HisKA (0.0000000000514381)~~679;X;730~~HATPase_c (1.71755E-26)~~831	KdpD protein
	0.0003	30.2	9.6	0.00046	29.8	6.7	1.2	1	Q1IPN8_KORVE	Uncharacterized protein	Acid345_2161	Koribacter versatilis (strain Ellin345)	138	204669	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Candidatus Koribacter, Candidatus Koribacter versatilis, Koribacter versatilis (strain Ellin345)	>tr|Q1IPN8|Q1IPN8_KORVE Uncharacterized protein OS=Koribacter versatilis (strain Ellin345) GN=Acid345_2161 PE=4 SV=1MCHWNCFGCPLLCEQRAGVNRQEHYRRHFLSLAGIVVSVLLAVFLIFSVRGTHRSLIVPVVFLVFIILCARYFGMLAGVVASIIASGLFAVFLFEPYGSLQIKDHQALWNLALMLFAGIALSYANSGNEDEPKAPKNS	32~~DUF4118 (0.0000981988)~~123	non-KdpD DUF4118 protein

	0.0004	30.1	10	0.00063	29.3	6.9	1.4	1	B5I2H9_9ACTN	Histidine kinase (EC 2.7.13.3)	SSEG_09855	Streptomyces sviceus ATCC 29083	851	463191	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sviceus, Streptomyces sviceus ATCC 29083	>tr|B5I2H9|B5I2H9_9ACTN Histidine kinase OS=Streptomyces sviceus ATCC 29083 GN=SSEG_09855 PE=4 SV=1MGRGRLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVGFVEHHGRPRTEVMLRGLEEMPRREIEYRDSVFTEMDVDAVLRRAPAVALVDELAHTNIPGSRNARRWQDVEELLAAGIDVVSTVNIQHLESLGDVVEAITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLKQYRSEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTSASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGVNATQVVLGSSRRKTWQYVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARSARRILWGWLVGLAAPVLLTLLLTTVDLGLANDMLLFAVVVAAALLGGLFPALASAAVGSLLLNYFYTPPLHRWTIADPKNIVAIVIFVGVGISVASVVDLAARRTHQAARLRAESEILSFLAGNVLRGETRLEELLERVRETFGMESAALLERAGDVEPWTCAGRAGLGPAVERPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLQEEADQSRALAEGNRIRTALLAAVSHDLRTPLAGIKAAVSLRSHDVAWSEEDQAELLEGIEEEGADRLDHLVGNLLDMSRLQTGTVTPLMQEVDLDEVVPMALGGVPPDSVALDIPETLPMVLADPGLLERLVANVVENAVKYSPPGTPVRVSASAIADRVEVRVVDRGPGVPDEAKERIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMNGTLNAEDTPGGGLTMVLTLRAADTHAQLLVDPFEEEAEPERQAT	1~~KdpD (2.10711E-123)~~211;X;233~~Usp(3.50986E-31)~~356;X;425~~DUF4118 (0.00682158)~~480;X(131);611~~HisKA (3.34852E-15)~~677;X;726~~HATPase_c (3.0061E-26)~~827	KdpD protein
	0.0004	30.1	8.7	0.00065	29.3	6	1.4	1	A0KED2_AERHH	Histidine kinase (EC 2.7.13.3)	AHA_0014	Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	862	380703	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Aeromonadales, Aeromonadaceae, Aeromonas, Aeromonas hydrophila, Aeromonas hydrophila subsp. hydrophila, Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240)	>tr|A0KED2|A0KED2_AERHH Histidine kinase OS=Aeromonas hydrophila subsp. hydrophila (strain ATCC 7966 / DSM 30187 / JCM 1027 / KCTC 2358 / NCIMB 9240) GN=AHA_0014 PE=4 SV=1MRDEVRADALLASLEQEHRGKLKVFLGAAPGVGKTYAMLQAVREQAKEGVDILIGVVETHGRQETLALLDKLAIQPRKLHLHRQQRLEEMDLDGLLARKPAIAVVDELAHSNAPGSRHEKRWQDVEELLGAGIDVYTTLNVQHLESLNDLVWQLTGVRVKETLPDQVLLEADSLVLIDLPPKELLGRLKEGKVYVPHQAKAALQSFFSLNNLTALRELAMQTAASHVEGDLQLQWQAAGKTTLPLRGKLMVCLGDQHGAALVRYGHRFAQRRQLPWLVVHIDSKGQRSVELEQALALASQLGAKVLTLSSPAVADTLLETAEQQQVSQLLLGKPHKAPWRRSLVQHLLKQAQGLEITLVDTEKRKPSLGLKPLHPKDIRQSLLAVAIMGTTSAAVWGLSHWLPPASLPMLFVLGVLATALTTSLMPAILAAVLGFVGHNLLFTAPYFSLSVASHSDLLTLFVLLIVGITAGRLASRQRQQLIGLRETQQLGNALLSLSQGLATASSPEEVLRQGSQAISLALGQPVFALDQHYQHRAGSTQHKPGQTDKAAIDWCLAQKQSAGAHTATLNAAEAQYHHLSDELVLGIVLANPLASSAEHQLQALLTDIRAALARIDLNERLADSQLQAETDRMRAALLSSVSHDLKTPLATIMGAGSTLLEYGDRISSEDRSELLHSVQDEARRLHSYVQNLLDMTRIGSPDFQLKRDWVDLADLVENARRRLDSSWRQHKLLVHFDQQQIPRLYVHGALIEQVLVNILDNASRYSPAGTPIEFKVMLADPDLILDIIDIGVGIAESDRDKIFNLFYTQPVGDCGSRGTGLGLAISRAMIEAHGGRIWAFSGPNGNGTCMRISLPLALNAAAA	17~~KdpD (1.60465E-116)~~227;X;248~~Usp(9.36775E-25)~~359;X;382~~DUF4118 (0.000000000008636 93)~~480;X(151);631~~HisKA (0.000000000045412)~~697;X;750~~HATPase_c (5.84817E-23)~~852	KdpD protein
	0.0004	30.1	10.7	0.00083	28.9	7.4	1.6	1	Q0SDF8_RHOJR	Sensor kinase, two-component system	RHA1_ro02623	Rhodococcus jostii (strain RHA1)	570	101510	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus jostii, Rhodococcus jostii (strain RHA1)	>tr|Q0SDF8|Q0SDF8_RHOJR Sensor kinase, two-component system OS=Rhodococcus jostii (strain RHA1) GN=RHA1_ro02623 PE=4 SV=1MRPDRQLDMMLIEVCPRTPRLIRACTMTRQWSRRSIGALARRGAASPRAVFDADAHQMPARLISLLVRPTTPPLWLGIVVAATVITVETVVVHQLDKVAPHNAFGAVFLLGVLVVSARWGFALSVMTTLVSALVYVYFHLQVEGTLVPAKASDWVAVVVFLPVALVANLMAGQARLRTAEAVLRRREAEASRDELAILAEHQAALRRVATLAARGVSPTEVFTAVAEELALWLHVVDAVLLRYEGDGTGTLVAVRYEPGESRMPVTGDTISTEGDDVGAIVLRTGHGARIDNHAHVGGAVATRIRAEGFGSIVGVPIVVDGRVWGAAIVGSRRTVPLPADTQTRLGDFADLVATAVANAATRAELIASRARIVAAADDARRRLERDLHDGAQQRLVSLGLEVRMAEASVPAEWVDVREQLSAIASGLTGVSEDLRELSHGIHPAILSKGGLGSAVRTLARRSAVPVALDVALEGRFTESVEVAAYYVVAEALTNAAKHARASEVAVSLRAEDGTLHLVIGDDGVGGASSGAGSGLIGLHDRVEALGGHMRITSPPGHGTTLDITIPVVGE	0.00000108599)~~167;X;217~~GAF (0.000132053)~~351;X;380~~HisKA (0.00000000301593)~~446;X;487~~HATPase_c (0.00000682722)~~565	non-KdpD DUF4118 protein
	0.0004	30.1	7.1	0.00064	29.3	4.9	1.4	1	G8X3F8_STREN	Histidine kinase (EC 2.7.13.3)	SCATT_46380	Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	874	1003195	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cattleya, Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	>tr|G8X3F8|G8X3F8_STREN Histidine kinase OS=Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057) GN=SCATT_46380 PE=4 SV=1MAFLRFAGFALRTLGDAGPFRRYEDGAMARGRLRIYLGAAPGVGKTYAMLSEGHRRLERGTDLVVGFVETHNRPRTEVMLHGLEQIPRRTLTYRGSRFTEMDVDAVLARRPEVALVDELPHTNVPGSRNAKRWQDVEELLEAGVDVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYQPDKIDAALANYFRPGNLTALRELALLWTADRVDEYLQQYRAEHRISSTWQARERIVVGLTGGPEGRTLIRRAARLAAKGSGSEILAVYVARSDGLASGSPKELTVQRTLVEDLGGSFHHVVGDDVPTALLDFARGVNATQIVLGTSRRKAWQYVLGPGVGATVARESGPDLDVHIVTHEEAAKGRGLPVARGARLGRARIALGWLVGCGGPALLTPLLLAFTPGLGLANDMLLYLATTVAAALVGGMLPALASAAVGSLLINYFFAPPVHRFTIADPHNIVAIVIFVAVAVSVASVVDLAARRTHQAARLRAEAEILSLLAGNVLRGETSLDALLERVRETFAMDSVALLERNDEYAPWTRAGGVGPTPCGRPDAADVAVPVGDRMSLALSGRVLPAEDRRLLSAFAAQAAVLLDRRRLVGEAEQARELAEGNRIRTALLAAVSHDLRTPLAAIKAAVSSLRSDDVAWSPEDEADLLEAIEEGADKLDHLVGNLLDMSRLQTGTVTPLMQEVDLDEVVPMALGGVPPDSVALDIPETLPMVLADPGLLERLVANVVENAVKYSGDAERVLVAASALRDRVELRIADRGPGVPDTAKERIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLVADDTPGGGLTMVLTLRAAGALDPSAPELPAEVTS	28~~KdpD (6.4028E-123)~~238;X;260~~Usp(6.96805E-30)~~383;X;438~~DUF4118 (0.000048136)~~492;X(147);639~~HisKA (0.000000000000113289)~~705;X;754~~HATPase_c (3.46044E-25)~~855	KdpD protein
	0.0004	30	10.8	0.00066	29.2	7.5	1.4	1	R4LG40_9ACTN	Histidine kinase (EC 2.7.13.3)	L083_0730	Actinoplanes sp. N902-109	812	649831	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	>tr|R4LG40|R4LG40_9ACTN Histidine kinase OS=Actinoplanes sp. N902-109 GN=L083_0730 PE=4 SV=1MARGELRIYLGAAPGVGKTYTMLAEAHRRAGRGTDVVVALVETHGRQHTEAMVGDLEVLPRRGGELDLDAVLARRPRLAVVDELAHTNGPGARHGKRWQDVQELLAAGIDVLTTVDVRHLESLNDVVTRITGVPQRETVPDAVVRSAGQVELVDMTPEALRRRLAHGNIFRPSQVDAALGSYFRAGNLTALRELALLWLADEVEAQLGRYRADHDIDAIWETRERVVVGLTGGPEGETLIRRAARIAARTRGTDVLAVHVARNDGLAGADPAGLARQRVLVERLGGSYHQVVGADVAQALLDFARAVNATQIVLGASSRGRLARLLSAGVGAATTALSGTIDVHLVPHERVAPGRRRARMPAALSRGRRLAGAAAAAVAGLPGLTALLKLSAGLSLTNDILFFLTATVGIALIGGLWPALLAAVVGGFLLLNWFFTPPYGRFLIAEADNLLALAIFVVVALAVSWVVDTAARSTRRAAQAGAEAQTLAAVAGSVLRGERPLTALLERLRETFSLESVELRQGGATVAAVGTSELPAEQVRVDDDLVMVLRGRPLAASDRRIAEAFAAQAAVALRQEQLSAEAATAKPLAEADRLRTALLAAVSHDLRTPLAAAKTAVASLRSADVEFGEQDRAELLETADESLDRLHRLVSNLLDMSRLQAGVLGVTLLPVGAEEVVPRALDDLGDAGRTVTAHIPDDLPALSADPGLLEQVLVNLLANALRYSPADRPPVVTASTLGDAVELRIVDHGPGIPKDRWDDVFLPFQRLGDRDNHTGVGLGLALARGLTEAMGGTLVPEETPGGGLTMVLALPHHTG	1~~KdpD (2.7459E-104)~~203;X;225~~Usp(8.19514E-20)~~347;X;394~~DUF4118 (0.00000000659303)~~469;X(120);589~~HisKA (0.000000000001912 03)~~655;X;706~~HATPase_c (2.43292E-23)~~807	KdpD protein

Disagreement between HMM and CDD prediction	0.0004	30	8.2	0.00056	29.5	5.7	1.2	1	D2B2J6_STRRD	Osmosensitive K+ channel histidine kinase-like protein	Sros_0446	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	246	479432	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	>tr|D2B2J6|D2B2J6_STRRD Osmosensitive K+ channel histidine kinase-like protein OS=Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100) GN=Sros_0446 PE=4 SV=1MPRYLDRDRIAIVAAVVVPLVVSAILVPFRESFSNTNVALVLVVTVVAVAANGHRLAGALAAVSAAVWFDFFFTRPYQRFTITKSADVQTAVLLLVVGLAVSQLAARARRLHLVAITDAGYLARLHDTAELAQSTKSPDTVVDHVAAQLTDLLGLRGCRFEYGSLIGHPPRLEQDGTVIWDRRRWDVERLGLPDREVELRTFGNGHFYGRFMLDPTPGTIPSLQARLVAVTLADQVGAALDTAGNG		No DUF4118 detected by NCBI CDD
	0.0004	30	9.2	0.00067	29.2	6.4	1.4	1	V5XHB1_MYCNE	Histidine kinase	D174_21905	Mycobacterium neoaurum VKM Ac-1815D	593	700508	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	>tr|V5XHB1|V5XHB1_MYCNE Histidine kinase OS=Mycobacterium neoaurum VKM Ac-1815D GN=D174_21905 PE=4 SV=1MGILGRKRADLRIYLGAAPGVGKTYSMLGEAQRRMSRGTDVVAAVIETHGRRHTAQQLAGIEMVPPIVIEYQGARHAEIDVEAVLARRPQVVLVDELAHTNTPGSRNAHRWQDVEEFLDAGITVISTVNVQHLESLHDVVGHITGITEQQRIPDEIVRAADQIELVDITPEALRRRITHGNVFGRDRIDAALDDYFRPGNLSALRQLALLWLADQVDAALAKYRTDKNITDTWEARERVVVAVSGGPESETLVRRASRIASRSGAELKVLHIVQGDGLVAITPQQKKMLRELAASLGATMHTVVGEDVAATLLDFARSANATQLVIGTSRRSRWARMFDEGIGAQVIAQSGNVDVHMVTHPEAHTGISWSRSSLLHRRRFWSWLTAVAIPAIICAATTGLPEGALGIGGQSALFFTGVVAVALIGGIAPAALCAVLSGVLLTYFLVSPVHSFAVYDSDSVVTIAVLLVVAVAVAVVVDRAAHRAAEARRAAREAELLALFADAALRDADLDVLLDRLREAYGQRAVSIVSADGTVLAGVGHDPCTDVEAADTAIDVADHDHWLLLSGKTLTTRDRRVLSAVAEQAVSMIRRQSA	7~~KdpD (1.88289E-107)~~216;X;238~~Usp(4.19507E-35)~~359;X;382~~DUF4118 (0.000008087)~~462	KdpD protein
Disagreement between HMM and CDD prediction	0.0004	30	6.8	0.00073	29.1	4.7	1.4	1	A0A0F4JNS4_9ACTN	Histidine kinase	VR44_08850	Streptomyces katrae	848	68223	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces katrae	>tr|A0A0F4JNS4|A0A0F4JNS4_9ACTN Histidine kinase OS=Streptomyces katrae GN=VR44_08850 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVGFVEHHNRPRTEVMLHGLELIERRELDYRGSTFTEMDVDAILARRPAVVLVDELAHTNVPGSRNAKRWQDVEELLQAGIDVVSTVNIQHLESLGDVVETITGVRQRETVPDEVARRADQIELVDMSPQALRRRMAHGNVYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYRGEHNIRSTWQARERIVVGITGGPEGRTLIRRAARLAEKGAGGEVLAVYIAASDGLTSASPKELAVQRTLVEDLGGTFHHVIGDNVPDALLEFARGVNATQIVLGVSRRRSWQSVFSPGVSATVARESGPDLDVHIVTHDEAAKGRRGLPVARGARLSRSRIIWGWAAGIAGPAVLAVLLSQFVPELGLANDMLLFLTFTVAAALLGGLLPALASAAFGSLLLNYYFTPPLHEFTVSDPKNIVAIAIFVGVAVSVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGEDSLDALLERLRETFAMQSVVLLERTSEVEPWTTAASVGTGPISRPEDADVDLPIGDNMALALAGRVLPAEDRRVLGAFAAQAAVVLDRQRLVDEAEKSRRLAEANRIRTALLAAVSHDLRTPLAGIKASVTSLRSDDVEWSEEDKAELLEGIEDGADRLAALIGNLLDMSRLNTGTVVPLIRETDLDEVVPMALGGVPEDSVGLDIPETLPMVAVDRGLLERAVANIVENAVKYSPHGQPVNVSASALGNRVELRVVDRGPGVPDEAKNRIFEPFQRHGDAPRGAGVGLGLAVARGFTEAIGGTLAAEDTPGGGLTMVLTLPVAGDGPPVSPEMPTSAVT	1~~KdpD (5.46546E-124)~~211;X;233~~Usp(1.36508E-32)~~356;X(257);613~~HisKA (0.000000000000143033)~~679;X;728~~HATPase_c (1.19484E-25)~~829	KdpD protein
	0.0004	30	11.1	0.00077	29	7.7	1.5	1	I0H1T1_ACTM4	Histidine kinase (EC 2.7.13.3)	AMIS_17480	Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	832	512565	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes missouriensis, Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	>tr|I0H1T1|I0H1T1_ACTM4 Histidine kinase OS=Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431) GN=AMIS_17480 PE=4 SV=1MARGELRIYLGAAPGVGKTYTMLEEAHRRGERGTDVVIALVETHGRKHTTAMTAGLEVVPRREVTYRGAAFAEMDLDAVLARRPELAVVDELAHSNVPGSRHAKRWQDVRELLEAGISVLTTVNVQHLESLNDVVARITGVPQRETVPDAVVRAAEQVELVDMTPEALRRRMAHGNIYRPEKVDAALGNYFRTGNLTALRELALLWLADKVEQQLGQYRADHDIDSTWETRERVVVALTGGPEGDTLIRRAARIAARSKGADLLAVHVARSDGLAGANPAELARQRVLAESLGGTYHQVVGADVPRALLDFARGVNATQIVLGASSRGRFAQLFAAGVGVTTIARSGSIDVHLVTHELAGRGRRRRGPLPPALSRKRRIIGFGVALLGLPLLTVALEAGPPLPLIDDILLFLVAVVGVALIGGLWPALLAAVGGSLLLNWFFTAPVGRFTIAEGQNLLALAIFVLVAVAVSWVVDTAARTTRQAARASAEAQTLAAVAGGVLRGERPLTALLDRLRETFALDSVTLVEKGPGGTGTVVASVGDPVCVSPGAADGEVTADGDLMILLRGRTLEASDRRIVEAFAAQAAVALRQERLAAEAATAKPLAEADRLRTALLAAVSHDLRTPLASAKAAVASLRSSEVEFDDEDRAELLATADESLERLDRLVANLLDMSRLQAGALGVVPIEVGAEEVVPRALDDCGPEGRKVAVRVPEDLPLLRADPGLLERVLVNLVANALRHSPPDAPPMITGSTHGDMVELRVIDHGPGIPADRWDDVFLPFQRLGDRDNHTGVGLGLALSRGLTEAMGGTLTPGETPGGGLTMVLALPVARLC	1~~KdpD (4.21641E-120)~~211;X;233~~Usp(6.96153E-22)~~355;X;383~~DUF4118 (0.000000000214841)~~478;X(130);608~~HisKA (0.000000000000342697)~~674;X;725~~HATPase_c (3.95475E-22)~~826	KdpD protein
	0.0004	29.9	12.5	0.00069	29.2	8.7	1.3	1	A8EUC4_ARCB4	Histidine kinase (EC 2.7.13.3)	kdpD Abu_1291	Arcobacter butzleri (strain RM4018)	342	367737	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Arcobacter, Arcobacter butzleri, Arcobacter butzleri (strain RM4018)	>tr|A8EUC4|A8EUC4_ARCB4 Histidine kinase OS=Arcobacter butzleri (strain RM4018) GN=kdpD PE=4 SV=1MKKIFIKYKEYSYIFKALAILTFITIICHIFREHLGIINIALIHIIPVIVVAIHGNIKATFFMTFLSVLFLNFLYIPPLYSFNVNNELYLWSFLIFGVVGLIITIQAKNLITQKKQNELKESLLHIISHDLRTPLSTIHGTINLILSNDKLDSKSLYPLLEDINYASISMKRLITNLLDSTRLSNKNFDLKQEWCDFEDIIGVALNEFSQKQNDEKLNIKIDELALFWGDNILLTQLIVNLLDNAFKYSKSDSKIDLEVENLNNFIRIKVFNETEYIDKKKLKNIFDKFYRLEDTNDISGSGIGLAICKSIVKLHNGEIKAVSKDNGILIEIELPIVKRVNL	14~~DUF4118 (0.00020634)~~103;X;117~~HisKA (0.00000000213852)~~182;X;234~~HATPase_c (2.04642E-20)~~334	non-KdpD DUF4118 protein

	0.0004	29.9	10.2	0.00074	29.1	7.1	1.4	1	Q21XK6_RHOFT	Multi-sensor hybrid histidine kinase (EC 2.7.3.-)	Rfer_1768	Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) (Albidiferax ferrireducens)	1033	338969	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Rhodoferax, Rhodoferax ferrireducens, Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) (Albidiferax ferrireducens)	>tr|Q21XK6|Q21XK6_RHOFT Multi-sensor hybrid histidine kinase OS=Rhodoferax ferrireducens (strain ATCC BAA-621 / DSM 15236 / T118) GN=Rfer_1768 PE=4 SV=1MNTSGKIQGNDDGKASDRSVSLLPNQELRHKHPAWNRLLNLLDRFYAKLAHSEHKGLYRYLLTLVLSVVALFARMVIAPEDAGLQFITFFPAVAISAVLFGTGPGLFTTFIGATMGTYFFFPPYEAFVFEFQHHTLISVVIFCADGLIVSLSIGAMRRYFSNYVITVAKLETALEQSRHNEAELTYQKYALDQHAIVAATDVRGTITYVNDLFCAISQYSRDELLGHNHRLLNSGAHPKEFFEAMYRTISSGEVWKGDICNRAKDGSLYWVSTTIVPYVNDSGKPIRYVAIRADITERKRAKEAAQAATLAKSQFLANMSHEIRTPMNAVLGLTRMVLESDLKPEQREQLIKVSKSGRALVRIINDILDFSRIEAGRLAIERIPLRVEAVLLEVADLFSAQAEEKGLELFLDIEPETPLQVIGDPLRLTQVLNNLVGNAIKFTDHGEIHIGVRVAHYGDATLTLCINVRDTGIGMAPEQIGVLFQSFTQADSSTTRNYGGSGLGLTIAKKLVELMGGQITLDSAVGQGTNVSFSVAVGMAPDDFRRVTHMGQDLQQMHGKRVLVVDDQATSRQILSRLLQAWGMEATEAESGPQALARVAEANRAGRPFHAVLLDWRMPGMSGLEVATALKAQDEAKGLPTPLQVLMVTAYDKQSLLQEPEAANIDGVLTKPVVPSYLFDALLQGEPRHPDASDELVAQRFDGVRVLLVEDNDLNQEVASSFLRKRGVSVTVAWHGGEAVELIQHQQFDLVLMDLHMPVMGGIEAARRIRELPQGKNLPIVAMTAAVMEEDRARCRAAGMNGFVAKPVEPEDLARVLVMYTRPGTQTPPATTPTIQAGEPVLDLVKGLRRLDGDRALQQRLLLGFVERHHDIVGRLDALLAEKNTTEAVDLIHTLKGVAANLGAVALAEASRRLIEELRSATPLASRFAFHTTLVETLTQMQQHIAGHVQTDLAEAAAVEPVSLEHTLLALEPFIVGQEVIPDALLVALQRISTADLPYSPLARQLRHHLDNFEHGEVLEAFKLLRVEQAVQG	59~~DUF4118 (0.0000000593175)~~157;X;194~~PAS (0.000000000000208013)~~295;X;311~~HisKA (7.50762E-14)~~372;X;428~~HATPase_c (6.80064E-31)~~535;X;563~~REC (3.68388E-22)~~682;X;707~~REC (1.06473E-30)~~817;X;841~~HPT (0.00000000731137)~~954	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0004	29.9	9.5	0.00075	29.1	6.6	1.4	1	Q2FWH7_STAA8	Histidine kinase (EC 2.7.13.3)	SAOUHSC_02314	Staphylococcus aureus (strain NCTC 8325)	885	93061	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Staphylococcaceae, Staphylococcus, Staphylococcus aureus, Staphylococcus aureus subsp. aureus, Staphylococcus aureus (strain NCTC 8325)	>tr|Q2FWH7|Q2FWH7_STAA8 Histidine kinase OS=Staphylococcus aureus (strain NCTC 8325) GN=SAOUHSC_02314 PE=4 SV=1MSNTESLNIGKKRGSLTIYIGYSPGVGKTFEMLSNAIELFQSNVDIKIGYIEPHQRDETNALAEQLPKITTNFTKHGSHHFQYLDVDRIIEESPTIVLIDELAHTNISRDRHEKRYMDIEEILNHGIDVHTTLNIQHIESLSSSQIELMTGVHVKERVPDYFIMSADVLEVVDISPEQLIKRLKAGKVYKKDRLDVAFSNFFTYAHLSELRTLTLRTVADLMSDKEKVRHNHKTSLKPHIAVAISGSIYNEAVIKEAFHIAQKEHAKFTAIYIDVFEKNRQYKDSQKQVHQHLMLAKSLGAKVKVVYSQTVALGLDEWCKNQDVTKLIIGQHIRNKWRDFFNTPLIDHLMSFEHSYKIEIVPIKQIPVELKMNKSPYRPKGKRFAIDMLKMILIQIICVMMGLWIYQLDKHESSTIILMIFLIGIILLSIWTRSFIIGFLAAIINVFVFNYFFTEPRYTFEVYRFDYPITFIVSILTSILTSALLKQIKFQYSITKKQLYRTDLLFQFNDSIKQTYTVENLLINAGYQINQLLQQSITIYVINQSKVIKTIPLQNHIDNTTQQHEQALSWVIKNERQAGATTDTFPGINKWLIPIGTSPIKGILAIDYQSSQVINPYDASILESMLNELSLAVENVTLLKQTRESMLQAERQLTHSNFLRSISHDIRTPLTTIMGNLDILVSHSKDMSIIEKEQLLVHSFQESQYLYLLVTNILSLTKLQSSNVQIKLQPYLVSELVEEIDMILERRHLKKRITVSSSVNLQFIHIDSKLILQALFNLIENAVKHTSTDTKINLSIRYASYEQIEFAVIDEGPGISLEEQQKIFEPFYTGSNKYFKDNQKESMGLGLYLVQTILHKHQSNLQYKPNQPHGSIFYFNIYTDFNEGDV	11~~KdpD (6.57295E117)~~221;X;238~~Usp(9.03504E-37)~~361;X(294);655~~HisKA (0.000000102517)~~717;X;770~~HATPase_c (6.12635E-20)~~876	KdpD protein
	0.0004	29.9	10.1	0.00084	28.9	7	1.4	1	K9U4Q9_9CYAN	Multi-sensor hybrid histidine kinase	Chro_4222	Chroococcidiopsis thermalis PCC 7203	1198	251229	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Chroococcidiopsis, Chroococcidiopsis thermalis, Chroococcidiopsis thermalis PCC 7203	>tr|K9U4Q9|K9U4Q9_9CYAN Multi-sensor hybrid histidine kinase OS=Chroococcidiopsis thermalis PCC 7203 GN=Chro_4222 PE=4 SV=1MPKVTRSQIASYGVAILAVMLALALMLGLDSWLGMTKTPFLLFYGAVAIAAWYGGLKPGIVATVLSILFSNYFFHYPTYTFIVDLPDLLRLGLFALQGVMISYLCEELRIAKHRAEIDRQREQKAKDRAEAMQQRLAFLDLANTVLTSSLDYETTLRSVVELTIPKFADLCTVDILPADMAINPLAAVQAKDPNRADLVRQLTATYPLDLNDQTHPITRVFHTGRSELIPEVTDANYVAMARDAEQLKFFRQLGIKSAICVPLIAGREVFGVLSLMLTTSQRHYCNEDLTLAEELGRRVGLAMENSRLHRQLKQAMQRQEATLALIDTWLASSPVGLAFLDTDLRYVHVNQALADINGIPLKDHFHRSVREVLPAWGDTLEPVLRQVMQTGEPLLNQELSGETNSPGVYYRHSLVNFYPVCLANGQTLGVGATVVDITQLKQTQTSLSQREAELSLITNTVPALIAYVDLNQRYRFVNRTYEQWFGHPATEICGRHIRQVLGEAAYEKIRPYVEQALAGRAVRYESQVPYQDGGVRYIEAVYIPQFDSRGQVEGFVSLVSDMTDRKRAELERDRLLQQEQAARQLAELNIQRVYQLQNLTAALAQALTTEQVREILLHQGLAAFNATRGWIGLLHKNGKTVEIVCSIGYQEAEIAPYRRVPLTTPLPLTDTIRTGEMVIARSPAEYQQLYPSLADTYIASGSQAIASLPLTIEGRTIGSLGLSFNQPRDFDVAERAFMMTLARQCAQALERSRLYAAEQVAREVAESANRIKDEFLAVLSHELRSPLNPILGWAKLLRSRQYNEAARNRALETIERNAKLQAQLVDDLLDVSRILRGKLALKFAPVNLVSTILAAMETVQLSAEAKQIHLVFEGAGTSWEQGRAGKDKGDKGDKGDKEAAITIQNPKSKIQNFPTPLVLGDSGRLQQVVWNLISNAVKFTPAGGRVEISLQLPNPDSHSPTPDSQKSVQIQVSDTGKGISPDFLPYVFDYFRQADSSTTRTFGGLGLGLAIVRHLVELHGGTVGVESLGEGQGATFTVTLPVLEGSRESGVGNREMHHSPSNSQQLPLQGVRVLAVDDDPDMREYVTCVLQQHGAEATVVSSAEDALVALSQQMPDIILSDIGMPLIDGYMFLEKVKNIMQSRSLSIPAIALTAYAGEYDQQKAITAGFQLHLPKPIDPDELVKAIAEMVSTTRSGDRS	8~~DUF4118 (0.000000358741)~~104;X;134~~GAF (0.000000001818960)~~315;X(146);461~~PAS (0.00000000889541)~~561;X;605~~GAF (0.000000000063283 1)~~749;X;768~~HisKA (1.54677E-14)~~832;X;924~~HATPase_c (5.19029E-32)~~1039;X;1073~~REC (1.18133E-24)~~1188	non-KdpD DUF4118 protein
	0.0004	29.9	10.4	0.0008	29	7.2	1.4	1	U5VZI3_9ACTN	Histidine kinase (EC 2.7.13.3)	AFR_13825	Actinoplanes friuliensis DSM 7358	824	1246995	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	>tr|U5VZI3|U5VZI3_9ACTN Histidine kinase OS=Actinoplanes friuliensis DSM 7358 GN=AFR_13825 PE=4 SV=1MARGELRIFLGAAPGVGKTYTMLEEAHRRVERGTDVVVAFVETHGRKHTQAMLADLETVPRCTVEYRGAEFTEMNLDAVLARRPEIAVVDELAHTNVPGSRNAKRWQDVQELLDAGIDVLTTVNVQHLESLNDVVARITGVEQRETVPDAVVRAAEQVELVDMTPEALRRRMAHGNIYRPEKIDAALGNYFRTGNLTALRELALLWLADKVEDQLGKYRADNNIDTTWETRERVVVALTGGAEGDTLIRRAARIAARDKGADLMAVHVTRNDGLTGADPAALSRQRVLVESLGGTYHQVVGADVPRALLDFARAVNATQIVLGVSSRGKLAQLFAAGVGVTTTAMSGSIDVHLVTHERAAQGRRAQRLPAALSRRRRVAGFAATIAGLPALTALLHVGPSLSLTNDILVFLVAVVGVSLIGGLWPALLAAIAGSLLLNYFFTSPIGRFTIAEVDNLLALAIFVVVALAVSWVVDTAARKTRQAAEAGADAQTLATVAGSVLRGDRPLIALLDRLRETFALQSVTLLEDGAVVANVGDTACTVAGEADAEVKVNDHLKMLLRGRPLEASARRIVEAFAAQAAVALRQERLSAEAASARPLAEADRMRTALLAAVSHDLRTPLASAKAAVAGLRSADVDFDDNDRGELLATADESLDRLDRLVANLLDMSRLQAGALGVIPIDVGVEDIVPRALDDLGPDGRTVAVHIPDDVPLVHADPGLLERIVVNLVANALRYSPAGQPPVVVTASALGDIVEVRVIDHGPGIPEDRWNDVFLPFQRLGDRDNHTGVGLGLALSRGLTEAMGGTLTPEETPAGGLTMILALPAS	1~~KdpD (4.09767E-121)~~211;X;233~~Usp(2.19735E-19)~~355;X;382~~DUF4118 (0.000000000057686 4)~~479;X(124);603~~HisKA (0.000000000037496 5)~~669;X;720~~HATPase_c (7.00154E-23)~~821	KdpD protein

	0.0004	29.8	12.8	0.00075	29.1	8.9	1.4	1	I5AVL8_EUBCE	Histidine kinase (EC 2.7.13.3)	EubceDRAFT1_2080	[Eubacterium] cellulosolvens 6	655	633697	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, Eubacterium cellulosolvens, [Eubacterium] cellulosolvens 6	>tr|I5AVL8|I5AVL8_EUBCE Histidine kinase OS=[Eubacterium] cellulosolvens 6 GN=EubceDRAFT1_2080 PE=4 SV=1MPEQRLKEEHVLVCLSSSPSNKRLIEKAAVLAKAFQGYFTALYIETPEDARMSEEDRQRLENNEKLAKKLGAKLEIIPGENVAYQIAEYTRVSGVTKLVIGRSVQEGRKGRGDRHFIDTLLMFVPDVDVYIIPDKRPRPAHEIPVRFPLKIKSGWPDFFFAILMLALCSVIACLVHMAGGAESSIVAFYILTVCLISVRTASWIYSLFAAGASVVIFNFLFTAPYYTLLAYDNRYTASFAVMFGIALLCGLLGAKQKLLARNASRMAFRIQVLYDMNQQLEKSGTSEEIIDLTAGQLCRLLQKNIVVYAAENGVLGEARVFASGRENAIDFVPADEREAAEKAFASMRKTGRGTGVMPDVHCIYYAVRLHEIGYGVIGIDVADRKLDPYADSIVVSILSEAAIALENKRNEEEKERARVMAKNEQLRADLLRRSISHDLRTPLTSISGAASLLLSDEAKIDEAARRQLHTNIYDDAMWLEDLVENLLAITRLGESQGMKIHASTELVSEVIAEACRHVDRRISEHTLSVGQSSDLLLAKMDLAHLIVQVIINLINNAVRYTPAGSHIRVYADREGGRIRIFVCDDGPGVAEEDREHIFEMFYSGKKKVADSRRRSLGLGLALCKAVIQAHGGEISYTDNQPSGSVFLFTLEAEEVPSNE	10~~Usp(4.79337E-32)~~133;X;158~~DUF4118 (0.000000000613499)~~257;X(167);424~~HisKA (0.000000000000581 74)~~490;X;543~~HATPase_c (2.86165E-28)~~646	non-KdpD DUF4118 protein
	0.0004	29.8	9.9	0.00068	29.2	6.8	1.3	1	D5V3L2_ARCNC	Histidine kinase (EC 2.7.13.3)	Arnit_0053	Arcobacter nitrofigilis (strain ATCC 33309 / DSM 7299 / LMG 7604 / NCTC 12251 / CI) (Campylobacter nitrofigilis)	343	572480	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Arcobacter, Arcobacter nitrofigilis, Arcobacter nitrofigilis (strain ATCC 33309 / DSM 7299 / LMG 7604 / NCTC 12251 / CI) (Campylobacter nitrofigilis)	>tr|D5V3L2|D5V3L2_ARCNC Histidine kinase OS=Arcobacter nitrofigilis (strain ATCC 33309 / DSM 7299 / LMG 7604 / NCTC 12251 / CI) GN=Arnit_0053 PE=4 SV=1MKNLLFPYRQYNYILKALVILLIITIISHMFRNSLDIINITLIHIIPVIVVAIHGKGKTTFFMTILCVVLLNFLYIPPIYSFSVHNELYIWSFLIFGIVGWIITYQAKSLNTQMKQNELRESLLHIISHDLRTPLSTIHGSINLILSNNELNETNKNSLLEDINYASIRMERLITNILDSTRLSSGNINLKLQWCDFEDIVGVALDEFSQKQSDEKVIVNIEETGLFWGDNTLLTQLVVNLLDNAFKYSTTNAKIDFEVLDYNNYIKIQVFNETEFIDEEKLKNIFDKFYRVEDTNDISGSGIGLAICKSIVKLHNGEIKAISQNNGILIEINLPVLKRAKLI	117~~HisKA (0.000000000012996 4)~~182;X;234~~HATPase_c (3.32653E-20)~~327	No DUF4118 detected by NCBI CDD
	0.0005	29.8	15.9	0.0023	27.5	7.1	2.5	2	R4KFM2_CLOPA	Diguanylate cyclase (GGDEF) domain-containing protein	Clopa_3623	Clostridium pasteurianum BC1	562	86416	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium pasteurianum, Clostridium pasteurianum BC1	>tr|R4KFM2|R4KFM2_CLOPA Diguanylate cyclase (GGDEF) domain-containing protein OS=Clostridium pasteurianum BC1 GN=Clopa_3623 PE=4 SV=1MNKIDNKRKQINDIVSVVKLTSLLFSGMGFYNFIFNKYKINISNFNYTLTIDVILFGVLVLTLVYSIWAFSTTKKFNEKYVARIQIIENYSFVLIFFVIVFLTGAHKSEFKFLFLFIIITTTIQSGIKQGVIIACISSIIVLIVDLVYGPYSGENIYFEKDLIMAGVFILTAWPLGFYVKTESDHIKKLESLANEDGLTEVYNHRYFHEALREKVTSYEKDNKPISLIFIDIDHFKNYNDLYGHQKGDEVLKIIGLLLKNNVRDGDVAARYGGEEFAIILPDTSEEDGIKIAENIRCKIEETHFDGEENQPKGKLTASIGISTFPDKAKSDVELIKSADDALYRAKFFNKNRVETYHSILDELKEDIEDRHIDLVTSIKTLISVINAKDRYTYGHVERVVISYSRLLADKLKLSEEDKKKLIYGAYMHDIGKINISKEILIKKMPLTKEQWEILKQHPENGVEIIKPVESLKNISPLILHHHERYDGKGYPGNLKGENIPYLARALTVVDSFDAMTSNRPYSKVKTYDEAMGELKKCSGTQFDPSIANAFIEVIKENKDNINY	85~~DUF4118 (0.000000000535836)~~179;X;196~~Nucleotidyl_cyc_III (6.5577E-62)~~353;X;390~~HDc (1.66465E-22)~~533	non-KdpD DUF4118 protein
	0.0005	29.8	11.1	0.0007	29.2	7.7	1.3	1	R5UHM0_9FIRM	Histidine kinase (EC 2.7.13.3)	BN481_01137	Ruminococcus gnavus CAG:126	356	1263106	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	>tr|R5UHM0|R5UHM0_9FIRM Histidine kinase OS=Ruminococcus gnavus CAG:126 GN=BN481_01137 PE=4 SV=1MKTFFKNLTFTFLCLGISTILAFFFFNLGQKNSVNTALIYILALILIAQNTTSYWYGAVASVFCVIAANYFFTYPYFKLNFILDGYPVTFIGMLAISLITSATASMLKKQKAIASERERKLAEAEREKIHANLLRAVSHDLRTPLTSIIGSSASYLDDAQNMSEQERMELISNINEDAQWLLNMVENLLSVTKIQNESSKVKKSQEIVEEVVSESIVRLQKRLPKIQIRVSMPEDFLMIPMDATLIEQVLINLMENAYVHSSSSDPIDLLITDQPDCVTFAVRDYGIGLDPDQIPFIFDGQYSSDTADGHKGIGIGLSICRTIIHAHDGVIHAANLDKGAEFSFTLPKEKENANYA	54~~DUF4118 (0.0000181387)~~110;X;133~~HisKA (0.000000000186241)~~193;X;246~~HATPase_c (1.80201E-22)~~346	non-KdpD DUF4118 protein
	0.0005	29.7	8.5	0.00048	29.7	5.9	2.5	1	Q8XK43_CLOPE	Uncharacterized protein	CPE1560	Clostridium perfringens (strain 13 / Type A)	563	195102	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium perfringens, Clostridium perfringens (strain 13 / Type A)	>tr|Q8XK43|Q8XK43_CLOPE Uncharacterized protein OS=Clostridium perfringens (strain 13 / Type A) GN=CPE1560 PE=4 SV=1MIRDVNDNKKKKVDEILSIVKVSSLLFSAMAFLQYTFNLTKYNNKFLAYYSILSILISIFLLSTIYILWSLASLNKYKDHINKIQLIEIILFMIIFIMAILVSGGNSSNNKFLFLFIIITSTIQGGMHRGCVVSVVSSAIILVIDLIYSGNADVNIYFQNDLILAGVFVLTAWTLGFYVKTENDHIKELQTLVNEDGLTGVYNHRYFYDKLREKMHISEVENEKLSLIFMDIDYFKHYNDLYGHQKGDEALKKIGKLLKNIARENDLVARYGGEEFAIILPNTSEEEATKIAERIRNKVEKTYFEGQENQPNANFTVSVGIAVFPDKAKSELELVKCADDALYRAKFFHKNRVETYVSVLDELKRDLNEEENTLVTSIKTLISIINAKDKYTYSHVERVVIYSRLMAKKLGLSEDEKKQLIYGAYMHDIGKINIPNEILTKKMRLTKEEWEILKQHPKDGVEIIKSVNSLKNVVPLILYHHERYDGFGYPVGLKEKEIPYLARVLTVIDSFDAMTSSRPYNKRKTYDEGLIELERCSGTQFDPEIVCIFSEVVKENINEIQDF	103~~DUF4118 (0.0000000439994)~~185;X;196~~Nucleotidyl_cyc_III (7.30175E-63)~~353;X;391~~HDc (1.31671E-24)~~528	non-KdpD DUF4118 protein
	0.0005	29.7	14.5	0.00089	28.8	10.1	1.4	1	K9WTP0_9NOST	PAS domain S-box	Cylst_1471	Cylindrospermum stagnale PCC 7417	1168	56107	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Cylindrospermum, Cylindrospermum stagnale, Cylindrospermum stagnale PCC 7417	>tr|K9WTP0|K9WTP0_9NOST PAS domain S-box OS=Cylindrospermum stagnale PCC 7417 GN=Cylst_1471 PE=4 SV=1MGTVPSASCTKGEATLKGIRSRLKFYAVAVLAVCIALLLTLLLQPLLNPTIFILFFAAVAVSAWYGGMEAGLLATALSTLAVSYFFLKPVFPLSVHALDSMIRLGLFLVLVTILISSLNSQLRTAKKRLELSMQQLQASEARFRRLTESNIIGVITADINGGIVEANDAFLKMVGYTREDLLAGRVRWRDIVSPEDLEMCALRSASLKENRSVTELDSRGVCQPFEKEYIRKDGSRIPLLTGSALLENNPEQVIGFVLDLSIRQQAQNALRESQSRFSALADATIEGVIIHENGKVLDANRAFAKMFGYEIDEVIGMSAADFLTPEGQKIFRENICNGDEKLYEMTGVKKDGTTFPLEIVGKSCIYQGRTVRVSASRDITERKQAEQALQDSQKRFSRLVESNIFGVAVSDFEGGIEYANDYFLNMVGYSREEMLAGEVRWDVMTPPEYIDLDQKAIAELLKHGVANPFEKEYIRKDGSRVPILIGIVLLQEPYNRQQEQIAFCLDLSQRKRAEKTLHQREEELSLITNAVPVLISYIDTQHCYRFNNKGYEELFGIPASETYGKHIREVLGESGYQFVRPYIEAVMSGEQVSFENQVIDKHGRYRDVSTTYIPQFSQHGQVEGFVALVRDITEQKQAEAALKQSEERFRKLTEKVHVIPWEANPTTGQFTYVGPQTVEILGYPSTDWYTDNFWVEHIHPEDREWTTKYCVERSLSLNNYEFEYRMLAADGRIVWLYEIVNVVRGEEDQPQLLHGFMIDISDRKQAEQEREQLLAREQMARTEAEALNCIKDEFLGTLSHELRTPLNAMLGWTQLLKSRKFDETTTAKALETIDRNSRSLAQLIDDVLDVSRIIRGELRLNLHRVELIPVVESAIDTIRPAADAKEIWIECRFDSALGAVIGDANRLQQVMWNLLTNAVKFTPKGGRVEVQLERMDSGVVQIRVSDNGGGITAEFLPHVFERFRQADSSTTRSHGGLGLGLAIVRHLVELHGGTVSVESPGIGKGTTFVVKLPMKAAPIEESSTPKQIAPTASAEVTKNSLPILEGVRVLVVDDEADTRHLLKTILGQYGAQVMAVASTFDALKALQQFHPNILVSDIGMPEEDGYALIRQLRALGQEQGGRIPAVALTAYATAEDRTQALLAGFQLHIPKPVNPAELAAVVANLAGRT	54~~DUF4118 (0.000000248863)~~122;X;152~~PAS (0.000000000026796)~~257;X;283~~PAS (0.000000602499)~~354;X;405~~PAS (0.000000000039320 4)~~506;X;531~~PAS (0.000000380082)~~631;X;667~~PAS (0.0000000271502)~~759;X;790~~HisKA (1.72867E-15)~~851;X;906~~HATPase_c (7.90941E-35)~~1011;X;1049~~REC (4.9276E-28)~~1165	non-KdpD DUF4118 protein

	0.0005	29.7	9.8	0.00091	28.8	6.8	1.4	1	A0A0D5AEG1_9NOCA	Histidine kinase (EC 2.7.13.3)	NY08_3522	Rhodococcus sp. B7740	817	1564114	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. B7740	>tr|A0A0D5AEG1|A0A0D5AEG1_9NOCA Histidine kinase OS=Rhodococcus sp. B7740 GN=NY08_3522 PE=4 SV=1MADRGELRIYLGAAPGVGKTFAMLGEAHRLRSRGCDVVAAVVETHGRARTIDALDGIEVLPMATVHYRGSSAQELDLDAVLARQPQVVLVDELAHTNTPGSVHGKRWQDVEVLLDAGIDVISTLNVQHLESLNDVVQQITGVPQRETVPDSVVRAADEVELVDITPEALRSRLRHGNVYAAEKVDAALSNYFRGGNLTALRELALLWIADQVDAALVKYRKDNRITDTWEARERVVVAVTGGPESETLLRRASRIASKSSAELMVLHIVRGDGLMGVSAPQMGSVRKLAAGLGASVHSVVGDDVPSTLLDFARGVNATQLVIGTSRRSRAARILDEGIGAAVVQNSGKIDVHMVTHAEQARRWGVQVDSGRRRILAWVAAVLVPCLAAAVLSTVGPDFDSSGESALFFMVVLCVALLGGVAPAALSALIAGFLLNYFFTTPRYSLTIAEPDNFVVTVVLLLVAVAVAALVDAAARRTRQARRATQEAELLTLFAGSVLRGADLTALLERARETYRQSGVALWDNQSGSIVGSAGAQAPVDRAGADTEVDAGDFTLLLVGERTHAHDRRVLAAVANQAAGMVRQGRLAEEASRANALAEADALRRALLSAVSHDLRTPLSAVKAASSSLRSTDVQFSPEDTDELLATIDESADQLTALVSNLLDSSRLQAGVVQPSLRPVFVDDVLGGALVGADDRVRVEVGDVEVLADPGLLERVLANLVNNSARYAPVGDITVSAAAHGEWASISVADHGPGIAEGAEDTMFDAFQRLGDRDNSVGVGLGLSVVRGFVRAMGGTVTASNTVGGGLTMTVELKAASR	4~~KdpD (1.1251E-117)~~212;X;234~~Usp(4.31873E-30)~~355;X;376~~DUF4118 (0.000082621)~~453;X(147);600~~HisKA (0.000000000000196 57)~~666;X;712~~HATPase_c (4.5382E-26)~~812	KdpD protein
	0.0005	29.6	11.9	0.0009	28.8	8.3	1.4	1	K9XDS4_9CHRO	Multi-sensor hybrid histidine kinase	Glo7428_2091	Gloeocapsa sp. PCC 7428	1786	1173026	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	>tr|K9XDS4|K9XDS4_9CHRO Multi-sensor hybrid histidine kinase OS=Gloeocapsa sp. PCC 7428 GN=Glo7428_2091 PE=4 SV=1MAQPKAVENQHLNAGMHRRSSLKQQLWNYAVAIALVLMALLLMLVLDPYIQVKNTTFLIFHTALVLAAWYGGRNTGILATVLSAFLATYFFGDPIFSLNVTFASGARILIFVLQGILISVLVGALRTAQQQSKQSLKLQEAVFCEQQAVLRELQQTEVALRDSEARFQGLVSNLPGMVYRYAPCADGTEVFTYVSSGSHELTELSPETILQDAGAFLALIHPDDLPSFRESVAIAVENAIWQWEGRIITRSGQLKWIQGRSRPQQTEDGEVWDGLLVDITDRKQAEEALRRSEERQAFLLKLNDTLRPLMDVEEIQYQAACVLGEYLGASRVGYAEDQADGDTIVVTQNYTNGVPGIEGRYRYDDYGAELLREFQAGRTVVRSNIANDPMLTDAEKAAHAVLQLGATVNVPLLKAGRLVAVLFAHYPVAHSWTEAEVSLIQEVVDRIWAAVERARAEAALRQSEERYRTLFESMDEGFCTIEMIFDADDRPIDYRFLITNPAFDRQTGTENAQGRTVREIAPNHEAYWFEIYGNIALTGEARRFENRAEEFHRWYDVHAFRVGEPDLRRVGILFNDITERKQSEAILQESETRFRTLADNMAQFAWMADETGWIFWYNQRWFDYTGTTLEEMQGWGWQQVHHPEHVDRVVERIRHCFETGEVWEDTFPLRGHDGQFRWFLSRAMPIHNDRGEVVRWFGTNTDITDRLEIEAALRDRENMLGGIVGSITDALMMFDNDWRYTFVNEEFLHRIGMSLTDVLGQNVWELFPDAVGNTAYTQLHRAMAERIPVEYEVFYEPYHRWYSDKAYPTPDGGLTVYSQDITDRKQAEIELQISQERLQLALSSAKLGMWFWDIEPDTLIWTERCKALFGLPLDDSAIAYADFMAVLHPDDRERTHEAVVRAIEERADYDIEYRAVWQDGSVHWIASKGSCVFDAAGKAVRMNGVVIDIDDRKQAEENLRDREAQLASEASALVRLNEASSRLWRKLSLSEGLQEMLVATIELLGADMGNIQLLDADQGILRIAVQQGFKQDFLDFFREVSAEDDSACGRTLRSGERTIIEDVETDAPFAPFRPVARAAGYRAVQSTPLMGRDGILLGMLSTHWRSPHRPSEQDLRRLDLYVRQAADFIESIRAETALRESEELLSSTFSGVEGAITVSEVLADDEFRFLSANRVCVEWSGVPLEKWIGSRSQDILSPQEAEAVCERYRSAVRTGQVVKYEERLTLPAGEIWTYTAVTPLRDPDGRITRVVATSIDITERKQAEAALRESEENLQAALEGGQMGAWAWNPMTNTTTRDRRVLELFGLDSEATMGDTTPIFDRIHPDDRSSVIAALEAAQQPGGEYRAEFRVLLPDGKTRWLAGAGRARFNAQGRATRVYGVNFDITERQQAAQEREQLLEREQTAREQAEAANRIKDEFLAVLSHELRSPLNPILGWSKLLQKGNLNPAKTKTALATIERNAQLQAQLIDDLLDIARILRGKLSLNEAAVDLGVVISSALETVRLAAEAKALHVKVNLPTQVRTAMGDAGRLQQVVWNLLSNAVKFTPQGGQITVALTQSESYAQIQVTDTGKGIHPDFLPYVFEHFRQEDGATTRKFGGLGLGLAIARQIVELHGGTIAVESAGEGQGATFTVQLPLAPLTDQQPPSESASIEIEDLSGIRIWVVDDEIDSREFVAFVLEQAGANVASFSSGIEVLQAIEQTIPDLIVSDIGMPEMDGYMLLQQIIRSSDQGRHIPAIALTAYAGEFDRQQALQAGFQQHIAKPVEPAQIVTSVARLCDQKGGTAA	47~~DUF4118 (0.00000580814)~~131;X;191~~PAS (0.000504933)~~281;X;311~~GAF (0.0000000263343)~~448;X(153);601~~PAS (1.05476E-15)~~703;X;727~~PAS (0.0000597765)~~838;X;848~~PAS (0.000000566018)~~949;X;987~~GAF (0.000000000023273 7)~~1130;X;1161~~PAS (0.000000231334)~~1257;X;1298~~PAS (0.000000215162)~~1385;X;1413~~HisKA (5.24674E-14)~~1477;X;1532~~HATPase_c (8.30181E-33)~~1636;X;1665~~REC (3.85489E-28)~~1777	non-KdpD DUF4118 protein
	0.0005	29.6	6.9	0.00065	29.3	4.8	1.2	1	G4RAP2_PELHB	Uncharacterized protein	KKY_2557	Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	174	1082931	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Pelagibacterium, Pelagibacterium halotolerans, Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2)	>tr|G4RAP2|G4RAP2_PELHB Uncharacterized protein OS=Pelagibacterium halotolerans (strain JCM 15775 / CGMCC 1.7692 / B2) GN=KKY_2557 PE=4 SV=1MNVHAPKRVVPRILLGERAPGSSNQWVGVVEGAVLIGGVFAIERLGLFDLGVLPIHPLVLAVALMAAQYGALGGIMTAVMATALALLGGMLPQRVVGEGYFEYLAAVWTTPLAWLIIAVLVGVVSDGHRRLLQRSELALFEAQKERELIAAQYEALAARAKRLERRVAGLENNS	30~~DUF4118 (0.00000179589)~~130	non-KdpD DUF4118 protein
	0.0005	29.6	10.7	0.00091	28.8	7.4	1.4	1	A0A0F0KN13_9MICO	Sensor protein KdpD (EC 2.7.13.3)	kdpD RL72_02373	Microbacterium azadirachtae	923	582680	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium azadirachtae	>tr|A0A0F0KN13|A0A0F0KN13_9MICO Sensor protein KdpD OS=Microbacterium azadirachtae GN=kdpD PE=4 SV=1MSVSEGVSAMAERRREGGSARGRLRVLLGAAPGVGKTYEMLGEGRRLDELGRDVVIGVVETHGRAATLAQTQGIEQVPRRIVSHRGVQLDELDLDAVLARRPELALIDEMAHTNAPGSRNAKRWQDVQELLDAGIDVITTVNVQHIESLNAVVEKITGVVQQETVPDEVIRDADEVEVVDLAPQTLRDRLSAGQVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALRSYRSQHGIDSAWQTRERVVVALTGGPEGETLLRRGARIAARSAGGELLAVHVTTQDGLRGDRPGALTQQRGLVESLGGSYHQLVGDDVAGTLVEFAQSVDASQLVIGVSRRSRLSAALTGPGIGAEIIRRSGDIDVHIVTHSAAGRRGPLPTIRGGALGWRRQLIGFAVALIGGPLLSWLLFSLKAPGSITSDVLSYQLLVVVVALIGGLRPALFAAVLSGFTLDFLFVEPLFTVTIADPLHALALVLYVVIAVLVSIVVDQAARRARAAQRASGEAELLAAVAGNVLRGDSAPTALVARAREAFGLSGIRLLSPDGDVLAVDGEPLGGNVPGGDPEHAAHDAHGPEARTTTATAGASATADGAQPPRPPRVETVPVGTAADGRPRAILELHGGDLDAAGRRLLDAIVAQLAAAIEHTDLRETAKEAAVLAETDQVRSALLSALSHDLRRPLAAAVAAVGGLRGAHRLSAEDRAELVETADESLATLSRLVTDLLDVSRVQAGVLAVSLGRVDAGGGVVSALDELSLGPDEVELALDPALPPLRADPVLLQRVLVNLLTNAVRHSPAGDRVIVSTSRLGERAEIRVADRGEGIPEDQRESAFLPFQRHGDTDNTTGLGLGLALSRGFAEGMGGTLTAEDTPGGGLTMVVSLPLDDAGLDVSTRPDPGAEYDTLRTSHREPRSDDEGGTR	19~~KdpD (4.96191E-115)~~229;X;251~~Usp(5.3398E-30)~~374;X;397~~DUF4118 (0.000000000006115 87)~~495;X(173);668~~HisKA (0.000266113)~~733;X;784~~HATPase_c (5.54073E-28)~~885	KdpD protein

