Genome-Wide Proteomics and Quantitative Analyses on Halophilic Archaea

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Genome-Wide Proteomics and Quantitative Analyses on Halophilic Archaea

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Erklärung

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„Ich liebe Den, dessen Seele sich verschwendet, der nicht Dank haben will und nicht zurückgiebt: denn er schenkt immer und will sich nicht bewahren.“

Friedrich Wilhelm Nietzsche *(1844-1900)*

”I love him whose soul is lavish, who wanteth no thanks and doth not give back: for he always bestoweth, and desireth not to keep for himself.”

Translated by Thomas Common (1850-1919)

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List of abbreviations

1-D	one dimensional
2-D	two dimensional
2-DE	two dimensional gel electrophoresis
ABC	ammonium bicarbonate
ACN	acetonitrile
AP	alkaline phosphatase
APS	ammonium peroxodisulfate
BCA	bichinconin acid
bp	base pairs
BSA	bovine serum albumine
C	Celsius
^{12}C-Nic-NHS	d0-/^{12}C-nicotinoyl-N-hydroxy-succinimide
^{13}C-Nic-NHS	d0-/^{13}C-nicotinoyl-N-hydroxy-succinimide
CAI	codon adaptation index
CBB	Coomassie brilliant blue
CHAPS	3[(3-cholamidopropyl)dimethylammonio]-1-propansulfonate
CHCA	α-cyano-4-hydroxy cinnamic acid
CID	collision induced dissociation
d4-Nic-NHS	d4-/^{12}C-nicotinoyl-N-hydroxy-succinimide
Da	dalton(s)
DEPC	diethyl pyrocarbonate
DIG	digoxigenin
DIGE	differential in gel electrophoresis
DMSO	dimethylsulfoxide
dATP	desoxyadenosine triphosphate
dCTP	desoxycytidine triphosphate
dGTP	desoxyguanosine triphosphate
dNTP	mix of the 4 deoxynucleotide triphosphates dATP, dTTP, dCTP, dGTP
DSMZ	"Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH"
DTT	1,4- dithiothreitol
dTTP	desoxythymidine triphosphate
EDTA	ethylenediamine tetraacetic acid
emPAI	exponentially modified protein abundance index
ESI	electrospray ionization
EtBr	ethydium bromide
EtOH	ethanol
FA	formic acid
fig.	figure
FT-ICR	Fourier transform ion cyclotron resonance
g	gram(s)
g	force of gravity
GRAVY	grand average of hydrophobicity
h	hour(s)
H_2O_{dest}	distilled water

Hbt.	*Halobacterium*
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
HOAc	acetic acid
IAA	iodaacetamide
ICAT	isotope coded affinity tag
ICPL	isotope coded protein label
IEF	isoelectric focusing
IMAC	immobilized metal ion affinity chromatography
IPG	immobilized pH gradient
iTRAQ	isotope tags for relative and absolute quantification
kbp	kilo base pairs
kDa	kilodalton(s)
L	liter
LC	liquid chromatography
LC-MS/MS	liquid chromatography with subsequent MS/MS measurement
log	logarithmic
m	meter(s)
M	molarity (molar concentration e.g. in mol/l)
mA	milliampere
MALDI	matrix assisted laser desorption/ionization
MeOH	methanol
mg	milligram(s)
Milli-Q	ultrapure laboratory grade water, filtered and purified by reverse osmosis
min	minute(s)
mL	milliliter(s)
mm	millimeter(s)
mM	millimolar
MTP	microtiter plate
MudPIT	multidimensional protein identification technology
µg	microgram(s)
µL	microliter(s)
µm	micrometer(s)
µM	micromolar
N	normality
nL	nanoliter(s)
nm	nanometer(s)
Nmn.	*Natronomonas*
MS	mass spectrometry
MS/MS	tandem mass spectrometry
MS/MS/MS	multiple mass spectrometry
Mw	molecular weight
m/z	mass-to-charge ratio
NHS	N-hydroxysuccinimide
Nic	nicotinic acid
Nic-NHS	nicotinoyl-N-hydroxy-succinimide (N-nicotinoyloxy-succinimide)
OD_{600}	optical density at 600 nm

ORF	open reading frame
PAA	polyacrylamide
PAGE	polyacrylamide gel electrophoresis
pI	isoelectric point
PMF	peptide mass fingerprint
ppm	parts per million
Q-TOF	quadrupol-time of flight
ρ (“rho”)	density
RP	reversed phase
rpm	rounds per minute
RT	room temperature
RTqPCR	real-time quantitative polymerase chain reaction
s	second(s)
SCX	strong cation exchange
SDS	sodium dodecyl sulfate
SDS-PAGE	sodium dodecyl sulfate polyacrylamide gel electrophoresis
SEC	size-exclusion chromatography
SILAC	stable isotope labeling with amino acids in cell culture
Taq	Thermophilus aquaticus
TCA	trichlor acetic acid
TCEP	tris-(2-carboxyethyl) phosphine, hydrochloride
TEMED	N,N,N',N'-tetramethylethylenediamine, [synonym: N,N,N',N'-Di-(dimethylamino) ethane]
TFA	trifluor acetic acid
TMD	transmembrane domain
TOF	time of flight
tricine	N-[tris (hydroxymethyl) methyl] glycine
Tris	tris (hydroxymethyl) aminomethane
V	volt(s)
W	watt(s)
v/v	volume per volume
w/v	weight per volume

1 Introduction

1.1 Microorganisms in hypersaline environments. Microorganisms adapted to life at high salt concentrations are widespread, both within the bacterial and the archaeal domain. As a result, highly diverse prokaryote communities can be found at all salt concentrations, from seawater up to about 340–350 g/liter (brines saturated with NaCl), in both thalassohaline and athalassohaline environments. A few microorganisms can adapt to life over the whole salt concentration range from near fresh water to halide saturation. In most cases, however, each organism has a relatively restricted salt concentration range enabling growth. Some bacteria and archaea are adapted to life in saturated and near-saturated brines, being unable to grow and even survive at NaCl concentrations below 15–20%. Most representatives of halophilic archaea of the order Halobacteriales show such a behavior [Oren 2006].

A cell not adapted to hypertonic surroundings would shrink without apparent readjustements afterwards and finally perish. Halophilic and halotolerant microorganisms encounter osmotic challenges by adjusting the amount of intracellular solutes, until the cytoplasm reaches a similar osmotic strength as the surrounding medium. Thereby, two strategies of osmoadaptation have emerged, the KCl-type and the organic-osmolyte type. Halobacteria belong to the first group, being able to accumulate 4-5 M KCl and 1-3 M NaCl in their cytosol [Ginzburg et al. 1970]. These high cytoplasmic ion concentrations are tolerated due to specially adapted enzymes and cell structures [Eisenberg and Wachtel 1987]. Stabilization of halophilic proteins in their physiological environment is due to a hydration network consisting of both water molecules and salt ions, attributed to an excess of acidic residues and a deficit of basic residues [Zaccai and Cendrin 1989]. Microorganisms employing the organic-osmolyte type of osmoadaptation are able to maintain a usual enzymatic machinery, as the so-called compatible solutes do not interfere with the cells' metabolism. Although production and accumulation of organic osmolytes are wide-spread among halophilic bacteria, and most archaeal halobacteria tolerate high cytoplasmic concentrations of KCl, there is no clear distinction between archaea and bacteria regarding the modes of osmoadaptation [Galinski 1993].

Different classification schemes have been designed to define the salt relationships of microorganisms. Because of the continuum of properties found within the prokaryote world, there will always be organisms that cannot be classified unequivocally within any of the groups defined. The most widely accepted classification according to salt dependence and salt tolerance is that of D. J. Kushner [Kushner 1978]. This scheme recognizes different categories of salt dependence (non-halophile for < 0.2 M salt; slight halophile for 0.2-0.5 M salt; moderate halophile for 0.5-2.5 M salt; borderline extreme halophile for 1.5-4.0 M salt; extreme halophile for 2.5-5.2 M salt; and halotolerant). Halotolerant microorganisms, while not requiring high salt concentrations for growth, are able to grow at high concentrations of NaCl and other salts. Classification should be based not only on the behavior toward NaCl but to other ions as well, especially for organisms adapted to life in athalassohaline environments [Edgerton and Brimblecombe 1981].

1.1.1 Characteristics of the halophilic archaea *Natronomonas pharaonis* and *Halobacterium salinarum*. Archaea constitute one of three phylogenetical distinct domains [Woese and Fox 1977] in addition to Bacteria and Eukarya. So far it was widely accepted that archaea are subdivided into two ubiquitously distributed major phyla, the Euryarchaeota and Crenarchaeota [Jurgens and Saano 1999]. Recent research shows that there is evidence for the introduction of a third phylum, which was proposed to be named Thaumarchaeota (Fig. 1) [Brochier-Armanet *et al.* 2008].

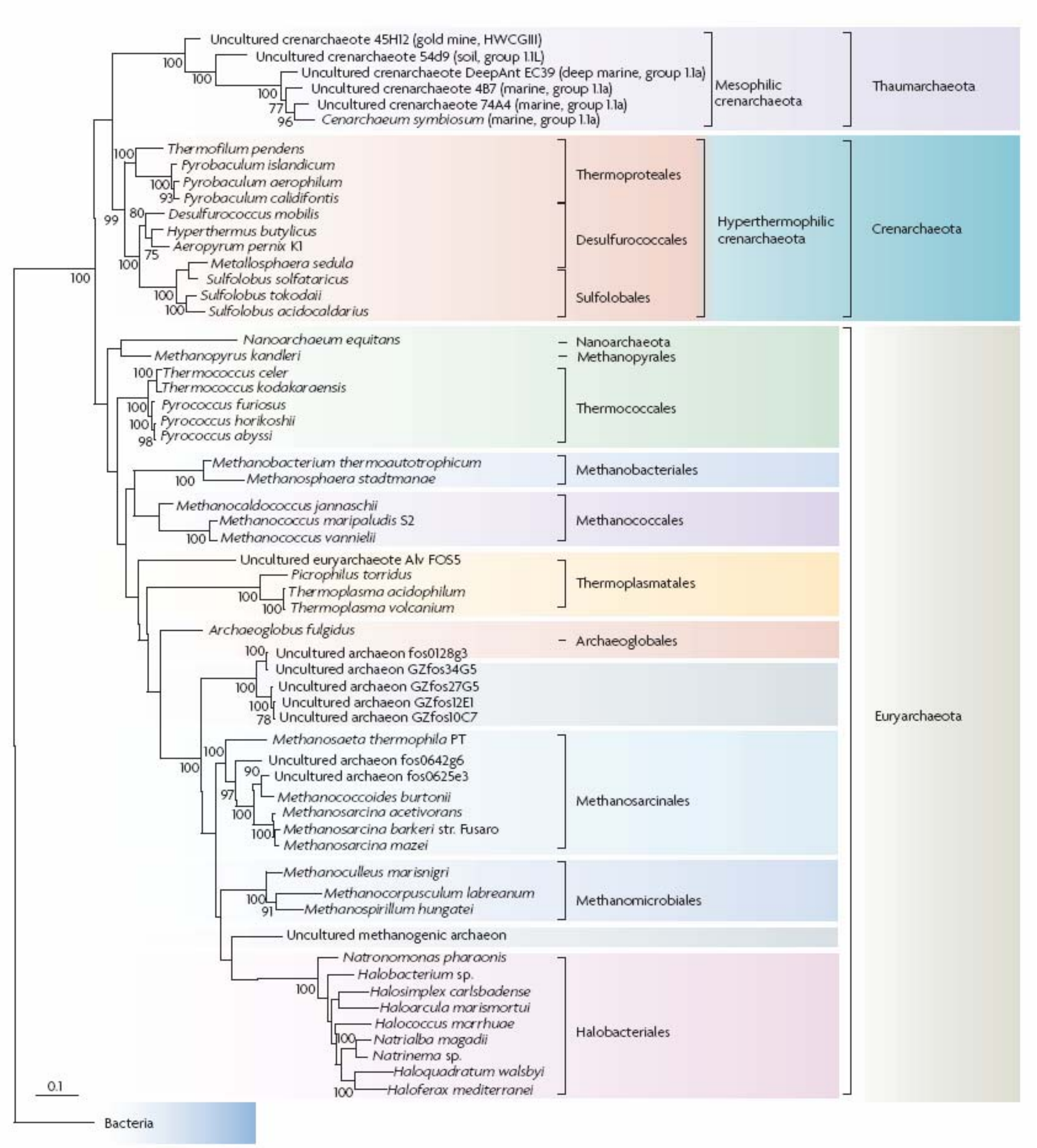


Figure 1. Phylogenetic tree, illustrating the classification of archaea into phyla (e.g. Euryarchaeota), orders (e.g. Halobacteriales) and species (e.g. *Natronomonas pharaonis*), based on recent research from Brochier-Armanet *et al*., 2008. Figure taken from Brochier-Armanet *et al*., 2008.

Strains of the extreme haloalkaliphilic archaeon *Nmn. pharaonis* were isolated originally from saline soda lakes in Egypt [Soliman and Trueper 1982] and Kenya [Tindall *et al.* 1984]. Growth occurs in media containing high concentrations of NaCl and Na_2CO_3. The cells thrive optimally in 3.5 M NaCl at a pH of 8.5-9.5 (surviving up to pH 11) and have a very low magnesium tolerance [Staley *et al.* 1989]. *Nmn. pharaonis* belongs to the halophilic branch of the Euryarchaeota which form a homogenous phylogenetic group according to rRNA analysis. The close phylogenetic relationship between the haloarchaea is further supported by the large number of highly homologous proteins. The genome of *Nmn. pharaonis* consists of a 2.6-Mb GC-rich chromosome and two plasmids of 131 kb and 23 kb [Falb *et al.* 2005]. From genome analysis it has been concluded that the metabolism of halophilic archaea is highly flexible [Falb *et al.* 2005] and reflects an adaptation to extreme habitats which share the characteristic of being hypersaline but include additional environmental threats like high alkalinity or high $MgCl_2$ concentrations, as in the case of *Natronomonas pharaonis* or *Haloquadratum walsbyi* [Bolhuis *et al.* 2006], respectively. This flexibility can originate from either (a) species-specific gene loss, or (b) genetic exchange with other organisms like halophilic bacteria and algae that live (or more likely died) in the hypersaline environments. Genetic exchange may originate from DNA uptake or may involve gene transfer via phages or mobile genetic elements affecting also larger genome regions. Consistent with this, most halophiles have megaplasmids (or small chromosomes) and genome regions that have a GC content deviating considerably from the chromosome average.

The theoretical proteome of *Nmn. pharaonis* consists of 2843 protein-coding genes according to detailed evaluation of automatic gene prediction data [Falb *et al.* 2005], which has confirmed that gene prediction in GC-rich genomes is error-prone [McHardy *et al.* 2004]. Due to the statistical bias of GC-rich genomes, which results in a scarcity of stop codons, the number of reading frames which are open for considerable length greatly exceeds the number of reading frames representing protein-coding genes. This results in a large number of so-called spurious ORFs, most of which are longer than 100 codons in *Natronomonas* but are assumed to not code for real proteins.

Most sequenced genomes contain a large number of organism-specific genes with neither sequence homology nor assigned function and it may be questioned if they are real genes.

Experimental validation and confirmation can be obtained by proteomic data which increase the reliability of the theoretical proteome.

Such a reliable proteome is also required for genome-wide analyses, e.g., metabolic reconstruction. *Natronomonas* shows a high nutritional self-sufficiency and thus is able to grow in a very simple synthetic medium [Falb *et al.* 2005], whereas organisms like *Halobacterium* require a rather complex set of nutrients for growth.

Proteomic investigations on *Hbt. salinarum* strain R1 have already confidentially verified the existence of 1992 proteins, representing 70.3% of the theoretical proteome (2784 protein-coding genes) [Klein *et al.* 2007; Klein *et al.* 2005; Tebbe *et al.* 2005]. This strain thrives optimally in 4 M NaCl, growing both under aerobic and anaerobic conditions being able to use e.g., DMSO as terminal electron acceptor [Oren and Truper 1990], to ferment arginine to ornithine [Hartmann *et al.* 1980; Ruepp *et al.* 1995], and to grow photosynthetically due to the retinal protein bacteriorhodopsin [Oesterhelt 1998]. Furthermore, it is able to respond to various environmental stimuli showing phototactic as well as chemotactic responses [Marwan and Oesterhelt 2000]. The genome of *Hbt. salinarum* strain R1, DSM 671, consists of a 2 Mbp chromosome and 4 megaplasmids ranging from 41 to 284 kbp [Pfeiffer *et al.* 2008a] and is very similar to that of the strain *Halobacterium sp.* NRC1 [Ng *et al.* 2000], especially in its chromosomal genes.

Depending on parameters like the shaking rate and thus aeration of the medium, generation times of 8 h [Oesterhelt and Stoeckenius 1974] to 10 h [Gonzalez *et al.* 2008] in complex and up to 14.5 h [Gonzalez *et al.* 2008] in synthetic medium have been reported. For the closely related *Halobacterium* sp. NRC-1 (*Hbt.* NRC-1), generation times of 1.86 h have been measured in GN101 medium, growing equally well within a temperature optimum range spanning 15 °C (35-50 °C) [Robinson *et al.* 2005]. The growth behavior of *Hbt. salinarum* strain R1 is shown in Fig. 2 (for growth conditions see chapter 2.2.1).

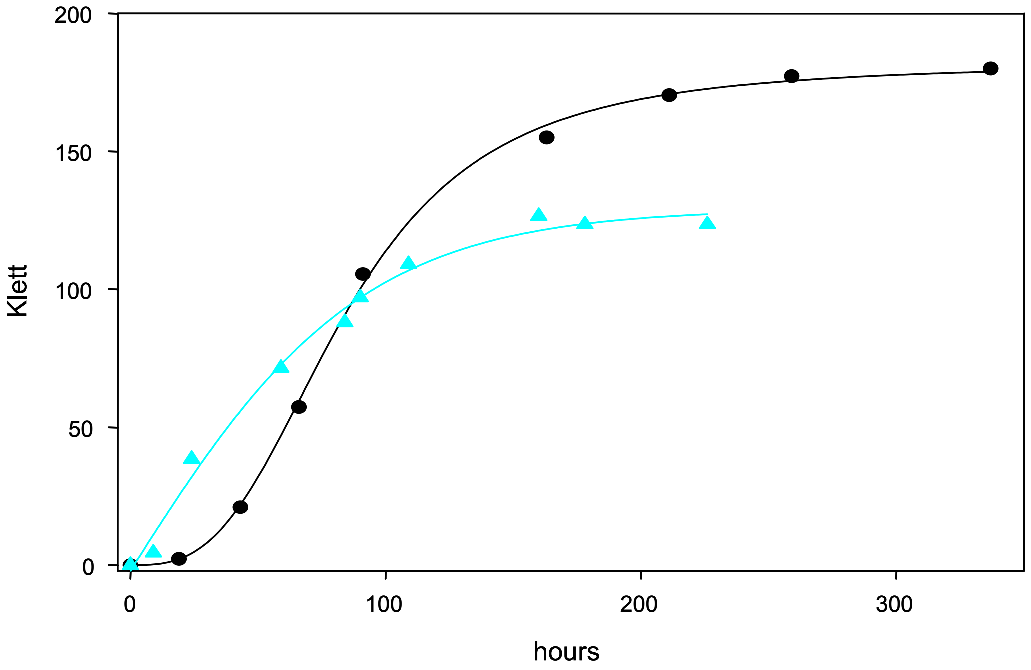


Figure 2. Growth curves of *Hbt. salinarum* strain R1 (cyan line) and *Nmn. pharaonis* (black line), respectively, determined under identical conditions of aeration and preparation of the inoculum (for growth conditions see chapter 2.2.1). *Hbt. salinarum* grows much faster directly after inoculation to standard medium, whereas *Nmn. pharaonis* grows to a higher density (complex medium for *Hbt. salinarum*; modified DSMZ medium 371 for *Nmn. pharaonis*; see chapter 2.1.5).

1.2 The transcription machinery of archaea. Concerning their molecular mechanisms, archaea are featuring both eukaryal and bacterial characteristics [Bell and Jackson 1998; Brown *et al.* 1989; Gribaldo and Brochier-Armanet 2006]. Substantial similarity between the archaeal and eukaryal DNA replication apparatus, ribosomal proteins, transcription, protein co-translational targeting, and RNA metabolism are opposed to aspects showing notable similarities to bacteria like the size and organization of archaeal chromosomes, the presence of polycistronic transcription units, and partly the utilization of Shine-Dalgarno sequences for the initiation of translation [Gribaldo and Brochier-Armanet 2006; Londei 2005].