	0.0005	29.5	4.2	0.00094	28.8	2.9	1.3	1	S6AHK8_9PROT	Diguanylate cyclase	SCD_n01825	Sulfuricella denitrificans skB26	284	1163617	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Sulfuricellales, Sulfuricellaceae, Sulfuricella, Sulfuricella denitrificans, Sulfuricella denitrificans skB26	>tr|S6AHK8|S6AHK8_9PROT Diguanylate cyclase OS=Sulfuricella denitrificans skB26 GN=SCD_n01825 PE=4 SV=1MSIDIFRIIRWKPAPGGRTVLYASTLATIIGATWVHYKLGQHYHIDMFFLLPVILMSWYGGRKAGNLLSLLSVAGWMIVDMGILHDSPFWAEFINNIFRFSVLLIVVQIASRLRIALDREHEMARQDNLTRLPNRRAFYEMGEVETERSRRYDRPFTAIFFDLDNFKTVNDTKGHGEGDRLLKTVAEILHSRLRTTDICGRLGGDEFAVLLPETGEEAAASFAAELRALRIEAMERHSWPVTFSIGVATFNTTPDSLDQLIKNADTLMYTVKQDGKNAIRQEVY	23~~DUF4118 (0.00000276383)~~114;X;125~~Nucleotidyl_cyc_III (8.49972E-57)~~280	non-KdpD DUF4118 protein
	0.0006	29.5	9.6	0.001	28.6	6.7	1.4	1	C7Q1T4_CATAD	Histidine kinase (EC 2.7.13.3)	Caci_6794	Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897)	891	479433	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Catenulisporales, Catenulisporaceae, Catenulispora, Catenulispora acidiphila, Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897)	>tr|C7Q1T4|C7Q1T4_CATAD Histidine kinase OS=Catenulispora acidiphila (strain DSM 44928 / NRRL B-24433 / NBRC 102108 / JCM 14897) GN=Caci_6794 PE=4 SV=1MSARGNLRVYLGAAPGVGKTYHMLDEAQRRAERGGDVVVGFVETHGRPHTQAMVDGLEIVPRRRMEYRGSDFEEMDIDAVLARQPSVVLIDELAHTNIPGSRNTKRWQDVEELLAAGIDVIASVNIQHLVSLNDVVQKITGVPQRETVPDEVVRSADQIELIDMAPEALRRRMAHGNIYQPEKIDAALSNYFRPGNLGALRELALLWVAGRVDEALQRYRDQHGIDKVWETRERIVVALTGGPEGATLIRRGARIAQRVGAKGSDLLAVHVARSDGLTGASPALLAEQRALVESLGGTFHSVVGDDIPNALLQFARAENATQLVIGVSSRRGLRERFLGGYGIGETVVQQSGDIDVHMVTHERSAADQSRWMWARRVLRQPETGPRWWGPVAGLIVPILLTLVLANVRSGLNLTNQVLVFLAGVVAVARLGGLLSAFFASLTASLLLNYYFIRPFYRLTINDPQNILALVVFALVALIVASVVDFASRQERRAGKASAEAETLSELARSVLRGDEAIGALLGRFRFETFGMESVALLERVEPGSPVLPDETDDPDAWRIVAATSAGGEMPCRTPGEGNVVVHAGPDAMLVLRGRALPAADQHVLTAFAAQAAVALERSRLARQAAEAVPLAAADKMRTALLAAVSHDLRTPLAAAKLSVASLRDTTVQWSEEDRADLLSGAEESLDRLSRLVENLLDMSRLQAGALNLRLEDVAIEDVAAMALDSLGIEGSLVEFGDLSGVSEVLADPVLLERAVANLIANALKHGSLNRPVLLAASELAGRVELRVTDRGPGVRPEDWERIFTPFQRLGDRDNTTGVGLGLALSRGLVEAMGGALTPEETPGGGMTMVVSLPAAGMAGNEDDSGDGTGNGSGDGEHDVEVTAALAAAEEPAR	2~~KdpD (1.2415E-118)~~212;X;234~~Usp(1.78287E-33)~~359;X;389~~DUF4118 (0.00000000168356)~~488;X(144);632~~HisKA (0.000000000000707417)~~698;X;749~~HATPase_c (2.92252E-22)~~850	KdpD protein
	0.0006	29.5	10	0.00099	28.7	6.9	1.4	1	F4GEN7_ALIDK	Histidine kinase (EC 2.7.13.3)	Alide2_1439	Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	909	596154	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Alicycliphilus, Alicycliphilus denitrificans, Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	>tr|F4GEN7|F4GEN7_ALIDK Histidine kinase OS=Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601) GN=Alide2_1439 PE=4 SV=1MGAENTQQADALVGELRRQAAGRLTVFLGAAPGVGKTYAMLARARELHRQGIDVVIGIVETHGRAETMALVEGLPQVPRRQVGYQGRMLDEMDLDGLLARRPAIALVDELAHRNAPGSRHERRWQDVQELLDAGIDVYTTVNVQHLESLNDVVHQITGIRVSETVPDAVFERLRDIRLVDLPARELIERLNQGKVYLPEQAAQALQAFFSPSNLTALRELAMQTVAEHVDADLRETRTARGLADIAIQRHVLVAIDGRGQSEYLVRAGARIAERRGAPWSVVSVDTGRSAGAALHAEDLERAAPGQARHSAAHAEQQRQRELDQAFALARSLGGETEALHNTDVTQALLDAAAARGARSIVIGRTRERPVARIFNRTLTQQLLQRGARYELTIVSTPQARQRALRLQGLAGERLARGEPALIALATLGATAAAALAERFVGLEDLSTVFLIAVLLVASRTRMVAAAITAVLCFLAYDFLFIEPRFTFLISAQRGVATVLLFLAAALIAGRLASRLRMQVIALRAANTHATAMQNLARQLSKAADLGQVITASASVLQSTLNAQAWIRINGESGPAAAAQHLDEKDKAAAEWSQQHGQPSGRYTDTLAHCAWWFLPVHSDRETLGVVGLRFPAGMGRLPFEQRRLAESMTEDIGQAALRARLVSELEAARVTGETERLRSALLSSVSHDLRSPLSSMIGAADSLARYGQDMGAQDRGSLLETIRVEGERLDRYIQNLLDMTRLGQQGLALSRDWIGVDELVGSAVRRLQRYEPAVKVESSIDAGIGPVHVHPALIEQAIFNVLENAAKFSPPGEPIRVQALREEEGGLLRIDISDRGPGIPEDERRRIFDMFYSVERGDRGKQGTGLGLTIVQGIVGAHMGRVEALPGPDGRGTTIRLTLPLGEPLPAQEG	22~~KdpD (1.31422E-119)~~229;X;250~~Usp(7.95852E-28)~~395;X;448~~DUF4118 (0.000186845)~~490;X(185);675~~HisKA (0.000000000028657 1)~~741;X;794~~HATPase_c (1.00441E-23)~~898	KdpD protein
	0.0006	29.5	11.6	0.001	28.6	8.1	1.4	1	A0A022LVB6_9MICO	Histidine kinase (EC 2.7.13.3)	H489_0104365	Curtobacterium flaccumfaciens UCD-AKU	830	1292022	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Curtobacterium, Curtobacterium flaccumfaciens, Curtobacterium flaccumfaciens UCD-AKU	>tr|A0A022LVB6|A0A022LVB6_9MICO Histidine kinase OS=Curtobacterium flaccumfaciens UCD-AKU GN=H489_0104365 PE=4 SV=1MKRGKLRVLLGAAPGVGKTYTMLEEGRRLLDEGRDVVVAVVETHERAATAALVNGLEVVPRRTVSHRGVDLDDLDLDAVIARAPEVALVDELAHTNAPGSPNEKRWQDVEALRDAGIDVISTVNVQHMQSLGDVVREITGTVQRETVPDAVVRAADQIEVVDLAPAALRERLSDGLVYPAARIDAALSNYFRLGNLTALREIALLWLADEVDDALKAYRAEHGIEHRWETRERVLVALTGGPEGETLLRRGARIAARSAGGELAAVHVTTNDGLRVRHPGALGKQRTLLEQLGGTYHQVVGDDVPSTLVRFARSIDATQIVIGVSRRSRLAAAMTGPGIGNTVIRESGDIDVHVVTHERAGGGITLPKLGGSLSRGRVIAGFVLSVLVGPLLTWVLSIGSDPDAITVDVLAYQLLVLVVALVGGMWPAVFAAVLSGLSLDYFFVQPLYMVTVQQPWHLFALVMYVISAVLVSFVVDRSARRSRAARRASAESGLLMGIAGSVLRGDDALQALLDRTREAFGFAGVRIRQGDEVPATSGEFGATPDASTTLASGAVLEFAGAPDDPTQRRLLRVVEQQLDAAVEHRELTRTAVGAERIAAADRVRSALLAAVGHDVRRPIAAASAAVQTLRAPDIDLSGPDREALLATADESLGQLAVLLADLLDVSRVQAGVLAVTPASIALETVVAPALDELELGPDDVDLDLPADLPPVLADPVLLQRVVVNLLANAARYAPDGTHVRVAASAFAGVVELRVADHGPGIPADRRDEVFQPFQRLGDTDNETGLGLGLALARGFTEGMGGTIEVDDTPGGGLTVVVRLPIAGHVGVEIR	1~~KdpD (8.19836E-108)~~211;X;233~~Usp(9.92023E-30)~~356;X;424~~DUF4118 (0.0000763709)~~476;X(242);718~~HATPase_c (6.11434E-27)~~819	KdpD protein
	0.0006	29.4	0.4	0.001	28.7	0.3	1.4	1	E1QKC5_DESB2	Histidine kinase (EC 2.7.13.3)	Deba_2664	Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	354	644282	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfarculales, Desulfarculaceae, Desulfarculus, Desulfarculus baarsii (Desulfovibrio baarsii), Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14)	>tr|E1QKC5|E1QKC5_DESB2 Histidine kinase OS=Desulfarculus baarsii (strain ATCC 33931 / DSM 2075 / VKM B-1802 / 2st14) GN=Deba_2664 PE=4 SV=1MVKQLLRGWKVVPLWLKVAPMIVLLAGLPLLQAYLEHHRPDLVPLMRHAYYLPLFMASVLFGLRGGLLCALAISFNFFEDVVGQRSVDLTQRLYMAAGVGVYFLVGGVTGFLVDREKREAQRLKHMQEMAALGQAAAALAHEMKTPLIAIGGFAQQIYRTLEDDHPHRAKLKIIVDQVAHMEQLMREVLDYARPMQLRLERAYLREVVEEARSLASLFAEQSGVSLELELPPQPVEALIDKGRLRQVLLNLMQNAIQASPRGARVIVSTAREGDFGLITVGDQGCGIAAEDLARIFNPFFTKRQGTGLGLAVAQKIVQAHGGGIESRSAPGQGSSFTVRLPLAGPAEPTAPAA	22~~DUF4118 (0.000267857)~~119;X;141~~HisKA (0.0000000540652)~~193;X;244~~HATPase_c (6.08102E-31)~~341	non-KdpD DUF4118 protein

Disagreement between HMM and CDD prediction	0.0006	29.4	3.1	0.0031	27.1	1.1	2.5	1	A0A0D5NJG3_9BACL	Uncharacterized protein	VN24_11430	Paenibacillus beijingensis	736	1126833	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus beijingensis	>tr|A0A0D5NJG3|A0A0D5NJG3_9BACL Uncharacterized protein OS=Paenibacillus beijingensis GN=VN24_11430 PE=4 SV=1MKILITGGYGFIGSFVAERFHKEGDQVFILDNLSSGSKSNVPFKHRGYILNVEDRNCDEIFRAHRFDVVVHLAAQVSVATSMIQPELDAKSNVLGLANMLTLARKYGIKKFIFASSAAVYGAPDEVPIREDAALNPISPYGINKMVGEIYCEKWKDLFGLDTLCFRFSNVYGPKQGNGGEGGVVSIFIERVLAQKEIHVYGDGGQTRDFIYVEDVADAIYRASYSSLSGVFNLSTCTENRVTDLIKHLQQLHGAIDVSYSQPREGDIYRSALDNRRIFQSLDWVPKYSLQEGLRKTYDWFKQNHRADHAKPGEQAKTRVDLKNRLAKLAKLAKPLLPSLENLFCFAVLLWITLKLQPVSSYSFDYSLLYILLIGLLHGSRQSMPATVLAFGLYIYRELESGRDLIALTYSSEFFFQLAVYLSAGLVVGYSIDHRTRKLRSQEEKLLEAEEKYSFLHHIFDETRLIKDELQQQILTNGHSFGKLHAVTKELETLEPEQIFTAAVGVLESIMNTDSVTIHTVNKQGNFLRLAAHSSGMTDVAKSVKVQDYPYLNELLVSHQLFVNKDLKADLPLLAAPVISAGQTVALVSVHTIEFERFTLYYQNLFKVAVDLISSALTRAHSYIEAVGTIRYVDGMQGKVLRHEVFAEIVINKQKASSRYGLDFILLTSLADGSSTDELADRIVASLRETDYMGMGRNGELLVLLSNTNKEEAQFVLERFQKQNIYMKVVEEGPEYV	2~~NADB_Rossmann (1.5348E-100)~~300;X(194);494~~GAF (3.93912E-17)~~618	No DUF4118 detected by NCBI CDD
	0.0006	29.4	11.5	0.0011	28.5	8	1.3	1	U2RI82_9FIRM	Histidine kinase (EC 2.7.13.3)	HMPREF1546_00017	Oscillibacter sp. KLE 1745	881	1226323	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter sp. KLE 1745	>tr|U2RI82|U2RI82_9FIRM Histidine kinase OS=Oscillibacter sp. KLE 1745 GN=HMPREF1546_00017 PE=4 SV=1METSAQVGRGERRRKGSLTIFAGYFSGTGKTYRMLEAAGRAVRAGEDVAVGLLSCSQWPQTQILADGFETLPLKAFSEAGKTVYELDVDTCLKRGPRLLLIDELSHENAGGSRHRKRCQDIEELLQAGIDIYTTLDVQHIESIQDTVSEILGAPAEERIPDRVFDQAARVEFVDCEPEDLRERLIRQDRTDLLSEYSQPKLSALRELALRRCADRTALDTQKSRGGERYRTREHVLVCLSAAPSNERVIRTAARMADAFRCGFTALFVETKNFQSIPQPDRNRLRANLRLAQQLGASVETVYGDDVAYQIAEFSRLSGVTKIVLGRGETSNRILFWKPSLTERLVELTPELDIHIIPDTGTARRFASHYKKELYAPAVPLLDLLKSTLLLVLSTLVGLIFYYLGLSEANIITVYILGVMLTSIFTKSAVCSFLNSVVGVLAFNFFFTEPRFSLHIYASDYMVTFLVMFLASLLTGSLAAKLKSLAKHSAQLAWRTKLLFETNQELQKAGTQDEILSVTARQLLKIFQRDIVTYRSDQGQLDAPKIFPVDDAFSESKYSAASEHQAAQWVLTNNKRAGAGTETFSDACCTYLAVRTAEQVYGVIGVAASGEEMDSFEGGLLLSILGECALAMENQKNLEEKEAAAVLAKNEQLRANLLRSISHDLRTPLTSISGNASNLLSNGDMFDAKTKHQMYVDIYDDAMWLINLVENLLSVSRLEGGQMNLHLSTELIGEVVAEALRHINRRSAEHHLHIQSGDEYLLAQMDAHLIVQVIINIVDNAIKYTPPGSDIEISWERQGRFAALSVADNGPGIPDSAKPRVFDMFYSASNRIADSRRSMGLGLALCKSIITAHGGEITVADHAPHGTVFTFTIPIEEVELHE	14~~KdpD (1.94904E72)~~215;X;234~~Usp(6.78806E-38)~~357;X;397~~DUF4118 (0.000000000915133)~~482;X;510~~GAF (0.0000671087)~~633;X;650~~HisKA (0.000000000905809)~~716;X;769~~HATPase_c (1.74529E-29)~~872	KdpD protein
	0.0006	29.4	5.8	0.0011	28.5	4	1.4	1	A0A0F5W4Y7_9ACTN	Histidine kinase	TN53_04920	Streptomyces sp. WM6386	847	1415558	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	>tr|A0A0F5W4Y7|A0A0F5W4Y7_9ACTN Histidine kinase OS=Streptomyces sp. WM6386 GN=TN53_04920 PE=4 SV=1MGRGRLRIYLGAAPGVGKTYAMLSEGHRRIERGTDCVVAFVEHHGRPRTEVMLHGLEQIPRRELAYRGSAFTEMDVDAVLHRAPAVALVDELAHTNVPGSRNAKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYRSDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLKQYRSEHQVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTAASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGANATQIILGSSRRKTWQYVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRARIIWGWAVGVVGPPVLAVLLNTVDLGLANDMLLFLTVTVAAALLGGVAPALASAAVGSLLLNYFYTPPLHHWTIADPKNIVAIAIFVGVGVSVSSVVDLAARRTHQAARLRAESEILSFLAGNVLRGETSLEELLERVRETFAMESAALLERVSDVEPWTCAGRAGLGRPVERPEDADVDVPVGDHMALTLTGRVLPAEDRRVLAAFAAQAAVALDRRRLQEEADQARTLAEGNRIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDQAELLEGIEEEGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEDSVELDIPETLPMVAVDPGLLERSVANLVENAVKYSPTGEAVLVSASAIADRVEVRVVIVSRLMAKKLELSEDEKKQLIYGAYMHDIGKINIPNEILTKKMRLTKEEWEILKQHPKDGVEIIKSVNSLKNVVPLILYHHERYDGFGYPVGLKEKEIPYLARVLTVIDSFDAMTSSRPYNKRKTYDEGLIELERCSGTQFDPEIVCIFSEVVKENINEIQDF	1~~KdpD (6.38632E-123)~~211;X;233~~Usp(1.00491E-31)~~356;X;381~~DUF4118 (0.0000212091)~~463;X(148);611~~HisKA (5.17576E-15)~~677;X;726~~HATPase_c (7.09831E-25)~~827	KdpD protein
	0.0006	29.3	9.5	0.00062	29.3	6.6	2.5	1	Q0SSR0_CLOPS	GGDEF/HD domain protein	CPR_1530	Clostridium perfringens (strain SM101 / Type A)	564	289380	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium perfringens, Clostridium perfringens (strain SM101 / Type A)	>tr|Q0SSR0|Q0SSR0_CLOPS GGDEF/HD domain protein OS=Clostridium perfringens (strain SM101 / Type A) GN=CPR_1530 PE=4 SV=1MIRDAGNNKKKKVDEILSIVKVSSLLFSAIAFLQYIFNIMSLHGEIPVYYGIVPAALVSIFLLSIIYILWSLASLNKYKGHINKIQLIETILFMIIFIMAILVSGGNSSNNKFLFLFIIITSTIQGGMHKGVLISVVSSAIILAIDLIFSVNADVNIYFQNDLILAGVFVLTAWTLGFYVKTENDHIKELQTLLNEDGLTGVYNHRYFYDKLREKMHISEVENEKLSLIFMDIDYFKHYNDLYGHQKGDEALKKIGKLLKNIARENDLVARYGGEEFAIILPNTSEEEATKIAERIRNKVEKTYFEGQENQPNANFTVSVGIAAFPDKAKSELELVKCADDALYRAKFFHKNRVETYVSVLDELKRDLNEEENTLVTSIKTLISIINAKDKYTYSHVERVVIYSRLMAKKLELSEDEKKQLIYGAYMHDIGKINIPNEILTKKMRLTKEEWEILKQHPKDGVEIIKSVNSLKNVVPLILYHHERYDGFGYPVGLKEKEIPYLARVLTVIDSFDAMTSSRPYNKRKTYDEGLIELERCSGTQFDPEIVCIFSEVVKENINEIQDF	86~~DUF4118 (0.0000000000594568)~~186;X;197~~Nucleotidyl_cyc_III (2.92137E-62)~~354;X;392~~HDc (1.84564E-23)~~529	non-KdpD DUF4118 protein
	0.0006	29.3	8.9	0.0012	28.4	6.1	1.3	1	D7BWR2_STRBB	Histidine kinase (EC 2.7.13.3)	SBI_00297	Streptomyces bingchenggensis (strain BCW-1)	823	749414	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	>tr|D7BWR2|D7BWR2_STRBB Histidine kinase OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_00297 PE=4 SV=1MNDVRPGRLKVYLGAAPGVGKTYRMLDEGRRRASRGADVVVGFVECHGRPRTEAMLDGLEVVPRAHCDYRGGKFQEMDLAAVLARRPQVAIVDEFAHSNVPGGHNSKRWQDVEELLAAGVDVITAVNIQHLASLNDVVEKITRVPQGETVPDEVVRRAQQIELVDMEPEGLRRRMAHGNIYAPEKVDAALANYFRPGNLTALRQLALLWVADQVDEALQMYRTEHGIGRVWETRERVVVALTGGLEGDTLIRRAARIADRSAGGDLLAVHVTRSDGLAVGSSHASLARQRRLVEDLGGSYHSVVGDDVGTALVEFARAEHATQLVLGTSRRGRIERFLGGCGTGETVVGMSGDIDVHMVTHERAGRGMLLPSRRRTLSLVRRVAGPVAGLVLPVLLTVLLDRARGTFNLTSEALLFLLTVVGVACIGGVASAVIASVTASLLLNYWFIPPIGAFTLDNADALVALGVFAIVAATVAGVVDRSLRLSRRSARATAEAETMSSLAGTIVRGGATIPALLERTREFTGMESADLVHHEQTPDEEGVTVVPAGPGAFLVLRGRTLPSSGRRVLAAFAAHVGSAVERTRLAEAAAEIEPVKAADRMRTALLRAVGHDLRTPLAAGWAAVTSLRSRDVEFSDEDRDELLATADESLAKLNRLVENLLDLSRLQAGVLTLDLRATTLEEVLPAALADIPDVEVRDLEEIPAVMADPPLLERVIANLVGNAARHSPPGGQVALTASAHAGRVEVRVVDRGPGLPQTGRERIFEPFQRLGDTDNTTGLGLGLALSKGLTEAMDGTLVPEDTPGGGLTMVLSLPFAERTVYSR	5~~KdpD (9.93707E-109)~~214;X;236~~Usp(2.35964E-28)~~360;X;414~~DUF4118 (0.000000242342)~~481;X(118);599~~HisKA (0.0000000028115)~~665;X;712~~HATPase_c (1.61192E-24)~~813	KdpD protein

	0.0006	29.3	10.4	0.0012	28.4	7.2	1.4	1	Q8YSJ3_NOSS1	Two-component hybrid sensor and regulator	alr3092	Nostoc sp. (strain PCC 7120 / UTEX 2576)	1290	103690	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	>tr|Q8YSJ3|Q8YSJ3_NOSS1 Two-component hybrid sensor and regulator OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=alr3092 PE=4 SV=1MSNIQRSHLQRYCISIVSVLLALLLGLTLGRYLKVEISPLFFASVVFSSWYGGLAPGLVATVLAILVKNYFFITPFNSIAVSQGNDLLNLIVFASVAVLISSLNLQVLTAREVSEAKLGKLKVNYRQLLETAYEGIWIFDSEGKTEYVSPQLAQILGYSVERIGEFSIFNFLEPQARLEIEQWLEQQQKYNHQTKQQFDLRLQRRDGASLWVIVSLSSILDKHRRFSGAVAMLTDITEHKHEQAEPDLERQRLRAILDILPMGVVISDAKGQLLEINPGVKAIWGEDAPLLDNTSQYHQYKGWWPDTGQPLTAAEWTLARTLATGEAIIGEEIDIATFDGKRKTILNSAVPIYDATGAIVNAVTVNVDITERKRVEAALRQSEALAKARAEELETIMETVPAAVWIAHDPLCHSMSVNRAAYDMMRVPPGSVMTATPASGGYPFPFKIQKNGQDIPLNELAMQQAGLTGQEVEAEVEFFFSPEDVRHIYGKAIPLCDPDGNVRGVIGAFLDVTERQQLMSLLQQKQEWLDLAQKSGKIGSFDWKLTSNINVWSQELEEIYGLQPGEFGGTFADWAKHVHPDDLARVEVELRELLNTGSKEFFSDFRIIRQDGSICWLQSRARVFYDDHGQPLRMVGVNVDVTERKQAEAALQQSEARLKRLLQSSIIGIIEADPERINFANDAFLKIVGYTHEDLLTGKLRWQDMTPPEYSELDQAKVEEVINSGFCIPFEKEYIRKDGSRVPILLGAARLSSSPLTWVCFILDLTERKQAQAALQQSELMFRTLADTMPQMFWITQPNGYHEYFNQRWYDYTGTTLEQTQGAGWQNILHPDDVQRTIEQWQDSLDTGKDYDIEYRLRRAADGEYRWHLGRAFPLRDENGRILKWFGSCTDIHDQKLAIEERAQAWEQERAARIELERANRMKDDFLAIVSHELRSPLNPILGWAKLLKSRKLDALKTNQALEVIERNAKLQARLIDDLLDVSRILRGKLSLNVCTVDLVTTIEAALETVRLTAESKSIHIQTELTSHVCRVEGDPNRLQQVVWNLLTNAVKFTPEGGQIEVSLERVGSLAHIQVRDTGKGISLDFLPYVFERFRQADEVTTRKFGGLGLGLAIVRHLVELHGGAVQVTSPGEGLGTTFTVKLPLIAVSQIYEEHFVADTTPNLQGLRMVVVDDDADTLELLSFILEQYGVEVKAVNSANEALEAIAHTKPDLLLSDIGMPEVDGYMLIKQIRSMEVASGTKLPAIALTAFAGETNFQKIMSAGFQRHLTKPVEPSELATAIANLIQSNS	40~~DUF4118 (0.000000267573)~~104;X;132~~PAS (0.000000000069924)~~236;X(303);539~~PAS (0.000000000236412)~~641;X;665~~PAS (0.00000000161224)~~765;X;789~~PAS (0.000000000015247 8)~~892;X;920~~HisKA (1.70581E-14)~~984;X;1039~~HATPase_c (1.06605E-33)~~1143;X;1171~~REC (3.70041E-27)~~1286	non-KdpD DUF4118 protein
	0.0007	29.3	7.3	0.0013	28.3	5.1	1.6	1	B7KJT7_CYAP7	Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(S)	PCC7424_1083	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	812	65393	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	>tr|B7KJT7|B7KJT7_CYAP7 Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(S) OS=Cyanothece sp. (strain PCC 7424) GN=PCC7424_1083 PE=4 SV=1MRQNFKPLKIPPYSLAIICPLLALGVRYLLNWALGNNAPLLIFIIPVIITAWYGGLLPGILSTVISAYLGNYFFIHPTEQFKILSLPETVRIIIFLSEGIFLSIFFEYYKRLNTKTSQIVESLRESEERYRLLVEGIEDYGIFMLDGQGRIISWNLGAERIQGYQSTEIIGRHYSIFFTTTDTSAKVPEKILQTALKQGRFKGEGWRRRKDGSLFWASIVLSPVFAQNRQLKGFAKITRDISERKQAEVQKNKLLKDLTDLKLALDQSAIVAVTNSQGIITAVNDQFCQISGYSKEELIGKTHRIINSGYHSKKFFQQLWATISQGKIWRGEICNRSKTGQFYWVATTIVPFLNQNNQPFQYFAIRFDITQRKLAEKRLRHEVLHDSLTGLPNRTLLIQRLEQVRHRAKRKANYCFALLFIDLDRFKNINDNLGHPIGDRVLITIASRLQECVRSLDTVARLGGDEFIILLDELEEEEKEIFKIIERIEKQLTTPMVIEGQTLSLTASIGIAFNDTNLSNSDLLRNADLAMYRVKNEGKAGYAIYQSEMYAQAQALWELENHLKLAIERQEFLLYYQPILSLKTLTVIGFEALIRWQHPQRGLISPVHFIPVAEETDLIVAIGEWVLQQSCQQLSAWREKYPQANHLTINVNLSNRQLEKDNFVYKLDNVLQQTGLPATQLKLEITETLLMTNLAAAIATLSQLKQRNINISIDDFGTGYSSLNYLCRLPVSSLKIDRSFVANVHEDSKNLQIIQTILSLGEQLMIEVIAEGIETQKHLEQLQELGCQYGQGYLFSKPVNCEAAEQLICAGLC	12~~DUF4118 (0.0000000228877)~~111;X;139~~PAS (0.000000000042552 7)~~241;X;268~~PAS (0.000000000000289671)~~369;X;384~~Nucleotidyl_cyc_III (1.4996E-53)~~542;X;560~~EAL (1.18291E-111)~~799	non-KdpD DUF4118 protein
	0.0007	29.2	11.4	0.0013	28.3	7.9	1.4	1	B7K8P7_CYAP7	Multi-sensor hybrid histidine kinase (EC 2.7.13.3)	PCC7424_2839	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	1478	65393	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	>tr|B7K8P7|B7K8P7_CYAP7 Multi-sensor hybrid histidine kinase OS=Cyanothece sp. (strain PCC 7424) GN=PCC7424_2839 PE=4 SV=1MTWQKVTRSPFFSYGVAVIAVLLAFLIMLMLDPWVSMVKSPFLLFLGAIVISAWYGGLKPGLLASFLSVILSHYFFLEPLYTFGLTLSEGIRIGLYFLQGVIVSLICEALRKAKRQAEVNLLKFKVSEERFRLALSNSNLCIFQQNQDLKYLWIHTSEGQVSPEEIIGKSDYDLFSQPEAQQLTAIKKRAIHSRQPLREEVCLTFGANPHYYELFIQPIASFDEQICGITCVAVDITERKHFEQQLHSATQQSSQILESLTDAFFALDQTWQFTYVNRHFEEISEHTREDLLGECIWDVFPEMRQSVFYEEFSLVFEQNLPISIEAINPINPEQWIEARAYPSAEGLCVYWQDITLRKETETERNQLLEREKTARAAAELMQQRLAFLDTASTILAGSLDYPTTLQTVVNLIVPDLADLCGLDILQEDRSVNPLIALKAKDQQEEELVRHFTRLYPLDLNDNHHPITRVFQTGLPETLYQITDEDYQAIAKDPQHLHYLRQLGMKSSICVPLKAHEEVFGVMTLALTKTERSYNDDDLRLALELGRRVGLAIENSRLHHQLQQATRQQQDSLTLLEAVIQQMPAGLAIVESKTGRIILQNDQLRQILGNRPLSTELLENYHHLYEVYHPNGHPYKIEELPLMRSRQQGEVVKSEEMLLVWTDGTQKTLLVDSSPIVNSQGEIEVAVATIYDITDYKQVVTDLKNRQEQLRLAVEGANLGMWNYDLLSGELIWSNRCKKMFGIAANTQISYEVFINALHPEDRLRVDQAVQHSISQRQNYDIEMRTQWPDGSLHWVRSIGHAYYNNEGVAHRMAGVVLDITGQKQAQEALRKSEERFRVAQELSLDGFTVLKSIRNQSGEIIDFEWTYVNPTAAKILRSQINDLIGKRLLEILPDNQSNSELFKRYVQVVETANSHDLELYYDSDEIVGWFRNMAVKLEDGVAVSFSDITERKQAEETLRENEQRLNIALKTAKLGSWHLDLSTMELFTSAQYKANFGLATDADLSYTTLFRLIHPEDRGYVSQMVQHAINTHTDYEAEYRSIWPDGSIHWINSQGCVLYSNTGIPLRIVGVNLDITGRKQAQEEQKRLLEREKLAREEAERVNRIKDEFLAVLSHELRSPLNPILGWAQLLRSGSFDKANQNKALEIIERNAKLQAQLIEDLLDVSRILRGKLSLNVTQLNLFFPIQGAIETVRLSAQAKSIEIKTNLATDVVQISGDAGRIQQIVWNLLSNAIKFTPEGGQIEIGLEQVNHQAQITVKDSGKGIDPQFLPHVFEHFRQADSTTTRKFGGLGLGLAIVRHLVEMHGGTVSAYSAGENQGSTFIVQFPLLKDQSNKIKPEIIDPFLFSVTQSALKGIRILAVDDDPDMRDYVTYVLEQSGAEVKVAGSANEALNILSHFKPDILLSDVGMPKIDGYRLLRQIRSLFPESNQTIPAIALTAYAGEYNQRQALAAGFERHLSKPVEPEQLIKAIVDLINLN	10~~DUF4118 (0.000000000287974)~~117;X(143);260~~PAS (0.00948414)~~354;X;400~~GAF (0.000000000097885 1)~~557;X(173);730~~PAS (0.00000935677)~~819;X(160);979~~PAS (0.00000790214)~~1075;X;1103~~HisKA (4.31027E-15)~~1167;X;1222~~HATPase_c (1.64101E-32)~~1326;X;1359~~REC (8.46256E-29)~~1475	non-KdpD DUF4118 protein
	0.0007	29.1	11.8	0.0013	28.3	8.2	1.4	1	B1MDK8_MYCA9	Histidine kinase (EC 2.7.13.3)	MAB_3251c	Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	835	561007	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium chelonae group, Mycobacterium abscessus subgroup, Mycobacterium abscessus, Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	>tr|B1MDK8|B1MDK8_MYCA9 Histidine kinase OS=Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543) GN=MAB_3251c PE=4 SV=1MPDGLRARGTLRIYLGAAPGVGKTFAMLNEAHRRAGRGTDVVAAVVETHGRSKTAELLDGLELIPPKEMVHRGTAMYELDVDAVLERRPALVLIDEMAHTNVPGSRNPKRWQDIDEILDAGIDVLTTINVQHLESLNDVVEQITGIVQRETVPDAVVRRAEQVELVDITPEALRRRMVHGNVYAPEKVGSALSNYFRTGNLTALRELALLWLADQVDAALAKYRSDNRITKTWEARERVVVAVTGGPESETLVRRASRIAAKSSAELLVVHVVRGDGLVGASTAVMTRVRRLANDIGASVQAVTGDDVPQTLLDFARGVNATQLVLGTSRRSRWARILDEGVAAAVIRDSGAIDVHMVTHGHTSGRLRSWSVPQDGRKRLIINWLAAILVPPATALFIHFFDTAFGVGSKSALFLIAVLGVSLLGGVSTALVSAVISGLLLNFLFVAPRYSFTIGETDNALTILMMMVTAVAVAALVDAAATRARQARRASREAELLALFAGGVLVNSDLSALLERVRTTYNQTAVSLLCAEGPAVASVGEDPPTRESEADSVFRVDDGAYALALNGPPVPSSDARVLQVVAGTAVGLVRSARLAEEASQASALAEADRLRRALLSAVSHDLRTPLAAVKAAVSSLRSPDIEFSPEDTAELLATVEESADQLTALVGNLLDSSRLAAGVVKPRAVPVYVDEIAQRALLGATENDRKRVHLDLGGAVVRADPGLLERVLANLVDNALRYSQGEVRVSHEEVDDRTLVIVADHGKGLEASKRGAAFDAFQRLGDRDNTVGVGLGLSVVKGFVEAMEGTVNATDTAGGGLTMIVDLPSAGSAPTGAIR	7~~KdpD (8.03994E-120)~~216;X;238~~Usp(1.48217E-32)~~359;X;383~~DUF4118 (0.00000114213)~~466;X(142);608~~HisKA (0.000000000001583 56)~~674;X;724~~HATPase_c (2.11814E-21)~~823	KdpD protein

	0.0007	29.1	13.6	0.0013	28.3	9.5	1.4	1	R5CKX2_9FIRM	Histidine kinase (EC 2.7.13.3)	BN785_01370	Firmicutes bacterium CAG:791	360	1262993	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:791	>tr|R5CKX2|R5CKX2_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:791 GN=BN785_01370 PE=4 SV=1MKNFDLYYFNLHPILKNSLLTSGILLVTSIFCFLLQQFVTADAYVPLIFILAIVLISRFTEGYSYGIVASFIAVFGVNCIFTFPYFSLNFSLTGYPLTFFVMLTVSIMISALTTQIKQQEQIKLQMEREQMRANLLRSVSHDIRTPLTSIVGSASAILDNYDTLDDEQKKTLTGDIKTEAQWLNRIVENILSITRISSGANAHITKTEELAEEIVSSTVQKFHKHSPSIPVEVKVPDEVLLVPMDPLIIEQVLLNLLDNSVMHGGNITRIVLHVMHIPGHAVFSVEDDGTGIDPQLLPHLFDGSLPLHAGDTRASGRSMQIGLSVCMTIVLAHHGTMHAENLPGGGARVWFELPLENTYA	19~~DUF4118 (0.00000000638831)~~119;X;129~~HisKA (0.000000000029337)~~195;X;249~~HATPase_c (2.13232E-21)~~353	non-KdpD DUF4118 protein
	0.0008	29	11.5	0.0012	28.4	7.9	1.3	1	D4J9A5_9FIRM	Histidine kinase (EC 2.7.13.3)	CC1_22400	Coprococcus catus GD/7	357	717962	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Coprococcus, Coprococcus catus, Coprococcus catus GD/7	>tr|D4J9A5|D4J9A5_9FIRM Histidine kinase OS=Coprococcus catus GD/7 GN=CC1_22400 PE=4 SV=1MKKKRHHLWKNIMIMAAVFLVASGSSIILQKTGVYEHITAIFIFAVFLTSILTDGYIYGIVSALVGTLAVNYAYTYPFYALNFRFQGNMVSAVVMMAIAVLTGMLTTQVKTHEAIKAESEKERMRANLLRAVSHDIRTPLTTIYGASTTLLESGDNYTKEQRIKILKGIQEDSDWLVRMVENLLSITRIDEGRIKIIKTPTVLDELIDSVMVKFHKRYPQQEVHLDLPEDIIVIPMDAILIEQVIFNLLENAVLHADGMTELILKVFVLGQQVVFEVSDDGCGIEKERLSGIFNGSYHLFEDKASSADSQKHNSGIGLSVCQTIIKAHDGVIAAENNAKGGAVFRFSLNREETSESE	11~~DUF4118 (0.0000000439908)~~112;X;122~~HisKA (0.000000000012518)~~188;X;241~~HATPase_c (5.63021E-20)~~348	non-KdpD DUF4118 protein
	0.0008	29	11.6	0.0012	28.4	8.1	1.3	1	A0A0E9M6M1_9PROT	Putative sensor histidine kinase pdtaS (EC 2.7.13.3)	pdtaS OYT1_00852	Ferriphaselus amnicola	586	1188319	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Gallionellales, Gallionellaceae, Ferriphaselus, Ferriphaselus amnicola	>tr|A0A0E9M6M1|A0A0E9M6M1_9PROT Putative sensor histidine kinase pdtaS OS=Ferriphaselus amnicola GN=pdtaS PE=4 SV=1MFTIDGVSQVFDYLGEGQPKFEGVFQYLMVCVLMGVALWVRLAVAPLDAGLQYLTLFPAVTLSAVIFGFRAGLFAVFIGICIATFIFVPPYYTISLHSVEVALWSNTVFLVDGLIVSLVVGAMHRYQEKLETAVKKFERAGEYLRDSQADLHRAQSMGKIGNWRLDVRHNQLNWSDENYRIFGIPVGNPLTYDNFLSIVHPDDRDYVDRMWQAALHGEPYDIEHRIIVNGAVRYVRENALLEFGESGELLGGFGTTQDITQSRLREMEYQGIIQTISEGFWFCDTTGRILEVNDSYCRMVGYTREEMLKMRIQDIEASESPQEVAKHIQRIVEVGHDLFETRHRRRKNGELIDFEISVNRSASRNDAIVVFARDITDRVKRNELRLIEIKQQRDVLIREVHHRIKNNLQGVVGLLRQHVSEHPNLAEVVDVIIGRIYSIAIIHGLQAQEMSEEVGLSPLMNLIIDASGTAVEYHDDLTHSLMLSRDEAVPIALVLNELFTNAGKHRSKQSTVAVRLEERGSHVIITLSNLFDARLTDEIKDGQGLSLVRSLLPRNSATLTMREAEGVFTAELDLAPPVVIHKQFDTQ	28~~DUF4118 (0.0000000182315)~~127;X(149);276~~PAS (0.000000000202398)~~374;X;398~~HWE_HK (0.000000000824243)~~483;X;487~~HATPase_c (0.00061573)~~574	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0009	28.9	3.4	0.0012	28.4	2.4	1.2	1	A0A0F4JQI4_9ACTN	Histidine kinase (Fragment)	VR44_08855	Streptomyces katrae	213	68223	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces katrae	>tr|A0A0F4JQI4|A0A0F4JQI4_9ACTN Histidine kinase (Fragment) OS=Streptomyces katrae GN=VR44_08855 PE=4 SV=1NAALILVVAVVAVAATGTRTAGAVAALSAAAWFDFFLTVPYQRFTITGRQDVETAVLLLVVGLIVSQLSVRARRLQTTVITDAARLASLRGTARLAEDGRSPEAVVEYVRRELVGLLGLRGCRFEYGNLMGGLPRLEHDGGVWLRRPDRVTEYADWPDDETELRVVGGGHYYGRFLLDPLPGPLPPEQDRLVAVALAAQAGSALDTAGLDRLG		No DUF4118 detected by NCBI CDD
	0.0009	28.9	8	0.0015	28.1	5.6	1.4	1	R6K1C2_9CLOT	Histidine kinase (EC 2.7.13.3)	BN486_03708	Clostridium clostridioforme CAG:132	510	1263065	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium clostridioforme CAG:132	>tr|R6K1C2|R6K1C2_9CLOT Histidine kinase OS=Clostridium clostridioforme CAG:132 GN=BN486_03708 PE=4 SV=1MARTRILDTLKTMAVLAAATAVGFLLETIGLSQANIITVYILGVLVVAAVTASRWYSISASLASVLLFNYIFTEPMFVLKAEDAGTQLTLLITFLAAVFTSSYTVQMKEKARLSQQDAYRSGVILDTSQMLQKAAAPADILSCTARQLNKLLKRDITCFEQDGAGLKSPLCFREYSSPATGRGPSPDTLEELTAARKCFREGKETGAATEVFPAAAYHFLPLQSSGAVYGVMGILVGNTPPGDFENSLAVAIIAQCSMALEKEYISRKREEEAAMARAEQLRSNLLRSISHDLRTPLTSISGNAGVLMSDGGSLTAEHRNRIYRDIYDDSMWLINLVENLLSITRMEGQGVHLHMETELLEEVIDEAMRHINRRHEHHTIKVNQIGDYILADMDARLIMQVITNLVDNAVKYTPEGSTIMVNSRQEGSSAVIDVSDNGPGIPDESKEKIFEMFYTTGHKSADGKRGMGLGLPLCRAILSAHRGTIEVLDNKPAGSIFRLTLPAKEVSLHE	10~~DUF4118 (0.0000000298253)~~110;X(170);280~~HisKA (0.000000000570914)~~345;X;398~~HATPase_c (1.46297E-28)~~501	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0009	28.9	6.7	0.0016	28	4.7	1.4	1	A0A0B5EJU1_9ACTN	Histidine kinase (EC 2.7.13.3)	SLNWT_1393	Streptomyces albus	847	1888	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albus	>tr|A0A0B5EJU1|A0A0B5EJU1_9ACTN Histidine kinase OS=Streptomyces albus GN=SLNWT_1393 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAYAEPHERPRTEILLHGLEQLPRRELCHRGAAFTEMDVDAALERRPAVALVDELAHTNIPGSRNAKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQQETVPDEVVRHADQIELVDMSPQALRRRMAHGNIYQPDRVDAALSNYFRPGNLTALRELALLWVADRVDEYLQQYRGEHDIRSTWQARERIVVGLTGGPEGRTLIRRASRMAAKGSGSEILAVYIARSDGLTAASPKELAVQRTLVEDLGGTFHHVIGDDIPSALLEFARGVNATQIVLGSSRRKAWQYVFGPGVGMTVARDSGPDLDVHIVTHEEAAKGRGLPVTRGARLGRPRLIAGWIIGVAGPALLALLHEFDSDLGLANDVLLFLSLTVAAALLGGLLPALASAAVGSLLLNWYFTPPVRRITIADPSNIVALVVFIAVAVAVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFAMDSVALLERESDVAPWTSAGSVGPNPCVRPEDADVDMPVRDTMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLQSEAEQARALAEGNRIRTALLAAVSHDLRTPLSAIKAAVSSLRSDDIAWSEQDQADLLEGIEDGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSVALDIPESLPMVAVDPGLLERAVANVVENAVKYSTGASRVLVAASALGDRVELRVVDRGPGVPEEAKDRIFEPFQRHGDAPRGAGVGLGLAVARGFAEAMGGTLAAEDTPGGGLTMVLTLRAPAPRPPAAAEPSGRAAR	1~~KdpD (4.07308E-122)~~211;X;233~~Usp(2.78521E-30)~~356;X(256);612~~HisKA (4.09453E-14)~~678;X;727~~HATPase_c (7.06519E-27)~~828	KdpD protein
	0.0009	28.8	8.1	0.0015	28.1	5.6	1.3	1	A0A0F2NAV2_9DELT	Universal stress protein UspA	VR65_21270	Desulfobulbaceae bacterium BRH_c16a	273	1629713	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, unclassified Desulfobulbaceae, Desulfobulbaceae bacterium BRH_c16a	>tr|A0A0F2NAV2|A0A0F2NAV2_9DELT Universal stress protein UspA OS=Desulfobulbaceae bacterium BRH_c16a GN=VR65_21270 PE=4 SV=1MIFFKKSYKIATVALLVLIIAFIDYTVTFRLSKIDLVYRDVYFIPILLGAYWFGKKGGLFTSLAASAFYLPCAILGNPLGSIIFFSNMLEIFFFIGVGYFVGSYRDLLRSQFVLTSNGYEEELYQPTKNVLFCIYSAENTFKAARYIADNFSHQSETTVTVMGLLRVKPQDFFATEEEFHTALEKSNAEMTTIVERAKAIIRQGGVSEPNIRERMITVEGENTAKIILKEQRRSHYDMIIAGCTKKTKAEEFLFGNTNVTLVREAPCPVLVVC	13~~DUF4118 (0.000000479232)~~111;X;129~~Usp(0.000000000334774)~~272	non-KdpD DUF4118 protein

	0.0009	28.8	11.1	0.0017	27.9	7.7	1.4	1	E2Q1F8_STRC2	Sensory histidine kinase in two-component regulatory system wtih KdpE (EC 2.7.13.3)	kdpD SCLAV_5517	Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	845	443255	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces clavuligerus, Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602)	>tr|E2Q1F8|E2Q1F8_STRC2 Sensory histidine kinase in two-component regulatory system wtih KdpE OS=Streptomyces clavuligerus (strain ATCC 27064 / DSM 738 / JCM 4710 / NBRC 13307 / NCIMB 12785 / NRRL 3585 / VKM Ac-602) GN=kdpD PE=4 SV=1MAQGRLRIYLGAAPGVGKTYAMLAEGRRLAAEGADVVVALVEPHGRRLTAAMAEGLPSVPRRRVVHRGVRLTEMDVAAVLARRPGIALVDELAHTTVPGSRNPRRWQDVEELLDAGIDVITTLNIQHLESLNDVVEEITGVRQHETLPDPVARRADQIELVDLEPEALRRRMTHGDIYPPDRIETALTHYFRVGNLTALRELALLWLADRVEEGLQRYRAEHGISAPWETRERILVGLTGGREGGTVIRRAARISARTPGSELLALHVVPGDGLADPVPLAEQRALVESLGGTYHQVTGDDIAAALLGFARTENVTQIVLGASRRGRVMSVVRTGVGRRTIRGSGPIDVHIVTHEEAGGPVPRPGSGSGRAPGPGRHRWSPYRDRRWWAALALAAVLPPALALVLTAPGTGVGPAGALLLCLLLVVVIALVGGLWPALLAAVVSAVLADRWFAAPGRSLSGARADELLAPAVFLAVAVLVGLAAGTAARRARRAGRAAAEAAALSRLATEMMRGRELPALVEQIRENFGLTSLSLLLRETAAGVRTRWYVVAAAGERPPERPEDADVEALADSGLTLAGRGRALGTDDYRVVFAACGAQLAVAYSRGVLARRAAETDTRATAERTRASLLLRAGRELRAVLRTADEALVRLGHGAGTRADEARLLGTAQLSVRRAERLVADLETLNRLHGGALATVLRPVDVGEVLTASLDELGPGGRTVEVSVPDGLPEVIADAAQLARALTALIADALRNSAPGAPPSVVARALPGKLAVRVTDGGSPAPPAGDRPPGARAEGIAQRLSRELTEAMGGALTAAGTRGGRFTVTLTLPAVAPPARPGPDGTPGPG	1~~KdpD (6.58844E-107)~~211;X;233~~Usp(5.12258E-26)~~353	KdpD protein
	0.0009	28.8	6.6	0.0016	28	4.6	1.3	1	R6SSY4_9CLOT	Universal stress family protein	BN719_02215	Clostridium sp. CAG:58	666	1262824	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	>tr|R6SSY4|R6SSY4_9CLOT Universal stress family protein OS=Clostridium sp. CAG:58 GN=BN719_02215 PE=4 SV=1MEEMRPDSEQLLKRIQYEEKREQEKNRGKMKVFLGYAAGTGKTYAMLEAAHEAEKSGIDVVAGYIEPHNRPDTEALREGLEEIPPLMVDYKGIQLREFDLDAALKRRPQLLLVDELAHTNVRGCRNEKRYQDVMELLQAGISVYSTVNIQHLESLNDLVGSITGIQVRERIPDYVFDQADQVEVIDIEPDDLIRRMKEGKIYGESQAERALSNFFRREKLVALREIALRRTADRVSRMAEEERSLSDNQDYHTGEHILVCITAAPSSAKVIRTAARLADAFRGRLTGLVVETAKIREADEKTKAALRENMEIAKVLGARVVTVCGSDVASQIAQYARISNVSKIVLGRTNHLTIRPMYRSELLEKLTYLAPNIDVYIIPDMRRQTKRYHPSQMEKRKKGDWRKTVLDLSLITAVMAAAAFLSLAFLKLGLSGTDQIILYLLGVLISSYIADRKIYSLYSALLSVVLYNFFCIEPLYSLKAYDRGDSVTFILLFFSGFFAAAMTRKLKQQNVESAKIAYRTGLLLENSQRLRRCRREKEVWALTAAQAGKLLNLSVLIYPVDKKGRLGTAMVFPRPGMSEEEFSVCLSTREKGVAQWTAANGHRAGASTHTLPDSLALYLPIQDEDQVKGVMGIYLEERRPIAEFEYNLLTAMLSEAAVKLKDTFPQE	25~~KdpD (8.78841E-124)~~235;X;256~~Usp(5.83135E-32)~~379;X;437~~DUF4118 (0.000000022686)~~508;X;537~~GAF (0.0000032983)~~659	KdpD protein
	0.001	28.7	8.2	0.0016	28	5.7	1.4	1	A6V7N5_PSEA7	Histidine kinase (EC 2.7.13.3)	PSPA7_3716	Pseudomonas aeruginosa (strain PA7)	914	381754	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	>tr|A6V7N5|A6V7N5_PSEA7 Histidine kinase OS=Pseudomonas aeruginosa (strain PA7) GN=PSPA7_3716 PE=4 SV=1MRAEQTEQADALLGELERQTAGRLTVFLGAAPGVGKTYAMLVRARELHHQGVDVVVGIVETHGRGETQTMVEGLSLLPRKKVEYQGRQLEEMDLDGLLARKPAIALVDELAHRNVPGSRHERRWQDVEELLDAGIDVYTTVNVQHLESVNDVVHQITGVRVSETVPDAVFERLRDIRLVDLPARELIERLNQGKVYLPEQAAQALQAFFSPSNLTALRELAMQTVAEHVDADLREKRAARGLEGISIQRHVLIAVDGRGHSEYLVRAGAKIAERRGAPWSVVTVETGRSADAALHTDEMDRAAPTLNRMARDEQQRLMEIDKAFALARNLGGETEVMHNTDVTQALLDAAAARGAKSIVIGRTRERPFARIFNRTLTQQLLLRGARYELTIISTPQARQRSLRLPDITGERLTWREALLILMASLGAVGTAALAERTLGLQDLSMVFLVAVILVASRTRMASAVITATLCFLAYNFFFIEPRYTFLISAHRGVATVMLFLAAALIAGRLASRLRMQVVALRAANTHAMAMQNLGRRLAKAADLGQVITAGASILQSTLHAEVWIRINGESGPATSAGRLADKDLTAADWTQQHDQASGRYTDTLTNSAWWFLPVSSDKDTLGVVGLRFPPNMGRLSFEQRRLAESMVEDIGQTALRTRLVSELEVARVTGETERLRSALLSSVSHDLRSPLSSMIGAADSLARYGKDMGLEDQQSLLETIHVEGERLDRYIQNLLDMTRLGQQGLTLTRDWIGIDELVGSASRRLQRYEPDARIEHEIPAELTPIHVHPALIEQALFNVMENAAKFSPPGEPVRVQVRRTNDDQLQIDVSDRGPGIPEEERRRIFDMFYSVERGDRGKQGTGLGLTIVQGIVGAHMGSVEALPGPEGRGTTIRLTLPWGGYSNQEAKENDGTSQ	22~~KdpD (9.77E-118)~~229;X;250~~Usp(1.81398E-26)~~393;X;414~~DUF4118 (0.000000000440189)~~514;X(159);673~~HisKA (0.000000000041507)~~739;X;792~~HATPase_c (1.8297E-23)~~896	KdpD protein
Disagreement between HMM and CDD prediction	0.001	28.7	7.5	0.002	27.7	5.2	1.4	1	B8HTL0_CYAP4	Multi-sensor hybrid histidine kinase (EC 2.7.13.3)	Cyan7425_3772	Cyanothece sp. (strain PCC 7425 / ATCC 29141)	934	395961	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7425 / ATCC 29141)	>tr|B8HTL0|B8HTL0_CYAP4 Multi-sensor hybrid histidine kinase OS=Cyanothece sp. (strain PCC 7425 / ATCC 29141) GN=Cyan7425_3772 PE=4 SV=1MIRLPPTAFHRYAVAIVLVGVSLVFMLLLDPFIGMTSTPFLLFFGALTISAWYGGRGAGILATLLSALLSEYFFIQPQHPFGFGLHFNDSLRTVLFILQGLLISHLCGALRLAQDRTRTTLEQLQANETRFRRLVDSNIIGVVGCDIKGAITSANDEFLRMTGFSRADVLAGRVRWDEMTPADLKPLDEPAMEELLSKGKNTAYEKALIGKDGRRVPVVVGAALLRNDPESVISFVLDLTRLRLTEQRLTVQYAVTRVLAEAVTVRESVAPILQALCQSLDWEFAIIWTVDQQAGVLRYLESWPTDTLLLDEFRSLKQPITFTPGMGLPGRIWATGQPAWIECLATDPNFPRAAAAQRAGLQSAMGFPIRLDDQVLGVIEGFSTHGRPPDQDLLQLMGAIGSQIGQFMERKRAEESLRQSQALFDRFMSHTPVAAWIVDQASRIVYLNPTYFRLFNFPAQDAIGKTVAELYPPQFAEQFLQNNRPVFTHQEVVETIETAPRTDGSTGEFLVYKFPIPQEPDELLLGGVALDITERKQAEAERERLLQREQEAREQAESANRIKDEFLAVLSHELRSPLNPILGWAKLLQTRPFAPEKAQQALQTIERNAKLQAQLIEDLLDVSRILRGKMVLNVCPVDLVTVIEAALETVQLSAEAKGIQLERHLANDIGFISGDAGRLQQIVWNLLSNAIKFSPPGHRVDIRLERVGAEAQMQVRDTGKGINPSFLPHVFEYFRQEDSRTTRKFGGLGLGLAIVRYLTELHGGTVQAESGGEGQGATFKVRLPLLKVGHSSEERSVSPPSPTSRLRGLRILAVDDEADMRDLLVTMLEDAGAVVKITASAVEALAALDSFHPDLLISDIGMAEVDGYMLLHQIRGLPPEQGGQIPALALTAYARDEDRQQVLAAGFQQHLPKPIEPDTLVAAVADLIRRSPTG	141~~PAS (0.00000000285928)~~242;X;272~~GAF (2.59349E-16)~~409;X;431~~PAS (0.00000000668579)~~532;X;560~~HisKA (1.85958E-15)~~624;X;679~~HATPase_c (1.52361E-30)~~783;X;812~~REC (1.57494E-28)~~928	No DUF4118 detected by NCBI CDD
	0.0011	28.6	8.5	0.0011	28.6	5.9	2.4	1	M1LSP9_9CLOT	Uncharacterized protein	Cspa_c22600	Clostridium saccharoperbutylacetonicum N1-4(HMT)	571	931276	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium saccharoperbutylacetonicum, Clostridium saccharoperbutylacetonicum N1-4, Clostridium saccharoperbutylacetonicum N1-4(HMT)	>tr|M1LSP9|M1LSP9_9CLOT Uncharacterized protein OS=Clostridium saccharoperbutylacetonicum N1-4(HMT) GN=Cspa_c22600 PE=4 SV=1MKKIINNKQKQINDIVSVVKLSTLLLIGIILSKTFVKNNSAIWESSTFYILIILFIPLMLFVLVYLAWSFSVENKIKNKYRNIFNIIEINFFLIVFSAIIWVCGVNGSQYKILYLFIIITTTIQYGMKRGLIVSIISSLIILGMDIMVVPNAYLNDFFQDDLILVGIFILTAWPLGFYVKIEGEHIKRLEEQINIDGLTELYNHRYFCDTLIEKVKAGERNNKPVSMIFIDIDYFKQYNDTYGHQKGDYVLRKVAEIIKGNIREGDLSARYGGEEFAVILPDTNEKEALNLAEHLRERIENTYFEGEDSQPNGKITASMGVSVYPDKAKDDIELIKSADDALYRAKFINKNKVESYTSILDEIKSNIDEKDVELVTSIKTLISVINAKDKYTYGHVERVVIYSRLIAEKLQLSKRNKEILIYGAYMHDIGKINTRKEVLVKKMKLTDEEWEELKQHPANGAEIIKSVESLKEITPLIISHHERYDGKGYPNRLKGDEIPFLARILTVVDSFDAMTSNRPYNTRKSYEDGIQELERCSGTQFDPEIVKAFVEVVRNDIEVSDLNGMNRKYAN	85~~DUF4118 (0.0000317474)~~185;X;194~~Nucleotidyl_cyc_III (5.35929E-62)~~353;X;391~~HDc (2.15953E-24)~~528	non-KdpD DUF4118 protein