The transcription machinery of archaea displays a level of complexity, which lies between that of eukarya and bacteria. Unlike archaea and bacteria, eukaryotes have three different RNA polymerases (RNAP I, II and III) to transcribe different gene classes encoding rRNAs, mRNAs, and tRNAs and other sRNAs, respectively [Best *et al.* 2004; Santangelo *et al.* 2007].

Archaea possess a subset of the eukaryal general transcription factors (GTFs) to constitute the core transcription apparatus, namely homologues of the TBP, of the TFIIB (termed TFB) [Thompson *et al.* 1999] and a protein with homology to the N-terminal half of the TFIIEα (termed TFE) [Bell *et al.* 2001]. Just as for the eukaryal RNAP II transcription apparatus, transcription from archaeal promoters is initiated by binding of a highly conserved TATA-box binding protein (TBP) to its recognition element [Langer *et al.* 1995]. Once bound, the TBP recruits the transcription factor TFB, which serves as a bridge between TBP and the RNAP.

The TFB determines transcription polarity in archaea by interaction with the B recognition element (BRE), a region immediately upstream of the TATA box [Bell *et al.* 1999; Littlefield *et al.* 1999]. Transcription initiation could be reconstituted from many archaeal promoters *in vitro* using TBP, TFB and RNAP. The TFE, however, has been suggested to stimulate transcription selectivity at weak archaeal promoters [Bell *et al.* 2001; Hanzelka *et al.* 2001].

The occurrence of multiple genes encoding TBP and TFB proteins in some archaea, especially in halophiles, led to the assumption that different combinations of these could selectively direct global transcription towards adaptation to changing environmental conditions, a strategy similar to the use of multiple σ-factors in bacterial cells [Thompson *et al.* 1999]. Recent studies revealed that multiple TFBs in *Hbt.* NRC-1 differentially recognize specific subsets of promoters [Facciotti *et al.* 2007]. *Tfb* deletion mutants of *Thermococcus kodakaraensis*, holding two genes encoding for different tfbs, but with exchangeable and overlapping functions, did not exhibit detectable growth defects. Unlike σ-factors in bacteria, these two TFBs do not function in promoter selection. Contrariwise, archaea with multiple GTFs like *Hbt.* NRC-1, which were reported to code for 6 TBP and 7 TFB proteins, are suggested to exhibit promoter specificity [Baliga *et al.* 2000; Facciotti *et al.* 2007; Coker *et al.* 2007a; Teufel *et al.* 2008].

Hbt. salinarum strain R1 (DSM 671), which is described in this work, has a virtually identical chromosomal genome composition to that of *Hbt.* NRC-1, and only differs by some sequence rearrangements when comparing the plasmid DNAs [Pfeiffer *et al.* 2008a;

Pfeiffer *et al.* 2008b; Teufel *et al.* 2008]. These rearrangements may have been caused by evolution in the laboratory [Pfeiffer *et al.* 2008b]. Examples for the genetic flexibility of halophilic archaea attributed to diverged evolution have been discussed previously [Konstantinidis *et al.* 2007]. In contrast to *Hbt.* NRC-1, *Hbt. salinarum* R1 codes for eight *tfb*s (*tfb*A-H), three located on the plasmid pHS2 and five on the chromosome . Two of the *tbp*s in the strain R1 (*tbp*B and *tbp*F) carry an ISH2 insertion and are not functional. From the four functional TBPs (*tbp*ACDE), three are encoded by plasmids (pHS1 or pHS4) and only one (*tbp*E) by the chromosome (www.halolex.mpg.de) [Pfeiffer *et al.* 2008a; Pfeiffer *et al.* 2008b]. Since formation of the preinitiation complex requires binding of a TBP with a TFB to recruit RNAP to the promoter, it seems possible that the four functional TBPs and eight TFBs interact in up to 32 different combinations, driving transcription from a diverse set of promoters. This number of possible combinations constitutes the second highest after that of *Hbt.* NRC-1, when comparing with to date fully archaeal sequenced genomes [Facciotti *et al.* 2007]. The quantity of different combinations and the possibility of interactions with different regulators may explain the diversity of halophilic promoters [Baliga and DasSarma 1999; Soppa 1999].

In archaea, upregulation of a *tfb* gene in response to heat shock has been noted on the transcriptional level in both *Haloferax volcanii* (*Hfx. volcanii*) [Thompson *et al.* 1999] and *Pyrococcus furiosus* [Shockley *et al.* 2003]. In *Hfx. volcanii*, Western analysis also proved TFB-protein level to be elevated, but to a much lesser extent (≈ twofold increase). In addition, exposure to heat shock induced transcription of the transcription regulator *phr* in *Pyrococcus furiosus*, with a concomitant weak stimulation of the Phr protein, also detected by Western blotting [Vierke *et al.* 2003]. Similarly, mRNA levels of a homologous transcriptional regulators (AF1298) in *Archaeoglobus fulgidus* [Rohlin *et al.* 2005] have also been found significant increased in response to heat shock.

1.3 Molecular chaperones. Prolonged exposure to elevated temperatures or other environmental impacts results in unfolding, misfolding and subsequent aggregation of proteins in living organisms. Hence, increased synthesis of molecular chaperones and proteases that contribute to repairing protein damage and assist in the recovery from denatured states, is rapidly induced [Morimoto 1998]. Members of the Hsp70 (DnaK) and

Hsp60 (GroEL; CCT) families can be involved in attaining correctly folded states and functional conformations during protein maturation or during recovery from denaturation [Georgopoulos and Welch 1993; Kubota *et al.* 1995]. Other molecular chaperones important in perventing protein aggregation under stress are members of the Hsp90 and Hsp100 families, as well as the so-called "small Hsps" [Schirmer *et al.* 1996; Jakob and Buchner 1994].

Folding of a subset of proteins depend on chaperonins (Hsp60), a family of structurally related chaperones, classified into two groups. Group I chaperonins were found in bacteria (GroEL) as well as in mitochondria and chloroplasts of eukarya. Archaea and the eukaryotic cytosol possess members of the Group II chaperonins, also known as thermosomes, like the archaeal "cytosolic chaperonin containing T complex polypeptide-1 (TCP-1)" CCT. Group II chaperonins form eight or nine membered rings and are independent of a general co-chaperonin like the GroEL cofactor GroES [Gutsche *et al.* 1999]. While some thermosomes are comprised of a single subunit, such as that of *Methanococcus jannaschii* [Bult *et al.* 1996], most consist of two homologous subunits in each of its rings (αβ-thermosomes as in the case of *Hbt. salinarum*) originating from gene duplications. Interestingly, two *Sulfolobus* species [Archibald *et al.* 1999] and *Haloferax volcanii* [Kuo *et al.* 1997; Thompson and Daniels 1998] possess even a third (γ) chaperonin gene.

The chaperone DnaK and its co-chaperones DnaJ and GrpE interact and cooperate in protein maturation [Bukau *et al.* 2000]. The co-chaperones stimulate the ATPase activity of DnaK with GrpE promoting nucleotide exchange and DnaJ enhancing the rate of ATP hydrolysis [Liberek *et al.* 1991; Panagiotidis *et al.* 1994]. This clustered operon is present in all bacterial and eukaryotic organisms reported to date, with GrpE being replaced by other molecules in eukarya [Macario *et al.* 2006]. In many archaea DnaK does not occur, like in members of the Crenarchaeota [Rohlin *et al.* 2005], whereas a few species, like the cyanobacterium *Synechococcus elongatus*, even encode for multiple copies [Sato *et al.* 2007].

Hsp70 interacts with nascent proteins to prevent premature folding, and some of the newly synthesized proteins are transferred to Hsp60 chaperonins to promote folding in an ATP-dependent manner [Georgopoulos and Welch 1993; Gutsche *et al.* 1999].

DNA-binding heat shock proteins also play a role in the control of DNA topology during thermal stress. They bind to nonspecific unfolded sites and have bending and unwinding properties through the action of DNA topoisomerases [Adamcik *et al.* 2002]. A similar interaction between DnaK and DNA gyrase has been observed during heat shock in *Escherichia coli*. After heat induced relaxation, the chaperone associates with the DNA and acts directly on DNA gyrase, thereby both contributing to the re-supercoiling of DNA [Ogata *et al.* 1996].

Microarray analyses of heat shock response in the archaeon *Methanosarcina barkeri* showed induction of the Hsp70 operon and two Hsp60 homologues, as well as of an AAA+ ATPase and a small heat shock protein (sHSP) [Zhang *et al.* 2006]. *Archaeoglobus fulgidus* and *Pyrococcus furiosus*, both lacking the *dnaK* operon, also showed induction of genes encoding HSP60 and sHSP20, as well as of molecular chaperones (VAT, VCP-like ATPase) belonging to the cdc48/p97 (cell division control protein48) branch of the AAA+ family.

1.4 Mass spectrometry. Mass spectrometry has its origins in the studies performed by J.J. Thomson and his student F.W. Aston around the turn of the 19th century [Griffiths *et al.* 2001]. It is an analytical method that can be used for determining the molecular weight of biological compounds, and hence an important tool in proteomics, where it is essential for the identification of proteins. A mass spectrometer is an instrument that produces ions from a sample, separates them according to their mass-to-charge ratio (m/z) and records the relative abundance of each of the ions to obtain a mass spectrum [Bonner *et al.* 2002]. The mass spectrometer can be divided into three basic components: the ion source, mass analyzer and the detector (Fig. 3). An advantage of a mass spectrometer over other analytical instruments is the high degree of accuracy (~0.01-0.001%) and sensitivity (detection of 10^{-9} - 10^{-18} mol of sample required) [Poland *et al.* 2001]. Until recently mass spectrometry was restricted in its use to determining the molecular weight of volatile compounds. The development of “soft ionization” techniques in the 1980s by J.B. Fenn permitted the ionization and vaporization of large, polar, and thermally labile biomolecules such as proteins and peptides without inducing fragmentation [Fenn *et al.* 1989; Poland *et al.* 2001]. The characterization and quantification of proteins has been greatly enhanced by the development of two critical "soft ionization" technologies: electrospray ionization mass spectrometry (ESI-MS) [Fenn *et al.* 1989] and matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS) [Karas *et al.* 1987].

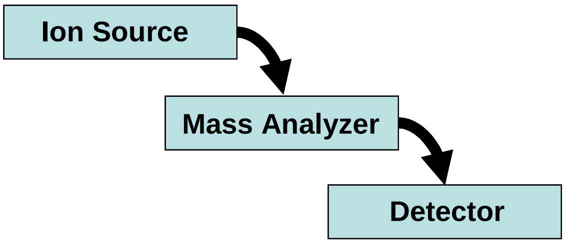


Figure 3. The three basic components of a mass spectrometer. Examples for ionization sources are ESI and MALDI. Some examples for mass analyzers are quadrupoles (Q), quadrupole and linear ion traps (IT, LIT), (tandem) time of flight (TOF, TOF/TOF), fournier transform ion cyclotron resonance (FT-ICR) and orbitraps. The electron multiplier and the array detector are examples for different detectors.

1.4.1 Ion Sources

1.4.1.1 Electrospray ionization (ESI). ESI is typically carried out in tandem with high performance liquid chromatography (HPLC) usually for proteomic applications in conjunction with a nano electrospray conformation [Mann *et al.* 2001]. ESI generates charged microdroplets containing analyte ions. The sample of interest is dissolved in a solvent and then pumped through a thin capillary or needle that is raised to a high potential that may be positive or negative. As a result of the electric field, the solution exits the tip of the capillary in the shape of a cone, known as the Taylor cone. At the apex of this cone charged droplets are sprayed from the capillary. These small charged droplets travel down a pressure and potential gradient towards an orifice in the mass spectrometer. As the droplets traverse this path they become desolvated and reduced in size while their charge remains constant [Cole 2000]. As the droplet shrinks, this increases the electrostatic stress near the surface of the droplet. The droplet can no longer sustain the charge when the force of electrostatic repulsion between like charges becomes equal to the surface tension force. At this juncture the droplet undergoes Coulombic fission, leading to the production of smaller droplets. This process continues until the point is reached that either an ion desorbs from the droplet or the solvent is completely removed [Griffiths *et al.* 2001] (Fig. 4). The gas phase ions are then detected as a series of multiply charged ions. To determine the molecular weight (Mr) of the compound, a simple algorithm transforms this ion series into a single Mr value. Under ESI, macromolecules such as proteins and peptides yield multiply charged ions, e.g., $(M+nH)^{n+}$. Electrospray ionization is characterized as a concentration sensitive methodology where signal strength is proportional to concentration [Cole 2000].

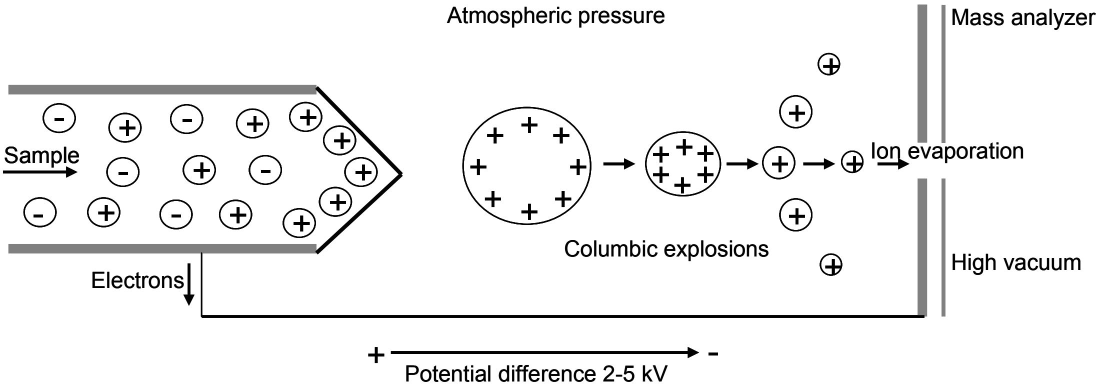


Figure 4. Schematic representation of the process of ESI.

1.4.1.2 Matrix-assisted laser desorption-ionization (MALDI). Matrix-assisted laser desorption-ionization (MALDI) is a method that was pioneered by Karas and Hillenkamp when in 1987 they utilized an ultraviolet laser to desorb intact molecular ions of proteins that were co-crystallised in a nicotinic acid matrix solution [Hillenkamp *et al.* 1991; Karas and Hillenkamp 1988]. Unlike ESI, generally only singly charged ions are observed for MALDI. In MALDI the analyte of interest is co-crystallised with an excess of matrix that is utilized as a diluent preventing the analyte from forming large aggregates that would otherwise be too large to desorb [Karas *et al.* 2000; Kicman *et al.* 2007]. The matrix also absorbs UV light from a laser thus facilitating analyte desorption and ionization [Karas *et al.* 2000]. There are a number of different matrixes that may be used in MALDI-MS. The standard matrix used for protein analysis is typically 3,5-dimethoxy-

4-hydroxy cinnamic acid (sinapinic acid) whilst α-cyano-4-hydroxy cinnamic acid (CHCA) is often used when analysing peptides. Analyte and matrix are both spotted onto a metal target plate which is then inserted into a high vacuum source region within the mass spectrometer [Kicman *et al.* 2007]. The target plate is subjected to laser bombardment and analyte molecules are vaporised along with the matrix molecules. The process of desorption and ionization in MALDI is not fully understood with several influencing factors such as laser wavelength, pulse width and chemical properties of the matrix and analyte. During laser irradiation a gas jet of matrix neutrals and surrounding analyte molecules is formed (Fig. 5). The matrix molecules are strongly excited at this stage and analyte molecules are thought to be ionized as a result of multi-step interactions with the matrix resulting in proton transfer yielding up both protonated and deprotonated analyte ions [Karas *et al.* 2000; Kicman *et al.* 2007].

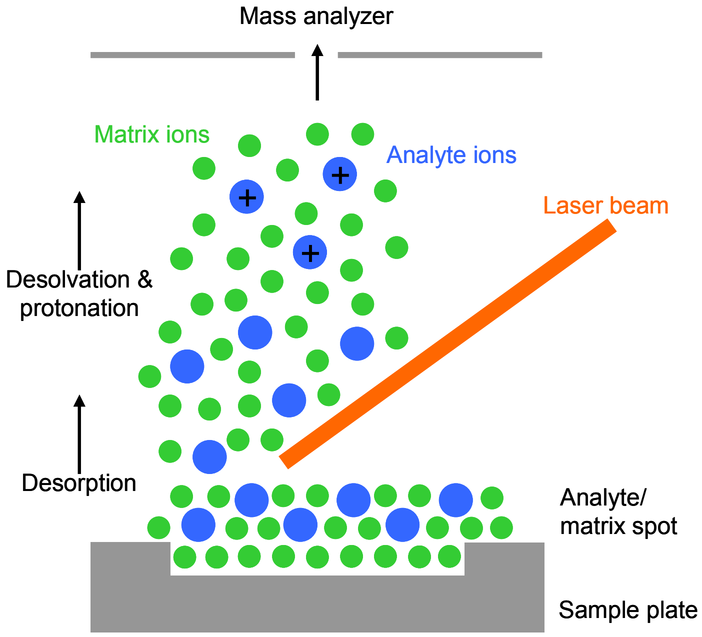


Figure 5. Schematic representation of the MALDI process.

1.4.2 Mass analyzers

1.4.2.1 Quadrupole mass spectrometers. The single quadrupole mass analyser consists of four circular metal rods placed equidistant from each other with an oscillating electric field applied through a combination of direct current (DC) and radio frequency (RF) to the rods. One pair of rods are supplied with a positive DC and RF voltage, whilst the second pair are supplied with a negative DC and RF voltage 180° out of phase with the first pair. This creates a quadrupolar electric field and for a particular amplitude of direct current and radio frequency, only ions of a given mass to charge (*m*/*z*) ratio will have a stable trajectory and therefore be able to pass through to the detector, all other ions will collide with the quadrupole rods. By adjusting the DC and RF voltages, ions of different *m*/*z* values can pass through to the detector. The ramping of these parameters can occur in less than 1/6th of a second, allowing ions over a wide *m*/*z* range to be scanned in the one mass spectrometry experiment. Today, however, it is unusual to see large scale proteomic or metabolomic studies carried out using a single quadrupole instrument. More typically the instruments of choice will be the hybrid quadrupole ion trap mass spectrometer or a triple quadrupole mass spectrometer. Triple quadrupole mass spectrometers allow for tandem mass spectrometry and consist of three sections (Q1, Q2 and Q3). Q1 acts as a mass filter allowing only ions of a certain mass to move further into the mass spectrometer. Q2 functions as a collision cell for fragmentation of the ions. Q3 acts as a second mass separating quadrupole allowing the fragment ions to be separated and resolved before they are measured by the detector [Mann *et al.* 2001].

1.4.2.2 Time of flight. A time of flight (TOF) mass spectrometer is one of the simplest analyzers available whereby ions are accelerated by an electric field into a long, straight, evacuated tube prior to detection. The distance of the tube to the detector is fixed and the ions are accelerated to the same energy. As the ions have the same kinetic energy, the smaller the mass the faster the ion will transverse the tube. The different velocities of the ions lead to a separation in space and time [Doroshenko and Cotter 1999]. The time taken for the ion to traverse the tube is proportional to its mass to charge ratio with each ion having a characteristic time of flight [Li *et al.* 2000; Mann *et al.* 2001].

A mass spectrometer that is extensively used in proteomics is the Q-TOF, a hybrid combining a triple quadropole instrument with a reflector TOF in place of Q3 (Fig. 6). This instrument has a wide dynamic range and also a high degree of mass accuracy [Aebersold and Mann 2003].