Disagreement between HMM and CDD prediction	0.0011	28.5	5.9	0.0021	27.6	4.1	1.5	1	V4IXB4_9ACTN	Histidine kinase (EC 2.7.13.3)	B590_05719	Streptomyces sp. PVA 94-07	852	1223307	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. PVA 94-07	>tr|V4IXB4|V4IXB4_9ACTN Histidine kinase OS=Streptomyces sp. PVA 94-07 GN=B590_05719 PE=4 SV=1MGRGTLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVIGFVAHHDRPRTRALLEGLELIEPLGGPDGDGGTPQTREMDVEAVLARRPAVALVDELAHTNASGARNAKRWQDVEELLAAGISVISTVNIQHLESLGDVVEAITGVRQQETVPDEVVRRADQIELVDMSPQALRRRLAHGNVYQSDKVDAALSNYFRPGNLTALRELALLWTADRADEYLQKYRGEHNIRSTWQARERIVVGLTGGPEGRTLLRRAARMAAKGSGSEILAVYIARRDGGLTTASPKELALQRTLVEDLGGSFHHVIGDDIPSALLEFARGVNATQIVLGSSRRKSWQYVFGPGVGATVARESTPDLDVHIVTHEEVGQGRGLPVARGARLGRSRILWGWFIAVCGPALLAIVLSSLDHGPGLANDVLLFLSLTVGAALVGGLLPALASAALCSALLNFYFTPPTRTLTISDPENIVAIVISFAVAVAVASAVDLAARRTHQAARLRAESEILSFLAGSVLRGATTLDALLERVRETFAMESVALLEREGDRTPWTCAGSVGPRPLERPEDADVDMPVGDHMALALCGRVLPAEDRRVLAAFAAQAAVVLDRQRLQDEADAQARRLAEGNRIRTALLAAVSHDLRTPLAAIKASVTSLRSDDVAWSEQDEAELLESIEHGADRLDHLVGNLLDMSRLQTGTVTPLIREIDLDEVVPMALGGVPEGSAQLDIPETLPMVAVDPGLLERSVANVVENAVKYAPEGAPVLVAASALGDRVELRVMDHGPGVPDDAKDRIFAPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLTLRAVTGPRAGARTVLPAQVTS	1~~KdpD (2.03489E-109)~~213;X;236~~Usp(1.50732E-29)~~360;X(256);616~~HisKA (0.000000000000137299)~~682;X;731~~HATPase_c (2.72648E-25)~~832	KdpD protein
Disagreement between HMM and CDD prediction	0.0011	28.5	8.4	0.0019	27.7	5.9	1.4	1	Q741U1_MYCPA	Histidine kinase (EC 2.7.13.3)	kdpD MAP_0996c	Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	858	262316	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium avium complex (MAC), Mycobacterium avium, Mycobacterium paratuberculosis, Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	>tr|Q741U1|Q741U1_MYCPA Histidine kinase OS=Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10) GN=kdpD PE=4 SV=1MMVDVTDVRDHHPKRGELRIYLGAAPGVGKTYSMLGEAHRRLERGTDLVAGVVETHGRAKTAELLEGIEIIPPRYIEYRGGRFPELDVPAVLARHPQVVLVDELAHTNTPGSKNPKRWQDVEELLDAGITVISTVNVQHLESLNDVVAQITGIEQKETVPDSVVRQASQVELIDITPEALRRRLSHGNVYAPDRIDAALSNYFRRGNLTALRELVLLWLADQVDTALAKYRAENKITDTWEARERVVVAVTGGPESETLVRRASRIASKSSAELMVVHVIRGDGLAGLSESRMAKIRELASSLDASLHTIVGDEVPAALLEFAREMNATQLVIGTSRRSRWARLFEEGIGPRIVELSGKIDVHLVTHEESKRGFRASSLAPRERRVASWLAALIVPSVICAVTVTWLDPYLDTGGESALFFVGVLLVGLLGGIAPAALSAVLSGLLLNYYLIAPRHSFTIAEPNSAITELVLLLIAVAVAVLVDFAAKRTREARRASQEAELLTLFAGSVLRGADLETLLERVRETYAQRSVSMLRESEDARAGGTKTQVVACVGRDPCVSVDAADTAIEVGGPDSSEFQMLLAGRKLSARDRRVLSAVARQAAGLIRQRELAEEASRTEAIVRADELRRSLLSAVSHDLRTPLAAAKVAVSSLRAEDVAFSPTDTAELLATIEESIDQLTALVGNLLDSSRLAAGAIHPDLRRVYLEEAVQRALVSIGKGATGFFRSAIDRVKVDVGDAMVMADAGLLERVLANLIDNALRYAPNCVVRVNAGQVGDRVLISVIDEGPGIPHGAEEQIFEAFQRLGDHDNTTGVGLGMSVARGFVEAMGGTITATDTPGGGLTVMVDMAAPQSEGAA	13~~KdpD (2.84277E122)~~223;X;245~~Usp(1.14912E-33)~~366;X(260);626~~HisKA (0.000000000039094 9)~~692;X;749~~HATPase_c (4.46982E-26)~~847	KdpD protein
	0.0011	28.5	10	0.0018	27.8	7	1.3	1	G4KZ26_OSCVS	Histidine kinase (EC 2.7.13.3)	OBV_40190	Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	361	693746	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Oscillospiraceae, Oscillibacter, Oscillibacter valericigenes, Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20)	>tr|G4KZ26|G4KZ26_OSCVS Histidine kinase OS=Oscillibacter valericigenes (strain DSM 18026 / NBRC 101213 / Sjm18-20) GN=OBV_40190 PE=4 SV=1MHSEESILKRLFPFRWQDLLVCVAILFCAATVCMILQSVSTSEGFASPIFVLAVLLISRLTNGYLFGLAASVVGVIAVNYTFTYPYGAIDFTLSGYPLTFLTFLMVSVVTSAMTTQVKQQERLRAENEKEKMRANLLRSVSHDIRTPLTSIVGSTSAILENPSISRAEQEDLLRDVRDEAQWLIRVVENLLSVTRIGENGQAQIAKKDEAAEEILGDAARKFRKRFPNVNITVEAPRELLLVPMDAILIEQVLVNLLENAVRHGETTTCVSLSVRRQGRLAKFSVRDNGRGIPRDQLPRLFDGTLKSSETSSGDGKRDMGLGLVVCLTIVRAHNGFMEAQNMEGGGAEFFFCLPLSEEEEQ	19~~DUF4118 (0.0000000876655)~~120;X;130~~HisKA (0.000000000006396 7)~~195;X;249~~HATPase_c (2.92777E-26)~~353	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0012	28.4	9.5	0.0019	27.8	6.6	1.3	1	F4CN81_PSEUX	Osmosensitive K+ channel histidine kinase-like protein	Psed_4967	Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	259	675635	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Pseudonocardia, Pseudonocardia dioxanivorans, Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	>tr|F4CN81|F4CN81_PSEUX Osmosensitive K+ channel histidine kinase-like protein OS=Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190) GN=Psed_4967 PE=4 SV=1MGTRTWAGPWALTWAVVLPVATAAVLGLLRAVVVNTSASLILVLVVTAVAVRAERAAGLLAAVIAALAFDFFLAPPFYELTIFERADLETTLLLLAVGAAVTELAQWGRRERARASRREGYVAGVAGVARMAVDGATSDLVTTVGAMIAEVLDLDRCEFRPGPRPDRPRLHPDGSVTWNRRPVDVGREGLPTMDRIELATGRGDGVYELTASTRVRRPDLERRLVAATLAEQVDTRPTASAHMSGSGVQDRGSGSGPS		No DUF4118 detected by NCBI CDD
	0.0012	28.4	17.2	0.0021	27.6	11.9	1.4	1	Q5YZH6_NOCFA	Histidine kinase (EC 2.7.13.3)	kdpD NFA_15690	Nocardia farcinica (strain IFM 10152)	828	247156	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia farcinica, Nocardia farcinica (strain IFM 10152)	>tr|Q5YZH6|Q5YZH6_NOCFA Histidine kinase OS=Nocardia farcinica (strain IFM 10152) GN=kdpD PE=4 SV=1MSTSDAPAPRRGRLRIYLGAAPGAGKTYAMLGEAQRRIARGGDVVVAIVNTHGRPRTEEQLAGLEVVPPRRITYRGVEFEELDLDAVLARRPAVALVDELAHTNVPGSRHAKRWQDVAELLAAGIDVLSTVNIQHLESLADVVEQITGVAQRERIPDAVVRRAEQIELVDITPQALRRRLAHGNVYAPEKVDAALRNYFREGNLTALREIALLWLADQVDLALAKYRGEHAITDTWEARERVVVAVTGGPESETLVRRASRIAAKAGADLLVVHVVRGDGLTTPEMGAVRELAAGLGADVHSVVGDDVPATLLDFARQVNATQLVVGTSRRSRWARILDEGIGAAVVRDSGKIDVHMVTHEHRVRGPRPALLGRHDRRPAAWLAAFLIPVAATAVMAAIVRLTGTAGLNALFFVAVLAVALFGGVGPAIVAALLSGLLLNYFFTEPLYSLTIAEPANFVTTVVLLVVAVAVAALVDTAAARAREAGSAAREAELLALFAGAVLRGADVPALLEKVRETYAQRGVSLVRLDGDRVEVLGTAGAEPPSTPAAADTRGDVEDSPYALLLAGPRLRPRDRRVLTAVAGQAAGLVRQRELAAEAARAAMLAETDRLRRLLLSAVSHDLRTPLAAVKAAAAGLRSTDVEFSPEDTAELLATIEESTDQLTRLVTNLLDSSRLAAGVVTPEPRPVYVDEVVHSALLSLGVDAGERLTLEGDTLVRADATLLERVLANLLDNALRYAPDGPIRVCATNSGERTTVTVADHGPGLDSGVTAFPRTGDQRTGGAGLGLVVARGFVEAMGGTLTAAETPGGGTTMIIDLPAVSTEAPA	9~~KdpD (3.08015E-118)~~219;X;241~~Usp(1.47463E-32)~~359;X;381~~DUF4118 (0.0000000847973)~~458;X(151);609~~HisKA (0.00000000248205)~~675;X;725~~HATPase_c (2.68741E-20)~~819	KdpD protein

	0.0013	28.3	3	0.0023	27.5	2.1	1.4	1	B5EGR2_GEOBB	Histidine kinase (EC 2.7.13.3)	Gbem_2537	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	675	404380	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	>tr|B5EGR2|B5EGR2_GEOBB Histidine kinase OS=Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622) GN=Gbem_2537 PE=4 SV=1MEKLTITSRLLRMVTSALLVFLATVVGVKLLQPLGLRHPLLIYYPAVAVSAIYLGLEGGLTATLLSALSAAYFSIEPRSNFAIRDFEEQLYVAVFVLEGCIISYAAYKMRRAETAEAQIKIAKERTLAAERLEESEIRLRLALEGAKMGMWTLDVTSNQCELSDQEYDLLGDTKGGGLEPVDAFFERVHPDDREEFKRLLSEVLDHGDNFSHEFRIVRPDGEIRWLAARARLSRSRKGKPIRMHGVNYDVTSQRRFEEQLRHSENEARARANELAVLMDTVPAITFIAHDPECRDMSGSRKSREMLRVVPEGKSVVSASAPEGEFANSFHGFKDGRELSPEELPVQMAARGQEVHDYELTLVFNDGTSCEVIGNAVPLFDGAGKARGAIGAFLDITEQKRIQRELEKVRDELDKRVKERTAELRQALETLQRETEERIESVNLLIHQSRLAAMGEMIGYIAHQWRQPLNIMGLIVQEMPMVYGGGEFTEEYLKAQMDKARQLVMHMSATIDDFRDFFKPSKEKEVFKAGEMIRKTLALIEGVLKTQQITVHADQSGDPDIYGYIGECCQVLLSLLVNSRDAFLAREEIANRAITIRTFSEDGKTVLTISDNAGGIPEEIRDKIFDAYFTTKPPEKGTGLGLSLARKIIEKRMNGRFTFRDIVDGAEFRIEIDSKPAA	12~~DUF4118 (0.0000000302147)~~112;X;146~~PAS (0.00000000106988)~~250;X(317);567~~HATPase_c (1.94104E-17)~~669	non-KdpD DUF4118 protein
	0.0014	28.2	13.7	0.0021	27.6	9.5	1.2	1	A7I7N8_METB6	Integral membrane sensor signal transduction histidine kinase	Mboo_1231	Methanoregula boonei (strain 6A8)	366	456442	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula boonei, Methanoregula boonei (strain 6A8)	>tr|A7I7N8|A7I7N8_METB6 Integral membrane sensor signal transduction histidine kinase OS=Methanoregula boonei (strain 6A8) GN=Mboo_1231 PE=4 SV=1MNETSSPGTLYNAPDRLKLIVLAILVLVGVFLEGIVHYLYHISAVYTQFYYLIVVVVCLWYGRAAIAIALFFGALQIAVSWLLAPDSLPYEAIIRALMLLLVAIVIWKIVEEMTGYYNRLLIQNAELKDLNARLDASREAFLTANKKLNLLSGITRHDIRNQLTALLAYIELSRMIQQDPEMTATIDKEELVANNILRQIEFTKDYEDIGVKTPTWNNVAEEMRILLPQLKSAGIALEISTGDLEIYADPLLEKVFENLVDNSLRHGEHVRHITVSYRKNPDGLALIYRDDGVGVAAAEKEKIFDRGFGKNTGLGLFISREILSITGLSISECGTPGTGVQFEIGVPEGRYRFIGSTESVNDGQGR	18~~DUF4118 (0.00000000284291)~~124;X(128);252~~HATPase_c (0.000000000000168994)~~344	non-KdpD DUF4118 protein
	0.0014	28.2	10.1	0.0025	27.4	7	1.4	1	D6ZE67_SEGRD	Histidine kinase (EC 2.7.13.3)	Srot_0870	Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	856	640132	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Segniliparaceae, Segniliparus, Segniliparus rotundus, Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	>tr|D6ZE67|D6ZE67_SEGRD Histidine kinase OS=Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578) GN=Srot_0870 PE=4 SV=1MESMSTEPAPDLQPTPPKRGQLRIYLGAAPGVGKTYAMLAEAHRCQEAGTDVVVAVVATHGREKTAALLDGLEIVPAARVSYRGTALEEMDLGAVLERAPQLALVDELAHTNAPGSAHEKRWQDVQVLLEAGIDVLSTVNVQHLESLNDVVAQITGATQQETVPDVFARSAAQVELVDITPEALRARMSHGEIYAPDKVDAALRNYFRAGNLTALRELALLWLADQVDAALAKYRREHRITDVWETRERVIVSVTGGPESQTLIRRARRIASRSGAELMVLHVVRGDGLASAAETELGRLREFSANVGASLHTVVGDDVPTTLLEFARAVNATQLVIGTSRRSRMAQLLDEGIGMRVVRESGKIDVHMVTHEEAGRRRALRPGLRSTRKTSWSAAVLAPPAAAWLMELAGPAVDFTSATAVFFAVVLLVSLLGGVAPAAFSAVVSGVLLNYFFAPPLRSFAVKSPGQVVTIFVMVGLGVAVAALVDFASSRARQRAAQEAELLTLFAGAVLRGADVSELLARAKETYGLRAVSLVRSGDVVSCAGEDAPTSEASARAAVQSPDGECVLLLDGPKTFAGRDRRVLEAVAAQAAALVRQADLAQEAAALADGLAEADKLRRALLSAVSHDLRTPLAAVKAAVSSLRSDDVEFSPEDVGELLATIEESADQLTALVGNLLDSSRLAAGVLAPQRRRVYVDEVAHRAILSLPAPRRARVQVQPDVNAVLADPGLLERVLANLIDNALRYAPDSQVTVRSERQEGEVVISVVDHGPGIRADQRERAFEPFGRLSSAPDGRGDRDNSVGVGLGLSVVRGFAESMGGQVVVTQTPGGGATLQIWLPDANTAKRHAAETGAKA	17~~KdpD (1.03598E108)~~227;X;249~~Usp(3.6815E-22)~~370;X;415~~DUF4118 (0.000000150364)~~486;X(130);616~~HisKA (0.000000000000270746)~~682;X;732~~HATPase_c (2.71338E-27)~~839	KdpD protein
	0.0014	28.2	12.1	0.0025	27.4	8.4	1.4	1	V2UDL0_9GAMM	Histidine kinase (EC 2.7.13.3)	P255_00724	Acinetobacter brisouii CIP 110357	881	1341683	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter brisouii, Acinetobacter brisouii CIP 110357	>tr|V2UDL0|V2UDL0_9GAMM Histidine kinase OS=Acinetobacter brisouii CIP 110357 GN=P255_00724 PE=4 SV=1MQIDRNNKADAWLAHSQREQSGRLTIFLGAAPGVGKTYAMLTRAHELMQQGQHVVVGVVETHGRSDTERLIQGLHVIPRKSLEYQGRMLEEMDLDQILKLKPQIVLVDELAHRNVPNSRHEYRWQDVNELLDAGIDVYSTLNIQHLESLNDVVYQITGIRVTETVPDALLKRLKDIRLVDLPVPELLERMNHGKIYFADVAPHALQGFFKAANLTALRDLAIQTVAGQVDIDYREKFVAQGQIIPIQNHVLLAIDGSEFSEDLVRRAHRIAERRNATWSVISIQKSKAETTQIFTVTKAFNLARKLGADTYLLYSNHIASTILQAAYDYGASNILLGKSPQKSLWQRLFSDHIADQLLEKQHPFEITFVQPLKAQNNQTSPNDAAHSSWREQGLAFTQREVFESIIIVLLGLIVAAISDHFIGYSDLALIFIVTVLLVAIRARMLITIISVFICFLLYNYFFIEPRFTFMISAERGVITIITFIVSALLVGRLANQLRAQVLSLRAANSVSLQLQELERKLSACVDIEQVLNVAKQHLETSLNATVWLKVENQSLGDPSVLNEKDQIAADWTQKNAKPCGRFTNTLTNSDWWFIPLNLVKEYGVIAIRFNQNAQTISFELQRLTELMIEDIAQTVARVQLSLQLENSRVVAETEKLRSALLSSVSHDLRSPLAAMIGSADTLKYYGEQMSESDRHELLDTIHIEGERLDRYIQNLLDMTRLGHQGLTLARDWIGVDELIGSATQRLKRYQPNVKIDVTLADDLPQLYVHPALIEQAIFNVLENAAKFSPDDMPIKISIQQEDDFLQINIEDQGVGIPEDEREQIFDMFYTMQRGDRGKTGTGLGLAIVKAIIGAHMGSIEALAGTHGQGTLIKIRLPLHQD	22~~KdpD (2.20983E103)~~229;X;249~~Usp(4.90384E-27)~~369;X;402~~DUF4118 (0.000000000865481)~~500;X(154);654~~HisKA (0.000000000018543)~~720;X;773~~HATPase_c (8.33256E-24)~~876	KdpD protein
	0.0014	28.2	7.9	0.0025	27.4	5.4	1.3	1	A0A0F2SES3_9FIRM	Kinase	VR66_13100	Peptococcaceae bacterium BRH_c23	373	1629714	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, unclassified Peptococcaceae, Peptococcaceae bacterium BRH_c23	>tr|A0A0F2SES3|A0A0F2SES3_9FIRM Kinase OS=Peptococcaceae bacterium BRH_c23 GN=VR66_13100 PE=4 SV=1MLNHEPPAQNRTRTLFDLIAIGLVVVILTAIHYTNYHYEMNYHILLQFAYYLPVIYAAMRFGPAGGIISSLVITVLILPLMIYLQAMAPSAMYMQWVEIGLINGIGWLTGFLIEQERKASRKHQLALLVQTQLVEKLKQEGQERERLEGEIRQTERLTALGHMSAGLAHEIRNPLGIMKVSIQLMAQEKSDDGVVSEYCRVLIEESERLNRLVSEFLFFARPKELVRGGIPLGKLLDEVVTLIRPALRQHHIELKQAPSQVGEQEVVVDPDQIKQVILNILLNAIDAQGEGGVILLEGVRQVGFVGFAVSDEGPGISLDVMPYIYDPFFTTKEKGTGLGLSVVHSILDQHGGKISTTNRRDGGVRVEILLPSI	15~~DUF4118 (0.0000208373)~~119;X;157~~HisKA (0.000000000000705008)~~221;X;273~~HATPase_c (1.40352E-21)~~370	non-KdpD DUF4118 protein
	0.0015	28.1	4.7	0.0026	27.3	3.2	1.4	1	G8NP68_GRAMM	Histidine kinase (EC 2.7.13.3)	AciX8_3984	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	480	682795	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	>tr|G8NP68|G8NP68_GRAMM Histidine kinase OS=Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8) GN=AciX8_3984 PE=4 SV=1MFARPIRLVLRRIAAGSSAAALLTFLAFRLHFNLSAATSVHFLLMSVIALRWGFLEASIVSILSVACLDYYFTDPIFAFYIRDSHDWIALATFEVAALLVSRLSNQMHRHARESELHQAHLQKLYALSQHILLLDREGAVEQQLVHIIRSSLQVEGIALWNGYDLHMYKSGTCNFDDDQVRSSFHMEADSDDASTGISRRVLRSGTRAIGAFALCGHSLDTTSVNAAASLVSVAIERARSFSTEANAVAARQTEQLRSAILDGMAHAFKSPLTTIRTSSSGLLAMNTLSGTEKKLVGLIDRHASHLNDLANHLLLTAKLDSGDIKVNREEIDLSQLVENSIESSSQELDGHAVEIRVTERPRIVYADRKLLQMALLQILDNAVKYGRPGSPVLIAVEKEGAELVIAIRNEGSFIPPEEREKVFQRFYRCSGSIRTISGTGIGLSVVRRIAEAHQGRVWVDSDVENGTTFSITLPSLALEG	24~~DUF4118 (0.000065695)~~104;X(150);254~~HisKA (0.0000131943)~~318;X;371~~HATPase_c (3.90314E-27)~~473	non-KdpD DUF4118 protein

	0.0015	28.1	7.1	0.0015	28.1	4.9	2.1	1	E8RCQ1_DESPD	Histidine kinase (EC 2.7.13.3)	Despr_1692	Desulfobulbus propionicus (strain ATCC 33891 / DSM 2032 / 1pr3)	872	577650	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfobulbus, Desulfobulbus propionicus, Desulfobulbus propionicus (strain ATCC 33891 / DSM 2032 / 1pr3)	>tr|E8RCQ1|E8RCQ1_DESPD Histidine kinase OS=Desulfobulbus propionicus (strain ATCC 33891 / DSM 2032 / 1pr3) GN=Despr_1692 PE=4 SV=1MTRRRYILVVTGGYVLLALAWILLSDQLLATVGDSQSIAWISRAKGVFFVLVTSMALFSVLHAVPAAESDIRATTMDEGLFDLVSAHPLPGWLAYILAAALTGVVLCLRLLLPVPIEKRPLMFMFALPIIVSALFGGLGPGLFATLVSTLLTLYALIPPAGSFTIGAEQDLFQLSLLIVNGLIISLVSGAVHRLRRKDRLRVHQLNEALAALQESAERFRTLFEAAPIAMTLTNEAKVFLARNARMEQLFGYTPAELVTVDDWWHLAYPDPVYRAEVQASWNAALSRLGPDNKTVMGGDFRVRCKDGTERLVRFFATLMPEGQLTILLDETDRHQAERRLRLWAESFDQAQLALVIADAQTNTIVAANPAFARQRGYGREELTGMPLSRLFPADRQQDLNDLVATLRSTSHGLFQTEHVTKEGHRFPVLIDITALYDQEGRPVNRIAYYVLDITEKEQAERALAEALERQRDGRIAALNQMQDANIARGKAEAVLAALRESEERLALFIEHAPAALAMFDRDMRYLAVSRRWLHNYSIGEAVVLGQCHYDIFPEIGPDWKELHRRGLAGEILHRDEDRFERANGQTQWERWEIRPWHTATGDIGGILIFSEDITRFKEAEMEIRQLNAELEQRVAERTAELTAANRELDSFAYAVSHDLRAPLRAMNGFSQALIEDYGDLLQGEARVYLEQIIIGSRKMGELIDGLLALSRSTRGELQRQRVNLSTMARQIMEDLAAAEPQRQVRWHIEPNLLVRGDRAMLEVVVRNLLANAWKYTCRRDEAIIRVFSRKEGDVTYMCIEDNGAGFDPAHADKLFQPFQRLHRQEEFPGIGIGLATVQRIVHRHGGRLHARGEKGQGATFCFSLSGEMSTMEE	94~~DUF4118 (0.000000229867)~~197;X(158);355~~PAS (0.000000000906938)~~452;X;511~~PAS (0.0000809989)~~612;X;644~~HisKA (0.0000000333587)~~710;X;760~~HATPase_c (1.32348E-24)~~863	non-KdpD DUF4118 protein
	0.0015	28.1	2.9	0.0029	27.2	2	1.5	1	Q9KM57_VIBCH	Histidine kinase (EC 2.7.13.3)	VC_A0531	Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	497	243277	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio, Vibrio cholerae, Vibrio cholerae O1, Vibrio cholerae O1 biovar El Tor, Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961)	>tr|Q9KM57|Q9KM57_VIBCH Histidine kinase OS=Vibrio cholerae serotype O1 (strain ATCC 39315 / El Tor Inaba N16961) GN=VC_A0531 PE=4 SV=1MVTRLNEAHKALILVALYAMVTVVGVMYRKDMIETDVAMLFLLLNILSASVLKPRNAYVMMGLSIIDYHYFLLPDYQSFRFENAQYVITYAVLAFSGIFAVNITQAQRKQIEKNKRLQQQHKKYYELACHLSALSTSEDIAQATVKFLSKEKGIVSAIALYQPQWQWVAQHADFPVAAIELPQPPLTDNTSTLVQDEQINAFTLVDRGTILGVIYFLRYPHERFASPEALRRESKIAPWVRSLLTLSLARAHAHRTLAHVEAEKQLESTRTTLLASVSHDLKTPLGAIIGSATTLTDPSLHLSTETQQELLTSIAEQGERLNRSLTKLLDITRYTASALVPKLDWVEPEELIGTVLSRLAPRLTHHKVQIESQPMLVELDSLLIEQVLINLVENAAKYTPRGSEIEIACAYQEQQFTLAVMDNGAGIPDEALPRIFDRFYRVEGNHADGTGLGLAICQVIVAAHQGSIRVHNRESGGACFTVTIPCRQYNLKELYEQ	12~~DUF4118 (0.0000580615)~~110;X(157);267~~HisKA (0.000000000026733)~~333;X;384~~HATPase_c (4.07088E-31)~~484	non-KdpD DUF4118 protein
	0.0016	28	5.9	0.0032	27	4.1	1.5	1	O54137_STRCO	Histidine kinase (EC 2.7.13.3)	SCO5871	Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	848	100226	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albidoflavus group, Streptomyces coelicolor, Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	>tr|O54137|O54137_STRCO Histidine kinase OS=Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145) GN=SCO5871 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVALVEHHGRARTEVMLRGLEQVPRREAEYRGAAFTELDLDAVLARAPRVALVDELAHTNVPGVRNAKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYQSDKVDAALSNYFRPGNLTALRELALLWVADRADEYLQQYRSEHRVSKIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTSASPKELAVQRTLVEDLGGTFHHVLGEDIPAALLDFARGVNATQIVLGSSRRKAWQYVFGPGVGATVARESGSDLDVHIVTHEEVAKGRGLPVARGARLGRSRIVWGWFAGLGGPVLLTLLLSTVHLGLANDVLVLYLALTVAAALLGGLYPALASAAVGSLLLNWYFTPPVNRITIADPRNMLALAIFVGVALSVASVVDVAARRTHQAARLRAESEILSFLAGDVLRGETSLETLLERVRETFGMESAALLEREGDVAPWTCAGRAGSGPPVDRPEDADVDMPVGDHMALALTGRVLPAEDRRVLAAFAAQAAVVLDRRRLREEADRARTLAEGNRIRTALAAVSHDLRTPLAGIKAAVTSLRSDDVAWSEEDRAELLEGIEEGADRLDHLVGNLLDMSRLQTGTVTPLIREIDVDEVAPMALGGVPEGSAELDIPETLPMVAVDAGLLERALANLVENAVKYSPDDRTVLVAASALADRVEVRVVDRGPGVPDEAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLTLRAVGSSAPTSRPATAERQAAL	1~~KdpD (2.50743E-123)~~210;X;233~~Usp(2.1904E-30)~~356;X;423~~DUF4118 (0.0000653967)~~480;X(131);611~~HisKA (4.42981E-14)~~677;X;726~~HATPase_c (2.00265E-27)~~827	KdpD protein
	0.0017	27.9	0.6	0.0023	27.5	0.4	1.2	1	A0A068NPU6_9BACT	Integral membrane sensor signal transduction histidine kinase	OP10G_2093	Fimbriimonas ginsengisoli Gsoil 348	183	661478	cellular organisms, Bacteria, Armatimonadetes, Fimbriimonadia, Fimbriimonadales, Fimbriimonadaceae, Fimbriimonas, Fimbriimonas ginsengisoli, Fimbriimonas ginsengisoli Gsoil 348	>tr|A0A068NPU6|A0A068NPU6_9BACT Integral membrane sensor signal transduction histidine kinase OS=Fimbriimonas ginsengisoli Gsoil 348 GN=OP10G_2093 PE=4 SV=1MVAQVESFDLASERWSPMEASKEHDSKPWGWRAVSPYIETVLLICILTYVRQLAAGILEDRARYTLFFIAPCYSVWRGGLISGCLALVATCYIGTYFFLPPDRTHAIEDIGDALSMLLYLGVGLVIVLLGEKERAERRQVLERDKELVIAHAQLAEANEKLEQAVARRTAQLEELRQWAADEL	36~~DUF4118 (0.0000246925)~~136	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0017	27.9	11.9	0.0039	26.8	8.2	1.5	1	K9U6R8_9CYAN	Signal transduction histidine kinase	Chro_4563	Chroococcidiopsis thermalis PCC 7203	598	251229	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Chroococcidiopsis, Chroococcidiopsis thermalis, Chroococcidiopsis thermalis PCC 7203	>tr|K9U6R8|K9U6R8_9CYAN Signal transduction histidine kinase OS=Chroococcidiopsis thermalis PCC 7203 GN=Chro_4563 PE=4 SV=1MVKRKSLFWRYGVAVLTVAIALVVTLFLATLIHKESPFMLFFIAILVSAWCGGMGAGLAATALAAILCNYFFLPPQYVLSIASWEQGLRLTIFVLEAICICTAIAILNSARVRAQQSQVAALHCQATLLQSEERFRLLIEGVKDYAIFMLDADGIVASWNAGAARITGYKAREAIGQHYSRFYTYTDIESGIPQQELQTAIAQERLETEGWRIRRDGSRFWANVVTTALKDSSGEIQGFSQVVRDVSDRQRSEELLRQSQERLHLTLEASQIGIWDWNLHTHELKWSLQQEALFDLAPGTFAGTYEAVLDRIYPEDRASFSEAITRALERTGEFEQEFRILSADGNIRWLAGQGKVFYDDADRAIWMTGINRNISEQKQAAARIQAVEREKDFLLKEVHHRVKNNLQMISSLLSLQTNYVSDRQTLEILKSGEARIFSMALVHDLLYRSQSQNFVQINLADYIETLVNNLYSTYDTAKLNCKQVTLKLATEPIWVSIDIAILCGLIINELTTNAMKHAFKKRQFGQICIAVQFEEPQTHNHVILKVSDDGIGLPLELNWQNTKSLGLQIVNILTNQLKGNIELTKKDFGTEFIVRFSI	144~~PAS (0.000000000264728)~~246;X;273~~PAS (0.0000151204)~~363;X;397~~HWE_HK (5.91509E-29)~~474;X;506~~HATPase_c (0.00000000169795)~~596	No DUF4118 detected by NCBI CDD
Disagreement between HMM and CDD prediction	0.0017	27.9	9	0.0017	27.9	6.3	2.3	1	Q8E0B7_STRA5	Membrane protein, putative	SAG0817	Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R)	187	208435	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Streptococcaceae, Streptococcus, Streptococcus agalactiae, Streptococcus agalactiae serogroup V, Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R)	>tr|Q8E0B7|Q8E0B7_STRA5 Membrane protein, putative OS=Streptococcus agalactiae serotype V (strain ATCC BAA-611 / 2603 V/R) GN=SAG0817 PE=4 SV=1MSKNNNTTCLIETAIFAALAMALSMIPDFASWFTPSFGAIPLILFALRRGTKYGLFAGLIWGLLHFVLSKVYYLSLSQVFIEYILAFISMGLAGVFSAKFKDALSSSSKTKALSLALSGAILATLVRYVWHYIAGVIFWASYAPKGMSATLYSLSVNGTAGLLTLFFVVISIIILVISYPSFFLPKK	7~~DUF3816 (1.02899E-53)~~184	No DUF4118 detected by NCBI CDD

	0.0017	27.9	7.6	0.0034	27	5.3	1.5	1	A0A0D4DG89_9ACTN	Histidine kinase (EC 2.7.13.3)	T261_13108	Streptomyces lydicus A02	848	1403539	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	>tr|A0A0D4DG89|A0A0D4DG89_9ACTN Histidine kinase OS=Streptomyces lydicus A02 GN=T261_1308 PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHDRPRTEVMLHGLEQVPRKELEYRGTS FTEMDVDAVLERAPAVALVDELPHTNIPGSRNAKRWQDIEELLAAGIHVISTCNIQHLESLGDIVESITGIRQKETVP DEVVRRADQIELVDMSPHALRRRMAHGNIYKPHKVDAALSNYFRPGNLTALRELALLWVADRVDEYLQEYRSEHQ VSKIWGSRERIVVGLTGGSEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTSGSPKELAVQRTLIEDLGGTFHHV MGEDIPSALLEFSRGVNATQIVLGTSRRKAWQYIFGPGVGATVARDSGPDLDVHIVTHEEAAKGRGLPVARGARL GRPRIIWGWLTGVAGPALLTLPLMYVGAGLGFANDVLLFLTLTVAAALLGGLLPALASAVVGSLLLNWFFTPPVGR LTIADPKNILALVIFLLVAASVASVVDVAARRTHQAARLRAESEILSFLAGSVLRGETTLDALLERVRETFAMDAVALL ERETETAPWTCSGSVGDASPLSRPEDADVDMPVGDHMALALSGRVLPAEDRRVLAAFAAQAAVVLDRQRLKSQ ADHARKLAEGNRIRTALLAAVSHDLRTPLASIKASVTSLRSDDVEWSDEDRAELLAGIEEGADRLDHLVGNLLDMS RVQTGTVTPLIREIDLDEVVPMALGGVPEDSVVLDIPEALPMVAVDPGLLERSVANIVENAVKYSPSDGETVLVSAST LGDRVEVRVADRGPGVPDDAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAEAIGATLTAEDTPGGGMTMVLTV PTAAGHLPAQPDLPAAVTS	1~~KdpD (6.52106E-122)~~211;X;233~~Usp(2.85697E-29)~~356;X;432~~DUF4118 (0.00123084)~~482;X(131);613~~HisKA (0.000000000000040627)~~679;X;728~~HATPase_c (1.45786E-24)~~829	KdpD protein
	0.0018	27.9	9.7	0.0035	26.9	6.7	1.5	1	Q2NCJ5_ERYLH	Histidine kinase (EC 2.7.13.3)	ELI_02520	Erythrobacter litoralis (strain HTCC2594)	511	314225	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Erythrobacteraceae, Erythrobacter, Erythrobacter litoralis, Erythrobacter litoralis (strain HTCC2594)	>tr|Q2NCJ5|Q2NCJ5_ERYLH Histidine kinase OS=Erythrobacter litoralis (strain HTCC2594) GN=ELI_02520 PE=4 SV=1MDAERAEFGYQPTMSLLRESPERSNLAVSLAIDFGVFFIAALVTWLAQYFDRPITAVLAFLTGVIMIAVHSGM TRAVIGAVAASIVYNFFLSEPVYQFGVTTADETIPLVAFNVSALLVGFVVGRLSDYASDAQTARAETQFLLTLSDKL QSAISFEDVELAINRALPMQGLESVKVYLSRGDAYVRPTTGEVEMESFSALIAENTDHPPGSRAKILELLGARGSLG LVKFQLVHTAKGEDVALRLQSITALIAVAIERCLLLDELAEARTAARSEELKDAILASVSHDLRTPITVIETAASALKSS DVSLDGEQRHKMLVSIVEQCHRLDRYTNQLLDVGRIQAGISKLRMGTVDLAEIAQLAIRHVRSGKPEVVFERNFPR ERCLVSGNEGMLENALFNLFDNAAKFGGADGPVTVEIAIEGRYARLSVSDRGPGIPAHELDTVFKRFHKSGRNTA NGGAGLGLFIARGFIEAANGSIAIESPVDGQHGTRATVRLDLAREPELREAAA	34~~DUF4118 (0.00000474907)~~129;X(147);276~~HisKA (0.000000000180339)~~342;X;395~~HATPase_c (2.25333E-24)~~498	non-KdpD DUF4118 protein
	0.0018	27.9	2.6	0.003	27.1	1.8	1.3	1	B8ICU5_METNO	Histidine kinase (EC 2.7.13.3)	Mnod_2540	Methylobacterium nodulans (strain ORS2060 / LMG 21967)	809	460265	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium nodulans, Methylobacterium nodulans (strain ORS2060 / LMG 21967)	>tr|B8ICU5|B8ICU5_METNO Histidine kinase OS=Methylobacterium nodulans (strain ORS2060 / LMG 21967) GN=Mnod_2540 PE=4 SV=1MLGLRSTQYGLAVLATTGAFLLRLGLDPVLGDRSPFLLFTLPILVTALSAGTRPALVAAVLGGLSGTYAFVPP NPSLRLVTPGDWLEVALFSITAALIIRVVNRRAALRAQHNQAVEELRTSEAIKAAILRGALDGIVTTTEDGRILAANPA FCRAFGFRAEDAVGRRLTDLLVVPAPSLLPGTSPERVVAALPGIRPDHRVEGEALRSDRSRFPAEIAMTFTRHQTH NQLTWFIRDVTERKAFEDALRRTTRQLTVVLENASESIFLLDEQGCCVYMNPSAESLTGFTLAEASGRSLHALIHHI GPDGSPCPEADCAIACASRGQTKRSGQEVLIRRNGDFVPVSYIASPIRDSSHAVIGAVIEIRDVTEERRRDALLDEN RRQLLRQQQALETLHRLGITIAAELHPDRLVQTVVDAGVTLSGAQVGAFFYNATNDTGDHYVLYALAGAERSAFD RFGLPRATPLFGPTFRGDGVIRSSDILQDPRYGKNAPHAGMPEGHIPVRSYLSVPVASRDGNVIGALFFGHAEPDI FDEAAERAVIGLAAHAAIGLDNARLFEAVEKAKQTLEEKVRTRTQALEEINAELDAFSYTVSHDLRAPLRAVQTLASI LLDDFGERLGETGRQYAERIVGAAQRMDDLVQGLLQYSRLARTDIQLQPISLRFVMEKVRQTLERNEELDDAVLDL SENLHTVYANPTILQQVLHNLVTNAIKYRHEERPARVKAWSELRNDRVVRIWIEDNGIGVAPDQLDKIFDVFYRAP GTMSRPGTGIGLAVVKKGTERMDGRCGVESRDGEGSRFWIELPTPN	12~~DUF4118 (0.00000075725)~~98;X;135~~PAS (0.00000283829)~~238;X;262~~PAS (0.000000000574326)~~369;X;406~~GAF (0.000000000015889)~~554;X;584~~HisKA (0.000000000122033)~~650;X;701~~HATPase_c (1.69369E-24)~~805	non-KdpD DUF4118 protein
	0.0018	27.8	11.6	0.005	26.4	8	1.8	1	A0A090K5S6_9GAMM	Histidine kinase (EC 2.7.13.3)	MVIS_1135	Moritella viscosa	343	80854	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Moritellaceae, Moritella, Moritella viscosa	>tr|A0A090K5S6|A0A090K5S6_9GAMM Histidine kinase OS=Moritella viscosa GN=MVIS_1135 PE=4 SV=1MMYKYWRSNLMFFTFVILMSALLSSIIIDLLFGATIAVLLILQLAVVVVALRCNAKFAYFAAIFEAVSFNLLFTTP RYSLQMFHMDDIVNLLVFVIVALTASQLAEHYQRQKNELKQAQLRNNILLSVSHDLRTPLATIIGTLTTLKEYMEKLS ESEKIELLDSATTESHRLHQYIENLLQATKLQHGALRFNKSTDSILNVVSQTIDRFPESRQRIKLIAATPLPTLQISSSL IEQAIFNVLDNALRYTPSDNMVNINAYQAGNDVILDIQDEGDGITIDQAVHIFDLFYSENTLKNNDSGTGLGLAVAKG ILTAHNGNVEAIPVTHGCLIRIRLPITKEEQ	11~~DUF4118 (0.00000102683)~~111;X;119~~HisKA (0.0000001498 63)~~184;X;235~~HATPase_c (1.75372E-19)~~336	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0019	27.8	7.8	0.0039	26.8	5.4	1.5	1	Q82KK7_STRAW	Histidine kinase (EC 2.7.13.3)	kdpD SAV_2396	Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	851	227882	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces avermitilis, Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	>tr|Q82KK7|Q82KK7_STRAW Histidine kinase OS=Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680) GN=kdpD PE=4 SV=1MARGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCVVAFVEHHGRPRTEVMLHGLEQVARRELAYRDTV FAEMDVDAVLRRAPAVALVDELAHTNVPGSRNAKRWQDVEELLAAGIDVVSTVNIQHLESLGDVVESITGVRQRE TVPDEMVRRADQIELVDMSPQALRRRMAHGNIYKPDKVDAALSNYFRPGNLTALRELALLWVADRVDAYLTEYRS EHRVSAIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVMAVYIARSDGLTSASPKELAVQRTLVEDLGGT FHHVVGDDIPSALLDFSRGVNATQIVLGSSRRKAWQYMFGPGVGATVARESGPDLDVHIVTHEEVAKGRGLPVA RGARLGRSRIIWGWLVGVAGPVVLALLLNTVDLGLANDMLLFLALTVAAALLGGLLPALASAAFGSLLLNYYYTPPL HRLTIADPKNIIAIAIFVGVAVSVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETSLDALLERVRETFGMESVA LLERESDVAPWTCAGSVGVRPLVDRPEDADVDMPVGDHMALALSGRVLPASDRRVLAAFAAQAAVVLDRQRLQ READQARTLAEGNSIRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDRAELLEGIEDGADRLDHLVGNLLD MSRLQTGTVTPLIREIDLDEVVPMALGGVPEDSVVLDIPESLPMVAVDPGLLERSVANLVENAVKYSPSDESVLVA ASALANRVELRVVDRGPGVPDEAKDRIFAPFQRYGDAPRGVGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTM VLTVGAAVDSPAGRPGLAHATAEROTRC	1~~KdpD (3.05015E-122)~~211;X;233~~Usp(6.96116E-32)~~356;X(255);611~~HisKA (0.000000000000042042)~~677;X;726~~HATPase_c (4.18087E-24)~~827	KdpD protein
	0.0019	27.8	6	0.0019	27.8	4.1	2.1	1	A0A0A7FW72_9CLOT	Diguanylate cyclase domain protein	U729_2381	Clostridium baratii str. Sullivan	566	1415775	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium baratii, Clostridium baratii str. Sullivan	>tr|A0A0A7FW72|A0A0A7FW72_9CLOT Diguanylate cyclase domain protein OS=Clostridium baratii str. Sullivan GN=U729_2381 PE=4 SV=1MSNIEKDKSKRINDIVAIVKLVSLLFTGMIFIQYAFKNDADIIDKLIYSESIVLGFSFLIMLLLSIYILWTLSIKNKMN EKSTMIVNVIERKIFIIVFTITIIISGGNTSQYKVLFLFIIITTTIQSGMKQGLLVAAISSFIILGMDIIYMPDSQVNVVYFEND LVLSGIFVLTALPLGFYVKIEGEHIKKLLSLANEDGLTGVYNHRYFYDSLSDKIKEADDTKTKLSMLFIDIDYFKQYND TYGHQAGDKVLRDMGAILKKSTREKDIVTRYGGEEFAIILPSTDENEASIIAEKIRDEVESTYFEGQENQPNKNLTVS IGISIYPDKARDSIDLIKSADDALYRAKFFNKNRVETYVSIFDEINKDITDEDVEVIASIKTLISVINAKDRYTYGHGERL VFYCKLLAEKLRLSKRDKMQLLRGAYVHDIGKINISKEILVKKMPLTNEEWNTLKEHPQNGVDILKPMKALNNLQEL VLYHHEKYDGTGYPKGLKGSEIPYLARILTVVDSFDAMTSNRPYNRRKSYEEAIKELRRCSGTQFDPDIAEAFIEVIK ENKDNLGNLV	105~~DUF4118 (0.0000000160384)~~187;X;198~~Nucleotidyl_cyc_III (1.13616E-62)~~355;X;392~~HDc (1.0843E-21)~~535	non-KdpD DUF4118 protein

Disagreement between HMM and CDD prediction	0.0019	27.8	10	0.0019	27.8	6.9	3	2	D7DKQ5_METV0	Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(S)	M301_2133	Methylotenera versatilis (strain 301)	879	666681	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylotenera, Methylotenera versatilis, Methylotenera versatilis (strain 301)	>tr|D7DKQ5|D7DKQ5_METV0 Diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(S) OS=Methylotenera versatilis (strain 301) GN=M301_2133 PE=4 SV=1MLLRNRYILLVTISYFVLALLWIFLSDQLLSIFTDINSIVWLSTAKGVFFVFASALGFFFALRAMPLSNDASNLRLQDVVFSGVLFERRSAWLTYVFAIIVTLLMLFVRMHMGLNADHRPLMILFMLPILLSALLGGLGPGLLATFLASIGTDYLVIQPLHSFEISDKYDLIQWSTLIFSGLILSIFSEMLMRMRARAENNLKLLNVAVSGTADAVFVKDKIGRYLIVNQAAANFAGMPMAEILGKDDYFLFPESSAKAVMLQDQKVMDSRRTQSHEESVVSFGGKSMVFDVTKGPMFDAAGNVIGLFGISRDITERKQAEINLQIAAVAFESQNSVMITDASLNILRVNKAFTDIFGYTAEEAVGKTAKLLRSGSQDADFYEHIWHEVNTTGSWQGEILNRHKNGQLLSNLLSISVVKSKDGVVTHYVGSHVDITERKAAADKILHIAFHDLLTQLPNRQLFNDRLKQAIASSARTSQIGALLLIDLDNFKTLNDTLGHDIGDLLLQQVAERLNLNVREGDTVARLGGDEFVILLEDLSDNALDAATSAEVLGDKILVALNQPYVLGSNHYHTTSSIGVTMFEGHQLMIADLLKQADISMYQAKKAGRNTLRFFDPKMQEAFNIRATLEIELRRALESKQFQLYYQVQVDQLARPFGAEVLIRWIHPERGMISPLDFIPLAEETGLILPIGEWVLDTACAQLEVWQKEKSTKNLTLSVNVSAKQFSQADFVRQVQAKLSRYNVKPQHLKLELTESILLEHVDNIVISMVALESIGVQFSLDDFGTGYSSLQYLKMLPLNQLKIDQSFVRDIVEDSNDRSIVGTIIAMAKNLGFEVIAEGVETEAQKELLLSKGCOHFOGYLFGKPMPIEOFGSLLKLK	212~~PAS (0.000097594)~~314;X;337~~PAS (0.000000563653)~~435;X;450~~Nucleotidyl_cyc_III (1.55388E57)~~613;X;632~~EAL (1.60657E-105)~~871	No DUF4118 detected by NCBI CDD
Disagreement between HMM and CDD prediction	0.0019	27.7	10.9	0.0031	27.1	7.6	1.3	1	V6KD09_STRRC	Uncharacterized protein	M878_19685	Streptomyces roseochromogenus subsp. oscitans DS 12.976	265	1352936	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces roseochromogenus, Streptomyces roseochromogenes subsp. oscitans, Streptomyces roseochromogenus subsp. oscitans DS 12.976	>tr|V6KD09|V6KD09_STRRC Uncharacterized protein OS=Streptomyces roseochromogenus subsp. oscitans DS 12.976 GN=M878_19685 PE=4 SV=1MSAVTGIWKPLRTEARVVWAWPLRDRLALAAAFVAPFLVALVLVPFRTSVTHTNAALILVVVVVAVAALGSRTAGVAAALSAAAWFDFFLTRPYETFDITASADIETAVLLLAVGVLVSQLAARARRLEVVTVTDAAHLARIHRTADLAKTANSADIVVDHVRRELTELLGLRACRFEYGTLLGKPPRLETDGGVTVGRRTWNPDTDGWPEGEIELRTYGNGHYVGRFMLTPGPGPVLPLQARLVAVTLADQTGAALDTAGPARR		No DUF4118 detected by NCBI CDD
	0.002	27.7	12.7	0.0038	26.8	8.8	1.5	1	B2FJW7_STRMK	Histidine kinase (EC 2.7.13.3)	kdpD Smlt0405	Stenotrophomonas maltophilia (strain K279a)	886	522373	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Stenotrophomonas, Stenotrophomonas maltophilia group, Stenotrophomonas maltophilia (Pseudomonas maltophilia) (Xanthomonas maltophilia), Stenotrophomonas maltophilia (strain K279a)	>tr|B2FJW7|B2FJW7_STRMK Histidine kinase OS=Stenotrophomonas maltophilia (strain K279a) GN=kdpD PE=4 SV=1MTDARTRQADALVEGLQREAGGKLTVFLGAAPGVGKTYAMLTRAQEQLRRGVDLVVGLVETHGRADTQALLEGLPQLPLKDVAYHGHALQEMDLDAVLARHPALVLVDELAHRNAPGSRHERRWQDVMELLDAGIDVWTTVNIQHLESLNDVVMRITGVRVSETVPDGVLDRLHDIVLVDLPPREIARLQQGKVYVPEQAAQALQAFFSPANLTALRELAMQEAADRVDSSLREARAARGESNLPLRRGVLVAIDGGGQSEYLVRVARRIAERRDAPWTVVTVQGRRQDEATRREIDAAFALARRLGGDAELLHGSSIADALLDHAAHNGVSTLVLGRTRERPLARMFNRTLTQQLIQRGAHYEITIISTPQARARSRREGLLPPMRGISYEPVQALIATALACAVAWLAERWVGMADLSMVFIVAVVLVAARTRASVAVMAAILCFLAYNFLFIAPRFTFAIGARQGVITVFLFLAAALVAGRLASRLRMQVIALRAANRHARARQQLGRQLASAAGNGEVAQAGRHALEQAMDVPAWLRIGADTATGGRSQPGDTDLAAADWALRHGQPSGRFTDTLAGAQWWFLPLLDGEDRAIGVAGLYLPGAQARLLPEQRQLAEAMVDDIAQAALRTRLVAELEQAHVSNETERLRSALLSSVSHDLRSPLAAMIGSADSLASYGAAMDTADRRALLDTILVEGERLDRYIQNLLDMTRLGHEGLKINRDWIGVDELIGSAARRLQRYQPKVRLELDIPATLAPIWVHPALVEQAVFNVMENAAKFSPPDAAVQVQARELDGQLRIDVIDAGPGPIDDERARIFDMFYSVERGDRGRHGTGLGLTICQGMVGAHGGSVQALPGRDGRGTLIRITLPLLKPASHDEPDSD	19~~KdpD (4.95346E123)~~229;X;251~~Usp(1.90056E-31)~~370;X;395~~DUF4118 (0.00000000206816)~~491;X(159);650~~HisKA (0.000000000160418)~~716;X;770~~HATPase_c (2.29384E-22)~~872	KdpD protein
Disagreement between HMM and CDD prediction	0.002	27.7	5.7	0.0029	27.2	4	1.2	1	A0A0A8F069_9ACTN	Osmosensitive K channel histidine kinase-like protein	GZL_08791	Streptomyces sp. 769	248	1262452	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	>tr|A0A0A8F069|A0A0A8F069_9ACTN Osmosensitive K channel histidine kinase-like protein OS=Streptomyces sp. 769 GN=GZL_08791 PE=4 SV=1MLRYLTRDQVALAAALVLPPAVCALLLPFRDRMSNTNAALVLVVVVVAVAVLGHRPAGALAALSAAVWFDFFLTRPYERFAITKSADIVTAVLLLAVGVAVSQLAARTRELKVIAITDDDYLAQIHHTARLVESAAGPDAVVDHVRRQLVGLLGLSGCRFEYGTLIGHPPRLMDDGSIAWGRRHWDVDRDGLPQEEVELRVSRGGRFHGRFLLQGAPGAAPPLAARLVAVTLANQVGAAYESVSPVRA		No DUF4118 detected by NCBI CDD
	0.0021	27.6	7.6	0.0041	26.7	5.3	1.4	1	A0A0C5FSD5_9ACTN	Histidine kinase (EC 2.7.13.3)	TU94_02380	Streptomyces cyaneogriseus subsp. noncyanogenus	857	477245	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cyaneogriseus, Streptomyces cyaneogriseus subsp. noncyanogenus	>tr|A0A0C5FSD5|A0A0C5FSD5_9ACTN Histidine kinase OS=Streptomyces cyaneogriseus subsp. noncyanogenus GN=TU94_02380 PE=4 SV=1MARGKLRIYLGAAPGVGKTCAMLSEAHRRAERGTDCVVAFVEHHHRPRTEVMLHGLEQIPRKEIEYRDTAFTEMDVDAVLARRPRVALVDELAHTNVPGSRNAKRWQDVEELLAAGIDVISTVNIQHLESLGDVVESITGVRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYRPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLNQYRSEHQVFRIWGSRERIVVGLTGGPEGHTLIRRAVRLAEKGAGGEVMAVYIARSDGLTSASPGELAVQRRLVEDLGGTFHQVVGDDVPAALLDFARGVNATQIVLGVSRRKSWQYVFGPGVGATVARDSGPDLDVHFVTHDAVGKGRGLPAAARGARLGRARVVWGWLVGVLGPALLTWMLTGAAVDVGLANDMLLLLTLTVAAALLGGLAPALASALVGSLLLNWYFTPPVRTLTIADPKNIVAIAVFVGVAVSVASVVDLAARRTHQAARLRAESEILSFLAGNVLRGETSLEALLERVRETFGMESAALLERTGETEPWTSAGSAGPRPARIPEEADVDVPVGDHMTLALSGGVLPAADRRVLAAFAAQAAVVLDRRRLRREADRARELAEGNRMRTALLAAVSHDLRTPLAGIKAAVSSLRSDDVAWSEEDQAELLAAIEEGADRLDHLVGNLLDMSRLQTGTVTPIIRETDLDEVVPMALGGVPEGSVELDIPETLPMVHVDRGLLERAVANIVENAVKYSPPGEKVLVSASALAGRVEVRVVDRGPGVPDAAKDRIFEPFQRYGDAPRGAGVGLGLAVARGFAETIGGTLDTEDTPGGGLTMVLAVPTAARORPDRPAAAATRGOEPPGAAGRP		KdpD protein