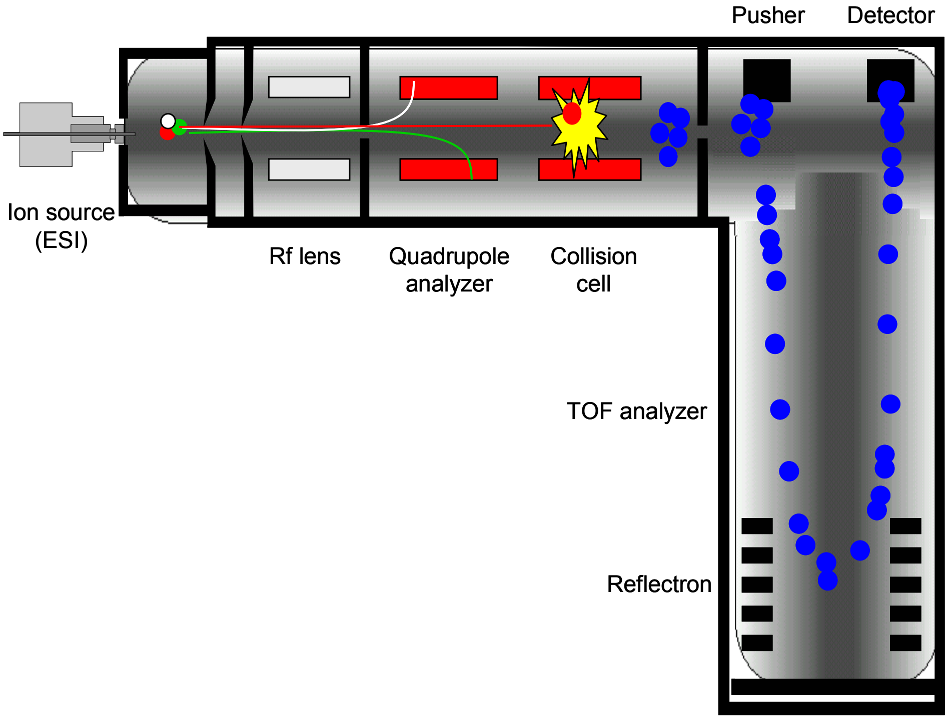


Figure 6. Operating mode of a Q-TOF mass spectrometer. In the "MS" mode**,** the sample is sprayed and ionized from the nanospray needle and the ions pass through the sampling cone, skimmer lenses, Rf hexapole focusing system, and the quadrupole analyzer. The quadrupole in this instance is not used as an analyzer, merely as a lens to focus the ion beam into the time of flight analyzer, which separates the ions according to their mass-to-charge ratio.

With the digest mixture still spraying into the mass spectrometer, the Q-TOF is switched into "MS/MS" mode**.** The protonated molecular ions of each of the digest fragments can be independently selected and transmitted through the quadrupole analyzer, which is now used to transmit solely the ions of interest into the collision cell. An inert gas such as argon is introduced into the collision cell and the sample ions are bombarded by the collision gas molecules, that cause them to fragment. The fragment ions are then analyzed by the time of flight analyzer. In this way an MS/MS spectrum is produced showing all the fragment ions that arise directly from the chosen parent or precursor ions.

1.4.2.3 Tandem mass spectrometry (MS/MS). In order to acquire peptide sequence information, it is necessary to induce fragmentation of the peptides of interest. Soft ionization techniques such as ESI and MALDI, in conjunction with tandem mass spectrometry (MS/MS) has allowed the elucidation of a wide range of peptides. MS/MS spectra of peptides, however, are often complex and difficult to interpret [Vachet *et al.* 1998]. In MS/MS, peptides are individually ionized in the source region using ESI or MALDI. These peptides are then further separated based on their *m*/*z* ratio. The selected precursor ions are allowed into a collision cell, which is filled with an inert gas such as xenon, argon or nitrogen. Collisions then occur between the precursor ion and inert-gas atoms (molecules). In these collisions, part of the precursor ion’s translational energy can be converted into internal energy, and as a result of single or multiple collisions, an unstable excited state is populated. Excited precursor ions decompose to produce product ions in a process termed “collision- induced dissociation” (CID) [Griffiths *et al.* 2001]. The types of fragment ions observed in a MS/MS spectrum depend on many factors, including the primary sequence of the peptide, the amount of internal energy and the charge state [Johnson *et al.* 1987]. The main types of ions observed in the fragmentation of protonated peptides are well established, noting that fragments can only be detected if they carry a charge. If the charge is retained on the N-terminal fragment, the ion is classified as a, b, or c; x, y, or z if the charge is carried on the C-terminal. The nomenclature for fragmentation ions has been described previously [Johnson *et al.* 1987] and is shown in Fig. 7. These product ions are then mass analysed, producing spectra [Griffiths *et al.* 2001]. The tandem mass spectrometry data can be used to elucidate the primary sequence of a peptide. The process of deducing an amino acid sequence from the tandem mass spectra is aided by the availability of protein and DNA databases [Eng *et al.* 1994].

1.5 Proteins and microbial proteomics. Since the publication of the first microbial genome sequence more than 10 years ago, science is moving towards a post genomic era with transcriptomics and proteomics offering insights into cellular processes and function, to analyze the physiology and metabolism of microorganisms. From this research it will be possible to move towards a systems biology understanding of a microorganism, where upon researchers can build a comprehensive cellular map for each microorganism that links an accurately annotated genome sequence to gene expression data, at a transcriptomic and proteomic level.

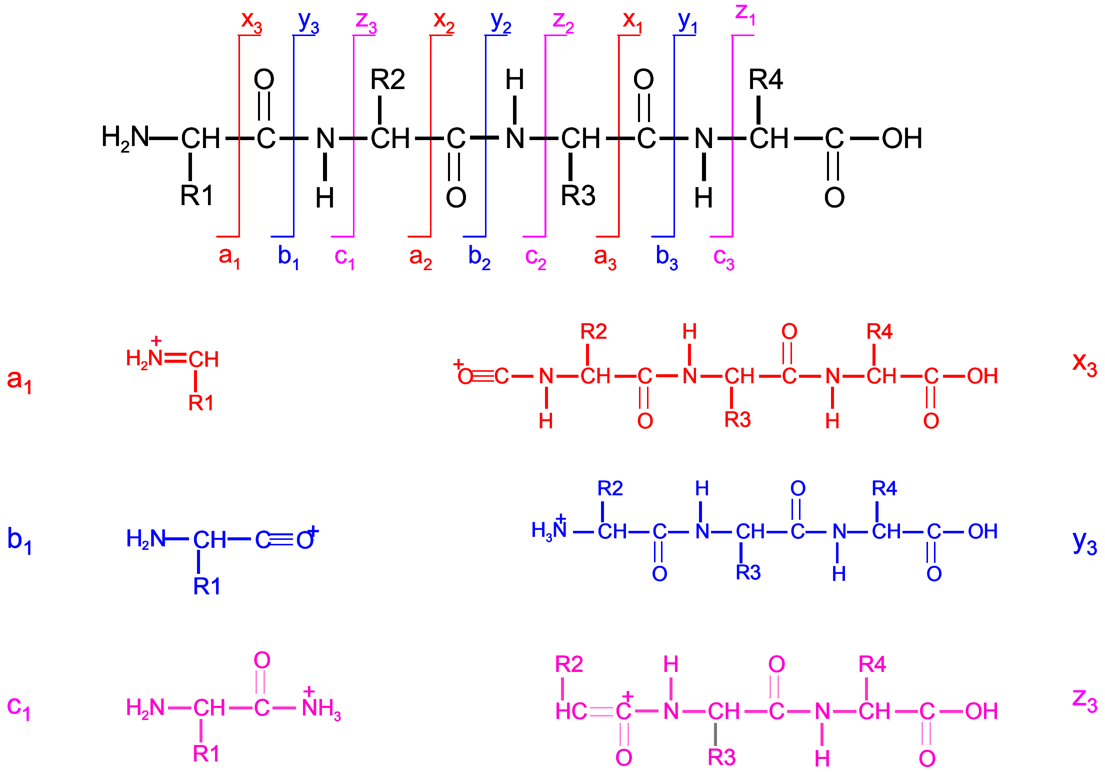


Figure 7. Ions generated from peptide backbone fragmentation by MS/MS. Peptide fragment ions are indicated by a, b, or c if the charge is retained on the N-terminus and by x, y or z if the charge is retained on the C-terminus. The subscript indicates the number of amino acid residues in the fragment.

Proteins are continuously synthesized and degraded according to the needs of the cell metabolism. Proteomic identification of proteins will therefore result in different proteomes depending on the time at which the protein complement of the cell is isolated. To yield information about the proteins, the protein mixture must be separated, broken down into peptides, and identified by mass spectrometry.

Separation of complex protein mixtures may be performed by gel-based electrophoresis. The separated proteins must be digested within the gel, ensuring the proteins are specifically degraded into fragments that fit the effective molecular mass separation range of the mass analyzers, before extraction of the resultant peptides. Destaining, reduction and alkylation of cysteines, enzymatic cleavage of proteins, and extraction of peptides from the gel are essential steps in obtaining high-quality mass spectra. For ESI-MS the procedure includes an additional desalting step which is optional for MALDI-MS. The identity of the peptide is determined by comparison of the mass spectral data with an in silico-generated protein data bank (Fig. 8).

Small proteins tend to escape proteomic identification and are generally underrepresented, as the likelihood of identification increases with the number of peptides generated from a protein, and because small proteins may show low gene expression levels as suggested by their low average codon adaptation index [Klein *et al.* 2007] (see chapter 1.6). For investigation of low molecular weight proteins (below 20 kDa) in *Hbt. salinarum*, an optimisation of common protocols has been established. The low molecular weight proteins were enriched by filter membrane centrifugation before subsequent tricine SDS-PAGE, they were not stained, and a shortened digestion protocol was applied to minimize loss of peptides [Klein *et al.* 2007]. Identification was performed by an FT-ICR mass spectrometer, which allows reliable protein identification by MS/MS/MS of a single peptide [Olsen *et al.* 2004a].

Membrane proteins are in general more difficult to handle than cytoplasmic proteins in terms of separation and identification by standard proteomic techniques [Santoni *et al.* 2000]. Several classes of membrane proteins can be distinguished according to their association with the cell membrane [Klein *et al.* 2005]. Integral membrane proteins are localized within the lipid bilayer and most of them have hydrophobic, membrane-spanning α-helices, called transmembrane domains (TMDs). A minority, found mostly in the outer membrane of bacteria, have hydrophilic membrane-spanning β-barrels. A simple bioinformatic prediction of an α-helical transmembrane domain involves a search for a hydrophobic stretch of 15-25 amino acids in length. The usual parameters to describe the character of membrane proteins are the “Grand Average of Hydrophobicity” (GRAVY), based on the empirical values of Kyte and Doolittle [Kyte and Doolittle 1982], and the number of transmembrane helices predicted by the algorithm TMHMM

[Krogh *et al.* 2001]. Discrimination between integral membrane proteins with one TMD and an exported protein with a hydrophobic signal sequence remains difficult.