	0.0021	27.6	9.5	0.0047	26.5	6.6	1.5	1	R4LLR9_9ACTN	Histidine kinase (EC 2.7.13.3)	L083_3149	Actinoplanes sp. N902-109	827	649831	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	>tr|R4LLR9|R4LLR9_9ACTN Histidine kinase OS=Actinoplanes sp. N902-109 GN=L083_3149 PE=4 SV=1MARGELRIHLGAAPGVGKTYTMLEEAHRRAERGTDVVIGLVETHGRKHTEAMIGELEVIPRTQLRYRGAGFTEMDLDAVLARRPELAVVDELAHSNVPGARNAKRWQDVQELLAAGIDVLTTVNVQHLESLNDVVAQITGVEQRETVPDAVVRAAEQVELVDMTPEALRRRMAHGNIYQPEKIDAALGNYFRAGNLTALRELALLWLADKVEDQLDKYRADHKIDTRWETRERVVVALTGGREGGTLIRRAARIAARNKGADLLAVHIARNDGLNGADPAALSRQRVLVESLGGSYHQVVGADVPQALLDFARAVNATQIVLGASSRGRLAQLFTAGVGVTTTALSGTIDVHLVPHERAGAGRRAGRVPAALSRRRRVAGLVTVLAGLPVLTALLSIGAGLTLANDILVFLAAVVAVSLIGGLWPALIAAAVAGSMLLNYFFTPPVRRFTIAEGENLLALGIFVVVALAVSWVVDTAARKTRQAAQAGADAQTLATVAGSVLRGDRPLIALMERLAEIFALRSVTLLDKRMRTALLAAVSHDLRTPLASAKASVASLRSGDVDFDEQDRAELLETADVSLDRLIRLVTNLLDMSRLQTGALGVSAEEIVPRALDDLGPAGRTVALHIPDDLPLLSADPGLLERVLVNLSANALRHSPPGHPPMITASTLGSTVEIRVVDRGPGIPEDRWEDVFAPFQRLGDRDNHTGVGLGLALSRGLTEAMGGTLTPEATPGGGLTMTVSLPTAEPR	1~~KdpD (5.08749E-119)~~211;X;233~~Usp(8.2928E-19)~~355;X;385~~DUF4118 (0.000000010335)~~479;X(124);603~~HisKA (0.000000000001891 01)~~669;X;720~~HATPase_c (7.61255E-22)~~821	KdpD protein
	0.0022	27.6	11	0.0041	26.7	7.6	1.4	1	B0VM40_ACIBS	Histidine kinase (EC 2.7.13.3)	kdpD ABSDF1600	Acinetobacter baumannii (strain SDF)	884	509170	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter calcoaceticus/baumannii complex, Acinetobacter baumannii, Acinetobacter baumannii (strain SDF)	>tr|B0VM40|B0VM40_ACIBS Histidine kinase OS=Acinetobacter baumannii (strain SDF) GN=kdpD PE=4 SV=1MQSNRENQAEALLNHVNRYQAGRLTVFLGAAPGVGKTYAMLARAKELFQQGTDVVVGIVETHGRIETLKILEGLPQIARKEMQYQRHTLEEMDLDAILLRHPQIVLVDELAHRNVPNSRHERRWQDVNELLDAGIDVFTTINIQHLESLNDVVYQITGIRVNETVPDRVFDRIRDIRLIDLPVSELIERLHQGKVYVPEQANLALQGFFSISNLTALRELAMQCVAEHVDSDLKESYASKGLKSISLQNELMIAIDGQGSSEYLVRAGCRLAERNGAIWTVVNVARSLDFGQSSGNSYKKEYIEIDRAFELARQLGGRTEVLYGHRVASVLMDAAVDRGISNLVIGKSISPWWLKLFKKNLAQQLLNQENSIALTILHPEQGTKKINQLEKPSFLSLKESVFVLAVTCASIFIAHFAEVLFGIEDFSVIFIISVLIVATKTRMLAAVVAAICFLAYNFFFIAPRYTFQISAHQGVVTVVAFFAAALIAGRLASQLRQQVLSLKAANAYTTVMQDLARKLSSAVNLEEVMQTGRMTLETQLQTKVWISIRDKVISSDIELNDKEKVTAEWCLKHRQPCGRFTDTLSQSNWCFLPLLEQKNSLGIVGIYFKDELVSLNFEQKKLTESVIEYIAQAVLRTQLVDELEQAKVISETERLRSALLSSVSHDLRSPLASIIGAADTLAHFKAEMTEQDQQDLLETIHLEGERLDRYIQNLLDMTRLGHEGLTLKRDWVGVDELIGSATRRLKRYKPDTQVVVQLPEQQISLYVHPALVEQAIFNVLENAANFSPPDEPVMIRAQLSSEDEVKIEIEDRGAGIPEDERHRIFDIFYTMERGDRGKFGTGLGLTIVKAIIGAHMGTIEAFSGRQNKGTLIQIKLPLHPVKE	22~~KdpD (3.59125E-117)~~229;X;251~~Usp(2.05575E-24)~~377;X;401~~DUF4118 (0.000000012037)~~499;X(155);654~~HisKA (0.000000000000941286)~~720;X;774~~HATPase_c (4.76603E-21)~~877	KdpD protein
	0.0024	27.4	16.7	0.0056	26.3	11.6	1.7	1	K9WFN6_9CYAN	PAS domain S-box	Mic7113_2785	Microcoleus sp. PCC 7113	1916	1173027	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	>tr|K9WFN6|K9WFN6_9CYAN PAS domain S-box OS=Microcoleus sp. PCC 7113 GN=Mic7113_2785 PE=4 SV=1MLKVIRSQPRAYVIAFLAWAIALGLTWVLEPLMSPTIFALFYPAVMVSSLYGGLPSGLLSILLAALATKYFFLPPLYSLAFTSASNLFRFTVLLLVALMISLVSTELLRAKQRMELSLSRLRRSEEQYRLIVETTNEGVWLVDEQARTTYVNAQMARLLGYSIQDMLGRSAFDYIYEKDRAEAERLMERRRQGISEELEFCLRCQDGSPIWVNCNVNSMLSDNGKCFAMLAMVTDVTERKRTEKRQRVQYAVTRILAEATTLADALPTILQSLCESLGWQVGMIWSLDRQGNLLRFVESWHTPTINVEEFTQINQQATFAPGIGLPGRIWASGQPAWISHLVEDNNFPRVELAAKAGLQGALGFPIRLDHEIVGVIECFSDTVQEPDQDLLQMMMSIGSQMGQFMERKRSEEALAENQALFLSFMNNIPGTAFIKDEQGRYLYTNPVAEKLVNCPPQALVGKTDFDILPTEVAQQVRENDRAVLAADEPKEIVEALPQEDGIHYWMSLRFPFKDGSGKQRLAGMSFDISDRQRAEDQIGTLNKDLNRRVNELQTTLDVIPMGIGIALKPDCRDIRMNPAFAEWLKLPSYTNGSTSQPNAEQLPYRVYRQGQELPPQEQPIQYAAAHGVIVRNVEIEIVHDDGRVLHLLANAAPLLDEEGQVRGCVGAFLDISERKQAEESLRASENLYRTLSEAVPDFIWSCNAQGQLDFVNSRWLEYAGMTVEDMNTGGFEQVYHPEDLSGAMEQWNQAIYQGEPFETESRFRGKDGVYRWFMVRAVPLKDAQGNILKWIGVTTDIHERKQTEEALSQSEERLRVALKHSPISVFNQDRELRYTWKYGSDFEDEVEDILGKRDIDLLTGADAEILTQIKRQVLETGMGTRQEVKISLHGQDWYYDLTVEPLRDAKNQIIGITCAAIDISERKQAQMKLQKSETVLHAFLASSPVGLAFLDRDLRYIHANQALAAINGIPLSEHLGRTLGDVLPQWAPQLAPILHRVMQTQEPLLNQEISGELNQPGVHRHCLVSYYPVCLPDGQVLGVGVTSMDVTQSKRVEQALRESESLFRRMADGAPVFIWMSGLDGHCTYFNQPWLDFVGQTLEEAVTLGWPDGIHPDDTEYCLETYLSAFNARQRFQIEYRHRRQDGEYRWLLDEGVPLFNEEGRFAGYIGSGIDITERRQTEKAQHYLAEASRVLSSSLDYQTTLASIAQLTVPELADWCTVHLIAEDGSLQPLVTAHVNPAKIAWANQNNQKYPVDPNDVRGVAQVLRTGQSEFYPDIPDHLLVEAARDQEHLQILREVGFKSVMIVPLLTRGRTVGTISFVAAESGRQYDSTDLALAEELARRAALAVENARLYQQAQQARQTAEQAADVTARLQSITAAFSEALTLDQVAEVVVNQGIAALGVSAGFVALLTDNDTSLEIVKSVGLPEHVIEDWKSFSITAPVPMAELARTGQPIFLENIAACPTQYPIVACVAKSTGYQAFACIPLTVEGRTLGGMSFSFACATSFSPEDRAFMLTLGHLCGQAIARARLYEAEQRARTEAEAANRIKDEFLAILSHELRSPLNPILGWTRLLRSRKFDEKATDRALEIIERNAKLQTQLIEDLLDVSRILRGKLVLNESPVNLVSTIEAALETVRLAAQTKEIQIQTVFEANAGQVSGDANRLQQVIWNLLSNAIKFTPSGGRVEVRVEQVGSQVQIHVQDTGKGISPEFLPYVFEYFRQENSSTTRQFGGLGLGLAIVRYLTELHGGSVHAESLGEGLGSTFTVTLPLMGTQAEVIPEPMPSRGAADLDGLRILMVDDETDIRELVAFILQQSGAEVTVAASAEEALAALNQSVPDVLLSDIGMPDLDGYMLMRQVRTFSAQQGGQIPAIALTAYAGEYNQQQALQAGFQLHISKPVEPEELVRAIARLVGRG	(0.00000273288)~~105;X;135~~PAS (1.23918E-15)~~236;X;259~~GAF (3.509E-17)~~406;X;433~~PAS (0.000016853)~~520;X(112);632~~PAC (0.000183531)~~674;X;696~~PAS (2.48944E-14)~~797;X(273);1070~~PAS (1.11647E-15)~~1172;X;1185~~GAF (7.32048E-14)~~1353;X;1383~~GAF (0.000000000000205929)~~1527;X;1546~~HisKA (0.000000000000113426)~~1610;X;1665~~HATPase_c (6.1785E-32)~~1769;X;1797~~REC (3.22523E-23)~~1912	non-KdpD DUF4118 protein
	0.0026	27.4	10.1	0.0042	26.7	7	1.4	1	Q2SJ20_HAHCH	Histidine kinase (EC 2.7.13.3)	HCH_02554	Hahella chejuensis (strain KCTC 2396)	527	349521	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Oceanospirillales, Hahellaceae, Hahella, Hahella chejuensis, Hahella chejuensis (strain KCTC 2396)	>tr|Q2SJ20|Q2SJ20_HAHCH Histidine kinase OS=Hahella chejuensis (strain KCTC 2396) GN=HCH_02554 PE=4 SV=1MLRNYCVLKDINAHFKPKDFWLATLIMLGAMLASLVITQVLAHPNVLLVLFLGVLAAGVKTSVWPALWSALLGFFAYNYFFTHPHYTLKVTHSEDLLTIIFFLLVSTISGNLAVRLKEQVLAIRESKREVEDLLSLSSKLSLAPDRRSIMEVALKEMAKLVSAPVLAFEKGLVEQGSALDARGEPFALPASELALARRIWEQSASDSSSARTSPEQPSQYKWLPVCSEMGVLCLLGVPDGAYKALDWELHNRISNLTQQLKLSLLRTKLNEELEEVRFQAETERLRAALLSSVSHDLKTPLAAMIGSAGSLLQYHDRLSDEDRKELMETTLQEAERLDRYIQNLLDMTRLGYGALKLHRDWTSLHDIVGAAVKRLVNELKPLKVNIELAPDIPLLYVHAALLEQALINILENAAKFSPEGGRIDILASVESTSLIIDVIDQGPGIPPEEREQVFNMFYSVTKGDRKPSTGLGLAICHGMIGAHGGSVEALDGKDGRGADIRIILPVDPQPESDPDGALDGDPAEGAE	64~~DUF4118 (0.000000167127)~~119;X(164);283~~HisKA (0.000000000000333 63)~~349;X;402~~HATPase_c (1.10629E-25)~~504	non-KdpD DUF4118 protein

	0.0026	27.3	6.8	0.005	26.4	4.7	1.4	1	Q0W6L0_METAR	Predicted signal transduction protein	RCIX576	Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	992	351160	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanocellales, Methanocellaceae, Methanocella, Methanocella arvoryzae, Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50)	>tr|Q0W6L0|Q0W6L0_METAR Predicted signal transduction protein OS=Methanocella arvoryzae (strain DSM 22066 / NBRC 105507 / MRE50) GN=RCIX576 PE=4 SV=1MRNCSYRVVRGDVVADKLSFRLSGKYKELILGSTLVITIFLAIYINLRLGIEIVYTHLFYVPIILAGVWYHRKGVLI AVFLGLLHIYLGWLAYNTIMPEPVIRALIFVIIAYVIGTLSERKDQLHDDLAESRAKLSESLRQLSNVIEFYPDATLIIDN NGRVVAWNKAIEDMTGVKAADMIGKGDNEYAVPFYGYRRSFLLNLVNLTADDLRDRYTDISVVNGRFEAVTADAT LKGRKVILHCTASKLYDDSGNVIGAIESIRDVTAQKKMEAELQQQYASLTAQHELLQQQTAEINRQNVELTRVHGLL KESEENYRAITTSVNDCILTTDLTGTCTYLNPRVTELTGYAPDDILNTPVNNLVAEESGEIVSSILSSVSRDERRSVEI WIHAKSGKKMLIELNTSIICDAAGNPVGIVGAFRDITERKLAEEKLIELSRAVEQSPSIVIITDARGKIDYVNPKYTQVS GYTLEDIKGYDPHKINAASLTSEQIQERNRALRQGNYWRGELSKRKKNGELYWVSASVSPVRNKDGEIIRYVDVE EDITERKMVEVALKHANDELVKANEVLENRVLERTEALTHAHNTLEAIMQNIQIGVVVVQRETGEVSYYTTKAMEIL SGPVMGIASPGRNRPYEFLKPDGSVLPDERQPLYRSLQHGENVRNEEVLIRRKDGSTVTVLMSSTPIVDPEGKVV SAVVGMLDITDRKRAEQAAGESQEKFRSIAENINDWIWEADENAVFTYSSPKIREILGYEPEEVIGKKLYDLMYPDE AKRFKKAIDLLYFTREPFTYLRTTLIGKGGTLATLEYSGRPIFDKAGTFRGYRGVSRDISERKRSENALLRSEARMK ALMSAAPGTIILVNKVGHFLDCKVEAGNHLFPKPDDIVAKNAYEVLPIDLARILIFNVNRALKTGKPQTFEYQFDAAG QTWYQKASCVACGGDEAIVFVQDNSPEDQKRATAAEPETRQEGRKPGPASRSRPQPDSEPGSSL	25~~DUF4118 (0.0000000387462)~~120;X;150~~PAS (0.00000234972)~~265;X;328~~PAS (0.000000000728995)~~425;X;445~~PAS (0.00000000099021)~~547;X(182);729~~PAS (0.000000000002082 31)~~832	non-KdpD DUF4118 protein
	0.0026	27.3	9.8	0.0045	26.6	6.8	1.4	1	E1VQU2_9GAMM	Histidine kinase (EC 2.7.13.3)	kdpD HDN1F_36010	gamma proteobacterium HdN1	903	83406	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, unclassified Gammaproteobacteria (miscellaneous), gamma proteobacterium HdN1	>tr|E1VQU2|E1VQU2_9GAMM Histidine kinase OS=gamma proteobacterium HdN1 GN=kdpD PE=4 SV=1MSSEQSIQANALLGEIRRQSGGRLTVFLGAAPGVGKTFAMLTRARELLRQGVDVVAGIIETHGRSETLALLD GLPVLPRKKLEYKGRWLEEMDLDGLLARRPAIALVDELAHSNVPGSRHEKRWQDVEELLDAGVDVYTTINVQHLE SLNDVVHQITGVRVSETVPDVVFSRLRDIRLVDLPARELIERLNQGKVYLPEQASQALQAFFSPSNLTALRELAMQT VAGHVDADLRETRMARGLENISIQHHVMIAIDGQGHSEYLVRAGARIAERRAASWSVVTVETGRAAIATLQVNDLE RAPRAHDPAARAEQQRLSEIDRAFALARNLGGETEALHNTDVTQALLDAAAVRNAKTIVIGRTRERPIARLFNRTM TQQLLQRGARYELTIISTPQMPARTRDWPLASHLRLPGRETLLILVASLGAVGIAAIAERYLDLQDLSLIFLVAVMLVA SRTRMLAAAIAAVLCFLAYNFFFIEPRFTLLISAHRGVATVLLFLAAALIAGRLASQLRMQVVALSAANTHTTLLQKLG HGLASAADLGQVMTAGTAVLQNTLSAQAWIRIDATRIPADLTFTEKDLMAADWTLQHGRECGRYTDTLGNCPWW FLPLQTDGNSFGVIGLKFPESAGRPTFEQRRLAESMVTDIGQAALRTRLVSELEAARVGGETERLKVALLSSVSHD LRSPLSSIIGSADSLVCYGKDMSEEDRQSLLEAIRLEGERLDRYIQNLLDMTRLGHEGMTLVRDWIGVDELVGSAS RRLQRYQPEVRIECSIPEDLPPIHVHPALIEQALFNVMENAARFSPRDEPVIVNVSGEPGAHLQIRISDAGPGIPEAE RSRIFDMFYSVERGDRGTQGTGLGLTIVQGIIGAHMGSVEALPGPDGRGTTIRLTLPWGHFPHRS	22~~KdpD (1.23489E121)~~229;X;250~~Usp(2.00488E-26)~~393;X;418~~DUF4118 (0.00000232402)~~483;X(188);671~~HisKA (0.000000000417354)~~737;X;790~~HATPase_c (2.54308E-22)~~894	KdpD protein
	0.0027	27.3	9.7	0.0055	26.3	6.7	1.5	1	K9PNP9_9CYAN	Multi-sensor hybrid histidine kinase	Cal7507_4004	Calothrix sp. PCC 7507	1230	99598	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix sp. PCC 7507	>tr|K9PNP9|K9PNP9_9CYAN Multi-sensor hybrid histidine kinase OS=Calothrix sp. PCC 7507 GN=Cal7507_4004 PE=4 SV=1MPHINNSQLRSYGIAVLVVAVALALMLMLDTWLGMSSTPFLLFFSAVMVSAWYGGWKSGLLATFLSVILSHY FFLAPTHHLTINLPNLVRLGLFASQGLLFSFLCEALRTAKRRTEVNLQKLKVSEARFRLALTSSDIFVFQQDRDLRY QWIHNSQGEDVAEALGKSDYELFPPTELEQLIAIKQKTLETGVSNREKICLTVRGEVRYYDLLVEPLKEMGDVQGII CVAVNITQLKQTEQALRESEAKFRSVVESNMIGIGFWERDGKITGANDALLDVLGYTLEELVNEKLNWVDLTPPEY LSLDEQALTQLQDSPFLTPFAKEYIRKDGSRIPVLVGGSHFEGTVDRGAFFVLDMTERHQAEDALRESEERFRAM FNQAAVGISLVGLDGQFLQINRALCEITGYSAAELMQMNFREITHPDDLAVDLSYARQVLAREMSGYSLEKRYIRK DGSTVWVNLTSSVVWDANGQPKYALGIIEDISDRKQAETAQQFLVETSTLLAASLDYEVTLANVANLAVPTLADFCI VDIFRADNSIQQIAIATADPLKKQTLQELRRRYPPNTEQEHYFLPKLQQGQSVFYLQVSDSFLTELAQDEEHLQLLR SLGVRSLMVIPLYSRQQLFGAISFVTAESSRFYGQADLALANDIARRAATAIDNARLYQETQQAKQAAEKVVSRIMR LQKITAAFSEALTPQEVADVVVSQGIAALGATSGSVVLLADGDTSLKVVKAIGYPQSIINVWTSFPLKADVPIAETVR TGQSIFLENPEALISKYPSLENSVEITNNQAFASIPLIVENKAIGALGLSFATAQVFSQEDRRFMLTLGQQCGQAIAR AQLYEAEKTARAEAETANRIKDEFLAVLSHEIRTPLNPILGWAKLLRTRKHDAATTLLGLETIERNAKLQTQLIEDLLD VSRILRGKLSLNIYAVDLKATITAALETVRLAAEAKSIQLQIALSDNTVQVMGDGNRLQQVVWNLLSNAVKFTPTGG RVEVSLLQIENDAQIQVIDTGKGITPEFLPHVFEYFRQADGKTTRVFGGLGLGLAIVRHLVELHGGTIEAESPGEGQ GATFKVRLPLLKNANLPDESIESPICTEDSILCGVQILLVDDQADVREFFSFALEQYGAIVKTVASASAALKALAESK PDILLSDIGMPEMDGYMLLREVRKWSVAEGGQIPAIALTAYAGEIDHRQALAAGFQKHIPKPVDPIELAVAIANLLGR K	41~~DUF4118 (0.0000907261)~~114;X(145);259~~PAS (0.00000000448039)~~355;X;381~~PAS (4.68165E-16)~~484;X;494~~GAF (0.000000000006912 97)~~671;X;685~~GAF (0.000000000001106 62)~~851;X;858~~HisKA (0.000000000000314 061)~~922;X;977~~HATPase_c (1.58268E-33)~~1081;X;1111~~REC (2.48827E-23)~~1227	non-KdpD DUF4118 protein
	0.0027	27.3	12.6	0.0042	26.7	8.7	1.3	1	E3H9C3_ILYPC	Uncharacterized protein	Ilyop_1251	Ilyobacter polytropus (strain DSM 2926 / CuHBu1)	405	572544	cellular organisms, Bacteria, Fusobacteria, Fusobacteriia, Fusobacteriales, Fusobacteriaceae, Ilyobacter, Ilyobacter polytropus, Ilyobacter polytropus (strain DSM 2926 / CuHBu1)	>tr|E3H9C3|E3H9C3_ILYPC Uncharacterized protein OS=Ilyobacter polytropus (strain DSM 2926 / CuHBu1) GN=Ilyop_1251 PE=4 SV=1MKSKTFNCFIESLLYTTAVYLVFFHFSSFKYSFLAMNLHPLLIVIAVISLKYGTYMSGFVVSFSIIYYILAYIGLGR DMIIFFSSFEYYKFILMFFFTALFLGKLRDTTDQKIMHLEGEVSKTREDYEKQKENNVKLITINSRLKKRIISSRESIVT LNQIKSSFANMNVEQIYTEAILVMRQFLESDVVSIYSFNHEKNFMRLKLRAGNGRIPGFLQVKKDSVFDEVIKAGAP MEFPLDIEGDSPIFVSPIKNNDEILGFINIERMSLEASERYSYEMFKIITHWLNEALSEAFVKEEKEIKENYLKDTKIFT MGYFNKIMSEEERRKKLLGMDFMAFETKIEGVTPDEVAEMIKGKVRESDFMAMDDNKLRILFPATTAASKELLMEK IASLFHGIEVDFYEI	9~~DUF4118 (0.0000000480729)~~107;X;169~~GAF (0.000000000497033)~~291	non-KdpD DUF4118 protein

	0.0027	27.3	6.6	0.0047	26.5	4.6	1.4	1	A0A0F7CQ87_9ACTN	Osmosensitive K channel His kinase sensor	SXIM_45970	Streptomyces xiamenensis	869	408015	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces xiamenensis	>tr|A0A0F7CQ87|A0A0F7CQ87_9ACTN Osmosensitive K channel His kinase sensor OS=Streptomyces xiamenensis GN=SXIM_45970 PE=4 SV=1MARRGTLRIYLGAAPGVGKTYAMLSEAHRRAERGTDIVVGFVETHDRPRTEALLRGLETVPRRPPPGAGRGEMDTEAVLRRAPAVACVDELAHSNAPGSRHDKRWRDIDTLLDAGIDVISTVNIQHLESLADVVAAITGVRQRETVPDAVVRRADQIELVDMTPEALRRRMAHGNIYAPDKVDAALSHYFRPGNLTALRELALLWTADRVDAYLQRYRTEQGIRSTWYARERIVVVALTGGPEGSTLIRRAARMAAKSSGGEILAVHVSRADRLTAVSPRELASQRTLVEQLGGTFHHVIGDDISSALLDFARGVNANQIVLGSSRRKTWQYAFGPGVGASVARDSGPDLDVHIVTHAEVARGRGLPNARGARLGRSRTVAGWLIGLAGPPLLTVLLAAPPRPLAEFASDVLLFLSVTVLAALVGGFYPGLVSAALATLLLDYFFTEPLREWGVGSGHDVITVVIFFAIALAVASVVDMSAQRTQQAARLRAESETLTVLAGSVLRGEDTLRALLGRARETFGMDCAALLERDHDGGRWRCVGSVSAIADNPRPLLRPQDADVDVPVGEHTMLVLSGRVLPAEDRRVLSAFAAQAATILDRQRLLTEAARAHKLAEGNRIRTALLAAVSHDLRTPLAAIKASVSSLRSDDVEWSPQDRAGLLESIEDGADRLDQLVGNLLDMSRLHTGTVRPLIRRTGLDEVVLRALAGVPVDVVDLDVPESLPWVAADPGLLERSVANIVENAVKYRPPDTRVLVRGSALGNQVELRVVDRGPGVPDADKGRIFEPFQRHGDIPRGNGVGLGLAVARGFTEAMGGTLDAEDTPGGGMTMVLTLPTDIPAPAAAGAGAPAERESEQGEQGGAHAPGTRGR	2~~KdpD (4.45641E-115)~~210;X;232~~Usp(3.7972E-29)~~355;X;382~~DUF4118 (0.000000836932)~~478;X(139);617~~HisKA (0.000000000000103023)~~683;X;732~~HATPase_c (5.61304E-24)~~833	KdpD protein
	0.0028	27.2	3.6	0.0043	26.6	2.5	1.2	1	A8MGT1_ALKOO	Histidine kinase (EC 2.7.13.3)	Clos_1078	Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	465	350688	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Alkaliphilus, Alkaliphilus oremlandii, Alkaliphilus oremlandii (strain OhILAs) (Clostridium oremlandii (strain OhILAs))	>tr|A8MGT1|A8MGT1_ALKOO Histidine kinase OS=Alkaliphilus oremlandii (strain OhILAs) GN=Clos_1078 PE=4 SV=1MNKDKKSKIVIILLLLLITILHYSTRLRPWGIHDFYRRLYYIPIILAAFKFRLKGGFIVSTLVVLIYAPHLLTYFGELNIEVINQFLESGMFMIIGLITGYLVEQDYKRGKALEHQVIKIANLENYTHNILESIDSGVMAFEANGSLQTINRHIEKILGSKEEVNRFLAQEDIIKQINRVLFGKEKVIKQELRYTKGKDHEIYLEITIYPIINTSKVQEGAVVVVQDVTIVKRLEAEVKRGERLAAVGQLASGIAHEIRNPLGIIKTISQTINQDIKDEEIKEGLDIIQHEIDRANKVIKGILDFARPNKIQDCKIDLEKLLNELVMVTRKFAQQQNVDLRFNILKQNKIQGDPDKLKQAFINIILNGIQAMKDGGKLEITLEESDKKWAVISFKDEGEGISDELLDKIFNPFFTTKESGTGLGLSITHSTIEEHNGKIEFNSKLGEGTNVKVYLPLMDKEDTNE	27~~DUF4118 (0.0000753113)~~103;X(141);244~~HisKA (0.000000000004461 93)~~307;X;357~~HATPase_c (3.46063E-22)~~455	non-KdpD DUF4118 protein
	0.0028	27.2	10.6	0.0028	27.2	7.4	1.6	1	C5AQE2_METEA	Putative transmembrane histidine kinase, putaive HK and ATPase domain but no sensory domain detected	MexAM1_META1p4572	Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	338	272630	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium extorquens group, Methylobacterium extorquens (Methylobacterium dichloromethanicum) (Protomonas extorquens), Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	>tr|C5AQE2|C5AQE2_METEA Putative transmembrane histidine kinase, putaive HK and ATPase domain but no sensory domain detected OS=Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1) GN=MexAM1_META1p4572 PE=4 SV=1MPSFLALAAGRLPAPPWFGDVAALGATGIAIALRHALDDVLPPGFPFLTFFPAVILTTFFFGLRPGIVCAVLSGLAAWYFFIGEANVFLFDAQTALALGFYAFIVTVDITLIHLMRVAGERLNAERAVSAQLYEQQRTMFQELQHRVANNMQFVAALLALQKRKVIDNPQEAADVFDEAQARLQTIARIHRRLYDPARADQPVGQYLQELCSDLLDATGARNIVCLVDAPPVRLDLARLTTLSLLVVEVVTNALKHAFHGTERGTITIRFETLGAGQASLSIADNGPGIPATFDPDTSRSLGFRIVQGLAGQLDGTLTYANEGGTVVRLVFVTGPTDA	21~~DUF4118 (0.0000159062)~~107;X;142~~HWE_HK (5.06288E-21)~~217;X;242~~HATPase_c (0.000000000000303 29)~~331	non-KdpD DUF4118 protein
	0.0029	27.2	10.6	0.0063	26.1	7.3	1.5	1	B2J1Y5_NOSP7	Multi-sensor hybrid histidine kinase	Npun_R3591	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	1039	63737	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	>tr|B2J1Y5|B2J1Y5_NOSP7 Multi-sensor hybrid histidine kinase OS=Nostoc punctiforme (strain ATCC 29133 / PCC 73102) GN=Npun_R3591 PE=4 SV=1MKGTRSLLAPYAVALLAVGSALLLTLLLQPLLKPTIFLLFFAAVAVSAWYGGMEAGLLATALSTLTVSYFFLEPVFSLSVASLDNIRRLGLFVLVTTFITLLNSELRTAKQHLQMSLQKLKVSEAKFRRLVESNIIGIIVANMDGAIAEANDAFLRMVGYSQEDLLAGRVRWRDMIPPKYIEANNSAIAELKAKGVCQPFENEYIRKDQNCVPILLGSALLENNSNDIISFVLDLSERKQVELALCQSEERYRAFLEQSSEGIWCIELEVPISPDCPEDEQIQHFYQYVYLAECNNVMAQMYGCSRAEEIINARLGDFLIPSDPHNIAYLRNFIRSNYRLIDAESHEIDKQGNSKYFLNNLVGIVENGLLVRAWGTQRDITERKQAEAALNQQEEQLRLITNAVPVQISYVDIQQLYRFNNKGYEDWFGLPASEIYGKHIREIMGESVYQSILPYVEAVLSGEEVTYETQLPHKDGTHHYINVSYVPQFSEQGKVEGFVALITDITLHKLAEAALKQSEKRLKTLTEKVRIIPWEVNATTGNFTYVGPQTVEILGYPLSDWYIDDFWQKHMHPEDREWAIQYCQESSLSLNNYEFEYRMLAADGRVVWLYDIINVVRDENGPQLLHGFMLDITDRKQAEQEREQLLEREKAARADAESANRMKDEFLATLSHELRTPLNAILGWTQLLRNRKFDEATTARALETIERNTKSLAQLIEDVLDVSRIIRGTLHLSIHRIKLVPLVEAAIDTVRPAAEAKEINIKCKFDPEVGIVVGDTNRLQQVVWNLLSNAVKFTSKGGSVDVQLERIESSVQIRVSDTGVGIAAEFLPHVFERFRQADSSSTRSHGGLGLGLAIVRHLVELHGGTVSVESLGVGQGATFIVNLPMKAVYVEANTAEQPSSLVDVPEANNYLPRLDDLRVLIVDDEADARHLLTTILGQYGAQVIAAASACEALALQQFRPHILVSDIGMPQQDGYALIRQVRALPTDQGGRIPAVALTAYARAEDRTQALLAGFQLHVPKPVNPSELAVVVANLTGRT	24~~DUF4118 (0.0000000133202)~~120;X;148~~PAS (9.84781E-16)~~250;X;282~~PAS (0.000000000002918 72)~~378;X;441~~PAS (1.74074E-14)~~544;X;552~~HisKA (2.32374E-17)~~617;X;671~~HATPase_c (1.54707E-30)~~786	non-KdpD DUF4118 protein
	0.0029	27.2	12.6	0.0051	26.4	8.7	1.4	1	K9ZLX8_ANACC	Histidine kinase (EC 2.7.13.3)	Anacy_4201	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	793	272123	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	>tr|K9ZLX8|K9ZLX8_ANACC Histidine kinase OS=Anabaena cylindrica (strain ATCC 27899 / PCC 7122) GN=Anacy_4201 PE=4 SV=1MKSAMNARIDQRFFPYIGAISSLAIAMLAVGTALFITWQLKSVLTNTIASFFFVAVAVSTWYGGLRLGLMTTILSVLTINYFFIPPIYNFTPATWNDFILLGLFFANSSIISLLSYDLQRSKKTLEQINQQLLGESTQRYASLAAAVPVGIFRTNLVGHCLYVNEQWCKITGMTFDQALGTGWVQALHPSDRDRIIQAWSQTTQNQEKSITVEFRFLRPDGVVTWVFTQAVVEQTNNGEVISYIGTVTDISESKQREEQLRLLESVIVTTNDAVLITAAEPIDLPGPKIVYVNPAFTQMTGYTSAEILGKTPRILQGEKTERAALDKIRANLQTWQPVQVEMINYRKDGSDFWVELNIIPVTDERGWFTHWIAIQRDITDRKQAETTLKLANVKLESRVALRTIELSQANAQLQLELKERQRAEVALRQSEAKFRSLSEFSPMGIFMNDAQGQCIYTNPRAQEIAGYTFAEALGFGWLEFVHPQDRKQITPQWIQAFSEQQGTVYEELRYVHKDGTIRYARVQSAPIFAENNKFIANVGTMEDITASRAIAQMKNEFISVVSHELRTPLTAIRGSLGLLAAGVYDKKPEKGKRMLQIASEQTDRLVRLVNDILDLGRLESGKMTLVMQSCDAATLIGKSVDAMQSSAEQNQITLSVNSPPSLQLWANPDAIIQTLTNLLSNAIKFSPPHTTIWINVECCEDIENVSGSSSPHSLVRFEVKDQQGRGIPLDKLEAIFDRFQQVDASDSREKGGTGLGLAICRRIIQQHDGNIWAESTMGEGSSFYFTLKRTGNSE	24~~DUF4118 (0.0000000133202)~~120;X;148~~PAS (9.84781E-16)~~250;X;282~~PAS (0.000000000002918 72)~~378;X;441~~PAS (1.74074E-14)~~544;X;552~~HisKA (2.32374E-17)~~617;X;671~~HATPase_c (1.54707E-30)~~786	non-KdpD DUF4118 protein

	0.0029	27.2	6.3	0.0043	26.6	4.4	1.3	1	A1SMW7_NOCSJ	Uncharacterized protein	Noca_3652	Nocardioides sp. (strain BAA-499 / JS614)	218	196162	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Nocardioides, Nocardioides sp. (strain BAA-499 / JS614)	>tr|A1SMW7|A1SMW7_NOCSJ Uncharacterized protein OS=Nocardioides sp. (strain BAA-499 / JS614) GN=Noca_3652 PE=4 SV=1MSTRSNAGRRRRGILGAMTLPGPSTGTATEAWFRRRPPLTWAAVAAMFVGVFLLRLSGGTVEDAYSMLYV FPVALVAFAFGLRKGAAAGVLAVLLIVVWAVARGVHLDPAGWASRILPILLLGVLLGDASDRLRRNEAERRRLETA ALLHRDAIEINDSLVQGMAAAKWSLEAGDVDTGLRTLNATISEAQELVSGLIRQAGMGGRTERPTESPTDQE	41~~DUF4118 (0.00038406)~~101	non-KdpD DUF4118 protein
	0.0029	27.2	9.9	0.0029	27.2	6.9	1.7	1	C6RQT2_ACIRA	Histidine kinase (EC 2.7.13.3)	ACIRA0001_0651	Acinetobacter radioresistens SK82	886	596318	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter radioresistens, Acinetobacter radioresistens SK82	>tr|C6RQT2|C6RQT2_ACIRA Histidine kinase OS=Acinetobacter radioresistens SK82 GN=ACIRA0001_0651 PE=4 SV=1MTNIQTNKADILLQQVKRHQTGHMTIFLGAAPGVGKTFAMLSRAHELYGQGQNVAIGYIETHGRLETEELVA GLPVIPRKIVEYKNHNLEEMDLDSILQIHPDIVLVDELAHQNIPGSRHKKRWQNINELLDAGIDVFTTMNIQHLESLND VIFQITGIRVKETVPDQILERIRDIRLIDLPVNELLERLNQGKVYVPDQAAHALKSFFNIANLTALRELAIQTVAHHIDID AREQFDVKGLSLTPLNNHVLIMIQGNQNSEALVRIGSRIAERRNAKWTVAAFLTTASGHNPISFETHSTGREIERAL HLARQLGGMTDILYGKNYAGTLYNFACERGISILVLEQESRPLFYSWLRPPLAHQLLKYQLAFELSIVPVQQGKPQ AYRFNRQNYVLNLKELIFVLITTITSILIAKLSVQYLKVEELSLIFITAVIFVAANTRMTAAMLAAILFFFAYNFFFIPPTLT FQISAHKSVITVVAFLAAALIAGRLASRLREQVVALRSANSYNSIMQDLGQKLSVAVDLQQVIEIGQNSLEKSLNVQV WFKLSDETALSSDENLLTEKEKISANWTLKNHQPSGRFTQTLSESAWWFLPLLASKECIGVIGLNISENQREMNIE QRRLAEAMVEYITQAITRTQLSKELEYANISSETEKLRSALLSSVSHDLRSPLAAMIGAADTIATYKSTMTEEDQLTL LETIGLEGERLDRYIQNLLDMTRLGYQGLKLTRDWIEVNELVDTATRRLKRYKPVVEFNIQRLLQELKIYVHPALIEQ ALFNVLENAAKFNPEDQPIDIILSQPDTAHIQFDISDQGKGIDIADREKIFDMFYTMHGDRNPTGTGLGLAIVKAIISA HIGSIKAQIGLKNKGTNIQIVLPVHISQD	22~~KdpD (4.5633E-111)~~229;X;250~~Usp(4.97552E-18)~~378;X;401~~DUF4118 (0.0000169944)~~500;X(157);657~~HisKA (0.000000000399039)~~723;X;776~~HATPase_c (4.73976E-21)~~879	KdpD protein
	0.003	27.1	9	0.0067	26	6.2	1.5	1	Q8YLT6_NOSS1	Two-component hybrid sensor and regulator	all5210	Nostoc sp. (strain PCC 7120 / UTEX 2576)	1558	103690	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	>tr|Q8YLT6|Q8YLT6_NOSS1 Two-component hybrid sensor and regulator OS=Nostoc sp. (strain PCC 7120 / UTEX 2576) GN=all5210 PE=4 SV=1MPNIPISALLRFGIVIFSVALACALMLLLDPWLGMTRTPFLLFFSAVMLSAWYGGFWSGMLGTFLSVILSNYF FFHPRYTLSIDTYNVVRIGLFAVQGWFFSFICETLRNTKKQDVVNLQKLRQSEERFRLALSNSDIVVFQQDRDLRY RWIHNYRGVASAEEIIGKSDNELFPTSVAEKLTAIKQKVLEKDISVHEEVSVIFHGEVVYYDLLAEPLTINGQIQGITC AAVDITERKRSELEKAKLQRKLQKAIQQQDEYLALLNAWLASSPVALAFLDTKLRYVYTNEALAAINGIPQSQHIGR TLREVLPEWATQLEPILQQVMATKEPLINQEVCGVTYPSGVHRCSLVNYYPVCLPDGKLLGVGVTGLDITERKQAE DALRYIAQTSNILSSSLDYEQTLAKIAKISVPQLADWCSIDIINQDGSIRRLPIAHVDPAKAELARLFQEYAPKSGSAS LVAKVLQTGEPLLVADIPDSLLAAATQNEEHLDLVRQIGIKSLMFLPLIAHEQVLGCITFVSAESGRSYNQSDLTLAK DIAYRAALAIENAQLYRDAHQALKHYAESLALLDALLAGAPVAVCFLDKELRYIRINQVLADVNGLSIEEHLGRKFRD VLPKMAEQFEAQLQQVLETGQPLLNLEVSGEALGRPEINSYWLGNYYPVYDSMGKTVGIGIILAEVTATKQVEIAL RESEERFRAMFDQAAVGITLVTLDGQFLQNNQALCDITGYSSEELSQMKFSDITHPDDVEADWVYAKQVLAREIN GYSLEKRYLRKDGTTVWVNLTASAVWNEQGEPKYALGIIEDINERKQAEAAQNFLVEASTLLAASLDYEVALNNVA HLAVPTIADWCTVDILQADWSIKRVAIACIDSAKLDTIEEIRYSYPPGTKGEHPFRDKLLKGESAFYPELPNSILVEM AKDERHLQLLQNLEMRSLMVVPLYSREQIFGVISFVTSISGRQFKQTDLALAEDIARRAATAIENARLYQETQQAKQ AAELAMSRMVRLQSITASLSEALTPQQVADVVVNQGLAALGASAGSVVLLTEGGTTLKIIQAIGYPESVQDAWETF PLTATVPIAETARTGEAIFLANIEEFAAKYPQIANVPSLTGNCAFACIPLIVEQQTIGVMALSFATAQKFNEEQQKFML TLGQQQCAQAIARSQLYEAEKNARAIAESTNRIKDEFLAVLSHELRTPLNPIMGWAKLLRTRTYKEETIKQGLETIERN AKLQTQLIDDLLDVSRILRGKLNLNVCLVDLRNTVQAGLETVRLAAEAKSIEIHTILSDEPVQVMGDGDRLQQVIWNL VSNAVKFTPSEGRVDVRLEQVGRDAQIQVIDTGKGITPEFLPYVFEYFRQADAKTTRVFGGLGLGLAIVHHLVELH GGTVVAESAGEDQGATFTVKLPLHKSADYQVQSAKSAVTELENQDSLLVGVQILLVDDQEDVREFFSFALEQCGA SVTAVASAIEALEALARSKPDVLLSDIGMPQIDGYMLLRQIRKWSPEQGGQIPAIALTAYAGEIDQRQAIAAGFQKHI PKPADPVELAEAIAQLLRRK	30~~DUF4118 (0.0000238698)~~109;X(290);399~~GAF (0.000000000000385814)~~555;X(151);706~~PAS (1.88157E-14)~~809;X;822~~GAF (0.00000000041043)~~996;X;1005~~GAF (0.000000000000235581)~~1176;X;1183~~HisKA (1.43285E-15)~~1247;X;1302~~HATPase_c (1.31124E-32)~~1406;X;1439~~REC (4.98938E-27)~~1555	non-KdpD DUF4118 protein
	0.0031	27.1	5.5	0.0071	25.9	3.8	1.5	1	E8X5D0_GRATM	Histidine kinase (EC 2.7.13.3)	AciX9_2442	Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9)	495	1198114	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella tundricola, Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9)	>tr|E8X5D0|E8X5D0_GRATM Histidine kinase OS=Granulicella tundricola (strain ATCC BAA-1859 / DSM 23138 / MP5ACTX9) GN=AciX9_2442 PE=4 SV=1MNLSFAKFEHAIARRITNPPHVEIARATIAVIITICLSASAFALHLNLASAISILLLATVVASIQWGVIQGTAVSLAA VGCLDFLFTAPLFKFSVHNRENWIALMTFEITALMVSRLSWKERLHAREQEYQRQGISKLYQLSNAILLVDTRSSW LEQLSALLREFFSVESVELWIAPDDRAFSATAEVNAVENAAYRVFAAGDDTDSVEGGWSHRVLRMGTSSIGGMV LQGWEVDPAIADAAGSLIAVAVERARSAQKESHAEAARNTEQLRTAVLDALAHGFKTPLTAIQTASSGLLAIGRLSE IQSELVEIIDQEVGMLAGLTSRLLRTAALDAREIKVRSSQVSLLPLVEGIVMEHDEETRRRIHIASPPVLMDIQADPQL LTLALAQVVDNASKYSTVGSRIDLRFIQDESRTIITVSNQSEPLRKEDLGRIFERYYRGAQAGKGPTGTGLGLSIVKK IAEAHGGDATATCQGNEISISLRLPGGTRLSNG	27~~DUF4118 (0.00000193071)~~122;X(147);269~~HisKA (0.000000321933)~~329;X;385~~HATPase_c (1.37016E-16)~~484	non-KdpD DUF4118 protein
	0.0033	27	11.3	0.0033	27	7.9	2.6	1	A0LU57_ACIC1	Histidine kinase (EC 2.7.13.3)	Acel_1195	Acidothermus cellulolyticus (strain ATCC 43068 / 11B)	609	351607	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Acidothermales, Acidothermaceae, Acidothermus, Acidothermus cellulolyticus, Acidothermus cellulolyticus (strain ATCC 43068 / 11B)	>tr|A0LU57|A0LU57_ACIC1 Histidine kinase OS=Acidothermus cellulolyticus (strain ATCC 43068 / 11B) GN=Acel_1195 PE=4 SV=1MRDSLPAAVALPALFVVSLLFAAFVVAVGGLPADAVTAGEAGIVGWFSFRSQPATAPLLGLLGWFFAASFSA QPFAAIHLSQAPVAAVVLGVVTSTASAAGAVRRRSASRATTNGSADSADGDAGILDDVAMARSAGTRRRPHALAS LSWRRQVLGLLTSAVLLPIATVLLTTTARHALADVALGYLLVVLVVTMIGGVWVAIAAALSAGLLINWYFSPPVHTW TIDAPENIASILLFVAVALSVSFLVHLSARRAQLAEARRREADLLLALAERLLGGDDSPQAVLDELAKETGSPVVLEE RCGGTWVTVAKAGSAAGGNDPQHAAILPAGAALRLVVGVSAESPPDRLLRAYAAQAAAALERQRLRIQASQAEA LAAGNRMRTALLAAVSHDLRTPLASIKAGVSTLRQTDIQWSPSDVAELLSSVDQATDQLDALIANLLDMSRIHTGAV QPFLRPTALEEVAPLALAGLADAERVQLDIPEDLPLIATDPGLLERVLANLVANALRHSPPHLPPAVVARIRGEKVRI DVVDHGPGIPPHARDRVFQPFQQLDDRRGGGVGLGLAVARGFVEALGGEIHVLETPGGGVTMRVELPISAYVPS DIDA	381~~HisKA (0.000000000000895843)~~447;X;497~~HATPase_c (3.53449E-16)~~597	No DUF4118 detected by NCBI CDD

	0.0033	27	1.8	0.0054	26.3	1.2	1.3	1	B1Y7N8_LEPCP	Histidine kinase (EC 2.7.13.3)	Lcho_0211	Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) (Leptothrix discophora (strain SP-6))	671	395495	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, unclassified Burkholderiales, Burkholderiales Genera incertae sedis, Leptothrix, Leptothrix cholodnii, Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) (Leptothrix discophora (strain SP-6))	>tr|B1Y7N8|B1Y7N8_LEPCP Histidine kinase OS=Leptothrix cholodnii (strain ATCC 51168 / LMG 8142 / SP-6) GN=Lcho_0211 PE=4 SV=1MTHRQAIGRASVVRRYGSATAAIAAVVGLRVLLAPSLGDQAQFAPVLCAVVFAAWHGGFGPALFAVLFGALATRYFVLEPIGSLAIDGRDQQVGLAVYLLSGLGIAALGGSMHKAERRANEVAEQLKLKGALIENALEPVLGWDWDGRITFWNRAAQRLYGYSRDDALGCTSHELLRTRVHGQGGAFMDRLAADGAFEGELRQRTRDGREIVVETRMVRVMRDDGSAYVIEANRDVTARTEAQAAMQQLNAELESRVRERTDALSRNNELLAASRARLASIVDSAMDAIVTLDGRQQIVLFNAAAERMFGLSAAQALGQPLERLIPPRFRGGHPAHVDGFDARGDSAAVRSMRATPSGGELLGLRADGTEFPVEASISRTDVNGDKLFTVILRDITERSRAEEAAVRLRIAEEQAVIAQRDSRMKSEFLASMSHELRTPLNAILGFTDLLLMKGAGPLTPDQEKKLRHIHAGGSRQLSLIGDLLDLARIEAGRFPVSIAQVVCTDVIQKVVRGLQPAVASKGLQLTADVPGSIEAVRSDAVVLAKIVRLLADNAVKFTEAGRVTLSVHQHREGAGVLVTGISVSDTGPGIRPEDQDKLFLAFIQGDGASTRQHGGLGLGLHLSNKLAGLIGAQIEFRSEFGQGSVFTLRLAQDEAAPASSPLSRTPVPDRP	(0.000254767)~~103;X;138~~PAS (0.00000000105051)~~226;X;287~~PAS (0.0000000862702)~~395;X;422~~HisKA (9.90664E-16)~~488;X;543~~HATPase_c (0.000000000000010298)~~650	non-KdpD DUF4118 protein
	0.0033	27	7.6	0.0057	26.2	5.3	1.3	1	R6CE13_9CLOT	Uncharacterized protein	BN687_01636	Clostridium sp. CAG:510	377	1262816	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:510	>tr|R6CE13|R6CE13_9CLOT Uncharacterized protein OS=Clostridium sp. CAG:510 GN=BN687_01636 PE=4 SV=1MFEKKKKKQTPPYAYMKDHNVPTNILITLGILLLFTAVSVVIYRLLPDSDGSHGVIYLVYSMALILIAMHTNGYVYSIVSSLICVVFINYAFTYPYHKLNFTLSGYPLIFSCMLVINLLSCTLTAQLRKQQKEIMEREALLRTAELEKMRANLLRAVSHDLRTPLTGIIGNSSLYLEQADVMADAEKKELIFSIQSDANWLLNLVENLLTVTRIQGDNLLINTRPEPVEEVVSEALERVKKRFPDVKIHASVPEEMLFIPMDPVLIEQVIINLIENAIVHSETNEPIDFTVSVTENKVSFCIKDYGKGIDPQKLPTLFDGGDVSGMNSYDSRRGMGIGLSICKTIVRAHHGEIYCKNHENGAAFCFVLPKGEINIES	35~~DUF4118 (0.0000243007)~~130;X;147~~HisKA (0.000000000002896)~~213;X;266~~HATPase_c (6.64402E-23)~~368	non-KdpD DUF4118 protein
	0.0034	27	9.1	0.0067	26	6.3	1.5	1	K9XEX3_9CHRO	Multi-sensor hybrid histidine kinase	Glo7428_2114	Gloeocapsa sp. PCC 7428	705	1173026	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	>tr|K9XEX3|K9XEX3_9CHRO Multi-sensor hybrid histidine kinase OS=Gloeocapsa sp. PCC 7428 GN=Glo7428_2114 PE=4 SV=1MLRTMRLHYMGYSVAVVAVIAFVLTKLVWQLTQPHVYPLFLAAVMVSSWYGGMKSGLFAAALSAVLCEYFFVPPLYTLLPTRQGISGVIQFVLVAGLITTLNTRLRSTQKLAQRNYEHLRQSQESLRHSEERYRILVEGVTDYAIFMLDSNGIFATWNVGSERILGYQEAEIIGQPFERIFTPEAIQQGLPEQVLQRAIATGFSRENRWHIRKDGTHFWTHCIVTALRDDNGNLRGFAKIMQDITQRKLAEEEREQLLLREQAARAEAEAANRAKDDFLAVVSHELRTPMTAIIGWAGMLRSGMLDESRAALAMETIERHANLQMQLIEDLLDISRIVRGDLALNFDKVDLVKVIAAAIEVVQPAANEKAIDLTFVQKLPTTNYPSAITRFFQIQVSDTGIGIDRGFLPYVFDRFRQADSTSARANKGLGLGLAIARHLVELHGGTIEVDSPGIGQGATFAINLPYYNTFPPENFTVTNPERSQSYVVGENTKTFNNPPRLDGLRVLIVDDEPDARQWISIVLHESGAEVIAVASVAEALTALAQQRPDVLVSDIGMPGEDGYALMRKIRELEPEMGGTIPAVALTGYAREEDYTKALAAGFQLHVAKPIRAAELIAVVSSLARMAGKS	36~~DUF4118 (0.00029914)~~107;X;142~~PAS (0.0000000004276 43)~~245;X;276~~HisKA (2.66773E-15)~~337;X;404~~HATPase_c (3.69126E-24)~~540;X;583~~REC (5.94618E-27)~~699	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0038	26.8	7.5	0.007	26	5.2	1.4	1	F5YTX1_MYCSD	Histidine kinase (EC 2.7.13.3)	kdpD JDM601_0994	Mycobacterium sinense (strain JDM601)	832	875328	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sinense (strain JDM601)	>tr|F5YTX1|F5YTX1_MYCSD Histidine kinase OS=Mycobacterium sinense (strain JDM601) GN=kdpD PE=4 SV=1MSVLSQRGELRIYLGASPGVGKTYAMLGEAHRRAERGTDVVAAAIETHGRSKTAELLRGIETVGDPSAELDVAAVLARRPRVVLVDDLAHTNAAGSRNPKRWQDIEELLDAGITVISTVNVQQLESLSDVVTKITGTTEHDTVPDAIVRQAAQIELIDVAPEALRRRLSHGNVYPPEKVDAALANYFRGETLTALRELALLWLAGQVDAALTKYRADKKITQTWEARERIVAAVTGGPPESETLVRRASRIASKAGGELLVLHVLGDGDSGAPAPRVGKIRQLAISLGASLHTVIGDDVPAALLEFARDVNATQLVIGSSRRSRWARILDEGVGAAVVQQSGDIDVHIVTDEDTKPNFRSVSISPRERRAVSWLAAVAVPCVMCAIVVGWLDRYLDTGQSALFVVGVLVVALLGGIAPAVLSALLSGVLLNYFLLAPRRGFTIAEHDAAVTEVVLLLVAVAVAVLVDSAAKRAREAGRASREAELMTLFAGSVLRGADLDTLLERVRETYAQRAVSLVRIPAGTARPEVVASVGEQPCTSVDLADTTIDVGDDEFWMLMVGRQLASRDRRVLSVVARQAAGLVRQEELAAEASRADAVMRTDELRRSLLLSAVSHDLRTPLAAAKAAVSSLRADDVAFSPDDTAELLATVEESVDQLTDLVGNLLDSSRLAAGVIRPALTKVYLEEVVQRALIGIGRRSNVFGRGRLDQVKVEVGPTVAMADAGLLERVLANVIDNALRYASDSVVRVTAGRVGDRVLVNIADEGRGLPPGGELHAFDPFQRLGDRDNTSGVGLGLSVARGFVEAMGGTLSATETPGGGLTMVVDLAAPAGEGG	5~~KdpD (5.80259E-96)~~207;X;229~~Usp(5.91313E-33)~~349;X(252);601~~HisKA (0.000000000096262 4)~~667;X;724~~HATPase_c (2.84019E-24)~~824	KdpD protein
	0.0039	26.8	10.3	0.0066	26	7.1	1.4	1	A0A088QFP9_9CORY	Histidine kinase (EC 2.7.13.3)	DR71_936	Corynebacterium sp. ATCC 6931	867	1487956	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium sp. ATCC 6931	>tr|A0A088QFP9|A0A088QFP9_9CORY Histidine kinase OS=Corynebacterium sp. ATCC 6931 GN=DR71_936 PE=4 SV=1MAKRGKLKVYLGFAPGVGKTCAMLSEGHDLYSRGHEVVIGLVEHHGRERTKKLIEGLPVLDCRKVSYRGNTYRELDVDAIIEMRPEVALVDELAHTVVTDEPDNEFVQQRKRWHDVYQLLDAGIDVISTMNIQHLESLNDVVAAVTGVRQMETVPDRVLRDADEIELIDLSPDALRIRLSRGEIYRKEQAELALRKYFRPGNLSALRELALLWLADKVEEVLDAYREDEEIDDHWTTRERVVVAVRDDENAESMIRRGARMTGRVAGREMIVVHITGEDDGLDRGYLRRLRKLQDLTESLGGQWRTIVGDDVPGILLEFSRTVNASQLVIGSERGLRRYYVGLSTSQRIIDQAGPIDVHIISSSSEKKAKRRKKLRSRFSKERRITGWLLALVGPVLLTLLLYQLDTGPEFLGVLLLTYLMPIVFAAMAAGLVPALAAVVVSSILANWYFTAPVNTLTITEPASLAQILLFGVIAAAVATVVERSERRREMADRSLHQAVVMSELAHGVVHDGDNMSNLVHSLADTFSMERVDVQRYSSERKKWLTIVTTAEHGLSEPWPTELPMTKVSSGDDLRFVLSGRELTAAETAMIAAHGSRIRALMDMEEIAAMRRATAALEAGNRVGSAVLTAVSHDLRTPLASIKAAISSMNMEDVELLDDETRLILMETIESSADRLEVVIGNLLDASRIDSSTKRVESVPVSVSDVVDAVCAELPEAAGHIDRDIDHDACMVEGDPGLIQRIVSNIVINGRQYAPESSLTIRTRPSERGVRGPADMPVMGSLGAIAASACIDILIIDHGKGIPEDKLEEIFQPFQRLGDYSAQSQGLGLGLAAASRFADAMGGAIRAEQTPGGGATFVLTLPRAMGERK	2~~KdpD (5.41434E-100)~~218;X;240~~Usp(2.40254E-23)~~361;X;418~~DUF4118 (0.0000103198)~~470;X(157);627~~HisKA (0.00000000682077)~~686;X;737~~HATPase_c (9.19647E-20)~~859	KdpD protein
	0.0039	26.8	7.5	0.0066	26	5.2	1.3	1	R6Z0D3_9FIRM	Histidine kinase (EC 2.7.13.3)	BN600_00679	Roseburia sp. CAG:309	312	1262945	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Roseburia, environmental samples, Roseburia sp. CAG:309	>tr|R6Z0D3|R6Z0D3_9FIRM Histidine kinase OS=Roseburia sp. CAG:309 GN=BN600_00679 PE=4 SV=1MAMAVFFVSRFTDGFVYGIIASLLSVLVLNFAFAFPYFAFNFSIPENIISAVIMLVITAMTSTITSQLKWQERVRAESINEKMRGNLLRAVSHDLRTPLTTIYGSSSAIVQNYEHLSEDQVVQLADGIREDARWLIGMVENILSITRIDNDGVKLVKTSTVLEELIDSVLTQFKKRYPDQKVNVSIPEEFTSIPMDAVLIEQVLMNLLENAVQHAKGMKTLELHVFVLGDKAVFEVRDDGCGIEKERMKGLFQDYFSVKDAPVDNQKRSMGIGLAVCASIIKAHGGAITAENRKEGGCCIRFALELEETENE	81~~HisKA (0.000000000239755)~~147;X;200~~HATPase_c (3.73952E-22)~~304	No DUF4118 detected by NCBI CDD

	0.0042	26.7	6.5	0.0062	26.1	4.5	1.3	1	G8AL95_AZOBR	Sensor protein (EC 2.7.13.3)	AZOBR_100393	Azospirillum brasilense Sp245	310	1064539	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum brasilense, Azospirillum brasilense Sp245	>tr|G8AL95|G8AL95_AZOBR Sensor protein OS=Azospirillum brasilense Sp245 GN=AZOBR_100393 PE=4 SV=1MIIAITTLLRYVLEPILSKYPFLLYIPAIFLVSLLFDRASGFIAVLLSGGFAAWLFMEPRGDLWIADHGDQLAFMIYVGLGLIAAITEMLRTTLEELCQSWEKLAASDREKDLMLQEIHHRIRNDLQMISAQLTLAAMRPENAQAMMQGTIERIGVLARIYGRLRRVDGASIVNVKEFLESLVEDLQLGMVGVRPIALSARADSVDLDMNTAVAVGTIANELVTNAVKYAFPDAQAGWVDLSFRQEADEYVLCVSDNGVGFTSDQPKGTGLGRQIVQQLALQLRGKLDIQSRTEGGIQAMLRFPVPRPG	2~~DUF4118 (0.00000132806)~~92;X;118~~HWE_HK (0.000000000000167751)~~187;X;219~~HATPase_c (0.000000000000222919)~~297	non-KdpD DUF4118 protein
	0.0043	26.6	11.7	0.0076	25.8	8.1	1.4	1	Q6F8D1_ACIAD	Histidine kinase (EC 2.7.13.3)	kdpD ACIAD2975	Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	881	62977	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1)	>tr|Q6F8D1|Q6F8D1_ACIAD Histidine kinase OS=Acinetobacter baylyi (strain ATCC 33305 / BD413 / ADP1) GN=kdpD PE=4 SV=1MMQIDRNEKADAWLAHTQREQSGRLTIFLGAAPGVGKTYAMLTRAHELMQQGKQVVVGVVETHGRADTARLIAGLNVIPRRVVEYQDRKLEEMDLDQILHIKPEIVLVDELAHRNVPGSRHEYRWQDVNEILDAGINVYSTLNIQHLESLNDVVYQITGIRVTETVPDALLKRLKDIRLVDLPVPELLERMKHGKIYLDDMAPHALQGFFKPAHLTALRDLAIQTVAGQVEIDYREKSVAQGRIVPIQNHVMLAIDGSVFAEDLVRRAHRIAERRNATWSVISIQKSKTSSAQSLAVSKAFNLARKLGADTYLLYSHQIAPTILQAAYDYGASNILLGKSPKKTLLERIRSEHIADQLLDKQHPFEITFVQPLKATSYSAQAAVPDQTWLQQYTHFQARELIESVLIVLAGFIIAVISDHFIGYTELALIFVVTVLVVAMRARMLMTLLSVFVCFLLYNYFFIEPRFTFRISAERGVITIVIFILSALLVGRLANQLRAQVLSLRVANSVSLQLQELERKLSTCVDIAQVLSVSKQHLESALKATAWLRVSELEAGDRSQLNHKDHIAADWTQKNGQPCGRFTNTLTQSEWWFNPLNLAGEHGVIALRFHPDLDVISFEQQRLAELMIEDIAQTLARVLLSFQLENSRVVAETEKLRSALLSSVSHDLRSPLAAMIGSADTLKYYSVQLSDTDRDSLLDTIHIEGERLDRYIQNLLDMTRLGHQGLTLSRAWISIDELIGSATQRLKRYQPNIQIDTHIAPNLPALYVHPALIEQALFNVLENAAKFSPDAVPIQVKISAVDEQFQIDIIDLGIGIPEQEREQIFDMFYTMQRGDRGKTGTGLGLAIVKAIIGAHMGSIEAMAGPYGQGTQIRIRLPQHQE	23~~KdpD (1.77243E-103)~~230;X;250~~Usp(6.35116E-28)~~370;X;401~~DUF4118 (0.000000000667026)~~500;X(154);654~~HisKA (0.000000000166456)~~720;X;773~~HATPase_c (0.000000000025519 2)~~876	KdpD protein
	0.0043	26.6	18.2	0.0076	25.8	12.6	1.4	1	A0A0F5L3G4_9RHIZ	Uncharacterized protein	VW35_16395	Devosia soli	332	361041	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Devosia, Devosia soli	>tr|A0A0F5L3G4|A0A0F5L3G4_9RHIZ Uncharacterized protein OS=Devosia soli GN=VW35_16395 PE=4 SV=1MQAAEWLRNRPIQAYAIALLAFLIALWLRFTVDHALPVGFPYLTFFPAVLLTAFFCGTGPGIVVAVLSVVSAWYWFIPPIASFELTSQSAIAVLFFVAILTADIFIIHVMHGALRRLVQEQARTAGLLEQQKTLFAELQHRTANNIAFISALLSMHKRKARGQADPVSVFDDATSRLESMARIHRRLYDPTNGDLQLDAYLAELVRDIFDSAGRERVDVSIVSRIEKLDVNRLITLSLVVSELATNALKHAFSNGTGRFAIELTPRGGSNVLRVRDNGPGFPHGFDPSGSDRLGFRVLYSFARNLNGTLDFRSDDGALVELVFPSNHQDKAA	137~~HWE_HK (1.93089E-15)~~212;X;236~~HATPase_c (0.00000000021173)~~316	No DUF4118 detected by NCBI CDD
	0.0044	26.6	9.7	0.0071	25.9	6.7	1.3	1	R4M4F5_MYCTX	Sensor protein kdpD	J113_07240	Mycobacterium tuberculosis CAS/NITR204	289	1310114	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex, Mycobacterium tuberculosis, Mycobacterium tuberculosis CAS, Mycobacterium tuberculosis CAS/NITR204	>tr|R4M4F5|R4M4F5_MYCTX Sensor protein kdpD OS=Mycobacterium tuberculosis CAS/NITR204 GN=J113_07240 PE=4 SV=1MNATQLVVGTSRRSRWARLFDEGIGARTVQEPGGIDVHMVTHPAASRASGWSRVSPRERHIASWLAALVVPSVICAITVAWLDRFMGIGGESALFFIGVLIVALLGGVAPAALSALLSGMLLNYFLTEPRYTWTIAEPDAAVTEFVLLAMAVAVAVLVDGAASRTREARRASQEAELLALFAGSVLRGADLATLLQRVRETYSQRAVTMLRVRQGASTGETVACVGTNPCRDVDSADTAIEVGDDEFWMLMAGRKLAARDRRVLTAVATQAAGLVKQRDAAGRPGRGHR	1~~Usp(0.00000000490033)~~41;X;64~~DUF4118 (0.0000246765)~~143	non-KdpD DUF4118 protein
	0.0044	26.6	11.5	0.0081	25.8	8	1.4	1	A3CUL8_METMJ	Multi-sensor signal transduction histidine kinase	Memar_1136	Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1)	608	368407	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanomicrobiaceae, Methanoculleus, Methanoculleus marisnigri, Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1)	>tr|A3CUL8|A3CUL8_METMJ Multi-sensor signal transduction histidine kinase OS=Methanoculleus marisnigri (strain ATCC 35101 / DSM 1498 / JR1) GN=Memar_1136 PE=4 SV=1MAPLPETIRTFIVGILIGISIVLTYYFHAVLSVGAVFSHFFYIPIILAALWWGRRGISVAFFLGGLVLISHFLLRTDVGTVNDYGRAVMFVVVAIVIAWLSERLKRQQKDTERERDRAQGYLDVAAVLLVVINADQTIGLVNRRGCELLGYREDELVGKNWFDVAIPERNREDARQVFARMISGAATTSPTDEIVIVTKDGDERTLIWKEAVLRDAGGRITGVLGSGKDITERIRAQEALQNREAQLRTIVENLNEGLGVFDLDGHPLQWNRAARESFGLFGFESAPGNVSEFDSLFEFTTTDGTVLPVEEWPLSRVLRGEQIRDVEVRTRRIGTDRQRVFNYGGTLVRGAGGSPFMAVVTFTDITDRKEAEEALLAANEVANLYLDIMVHDINNANAIALGYSEILAEDLEGTNREMIQKVRSAVSQSIEIIQNVSTIRRLRSLTPPLRPVDLDAVIRAEIRQHRETDIRYDGRPVTVLADDLLPEVFTNLVGNSIKFGDPDVTVAIRVEDQDGEVLVSVEDTGPGIPDDVKPALFSRFRKGKSSKSGKGLGLYIVRMLVTRYGGSIRVEDRVPGATEEGAAFRFTLKKAAREEPETPAIPEARPPM	15~~DUF4118 (0.00000000853683)~~107;X;125~~PAS (0.00000000233523)~~230;X(258);488~~HATPase_c (8.59705E-17)~~588	non-KdpD DUF4118 protein
	0.0045	26.6	9.3	0.0083	25.7	6.4	1.4	1	A0A0F5VH18_9GAMM	Histidine kinase	KY46_04830	Photobacterium halotolerans	349	265726	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Photobacterium, Photobacterium halotolerans	>tr|A0A0F5VH18|A0A0F5VH18_9GAMM Histidine kinase OS=Photobacterium halotolerans GN=KY46_04830 PE=4 SV=1MLTYWRKSHFLFSFIVLASALSVSWLIDQVLGSTIAVLLVLQLAVVVVALQCTSHFAYGFAVIEAMSFNFLFTTPRYSLQMFHAEDIINLVVFVLVALTTSQLAEHYRRQQDELKKAKLRNSILLSVSHDLRTPLATIIGTLTTLNEYMPKLSEGEKSELLNSATAESHRLHQYIENLLQATKLQHGALKITRNDESIIHIINNAVLRLPYSQERVRVQVQGQLSHISVSAIFIEQALFNVLDNALRFSPKHQSVVVTLFQESAFIVIDIQDKGVGIKRDEAARIFDLFYSSATKKTADSGSGLGLAVAKGIITAHQGQIESVPVSEGCLIRIRLPIDQPSSSPQGEQS	118~~HisKA (0.0000000289791)~~183;X;234~~HATPase_c (1.35602E-21)~~335	No DUF4118 detected by NCBI CDD

	0.0046	26.5	8.9	0.0091	25.6	5.9	1.7	1	N8ZKG9_9GAMM	Histidine kinase (EC 2.7.13.3)	F960_01562	Acinetobacter gerneri DSM 14967 = CIP 107464	888	1120926	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter gerneri, Acinetobacter gerneri DSM 14967 = CIP 107464	>tr|N8ZKG9|N8ZKG9_9GAMM Histidine kinase OS=Acinetobacter gerneri DSM 14967 = CIP 107464 GN=F960_01562 PE=4 SV=1MSENRDNKADVLLQHTKRYQSGRLTIFLGAAPGVGKTYAMLVRAHDLFQQGVDIVIAYVETHGRAETDHLVDGLPIIARKMVSYQGHQLQEMDLDAVLEKKPHIVLVDEFAHTNMPGSRHEKRWQDINELLDAGIDVFTTMNIQHLESLNDVVLQITGVRVLETVPDRVFERIRDIRLIDLPVNELIERLNQGKVYVPEQASHALKGFFTPSNLTALRELAMQTVASHVDSDVRENFAIQGIAPIPLKNHILVLIEAKGKAEALVRAGCRLAENRLATWTVVAFFKDNATSDALKLDEHSREIETALNLARQLGGMTEILYGEKHAKVLSEYAIERGISTIVLAQQNESILQKYFQPSLIDHLLKNHPKFELSIVPIQENHQVKSKHLNKRYLLSLSETLFVLLITICSIAIASLSEKYLGISEISIIFITAVVFIASKTRMMAATTAAILLFLSYDFFFILPKFTFDISAPKGFITIVAFLAAALIASRLASRLKEQVNALKAANRYNSIMQDLSQKLSVAANLEQVLDIALNQLSQNLKAKIWFNLAENAPYLEQINHHTLSQKEKISADWTFKNSQPSGKFTQTLTENEWWFLPLLASKQCLGVVGIKFEYSISQMTLEQKRLAEAMIENIAQAISRTQLTQDLELAKVSSETEKLRSALLSSVSHDLRSPLASMIGAADTLSNYRHNMNQDDQDDLLQAIHLEGERLDRYIQNLLDMTRLGHEGLTLRRDWIGVDELVGSAVRRLKRYLPKIKVNVKFSEANLSLFVHAALIEQAIFNVLENAAKFSPEDEAVELDVEKLNDQQIQISITDQGQGIPEDERNRIFDMFYTMQRGDRGQYGTGLGLTIVKAIIGAHMGQISASSGRQQKGTCIRIVLPIQQMISA	22~~KdpD (3.58707E-120)~~229;X;250~~Usp(2.37184E-19)~~376;X;399~~DUF4118 (0.00000000348473)~~498;X;524~~GAF (0.000318654)~~640;X;657~~HisKA (0.000000000254543)~~723;X;776~~HATPase_c (2.22521E-23)~~880	KdpD protein
	0.0046	26.5	5.2	0.01	25.4	3.6	1.6	1	K9QM52_NOSS7	PAS domain S-box	Nos7524_0242	Nostoc sp. (strain ATCC 29411 / PCC 7524)	1249	28072	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain ATCC 29411 / PCC 7524)	>tr|K9QM52|K9QM52_NOSS7 PAS domain S-box OS=Nostoc sp. (strain ATCC 29411 / PCC 7524) GN=Nos7524_0242 PE=4 SV=1MPNIAGYSWLRCSIALINVAFALMLMLLLDPWVKMSGTPFLLFFSAVMVSAWYGSWKGGVLATCLSAFVSDYFFLEPQYNLSVDLSNAVKIGLFAVQGLLFTILCVALKNAKRRDEANLHKLKESEERFQLALSSSDIVVFQQDSNLLYRWIHNPQGGTTTEDILGKSDYDLFPFSVAEQLTAIKQRVLETDVSEHEEVYIILQGKVLYYDLLVEPLKVNGRIQGITCVAINISERKQVEQEKAKLRQELQQAMQQKEESLALLNAWLASSPVALAFLDQELRYVYANEALAAINGVPQDQHIGYTIREVLPEWAAQIEPILYEVMQTKEPLLNQEVMGETHPTGVYRCGLVSYYPVCLPDGQLLGVGVTGIDITQQKKTQQALRESEARFRTMFNQAALGIALISLDGKFLQVNPALCQLVGYSYDEFIQMSFQDITHPDDLETDWNYGQKVLTREIINCYSLEKRYIRKDGGIVWVNVTSSVVCDDDGEPKYALGIVEDISQRKQAQATQNFLVEASTILAASLDYEVTLSNVAKLTVPTLADWCIVDILQPDWSIKRVAIACHNPQKRQIIEEIQQRYPPRSDGNHPFRQTLIQGKSVFYPELPTSTLVEMARDEEHLQLLQSLGMRSVMVIPFYSRERLFGVISFVTGESGRQFQATDLALAEDIARRAATAIDNARLYQETQQAKQAAEMAVSRTARLQSITSALSEALTPQQVADVIVNQGIAALGASGGSVVLIEGDSELKILEAVGYPQSVRENWASFPITANVPIAVAARTKEPIFLANTEILADQYPEIANIPALTGNCAFACIPLIVEQQTIGVLALSFATTQIFTAEDQRFMLTLAQQCAQAIARAQLYEAERNARAAAESANRIKDEFLTVLSHELRTPLNPILGWAKLLRTRKHNEATIIQALETIERNAKLQTQLIDDLLDVSRILRGKLQLNIRAVDLRTTITAALETVRLAAEAKSIEMITCLDAPVGQVMGDSDRLQQVVWNLLSNAVKFTPPNGQVQVTLEQVGLEAQIQVIDTGKGITPEFLPHVFEYFRQADSKTTRIFGGLGLGLAIVRHFVELHGGTVQAESAGDEQGATFTVKLPLTKNTEDRLLSADSAIAESEIQDSLLTGVQILLVDDQPDVREFFSFALEQYGANVTTVESALAALKILADTKPDVLLSDIGMPEMDGYMLVRQIRKWSPEQGGQIPAIALTAYAGEIDHQQALAAGFQKHIPKPAETVELVMAIAQLLGRN	401~~PAS (1.28565E-16)~~501;X;514~~GAF (0.00000000065008)~~688;X;712~~GAF (2.32477E-15)~~855;X;874~~HisKA (9.02831E-15)~~938;X;993~~HATPase_c (3.14381E-33)~~1097;X;1130~~REC (3.48121E-28)~~1246	No DUF4118 detected by NCBI CDD
	0.0048	26.5	8.2	0.0085	25.7	5.7	1.4	1	K9XIJ1_9CHRO	Signal transduction histidine kinase	Glo7428_3882	Gloeocapsa sp. PCC 7428	870	1173026	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	>tr|K9XIJ1|K9XIJ1_9CHRO Signal transduction histidine kinase OS=Gloeocapsa sp. PCC 7428 GN=Glo7428_3882 PE=4 SV=1MHICIKVLLTKVVSRATKASYMSVYGWRRKHFLWSRYCVAVAAIAITLLVKLLLAPIIDNESPFLLFFFAIVVSTWYGGRTTGILATVLAALCADYFFIPPFHSFLVDTVGFCIRLGLFIFEGTAITYVVAELNTTKQQAETRRLEALRYQETLQQSEERFRLFVESVGEYAIFMLDADANIVSWNVGAENLFGYKEAEILGKHFSSLFTLDDIRSGKPQHEIEQAIAQGRAEAQTWHLRSNGTWFWANCVITALRDNNGCLRGFAKVIHDFTEHHQVEVVLQKANEELELRVQSRTFELQNANEQLCNEIIERQQIEEALLDSQTRLQLINSISTAMMLGMSVEQIIKRTVRQISECFPSLRVAYSIIDQNGTLMVVHSLEPEGIPSLQGVTFDLQTMPDYLQAIQMNVPIVVEDIAQDLRFSPQNCALFRTYGIQAFVDVPLQYSKQLIGLLCFDSAQPRKWSNHEIGTLIVITQYLSIIIKNAQTQQERDRAELALQQAHDELELRVRNRTAQLAKANEELKTEIYERRRVEESLRQSEERLRFALSAADMVAWDWNTSTDEISYSDNAHSAIRLPSKTKINTATEFFNLIYPEDRDRVLQELRFQCTSANRNLYSTEFRLVHPDGSIHWMANQGKVSYDSAGKVIRVSGILRDITKQKQIADQIQASLVEKEVLLKEIHHRVKNNLQIISSLLSLQSGYIEDQQTLEILKAGENRIASMALIHEQLYQSQDLAKIDFPDYIQNLVANLFSSYDVSSEKIILHSNIERILLSLDIAIPCGLIINELISNSLKHAFPNNKKGNIYIKLSAIDDRYHLSIRDDGVGLPKNIDPNNTDSLGLQIVAALTQQLEGSLDIHSHNGTEFKIKF	(0.0000000687541)~~121;X;172~~PAS (0.00000000105874)~~271;X;343~~GAF (5.36413E-15)~~483;X;557~~PAS (0.0000121947)~~658;X;681~~HWE_HK (9.6781E-35)~~756;X;785~~HATPase_c (0.000000000000279423)~~870	non-KdpD DUF4118 protein
	0.0048	26.5	9.9	0.035	23.7	7.1	2.1	2	Q8EKN2_SHEON	Histidine kinase (EC 2.7.13.3)	kdpD SO_0060	Shewanella oneidensis (strain MR-1)	348	211586	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Alteromonadales, Shewanellaceae, Shewanella, Shewanella oneidensis, Shewanella oneidensis (strain MR-1)	>tr|Q8EKN2|Q8EKN2_SHEON Histidine kinase OS=Shewanella oneidensis (strain MR-1) GN=kdpD PE=4 SV=1MTFANTASINHYWRTHPALFTAMLLVVVLITSYFIDVFSGSAIAVLLILQLAVVVVALQCSANYAYFVAVFGAVSFNFLFTAPRYSLQMLNVEDIVNLTVFLLAALTSSKLAKHYRRQQDALEQAQLRNSILLSVSHDLRTPLATIIGTLTTLKEYQPKLSPAQTEELIDSAAAESHRLHQYIENLLQANKLQHGALKFSLDEANIREVLQRTIARFQTEQPRIQISEPELPSLMICSSLIEQAIFNVLDNALHYSPATQPVTVSLYRHQHMLRIDIQDQGKGIAPSQTGAIFELFYRQHPTTDGGAGLGLPVAKGIITAHNGTISAEKVAHGSLIRIALPITKESA	17~~DUF4118 (0.0000155104)~~118;X;126~~HisKA (0.0000000814345)~~191;X;242~~HATPase_c (2.00496E-22)~~341	non-KdpD DUF4118 protein

	0.0051	26.4	9.9	0.0091	25.6	6.9	1.3	1	A0A0F2J2H6_9BACT	Osmosensitive K+ channel Signal transduction histidine kinase	MCHI_002510	Candidatus Magnetoovum chiemensis	896	1609970	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Candidatus Magnetoovum, Candidatus Magnetoovum chiemensis	>tr|A0A0F2J2H6|A0A0F2J2H6_9BACT Osmosensitive K+ channel Signal transduction histidine kinase OS=Candidatus Magnetoovum chiemensis GN=MCHI_002510 PE=4 SV=1MSDNDLDKLISPDNLLEAVRKKESRTLEGKLKIFIGMAAGVGKTYAMVSEALAHHKNGIDIAVGLVETHKRKETQNLLRGLPVIKQKEYLYKGMKVSEIDIDAIIKRKPKIALIDELAHTNISECRHNKRYQDVLEILSHGIDVHTCVNIQHIESLNDQIRRITGVRVLETVPDSFFDRADEIVIIDLPPVDLLQRLREGKIYLGDNIARSLENFFKEDKLSLLRETALRFAAERVNIETQDFRLLNSITGAEQVKRKLMVGIFSSPYSEMLIRCTRRLAQALSTNWIGVYVDTDRELSDEEKELLEKNMNFVRQLGGEVVIAKDNDVVNGILRAARRQNVTQIIVGKSRRNLFSSIFAGKSLIDRLFRESREIDIYMVCTDANTCAKKPSIPPKRRLPKFNKLSLGLLFVSILTAASFLIIPQSGYRIMGYIYIIFVTLSATYFPLDVVIVLSILCGVLWNFFFIPPRFTFTIAKNEDWMLVLVVLITASIAGILTSKLKKKQKLIIEREEKTNALYQFTKQLSVSKNLAEIIENAAEILSKVFQTKIGIFVKNDNDELTFTNRQKITLSEKDKTTALWVYHNRKHAGKFTDTLPVSDFYFTPLNTAQNDLGVLCTDLSGSKVFTHQQQALLSNFANQLTLTIEKEILHLRLNKTKLEKQSELIFKTLMDSVSHELKTPLSTIHGCASALLEPSISSNPNTVAELANEIVVGSRRMNSMVQNLLDMSRIESGQMRIVLSPVDLSDLIGVSIEKVSKIAQNRKITVYIDSDTPLMNLDFVLFEQAVTNILTNACLYTQQDGIIKITVKSMTDAVSMIIEDNGLGIPLEYKDKVFDKFFRANASKTGGTGLGLTIARSIIELHKAGITAQSVKGEGAKFIITLPKEVFFINENTSNR	29~~KdpD (2.169E-111)~~236;X;258~~Usp(6.81175E-33)~~379;X;408~~DUF4118 (0.0000000301924)~~498;X;529~~GAF (0.0000000390091)~~646;X;667~~HisKA (0.0000000103081)~~729;X;782~~HATPase_c (2.22492E-24)~~882	KdpD protein
	0.0053	26.3	7	0.0084	25.7	4.9	1.3	1	A0A068SQE7_RHIGA	Histidine kinase (EC 2.7.13.3)	fixL RG540_CH22400	Rhizobium galegae	505	399	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Neorhizobium, Rhizobium galegae	>tr|A0A068SQE7|A0A068SQE7_RHIGA Histidine kinase OS=Rhizobium galegae GN=fixL PE=4 SV=1MASRTFAEKKDDYIQSFLSRRFSAAEVYFIATICVLVAFALRFSLHGVLDDKAPFTFFIPPILVAALIGGMRASLFAVVLSVLAAYVIKELTPRGANFTEMAMIGIVGVVIALLGEILHSARKAIGKAQAKADSREAHLRSVLDTVLDASIVSTRDGTIVSFNAAAIRQFGYGEDEVVGQNLRMLMPEPYHREHDGYMERYLRTGEKRIIGMDRVVVGRRKDGSTFPMKLAVGETHTGGETFFTGFVRDLTEREESAARLQEIQGELARLARLNEMGEMASTLAHELNQPLSAIANYVHGCARLLRDMDEAVAVRMREALEETANQSLRAGQIIKHLREFVTKGETEKAPENIRRLVEEAGALALVGSREKGVRAIFEFAQGPEMVTVDRIQVQQVLTNLMRNAIEAMRDSQRRELVIRTLQENEDMIQVIVQDTGPGIPEEIAGQLFKPFITTKAGGMGIGLSISKRIVEAHGGEMTVTRNAAGGATFRFTLPIDKEERENADG	2~~DUF4118 (0.000000624752)~~118;X;148~~PAS (0.000000000377821)~~250;X;273~~HisKA (0.00000137294)~~340;X;394~~HATPase_c (1.21684E-27)~~493	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0059	26.2	6.2	0.011	25.3	4.3	1.4	1	D7B3Y2_NOCDD	Histidine kinase (EC 2.7.13.3)	Ndas_1513	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	832	446468	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	>tr|D7B3Y2|D7B3Y2_NOCDD Histidine kinase OS=Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) GN=Ndas_1513 PE=4 SV=1MRRGRLRVFLGAAPGVGKTHTMLEEGRRLRDEGRDVVVAIVETHGREAVAALLDGMETVPRTAVSHRGVGLTEMDLDAVLARRPQVALVDEFAHTNAPGARHGKRWEDVARLCAAGVDVITTVNIQHIESLNDVVQRITGAPQRETVPDRVLRAADQIELVDLAPQALRDRLAAGRVYPAERIDAALSNYFRLGNLTALRELALLWLADEVDSALMDYRAEHRIDSTWEARERVVVALTGGPEGETLLRRGARIAARSGSGELLALHVSGQEGLRDARPEALAAQRVLTERLGGTFHQVVGDDIPRSLVEFARAVNATQLVIGISRRGRLLTALTGPGVGATVIRESGPIDVHMVVNHAAAARGPALPRLGGALSLRRRLAGFALSLVAGPLLTWMLAAERSPEALVADVLTYQLLVVVVALVGGIWPALYTAVMSAVTLDLLFIEPVLQIRIDHPVHLGALVLYALNAVLVSYVVDQAARRTRAAQRAGAEFELLATVAGSVLRGQDALRALVGRTREAFALDAVRLRSDGAVLSSAGEAPPGAEPTVVAVGERASLELHGAELGASERRLLEVIATQIDAALEHQDLRATASEVGPLAENDQVRSALLSAVSHDLRRPLAAVTTAVSSLRLSGVDWSPGDRDELLATAEESLATLTALVTDLLDVSRLQAGVLAVSAHDTDVDEVILPALDELGLGPADVDLELDPDLPAVRADAGLLQRAIVNLLANAVRFSPPGRGARVATSAFGAAAQIRVIDHGPGVSPDRLDQLFVPFQRLGDTDNTTGLGLGLALSRGFVEGMGGRLTAEDTPGGGLTMVISLPLAERPGPGEDA	1~~KdpD (1.81407E-112)~~211;X;233~~Usp(9.35595E-29)~~356;X(246);602~~HisKA (0.00000000425132)~~668;X;719~~HATPase_c (4.64181E-26)~~820	KdpD protein
	0.0059	26.2	8.8	0.009	25.6	6.1	1.3	1	R5TMK1_9CLOT	Histidine kinase (EC 2.7.13.3)	BN544_02010	Clostridium hathewayi CAG:224	496	1263067	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	>tr|R5TMK1|R5TMK1_9CLOT Histidine kinase OS=Clostridium hathewayi CAG:224 GN=BN544_02010 PE=4 SV=1MRNDIASAEHIVKILKNASKVAVIWVLSTMFAIVLNHMGVRIENLLLIYVVGVVICSVETSSMCWGIGSSVVFVFTFNFLFTAPKFTFQVDDPNYVISLMIFIIVAFIVASLTVKLQRQMDIANRRTEITTKLNAIGSGFLNLAGRPAIARYSCDSLKKLTEKRVDILIRSSDNEEFSDSIAEWCYRNSMICGHGEAQFGENTSLYVPIKNSNKTYGVIIFDCCDGDLEEEERVYVDTVISQITLVLERERLNEEKEETKIQIEKERLKSTLLRSISHDLRTPLTGIAGSSNFLYDNYGSLDEETAKSMLNDICTDAEWLNSMVENLLNMTRIQEGRLDIQKKKEVVDDLISGAVTLVSKRLGDHRLKTVTPHDIVLLPVDARLFTQVLVNLIDNAIRHSGNDTTITVSARVMGNFITFKVADNGSGIPEERLDKIFDNFFTTAYENGDKQRGVGLGLTICKAIVEAHGGHIKAVNNEGGGTTFQVDMPMEVRQNE	21~~DUF4118 (0.0000000139275)~~119;X(147);266~~HisKA (0.000000000015777 9)~~332;X;387~~HATPase_c (2.08715E-29)~~486	non-KdpD DUF4118 protein
	0.0061	26.1	9.8	0.01	25.4	6.8	1.3	1	D3HKC7_LEGLN	Putative osmosensitive K+ channel His-kinase sensor (EC 2.7.13.3)	LLO_2471	Legionella longbeachae serogroup 1 (strain NSW150)	653	661367	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella longbeachae, Legionella longbeachae serogroup 1 (strain NSW150)	>tr|D3HKC7|D3HKC7_LEGLN Putative osmosensitive K+ channel His-kinase sensor OS=Legionella longbeachae serogroup 1 (strain NSW150) GN=LLO_2471 PE=4 SV=1MNDSRPNPNALLQQVLEEEKQQQRGKLKIFLGAAPGVGKTHSMLHEALEEQAKGLDIIVGIVESHGRSEIVEILKNFVILPKVTIDYHGKKLQEFDLDAALKRNPGLIIMDEMAHTNVTGVRHKKRWQDIKELLDRGIDVYTTLNVQHIESLNNDVSQIIHAPVQETVPDFMIESANTIELVDLAPEDLLKRLAEGKVYVPKQAQLAAEFYFRKGNLMALRELALRTLAKRVNTQVLLYRQGQGIKSIWHIMEKILVCVGPGPESHKLIRSAKKIATSFQADWMAVYVDSPRTQLSRTQRNQAIKNLFFAEQLGAETHILMGYDLVKEILNFAREQNVTLIMINKRIQTRWRNFFARSLADEVLRYSSDIDVYTITEMAKKPQKKALNKPLTSWFPYFLSISIVSVTTLFNFLLYSLVPDANLIMVYLIGMIAIASLGRTGPTISGIFLSLLAYDFFFVPPYYSFLPNDADYIFNLVMMLVIAVIICQLTLVTRRQSEIARLAEYQTSTLYTLSRRLSRTRGIVRLLRTGINYISEIFHCEIIALLPKDTRLVIRARSKSHQELDDKEYSIAQWVYELGQKAGLGTDTLSFSTAIFIPLLGSRGTIGVLRIQPFNSDEWATPEKIQLLESCANQMALAIEVDSLQEESHKNKA	23~~KdpD (4.50543E-104)~~232;X;254~~Usp(5.74687E-34)~~376;X;396~~DUF4118 (0.0000000352323)~~496;X;526~~GAF (2.94309E-14)~~640	KdpD protein

	0.0062	26.1	5.5	0.011	25.3	3.8	1.4	1	I3Y9Y4_THIV6	PAS domain S-box	Thivi_1831	Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	1115	765911	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Thiocystis, Thiocystis violascens, Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) (Chromatium violascens)	>tr|I3Y9Y4|I3Y9Y4_THIV6 PAS domain S-box OS=Thiocystis violascens (strain ATCC 17096 / DSM 198 / 6111) GN=Thivi_1831 PE=4 SV=1MIPPARLAVRRWPRWSIYLLAIAMTVATLALRAKIAVSFGEQPLLILFMFPILLSAILGGFGPGLIATLGAALGTAYDAIPPTGSFAITARHDLLQWGFLILSGLLASLVSELMHRARRRAESNLRLQSATLACIPDLVWLKDPEGVFLACNPRFEQFFGAPESAIVGKTDYDFVTRELADFFRENDRLAIASDGPSLNEEAIRFANDGHRAWVETIKTPMRDLNGRLVGVLGISRDITEARATTAALRESESRYRDLFDSMREGFYLAELIYSEAGEPVDWRFLDVNPAHSRIIGLPREAVVGHTVRELFPSLEPFWFETTARVALTREPVSLEGFVAATGRWYRNHYYSPRAGQFACVFSDITERKLAEEQLRKLSLAVEQSPVGILITDATTRIEYLNQAFLDQTGYAQEELIGQTPDLLRSGKTQPETYEALREARRRGAIWKGEFHNRRKDGSEYTGFSIIAPIRQADGRISHFVAVQEDVTERKRLGEELDRHRHHLQDLVAQRTAELAEARERAESANRAKSAFLANMSHEIRTPMNAIVGLTDLLRREITDAAQSERLAKIEAAAHHLLNIINDILDLSKIDADRLQLEETDFALAEVLEAVMALIAEGLAAKGLTLAMVSDGVPAWLRGDPTRLRQALLNYAANALKFTEQGGIRLVRATLEDDGERLLVRFEVSDSGIGIAPEILPKLFSAFEQADSSTTRQFGGTGLGLAITRRLARLMGGETGVESQIGQGSTFWFTARLAHGRESTTPRAPMPARDAESALSLFPGARRVLLAEDNPINREVAVELLTRVGLRVDTAADGIEAVARAREDNPDLILMDVQMPHLDGLEATRRIRALPGWQSRPILAMTANVFVEDRRDCTAAGMNDFIAKPIDPQQLYAALLKWLPTDRPAPDERRTTAGAARSEEDDNWRARLAMIAGLDLDAALALLPGNSALLASLLGILADHHGDDVSRIRRCLAENDPDTAQRLAHTLKGAAGNLGAHRLQSAAAALDTHLREGAPRNRVERAIADLELELAQLIADIRHHVLPVVEEVGAVDRARADAVLARLTSWLEKGDMAANELIRAEAGLLLAALGEDGRTLARLIERFDYRGALALLRRHA	18~~DUF4118 (0.00000015353)~~120;X;135~~PAS (0.000000000163436)~~238;X(146);384~~PAS (1.63092E-14)~~486;X;525~~HisKA (4.52589E-15)~~588;X;643~~HATPase_c (4.18087E-29)~~749;X;784~~REC (1.29138E-32)~~898;X;962~~HPT (0.00000196994)~~1035	non-KdpD DUF4118 protein
	0.0066	26	8.7	0.012	25.1	6	1.4	1	K9WCX2_9CYAN	Histidine kinase (EC 2.7.13.3)	Mic7113_2453	Microcoleus sp. PCC 7113	1178	1173027	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	>tr|K9WCX2|K9WCX2_9CYAN Histidine kinase OS=Microcoleus sp. PCC 7113 GN=Mic7113_2453 PE=4 SV=1MVRATQSQMQPYGVAVLAVGLAMLLMRLLNSWVTMSHSPFLMFFGAVMVSAWYGGMGAGLFATFLSALLSTYFIDSPSHGLAFSLSNSLRLSVFVLEGILISGLCETLLTTNRQLQVSVRKLRESEERYRRVLDTAYEGIWTVDAQGQINYVNQRIAEILGYTMQNMLARPMFDFMDEEAQSEANHYLERQQQGIKEQYDFRFRHQDGSSVWAIVSTSPICSETGEFQGAIAMITDVSERKRAEESLREQAATLQNQQSWLESVLNFLPSPLLIEPGTARVTFANQAADQMAGGEFPKNKPSEEYHTVYYCTDAKGERIPDDQMPGVRVARGEQLKGFEMDWHTPEGIRSLIIFADTLSPMYGHPPTCVLVFQDISERKRVEQALELRLQQQAIVAQLSQRALSGIELSTLIDEVPILVAQSLDVEYCKVLELLPDGKALLLRSGVGWHPGLVGHATVGSETHSQAGYTLLSSQPVIVEDLRKETRFNGPPLLHEHQVISGMSVIIHGQNRPFGVFGVHTTRKQKFSQNDINFLQAVANVLAIAIEIERKRAEEAMRESQELFERFMSHAPVVAFIKDEQGRFLYVNSLLERTWNRPLADWLGKTDFDLFPAEQAQQWRDNDTAVLAGDKAVQLLETSVNQDRVQSWLSFKFPFIDASGRRFLAGMSLDISDRKRLEDELRQSEAKFRRLFDANIVGIIFSDFSGKILEANDAFLEMVGYTREDLHAGRVCWDTMTPSEYKPLDELAIAELRTSGVCTAFEKEYIRQDGSRVPVLLIGALLEGEPEQAVSFILDLSDRKQALAELRESESRFRNMADTAPVLIWMSGTDKLCNYFNQPWLDFTGRTMEQEFGNGWAEGVHPDDYQRCLNTYMNAFDARQSFRMDYRLRRFDGEYRWVLDTGIPRFTPDGGFLGYIGSCIDISDRVLAEEEVVKLNHSLEQRVKERTAQLEAANQELESFSYSVSHDLRAPLRHINGFVDLLQKQAATTLDERSLRYLSIITETTKQAGKLVDDLLSFSRMGRTEMRYIKVNMTLLIQEVKRDIEQDICGRNITWQIEDLPQVYGDPSMLRLVVHNLIDNAVKYTAKRDRAEIKIGSTETEDEFVFFVRDNGVGFDMRYVHKLFGVFQRLHSFQEFEGTGIGLANVKRIIDRHKGRTWAESVVKKGASFYFSLPKLNNKI	11~~DUF4118 (0.0000121981)~~102;X;136~~PAS (0.000000000000194385)~~237;X(154);391~~GAF (8.8576E-18)~~558;X(136);694~~PAS (0.000000000465338)~~796;X;818~~PAS (0.000000000111013)~~920;X;952~~HisKA (0.000000000260621)~~1018;X;1068~~HATPase_c (6.77977E-25)~~1171	non-KdpD DUF4118 protein
	0.0073	25.9	14.2	0.011	25.3	9.8	1.3	1	R7AGC1_9CLOT	Histidine kinase (EC 2.7.13.3)	BN653_00264	Clostridium sp. CAG:43	421	1262805	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:43	>tr|R7AGC1|R7AGC1_9CLOT Histidine kinase OS=Clostridium sp. CAG:43 GN=BN653_00264 PE=4 SV=1MKHSSKPSVPGTSNETFPKTESTSSLQGSAEPSSPDTSISNGGETHPSKIDALKNWFRTRPIVEKFCALPTYIQSWGLTLFFMGTATIIAFCFFYVLKNPTANIALTYILAVFLVARFTDGYSFGLFSSFVGVVCVNFLFTYPYFALDFTMAGYPITFVAMFSISSITSAITSNMKTQARVLAEREKKLMEAEKEKMRANLLRAISHDLRTPLTSIIGSSTVYLENGSSLPEVEKNALVRHILEDSNWLLNMVENLLSVTRINNETAKVTKTSEPVEEVLSEAMIRLKKRLPDANIHVRVPEEFLMVPMDAVLIEQVLINLLENAVVHAESTEPIECYVESLSDYAVFHVRDYGVGIPPEKLATIFDGSSSTTSTSPDGRKGMGIGLSICKTIILAHGGEIKAINHTRGAEFYFTLPKEDK	76~~DUF4118 (0.00000010485)~~178;X;195~~HisKA (0.000000000008090)~~261;X;314~~HATPase_c (3.03796E-24)~~416	non-KdpD DUF4118 protein
	0.0073	25.9	12.9	0.012	25.2	9	1.3	1	R6EM10_9FIRM	Histidine kinase (EC 2.7.13.3)	BN538_00485	Lachnospiraceae bacterium CAG:215	512	1262985	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:215	>tr|R6EM10|R6EM10_9FIRM Histidine kinase OS=Lachnospiraceae bacterium CAG:215 GN=BN538_00485 PE=4 SV=1MQIFNRKKKLECLRDFLITAGILAAATGIGFGFYTLGFSEENIIIVYLLGAMIVAVLTASRVWSGLAALFSVLLFNYLFTVPRFSFSAYGSGYPVTFVIAFIAAMIVGNLAVQLKRQAERSDKMAYRTQILLETNQMLQRAANEKEIVEETAGQIVKLFGRSVVCYRRNKKNLENPVVYPAGQENDLSVYFSDEERETALWAFRNHKRAGAGTDILSGAVCLYLTIRNKNNVYGVVGIDLREMVLTTAEQNLLLSVLGECALALEKEHYNRKQAEAATKAKNEQLRANLLRSISHDLRTPLTSISGNADILLQNHLDEEQRKRTCTYIYEDAIWMINLVENLLSATRIENGTMQLTKHAELLEDIIDEALKHISRKSKEYEIKKELPDEVLLVNVDSRLILQVFINLLDNAVKYTPPGGTISIETETETKFVHVRIADSGIGISEEKKKHIFDMFYMANEKIVDSRRSLGLGLALCRSIVTAHGGTIRVYDNHPKGSVFDFTLPLEEVAIHE	16~~DUF4118 (0.000000000122397)~~117;X;143~~GAF (0.000688941)~~266;X;283~~HisKA (0.000000000001115)~~347;X;400~~HATPase_c (9.25173E-28)~~503	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0076	25.8	9	0.012	25.2	6.2	1.2	1	A0A059VU36_STRA9	Osmosensitive K+ channel histidine kinase-like protein	DC74_377	Streptomyces albulus	248	68570	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	>tr|A0A059VU36|A0A059VU36_STRA9 Osmosensitive K+ channel histidine kinase-like protein OS=Streptomyces albulus GN=DC74_377 PE=4 SV=1MVRYLSRDRVALAAALVLPPAFCALLLPFRGWLSNTNAALLLVVVVVAVAVLGHRLAGALAALSAAVWFDFFLTRPYERFAITKSADLATAVLLLAVGVAVSQLAARTRELTVIAITDDDYLAQIHHTARLVESAAGPDAVVNHVRHQLVGLLGLSGCRFEYGTLIGHPPRLLEDGSLTWGRRRWDADRDGLPAEEVELRVSRGGRFHGRFMLRGAPGSVPPLAARLVAVTLANQVGAAFDAVTTARA		No DUF4118 detected by NCBI CDD

	0.0077	25.8	6.7	0.012	25.2	4.6	1.3	1	M1PTC2_DESSD	Histidine kinase (EC 2.7.13.3)	UWK_03047	Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	347	1167006	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfobacterales, Desulfobulbaceae, Desulfocapsa, Desulfocapsa sulfexigens, Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1)	>tr|M1PTC2|M1PTC2_DESSD Histidine kinase OS=Desulfocapsa sulfexigens (strain DSM 10523 / SB164P1) GN=UWK_03047 PE=4 SV=1MKNNKSNLAQKWAILAVLTVGITLLHYNTEQSLYYFHVFYGELYCIPIVLAGFWFGLRGALLVSTTITVFYLPFIYWHWQGLSPNALDSILSLCLYNGLALLTGALKDRETATREMVLQTDNLIVMGKSLAAAAHDMRSPLMLIGGFARRILKNMDDHDPARPKLTLIIQETEKMERMAEDMLDFSKPLALTKVRGNIDTTVRNGLAKVQEAARKKRVSVEYHPSPEPVDIKFDSVRFEQALINLIQNAVEASPEGDTVTIALSVSSLGSPFLDVADNGSGIPLAKRQKVFDPFFTTKKEGTGLGLPIVKKIIDAHGWSLQILDNNGGGTICRIMLKEGNGHDCIHQ	130~~HisKA (0.00000000002607)~~187;X;238~~HATPase_c (5.28759E-25)~~336	No DUF4118 detected by NCBI CDD
	0.0079	25.8	9.4	0.014	25	6.5	1.3	1	R7G954_9FIRM	Universal stress family protein	BN631_00316	Eubacterium dolichum CAG:375	629	1263076	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium dolichum CAG:375	>tr|R7G954|R7G954_9FIRM Universal stress family protein OS=Eubacterium dolichum CAG:375 GN=BN631_00316 PE=4 SV=1MQRKGRLKIFFGYCAGVGKTYSMLKEAHEKAQEGVDVVIGYIEPHDRKETISLIDGLEQLDKKEILYKKHRFYELDLDLALQRHPKLILVDELAHTNAIGSRHKKRYSDIEELLRAGIDVYTTINVQHLESLHDTVAMITRIQVNERIPDHIFDDADDVKLVDIEVDDLIQRLKDGKIYHKNQTKRALENFFVRDNLIALREIAMRRCADRINLITSTANKAFSKEHIMVCLGASPTNQKVIRTAARMVQAFHADFTALYVETSQADWITQKAKNQLQANLELARHLKADIVSTYGDDIAYQISQYAKNAHVSKLVLGRSYQKPSIFRKTTLVDQLSKLAPEIEIYIIPDQQSGAMKKKYRTLLKSKFNMQEAIITVLLVTTLFAIFLDSFHVHITSIVLLYVLASCFIGMMTFYPLYNLIATLLSLLLIDIFFVEPRFSLLMDSKEYPIMFLVMMIVSLSISMMGHRLKKEKMLASLHAHSMEVILQTSQRLQVLNTYHEIMEETCYQLFQLLHRPIIFYPVKHQELQDGVLYKACDFPAIKEQLTSIEEIAVAKWVFTNNKNAGATTNTLSHSKALYLAIRKGSCVYGVVGIRINTSNDLLPFEKNLLKAILNETALAMSSIAQQ	3~~KdpD (2.50056E-117)~~212;X;227~~Usp(9.82308E-32)~~349;X;372~~DUF4118 (0.0000344375)~~474	KdpD protein
	0.0079	25.8	10.3	0.017	24.7	7.1	1.5	1	D7C419_STRBB	Sensory histidine kinase in two-component regulatory system wtih KdpE, regulation of potassium translocation	SBI_09267	Streptomyces bingchenggensis (strain BCW-1)	758	749414	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	>tr|D7C419|D7C419_STRBB Sensory histidine kinase in two-component regulatory system wtih KdpE, regulation of potassium translocation OS=Streptomyces bingchenggensis (strain BCW-1) GN=SBI_09267 PE=4 SV=1MARGRLRIHLGAAPGVGKTYAMLQEGQRLRSLGTEVVIGLVEPHGRRPTAALAEGLETIPRHTLVHRGVSFTEMDLDAVLARRPQVALVDELAHTNVPGSRNAKRWQDVEELLEAGIDVVTTLNVQHLESLNDVVRQITGVTQHETLPDEVARRADQIELVDLLPETLRRRLVHGDVYPPDRIEAALTHYFRVGNLTALRELALLWLADRVEEGLQRYRAEHGITAPWETRERILVGLTGGPEGETLIRRAARITACTPGSELLALHVVPGDGLARGDPAALSGQRSLVESMGGSYHQMTGEDIPEALLQFAEAENITQVVLGASRRGRFSLLLHAGVGQRTIHDSGPIDVHIVTHEAAAGASAPRLPRPGHGGTGPVRYWSALVGAALLLPLMTLVLTGLRTGVGLSGALVLYLLAVVLAGLVGGRLPALLTAVAAGLLTDYYFTPPLHSFKVERGVDVVGLVVFLAAAWLVGSAAGTAARHTYQAVRATSEARALSRMAAAMMRGEPLPTLLEQVRENFSLTAVSLLERGTDHGPEPRWYVVASTGVRPPERPYDADVEAPIDDRLTLAARGRGLSGDDRRILTACAAQIGVAHTQGGLARRGAGTDLDEQGRPRAAALYLRPVDLDEALTAALDDLGPGGHSISLRLPERLPDVIADAALLARVLATLVADALRHSPPDAPPTLTAEALPDRLTVRIAGDTTGGAVDGERESPSLRLARDLTEAMGGTVEHTSGGGAASVTITLPTVAQHPDPEG	1~~KdpD (1.63608E-118)~~211;X;233~~Usp(1.06926E-26)~~355;X(309);664~~HATPase_c (0.000149664)~~747	KdpD protein
	0.0082	25.7	6.3	0.017	24.7	4.3	1.5	1	A0A0B5DGU4_9ACTN	Histidine kinase (EC 2.7.13.3)	SNOD_25015	Streptomyces nodosus	847	40318	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces nodosus	>tr|A0A0B5DGU4|A0A0B5DGU4_9ACTN Histidine kinase OS=Streptomyces nodosus GN=SNOD_25015 PE=4 SV=1MGRGKLRIYLGAAPGVGKTYAMLSEAHRRVERGTDCAVAFVEHHDRPRTEVMLHGLEQIPRKELVHRGSVFTEMDVDAVLHRAPAVALVDELAHTNVPGSRNAKRWQDVEELLAAGINVVSTVNIQHLESLGDVVESITGIRQRETVPDEVVRRADQIELVDMSPQALRRRMAHGNIYQPDKVDAALSNYFRPGNLTALRELALLWVADRVDEYLTEYRSQHKVSTIWGSRERIVVGLTGGPEGRTLIRRAARLAEKGAGGEVLAVYIARSDGLTSASPKELAVQRTLVEDLGGTFHHVVGDDIPAALLDFARGVNATQIILGSSRRKAWQYVFGPGVGATVARESGPDLDVHIVTHDEVAKGRGLPVARGARLGRTRIVAGWLTGVLGPVVLALLLNSVRLGLANDMLLFLTLTVAAALLGGLFPALASAAFGSLLLNYYYTPPLHRLTIADPKNIVAIAIFVGVAVSVASVVDLAARRTHQAARLRAESEILSFLAGSVLRGETSLEALLERVRETFGMESAALLERTSEVDPWTCAGSVGLSAPVARPDDADVDVPAGDHMALALSGRVLPASDRRVLAAFAAQAAVVLDRQRLQQEAEQARALAEGNRIRTALLAAVSHDLRTPLAGIKASVTSLRSDDVEWSEEDRAELLAAIEEGADRLDHLVGNLLDMSRLQTGTVTPLIREVDLDEVVPMALGGVPEDSVELDIPESLPIVAVDAGLLERAVANLVENAVKYSSLGTPVLVSASAALADRVEVRVVDRGPGVPDDAKERIFEPFQRHGDAPRGAGVGLGLAVARGFAEAMGGTLNAEDTPGGGLTMVLTLRAVQGRQDPARLAEAERQTT	1~~KdpD (1.13503E-122)~~211;X;233~~Usp(1.10782E-31)~~356;X;391~~DUF4118 (0.0000297384)~~463;X(148);611~~HisKA (0.00000000000101041)~~677;X;726~~HATPase_c (5.12702E-27)~~827	KdpD protein
Disagreement between HMM and CDD prediction	0.0082	25.7	8.4	0.013	25	5.8	1.4	1	Q6ABI9_PROAC	Histidine kinase (EC 2.7.13.3)	PPA0118	Propionibacterium acnes (strain KPA171202 / DSM 16379)	830	267747	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Propionibacterium, Propionibacterium acnes, Propionibacterium acnes (strain KPA171202 / DSM 16379)	>tr|Q6ABI9|Q6ABI9_PROAC Histidine kinase OS=Propionibacterium acnes (strain KPA171202 / DSM 16379) GN=PPA0118 PE=4 SV=1MAVRGRLRVLLGAAPGVGKTYAMLDEGKHLRAGGSDVVIAVVETHGRAATAAMTEGMEVIPRHYVECRGIELPEMDLDGVLAQHPDVALVDELAHTNAPGSRNEKRWQDVEELLEAGIDVISTVNIQHIESLNDVVEQITGVPQRETVPDTVLRRASQVEVVDLAPQALRDRLSSGKVYPAERIDAALSNYFRLGNLTALRELALLWVADEVDHALADYRSEHGIDSRWEARERVVVALTGGREGETLLRRGARIAVRAGGGELLAVHVTTEDGLRSPHPGELARQRGLVDKLGGSFHQLVGDDIPETLIEFAKSVNATQLVIGASRRGKLSRLLTGHDVEADIIRASGAIDVHIVSHDAQAKALRLPRMGGSLSTRRRIAGFAVLAVLGPLLTLLLVSSRSPEALTTDVLAYELLAVVVALVGGAFSSLIAALASGFALDYFFTKPFYTVTVNEPLHLVALLLYLLTAALVSVVVDRAARKTRVARRAAAESGLLQSVAGLVLRGEDAVESLLSRATEAFGLSGARLMTDGKVVANWGTTSDQVTEHRIDDHTVVEFHGPEPDASERRLMSVIAAQLGTALEQHQLEETAKAVEPLAATDRVRTALLSAVGHDLRRPLAAATAAVSGLRSEWSKLSDQDRADLLETADEALSQLANLVTDLLDVSRLQSGVLGVSVMPVDPAEVIMPALDELSLGPADVEIDLGSDVPEMVADPALLQRVVVNLLSNALRYEPAGSRVRLAESSFANQVEIRVIDHGPGIPEDRRDDVMVPFQRLGDTDSSVGLGLALSKGFVEGMDGTLALEDTPGGGLTMVISLPRVGVEEASVQ	4~~KdpD (9.90711E-119)~~212;X;234~~Usp(6.61465E-32)~~357;X(244);601~~HisKA (0.00000000318754)~~667;X;718~~HATPase_c (5.57946E-23)~~819	KdpD protein
Disagreement between HMM and CDD prediction	0.0084	25.7	5.7	0.0084	25.7	4	2.1	1	I4B5K0_TURPD	Uncharacterized protein	Turpa_1910	Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) (Leptospira parva)	206	869212	cellular organisms, Bacteria, Spirochaetes, Spirochaetia, Leptospirales, Leptospiraceae, Turneriella, Turneriella parva, Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) (Leptospira parva)	>tr|I4B5K0|I4B5K0_TURPD Uncharacterized protein OS=Turneriella parva (strain ATCC BAA-1111 / DSM 21527 / NCTC 11395 / H) GN=Turpa_1910 PE=4 SV=1MNRNRAIWEIRNEKNKASVRWVLVFAIGGYLTYLLETGKAAAVGSAPIFNGTYIMSVLAFAIAFNALVALQVHRAAARESIGRWVKYATMACDFLLVALVLIPTGGSQSLLYPLNYVIIVSNALRYGMSVAIAGTIIMNIFYLALLAYQYYPQTEIPGFHQEVLKIAGFWLVGVYTGYLSRRYEVLRGEVERYQELLAGALKKNAA		No DUF4118 detected by NCBI CDD