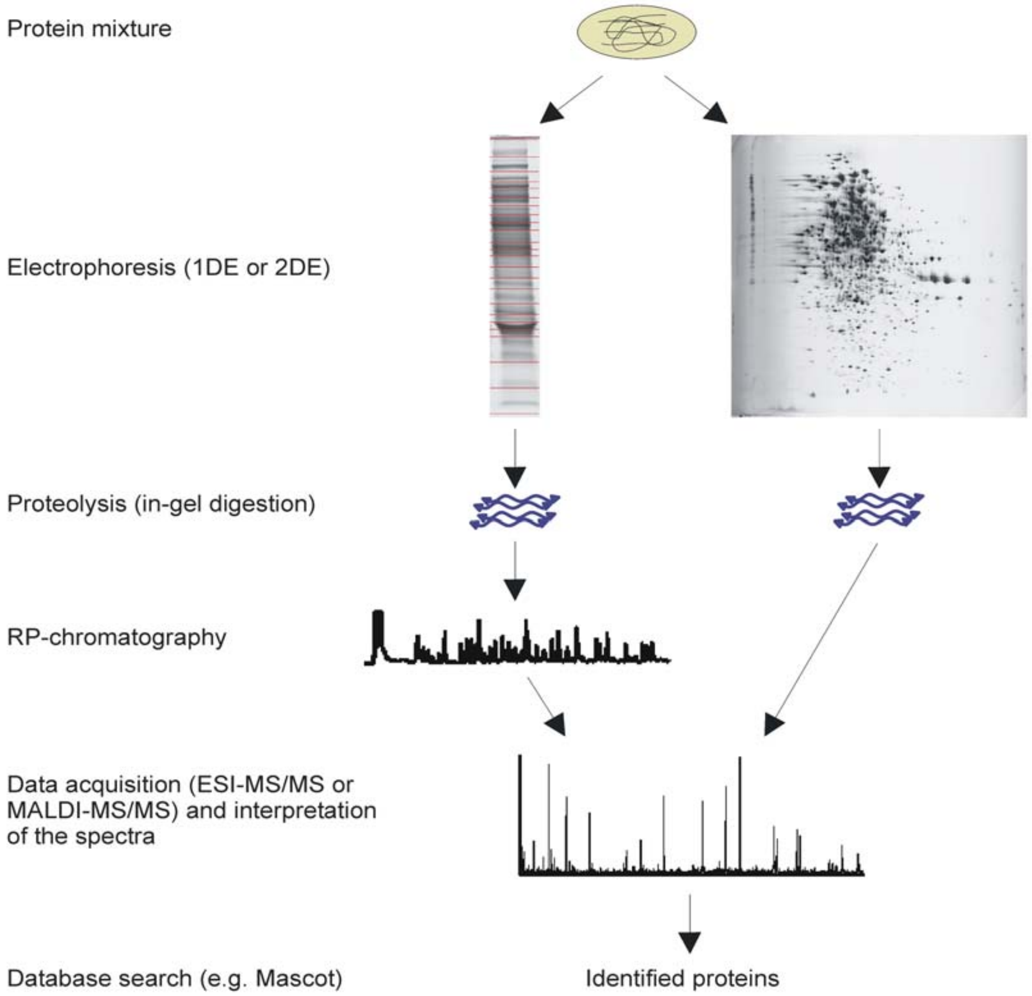


Figure 8. Workflow for sample processing, protein separation by electrophoresis and identification of proteins by mass spectrometry. After cell lysis, the proteome of a cell can be separated by 1-D or 2-D electrophoresis and the proteins excised subsequent to gel staining. In-gel digestion results in production of peptides that are processed for mass spectrometric analysis by RP-ESI-MS/MS or MALDI-MS/MS. The proteins are usually identified by comparison of the MS/MS spectra with proteome database entries.

Peripheral membrane proteins do not contain membrane-spanning domains and can be divided into two groups. The first group are lipoproteins, covalently bound by a cysteine residue (thioether linkage) in the amino-terminal region of the protein to a lipid anchor in the membrane. The cysteine is part of a “LAGC motif” and becomes the amino-terminal residue after cleavage by signal peptidase II [Hayashi and Wu 1990]. The second group lacks a lipid anchor and interact predominantly electrostatically with the exposed domain of integral membrane proteins. The most prominent members are subunits of membrane-associated complexes. In principle peripheral membrane proteins behave like soluble proteins [Klein *et al.* 2005].

1.5.1 Proteomic techniques for the large scale analysis of microorganisms. Until recently, the study of global protein expression was performed nearly exclusively using two-dimensional gel electrophoresis (2-DE), a technique developed in the 1970s [O'Farrell 1975] with significant advances in the intervening decades [Gorg *et al.* 2004]. The strength of 2-DE is that it can separate up to 10 000 proteins in one gel [Link *et al.* 1999]. Every component is fractionated on the first dimension, by isoelectric focusing and then further resolved according to molecular weight in the second dimension [Lin *et al.* 2003; O'Farrell 1975]. A limitation of 2-DE is typically that many more spots are resolved on the gel than are actually identified [Futcher *et al.* 1999; Regnier and Huang 1996], due to the very time-consuming [Link *et al.* 1999; Regnier and Huang 1996] protein processing, in which proteins have to be excised from the gel before subjected to proteolytic digestion, despite the advent of computerised gel visualisation and robotic spot excision equipment [Gorg *et al.* 2004]. The 2-DE methodology has traditionally had a number of practical limitations, with the main issue being the wide dynamic range of proteins present within a biological sample. Thus proteins present in low copy numbers, and therefore low concentration, are often not visualised on 2-D gels [Link *et al.* 1999; Regnier and Huang 1996]. A number of additional limitations can be encountered such as: most isoelectric focusing gels can only focus proteins between the pI ranges 3-10, so proteins with extreme pI will not be seen on the gels. Most 2-D gels cannot resolve proteins smaller than 10 kDa and above 200 kDa. Due to the nature of the buffers used in isoelectric focusing, the range of solubilising detergents that can be used in this methodology are restricted, thus making it difficult to solubilise certain membrane proteins [Rabilloud *et al.* 1990]. Furthermore, it could be shown that integral membrane proteins tend to irreversibly precipitate upon isoelectric focussing and therefore cannot be transferred into the second dimension [Klein *et al.* 2005].

An alternative to the traditional 2-DE technology for microbial proteome analysis is the high throughput approach of SDS-PAGE followed by liquid chromatography coupled to tandem mass spectrometry [Lin *et al.* 2003]. After SDS-PAGE of a complex protein mixture the lane is cut into a number of slices. The proteins in the slices are reduced, alkylated and tryptically digested. A second separation step is done by liquid chromatography (LC), analysing the resulting peptide mixture on a reverse phase (RP) column. The eluted peptides are then passed directly into the mass spectrometer where tandem mass spectrometry profiles are generated for each peptide. This process has a high throughput achieved in a short time and can be seen as complimentary to 2-DE as it overcomes many of the problems and limitations of that technique, i.e., identifying proteins with extreme pI, integral membrane proteins and lower abundant proteins [Washburn *et al.* 2001].

Further alternative strategies, complementing the standard LC-MS approach, are targeted at the isolation of specific classes of proteins/peptides by prefractionation or selective enrichment. One prefractionation method applied for additional separation of complex protein and peptide mixtures is integrated in the "multidimensional protein identification technology" (MudPIT) [Link *et al.* 1999], in which peptides are separated by strong cation exchange (SCX) prior to RP-LC. Peptides are bumped off the SCX column by an increase in salt concentration and progressively eluted from the RP column into the ion source by a gradient of increasing hydrophobicity. Another prefractionation method is to separate proteins and protein complexes by size (size-exclusion chromatography; SEC).

Selective enrichment strategies are often required to capture proteins of low abundance and high biological importance, as in the case of phosphopeptides, which can be selectively enriched amongst others by "immobilized metal ion affinity chromatography" (IMAC) or TiO_2 chromatography, utilizing the binding affinity of phosphopeptides towards metal ions such as Fe^{3+} and Ga^{3+}, or the property of titanium oxide to selectively absorb water-soluble organic phosphates [Pinske *et al.* 2004].

1.5.2 Staining and destaining of proteins. Proteins separated by electrophoresis and intended for in-gel digestion can be visualized for isolation by use of several staining methods. Proteins can be visualized amongst others by Coomassie brillant blue (CBB) [Tal *et al.* 1985; Wilson 1979], by which protein amounts of approximately 30 ng can be detected, and by the more sensitive silver method detecting up to 0.5 ng of protein [Mortz *et al.* 2001; Rabilloud 1990; Shevchenko *et al.* 1996].

Silver staining is based on binding of silver ions, mainly to sulfhydryl (R–SH) and carboxyl (R–COOH) groups of amino acid side chains [Merril and Pratt 1986; Rabilloud 1990], and reduction to metallic silver at alkaline pH. In silverstaining procedures, which are regarded as compatible with protein digestion and mass spectrometric analysis, glutaraldehyde in the developer has been replaced by formaldehyde [Mortz *et al.* 2001; Shevchenko *et al.* 1996]. Formaldehyde remains a major interfering compound during in-gel digestion of proteins, however. In a side-reaction, aldehydes can crosslink reactive side chains of amino acids (lysine, cysteine, and, to a lesser extent, serine and threonine) leading to protein reticulation by methylene bridges. Hence, cutting sites for the protease are partially blocked and peptide extraction is significantly reduced. Because the crosslinking reaction is a slow process, gels should be processed directly after staining. Peptide yield and sequence coverage can be additionally enhanced by a silver destaining step before in-gel digestion [Gharahdaghi *et al.* 1999; Richert *et al.* 2004; Sumner *et al.* 2002]. Destaining of silver-stained proteins entails oxidation of metallic silver and complexation of the released ions by the remaining formaldehyde. Destaining of CBB stained proteins is easily achieved by incubation of excised gel bands in a mixture of an organic solvent and ammonium bicarbonate.