	0.0086	25.7	11.7	0.014	25	8.1	1.4	1	S6C135_9ACTN	Histidine kinase (EC 2.7.13.3)	AEQU_1604	Adlercreutzia equolifaciens DSM 19450	943	1384484	cellular organisms, Bacteria, Actinobacteria, Coriobacteriia, Eggerthellales, Eggerthellaceae, Adlercreutzia, Adlercreutzia equolifaciens, Adlercreutzia equolifaciens DSM 19450	>tr|S6C135|S6C135_9ACTN Histidine kinase OS=Adlercreutzia equolifaciens DSM 19450 GN=AEQU_1604 PE=4 SV=1MAEVRERWEIGGGRGDPDAILQRIREEEEAGEAERFEGRGRLKVFFGYAAGVGKTFAMLTEAHRVQDEGVDVVVGYVEPHTRADTLALLDGLEVLPVKSVKHRNVALREFDLDVALKRRPQVVLVDELAHTNAPGCRHRKRYQDVEELLRAGIDVYTTVNVQHLEGLNDKIASVTAVAPSERIPDRVFDAADSVEVVDLEPADLIKRLRSGKIYAPERIGSALSHFFSRSNLAALREIALRRAADRLTRASAATVPHAAGGEDVLVLVTADAAAPRVIRAAAGMAEAFGGSCTALVVESGGEGAEGRSKGDAALARSIALAEEMGAHIVTLTGDDPVQPVALYAAAAGIRRIVVPSMPGRIGLLLGCGDVASRLMRAAPEAMVTAVPAVDAPSVLERLRTYASFRLTASDVFRALLAIAVATALGEVAWLASPTPSIILMTYLLVALLLATRADGFLYAVLVALGSVVAYSFFFTAPRYTFHAYSLSAPIIFTVLLIGTLGASSLAIRLKRQATTAARRAYRTEVLLESSREFQAVVSLGACLETAAAQVVKILDRPVVMYQVDGAAHGGLLPPRVFDVPGSGGGDAEKLDLAAPGEMAVASWVAANGEAAGATTDTLREARCLYLPIRSKDRVFGVAGLVMEQGDDDFGSFERNLLVALLDECGQAAEALALASERKNLAVKAEKEALRSNLLRAISHDLRTPLTSISGDADMLLASGDVLDEAQRKRLTSDIHEDANWLINLVENLLSVTRLDDGDVEVSRAPELVSDVLADALRHVSRSVSEHRLTVEIEDEFLLAQMDGRLIVQVVVNLLNNAIAYTPAGSSIRLTAHRERSASGDRVVVAVADDGPGIPPAEQARVFDLFYHGGRVGTGCEDGEGGDARRGMGLGLSLCRSILRAHGSDIVLRDAYPHGCVFSFALPAAELREEAPVGVVEEGSADVER	38~~KdpD (2.04428E116)~~247;X;264~~Usp(0.000000000002 91302)~~386;X;413~~DUF4118 (0.0000000310886)~~511;X(175);686~~HisKA (0.000000000116721)~~752;X;805~~HATPase_c (4.00038E-23)~~920	KdpD protein
	0.0089	25.6	12.5	0.014	24.9	8.6	1.3	1	R7BDZ1_9FIRM	Histidine kinase (EC 2.7.13.3)	BN803_01460	Firmicutes bacterium CAG:882	352	1262991	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:882	>tr|R7BDZ1|R7BDZ1_9FIRM Histidine kinase OS=Firmicutes bacterium CAG:882 GN=BN803_01460 PE=4 SV=1MRVVKNILRMVITLFVGFMTCLAIQYFFDNDFLIPTLLVLCVFLISVYTDGYIYGTVGAVISVFIVNVAFTFPYFRISLSVSENVVSMFIMLAITLVTSYLTSKIRYQEQIKAESEKEKMRANLLRAVSHDLRTPLTTIYGASSALLEKGNDFSDEQKNKLLAGIEEDSQWLCRMVENLLSVTRLDGDNVRIAKTPIALDELIDSVLVKFHKHYPDTEVNVILPDDIVVIPMDAILMEQVIMNILENAVLHADGMDRLELEVYTQEHRAVFEIRDNGCGIPADIINNIFTGGYARQNTVADGRKGNAGIGLTVCATIVKAHGGRISVENRKTGGACFRIELELEDEYEEQQI	2~~DUF4118 (0.0000105484)~~108;X;118~~HisKA (0.000000000094064 2)~~184;X;237~~HATPase_c (4.2921E-23)~~339	non-KdpD DUF4118 protein
	0.009	25.6	12.8	0.013	25.1	8.9	1.3	1	F2IES1_FLUTR	Histidine kinase (EC 2.7.13.3)	Fluta_3669	Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	340	755732	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Cryomorphaceae, Fluviicola, Fluviicola taffensis, Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	>tr|F2IES1|F2IES1_FLUTR Histidine kinase OS=Fluviicola taffensis (strain DSM 16823 / RW262 / RW262) GN=Fluta_3669 PE=4 SV=1MLILSVAGICYYFNDLFNYKIVALILLMTVSLSAMVFNIWPVLLGATLSAFIWNFFFIEPLFNIHINQAEDFLTFLMYFFIAFINAVLTFQIRRAEKKARNKEEKEKEVKLYNTLFNSLSHELKTPLSTILGSVDMLKENRSKLTSEQEVELLHAIDKSSLRLQRQVENLLNMSRLENDMLQLKLDWTDMNEVVHQLIQRHSEFKNHPIVYQSNDSLPLMKVDSGILETVLDNIIHNAIQYTPSNSSIEIILRSENNWCILEISDAGPGFPLESLPNVFDKFYRLPESKAGGTGLGLSIVKGFIEAHQGTVTVRNRLEGGAQFLITLPVEVSFMNNLNNE	2~~DUF4118 (0.0000819788)~~95;X;113~~HisKA (0.000000000015150 6)~~175;X;227~~HATPase_c (6.36127E-29)~~327	non-KdpD DUF4118 protein
	0.0092	25.6	8	0.015	24.9	5.5	1.3	1	A0A0G0JLF8_9BACT	Multi-sensor hybrid histidine kinase	US53_C0015G0001	Microgenomates (Woesebacteria) bacterium GW2011_GWA1_37_7	265	1618545	cellular organisms, Bacteria, unclassified Bacteria, Microgenomates, unclassified Microgenomates, Microgenomates (Woesebacteria) bacterium GW2011_GWA1_37_7	>tr|A0A0G0JLF8|A0A0G0JLF8_9BACT Multi-sensor hybrid histidine kinase OS=Microgenomates (Woesebacteria) bacterium GW2011_GWA1_37_7 GN=US53_C0015G0001 PE=4 SV=1MNKDQLKILASILFYLVITFSLHPIVGNLVGMFILVPIVVSAWVYGKKGGLITGIVLAVLNYMLLRTLNILVTRDLIQIMMGSVAGIIIGFSFGFTRDKLSELENLRNQLIGLKLGVERSKDVIFITNKNGIITYANTAFTKTYGYTSDEWKGKTPRLIKSGKQTTQFYENFWGKIKSGQTIELSIINKTKDGRFISMEASVNPIISESQGILGFLAIQRDVTEKKRLDESLLSRSGELERLNSLMVDRELKMIELKDNLKNKTH	7~~DUF4118 (0.0000231399)~~91;X;120~~PAS (0.000000000627486)~~222	non-KdpD DUF4118 protein
	0.0094	25.5	9.1	0.016	24.8	6.3	1.4	1	N9GJ29_ACIHA	Histidine kinase (EC 2.7.13.3)	F927_02454	Acinetobacter haemolyticus CIP 64.3	878	1217659	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter haemolyticus, Acinetobacter haemolyticus CIP 64.3	>tr|N9GJ29|N9GJ29_ACIHA Histidine kinase OS=Acinetobacter haemolyticus CIP 64.3 GN=F927_02454 PE=4 SV=1MQIDRNNKADAWLAHSQREQSGRLTIFLGAAPGVGKTYAMLTRAHELMQQGHHVVVGVVETHGRADTQALIHGLNVIPRKSVEYQGRFLDEMDLDQILKLKPEIVLVDELAHRNVPTSRHEYRWQDVNELLDAGINVYSTLNIQHLESLNDVVYQITGIRVTETVPDVLLKRLKDIRLVDLPVPELLERMNHGKIYLADVAPHALQGFFKPANLTALRDLAIQTVAGQVDIDYREKFVAQGQIIPIQNHIMLAIDGTEFSEDLVRRAHRIAERRNATWSVISIQKSKIENTQTFAVSKAFNLARKLGADTHLLYSNHIAATILQAAYDCGASNILLGKSPQKSFWQRLFSDHIADQLLEKQHPFEITFVQPLKTKQQDRKKSLDDLSERGLDLHQREVIESSLIILAGFIVAAISDRFIGYSDLALIFIITVLLVAIRAKMLITIASVLICFLLYNYFFIEPRYTFLISAERGVITITLLVAIRAKMLITIASVLICFLLYNYFFIEPRYTFLISAERGVITIRLPLHQD	22~~KdpD (1.91235E102)~~229;X;249~~Usp(4.01278E-26)~~369;X;399~~DUF4118 (0.00000000767007)~~497;X(154);651~~HisKA (0.000000000020894 5)~~717;X;770~~HATPase_c (3.23826E-24)~~873	KdpD protein
	0.0094	25.5	9.1	0.015	24.9	6.3	1.3	1	B8GSR2_THISH	Histidine kinase (EC 2.7.13.3)	Tgr7_1885	Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	913	396588	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Thioalkalivibrio, Thioalkalivibrio sulfidiphilus, Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	>tr|B8GSR2|B8GSR2_THISH Histidine kinase OS=Thioalkalivibrio sulfidiphilus (strain HL-EbGR7) GN=Tgr7_1885 PE=4 SV=1MGTEHTGQADALLGEIKRQTAGRLTVFLGAAPGVGKTYAMLARARELHRQGVDVVIGIVETHGRSETQTMVEGLPLLPRKKVEYQGRQLEEMDLDGLLGRKPAIALVDELAHRNAPGSRHERRWQDVEELLNAGIDVYTTVNIQHLESLNDVVHQITGIRVSETVPDAVFERLRDIRLVDLPARELIERLNDGKVYLPEQAAQALQAFFSPSNLTALRELAMQTVADHVDADLRETRAARGLEGISIQRHVLIAIDGRGQSEYLVRAGARIAERRGAPWSVVVTVETGRSADAALHTDDLYRTAPTRNMVARAEQQRLIEIDKAFALARNLGGETEVLHNTDVTQALLDAAEARGARSIVIGRTRERPIVRIFNRTLTQQLLQRGARYELTIVSTPQARQRAMELQGLASGRLTGREVVLILLASVGAVGAAALAERTLGLQDLSLIFLVAVMLVASRTRMLSAVITAGLCFVAYNFFFIEPRYTFLISAHRGVATVLLFLAAALIAGRLASQLRMQVVALRAANTHATAMQNLGRHLAKAADLGQVIASGSSVLQSTLHAEAWIRINGEAGPTTAANHLTEKDLMAADWTQQHGQASGHYTDTLTHSSWLFLPVHSDKNTLGVAGLRFPSGMGRLSFEQRRLAESMVEDIGQAAQRTRLVSELEEARVTGETERLRSALLSSVSHDLRSPLSSMIGAADSLARYAKDMGPEDQKSLLETIHVEGERLDRYIQNLLDMTRLGQQGLTLTRDWIGIDELVGSASRRLQRYEPDVRIEHDIPPDLPPIHVHPALIEQALFNVMENAAKFSPPGVPIRVQIRRTEDDQLRIDISDRGPGIPEDERRRIFDMFYSVERGDRGKQGTGLGLTIVQGIVGAHMGSVQALPGPEGKGTTIRLTLPWGGYANQEAKEHDGTS	22~~KdpD (2.60486E120)~~229;X;250~~Usp(2.21692E-28)~~393;X;445~~DUF4118 (0.000141531)~~488;X(185);673~~HisKA (0.000000000017183 8)~~739;X;792~~HATPase_c (7.54832E-23)~~896	KdpD protein

	0.0095	25.5	12.1	0.015	24.8	8.4	1.3	1	E4T4P9_PALPW	Histidine kinase (EC 2.7.13.3)	Palpr_1547	Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	395	694427	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Paludibacter, Paludibacter propionicigenes, Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	>tr|E4T4P9|E4T4P9_PALPW Histidine kinase OS=Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4) GN=Palpr_1547 PE=4 SV=1MKLNYFHQSMFKQVVISNLSVVLVALICYASLNYIGYHSVALLLLATVSVLSIFFTIYPVLSAAAMSAIIWDFFFIPPHFTLHITNSEDALLLLMYFVIALTSGILTSKVRELEKQEFLKEERSHTLRLYKTLFDSISHELRTPIATIVGASDNLLQNDVKIAEKDKLELVDQISVAAFRLNRLIDNLLNMQRVESGMLEIKPDWCEVSELINSPVNRLKNELVGHNVEVNIQPEMPIVRIDFGLIEQSVFNLLHNEVLYTQPDSTISINASYDGKNLIITIADNGKGFSEEELKLLFTKFYRISVNKTGGTGLGLSIVKGFVEAHNGTVKVENNTPNGAKFTIVIPVETLMLQDYMDFSNIAVKMNAQYETLTETYRPKQFGKTKDSTTDNSEE	19~~DUF4118 (0.0000000352588)~~112;X;127~~HisKA (0.000000000679838)~~193;X;246~~HATPase_c (1.3203E-25)~~346	non-KdpD DUF4118 protein
Disagreement between HMM and CDD prediction	0.0096	25.5	11.2	0.0096	25.5	7.8	2.3	1	A8AD85_CITK8	Uncharacterized protein	CKO_00285	Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	749	290338	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Citrobacter, Citrobacter koseri (Citrobacter diversus), Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696)	>tr|A8AD85|A8AD85_CITK8 Uncharacterized protein OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=CKO_00285 PE=4 SV=1MKLNQTYIKIRDKWWVLPLILPSLLLPILSIANTYAHTNTGSGNVTLFYLPLAFTISLMSFFDWAALPGIAVAIFWNRYPIVGLYETLSIIGHFIIPVVLCWGGYRVFTPRRNQVSHGDAHLMFQRMFWQVFCPATLFLVLFQFAAFLGMYASKSSMMGVMPFNINTLINYQALLVGNLIGVPLCYFIIRTVRNPLYLRGYYAQLKQQFDKKVTKKEVVIWLLLVLTLLMTMLCMPLNENSSIFSTNYTLSLLLPVMLWGAMRYGYRFISLIWSAVLITAIHYYQSYMPYYSGYDTQLTITSSSYLVFSFIVSYMAVLATRQRIVSGRARRLAYLDPVVHLPNLRALNRVVLKNSPWSALCFLRVPGLELLGKNYGVMLRIQYKQKLSHWINTLLAPGECVYQLSGHDLILRLNMESHQQRIEALDNHIKQFRFMWDDMPLQPQVGVSYCYVRSPVSHIYLLLGELSTIADLSLMTNKPENMQRRGAMHLQRDLKDKVAMMNRLQYALEHDHFCLMAQPISGIRGDVYHEILLRLKDDNGGMINPDGFLPVAHEFGLSSSIDLWVIENTLRFMAENRDKLPAHRFAINLSPTSVCRAQFPIDVSNLLSQYEVEAWQLIFEVTESNAFTNAEQGQATLSQLQQLGCQIAIDDFGTGYASYARLKNVSANILKIDGSFIRNIVSNSLDYQIVASICHLARMKNMQVVAEYVESEEIRSAVSALGIDYLQGYLLGEPRPLAATLEEVQAPLSGA	42~~MASE1 (1.42556E-40)~~322;X;330~~Nucleotidyl_cyc_III (3.85119E-20)~~476;X;500~~EAL (5.12044E-82)~~737	No DUF4118 detected by NCBI CDD
	0.0098	25.5	9.1	0.016	24.8	6.3	1.3	1	A0A0F6YNI6_9DELT	Chemotaxis protein methyltransferase CheR	DB32_007637	Sandaracinus amylolyticus	536	927083	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Sorangiineae, Sandaracinaceae, Sandaracinus, Sandaracinus amylolyticus	>tr|A0A0F6YNI6|A0A0F6YNI6_9DELT Chemotaxis protein methyltransferase CheR OS=Sandaracinus amylolyticus GN=DB32_007637 PE=4 SV=1MRTNARARRALRALAIASVATLVVALLHVWLRPWLGSTASLMLFLLAVYVSASVAGMLGGSIAAVLGVLVGSVFFMGRPGELGPLASGDQVRVVFFLAVAIAMSATSELLLRTRRRLQREVDARSDALAERERKLLLRERDARANAESMARLRDEFVGTVSHELRTPVNAILGFAVLLRQRASVDPKIVRGLEVIERNARAQARLIDDMLDLGRILGGKMALVPERLDLRVPIRDALESVRMSARAKHLVLEIDLGEEAVPVMGDAGRLQQVAWNLLSNALKFTPSGGRVRVALRREDERAVLDVIDTGEGIDPAFLPHVFDRFRQQDASSTRVHGGMGIGLAITRQLIELHGGRVRAESAGRGRGARFEVSLPIAEPGAQPHAEEAMPTRPSAVTPVPLAHGLLEGARVLLVEDDPDSREAVREGLRSSGAMVDAADAAEPALALLDRGRYDVLVSDIGMPGHDGWWLMREVRRAAAQYSRIPAIAISGFVREEDARASSEAGFDRHVGKPLDPIELAREIARMIGRPSDVTSAPS	19~~DUF4118 (0.00000648862)~~104;X;150~~HisKA (0.000000000000114082)~~213;X;268~~HATPase_c (2.31529E-32)~~372;X;410~~REC (7.81094E-16)~~525	non-KdpD DUF4118 protein
	0.0098	25.5	0.4	0.0098	25.5	0.3	2.5	1	F5LGN2_9BACL	Diguanylate cyclase (GGDEF) domain protein	HMPREF9413_0244	Paenibacillus sp. HGF7	371	944559	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. HGF7	>tr|F5LGN2|F5LGN2_9BACL Diguanylate cyclase (GGDEF) domain protein OS=Paenibacillus sp. HGF7 GN=HMPREF9413_0244 PE=4 SV=1MSEYLVALTIACTLVTLSYLALKIQRMHFFENYEKIASPVLTGLACILLMQQPLSLDTGAVDLRYLPVVMAGLRYGLGNALFSTLLPTLYCFLTAEDSMWVMQTLQSLIIPAVLSSGFHRSEFRTGSKPIPIWAGLKISVLLFLTQVVIYAAVHTGRHALSESYPLLFMSVVSAVSCLLIGMSNDENAKWLTQRKLEMKASQDLLTGLPNLRSFFEIAGRTLGFRAVSIFMIDIDNFKQYNDCWGHLHGDQLLRETGRLLKNVVAEHDYIARYGGEEFILMSTETDPVKLREYAEKIRLAVAAYPFEHAETTPVTVSIGISAAADAAADLQLLIDEADRALYISKNTGKNRITLCSESPEPALLEQQNAY	204~~Nucleotidyl_cyc_III (1.34571E-51)~~353	No DUF4118 detected by NCBI CDD

Sheet 7

Leave Identifier	Organism	Taxonomic lineage (ALL)	KdpD group
A0A0A1DR30	Nocardioides simplex (Arthrobacter simplex)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Pimelobacter, Nocardioides simplex (Arthrobacter simplex)	kinase
F5XJC8	Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Microlunatus, Microlunatus phosphovorus, Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)	kinase
A0A075JHN9	Dermacoccus nishinomiyaensis	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Dermacoccaceae, Dermacoccus, Dermacoccus nishinomiyaensis	kinase
D5UVQ0	Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Tsukamurellaceae, Tsukamurella, Tsukamurella paurometabola (Corynebacterium paurometabolum), Tsukamurella paurometabola (strain ATCC 8368 / DSM 20162 / JCM 10117 / NBRC 16120 / NCTC 13040) (Corynebacterium paurometabolum)	kinase
A6W6R8	Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Kineosporiales, Kineosporiaceae, Kineococcus, Kineococcus radiotolerans, Kineococcus radiotolerans (strain ATCC BAA-149 / DSM 14245 / SRS30216)	kinase
C5C3W2	Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Beutenbergiaceae, Beutenbergia, Beutenbergia cavernae, Beutenbergia cavernae (strain ATCC BAA-8 / DSM 12333 / NBRC 16432)	kinase
D7C8J1	Streptomyces bingchenggensis (strain BCW-1)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	kinase
G2P2E4	Streptomyces violaceusniger Tu 4113	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces violaceusniger, Streptomyces violaceusniger Tu 4113	kinase
F2R822	Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces venezuelae, Streptomyces venezuelae (strain ATCC 10712 / CBS 650.69 / DSM 40230 / JCM 4526 / NBRC 13096 / PD 04745)	kinase
B5H8P9	Streptomyces pristinaespiralis ATCC 25486	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pristinaespiralis, Streptomyces pristinaespiralis ATCC 25486	kinase
A0A0A8EGX6	Streptomyces sp. 769	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	kinase
A0A059W4G8	Streptomyces albulus	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	kinase
A0A0D4DJP8	Streptomyces lydicus A02	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces lydicus, Streptomyces lydicus A02	kinase
K4R5Q9	Streptomyces davawensis JCM 4913	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces davawensis, Streptomyces davawensis JCM 4913	kinase
K4R0W2	Streptomyces davawensis JCM 4913	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces davawensis, Streptomyces davawensis JCM 4913	kinase
A0A0C5FSD5	Streptomyces cyaneogriseus subsp. noncyanogenus	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cyaneogriseus, Streptomyces cyaneogriseus subsp. noncyanogenus	kinase
D7BWQ6	Streptomyces bingchenggensis (strain BCW-1)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	kinase
H2K2C9	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	kinase
S5VP11	Streptomyces collinus Tu 365	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces collinus, Streptomyces collinus Tu 365	kinase
A0A0B5DGU4	Streptomyces nodosus	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces nodosus	kinase
O54137	Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albidoflavus group, Streptomyces coelicolor, Streptomyces coelicolor (strain ATCC BAA-471 / A3(2) / M145)	kinase
Q82KK7	Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces avermitilis, Streptomyces avermitilis (strain ATCC 31267 / DSM 46492 / JCM 5070 / NBRC 14893 / NCIMB 12804 / NRRL 8165 / MA-4680)	kinase
C9Z0G1	Streptomyces scabiei (strain 87.22)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces scabiei, Streptomyces scabiei (strain 87.22)	kinase
B1VXM4	Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces griseus group, Streptomyces griseus subgroup, Streptomyces griseus, Streptomyces griseus subsp. griseus, Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350)	kinase
A0A0F7NCT0	Streptomyces sp. CNQ-509	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. CNQ-509	kinase
G8X3F8	Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces cattleya, Streptomyces cattleya (strain ATCC 35852 / DSM 46488 / JCM 4925 / NBRC 14057 / NRRL 8057)	kinase
A0A0F7CQ87	Streptomyces xiamenensis	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces xiamenensis	kinase
E4NB97	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Kitasatospora, Kitasatospora setae, Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	kinase
D6ZE67	Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Segniliparaceae, Segniliparus, Segniliparus rotundus, Segniliparus rotundus (strain ATCC BAA-972 / CDC 1076 / CIP 108378 / DSM 44985 / JCM 13578)	kinase

A0A0D5AEG1	Rhodococcus sp. B7740	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus sp. B7740	kinase
C1A1E6	Rhodococcus erythropolis (strain PR4 / NBRC 100887)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus erythropolis (Arthrobacter picolinophilus), Rhodococcus erythropolis (strain PR4 / NBRC 100887)	kinase
Q0SHD3	Rhodococcus jostii (strain RHA1)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Rhodococcus, Rhodococcus jostii, Rhodococcus jostii (strain RHA1)	kinase
A0A0A1FTM0	Mycobacterium sp. VKM Ac-1817D	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. VKM Ac-1817D	kinase
U5WM98	Mycobacterium kansasii ATCC 12478	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium kansasii, Mycobacterium kansasii ATCC 12478	kinase
Q741U1	Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium avium complex (MAC), Mycobacterium avium, Mycobacterium paratuberculosis, Mycobacterium paratuberculosis (strain ATCC BAA-968 / K-10)	kinase
A0R398	Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)	kinase
B2HPR8	Mycobacterium marinum (strain ATCC BAA-535 / M)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium marinum, Mycobacterium marinum (strain ATCC BAA-535 / M)	kinase
P9WGL3	Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex, Mycobacterium tuberculosis, Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)	kinase
G8RR39	Mycobacterium rhodesiae (strain NBB3)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium rhodesiae, Mycobacterium rhodesiae (strain NBB3)	kinase
A1TED5	Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium vanbaalenii, Mycobacterium vanbaalenii (strain DSM 7251 / PYR-1)	kinase
L0J3C9	Mycobacterium smegmatis JS623	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium smegmatis, Mycobacterium smegmatis JS623	kinase
V5XI24	Mycobacterium neoaurum VKM Ac-1815D	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	kinase
A1UKX9	Mycobacterium sp. (strain KMS)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium sp. (strain KMS)	kinase
V5XHB1	Mycobacterium neoaurum VKM Ac-1815D	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	non-kinase
W5TT91	Nocardia nova SH22a	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia nova, Nocardia nova SH22a	kinase
H6R5W2	Nocardia cyriacigeorgica (strain GUH-2)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia cyriacigeorgica, Nocardia cyriacigeorgica (strain GUH-2)	kinase
B1MDK8	Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium chelonae group, Mycobacterium abscessus subgroup, Mycobacterium abscessus, Mycobacterium abscessus (strain ATCC 19977 / DSM 44196 / CIP 104536 / JCM 13569 / NCTC 13031 / TMC 1543)	kinase
Q5YZH6	Nocardia farcinica (strain IFM 10152)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Nocardiaceae, Nocardia, Nocardia farcinica, Nocardia farcinica (strain IFM 10152)	kinase
G0FV52	Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis mediterranei (Nocardia mediterranei), Amycolatopsis mediterranei (strain S699) (Nocardia mediterranei)	kinase
R4T157	Amycolatopsis orientalis HCCB10007	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Amycolatopsis, Amycolatopsis orientalis (Nocardia orientalis), Amycolatopsis orientalis HCCB10007	kinase
K0K8R8	Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Saccharothrix, Saccharothrix espanaensis, Saccharothrix espanaensis (strain ATCC 51144 / DSM 44229 / JCM 9112 / NBRC 15066 / NRRL 15764)	kinase
F4CT89	Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Pseudonocardiales, Pseudonocardiaceae, Pseudonocardia, Pseudonocardia dioxanivorans, Pseudonocardia dioxanivorans (strain ATCC 55486 / DSM 44775 / JCM 13855 / CB1190)	kinase
I4ETM6	Modestobacter marinus (strain BC501)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Geodermatophilales, Geodermatophilaceae, Modestobacter, Modestobacter multiseptatus, Modestobacter marinus (strain BC501)	kinase
D7C419	Streptomyces bingchenggensis (strain BCW-1)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	semi-kinase
D2ATK3	Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Streptosporangiaceae, Streptosporangium, Streptosporangium roseum, Streptosporangium roseum (strain ATCC 12428 / DSM 43021 / JCM 3005 / NI 9100)	kinase
C8XB10	Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Nakamurellales, Nakamurellaceae, Nakamurella, Nakamurella multipartita, Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / JCM 9543 / Y-104) (Microsphaera multipartita)	semi-kinase
I0H1T1	Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes missouriensis, Actinoplanes missouriensis (strain ATCC 14538 / DSM 43046 / CBS 188.64 / JCM 3121 / NCIMB 12654 / NBRC 102363 / 431)	kinase
U5VTG1	Actinoplanes friuliensis DSM 7358	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	kinase
R4LG40	Actinoplanes sp. N902-109	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	kinase
R4LLR9	Actinoplanes sp. N902-109	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes sp. N902-109	kinase

U5VZI3	Actinoplanes friuliensis DSM 7358	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Actinoplanes, Actinoplanes friuliensis, Actinoplanes friuliensis DSM 7358	kinase
F4F4Z0	Verrucosispora maris (strain AB-18-032)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Verrucosispora, Verrucosispora maris, Verrucosispora maris (strain AB-18-032)	kinase
D9T8N8	Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micromonosporales, Micromonosporaceae, Micromonospora, Micromonospora aurantiaca, Micromonospora aurantiaca (strain ATCC 27029 / DSM 43813 / JCM 10878 / NBRC 16125 / INA 9442)	kinase
E3JB50	Frankia sp. (strain EuI1c)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain EuI1c)	kinase
Q0RF14	Frankia alni (strain ACN14a)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia alni, Frankia alni (strain ACN14a)	kinase
F8AWU8	Frankia symbiont subsp. Datisca glomerata	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia symbiont subsp. Datisca glomerata	kinase
Q2J7V2	Frankia sp. (strain CcI3)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Frankiales, Frankiaceae, Frankia, Frankia sp. (strain CcI3)	kinase
D2Q286	Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Nocardioidaceae, Kribbella, Kribbella flavida, Kribbella flavida (strain DSM 17836 / JCM 10339 / NBRC 14399)	kinase
E4NDZ4	Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Kitasatospora, Kitasatospora setae, Kitasatospora setae (strain ATCC 33774 / DSM 43861 / JCM 3304 / KCC A-0304 / NBRC 14216 / KM-6054) (Streptomyces setae)	kinase
H2JYA4	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	kinase
D7BWR2	Streptomyces bingchenggensis (strain BCW-1)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces bingchenggensis, Streptomyces bingchenggensis (strain BCW-1)	kinase
A0A059VV35	Streptomyces albulus	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces albulus	kinase
A0JW43	Arthrobacter sp. (strain FB24)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter sp. (strain FB24)	kinase
B8H6X0	Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Micrococcaceae, Arthrobacter, Arthrobacter chlorophenolicus, Arthrobacter chlorophenolicus (strain ATCC 700700 / DSM 12829 / JCM 12360 / NCIMB 13794 / A6)	kinase
E8N7S7	Microbacterium testaceum (strain StLB037)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Micrococcales, Microbacteriaceae, Microbacterium, Microbacterium testaceum (Aureobacterium testaceum) (Brevibacterium testaceum), Microbacterium testaceum (strain StLB037)	kinase
D7B3Y2	Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptosporangiales, Nocardiopsaceae, Nocardiopsis, Nocardiopsis dassonvillei, Nocardiopsis dassonvillei subsp. dassonvillei, Nocardiopsis dassonvillei (strain ATCC 23218 / DSM 43111 / IMRU 509 / JCM 7437 / NCTC 10488) (Actinomadura dassonvillei)	kinase
Q6ABI9	Propionibacterium acnes (strain KPA171202 / DSM 16379)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Propionibacteriales, Propionibacteriaceae, Propionibacterium, Propionibacterium acnes, Propionibacterium acnes (strain KPA171202 / DSM 16379)	kinase
Q4JUR7	Corynebacterium jeikeium (strain K411)	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Corynebacteriaceae, Corynebacterium, Corynebacterium jeikeium, Corynebacterium jeikeium (strain K411)	kinase
D1CGX0	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	cellular organisms, Bacteria, unclassified Bacteria, Thermobaculum, Thermobaculum terrenum, Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	non-kinase
Q2W609	Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum magneticum, Magnetospirillum magneticum (strain AMB-1 / ATCC 700264)	kinase
V6F0X5	Magnetospirillum gryphiswaldense MSR-1 v2	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Magnetospirillum, Magnetospirillum gryphiswaldense, Magnetospirillum gryphiswaldense MSR-1, Magnetospirillum gryphiswaldense MSR-1 v2	kinase
D3P2B3	Azospirillum sp. (strain B510)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Azospirillum, Azospirillum lipoferum, Azospirillum sp. (strain B510)	kinase
A0A023NTT4	Dyella jiangningensis	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Dyella, Dyella jiangningensis	kinase
Q8PCL9	Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas campestris, Xanthomonas campestris pv. campestris, Xanthomonas campestris pv. campestris (strain ATCC 33913 / DSM 3586 / NCPPB 528 / LMG 568 / P 25)	kinase
A0A0A8DVX1	Xanthomonas sacchari	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Xanthomonas, Xanthomonas sacchari	kinase
B2FJW7	Stenotrophomonas maltophilia (strain K279a)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales, Xanthomonadaceae, Stenotrophomonas, Stenotrophomonas maltophilia group, Stenotrophomonas maltophilia (Pseudomonas maltophilia) (Xanthomonas maltophilia), Stenotrophomonas maltophilia (strain K279a)	kinase
B0VM40	Acinetobacter baumannii (strain SDF)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Moraxellaceae, Acinetobacter, Acinetobacter calcoaceticus/baumannii complex, Acinetobacter baumannii, Acinetobacter baumannii (strain SDF)	kinase
E1VQU2	gamma proteobacterium HdN1	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, unclassified Gammaproteobacteria, unclassified Gammaproteobacteria (miscellaneous), gamma proteobacterium HdN1	kinase
A6V7N5	Pseudomonas aeruginosa (strain PA7)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	kinase
B8GSR2	Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Ectothiorhodospiraceae (purple sulfur bacteria), Thioalkalivibrio, Thioalkalivibrio sulfidiphilus, Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)	kinase
F4GEN7	Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Alicycliphilus, Alicycliphilus denitrificans, Alicycliphilus denitrificans (strain DSM 14773 / CIP 107495 / K601)	kinase

D3RSE1	Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Chromatiales, Chromatiaceae, Allochromatium, Allochromatium vinosum (Chromatium vinosum), Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / NCIMB 10441 / D) (Chromatium vinosum)	kinase
G8Q1U4	Pseudomonas fluorescens F113	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens F113	kinase
C3K5J9	Pseudomonas fluorescens (strain SBW25)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas fluorescens, Pseudomonas fluorescens (strain SBW25)	kinase
Q4K8P7	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	kinase
Q88FD9	Pseudomonas putida (strain KT2440)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas putida group, Pseudomonas putida (Arthrobacter siderocapsulatus), Pseudomonas putida (strain KT2440)	kinase
A0A077LKJ0	Pseudomonas sp. StFLB209	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. StFLB209	kinase
Q883V3	Pseudomonas syringae pv. tomato (strain DC3000)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas syringae group, Pseudomonas syringae group genomosp. 3, Pseudomonas syringae pv. tomato, Pseudomonas syringae pv. tomato (strain DC3000)	kinase
A6V7F6	Pseudomonas aeruginosa (strain PA7)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain PA7)	kinase
Q9I389	Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas aeruginosa group, Pseudomonas aeruginosa, Pseudomonas aeruginosa (strain ATCC 15692 / PAO1 / 1C / PRS 101 / LMG 12228)	kinase
Q3IYD7	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodobacterales, Rhodobacteraceae, Rhodobacter, Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides), Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)	kinase
A0A0B4Y426	Thalassospira xiamenensis M-5 = DSM 17429	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), Thalassospira, Thalassospira xiamenensis, Thalassospira xiamenensis M-5 = DSM 17429	kinase
Q89FC5	Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium diazoefficiens, Bradyrhizobium diazoefficiens (strain JCM 10833 / IAM 13628 / NBRC 14792 / USDA 110)	kinase
A4Z015	Bradyrhizobium sp. (strain ORS278)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Bradyrhizobium, Bradyrhizobium sp. (strain ORS278)	kinase
Q6N5H3	Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Rhodopseudomonas, Rhodopseudomonas palustris, Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)	kinase
F8JAZ5	Hyphomicrobium sp. (strain MC1)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium sp. (strain MC1)	kinase
A0A0D5LMW2	Martelella endophytica	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Aurantimonadaceae, Martelella, Martelella endophytica	kinase
A7IKC2	Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Xanthobacteraceae, Xanthobacter, Xanthobacter autotrophicus, Xanthobacter autotrophicus (strain ATCC BAA-1158 / Py2)	kinase
E3I288	Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Rhodomicrobium, Rhodomicrobium vannielii, Rhodomicrobium vannielii (strain ATCC 17100 / ATH 3.1.1 / DSM 162 / LMG 4299)	kinase
B1M7D3	Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium radiotolerans, Methylobacterium radiotolerans (strain ATCC 27329 / DSM 1819 / JCM 2831)	kinase
C5APB1	Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Methylobacteriaceae, Methylobacterium, Methylobacterium extorquens group, Methylobacterium extorquens (Methylobacterium dichloromethanicum) (Protomonas extorquens), Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1)	kinase
C3KRJ3	Rhizobium sp. (strain NGR234)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Sinorhizobium fredii group, Rhizobium fredii (Sinorhizobium fredii), Rhizobium sp. (strain NGR234)	kinase
A0A068SL95	Rhizobium galegae	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Neorhizobium, Rhizobium galegae	kinase
Q7CTB1	Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Agrobacterium fabrum, Agrobacterium fabrum (strain C58 / ATCC 33970) (Agrobacterium tumefaciens (strain C58))	kinase
B6JA61	Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Bradyrhizobiaceae, Oligotropha, Oligotropha carboxidovorans (Pseudomonas carboxydovorans), Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5)	kinase
A6X5I1	Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Brucellaceae, Ochrobactrum, Ochrobactrum anthropi, Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / NCTC 12168)	kinase
Q98GX8	Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae, Mesorhizobium, Rhizobium loti (Mesorhizobium loti), Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)	kinase
B9JKR0	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium tumefaciens complex, Rhizobium radiobacter (Agrobacterium tumefaciens) (Agrobacterium radiobacter), Agrobacterium radiobacter (strain K84 / ATCC BAA-868)	kinase
W6RZV1	Rhizobium sp. LPU83	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium sp. LPU83	kinase
Q2K0Q3	Rhizobium etli (strain CFN 42 / ATCC 51251)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Rhizobium, Rhizobium etli, Rhizobium etli (strain CFN 42 / ATCC 51251)	kinase
B8ET99	Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Beijerinckiaceae, Methylocella, Methylocella silvestris, Methylocella silvestris (strain BL2 / DSM 15510 / NCIMB 13906)	kinase
A5V6B3	Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales, Sphingomonadaceae, Sphingomonas, Sphingomonas wittichii, Sphingomonas wittichii (strain RW1 / DSM 6014 / JCM 10273)	kinase
Q92XJ2	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Rhizobium meliloti (Ensifer meliloti) (Sinorhizobium meliloti), Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)	kinase

C3MF86	Rhizobium sp. (strain NGR234)	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium, Sinorhizobium fredii group, Rhizobium fredii (Sinorhizobium fredii), Rhizobium sp. (strain NGR234)	kinase
B9K2I0	Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Rhizobium/Agrobacterium group, Agrobacterium, Agrobacterium vitis (Rhizobium vitis), Agrobacterium vitis (strain S4 / ATCC BAA-846) (Rhizobium vitis (strain S4))	kinase
N0B533	Hyphomicrobium denitrificans 1NES1	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Hyphomicrobiaceae, Hyphomicrobium, Hyphomicrobium denitrificans, Hyphomicrobium denitrificans 1NES1	kinase
B5EH77	Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter bemidjiensis, Geobacter bemidjiensis (strain Bem / ATCC BAA-1014 / DSM 16622)	kinase
Q39SW3	Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter metallireducens, Geobacter metallireducens (strain GS-15 / ATCC 53774 / DSM 7210)	kinase
B3EAQ0	Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfuromonadales, Geobacteraceae, Geobacter, Geobacter lovleyi, Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)	kinase
D5SYH6	Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Planctopirus, Planctopirus limnophila (Planctomyces limnophilus), Planctopirus limnophila (strain ATCC 43296 / DSM 3776 / IFAM 1008 / 290) (Planctomyces limnophilus)	kinase
D2R314	Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Pirellula, Pirellula staleyi, Pirellula staleyi (strain ATCC 27377 / DSM 6068 / ICPB 4128) (Pirella staleyi)	kinase
D5WU13	Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Alicyclobacillaceae, Kyrpidia, Kyrpidia tusciae, Kyrpidia tusciae (strain DSM 2912 / NBRC 15312 / T2) (Bacillus tusciae)	kinase
A0A068NN19	Fimbriimonas ginsengisoli Gsoil 348	cellular organisms, Bacteria, Armatimonadetes, Fimbriimonadia, Fimbriimonadales, Fimbriimonadaceae, Fimbriimonas, Fimbriimonas ginsengisoli, Fimbriimonas ginsengisoli Gsoil 348	kinase
A9AXU7	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Herpetosiphonales, Herpetosiphonaceae, Herpetosiphon, Herpetosiphon aurantiacus (Herpetosiphon giganteus), Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	kinase
D5MJR3	Candidatus Methylomirabilis oxyfera	cellular organisms, Bacteria, unclassified Bacteria, candidate division NC10, Candidatus Methylomirabilis, Candidatus Methylomirabilis oxyfera	kinase
G8M761	Burkholderia sp. YI23	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia sp. YI23	kinase
F2LE20	Burkholderia gladioli (strain BSR3)	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia gladioli (Pseudomonas marginata) (Phytomonas marginata), Burkholderia gladioli (strain BSR3)	kinase
C5AAP0	Burkholderia glumae (strain BGR1)	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia glumae (Pseudomonas glumae), Burkholderia glumae (strain BGR1)	kinase
A0A0D5EL36	Burkholderia ubonensis MSMB22	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia ubonensis, Burkholderia ubonensis MSMB22	kinase
A0A0D5V8M9	Burkholderia fungorum	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia fungorum	kinase
Q142K6	Burkholderia xenovorans (strain LB400)	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Burkholderiaceae, Burkholderia, Burkholderia xenovorans, Burkholderia xenovorans (strain LB400)	kinase
Q7NXN0	Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales, Chromobacteriaceae, Chromobacterium group, Chromobacterium, Chromobacterium violaceum, Chromobacterium violaceum (strain ATCC 12472 / DSM 30191 / JCM 1249 / NBRC 12614 / NCIMB 9131 / NCTC 9757)	kinase
Q4K7X9	Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas fluorescens group (fluorescent pseudomonads), Pseudomonas protegens, Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477)	kinase
D0IYP3	Comamonas testosteroni (strain CNB-2)	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Comamonadaceae, Comamonas, Comamonas testosteroni (Pseudomonas testosteroni), Comamonas testosteroni CNB-1, Comamonas testosteroni (strain CNB-2)	kinase
D8IRC8	Herbaspirillum seropedicae (strain SmR1)	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Oxalobacteraceae, Herbaspirillum, Herbaspirillum seropedicae, Herbaspirillum seropedicae (strain SmR1)	kinase
E1SHK7	Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea vagans, Pantoea vagans (strain C9-1) (Pantoea agglomerans (strain C9-1))	kinase
D4GDC9	Pantoea ananatis (strain LMG 20103)	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Pantoea, Pantoea ananas (Erwinia uredovora), Pantoea ananatis (strain LMG 20103)	kinase
B7J5L6	Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Acidithiobacillales, Acidithiobacillaceae, Acidithiobacillus, Acidithiobacillus ferrooxidans (Thiobacillus ferrooxidans), Acidithiobacillus ferrooxidans (strain ATCC 23270 / DSM 14882 / CIP 104768 / NCIMB 8455) (Ferrobacillus ferrooxidans (strain ATCC 23270))	kinase
C4XK61	Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio magneticus, Desulfovibrio magneticus (strain ATCC 700980 / DSM 13731 / RS-1)	kinase
M0QSC5	Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus stipitatus, Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	non-kinase
Q1DFX3	Myxococcus xanthus (strain DK 1622)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus xanthus, Myxococcus xanthus (strain DK 1622)	non-kinase
Q09AI1	Stigmatella aurantiaca (strain DW4/3-1)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Cystobacteraceae, Stigmatella, Stigmatella aurantiaca, Stigmatella aurantiaca (strain DW4/3-1)	non-kinase
H8MWB8	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, Corallococcus coralloides (Myxococcus coralloides), Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	non-kinase
F2NIP5	Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfobacca, Desulfobacca acetoxidans, Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	non-kinase

C1ABQ9	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadetes, Gemmatimonadales, Gemmatimonadaceae, Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	non-kinase
L0DJW0	Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	cellular organisms, Bacteria, Planctomycetes, Planctomycetia, Planctomycetales, Planctomycetaceae, Singulisphaera, Singulisphaera acidiphila, Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	non-kinase
C1F834	Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Acidobacterium, Acidobacterium capsulatum, Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	non-kinase
Q9RZN5	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus radiodurans, Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	non-kinase
Q1J2K3	Deinococcus geothermalis (strain DSM 11300)	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus geothermalis, Deinococcus geothermalis (strain DSM 11300)	non-kinase
L0A4X7	Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus peraridilitoris, Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	non-kinase
E8U858	Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	cellular organisms, Bacteria, Deinococcus-Thermus, Deinococci, Deinococcales, Deinococcaceae, Deinococcus, Deinococcus maricopensis, Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	non-kinase
Q31MG0	Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus elongatus, Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	non-kinase
Q1IUD7	Koribacter versatilis (strain Ellin345)	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Candidatus Koribacter, Candidatus Koribacter versatilis, Koribacter versatilis (strain Ellin345)	non-kinase
S0EVC4	Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	cellular organisms, Bacteria, Armatimonadetes, Chthonomonadetes, Chthonomonadales, Chthonomonadaceae, Chthonomonas, Chthonomonas calidirosea, Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	non-kinase
E6U9J4	Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ethanoligenens, Ethanoligenens harbinense, Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	non-kinase
F8I8U6	Sulfobacillus acidophilus (strain TPY)	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiales incertae sedis, Clostridiales Family XVII. Incertae Sedis, Sulfobacillus, Sulfobacillus acidophilus, Sulfobacillus acidophilus (strain TPY)	non-kinase
E0UCQ0	Cyanothece sp. (strain PCC 7822)	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7822)	non-kinase
K9XY83	Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Stanieria, Stanieria cyanosphaera, Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	non-kinase
K9TR56	Oscillatoria acuminata PCC 6304	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria acuminata, Oscillatoria acuminata PCC 6304	non-kinase
K9U0M1	Chroococcidiopsis thermalis PCC 7203	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Chroococcidiopsis, Chroococcidiopsis thermalis, Chroococcidiopsis thermalis PCC 7203	non-kinase
K9X9B6	Gloeocapsa sp. PCC 7428	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	non-kinase
K9QY28	Nostoc sp. (strain ATCC 29411 / PCC 7524)	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain ATCC 29411 / PCC 7524)	non-kinase
Q8YPF2	Nostoc sp. (strain PCC 7120 / UTEX 2576)	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	non-kinase
K9QGM4	Nostoc sp. PCC 7107	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	non-kinase
K9WYH7	Cylindrospermum stagnale PCC 7417	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Cylindrospermum, Cylindrospermum stagnale, Cylindrospermum stagnale PCC 7417	non-kinase
B2J4W2	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	non-kinase
K9PJF7	Calothrix sp. PCC 7507	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix sp. PCC 7507	non-kinase
K9ZA22	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	non-kinase
K7W0T7	Anabaena sp. 90	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena sp. 90	non-kinase
B0JYA9	Microcystis aeruginosa (strain NIES-843)	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Microcystis, Microcystis aeruginosa, Microcystis aeruginosa (strain NIES-843)	non-kinase
K9Z6H6	Cyanobacterium aponinum (strain PCC 10605)	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobacterium, Cyanobacterium aponinum, Cyanobacterium aponinum (strain PCC 10605)	non-kinase
K9VHA8	Oscillatoria nigro-viridis PCC 7112	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria nigro-viridis, Oscillatoria nigro-viridis PCC 7112	non-kinase
K9STD0	Synechococcus sp. PCC 7502	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. PCC 7502	non-kinase
K9RWZ7	Synechococcus sp. (strain ATCC 27167 / PCC 6312)	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27167 / PCC 6312)	non-kinase
B1XRS4	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Synechococcus, Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	non-kinase

B7JXL2	Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	non-kinase
B1WP54	Cyanothece sp. (strain ATCC 51142)	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain ATCC 51142)	non-kinase
B7KBV1	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	non-kinase
A0A0A7FZ16	Clostridium baratii str. Sullivan	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium baratii, Clostridium baratii str. Sullivan	non-kinase
Q8R869	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	non-kinase
B0KD64	Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Thermoanaerobacter, Thermoanaerobacter pseudethanolicus, Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	non-kinase
I3VXZ5	Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacterales Family III. Incertae Sedis, Thermoanaerobacterium, Thermoanaerobacterium saccharolyticum, Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	non-kinase
M4V6P6	Bdellovibrio exovorus JSS	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Bdellovibrionales, Bdellovibrionaceae, Bdellovibrio, Bdellovibrio exovorus, Bdellovibrio exovorus JSS	kinase
B3E0Q9	Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, unclassified Verrucomicrobia, Methylacidiphilales, Methylacidiphilaceae, Methylacidiphilum, Methylacidiphilum infernorum, Methylacidiphilum infernorum (isolate V4) (Methylokorus infernorum (strain V4))	kinase
F8L2N8	Parachlamydia acanthamoebae (strain UV7)	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Chlamydiae, Chlamydia, Chlamydiales, Parachlamydiaceae, Parachlamydia, Parachlamydia acanthamoebae, Parachlamydia acanthamoebae (strain UV7)	kinase
E4T7V3	Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Paludibacter, Paludibacter propionicigenes, Paludibacter propionicigenes (strain DSM 17365 / JCM 13257 / WB4)	kinase
D4KH79	Megamonas hypermegale ART12/1	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	non-kinase
R7RTY1	Carnobacterium maltaromaticum LMA28	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Carnobacteriaceae, Carnobacterium, Carnobacterium maltaromaticum (Carnobacterium piscicola), Carnobacterium maltaromaticum LMA28	kinase
H6LIZ9	Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Acetobacterium, Acetobacterium woodii, Acetobacterium woodii (strain ATCC 29683 / DSM 1030 / JCM 2381 / KCTC 1655)	kinase
Q8Y3Z9	Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Listeriaceae, Listeria, Listeria monocytogenes, Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)	kinase
J7IUW2	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	kinase
J7J0P9	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	non-kinase
I4D558	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	kinase
A0A075K9I1	Pelosinus sp. UFO1	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Pelosinus, Pelosinus sp. UFO1	kinase
I4D2C8	Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus acidiphilus, Desulfosporosinus acidiphilus (strain DSM 22704 / JCM 16185 / SJ4)	kinase
F0S644	Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Pseudopedobacter, Pseudopedobacter saltans, Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	non-kinase
C6VYH1	Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Dyadobacter, Dyadobacter fermentans, Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	non-kinase
D6D7W0	Bacteroides xylanisolvens XB1A	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides xylanisolvens, Bacteroides xylanisolvens XB1A	non-kinase
Q8R8I8	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	non-kinase
Q5KUV6	Geobacillus kaustophilus (strain HTA426)	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Geobacillus, Geobacillus kaustophilus, Geobacillus kaustophilus (strain HTA426)	non-kinase
B1YM39	Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sibiricum, Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	non-kinase
C4KYL1	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillales incertae sedis, Bacillales Family XII. Incertae Sedis, Exiguobacterium, Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	non-kinase
U5LHJ2	Bacillus infantis NRRL B-14911	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus infantis, Bacillus infantis NRRL B-14911	non-kinase
A7GLG6	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cytotoxicus, Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	non-kinase
Q81UW4	Bacillus anthracis	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus anthracis	non-kinase

Q81HP8	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae, Bacillus, Bacillus cereus group, Bacillus cereus, Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	non-kinase