1.5.3 Reduction and alkylation of proteins. Reduction and alkylation of cysteine residues is intended to ensure maximum sequence coverage and to secure identification of proteins with a large number of disulfide bridges [Hale *et al.* 2004; Katayama *et al.* 2004]. Reduction of disulfide bridges (e.g. with dithiothreitol) and successive alkylation of the SH groups ($S\text{-}CH_2\text{-}CONH_2$) can be performed in principle either before electrophoresis, or after staining and destaining of the proteins, respectively. On alkylation with iodoacetamide, cysteine is transformed into carboxyamidomethylcysteine, with a mass change of +57.022 Da, so the specific mass of the amino acid cysteine is increased from 103.009 Da to 160.031 Da. Quantitative alkylation of cysteines is not achieved after PAGE, because acrylamide monomers may also modify cysteines during electrophoretic separation leading to cysteine acrylamide adducts [Hamdan *et al.* 2001; Mineki *et al.* 2002]. On adduct formation the molecular mass of the cysteine is changed to 174.046 Da. To generate mass spectra with consistent signals for cysteine-containing peptides, alkylation must be homogenous. This is best achieved when reduction and alkylation are performed before denaturing electrophoretic separation of the proteins [Herbert *et al.* 2001; Sechi and Chait 1998].

1.5.4 In-gel digestion of proteins. For proteomic studies the serine protease trypsin is most frequently used. Trypsin cleaves peptide bonds specifically after the carboxyl group of arginine and lysine. Because of the biological distribution of arginine and lysine residues, especially in soluble proteins, the resulting peptide masses usually fit the range required for analysis by mass spectrometry [Olsen *et al.* 2004b]. The rate of peptide hydrolysis is reduced if an acidic amino acid is placed next to the cleavage site. If a proline is positioned at the C-terminal side of the trypsin site, no cleavage will occur [Thiede *et al.* 2000], implying that digestion can never be totally complete. Trypsin autolysis occurs in parallel with tryptic protein cleavage, leading to undesirable peaks in the mass spectra. Nowadays modified trypsin is usually used to reduce autolysis. Selective methylation of lysine residues within trypsin restricts the autolysis reaction to the arginines [Rice *et al.* 1977]. In contrast to unmodified trypsin, this modification leads to an increase in the optimum catalytic temperature from between 35 °C and 45 ° C to between 50° and 55 °C [Finehout *et al.* 2005; Havlis *et al.* 2003; Terry *et al.* 2004; Venkatesh and Sundaram 1998].

Although trypsin is active over a wide pH range (7–9), the optimum pH for digestion with modified trypsin is between 7.8 and 8.1 [Finehout *et al.* 2005]. Ammonium bicarbonate (NH_4HCO_3) and Tris/HCl are commonly used as inorganic buffer salts. Because of its properties, ammonium bicarbonate can be removed completely during iterative evaporation in a vacuum concentrator - the salt is decomposed into NH_3, CO_2, and H_2O.

After PAGE, proteins are embedded in the gel matrix. To digest the proteins within the acrylamide matrix, the protease must enter the gel to make contact with the protein. The protease must therefore be small enough to penetrate the matrix of the gel [Elder *et al.* 1977]. On the basis of the assumption that rehydration generates a directional process whereby penetration of the gel matrix by the protease is improved, most procedures include a dehydration step with acetonitrile before digestion of the proteins in a gel plug [Hellman *et al.* 1995]. Another way of increasing the efficiency of the in-gel digestion process is to minimize the diffusion distance by cutting the gel matrix into smaller pieces.

1.5.5 Extraction, concentration and desalting of peptides from polyacrylamide gels.

After protein digestion and elution of peptides, solutions may contain 30–50% (v/v) organic solvent (e.g. acetonitrile). The organic solvent is added to increase the solubility of (hydrophobic) peptides and to minimize adsorption of the peptides by surfaces of reaction vessels and pipette-tips [Castellanos-Serra *et al.* 2005; Erdjument-Bromage *et al.* 1998]. To concentrate the diluted peptide solution and to remove the acetonitrile, a vacuum centrifugation step is typically performed before MS analysis. If a volatile buffer salt (e.g. ammonium bicarbonate) was used, the salt can also be partially removed during the evaporation process. Consecutive cycles of water addition and evaporation are required, however, to remove volatile buffer salts from the protein digest completely [Maynard *et al.* 2004]. Salts are a major cause of low signal-to-noise ratio and sensitivity in electrospray ionization (ESI). Although MALDI-MS is usually regarded as tolerant of impurities in the samples, the quality of MALDI mass spectra can be significantly improved by use of desalted sample material [Bagshaw *et al.* 2000]. Purification and concentration of the peptide solution are therefore advantageous for all mass spectral applications.

Reversed-phase (RP) microcolumns are commonly used for concentration and desalting of peptide mixtures before mass spectrometric analysis [Lim *et al.* 2003; Stewart *et al.* 2001; Terry *et al.* 2004; Wa *et al.* 2006]. Binding of peptides to the alkyl-chain (C_4–C_{18}) of the matrix is a result of hydrophobic interactions. Depending on the hydrophobic properties and the size of the analyte matrices, different alkyl-chain lengths are used. For efficient binding to the RP material, sample solutions must be free from any organic solvent, because even a small proportion of organic solvent reduces adsorption of the peptides. The on column desalting and concentration procedure starts with activation of the reversed-phase matrix in an organic solvent, for example acetonitrile or methanol. After equilibration of the activated matrix with an aqueous buffer, the peptide analyte molecules are loaded. Because a hydrate shell covers the ionic salt molecules and hydrophilic parts of the peptide, the interaction with the organic phase is low. Side chains of the hydrophobic amino acid residues in peptides are, however, accessible for interaction with the organic phase. These hydrophobic interactions retard molecule mobility during liquid flow through the column. After several washing steps, peptides retarded on the column can be eluted in a small volume (1–5 µL) of organic solution containing at least 50% acetonitrile or methanol. A disadvantage is loss of peptides as a result of irreversible adsorption, especially of long and hydrophobic compounds [Stewart *et al.* 2001].

In MALDI-MS, desalting and concentration of peptide samples can be performed directly after spotting on the target. α-Cyano-4-hydroxycinnamic acid (CHCA) is commonly used as matrix for MALDI-MS of peptides. Contamination of MALDI samples with salts results in reduced sensitivity and causes matrix cluster formation. These background signals emerge mainly in the range below m/z 1200 in MALDI spectra. Salt contaminants can be removed by washing matrix/sample spots after peptide cocrystallization on the MALDI target with deionized water before analysis [Keller and Li 2000]. The simple procedure entails addition of a water droplet on the crystal surface; it can be removed by compressed air or pipetting after incubation for a few seconds. The method is based on the low solubility of many matrices (e.g., CHCA) in water, compared to salts and surfactants.

1.5.6 Identification of proteins by mass spectrometry. For identification of proteins in a mass spectrometer after in-gel digestion, peptides must be charged and ionized before separation and detection by a mass analyser/detector system is possible. With ESI (electrospray ionization) and MALDI (matrix-assisted laser desorption and ionization) two well established methods are available for ionization and dispersion of proteins and peptides [Shevchenko *et al.* 1997; Wilm *et al.* 1996]. In combination with a mass analyser such as TOF (time of flight), quadrupole, or ion trap, characterization of fmol amounts of peptides is possible [Shevchenko *et al.* 1996; Wilm *et al.* 1996]. A rapid and very simple method for determination of the identity of a protein by mass analysis is the recording of a peptide mass fingerprint (PMF) [Cottrell 1994; Henzel *et al.* 1993; James *et al.* 1993; Yates *et al.* 1993]. The basis of the PMF is the number and molecular mass of peptides produced by the catalytic activity of an endoprotease such as trypsin. The molecular masses detected in the mass spectra after MALDI are compared with theoretical masses generated by an in silico-generated protein database. Correlating masses are statistically evaluated and a likelihood number for identification of that protein is given. Often, however, the information from PMF measurements is insufficient to identify the proteins. The result of the database search is not significant if the number of assigned peptides is low, and a correlation may not be achieved if more than one protein is present in the excised gel spot. No correlation can be achieved, as it is also the case for MS/MS analyses, if the protein is not present in the database, or if modification of the amino acids shifts the detected mass values relative to the in silico-generated database information.

Another approach uses MS/MS data for direct protein identification in databases (e.g., Sequest or Mascot) [MacCoss *et al.* 2002; McCormack *et al.* 1997; Perkins *et al.* 1999]. The analysis strategy uses the MS/MS data for comparison with protein database entries. In a first step, potential peptide sequences are identified in a protein database by matching the molecular mass of the acquired peptide with amino acid sequences from the database entries. Information of fragment ion signals is subsequently compared with the predicted fragment ions of the sequences derived from the database. Best fits are scored and ranked in a list. MS/MS data can also be used for identification of target proteins by de novo sequencing of peptides [Mann and Wilm 1994; Rowley *et al.* 2000; Yates *et al.* 1995; Zhang and McElvain 2000].

For analysis of complex samples and/or if only small amounts of sample are available, mass spectrometric analysis by ESI-MS/MS can be coupled with reversed-phase liquid chromatography (RP-LC) [Lahm and Langen 2000]. The peptide solution is acidified by addition of 0.1% FA (or TFA) and loaded on to a C_{18}-based desalting and concentrating precolumn. The system enables automatic desalting and concentration with a high flow rate of a weakly acidic aqueous solution (e.g. 0.1% FA). Subsequent separation on an analytical column results in an increased concentration of the peptide and therefore leads to a large increase in detection sensitivity. Disadvantages are the long time required and the difficulty of the procedure. Small and/or extremely hydrophilic peptides can be lost during sample preparation on RP-microcolumns. In contrary, for analysis of hydrophobic proteins like membrane proteins, RP microcolumns with shorter alkyl-chains (C_4) should be used to prevent irreversible hydrophobic interactions [Klein *et al.* 2005].

The technique of de novo sequencing is capable of assigning peptide sequences to fragments in mass spectra without the need for any information from databases [Mann and Wilm 1994]. In principle, de novo sequencing of a peptide starts with the generation of an MS/MS spectrum and a search for probable candidates fitting into the y-ion or b-ion series within the spectrum (Fig. 7). It is assumed that these signals are commonly the most intense signals in MS/MS spectra. Complete or partial amino acid sequences of the fragmented peptide may be obtained by calculation of the mass differences between adjacent signals of the same ion series. Fragmentation of the peptides by ESI-CID (collision-induced dissociation) has proved to be one of the most efficient techniques for the de novo sequencing of peptides [Jensen *et al.* 1999; Shevchenko *et al.* 2000; Shevchenko *et al.* 1997]. With MALDI-MS, peptide fragmentation is also possible by MALDI post-source decay. Interpretation of resulting spectra is difficult, however, because of the poor quality of the fragment signals [Spengler *et al.* 1992].