Sheet 8

Uniprot entry name	Gene name	Organism (and Synonym)	Protein length		Taxonomic lineage (ALL)	Phylum/group	*hk*$^{K+}$ locus	HK^{K+} transmembrane type	HK^{K+} domain architecture	*rr*$^{K+}$ locus	RR^{K+} type
Q02CX3_SOLUE	Acid_0077	Solibacter usitatus (strain Ellin6076)	345	2~~KdpD (6.26984E-117) ~~212,224~~Usp (1.54758E-27) ~~341	Cellular organisms; Bacteria; Fibrobacteres/Acidobacteria group; Acidobacteria; Solibacteres, Solibacterales, Solibacteraceae, Candidatus Solibacter, Solibacter usitatus, Solibacter usitatus (strain Ellin6076)	Fibrobacteres/Acidobacteria group	Acid_0070	4TM	DUF4118,GAF hk	Acid_0071	rr (sigma70 related)
S0EVC4_CHTCT	CCALI_01549	Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	382	26~~KdpD (8.07489E-121) ~~234,256~~Usp (8.03126E-35) ~~375	Cellular organisms; Bacteria; Armatimonadetes; Chthonomonadetes, Chthonomonadales, Chthonomonadaceae, Chthonomonas, Chthonomonas calidirosea, Chthonomonas calidirosea (strain DSM 23976 / ICMP 18418 / T49)	Armatimonadetes	CCALI_01551	2TM	HAMP,PAS hk	CCALI_01550	rr (sigma70 related)
A0A068NUV8_9BACT	OP10G_3863	Fimbriimonas ginsengisoli Gsoil 348	331	1~~KdpD (7.62921E-75) ~~182,204~~Usp (1.08454E-32) ~~323	Cellular organisms; Bacteria; Armatimonadetes; Fimbriimonadia; Fimbriimonadales, Fimbriimonadaceae, Fimbriimonas, Fimbriimonas ginsengisoli, Fimbriimonas ginsengisoli Gsoil 348	Armatimonadetes	OP10G_3865	2TM	HAMP,PAS hk	OP10G_3864	rr (sigma70 related)
Q1IUD7_KORVE	Acid345_0508	Koribacter versatilis (strain Ellin345)	373	16~~KdpD (1.71949E-110) ~~226,248~~Usp (5.57085E-30) ~~369	Cellular organisms; Bacteria; Fibrobacteres/Acidobacteria group; Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Candidatus Koribacter, Candidatus Koribacter versatilis, Koribacter versatilis (strain Ellin345)	Fibrobacteres/Acidobacteria group	Acid345_0507	4TM	DUF4118,Xhk	Acid345_0509	rr (sigma70 related)
G8P0S1_GRAMM	AciX8_0324	Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	380	23~~KdpD (5.26022E-110) ~~233,255~~Usp (5.52697E-25) ~~376	Cellular organisms; Bacteria; Fibrobacteres/Acidobacteria group; Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Granulicella, Granulicella mallensis, Granulicella mallensis (strain ATCC BAA-1857 / DSM 23137 / MP5ACTX8)	Fibrobacteres/Acidobacteria group	AciX8_0323	4TM	DUF4118,Xhk	unknown	rr (sigma70 related)
E8V6Y1_TERSS	AciPR4_4262	Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	382	20~~KdpD (5.98867E-108) ~~230,252~~Usp (6.80042E-27) ~~373	Cellular organisms; Bacteria; Fibrobacteres/Acidobacteria group; Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus saanensis, Terriglobus saanensis (strain ATCC BAA-1853 / DSM 23119 / SP1PR4)	Fibrobacteres/Acidobacteria group	AciPR4_4263	4TM	DUF4118,Xhk	AciPR4_4261	rr (sigma70 related)
I3ZHZ0_TERRK	Terro_2254	Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63)	377	20~~KdpD (4.75761E-102) ~~230,252~~Usp (3.93584E-28) ~~373	Cellular organisms; Bacteria; Fibrobacteres/Acidobacteria group; Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Terriglobus, Terriglobus roseus, Terriglobus roseus (strain DSM 18391 / NRRL B-41598 / KBS 63)	Fibrobacteres/Acidobacteria group	Terro_2253	4TM	hk	Terro_2255	rr (sigma70 related)
E6U9J4_ETHHY	Ethha_1754	Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	377	20~~KdpD (2.3756E-119) ~~228,250~~Usp (4.08413E-43) ~~375	Cellular organisms; Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae, Ethanoligenens, Ethanoligenens harbinense, Ethanoligenens harbinense (strain DSM 18485 / JCM 12961 / CGMCC 1.5033 / YUAN-3)	Firmicutes	unknown		unknown	unknown	unknown
A0A0A7PZ16_9CLOT	U729_174	Clostridium baratii str. Sullivan	376	18~~KdpD (1.63698E-111) ~~227,249~~Usp (3.60018E-35) ~~374	Cellular organisms; Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae, Clostridium, Clostridium baratii, Clostridium baratii str. Sullivan	Firmicutes	U729_172	2TM	HAMP,PAS hk	U729_173	rr (sigma70 related)
I3VXZ5_THESW	Tsac_2388	Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	379	20~~KdpD (2.14748E-127) ~~230,252~~Usp (3.59439E-47) ~~377	Cellular organisms; Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacterales Family III. Incertae Sedis, Thermoanaerobacterium, Thermoanaerobacterium saccharolyticum, Thermoanaerobacterium saccharolyticum (strain DSM 8691 / JW/SL-YS485)	Firmicutes	LFE_1173	4TM	hk	Tsac_2383	rr (sigma70 related)
B0KD64_THEP3	Teth39_0496	Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	379	21~~KdpD (2.78624E-133) ~~230,252~~Usp (2.78451E-40) ~~377	Cellular organisms; Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacteraceae, Thermoanaerobacter, Thermoanaerobacter pseudethanolicus, Thermoanaerobacter pseudethanolicus (strain ATCC 33223 / 39E) (Clostridium thermohydrosulfuricum)	Firmicutes	unknown		unknown	unknown	unknown
Q8R869_CALS4	TTE2155	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	380	20~~KdpD (6.7387E-135) ~~230,252~~Usp (4.42212E-41) ~~377	Cellular organisms; Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	Firmicutes	unknown		unknown	unknown	unknown
F8I8U6_SULAT	TPY_3241	Sulfobacillus acidophilus (strain TPY)	360	7~~KdpD (2.10485E-117) ~~214,228~~Usp (4.71039E-32) ~~352	Cellular organisms; Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiales Incertae sedis, Clostridiales Family XVII. Incertae Sedis, Sulfobacillus, Sulfobacillus acidophilus, Sulfobacillus acidophilus (strain TPY)	Firmicutes	unknown		unknown	unknown	unknown
C8WRB1_ALIAD	Aaci_0254	Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	754	21~~KdpD (7.46611E-97) ~~224,247~~Usp (7.8134E-35) ~~373,400~~KdpD (6.11315E-106) ~~607,621~~Usp (5.65694E-34) ~~744	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Alicyclobacillaceae, Alicyclobacillus, Alicyclobacillus acidocaldarius, Alicyclobacillus acidocaldarius (Bacillus acidocaldarius), Alicyclobacillus acidocaldarius subsp. acidocaldarius (strain ATCC 27009 / DSM 446 / JCM 5260 / NBRC 15652 / NCIMB 11725 / NRRL B-14509 / 104-1A) (Bacillus acidocaldarius)	Firmicutes	Aaci_0250	4TM	DU4118,GAF hk	Aaci_0249	rr (sigma70 related)
F8I8U7_SULAT	TPY_3242	Sulfobacillus acidophilus (strain TPY)	371	10~~KdpD (1.86476E-93) ~~217,240~~Usp (1.53949E-27) ~~364	Cellular organisms; Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiales Incertae sedis, Clostridiales Family XVII. Incertae Sedis, Sulfobacillus, Sulfobacillus acidophilus, Sulfobacillus acidophilus (strain TPY)	Firmicutes	unknown		unknown	unknown	unknown
Q5KUV0_GEOKA	GK3245	Geobacillus kaustophilus (strain HTA426)	374	20~~KdpD (5.47856E-121) ~~230,252~~Usp (1.31718E-38) ~~372	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae, Geobacillus, Geobacillus kaustophilus, Geobacillus kaustophilus (strain HTA426)	Firmicutes	unknown		unknown	unknown	unknown
Q8R8I8_CALS4	TTE2009	Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	365	7~~KdpD (3.07006E-128) ~~217,239~~Usp (2.79724E-42) ~~361	Cellular organisms; Bacteria; Firmicutes; Clostridia; Thermoanaerobacterales; Thermoanaerobacteraceae, Caldanaerobacter, Caldanaerobacter subterraneus, Caldanaerobacter subterraneus subsp. tengcongensis, Caldanaerobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11007 / NBRC 100824 / MB4) (Thermoanaerobacter tengcongensis)	Firmicutes	unknown		unknown	unknown	unknown
A0A0D1XG31_ANEMI	AP333_0307	Aneurinibacillus migulanus (Bacillus migulanus)	383	19~~KdpD (6.33087E-119) ~~229,251~~Usp (2.2003E-39) ~~376	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Paenibacillaceae, Aneurinibacillus group, Aneurinibacillus, Aneurinibacillus migulanus (Bacillus migulanus)	Firmicutes	unknown		unknown	unknown	unknown
A0A099W3W6_9LIST	EP56_12795	Listeriaceae bacterium FSL A5-0209	383	25~~KdpD (2.21842E-111) ~~229,253~~Usp (4.42511E-35) ~~378	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Listeriaceae, unclassified Listeriaceae, Listeriaceae bacterium FSL A5-0209	Firmicutes	unknown		unknown	unknown	unknown

C4KYL1_EXISA	EAT1b_1247	Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	359	2~~KdpD (2.82524E-109) ~~210,231~~Usp (2.02404E-30) ~~356	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillales Incertae Sedis; Bacillales Family XII. Incertae Sedis; Exiguobacterium; Exiguobacterium sp. (strain ATCC BAA-1283 / AT1b)	Firmicutes	EAT1b_1260	2TM	HAMP hk	EAT1b_1259	rr (sigma70 related)
B1YM39_EXIS2	Exig_2548	Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	361	3~~KdpD (4.42688E-109) ~~211,232~~Usp (2.55099E-39) ~~357	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillales Incertae Sedis; Bacillales Family XII. Incertae Sedis; Exiguobacterium; Exiguobacterium sibiricum; Exiguobacterium sibiricum (strain DSM 17290 / JCM 13490 / 255-15)	Firmicutes	unknown		unknown	unknown	unknown
U5LH92_9BACI	N288_25405	Bacillus infantis NRRL B-14911	382	23~~KdpD (1.72478E-115) ~~233,254~~Usp (4.30831E-40) ~~379	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus infantis; Bacillus infantis NRRL B-14911	Firmicutes	N288_25380	2TM	HAMP hk	unknown	rr (sigma70 related)
A7GLG6_BACCN	Bcer98_0627	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	381	25~~KdpD (4.19754E-111) ~~235,252~~Usp (3.95331E-39) ~~377	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cytotoxicus; Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)	Firmicutes	unknown		unknown	unknown	unknown
C2W4C0_BACCE	bcere0022_0220	Bacillus cereus Rock3-44	381	25~~KdpD (3.97819E-113) ~~235,252~~Usp (2.04434E-41) ~~377	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus; Bacillus cereus Rock3-44	Firmicutes	unknown		unknown	unknown	unknown
Q81HP8_BACCR	BC_0756	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	381	26~~KdpD (4.78423E-112) ~~235,252~~Usp (5.12353E-45) ~~377	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus; Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)	Firmicutes	unknown		unknown	unknown	unknown
Q81UW4_BACAN	GBAA_0742	Bacillus anthracis	384	29~~KdpD (8.00965E-113) ~~238,255~~Usp (7.77947E-45) ~~380	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus anthracis	Firmicutes	unknown		unknown	unknown	unknown
C2WTK6_BACCE	bcere0024_0410	Bacillus cereus Rock4-18	384	29~~KdpD (4.5536E-113) ~~238,255~~Usp (8.72934E-45) ~~380	Cellular organisms; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group; Bacillus cereus; Bacillus cereus Rock4-18	Firmicutes	unknown		unknown	unknown	unknown
D3F9J1_CONWI	Cwoe_0725	Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	391	7~~KdpD (1.22714E-108) ~~217,249~~Usp (5.87203E-22) ~~372	Cellular organisms; Bacteria; Actinobacteria; Thermoleophilia; Solirubrobacterales; Conexibacteraceae; Conexibacter; Conexibacter woesei; Conexibacter woesei (strain DSM 14684 / JCM 11494 / NBRC 100937 / ID131577)	Actinobacteria	Cwoe_0719	4TM	DUF4118,Xhk	Cwoe_0720	rr (sigma70 related)
D7BJE2_MEISD	Mesil_3494	Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	370	18~~KdpD (4.77796E-120) ~~228,244~~Usp (1.20881E-36) ~~362	Cellular organisms; Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Meiothermus; Meiothermus silvanus; Meiothermus silvanus (strain ATCC 700542 / DSM 9946 / VI-R2) (Thermus silvanus)	Deinococcus-Thermus	Mesil_3487	4TM	hk	Mesil_3486	rr (sigma70 related)
E8U858_DEIML	Deima_1598	Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	371	21~~KdpD (3.78352E-113) ~~230,247~~Usp (1.11066E-33) ~~368	Cellular organisms; Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus; Deinococcus maricopensis; Deinococcus maricopensis (strain DSM 21211 / LMG 22137 / NRRL B-23946 / LB-34)	Deinococcus-Thermus	Deima_1590		hk	Deima_1589	rr (sigma70 related)
L0A4X7_DEIPD	Deipe_3483	Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	367	23~~KdpD (1.54277E-108) ~~231,244~~Usp (1.14636E-29) ~~365	Cellular organisms; Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus; Deinococcus peraridilitoris; Deinococcus peraridilitoris (strain DSM 19664 / LMG 22246 / CIP 109416 / KR-200)	Deinococcus-Thermus	unknown		unknown	unknown	unknown
Q1J2K3_DEIGD	Dgeo_2852	Deinococcus geothermalis (strain DSM 11300)	365	19~~KdpD (9.88835E-120) ~~228,243~~Usp (1.32287E-33) ~~363	Cellular organisms; Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus; Deinococcus geothermalis; Deinococcus geothermalis (strain DSM 11300)	Deinococcus-Thermus	Dgeo_2847	4TM	hk	Dgeo_2846	rr (sigma70 related)
Q9RZN5_DEIRA	DR_B0088	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	365	18~~KdpD (1.59463E-122) ~~228,243~~Usp (4.84692E-33) ~~363	Cellular organisms; Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus; Deinococcus radiodurans; Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)	Deinococcus-Thermus	DR_B0090	2TM	hk	DR_B0091	rr (sigma70 related)
H8GX33_DEIGI	DGo_CA0646	Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	339	2~~KdpD (1.21385E-107) ~~202,216~~Usp (4.09603E-28) ~~337	Cellular organisms; Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus; Deinococcus gobiensis; Deinococcus gobiensis (strain DSM 21396 / JCM 16679 / CGMCC 1.7299 / I-0)	Deinococcus-Thermus	DGo_CA0650	3TM	hk	DGo_CA0651	rr (sigma70 related)
A0A0F7SPZ3_9DEIO	SY84_13275	'Deinococcus soli' Cha et al. 2014	360	7~~KdpD (1.15587E-103) ~~214,237~~Usp (9.49576E-27) ~~358	Cellular organisms; Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus; 'Deinococcus soli' Cha et al. 2014	Deinococcus-Thermus	SY84_13295	4TM	hk	SY84_13300	rr (sigma70 related)
K9PA36_CYAGP	Cyagr_3178	Cyanobium gracile (strain ATCC 27147 / PCC 6307)	364	7~~KdpD (4.07094E-121) ~~216,229~~Usp (1.58029E-25) ~~353	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Chroococcales; Cyanobium; Cyanobium gracile; Cyanobium gracile (strain ATCC 27147 / PCC 6307)	Cyanobacteria	Cyagr_3177	4TM	hk	Cyagr_3176	rr (sigma70 related)
Q31MG0_SYNE7	Synpcc7942_1729	Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	370	7~~KdpD (8.26272E-110) ~~217,234~~Usp (9.25394E-37) ~~358	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Chroococcales; Synechococcus; Synechococcus elongatus; Synechococcus elongatus (strain PCC 7942) (Anacystis nidulans R2)	Cyanobacteria	unknown		unknown	unknown	unknown
K9RW27_SYNP3	Syn6312_2733	Synechococcus sp. (strain ATCC 27167 / PCC 6312)	373	21~~KdpD (1.58582E-116) ~~231,248~~Usp (1.64414E-44) ~~370	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Chroococcales; Synechococcus; Synechococcus sp. (strain ATCC 27167 / PCC 6312)	Cyanobacteria	Syn6312_2726	4TM	hk	Syn6312_2725	rr (sigma70 related)
B1XRS4_SYNP2	SYNPCC7002_G0054	Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	368	16~~KdpD (3.85165E-128) ~~226,244~~Usp (6.99861E-42) ~~366	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Chroococcales; Synechococcus; Synechococcus sp. (strain ATCC 27264 / PCC 7002 / PR-6) (Agmenellum quadruplicatum)	Cyanobacteria	SYNPCC7002_G0061	4TM	hk	SYNPCC7002_G0062	rr (sigma70 related)
KDPD_SYNY3	slr1731(kdpD)	Synechocystis sp. (strain PCC 6803 / Kazusa)	370	18~~KdpD (3.52355E-120) ~~228,246~~Usp (1.82614E-44) ~~368	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Chroococcales; Synechocystis; Synechocystis sp. PCC 6803; Synechocystis sp. (strain PCC 6803 / Kazusa)	Cyanobacteria	sll1590	4TM	hk	sll1592	rr (sigma70 related)
D4ZNR6_ARTPN	NIES39_O07180	Arthrospira platensis (strain NIES-39 / IAM M-135) (Spirulina platensis)	370	20~~KdpD (2.21518E-122) ~~227,245~~Usp (1.176E-45) ~~367	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Oscillatoriales; Arthrospira; Arthrospira platensis (Spirulina platensis); Arthrospira platensis (strain NIES-39 / IAM M-135) (Spirulina platensis)	Cyanobacteria	unknown		unknown	unknown	unknown
K9UP76_9CHRO	Cha6605_2200	Chamaesiphon minutus PCC 6605	365	5~~KdpD (4.61773E-120) ~~214,236~~Usp (1.65374E-43) ~~358	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Chroococcales; Chamaesiphon; Chamaesiphon minutus; Chamaesiphon minutus PCC 6605	Cyanobacteria	Cha6605_2205	4TM	hk	Cha6605_2206	rr (sigma70 related)
K9TDB0_9SYNE	Sym7502_01086	Synechococcus sp. PCC 7502	361	5~~KdpD (1.14486E-127) ~~214,234~~Usp (6.54485E-42) ~~356	Cellular organisms; Bacteria; Cyanobacteria; Oscillatoriophycideae; Chroococcales; Synechococcus; Synechococcus sp. PCC 7502	Cyanobacteria	Sym7502_01085	4TM	hk	Sym7502_01084	rr (sigma70 related)
K9VSI3_9CYAN	Cal6303_4152	Calothrix sp. PCC 6303	369	13~~KdpD (5.56341E-127) ~~223,242~~Usp (3.90014E-40) ~~366	Cellular organisms; Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Calothrix; Calothrix parietina; Calothrix sp. PCC 6303	Cyanobacteria	unknown		unknown	unknown	unknown

K7W0T7_9NOST	ANA_C11902	Anabaena sp. 90	373	17~~KdpD (1.6718E-128) ~~227,246~~Usp (8.12645E-41) ~~370	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena sp. 90	Cyanobacteria	ANA_C11907	4TM	hk	ANA_C11908	rr (sigma70 related)
K9Z6H6_CYAAP	Cyan10605_2262	Cyanobacterium aponinum (strain PCC 10605)	359	4~~KdpD (1.77855E-123) ~~213,232~~Usp (8.88706E-30) ~~356	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanobacterium, Cyanobacterium aponinum, Cyanobacterium aponinum (strain PCC 10605)	Cyanobacteria	Cyan10605_2260	4TM	hk	Cyan10605_2261	rr (sigma70 related)
B0JTA9_MICAN	MAE_53250	Microcystis aeruginosa (strain NIES-843)	372	1~~KdpD (5.71467E-123) ~~211,231~~Usp (6.14856E-35) ~~355	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Microcystis, Microcystis aeruginosa, Microcystis aeruginosa (strain NIES-843)	Cyanobacteria	unknown		unknown	unknown	unknown
K8GCX6_9CYAN	OsccyDRAFT_4627	Oscillatoriales cyanobacterium JSC-12	377	17~~KdpD (9.1245E-120) ~~226,250~~Usp (3.49737E-49) ~~372	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, unclassified Oscillatoriales, Oscillatoriales cyanobacterium JSC-12	Cyanobacteria	OsccyDRAFT_4622	4TM	hk	OsccyDRAFT_4621	rr (sigma70 related)
K9TR36_9CYAN	Oscil6304_4995	Oscillatoria acuminata PCC 6304	375	19~~KdpD (4.05718E-126) ~~228,247~~Usp (1.67844E-44) ~~369	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria acuminata, Oscillatoria acuminata PCC 6304	Cyanobacteria	Oscil6304_4989	4TM	hk	Oscil6304_4988	rr (sigma70 related)
K9VAD6_9CYAN	Cri9333_1267	Crinalium epipsammum PCC 9333	383	20~~KdpD (1.12415E-128) ~~230,249~~Usp (9.29474E-44) ~~371	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Crinalium, Crinalium epipsammum, Crinalium epipsammum PCC 9333	Cyanobacteria	Cri9333_1262	4TM	hk	Cri9333_1261	rr (sigma70 related)
K9WPQ8_9CYAN	Mic7113_5929	Microcoleus sp. PCC 7113	384	24~~KdpD (2.98303E-127) ~~233,253~~Usp (2.93248E-42) ~~375	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Microcoleus, Microcoleus sp. PCC 7113	Cyanobacteria	Mic7113_5927	2TM	HAMP,PAS hk	Mic7113_5925	rr (sigma70 related)
E0UCQ0_CYAP2	Cyan7822_3294	Cyanothece sp. (strain PCC 7822)	378	22~~KdpD (3.34227E-122) ~~232,251~~Usp (1.84335E-43) ~~373	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7822)	Cyanobacteria	Cyan7822_3299	4TM	hk	Cyan7822_3300	rr (sigma70 related)
K9XT83_STAC7	Sta7437_4020	Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	374	18~~KdpD (7.34473E-117) ~~227,246~~Usp (2.95741E-44) ~~368	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Stanieria, Stanieria cyanosphaera, Stanieria cyanosphaera (strain ATCC 29371 / PCC 7437)	Cyanobacteria	Sta7437_4002	4TM	hk	Sta7437_4000	rr (sigma70 related)
B7KBV1_CYAP7	PCC7424_4719	Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	377	15~~KdpD (2.0957E-121) ~~219,240~~Usp (1.87622E-42) ~~362	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 7424) (Synechococcus sp. (strain ATCC 29155))	Cyanobacteria	unknown		unknown	unknown	unknown
B7JXL2_CYAP8	PCC8801_0684	Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	368	15~~KdpD (1.29821E-112) ~~225,244~~Usp (1.24281E-41) ~~366	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain PCC 8801) (Synechococcus sp. (strain PCC 8801 / RF-1))	Cyanobacteria	unknown		unknown	unknown	unknown
B1WPS4_CYAA5	cce_3885	Cyanothece sp. (strain ATCC 51142)	370	15~~KdpD (1.80841E-121) ~~225,244~~Usp (2.99637E-42) ~~366	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Cyanothece, Cyanothece sp. (strain ATCC 51142)	Cyanobacteria	cce_3894	4TM	hk	cce_3895	rr (sigma70 related)
K9U0M1_9CYAN	Chro_3177	Chroococcidiopsis thermalis PCC 7203	367	2~~KdpD (1.58093E-120) ~~212,238~~Usp (3.22796E-48) ~~360	cellular organisms, Bacteria, Cyanobacteria, Pleurocapsales, Chroococcidiopsis, Chroococcidiopsis thermalis, Chroococcidiopsis thermalis PCC 7203	Cyanobacteria	Chro_3172	3TM	hk	Chro_3171	rr (sigma70 related)
K9X5B0_9CYRO	Glo7428_0033	Gloeocapsa sp. PCC 7428	390	18~~KdpD (4.8505E-131) ~~228,254~~Usp (4.6782E-49) ~~376	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Chroococcales, Gloeocapsa, Gloeocapsa sp. PCC 7428	Cyanobacteria	Glo7428_0026	4TM	hk	Glo7428_0025	rr (sigma70 related)
K9VHA6_9CYAN	Osc7112_2130	Oscillatoria nigro-viridis PCC 7112	383	26~~KdpD (3.62407E-129) ~~236,253~~Usp (3.16567E-44) ~~375	cellular organisms, Bacteria, Cyanobacteria, Oscillatoriophycideae, Oscillatoriales, Oscillatoria, Oscillatoria nigro-viridis, Oscillatoria nigro-viridis PCC 7112	Cyanobacteria	Osc7112_2125	4TM	hk	Osc7112_2124	rr (sigma70 related)
K9QGM4_9NOSO	Nos7107_3963	Nostoc sp. PCC 7107	386	18~~KdpD (3.53377E-120) ~~236,255~~Usp (1.46011E-47) ~~377	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. PCC 7107	Cyanobacteria	unknown		unknown	unknown	unknown
K9QY28_NOSS7	Nos7524_4781	Nostoc sp. (strain ATCC 29411 / PCC 7524)	362	5~~KdpD (1.07578E-127) ~~214,233~~Usp (8.79033E-49) ~~355	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain ATCC 29411 / PCC 7524)	Cyanobacteria	unknown		unknown	unknown	unknown
Q8YPP2_NOSS1	all4242	Nostoc sp. (strain PCC 7120 / UTEX 2576)	377	5~~KdpD (7.48427E-124) ~~223,246~~Usp (3.34889E-48) ~~368	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc sp. (strain PCC 7120 / UTEX 2576)	Cyanobacteria	unknown		unknown	unknown	unknown
K9PJP7_9CYAN	Cal7507_2475	Calothrix sp. PCC 7507	350	1~~KdpD (4.60856E-121) ~~200,219~~Usp (1.44753E-45) ~~341	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Rivulariaceae, Calothrix, Calothrix sp. PCC 7507	Cyanobacteria	Cal7507_2480	4TM	hk	Cal7507_2481	rr (sigma70 related)
B2J4W2_NOSP7	Npun_R0299	Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	384	26~~KdpD (9.11975E-130) ~~235,254~~Usp (9.49215E-45) ~~376	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Nostoc, Nostoc punctiforme, Nostoc punctiforme (strain ATCC 29133 / PCC 73102)	Cyanobacteria	Npun_F0303	4TM	hk	Npun_F0304	rr (sigma70 related)
K9WYA7_9NOST	Cylst_2653	Cylindrospermum stagnale PCC 7417	396	32~~KdpD (4.10847E-119) ~~242,261~~Usp (3.81575E-45) ~~383	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Cylindrospermum, Cylindrospermum stagnale, Cylindrospermum stagnale PCC 7417	Cyanobacteria	Cylst_2648	4TM	hk	Cylst_2647	rr (sigma70 related)
K9ZA22_ANACC	Anacy_0431	Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	372	12~~KdpD (4.13238E-125) ~~222,241~~Usp (8.83841E-47) ~~363	cellular organisms, Bacteria, Cyanobacteria, Nostocales, Nostocaceae, Anabaena, Anabaena cylindrica, Anabaena cylindrica (strain ATCC 27899 / PCC 7122)	Cyanobacteria	unknown		unknown	unknown	unknown
U5QMZ5_9CYAN	GKIL_2723	Gloeobacter kilaueensis JS1	753	24~~KdpD (1.40005E-88) ~~228,249~~Usp (9.2622E-38) ~~370,405~~KdpD (2.02942E-110) ~~610,626~~Usp (4.61773E-23) ~~748	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter kilaueensis, Gloeobacter kilaueensis JS1	Cyanobacteria	GKIL_2721	4TM	hk	GKIL_2722	rr (sigma70 related)
Q7NN44_GLOVI	gll0570(kdpD)	Gloeobacter violaceus (strain PCC 7421)	754	23~~KdpD (1.16945E-86) ~~228,248~~Usp (1.76104E-37) ~~369,406~~KdpD (4.06369E-107) ~~611,628~~Usp (6.55657E-34) ~~749	cellular organisms, Bacteria, Cyanobacteria, Gloeobacteria, Gloeobacterales, Gloeobacter, Gloeobacter violaceus, Gloeobacter violaceus (strain PCC 7421)	Cyanobacteria	gll0572	4TM	hk	gll0571	rr (sigma70 related)
I0INM1_LEPFC	LFE_1179	Leptospirillum ferrooxidans (strain C2-3)	740	21~~KdpD (1.25351E-76) ~~224,247~~Usp (0.000036151) ~~371,396~~KdpD (2.30841E-103) ~~598,616~~Usp (0.000000000110241) ~~730	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Leptospirillum, Leptospirillum sp. Group I, Leptospirillum ferrooxidans, Leptospirillum ferrooxidans (strain C2-3)	Nitrospirae	LFE_1173	4TM	hk	LFE_1172	rr (sigma70 related)
C0ZJR1_BREBN	BBR47_03850	Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	776	20~~KdpD (5.81109E-46) ~~225,250~~Usp (3.51347E-20) ~~375,415~~KdpD (1.85055E-114) ~~624,646~~Usp (1.3597E-32) ~~769	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus brevis (Bacillus brevis), Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599)	Firmicutes	unknown		unknown	unknown	unknown
A0A075QZZ7_BRELA	BRLA_c003560	Brevibacillus laterosporus LMG 15441	790	20~~KdpD (5.51897E-54) ~~241,263~~Usp (8.43389E-24) ~~388,428~~KdpD (1.58711E-110) ~~637,660~~Usp (1.30528E-29) ~~783	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Brevibacillus, Brevibacillus laterosporus (Bacillus laterosporus), Brevibacillus laterosporus LMG 15441	Firmicutes	unknown		unknown	unknown	unknown

A0A089ML71_9BACL	deleted	Paenibacillus odorifer	774	20~~KdpD (1.28141E-58) ~~224,246~~Usp (2.55185E-17) ~~371,412~~KdpD (5.21805E-117) ~~621,644~~Usp (4.75109E-27) ~~767	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus odorifer	Firmicutes	unknown		unknown	unknown	unknown
D3EAK7_GEOS4	GYMC10_0435	Geobacillus sp. (strain Y412MC10)	775	20~~KdpD (1.28074E-54) ~~221,243~~Usp (8.19054E-17) ~~368,409~~KdpD (6.98031E-113) ~~618,641~~Usp (4.20678E-20) ~~769	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Geobacillus sp. (strain Y412MC10)	Firmicutes	unknown		unknown	unknown	unknown
A0A0D3VH18_9BACL	UB51_10565	Paenibacillus sp. IHBB 10380	773	20~~KdpD (5.00442E-59) ~~223,245~~Usp (3.59779E-19) ~~370,411~~KdpD (1.77021E-109) ~~620,643~~Usp (2.09691E-26) ~~767	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. IHBB 10380	Firmicutes	UB51_10540	2TM	HAMP hk	UB51_10545	rr (sigma70 related)
A0A089ME28_9BACL	PGRAT_25535	Paenibacillus graminis	785	20~~KdpD (1.36979E-58) ~~224,246~~Usp (9.72001E-21) ~~371,411~~KdpD (3.84259E-112) ~~620,643~~Usp (7.47441E-24) ~~767	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus graminis	Firmicutes	PGRAT_25515	2TM	hk	PGRAT_25520	rr (sigma70 related)
V9VZT0_9BACL	ERIC2_c03150	Paenibacillus larvae subsp. larvae DSM 25430	769	20~~KdpD (5.10518E-60) ~~224,246~~Usp (1.71023E-14) ~~371,412~~KdpD (2.318E-114) ~~621,644~~Usp (4.54747E-26) ~~765	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus larvae, Paenibacillus larvae subsp. larvae, Paenibacillus larvae subsp. larvae DSM 25430	Firmicutes	unknown		unknown	ERIC2_c03080	rr (sigma70 related)
F5LL22_9BACL	HMPREF9413_0622	Paenibacillus sp. HGF7	784	20~~KdpD (4.38902E-53) ~~226,248~~Usp (2.82796E-16) ~~373,414~~KdpD (2.8619E-108) ~~624,647~~Usp (1.54678E-26) ~~769	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. HGF7	Firmicutes	unknown		unknown	unknown	unknown
A0A0A2UAK1_9BACL	P364_0106835	Paenibacillus sp. MAEPY2	779	21~~KdpD (3.12895E-57) ~~227,249~~Usp (1.84461E-18) ~~374,413~~KdpD (2.69567E-105) ~~622,645~~Usp (3.65951E-23) ~~770	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. MAEPY2	Firmicutes	P364_0106830	4TM	DUF4118,GAF hk	P364_0106825	rr (sigma70 related)
C6D694_PAESJ	Pjdr2_5993	Paenibacillus sp. (strain JDR-2)	775	21~~KdpD (2.57283E-57) ~~225,247~~Usp (1.79906E-14) ~~374,413~~KdpD (4.75319E-107) ~~622,645~~Usp (3.94183E-19) ~~768	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. (strain JDR-2)	Firmicutes	unknown		unknown	unknown	unknown
H6NGY0_9BACL	PM3016_1497	Paenibacillus mucilaginosus 3016	772	20~~KdpD (1.1717E-58) ~~223,245~~Usp (2.99918E-16) ~~366,410~~KdpD (6.43534E-107) ~~619,642~~Usp (2.02956E-25) ~~765	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus mucilaginosus, Paenibacillus mucilaginosus 3016	Firmicutes	PM3016_1498	4TM	DUF4118,GAF hk	PM3016_1499	rr (sigma70 related)
E3EDL7_PAEPS	PPSC2_06480	Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	775	20~~KdpD (3.10657E-53) ~~223,245~~Usp (4.51981E-15) ~~370,411~~KdpD (1.0726E-110) ~~619,642~~Usp (5.54451E-18) ~~763	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus polymyxa (Bacillus polymyxa), Paenibacillus polymyxa (strain SC2) (Bacillus polymyxa)	Firmicutes	unknown		unknown	unknown	unknown
A0A089L2I9_9BACL	R70331_28055	Paenibacillus sp. FSL R7-0331	779	20~~KdpD (1.65654E-48) ~~224,246~~Usp (3.5476E-16) ~~371,411~~KdpD (1.30241E-109) ~~620,643~~Usp (2.54387E-25) ~~766	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sp. FSL R7-0331	Firmicutes	R70331_28005	2TM	HAMP hk	R70331_28010	rr (sigma70 related)
X4ZZ42_9BACL	PSAB_12625	Paenibacillus sabinae T27	776	20~~KdpD (3.41229E-53) ~~224,246~~Usp (7.19502E-18) ~~371,410~~KdpD (1.06712E-105) ~~619,642~~Usp (1.27313E-27) ~~765	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus sabinae, Paenibacillus sabinae T27	Firmicutes	unknown		unknown	unknown	unknown
A0A089LVB4_9BACL	PSTEL_14245	Paenibacillus stellifer	777	20~~KdpD (9.24133E-52) ~~224,246~~Usp (1.50538E-17) ~~371,411~~KdpD (6.73824E-109) ~~620,643~~Usp (3.46385E-28) ~~766	cellular organisms, Bacteria, Firmicutes, Bacilli, Bacillales, Paenibacillaceae, Paenibacillus, Paenibacillus stellifer	Firmicutes	unknown		unknown	unknown	unknown
C1F834_ACIC5	ACP_0080	Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	387	28~~KdpD (1.05465E-116) ~~234,255~~Usp (1.73952E-32) ~~380	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Acidobacteriia, Acidobacteriales, Acidobacteriaceae, Acidobacterium, Acidobacterium capsulatum, Acidobacterium capsulatum (strain ATCC 51196 / DSM 11244 / JCM 7670 / NBRC 15755 / NCIMB 13165 / 161)	Fibrobacteres/Acidobacteria group	ACP_0081	2TM	HAMP,PAS hk	unknown	unknown
C1ABQ9_GEMAT	GAU_2894	Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	381	22~~KdpD (3.75106E-108) ~~231,255~~Usp (2.89543E-32) ~~381	cellular organisms, Bacteria, Gemmatimonadetes, Gemmatimonadaceae, Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	Gemmatimonadetes	GAU_2888	4TM	DUF4118 hk	GAU_2887	rr (sigma70 related)
F2NIP5_DESAR	Desac_2706	Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	383	18~~KdpD (1.7293E-113) ~~228,252~~Usp (1.85572E-40) ~~378	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfobacca, Desulfobacca acetoxidans, Desulfobacca acetoxidans (strain ATCC 700848 / DSM 11109 / ASRB2)	Deltaproteobacteria	Desac_2707	2TM	HAMP,X hk	Desac_2703	sigma54 dependent RR
Q09AI1_STIAD	STAUR_0220	Stigmatella aurantiaca (strain DW4/3-1)	390	20~~KdpD (6.93272E-118) ~~230,254~~Usp (4.00516E-43) ~~380	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Cystobacteraceae, Stigmatella, Stigmatella aurantiaca, Stigmatella aurantiaca (strain DW4/3-1)	Deltaproteobacteria	STAUR_0221	2TM	HAMP,PAS hk	STAUR_0222	sigma54 dependent RR
H8MWB8_CORCM	COCOR_07863	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	387	18~~KdpD (2.70358E-119) ~~228,252~~Usp (7.46163E-39) ~~378	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, Corallococcus coralloides (Myxococcus coralloides), Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	Deltaproteobacteria	COCOR_07862	2TM	HAMP,PAS hk	COCOR_07860	sigma54 dependent RR
M0QSC5_MYXSD	MYSTI_00155	Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	388	18~~KdpD (2.62928E-117) ~~228,252~~Usp (1.49994E-40) ~~378	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus stipitatus, Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)	Deltaproteobacteria	MYSTI_00156	2TM	HAMP,PAS hk	MYSTI_00160	sigma54 dependent RR
Q1DFX3_MYXXD	MXAN_0167	Myxococcus xanthus (strain DK 1622)	389	19~~KdpD (8.28285E-121) ~~229,253~~Usp (5.58921E-41) ~~379	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Myxococcus, Myxococcus xanthus, Myxococcus xanthus (strain DK 1622)	Deltaproteobacteria	MXAN_0168	2TM	HAMP,PAS hk	MXAN_0172	sigma54 dependent RR

G1UPR9_9DELT	HMPREF1022_00592	Desulfovibrio sp. 6_1_46AFAA	374	11~~KdpD (1.71715E-107) ~~218,243~~Usp (1.77831E-32) ~~368	Cellular organisms; Bacteria; Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio sp. 6_1_46AFAA	Deltaproteobacteria	HMPREF1022_00591	2TM	PAS hk	HMPREF1022_00590	sigma54 dependent RR
Q725T9_DESVH	DVU_3336	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	379	11~~KdpD (1.34359E-106) ~~222,243~~Usp (8.37802E-39) ~~368	Cellular organisms; Bacteria; Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	Deltaproteobacteria	DVU_3335	2TM	PAS hk	DVU_3334	sigma54 dependent RR
B8DR35_DESVM	DvMF_2574	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	375	11~~KdpD (3.02387E-103) ~~222,243~~Usp (4.34454E-38) ~~368	Cellular organisms; Bacteria; Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	Deltaproteobacteria	DvMF_2573	2TM	PAS hk	DvMF_2572	sigma54 dependent RR
A0LLJ3_SYNFM	Sfum_2617	Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	388	16~~KdpD (5.45009E-113) ~~226,245~~Usp (3.45572E-27) ~~371	Cellular organisms; Bacteria; Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria, Syntrophobacterales, Syntrophobacteraceae, Syntrophobacter, Syntrophobacter fumaroxidans, Syntrophobacter fumaroxidans (strain DSM 10017 / MPOB)	Deltaproteobacteria	Sfum_2621	2TM	HAMP,PAS hk	Sfum_2622	sigma54 dependent RR
I4C4T7_DESTA	Desti_1870	Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	551	18~~KdpD (4.37476E-110) ~~228,247~~Usp (3.2764E-28) ~~373,403~~PTS_IIA_fru (1.13785E-14) ~~546	Cellular organisms; Bacteria; Proteobacteria; delta/epsilon subdivisions; Deltaproteobacteria, Syntrophobacterales, Syntrophaceae, Desulfomonile, Desulfomonile tiedjei, Desulfomonile tiedjei (strain ATCC 49306 / DSM 6799 / DCB-1)	Deltaproteobacteria	Desti_1866	2TM	HAMP,X hk	Desti_1865	sigma54 dependent RR
L0DJW0_SINAD	Sinac_5539	Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	377	22~~KdpD (2.29166E-115) ~~228,250~~Usp (3.14704E-34) ~~375	Cellular organisms; Bacteria; Planctomycetes; Planctomycetia; Planctomycetales; Planctomycetaceae, Singulisphaera, Singulisphaera acidiphila, Singulisphaera acidiphila (strain ATCC BAA-1392 / DSM 18658 / VKM B-2454 / MOB10)	Planctomycetes	Sinac_5540	2TM	HAMP,X hk	Sinac_5541	rr (sigma70 related)
W8EUK8_9BACT	Hsw_0623	Hymenobacter swuensis DY53	391	26~~KdpD (4.8669E-108) ~~235,258~~Usp (1.44936E-26) ~~390	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales, Cytophagaceae, Hymenobacter, Hymenobacter swuensis, Hymenobacter swuensis DY53	Bacteroidetes/Chlorobi group	Hsw_0624	2TM	HAMP,PAS hk	Hsw_0616	sigma54 dependent RR
F4KRA6_HALH1	Halhy_6477	Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	397	19~~KdpD (4.12064E-115) ~~229,247~~Usp (1.88033E-27) ~~397	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Saprospiraceae, Haliscomenobacter, Haliscomenobacter hydrossis, Haliscomenobacter hydrossis (strain ATCC 27775 / DSM 1100 / LMG 10767 / O)	Bacteroidetes/Chlorobi group	Halhy_6476	2TM	HAMP,PAS hk	Halhy_6484	sigma54 dependent RR
A0A0E9MTD1_9SPHI	FPE01S_01_00290	Flavihumibacter petaseus NBRC 106054	371	14~~KdpD (2.0536E-115) ~~224,243~~Usp (2.37336E-30) ~~371	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Flavihumibacter, Flavihumibacter petaseus, Flavihumibacter petaseus NBRC 106054	Bacteroidetes/Chlorobi group	FPE01S_01_00300	2TM	HAMP,PAS hk	FPE01S_01_00230	sigma54 dependent RR
G8TDF4_NIAKG	Niako_4128	Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10)	377	23~~KdpD (3.81909E-115) ~~231,249~~Usp (4.96541E-34) ~~377	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Niastella, Niastella koreensis, Niastella koreensis (strain DSM 17620 / KACC 11465 / GR20-10)	Bacteroidetes/Chlorobi group	Niako_4127	2TM	HAMP,PAS hk	Niako_4135	sigma54 dependent RR
C7PUS6_CHIPD	Cpin_3612	Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)	374	18~~KdpD (2.56769E-115) ~~228,246~~Usp (1.93492E-28) ~~374	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Chitinophaga, Chitinophaga pinensis, Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)	Bacteroidetes/Chlorobi group	Cpin_3611	2TM	HAMP,PAS hk	Cpin_3620	sigma54 dependent RR
D2QBF8_SPILD	Slin_0067	Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896)	374	18~~KdpD (2.86999E-111) ~~228,246~~Usp (3.04737E-25) ~~374	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales, Cytophagaceae, Spirosoma, Spirosoma linguale, Spirosoma linguale (strain ATCC 33905 / DSM 74 / LMG 10896)	Bacteroidetes/Chlorobi group	Slin_0068	2TM	HAMP,PAS hk	Slin_0059	sigma54 dependent RR
I0K509_9BACT	FAES_1202	Fibrella aestuarina BUZ 2	374	18~~KdpD (1.44758E-110) ~~228,246~~Usp (2.15632E-28) ~~374	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Cytophagia; Cytophagales, Cytophagaceae, Fibrella, Fibrella aestuarina, Fibrella aestuarina BUZ 2	Bacteroidetes/Chlorobi group	FAES_1203	2TM	HAMP,PAS hk	FAES_1195	sigma54 dependent RR
F8EK06_RUNSL	Runsl_3028	Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	375	19~~KdpD (1.05356E-116) ~~229,247~~Usp (4.48656E-32) ~~375	Gemmatimonadetes; Gemmatimonadaceae; Gemmatimonas, Gemmatimonas aurantiaca, Gemmatimonas aurantiaca (strain T-27 / DSM 14586 / JCM 11422 / NBRC 100505)	Bacteroidetes/Chlorobi group	Runsl_3027	2TM	HAMP,PAS hk	Runsl_3035	sigma54 dependent RR
H8KMI4_SOLCM	Solca_3779	Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) (Flexibacter canadensis)	368	12~~KdpD (5.477E-116) ~~222,241~~Usp (6.4898E-29) ~~368	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Solitalea, Solitalea canadensis (Flexibacter canadensis), Solitalea canadensis (strain ATCC 29591 / DSM 3403 / NBRC 15130 / NCIMB 12057 / USAM 9D) (Flexibacter canadensis)	Bacteroidetes/Chlorobi group	Solca_3781	2TM	HAMP,PAS hk	Solca_3771	sigma54 dependent RR
C6XZL2_PEDHD	Phep_2504	Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290)	376	20~~KdpD (1.13123E-110) ~~227,248~~Usp (8.08843E-28) ~~376	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Pedobacter, Pedobacter heparinus (Flavobacterium heparinum), Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / NCIB 9290)	Bacteroidetes/Chlorobi group	Phep_2503	2TM	HAMP,PAS hk	Phep_2510	sigma54 dependent RR
H1YB16_9SPHI	Mucpa_5990	Mucilaginibacter paludis DSM 18603	373	17~~KdpD (8.65563E-115) ~~224,246~~Usp (6.70394E-28) ~~373	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Mucilaginibacter, Mucilaginibacter paludis, Mucilaginibacter paludis DSM 18603	Bacteroidetes/Chlorobi group	Mucpa_5991	2TM	HAMP,PAS hk	unknown	unknown
A0A077EBR1_9FLAO	BD94_1137	Elizabethkingia anophelis NUHP1	345	1~~KdpD (1.36614E-110) ~~200,217~~Usp (5.5713E-31) ~~345	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Elizabethkingia, Elizabethkingia anophelis, Elizabethkingia anophelis NUHP1	Bacteroidetes/Chlorobi group	BD94_1136	2TM	HAMP,PAS hk	BD94_1143	sigma54 dependent RR
A0A077KDX1_9FLAO	CHSO_1293	Chryseobacterium sp. StRB126	335	1~~KdpD (9.39232E-105) ~~190,207~~Usp (5.80053E-29) ~~335	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Chryseobacterium, Chryseobacterium sp. StRB126	Bacteroidetes/Chlorobi group	CHSO_1294	2TM	HAMP,PAS hk	CHSO_1288	sigma54 dependent RR
F4C639_SPHS2	Sph21_4258	Sphingobacterium sp. (strain 21)	374	18~~KdpD (3.16297E-113) ~~228,246~~Usp (2.53333E-29) ~~374	Cellular organisms; Bacteria; Bacteroidetes/Chlorobi group; Bacteroidetes; Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. (strain 21)	Bacteroidetes/Chlorobi group	Sph21_4259	2TM	HAMP,PAS hk	Sph21_4268	sigma54 dependent RR

C6VYH1_DYAFD	Dfer_0381	Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	371	15~~KdpD (1.0034E-119) ~~225,243~~Usp (5.90423E-29) ~~371	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Dyadobacter, Dyadobacter fermentans, Dyadobacter fermentans (strain ATCC 700827 / DSM 18053 / NS114)	Bacteroidetes/ Chlorobi group	Dfer_0382	2TM	HAMP,PAS hk	Dfer_0373	sigma54 dependent RR
Q11TL2_CYTH3	CHU_1986	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	374	18~~KdpD (8.77212E-120) ~~228,246~~Usp (8.10779E-37) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Cytophaga, Cytophaga hutchinsonii, Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	Bacteroidetes/ Chlorobi group	CHU_1987	2TM	HAMP,PAS hk	CHU_1981	sigma54 dependent RR
C6X583_FLAB3	FIC_01121	Flavobacteriaceae bacterium (strain 3519-10)	416	60~~KdpD (2.40343E-118) ~~270,288~~Usp (1.4488E-22) ~~392	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, unclassified Flavobacteriaceae, Flavobacteriaceae bacterium (strain 3519-10)	Bacteroidetes/ Chlorobi group	FIC_01120	2TM	HAMP,PAS hk	FIC_01129	sigma54 dependent RR
W0F294_9SPHI	NIASO_10395	Niabella soli DSM 19437	374	18~~KdpD (6.22645E-118) ~~228,246~~Usp (8.24069E-31) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Niabella, Niabella soli, Niabella soli DSM 19437	Bacteroidetes/ Chlorobi group	NIASO_10390	2TM	HAMP,PAS hk	NIASO_10420	sigma54 dependent RR
F0S644_PSESL	Pedsa_1588	Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	374	18~~KdpD (1.94538E-118) ~~228,246~~Usp (9.8028E-32) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Pseudopedobacter, Pseudopedobacter saltans, Pseudopedobacter saltans (strain ATCC 51119 / DSM 12145 / JCM 21818 / LMG 10337 / NBRC 100064 / NCIMB 13643) (Pedobacter saltans)	Bacteroidetes/ Chlorobi group	Pedsa_1589	2TM	HAMP,PAS hk	Pedsa_1581	sigma54 dependent RR
H1ZCI4_MYROD	Myrod_0222	Myroides odoratus DSM 2801	376	19~~KdpD (4.18219E-118) ~~229,247~~Usp (1.89891E-30) ~~375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Myroides, Myroides odoratus (Flavobacterium odoratum), Myroides odoratus DSM 2801	Bacteroidetes/ Chlorobi group	Myrod_0221	2TM	HAMP,PAS hk	Myrod_0227	sigma54 dependent RR
A0A088EZ71_9SPHI	KO02_07000	Sphingobacterium sp. ML3W	373	17~~KdpD (8.12761E-111) ~~227,246~~Usp (2.14067E-28) ~~373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Sphingobacteriaceae, Sphingobacterium, Sphingobacterium sp. ML3W	Bacteroidetes/ Chlorobi group	KO02_07005	2TM	HAMP,PAS hk	KO02_06965	sigma54 dependent RR
A6H082_FLAPJ	FP1688	Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	375	19~~KdpD (1.22434E-117) ~~229,247~~Usp (6.13607E-30) ~~375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium psychrophilum, Flavobacterium psychrophilum (strain JIP02/86 / ATCC 49511)	Bacteroidetes/ Chlorobi group	FP1687	2TM	HAMP,PAS hk	FP1694	sigma54 dependent RR
A0A0C1FPQ1_9FLAO	OA93_21600	Flavobacterium sp. KMS	375	19~~KdpD (8.29478E-117) ~~229,247~~Usp (1.14568E-29) ~~375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium sp. KMS	Bacteroidetes/ Chlorobi group	OA93_21595	2TM	HAMP,PAS hk	OA93_21630	sigma54 dependent RR
A5FIH2_FLAJ1	Fjoh_1971	Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) (Cytophaga johnsonae)	374	18~~KdpD (2.76634E-116) ~~228,246~~Usp (6.88482E-28) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Flavobacterium, Flavobacterium johnsoniae (Cytophaga johnsonae), Flavobacterium johnsoniae (strain ATCC 17061 / DSM 2064 / UW101) (Cytophaga johnsonae)	Bacteroidetes/ Chlorobi group	Fjoh_1970	2TM	HAMP,PAS hk	Fjoh_1977	sigma54 dependent RR
F2IFU5_FLUTR	Fluta_0548	Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	374	18~~KdpD (1.55641E-120) ~~228,246~~Usp (1.3562E-30) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Cryomorphaceae, Fluviicola, Fluviicola taffensis, Fluviicola taffensis (strain DSM 16823 / RW262 / RW262)	Bacteroidetes/ Chlorobi group	Fluta_0549	2TM	HAMP,PAS hk	Fluta_0542	sigma54 dependent RR
R9W556_9BACT	BN505_00832	Alistipes sp. CAG:157	370	17~~KdpD (1.67581E-121) ~~227,245~~Usp (1.00336E-21) ~~370	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, environmental samples, Alistipes sp. CAG:157	Bacteroidetes/ Chlorobi group	BN505_00833	2TM	HAMP,PAS hk	unknown	unknown
D4JZ0_9BACT	AL1_06430	Alistipes shahii WAL 8301	373	17~~KdpD (6.7923E-117) ~~227,245~~Usp (1.09477E-19) ~~373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Rikenellaceae, Alistipes, Alistipes shahii, Alistipes shahii WAL 8301	Bacteroidetes/ Chlorobi group	AL1_06440	2TM	HAMP,PAS hk	AL1_06360	sigma54 dependent RR
S0GLV5_9PORP	C803_05528	Parabacteroides goldsteinii dnLKV18	373	17~~KdpD (5.10234E-122) ~~227,245~~Usp (2.60035E-27) ~~342	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides goldsteinii, Parabacteroides goldsteinii dnLKV18	Bacteroidetes/ Chlorobi group	C803_05529	2TM	HAMP,PAS hk	C803_05519	sigma54 dependent RR
A6LIV0_PARD8	BDI_3934	Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	373	17~~KdpD (5.08099E-120) ~~227,245~~Usp (4.75161E-28) ~~373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides distasonis, Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / NCTC 11152)	Bacteroidetes/ Chlorobi group	BDI_3935	2TM	HAMP,PAS hk	unknown	unknown
R6XE34_9PORP	BN675_02911	Parabacteroides merdae CAG:48	346	1~~KdpD (3.90493E-113) ~~200,218~~Usp (7.79875E-28) ~~314	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides merdae CAG:48	Bacteroidetes/ Chlorobi group	BN675_02912	2TM	HAMP,PAS hk	unknown	unknown
R5VP67_9PORP	BN709_01654	Odoribacter laneus CAG:561	375	17~~KdpD (1.04744E-122) ~~227,245~~Usp (1.03003E-26) ~~373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter laneus CAG:561	Bacteroidetes/ Chlorobi group	BN709_01655	2TM	HAMP,PAS hk	unknown	unknown
A0A0C5NCU2_9PORP	BA92_10910	Sanguibacteroides justesenii	373	17~~KdpD (9.7547E-115) ~~227,245~~Usp (3.20966E-25) ~~341	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Sanguibacteroides, Sanguibacteroides justesenii	Bacteroidetes/ Chlorobi group	BA92_10915	2TM	HAMP,PAS hk	BA92_10880	sigma54 dependent RR
R7DKZ6_9PORP	BN686_00682	Tannerella sp. CAG:51	374	17~~KdpD (2.2949E-121) ~~227,246~~Usp (2.24863E-24) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:51	Bacteroidetes/ Chlorobi group	BN686_00681	2TM	HAMP,PAS hk	unknown	unknown
R5I937_9PORP	BN472_02765	Tannerella sp. CAG:118	374	17~~KdpD (5.67491E-128) ~~227,246~~Usp (1.11426E-28) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:118	Bacteroidetes/ Chlorobi group	BN472_02764	2TM(?no unpredicted periplasmic domain)	HAMP,PAS hk	BN472_02770	sigma54 dependent RR

R5Y2K9_9BACE	BN496_01537	Bacteroides sp. CAG:144	377	19~~KdpD (2.4606E-127) ~~229,249~~Usp (2.55758E-25) ~~345	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:144	Bacteroidetes/ Chlorobi group	BN496_01536	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	BN496_01542	sigma54 dependent RR
R5NG41_9BACT	BN471_01401	Paraprevotella clara CAG:116	377	19~~KdpD (7.67789E-123) ~~229,249~~Usp (1.72681E-23) ~~377	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Paraprevotella, environmental samples, Paraprevotella clara CAG:116	Bacteroidetes/ Chlorobi group	BN471_01402	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	BN471_01391	sigma54 dependent RR
R5PNT1_9PORP	BN783_01721	Odoribacter sp. CAG:788	374	17~~KdpD (2.99731E-125) ~~227,246~~Usp (1.70723E-25) ~~343	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter sp. CAG:788	Bacteroidetes/ Chlorobi group	BN783_01722	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	BN783_01716	sigma54 dependent RR
R7JDL5_9PORP	BN646_01831	Parabacteroides sp. CAG:409	375	18~~KdpD (4.56377E-124) ~~228,249~~Usp (2.90379E-29) ~~371	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides sp. CAG:409	Bacteroidetes/ Chlorobi group	BN646_01830	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	BN646_01829	sigma54 dependent RR
R7LGH1_9BACT	BN805_00525	Prevotella sp. CAG:891	379	21~~KdpD (3.19994E-119) ~~231,250~~Usp (9.19462E-28) ~~347	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:891	Bacteroidetes/ Chlorobi group	BN805_00524	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	BN805_00532	sigma54 dependent RR
R7NT34_9BACE	BN821_00360	Bacteroides sp. CAG:98	374	17~~KdpD (4.21823E-124) ~~227,246~~Usp (3.76923E-26) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:98	Bacteroidetes/ Chlorobi group	BN821_00359	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	unknown	unknown
A6L5B7_BACV8	BVU_3252	Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	375	18~~KdpD (3.96982E-126) ~~228,247~~Usp (1.04734E-27) ~~375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides vulgatus, Bacteroides vulgatus (strain ATCC 8482 / DSM 1447 / NCTC 11154)	Bacteroidetes/ Chlorobi group	BVU_3251	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	unknown	unknown
R5MM88_9BACE	BN711_02301	Bacteroides intestinalis CAG:564	374	17~~KdpD (6.25348E-126) ~~227,246~~Usp (2.19921E-28) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides intestinalis CAG:564	Bacteroidetes/ Chlorobi group	unknown		unknown	unknown	unknown
R6KEZ9_9BACE	BN506_01194	Bacteroides cellulosilyticus CAG:158	374	17~~KdpD (1.86511E-124) ~~227,246~~Usp (1.31757E-28) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides cellulosilyticus CAG:158	Bacteroidetes/ Chlorobi group	BN506_01193	2 HMM(no unpredicted periplasmic domain)	HAMP,PAS hk	BN506_01200	sigma54 dependent RR

R6LFS2_9BACE	BN507_02372	Bacteroides clarus CAG:160	374	17~~KdpD (1.29041E-126) ~~227,246~~Usp (1.86086E-26) ~~374	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides clarus CAG:160	Bacteroidetes/ Chlorobi group	BN507_02371	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	BN507_02377	sigma54 dependent RR
R7EMA6_9BACE	BN594_00615	Bacteroides uniformis CAG:3	373	17~~KdpD (1.33729E-127) ~~227,245~~Usp (5.59695E-29) ~~373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides uniformis CAG:3	Bacteroidetes/ Chlorobi group	BN594_00614	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	unknown	unknown
E6STB8_BACT6	Bache_0219	Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	373	17~~KdpD (1.33326E-123) ~~227,245~~Usp (3.67174E-26) ~~373	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides helcogenes, Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	Bacteroidetes/ Chlorobi group	Bache_0218	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	Bache_0223	sigma54 dependent RR
Q5LHU3_BACFN	BF9343_0508	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	375	17~~KdpD (1.40916E-124) ~~227,247~~Usp (2.76189E-24) ~~375	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides fragilis, Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	Bacteroidetes/ Chlorobi group	BF9343_0509	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	BF9343_0503	sigma54 dependent RR
R5J7D2_9BACE	BN523_02396	Bacteroides sp. CAG:189	375	17~~KdpD (8.67199E-124) ~~227,245~~Usp (7.64832E-28) ~~344	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:189	Bacteroidetes/ Chlorobi group	BN523_02397	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	BN523_02391	sigma54 dependent RR
R6DK25_9BACE	BN772_03518	Bacteroides sp. CAG:754	376	18~~KdpD (1.09008E-126) ~~228,248~~Usp (6.84439E-28) ~~376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:754	Bacteroidetes/ Chlorobi group	BN772_03519	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	unknown	unknown
R5V113_9BACE	BN535_00850	Bacteroides caccae CAG:21	376	18~~KdpD (6.88942E-125) ~~228,248~~Usp (3.39384E-24) ~~376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides caccae CAG:21	Bacteroidetes/ Chlorobi group	BN535_00849	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	unknown	unknown
Q8A523_BACTN	BT_2421	Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	377	19~~KdpD (4.88474E-127) ~~229,249~~Usp (7.6806E-29) ~~377	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides thetaiotaomicron, Bacteroides thetaiotaomicron (strain ATCC 29148 / DSM 2079 / NCTC 10582 / E50 / VPI-5482)	Bacteroidetes/ Chlorobi group	BT_2420	2-TM-(no unpredicted periplasmic domain)	HAMP,PAS hk	unknown	unknown

D6D7W0_9BACE	BXY_09400	Bacteroides xylanisolvens XB1A	376	18~~KdpD (1.70316E-126) ~~228,248~~Usp (7.25998E-28) ~~376	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides xylanisolvens, Bacteroides xylanisolvens XB1A	Bacteroidetes/ Chlorobi group	BXY_09410	2TM,no unpredicted periplasmic domain)	HAMP,PAS hk	unknown	unknown
R7G954_9FIRM	BN631_00316	Eubacterium dolichum CAG:375	629	3~~KdpD (2.50056E-117) ~~212,227~~Usp (9.82308E-32) ~~349,372~~DUF4118 (0.0000344375) ~~474,503~~GAF (0.00135929) ~~623	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium dolichum CAG:375	Firmicutes	unknown		unknown	unknown	unknown
R6VWM4_9FIRM	BN746_00939	Erysipelotrichaceae bacterium CAG:64	635	1~~KdpD (1.9228E-116) ~~211,226~~Usp (1.31271E-26) ~~347,372~~DUF4118 (1.24609E-14) ~~471,499~~GAF (0.0000250014) ~~623	cellular organisms, Bacteria, Firmicutes, Erysipelotrichia, Erysipelotrichales, Erysipelotrichaceae, environmental samples, Erysipelotrichaceae bacterium CAG:64	Firmicutes	BN746_00932	4TM	DUF4118,XHK	BN746_00931	rr (sigma70 related)
R5T4S6_9CLOT	BN544_02002	Clostridium hathewayi CAG:224	680	35~~KdpD (2.39703E-123) ~~245,265~~Usp (6.15466E-36) ~~391,422~~DUF4118 (0.000000000388533) ~~521,547~~GAF (0.0000372185) ~~671	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium hathewayi CAG:224	Firmicutes	BN544_02010	4TM	DUF4118,GAF HK	BN544_02009	rr (sigma70 related)
A0A0F0CBD6_9CLOT	CLFS41_46290	Clostridium sp. FS41	663	25~~KdpD (2.54532E-113) ~~235,255~~Usp (3.67268E-34) ~~378,401~~DUF4118 (0.0000000000460281) ~~502,530~~GAF (0.0000679823) ~~651	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, Clostridium sp. FS41	Firmicutes	CLFS41_46250	4TM	DUF4118,GAF HK	CLFS41_46240	rr (sigma70 related)
R5FAQ5_9CLOT	BN723_02738	Clostridium bolteae CAG:59	664	25~~KdpD (1.4993E-117) ~~235,255~~Usp (4.43648E-38) ~~378,401~~DUF4118 (0.00000000000901618) ~~502,530~~GAF (0.000170915) ~~651	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium bolteae CAG:59	Firmicutes	BN723_02742	4TM	hk	BN723_02743	rr (sigma70 related)
R5C547_9FIRM	BN499_00280	Blautia hydrogenotrophica CAG:147	516	2~~KdpD (3.14363E-30) ~~69,90~~Usp (6.57176E-34) ~~213,248~~DUF4118 (0.000000000000663217) ~~345,371~~GAF (0.000000184807) ~~497	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia hydrogenotrophica CAG:147	Firmicutes	BN499_00279	4TM	Usp,DUF4118,X hk	BN499_00278	rr (sigma70 related)
R6N6Z4_9FIRM	BN627_01443	Lachnospiraceae bacterium CAG:364	675	25~~KdpD (1.98856E-116) ~~235,259~~Usp (7.59823E-33) ~~382,417~~DUF4118 (0.00000235999) ~~499,540~~GAF (0.000000646184) ~~666	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, environmental samples, Lachnospiraceae bacterium CAG:364	Firmicutes	BN627_01442	4TM	DUF4118,GAF HK	BN627_01441	rr (sigma70 related)
Q0PAK0_CAMJE	Cj0679	Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	606	27~~KdpD (4.48022E-117) ~~233,254~~Usp (7.10705E-18) ~~337,386~~DUF4118 (0.000000000000051276) ~~485	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Epsilonproteobacteria, Campylobacterales, Campylobacteraceae, Campylobacter, Campylobacter jejuni, Campylobacter jejuni subsp. jejuni, Campylobacter jejuni subsp. jejuni serotype O:2 (strain NCTC 11168)	Epsilonproteobacteria	unknown		unknown	unknown	unknown
R5TPN1_9FIRM	BN481_00424	Ruminococcus gnavus CAG:126	550	31~~KdpD (8.17056E-121) ~~236,257~~Usp (1.82744E-35) ~~380,408~~DUF4118 (4.16815E-15) ~~509	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus gnavus CAG:126	Firmicutes	BN481_00424		unknown	BN481_00435	rr (sigma70 related)
R6R2Y2_9FIRM	BN652_02355	Firmicutes bacterium CAG:424	675	28~~KdpD (9.08415E-122) ~~238,259~~Usp (3.40886E-37) ~~382,411~~DUF4118 (0.00000000000078062) ~~512,540~~GAF (0.000000440509) ~~664	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:424	Firmicutes	unknown		unknown	unknown	unknown
R6Q206_9CLOT	BN618_00210	Clostridium nexile CAG:348	664	28~~KdpD (3.70712E-123) ~~234,255~~Usp (6.04674E-32) ~~378,407~~DUF4118 (6.86056E-16) ~~504,537~~GAF (0.0000482837) ~~660	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium nexile CAG:348	Firmicutes	BN618_00211	4TM	DUF4118,XHK	BN618_00212	rr (sigma70 related)
R5WPC9_9FIRM	BN568_01735	Blautia sp. CAG:257	666	32~~KdpD (1.56142E-119) ~~235,256~~Usp (3.21524E-31) ~~379,415~~DUF4118 (7.52405E-15) ~~507,415~~DUF3792 (0.00369447) ~~456,537~~GAF (0.00000373654) ~~662	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Blautia, environmental samples, Blautia sp. CAG:257	Firmicutes	unknown		unknown	unknown	unknown
R5RKN9_9FIRM	BN747_02091	Firmicutes bacterium CAG:646	672	32~~KdpD (2.09455E-119) ~~235,256~~Usp (2.33555E-33) ~~379,411~~DUF4118 (4.06471E-15) ~~509,539~~GAF (0.000198843) ~~661	cellular organisms, Bacteria, Firmicutes, environmental samples, Firmicutes bacterium CAG:646	Firmicutes	BN747_02095	4TM	DUF4118,GAF HK	BN747_02096	rr (sigma70 related)
R6SSY4_9CLOT	BN719_02215	Clostridium sp. CAG:58	666	25~~KdpD (8.78841E-124) ~~235,256~~Usp (5.83135E-32) ~~379,437~~DUF4118 (0.000000022686) ~~508,537~~GAF (0.0000032983) ~~659	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:58	Firmicutes	unknown		unknown	unknown	unknown
R6ZQF8_9CLOT	BN593_00577	Clostridium sp. CAG:299	666	27~~KdpD (4.41402E-124) ~~235,256~~Usp (1.60928E-33) ~~379,431~~DUF4118 (0.00000000000231714) ~~508,536~~GAF (0.0000253269) ~~657	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium, environmental samples, Clostridium sp. CAG:299	Firmicutes	BN593_00580	2TM	hk	BN593_00581	rr (sigma70 related)
J9ZAA5_LEPFM	LFML04_0561	Leptospirillum ferriphilum (strain ML-04)	741	24~~KdpD (7.4817E-57) ~~228,247~~Usp (0.0000714438) ~~368,394~~KdpD (1.80584E-106) ~~602,617~~Usp (0.00470996) ~~729	cellular organisms, Bacteria, Nitrospirae, Nitrospira, Nitrospirales, Nitrospiraceae, Leptospirillum, Leptospirillum sp. Group III, Leptospirillum ferriphilum, Leptospirillum ferriphilum (strain ML-04)	Nitrospirae	LFML04_0548	4TM	hk	LFML04_0547	

C9R8E9_AMMDK	Adeg_1482	Ammonifex degensii (strain DSM 10501 / KC4)	731	4~~KdpD (2.63127E-26) ~~164,251~~Usp (0.0000000000483919) ~~346,372~~KdpD (6.77887E-115) ~~577,594~~Usp (6.12816E-28) ~~719	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermoanaerobacteraceae, Moorella group, Ammonifex, Ammonifex degensii, Ammonifex degensii (strain DSM 10501 / KC4)	Firmicutes	unknown			unknown	
A0A0F4SDE3_9ACTN	VR44_18800	Streptomyces katrae	310	1~~KdpD (7.16031E-130) ~~210,233~~Usp (1.28169E-14) ~~310	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces katrae	Actinobacteria	VR44_18840	2TM	HAMP hk	VR44_18845	rr (sigma70 related)
R4M6T0_MYCTX	J113_07245	Mycobacterium tuberculosis CAS/NITR204	334	8~~KdpD (5.12193E-127) ~~217,239~~Usp (0.0000000144775) ~~279	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium tuberculosis complex, Mycobacterium tuberculosis, Mycobacterium tuberculosis CAS, Mycobacterium tuberculosis CAS/NITR204	Actinobacteria	J113_07240	4TM	hk	J113_07230	rr (sigma70 related)
K8W5U1_9ENTR	OO7_12934	Providencia sneebia DSM 19967	266	22~~KdpD (1.48834E-128) ~~231	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales, Enterobacteriaceae, Providencia, Providencia sneebia, Providencia sneebia DSM 19967	Gammaproteobacteria	OO7_12959	4TM	Usp,DUF4118,GAF hk	OO7_12944	rr (sigma70 related)
A7I6Q3_METB6	Mboo_0896	Methanoregula boonei (strain 6A8)	658	31~~KdpD (4.96405E-125) ~~239,262~~Usp (1.00358E-45) ~~384,408~~DUF4118 (1.45741E-18) ~~501,533~~GAF (0.0000000000176199) ~~651	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanoregula, Methanoregula boonei, Methanoregula boonei (strain 6A8)	Archaea	unknown			unknown	
D4KH79_9FIRM	MHY_04990	Megamonas hypermegale ART12/1	516	29~~KdpD (2.23349E-127) ~~239,259~~Usp (2.30323E-37) ~~383,421~~DUF4118 (0.00000000000885699) ~~510	cellular organisms, Bacteria, Firmicutes, Negativicutes, Selenomonadales, Veillonellaceae, Megamonas, Megamonas hypermegale, Megamonas hypermegale ART12/1	Firmicutes	unknown			MHY_04970	rr (sigma70 related)
A0A0C1Q9F8_9ACTN	LK07_36815	Streptomyces pluripotens	606	23~~KdpD (1.06624E-118) ~~233,256~~Usp (8.67786E-30) ~~390,432~~DUF4118 (2.39327E-23) ~~532	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces pluripotens	Actinobacteria					
J7J0P9_DESMD	Desmer_2979	Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	671	22~~KdpD (3.47022E-122) ~~229,251~~Usp (2.55415E-59) ~~375,407~~DUF4118 (1.25163E-16) ~~507,534~~GAF (6.04295E-14) ~~653	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Peptococcaceae, Desulfosporosinus, Desulfosporosinus meridiei, Desulfosporosinus meridiei (strain ATCC BAA-275 / DSM 13257 / NCIMB 13706 / S10)	Firmicutes	Desmer_2990	2TM	HAMP hk	Desmer_2989	rr (sigma70 related)
A0A0A8F065_9ACTN	GZL_08794	Streptomyces sp. 769	837	1~~KdpD (3.10106E-115) ~~211,233~~Usp (6.44063E-28) ~~355	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. 769	Actinobacteria	unknown			unknown	
A0A0F2Q2Q0_9PSED	VR76_04385	Pseudomonas sp. BRH_c35	364	17~~KdpD (2.98086E-120) ~~227,248~~Usp (4.85552E-24) ~~358	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas sp. BRH_c35	Gammaproteobacteria	unknown			unknown	
D1CGX0_THET1	Tter_2088	Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	384	22~~KdpD (2.2724E-113) ~~232,255~~Usp (6.62116E-34) ~~378	cellular organisms, Bacteria, unclassified Bacteria, Thermobaculum, Thermobaculum terrenum, Thermobaculum terrenum (strain ATCC BAA-798 / YNP1)	unclassified Bacteria	Tter_2095	4TM	DUF4118,GAF HK	Tter_2094	
F6D4T4_METPW	MSWAN_1124	Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	651	26~~KdpD (2.65272E-113) ~~235,257~~Usp (8.82855E-35) ~~373,404~~DUF4118 (1.10651E-18) ~~504,412~~DUF3816 (0.0075837) ~~505,530~~GAF (0.000000000525271) ~~647	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium paludis (strain DSM 25820 / JCM 18151 / SWAN1)	Archaea	unknown			unknown	
B2UR94_AKKM8	Amuc_1154	Akkermansia muciniphila (strain ATCC BAA-835 / Muc)	375	18~~KdpD (1.10599E-122) ~~228,247~~Usp (5.67198E-26) ~~375	cellular organisms, Bacteria, Chlamydiae/Verrucomicrobia group, Verrucomicrobia, Verrucomicrobiae, Verrucomicrobiales, Akkermansiaceae, Akkermansia, Akkermansia muciniphila, Akkermansia muciniphila (strain ATCC BAA-835 / Muc)		unknown			unknown	
W0JK97_DESAE	DESACE_07650	Desulfurella acetivorans A63	652	27~~KdpD (1.52678E-113) ~~236,258~~Usp (5.02857E-32) ~~378,401~~DUF4118 (0.0000000321014) ~~500,528~~GAF (0.0000000371551) ~~645	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfurellales, Desulfurellaceae, Desulfurella, Desulfurella acetivorans, Desulfurella acetivorans A63	Deltaproteobacteria	unknown			unknown	
X1X445_ACYPI	unknow	Acyrthosiphon pisum (Pea aphid)	517	14~~KdpD (3.83911E-122) ~~222,245~~Usp (6.83984E-42) ~~364	cellular organisms, Eukaryota, Opisthokonta, Metazoa, Eumetazoa, Bilateria, Protostomia, Ecdysozoa, Panarthropoda, Arthropoda, Mandibulata, Pancrustacea, Hexapoda, Insecta, Dicondylia, Pterygota (winged insects), Neoptera, Paraneoptera, Hemiptera, Sternorrhyncha, Aphidiformes, Aphidomorpha (aphids), Aphidoidea, Aphididae (aphids), Aphidinae, Macrosiphini, Acyrthosiphon, Acyrthosiphon pisum (Pea aphid)	Eukaryota	unknown			unknown	
V5XHB1_MYCNE	D174_RS21460	Mycobacterium neoaurum VKM Ac-1815D	593	7~~KdpD (1.88289E-107) ~~216,238~~Usp (4.19507E-35) ~~359,382~~DUF4118 (0.000008087) ~~462,382~~DUF4203 (0.00964245) ~~464	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Corynebacteriales, Mycobacteriaceae, Mycobacterium, Mycobacterium neoaurum, Mycobacterium neoaurum VKM Ac-1815D	Actinobacteria	unknown			unknown	
F0TA31_METLA	Metbo_1758	Methanobacterium lacus (strain AL-21)	651	26~~KdpD (2.09484E-113) ~~236,258~~Usp (1.13074E-33) ~~378,405~~DUF4118 (7.10739E-20) ~~505,531~~GAF (0.0000000000270243) ~~647	cellular organisms, Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales, Methanobacteriaceae, Methanobacterium, Methanobacterium lacus (strain AL-21)	Archaea	unknown			unknown	
M1E8G4_9FIRM	Thena_0832	Thermodesulfobium narugense DSM 14796	644	24~~KdpD (5.14668E-112) ~~234,256~~Usp (1.7135E-30) ~~375,396~~DUF4118 (0.000000492008) ~~494,522~~GAF (0.0000227208) ~~639	cellular organisms, Bacteria, Firmicutes, Clostridia, Thermoanaerobacterales, Thermodesulfobiaceae, Thermodesulfobium, Thermodesulfobium narugense, Thermodesulfobium narugense DSM 14796	Firmicutes	unknown			unknown	
A0A024HDR4_PSEKB	kdpd1 PKB_1850	Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	473	18~~KdpD (2.00005E-126) ~~227,248~~Usp (4.87669E-35) ~~365	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas, Pseudomonas knackmussii, Pseudomonas knackmussii (strain DSM 6978 / LMG 23759 / B13)	Gammaproteobacteria	PKB_1851 (PKB_1844)	0 (2TM)	hk (HAMP, hk)	PKB_1852 (PKB_1845)	rr (sigma70 related) (rr (sigma70 related)))

B4U8E6_HYDS0	HY04AAS1_0720	Hydrogenobaculum sp. (strain Y04AAS1)	643	20~~KdpD (2.96922E-115) ~~227,251~~Usp (4.60725E-34) ~~367,447~~DUF4118 (0.00105819) ~~499,525~~GAF (0.0000000464438) ~~639	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Aquificaceae, Hydrogenobaculum, Hydrogenobaculum sp. (strain Y04AAS1)	Aquificae	unknown			unknown	
[illegible]T	PrevDRAFT_1321	Prevotella bivia DSM 20514	378	20~~KdpD (5.45174E-118) ~~229,251~~Usp (1.96366E-24) ~~378	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, Prevotella bivia, Prevotella bivia DSM 20514	Bacteroidetes/Chlorobi group	PrevDRAFT_1319	2TM	[illegible],PAS hk	PrevDRAFT_1320	sigma54 dependent RR
T0VE02_9ENTE	HSIEG1_1767	Enterococcus sp. HSIEG1	492	16~~KdpD (9.28329E-124) ~~224,247~~Usp (2.57026E-27) ~~352,375~~DUF4118 (6.33329E-14) ~~476	cellular organisms, Bacteria, Firmicutes, Bacilli, Lactobacillales, Enterococcaceae, Enterococcus, Enterococcus sp. HSIEG1	Firmicutes					
A0A0A8UNS1_LEGHA	kdpD LHA_1369	Legionella hackeliae	648	23~~KdpD (4.24452E-107) ~~229,254~~Usp (1.82225E-36) ~~376,397~~DUF4118 (5.92764E-14) ~~496,524~~GAF (0.0000000000121863) ~~640	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella hackeliae		unknown			unknown	
E7GKG0_CLOSY	HMPREF9474_01405	[Clostridium] symbiosum WAL-14163	231	22~~KdpD (2.53521E-117) ~~213	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Lachnospiraceae, Lachnoclostridium, Clostridium symbiosum (Bacteroides symbiosus), [Clostridium] symbiosum WAL-14163	Firmicutes	HMPREF9474_01404	4TM	Usp,DUF4118,GAF hk	HMPREF9474_01403	
D3HKC7_LEGLN	LLO_2471	Legionella longbeachae serogroup 1 (strain NSW150)	653	23~~KdpD (4.50543E-104) ~~232,254~~Usp (5.74687E-34) ~~376,396~~DUF4118 (0.00000000352323) ~~496,526~~GAF (2.94309E-14) ~~640	cellular organisms, Bacteria, Proteobacteria, Gammaproteobacteria, Legionellales, Legionellaceae, Legionella, Legionella longbeachae, Legionella longbeachae serogroup 1 (strain NSW150)	Gammaproteobacteria	unknown			unknown	
B8GEQ9_METPE	Mpal_2485	Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	637	27~~KdpD (1.95024E-97) ~~231,256~~Usp (5.30027E-29) ~~374,399~~DUF4118 (3.42679E-14) ~~494,523~~GAF (0.00072878) ~~635	cellular organisms, Archaea, Euryarchaeota, Methanomicrobia, Methanomicrobiales, Methanoregulaceae, Methanosphaerula, Methanosphaerula palustris, Methanosphaerula palustris (strain ATCC BAA-1556 / DSM 19958 / E1-9c)	Archaea	unknown			unknown	
A0A0F7FRR0_9ACTN	SXIM_13900	Streptomyces xiamenensis	351	2~~KdpD (2.95133E-101) ~~196,218~~Usp (4.88072E-25) ~~342	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces xiamenensis	Actinobacteria	unknown			unknown	
D3DFQ0_HYDTT	kdpD HTH_0185	Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6)	408	28~~KdpD (3.4511E-101) ~~237,259~~Usp (8.35537E-30) ~~380	cellular organisms, Bacteria, Aquificae, Aquificae, Aquificales, Aquificaceae, Hydrogenobacter, Hydrogenobacter thermophilus, Hydrogenobacter thermophilus (strain DSM 6534 / IAM 12695 / TK-6)	Aquificae	unknown			unknown	
C7LZE9_ACIFD	Afer_1175	Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)	389	22~~KdpD (2.78663E-97) ~~228,253~~Usp (1.12582E-27) ~~376	cellular organisms, Bacteria, Actinobacteria, Acidimicrobiia, Acidimicrobiales, Acidimicrobiaceae, Acidimicrobium, Acidimicrobium ferrooxidans, Acidimicrobium ferrooxidans (strain DSM 10331 / JCM 15462 / NBRC 103882 / ICP)	Actinobacteria	Afer_1174	4TM	hk	Afer_1173	rr (sigma70 related) (rr (sigma70 related)))
R5E231_9FIRM	BN462_00740	Ruminococcus sp. CAG:108	188	23~~KdpD (5.43995E-97) ~~188	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Ruminococcaceae, Ruminococcus, environmental samples, Ruminococcus sp. CAG:108	Firmicutes	unknown			unknown	
D7DKJ9_METV0	M301_2076	Methylotenera versatilis (strain 301)	176	23~~KdpD (5.35182E-90) ~~174	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales, Methylophilaceae, Methylotenera, Methylotenera versatilis, Methylotenera versatilis (strain 301)	Betaproteobacteria	unknown			unknown	
H2JY98_STRHJ	SHJG_2394	Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	166	1~~KdpD (1.79526E-79) ~~155	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces hygroscopicus, Streptomyces hygroscopicus subsp. jinggangensis, Streptomyces hygroscopicus subsp. jinggangensis (strain 5008)	Actinobacteria	unknown			SHJG_2395	
A0A0F5VIN1_9ACTN	TN53_42855	Streptomyces sp. WM6386	124	1~~KdpD (1.04605E-69) ~~124	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	Actinobacteria	unknown			unknown	
Q02CX4_SOLUE	Acid_0076	Solibacter usitatus (strain Ellin6076)	346	30~~KdpD (4.00455E-44) ~~182,228~~Usp (1.65258E-24) ~~341	cellular organisms, Bacteria, Fibrobacteres/Acidobacteria group, Acidobacteria, Solibacteres, Solibacterales, Solibacteraceae, Candidatus Solibacter, Solibacter usitatus, Solibacter usitatus (strain Ellin6076)	Fibrobacteres/Acidobacteria group	Acid_0070	4TM	DUF4118,hk	Acid_0071	rr (sigma70 related) (rr (sigma70 related)))
R0PM03_9FIRM	BN323_01006	Eubacterium sp. CAG:192	208	2~~KdpD (1.29702E-29) ~~164	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:192	Firmicutes	unknown			unknown	
R5R754_9FIRM	BN506_00513	Eubacterium sp. CAG:161	207	2~~KdpD (1.13859E-27) ~~192	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:161	Firmicutes	unknown			unknown	
A9B064_HERA2	Haur_2535	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)	351	9~~KdpD (1.82684E-24) ~~205,226~~Usp (1.64015E-20) ~~347	cellular organisms, Bacteria, Chloroflexi, Chloroflexia, Herpetosiphonales, Herpetosiphonaceae, Herpetosiphon, Herpetosiphon aurantiacus (Herpetosiphon giganteus), Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)		unknown			unknown	
A0A0F2RLL4_9PROT	VR70_07975	Rhodospirillaceae bacterium BRH_c57	173	78~~KdpD (1.48522E-24) ~~173	cellular organisms, Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales, Rhodospirillaceae (purple nonsulfur bacteria), unclassified Rhodospirillaceae, Rhodospirillaceae bacterium BRH_c57	Alphaproteobacteria	unknown			unknown	
I3UFD3_ADVKW	TKWG_19635	Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	144	24~~KdpD (4.99459E-31) ~~102	cellular organisms, Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiales, Alcaligenaceae, Advenella, Advenella kashmirensis, Advenella kashmirensis (strain DSM 17095 / LMG 22695 / WT001) (Tetrathiobacter kashmirensis)	Betaproteobacteria	unknown			TKWG_19620	
A0A0F5VLI6_9ACTN	TN53_41240	Streptomyces sp. WM6386	279	1~~KdpD (2.39862E-24) ~~54,76~~Usp (3.92925E-33) ~~199	cellular organisms, Bacteria, Actinobacteria, Actinobacteria (high G+C Gram-positive bacteria), Streptomycetales, Streptomycetaceae, Streptomyces, Streptomyces sp. WM6386	Actinobacteria	unknown			unknown	
R0M394_9FIRM	BN331_00632	Eubacterium sp. CAG:202	391	2~~KdpD (9.80095E-19) ~~48,68~~Usp (4.15249E-42) ~~191,218~~DUF4118 (1.68135E-14) ~~319	cellular organisms, Bacteria, Firmicutes, Clostridia, Clostridiales, Eubacteriaceae, Eubacterium, environmental samples, Eubacterium sp. CAG:202	Firmicutes	unknown			unknown	

Sheet 9

Uniprot entry of the correspond non-kinase KdpD	500bp upsteam of *kdp* start codon	Species name	Taxonomy lineage	Predicted sigma54 promoter motif	Start	Stop	E-value
B8DR35_DESVM	GCGCCACGCCACGCAACTCCCCGTCGCTGCTGCATTTCCTCTTTCGCTCCGCCCTTGGCACGCCGCATGCTCTACCGGTGACGTCCGGCAC CCGCCGGGCCGGGTACGCCTTCTTCCGCCGACACAGGCAGGAACGGCCCCCGCGCACCTCCATCCGCGCCCTGCCGGGCGCGCCGGAGC GCACCATGGAACTGTACGACGCCATCGGCATCGCCTTTGCGGCGGGCCTGTTCGTCTATCTCGTGTATGCGTTGTTTCGACCCGACAAGTTC TAGAGGGTGCTTCCCAATGGCCTTTTCGCCCGTTGGCTTCGCCAGACTTCGCCTGCCATCTCGGTTGAATGCGAGAAGGGCACGCAGTGCG GTGGACATCCGGGAGGCTCGCTTCGCTCCCGCATGGCACGCTCGTCTTCCTCGCCAACGAACGAAAAACCTCACGCAGAAACACCCCCCTG AGCACAAACACCTCCCTGTCGGACCCGCCCCATACCGGAGACCATCATG	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	ttggcacgccgcatgctctaccggtgacgtccg gcacccgccgggccgggtacgccttcttccgc cgacacaggcaggaacggccccgcg	45	155	1.10E+00
W0F294_9SPHI	CTTCCGGTTGCCGGGGGAAAAGTGCTGTCTGCTTTTGATCTGGCCAGCGCTGAAAAGATCCACATCCAGAAAGTTTTGAATTACACCAACGG CAATAAAACCGAAACGGCAAAATTGCTGAATATAGCTTTAACCACGCTTTATCGGAAGATAGAAGAATATTATATAAAGTAACCCTTTCAAAAC GATAGTGGGCACCCTTTCATTTTGAAAGGGTTTTTATTGCCACGGCTGTGGCAAAAGAAATTACAACTCAGTACAGCAGCGCGTTCCGGCAG ATCCGGATTTTGTTGGAACGGGGATTGCATCCCTGTTGGCATATCAAATTATAATTCGTTATGCTCACATTCATTTTAATTCTCGCGGGGCTTT TAGGATTTGCCCTCTTTTTTTTTATCAATAAAATATTTTGAAAAGATATGACAGCATTATTCATCGTAGCCATCGCCGTATTTGTGTATATGTGTT ATGTATTGGTAAAACCGGAAAAATTTTAAAACAATG	Niabella soli DSM 19437	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Sphingobacteriia, Sphingobacteriales, Chitinophagaceae, Niabella, Niabella soli, Niabella soli DSM 19437	ttggaacggggattgca	244	354	2.70E+00
Q5LHU3_BACFN	CGTTTACTGAAAATCGGATTGACTACTTTATACCGAAAAATAGAAGAATATAAGCTCTGAGTCGCGCGTGAATATCGTTGCCTGAGTTTTATGC TTCTTTCCTTTTCAAAATAAAACGAACCTTTTCATAATGATAGGGTATCTTCGTACAAGACGAAGATACCCTATTTGTTTTATATCTCTGTATGAT AGTGACTTATCTTATCCTTGACTGTTTCTGGCACGCATTTGGCATGAAGAGTTACAGGTAAAAAACATAAGTATAAACATTTTAATTAAAAGGTA AAAAACATGGGAATAACAGTTTCATTTATTTTCTGCCTGTTGAGCGGGTTTGCCTGCTTCTGGCTGTTTTGGAAATGCGTTGACTGGTTTGAA ACAATTTAGAGAGGAGAATTTATTTTATGTACACAACACTATTTGTAGTAGGTATCATACTTTTCAGTTATTTGACGTATGTGCTCATTCGTCCA GAGAAGTTTTAATTTGAAAATAAAGCAATG	Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides fragilis, Bacteroides fragilis (strain ATCC 25285 / DSM 2151 / JCM 11019 / NCTC 9343)	ctggcacgcatttggca	171	281	3.20E+00
G1UPR9_9DELT	GGCAATCTGCTTAGACCGATCAGCTTTCTCATTCTGTTTCCCGACGCGCGTCGTCCCTTGTGGGCGACGCGCGTTTTGCGTTTTCAATAGTG CCGGATCTTTTCCTTCGTCTTCCCCGTGACGCTCCCCACCGCCTTACATTTTGTAATCCGGACTTCATCGGAGGTTACAAAATGTAAGATTTTT CCACACCGGGGAAATTATATCTATTTGAAATACAACATAAATTATGTTTGGTACAAGCCTTGCTCAGAGTGGAGACGCGCCGGGCCGACGCC GGGCGCGATCACTGACGTAAGGAGGAATCATGTTTGTCATCTGTTTAGTGCTGGGGCTGACCGTCTTCGCCGGTATGGCCCTGCTGACCCT GGCCTGTGCCAAATTGTAAGAAGAAAATGGAGAGCATCATGTTGTATGTTTCGGGGCTGGCATTGCTGTTCTGCATTGCCTATCTCGTCTGG GTCATTCTGAATACGGAAAAACTGTAGGAGAAGGCGGCCATG	Desulfovibrio sp. 6_1_46AFAA	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio sp. 6_1_46AFAA	ttggtacaaggccttgct	187	297	3.20E+00
S0GLV5_9PORP	ATAGGCTACCTTTACTTTTATTAAAGCCCCGGGCCCTATACAAGCCGGGGCTTTATTTTTATTCTCTCACTCTCTTTTTCATCTTTCCGTTTTGA TATACTTTACCGTTTTGACAGGCTGACCTTTTCAAAATGGAAGGGTTACCTCTTCCGACGTTATGCTGCGTTTTTCTGATAAGTATTTGTGATA CAGGTTTTAACATGTTGTTGTCTCCGCTTTGGCACGGCTTTGGCATATAGAAGGGCAAAATGATTTGTATAAACGATTAAAAGACAAAGCTAT GTTAGAGAATGAAATTGTATCATTTATTTTTTATGTGCGGTAGGTAGCCTTTGCTACTGGTTTTTTTTCAAGTGTGTAGATTGGTTCGAAAAGA TTTAAAGGAAGGAGGAGAGATATGTTCGTAGCACTGTTTATACTCTGCCTGGTTATCTTCGGGTATCTGATGTATGTGTTGATTAAGCCCGAA AAGTTTTAAACAAATAATGATGGTAAAAAGATG	Parabacteroides goldsteinii dnLKV18	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, Parabacteroides goldsteinii, Parabacteroides goldsteinii dnLKV18	ttggcacggctttggca	171	281	3.50E+00
R7LGH1_9BACT	CCCATGGAAACAAGACAGAAACAGCTCGTCTACTGAAAATCGGTCTTGCCACTTTATACCGAAAAATAGACTCCTACGGCATCCAATAACATA AAACATCCGTTTCTTTACCATTTCATTTTAAGAGAGCGACCTTCTCATTCTGAGAGGGCCGCTCTTTTGCTTTATAGTCAGTTGAATTTTTTTTA TAGCTGATACACAGTCTGTTTGTTCTTGATTTTTTTTCTTGGCACATCCCTTGCCTATATAATGCCATCATGTATAACTCATAATAATTGTAATAA CTAAAATGAAAAGAAAATGAACGAAATGATTGGAATCGCCATCTGTGTAGCCAGCGGATTGGCCTGTTTTAAACTGTTTATGAAGTGTATTGA TTGGTTCGACAACCTATAAAAAAGAGAAAGGTATGTATACAGCATTGTTTATCGTAGGTATTATCTTGTTCGGCTATCTTGCTTATGTCTTGGTT AAGCCGGAAAAATTCTAAAAAAAGAAATTATG	Prevotella sp. CAG:891	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Prevotellaceae, Prevotella, environmental samples, Prevotella sp. CAG:891	ttggcacatcccttgcc	180	290	4.70E+00
R6KEZ9_9BACE	TTGCACAAAGTCCGATAGAAAAGTTCGACGCATGCAACGGGGGTATTGAGTAATCCGGAATCAGACAGAAATCGCCCAATAGTATTGTTTCTT TTTCTTATTCTTTCCCTCAATTCTTTTCAAAATAGATAATACCTTTTCATTTTGAAAGGGTGCTCTTTAAGGGAGTATCCTGATTCGCTTGTTGC ATAAGGCTGTTTATTAGATGCTTATGAGTTTGTCCATCCTTCTGGCACGCTATTGGCACATAACCTTCCGATAAAATAAATAGTATTAATTCAAT AAAGGTAAAAAACATGGGACTAACGATTTCATTTATTTTCTGCCTGCTGAGTGGCTTGTTCGCTTTCTGGCTGTTTTGGAAATGTGTGGACTG GTTTGAAAAGATTTAAGAAGGAGAGAGAATTATGTATACAGCATTATTTGTATTGGGTATTGCGGTTTTCGGGTATTTGCTTTATGTACTTGTG AGACCGGAGAAGTTTTAAAGTAGAAAGAAAATG	Bacteroides cellulosilyticus CAG:158	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides cellulosilyticus CAG:158	ctggcacgctattggca	183	293	4.70E+00
H1ZCI4_MYROD	TTGTTGTGTTTTTTTTATAAGATATTGATTTGTATGTAGTTGTGTTGTTGGTGTGAAAGCTGGTATGGCATTCGCTTATACCTAGGCAAAATAAT ACATCATGAAAGCACCATATGCAGTACAAAGCAGGCGTAGCCCAAAGCGACTACACAACACAGAATGCGCAGTTCACGCAATCAATCACAAG TTTACTCTAACTTAAAAACAAACCCATGACCATTTTAGCGTGTATCCTTTTAGGCGTTGTGTGCTTTGTCTTGTTTTACAAAGCCATTCAATTTT TTGATAATCTATAATTTATTAGCCCCATGATTTTATTGTTCCTTATTGCGTTGGCAGTATTTGCTTATTTGTGCTATGTCCTACTCAAGCCCGAA AAGTTTTAAAGACAGCTTGAAAGAGACTGTAAAGAAGTAGGTCTAACCCTACTAATCTTTACGATGGTATACGGTATGGTATACCTCATTCAT CAGATTTTATTATTAATTGATTAATTAAAATG	Myroides odoratus DSM 2801	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Myroides, Myroides odoratus (Flavobacterium odoratum), Myroides odoratus DSM 2801	ctggtatggcattcgct	13	123	6.40E+00
Q725T9_DESVH	ATCATGCCAGATTCAAAGATGAATCGAATCTTGTTTCCGGAAGGGGCCATGTTGTGACGGGGCTTGCGTGATGATTACTCTACGATTTTTAGA AAGATGTGGGATAGATACTCTATCATATTCCGTATCATGCTGTCCTGAAAGATGAAAACAGGACTAAAAATATAAGAGTGGCATCATGGGGCG GGCTGTACACGGATGCCCTGCCGGGTGCCCCCCTCTGGTCCAGCAATATGAGGAAACGAAAGGCTCCCGTTACATTTTGTAACGGGAGCCT TTCATTTTGATACGCCGCGCACGCATAGCAGGAAGGCAAATTCTTTAAAATCATGGTGTTACTAAGTGGCACGTCAAATGCTCTTCGACTGGT GACCCTCAGCACAACATGCAAGGAGATGCCCCATGGATCTGCTCGATATCATCGGTCTCATATGCGCTGCGGCCCTCTACCTGTATGTCGGG TACGCATTGCTCTTCCCTGAACGCTTCTAGGAGTCGACATG	Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Hildenborough / ATCC 29579 / NCIMB 8303)	gtggcacgtcaaatgct	296	406	6.60E+00
R6LFS2_9BACE	GGCATGGAACAAAGTGTTCCGCAGCGGGAAACACTCCGTTTCATGCCGGGGAACTCTCGTTCCCAACCGTTGGAACAAATGGTTCCGCCGG ATGAACCCCGAATCATGCAGTATTCCTTTTCTATTTTGATAAGCACCCTTTCATTTTGGAAGGGTGTTTTCTTTTTCTGTAAGTCCCTGTTTTGC TTTATTCCTTTAGAAATCAAAATCTTATCTTTTTAGCTTCTCTTTTGGCACGCATTTGGCGATTATGAGGGCGGTAAAACATGAATATTAATTTA ACAAAGTAAAAACATGGGAGTAACGATTTCATTTATTTTCTGCCTGTTAAGCGGGTTTCTCGCTTTCTGGCTATTCTGGAAATGTGTGGATTGG TTTGAGAAGATTTAAAGAGGAGAGAAAAGATTATGTACACAGTATTATTTGTATTAGGTGTTGCAGTGTTCGGGTACCTGATGTATGTTCTGGT GAGACCCGAAAAGTTCTAAAAGATTAAAGAAATG	Bacteroides clarus CAG:160	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides clarus CAG:160	ttggcacgcatttggcg	184	294	8.20E+00
R5PNT1_9PORP	TGCTGTCGCTGTATTTCAGTGTGTAAATTGTTTGACAGCCTGATTTGTTATCGGATTTTTCGAATCTGCAATCGTCAATCTACAATCACGAATC GTGATTTATAAATTAAAAACTGTATCATTTTGGTAAGGGACCTTTTCATTTTGGAAAGGTCTTTTTGTTTTTATTATTACCCTTCTCTCTGTATCT ATTTATCTATCAAAATGTTTTGAATGCTGTCGTCGTTGTGGCACGAGCTTGGCATATTCGCTTAATGATAATATTTATTTAATAAAAT GATTATGGACTTCATTTCGATTGGATTTTTAGTGTGTGTACTGAGCGGGATTGCTTGCTTTTGGTTTTTCTTCAAATGCATAGATTGGTTTGAA AAGATTTAATAAAAAGGAGGAATTATAAGATGTACACGGTTTTATTTATTCTAAGTATTGTGATGTTCGGGTATCTGCTGTATGTGCTGGTAAA GCCCGAAGAATTTTAAAATGATGTAGTATG	Odoribacter sp. CAG:788	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Odoribacter, environmental samples, Odoribacter sp. CAG:788	gtggcacgagcttggca	181	291	9.20E+00

A0A0C3NCU2_9PORP	TAAGATAGAGGAGTACGGGTTAGGTGAAAAATAGCGGCTGGTCTGTTTTTTTTGATTGCAGATCGATATGCTATTATGATATGGTACCTTTTCAAAATGAAAAGGTGATAGACGGATAGAATATTCCATTCTATCCGTCTATTTATTTTATATACAATTAGTTATCTTTTGTGGTGATTCCGATGGCATGGCTTTGGCATAGGGAGAAACGAAAACTTAAATTAAATTGAAAAGTCATGGAAGAAGTATTATCATTTATTTTTTTAGGTATGGTTGGTGTTATTTGTTACTGGTTCTTTTTCAAGTGTATTTATTGGTTTGAAAAAATCTGAAAAGGAGGGAGGTTATGTTTACGGTATTGTTTATACTAAGTGTGATGATGTTCGGGTATATGATGTACGTGTTGGTAAAACCCGAAAAATTTTAGAAAGAGTATCAAGCGAATGTAGAAACGAGATAGAAATCCCGGATAACGGGAAATCGTAGTAATGTTTTAAAAGATG	Sanguibacteroides justesenii	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Sanguibacteroides, Sanguibacteroides justesenii	atggcatggctttggca	136	246	1.20E+01
H8MWB8_CORCM	AACCAGTGCCGCAGGCTCTGCACCGCGGCAGGCGGCATCCGGGTGGCACGCAACCGGCGCATGCGCTCGGTCGCCTGCTGAAGCCTGGGTTCGATGCTCTCGCTCCACCGGTACCGATGCACGCCAACCACCTCCGCTCCCCACTGTAACGCCGTCGCCCCCTTTCACCTCGCAGGGGCGCACGGAGCCGGTTCGTGCACATTGCAACCTGGACGTGAGTGCCGCGTCCGCAACCCCTCGGAATGCCTGGGCCTGACGCAAGGCCCGCTCCGGTACGGCGGATGCTCATGCTCCTGGAGTCATGAGCTTCGAATACTCCGCTGGGGCCGCGCTCGCGGTCCTCCTCTCCGTCTACCTCGTCTACGCCCTGCTTCGGCCCGAGCGCTTCTAGGAGCCCGCCATG	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, Corallococcus coralloides (Myxococcus coralloides), Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	cggaatgcctgggcctgacgcaaggcccgctccggtacggcggatgct	208	318	1.20E+01
F8EK06_RUNSL	ACGCAAGGCAACAAAACCGAAACCGCCCGTCTTCTTGGCATTGGCCTCACGACGCTATACCGAAAGATTGAGGAATATGATTTGTAGAAAGGCCGGAGATGGCAGACTCACTCTTCCAAAATGAAAATCAACCCTTCCAAAATGGAAGGGTTTTTTATTGTCCGCTAAGAGTCCCAATCCACAAAATACTGCTTTTCAACCATTTACTCTTCCCCTGATTTGTCGGGCACAGCTTTGGCATACCCACCTATATCTCATTAAACAGATTTTCGCTATGGTTATGCTCATCAGTCTTCTTTTAGCAGGTATTGGGTGTTTTGCTCTGTTCTTTGGTTCTATTCGATTCTTTGAAAAAATCTAACCCTATGTTCACTGTTCTGTTCATCCTCTCATTGGCTGTGTTTTGCTACTTGGTGTACGTTTTACTCAAGCCTGAAAAATTTTAGAAACCCCACCCCTGCCTCTCCCCTGCGAGGGAGGGGTAATACACTTTTACTACTATG	Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Runella, Runella slithyformis, Runella slithyformis (strain ATCC 29530 / DSM 19594 / LMG 11500 / NCIMB 11436 / LSU 4)	cgggcacacgctttggca	177	287	1.20E+01
R7JDL5_9PORP	ATTTATCCATTCCTGCTTTTAGCATTATTCTATACTGTTATGGAAGGATTTCCTTCCGATAGAGTTTAACCGTTTTCAGATAGATCATCTCACAATAATAATATCAGTTTATCAAATTGAGAAAGTTAAAATAGCATTGGAAGTAAATTGAATATTTATATTTCTCTAATATTCAATTGATTATATTCTTTATTCCTTTTATGGCATACCAATTGTATAAGTAAAGATGAATTTTAAAACATAAAAATATGGAACTATTTACAATTGGTTTTGTAGTCTGCCTGCTAATAGGCATGAGCTGCTTTGGATTATTCGAGAAATGTATTGATTGGTTTGAAAACATTTAAAATGAAAAGGAGGAAATATAGATGTACACAGTATTATTTATTGTAGGTCTGATTATGTTTGGCTATTTAATGTATGTCCTGGTTAAGCCGGAAAAGTTCTAAGTAAGTGAGTTGACAATGTATTAAGGCTATCTGCTAAAAAATAATTTAAGTATG	Parabacteroides sp. CAG:409	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Parabacteroides, environmental samples, Parabacteroides sp. CAG:409	atggcataccaattgta	154	264	1.50E+01
R5J7D2_9BACE	AATGATGCATTGATAGGGTGTGATACTGTTATACCTTTTTAATTAATCCGATATATATCCGTTAGGAAAAGTCGATATGGTACAAGTGTGCCGGGGCTTTTCAAAATAGTGTAATCCTTTTCAAAATGGAAGGGTTACACTATTTTTGTGTGTGCCTATCGTTGAACCTAATTTATTGATATATAATTGATTGTGATATAATCTTCTCTTTTGGCATATATTTGGCATATAGCAAGTCTGGTAAAAACAATTAATAACAATTTAAAAACAAGGTAAAAACATGGGAATAACATTATCATTCATTTTCTGCCTGTTTAGCGGCTTTGCTTGCTTCTGGCTATTTTGGAAATGCGTAGATTGGTTTGAGAATATTTAGAAAGAGGAGAATTAGAATTATGTATACAATACTATTTGTAATAGGTATCGCAATCTTCGGTTATCTGATGTATGTGCTCATCAGACCCGAAAAGTTTTAAACTACTTTTTATCGTATTAAAGCAATG	Bacteroides sp. CAG:189	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, environmental samples, Bacteroides sp. CAG:189	ttggcatatatttggca	164	274	1.60E+01
B8DR35_DESVM	GCGCCACGCCACGCAACTCCCCGTCGCTGCTGCATTTCCTCTTTCGCTCCGCCCTTGGCACGCCGCATGCTCTACCGGTGACGTCCGGCACCCGCCGGGCCGGGTACGCCTTCTTCCGCCGACACAGGCAGGAACGGCCCCCGCGCACCTCCATCCGCGCCCTGCCGGGCGCGCCGGAGCGCACCATGGAACTGTACGACGCCATCGGCATCGCCTTTGCGGCGGGCCTGTTCGTCTATCTCGTGTATGCGTTGTTTCGACCCGACAAGTTCTAGAGGGTGCTTCCCAATGGCCTTTTCGCCCGTTGGCTTCGCCAGACTTCGCCTGCCATCTCGGTTGAATGCGAGAAGGGCACGCAGTGCGGTGGACATCCGGGAGGCTCGCTTCGCTCCCGCATGGCACGCTCGTCTTCCTCGCCAACGAACGAAAAACCTCACGCAGAAACACCCCCCTGAGCACAAACACCTCCCTGTCGGACCCGCCCCATACCGGAGACCATCATG	Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Desulfovibrionales, Desulfovibrionaceae, Desulfovibrio, Desulfovibrio vulgaris, Desulfovibrio vulgaris (strain Miyazaki F / DSM 19637)	tcggcatcgcctttgcg	158	268	1.60E+01
Q11TL2_CYTH3	TCTATTGATAAGAATGGAAAACAACTTTCCGCTTTCGACCTGGCAAGCGCAGAAAAAATCCATATTCAAAAAGTGTTGAATTATACGAATGGAAATAAAACAAAAGCATCTGAATTATTAAATATTGCGCTGACTACCCTTTACCGAAAATTAGAAGAATATAAAATAAGCTGACGCCTTTCCCTAGCGAAACGATCGTGTAAACCCTTTCAAAATGAAAGGGTTTTTTATTGCCCGGTTGTATAAAAAAGTATTAAATAACACATTTCCAAAGTTTTACCACACACTAATGTATGCTGGTACAAGAGTTGAAAAAGATCATGTAGTTGACTAAACAAGTAAACTACATCATTGAAATTACTAAAAATACACAACACCATGATCACAGGAATTCTTATTACAACAGGCATCATCATGTATGCACTCTTTTATACATCCATTAACTGGTTTGAAAAAATCTAATCCTATGGCAGCATTATTTATTATCGCACTTGCAGTATTTG	Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Cytophagia, Cytophagales, Cytophagaceae, Cytophaga, Cytophaga hutchinsonii, Cytophaga hutchinsonii (strain ATCC 33406 / NCIMB 9469)	ctggtacaagagagttgaa	250	360	1.60E+01
Q09AI1_STIAD	CTGCGCGAAGAGCTGCTGGCCACCCCCACGGCCGCCGGGATTCTCCAGCTCCTCGTCCAGGCCGAGGAGTCCCATGTGGCGCGGATGGCCCGCCCGGGGAGGCCTGGTGCTCGTCGAGGGGGCGGGCTCTGGCCACGCCTGACAGGCCTTCGGGTTTCACCGCGCACGGCCTGGCCGGGGGCGTTTCGTGCAAGGTGCAACCCCGGCCGTCCGGAGGGGCTCGTAAGTCGCCGGAAAGACTGAGGAATTGCCAGGGCAGGGGGGGTACGGCCCGTGCTCTGGAAGGAGGGGCACTGGGAGCCCCTCCTTATATATGGCGATCTTCGAAATCACGTCCCTGCGGTTGAGCCAGACGGCTGCCGCGCCCCCCGCGTCCCGCTTTGAGGGAGAGGACGTCTTCCCATGACCTTCGACTACGCCGCGGGCGCCGTGCTGTCGGTGCTGCTCGCCCGTCTACCTCGTCTACGCCCTGCTCCGGCCAGAGCGCTTCTAGGGGCCGTGCCATG	Stigmatella aurantiaca (strain DW4/3-1)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Cystobacteraceae, Stigmatella, Stigmatella aurantiaca, Stigmatella aurantiaca (strain DW4/3-1)	ggggtacggcccgtgct	213	323	1.80E+01
R5I937_9PORP	GCGCCATATCAGTCGAGTATTAGAATATACTAAAGGAAACAAAACCGAAACTGCCAGATTGCTGAAAATCGGCTTAACTACTTTATATCGAAAAATAGAAGAATACAAAATATTGTCATAATAGAACAAGACTTTACCAAAATGAAAAGGTTGTAACAGTGATACTGTTACAACCTTTTTCATATACAACTGATAAACAAAACATTACAATATCACACTCATCTTTGGCATATTTTTGGCATAAAAGCCCGCGTAAATATTTTATTAATTAAAAATAATAAGAAATGGAAATTACACTAAACTTTATTTTTTGCCTGCTAAGCGGGTTTGCCTGTTTCTGGCTCTTTTACAAATGTGTCGACTGGTTTGAGAAAATCTAAAAAAAGGAGGTAACAATGTACACAGCACTATTTATAATTGGGTTAATCATTTTCGGTTATATGATGTATGTACTTATCAAACCGGAAAAGTTTTAAAAATTCATTAAGACAAACTAAACAATG	Tannerella sp. CAG:118	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Porphyromonadaceae, Tannerella, environmental samples, Tannerella sp. CAG:118	ttggcatatttttggca	178	288	1.80E+01
H8MWB8_CORCM	AACCAGTGCCGCAGGCTCTGCACCGCGGCAGGCGGCATCCGGGTGGCACGCAACCGGCGCATGCGCTCGGTCGCCTGCTGAAGCCTGGGTTCGATGCTCTCGCTCCACCGGTACCGATGCACGCCAACCACCTCCGCTCCCCACTGTAACGCCGTCGCCCCCTTTCACCTCGCAGGGGCGCACGGAGCCGGTTCGTGCACATTGCAACCTGGACGTGAGTGCCGCGTCCGCAACCCCTCGGAATGCCTGGGCCTGACGCAAGGCCCGCTCCGGTACGGCGGATGCTCATGCTCCTGGAGTCATGAGCTTCGAATACTCCGCTGGGGCCGCGCTCGCGGTCCTCCTCTCCGTCTACCTCGTCTACGCCCTGCTTCGGCCCGAGCGCTTCTAGGAGCCCGCCATG	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	cellular organisms, Bacteria, Proteobacteria, delta/epsilon subdivisions, Deltaproteobacteria, Myxococcales (fruiting gliding bacteria), Cystobacterineae, Myxococcaceae, Corallococcus, Corallococcus coralloides (Myxococcus coralloides), Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)	gtggcacgcaaccggcg	1	111	2.10E+01
A0A077EBR1_9FLAO	ATTCACTCTGTTAAGAAATATCATATCATCTTAAAAAAATCTCATTTTCAGTAACCCGTTTTTATCATTTTGAATATAAGCCTATCATTTTGATAAGCTTTTCTTATTTAACGAGCTTTCAAAAACCAAAATAAAACACTGTAAAACAATAATTTAAAAAAAATTGAAGCTAATTGGAATTGGTTTTGGCATATATCGTTCAGATAAAAATTATGAAAAATGACAACTTTAAAAAAAACCAGTCAGAAGCCCAGCCAGTCTTCTTATACCTGGTTACTGACGTTTCTGGCAGCACTCGTGGTCTTAACCTTAATTATTAGAATAATATGATGCTTTTAGTCCTTTTATTACTCAGTATTGTTTTATTCTGGCTTTTATATAAAACAGTTCAATTTTTTGATAAAATATAACATATCATGTGGAGTTTATTCATCCTTTCCGTTCTGGCATTCATTTACATCTGTTATGTGCTTATGAAGCCTGAAAAATTTTAAATTATTATG	Elizabethkingia anophelis NUHP1	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Flavobacteriia, Flavobacteriales, Flavobacteriaceae, Elizabethkingia, Elizabethkingia anophelis, Elizabethkingia anophelis NUHP1	ttggcatatatcgttca	139	249	2.20E+01

E6STB8_BACT6	GGCTGACTACTCTTTACCGGAAGATCGAAGAATATAAGATATAAGTCTGATTCCACAATGAATTATCATTTATGCCGGAATCACTGCCGATAGAGTCCCGATATTATCTTCTTTCCTCCCTTTCATTTTGGTAATTCCCTCTTTTCATTTTGGAAAGGTTTCTTTTCTTTCCTTTTTTCAGTGTTTTTTCTATAAGGTTCATGGTCAGATTGTTGTATCCGCATGTCTGTTTCTGGCACACATTTGGTATATAGATAGCAGATAAAGACGGACAATAATTTTTTAAAAGGTAAAAGAATATGGGAACAATGTTATCATTTATTTTCTGCTTGTCGAACGGTTTGTTCGCTTTCTGGCTCTTCGGGAAATTTGTGGATTGGTTTGGCAGGATTTAAAGCGAGGGAATATGTACACGATTTTGTTTGTACTGGGTATTGCAGTGTTCGGGTACTTGATATATGTACTCGTGGAACCTGGGAAGTTTTAAATACTTGAACGAGATG	Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	cellular organisms, Bacteria, Bacteroidetes/Chlorobi group, Bacteroidetes, Bacteroidia, Bacteroidales, Bacteroidaceae, Bacteroides, Bacteroides helcogenes, Bacteroides helcogenes (strain ATCC 35417 / DSM 20613 / JCM 6297 / P 36-108)	ctgcacacatttggta	186	296	2.20E+01