1.5.7 Expressional proteomics. Assessing the quantitative change in protein expression patterns by comparing different cell states is fundamental for the analysis of microbial systems. There are presently several methodologies that attempt to provide quantitative expressional analysis. These include, in addition to label free, also label based techniques using isotope labels such as ICAT, iTRAQ or ICPL, and furthermore, metabolic labeling (e.g., SILAC) as well as gel-based differential in gel electrophoresis (DIGE), allowing to monitor the dynamics of protein expression levels over time. A detailed description of ICPL and SILAC labeling is given in the chapters 2.2.3.3 (Fig. 15) and 2.2.3.4 (Fig. 16), respectively.

The exponentially modified protein abundance index (emPAI) is a label free methodology for estimating absolute protein abundance in a sample. This methodology is a simple calculation that utilizes the output information obtained when tandem mass spectrometry data is processed through database search engines, and is based on the number of observed peptides determined by mass spectrometry divided by the number of observable peptides per protein. Other label free methods for performing quantitative analyses of LC-MS experiments are the computational extraction of peptide ion intensities, thus comparing peak areas from LC-MS chromatograms [Chelius and Bondarenko 2002], and spectral counting [Liu *et al.* 2004]. The spectral count for a protein refers to the number of MS/MS spectra acquired from its peptide ions during a LC-MS/MS run. More abundand peptides will be more likely selected for MS/MS analysis.

The aim of any labeling strategy is to derivatize specific proteins/peptides in a sample to allow their analysis [Romijn *et al.* 2003]. Typically, protein mixtures from at least two states are labeled separately, one with a light reagent and one with a heavy (see chapter 2.2.3.3.1). The two samples are then mixed, tryptically digested and separated on a C_{18} column before analysis in a mass spectrometer. The relative abundance of the light and heavy versions of the peptides can then be compared and information on the protein expressional changes obtained [Goshe and Smith 2003; Gygi *et al.* 1999]. The iTRAQ reagent [Ross *et al.* 2004] has the advantage that up to eight states rather than only two can be measured in one experiment. Here, protein samples are first trypsinised, resulting in a peptide mixture with each cleaved peptide having a free amine group. Each sample is then labeled with one of the specific reagents by attachment of the label to the amine specific reactive group.

Metabolic labeling (see chapter 2.2.3.4) offers one of the most comprehensive methods of investigating microbial proteomes. Unlike other labeling technologies, samples to be analyzed can be combined before protein extraction thus removing the main source of sample variation (Fig. 9), which is the protein extraction process itself [Romijn *et al.* 2003]. The simplest methodology involves comparison of "normal" and "stress" states by growth of the microorganism on media enriched with N^{15} for one state and on media containing the naturally abundant isotope N^{14} for the other state. The ratio of N^{14}/N^{15}

containing proteins from the two conditions are measured and changes in protein expression levels can be identified [Goshe and Smith 2003; Romijn *et al.* 2003]. Additional isotopic variants such as deuterium and C^{13} enriched media can also be utilized for metabolic labeling [Cliff *et al.* 2002; Snijders *et al.* 2005]. In case of LC-MS/MS experiments, light and heavy labeling is commonly done with C^{12}/C^{13} or $^{14}N/^{15}N$ to prevent problems with the shifted elution peaks observed when using hydrogen/deuterium as label isotopes. [Goshe and Smith 2003; Tao and Aebersold 2003].

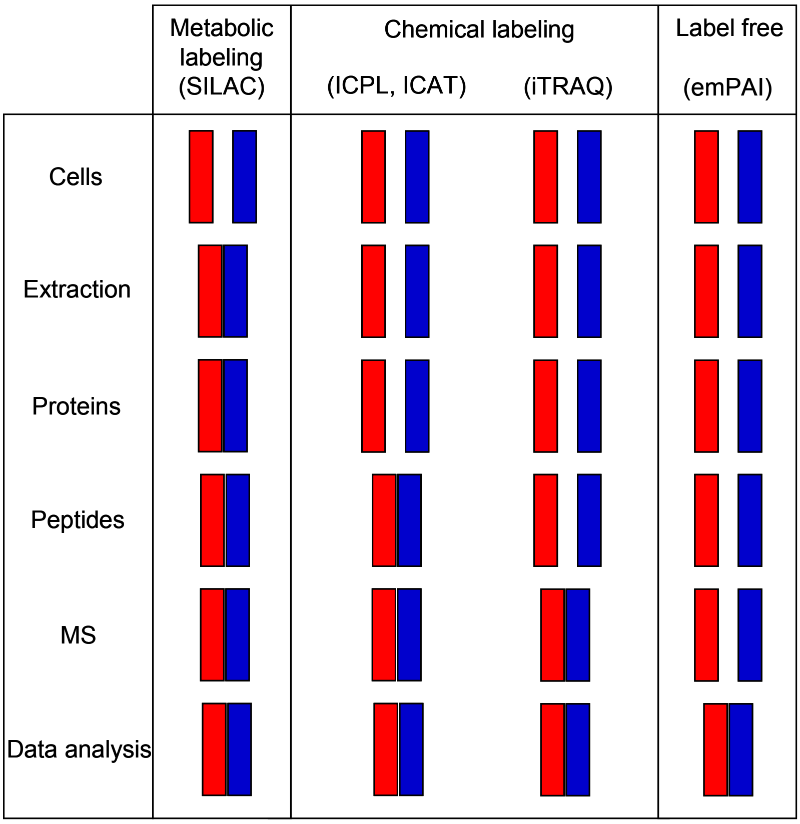


Figure 9. Comparison of different quantitative proteomics workflows. The different colors represent the two different experimental conditions. Experimental variations can occur until samples are combined (merged boxes).

1.6 Codon adaptation index (CAI). The genetic code associates a set of sibling codons to the same amino acid, of which some codons occurre more frequently than others in gene sequences [Carbone *et al.* 2003; Wada *et al.* 1990]. Among prokaryotes it has been established that codon usage arises from mutational bias and natural selection for optimization of translation [Akashi and Eyre-Walker 1998; Bulmer 1991; Musto *et al.* 2003]. The codon bias value for a gene is its propensity to use preferentially one of several codons to incorporate a given amino acid into the polypeptide chain. The CAI reflects the ratios of the usage of each codon to that of the most abundant codon for the same amino acid [Sharp and Li 1987]. Highly expressed genes tend to use a limited number of codons and display CAI values reaching a maximum of 1, whereas in lowly expressed genes with random codon usage the values may converge towards 0 [Carbone *et al.* 2003]. Preferred codons and iso-acceptor tRNA content exhibit a strong positive correlation, meaning that highly expressed genes selectively use codons recognized by the most abundant iso-acceptors, but almost completely avoid using codons of other iso-acceptors [Carbone *et al.* 2003; Ikemura 1985]. Thus the CAI reflects the expression rates by determining the non-random usage of synonymous codons.

Previous codon usage analyses showed that codon usage bias is associated not only with gene expression level but also with GC composition and other biological factors such as gene length, gene translation initiation signal, protein amino acid composition, protein structure as well as mutation frequency and patterns [Wan *et al.* 2004].

1.7 Objective. Classically, large-scale proteomic data are obtained by two-dimensional gel electrophoresis (2-DE) with subsequent mass spectrometric identification [Hecker 2003; Tebbe *et al.* 2005]. While the obsolete peptide mass fingerprinting (PMF) analysis requires a rather pure protein sample such as obtained from 2-D gel spots, LC-MS/MS permits the rapid identification of a wide range of proteins from a complex mixture. A limiting factor for protein identification may be a vast complexity of the sample, and several approaches were developed to solve this problem. One possibility to extend identification rate is to multiple prefractionate proteins prior to LC-MS/MS analysis.

The first part of this work describes the investigation of the cytosolic protein inventory of *Nmn. pharaonis* by nanoLC-MS/MS, to reach conclusions about the cellular physiology of the archaeon. Furthermore, it compares approaches with and without prefractionation of proteins by size-exclusion chromatography, before further separation by SDS-PAGE.

The second part comprises a comprehensive analysis of the heat shock response in *Hbt. salinarum* based on different approaches with regard to both the protein and transcript level. The goal of performing multiple approaches was to expand the identification of significantly regulated genes, and to either validate the results obtained by one approach, or to single out translational regulation. In addition, growth on different media was implemented to gain clues about the differential needs under varying environmental conditions. The results obtained are discussed in correlation to previous publications and thereof diverging regulation information substantiated by the multiplicity of approaches.

2 Materials and Methods

2.1 Materials and Devices

2.1.1 Materials/Chemicals

Material	**Company**
acetic acid 100%	Merck
acetone	Riedel-de-Haen
acetonitrile	Merck
N-acetyl cysteine	Sigma-Aldrich
acrylamide/methylene bisacrylamide (ProtoGel) (37.5:1) 30% (w/v)	NationalDiagnostic
agarose	Gibco
Amicon centrifugal filter devices YM-30	Millipore
ammonium bicarbonate	Fluka
ammonium chloride	Merck
ammonium peroxodisulfate	BioRad
ammonium sulfate	Merck
ascorbic acid	Merck
benzonase	Merck
BCA protein assay	Pierce
biotin D (+)	Fluka
„bis“: N, N’-methylene bisacrylamide	BioRad
boric acid	Fluka
brom phenol blue	Sigma-Aldrich
2-butanol	Merck
^{13}C6-leucine	Cambridge Isotope Laboratories
C_{18}-extraction disks	3M Empore
calcium chloride	Merck
calcium sulfate	Merck
casamino acids	Difco
centrifuge tubes, conical 15 mL, 50 mL	Techno Plastic Products
centrifuge tubes 1.5 mL	Beckman
centrifuge tubes safe lock 0.5, 1.5 and 2 mL	Eppendorf
CHAPS	Sigma-Aldrich
chloroform	Merck
citric acid monohydrate	Merck
cobalt chloride	Merck
Coomassie brilliant blue G-250	Serva
Coomassie brilliant blue R-250	Serva
copper chloride	Merck
copper sulfate	Merck
cover fluid, drystrip (plus one)	Amersham Biosciences
cuvettes, semi-micro, crystal-clear	Greiner Bio-One
α-cyano-4-hydroxy cinnamic acid	Sigma-Aldrich

CyScribe First-Strand cDNA Synthesis Kit	Amersham Biosciences
d0-/^{12}C-Nicotinoyl-N-hydroxy-succinimide	Toplab GmbH
d0-/^{13}C-Nicotinoyl-N-hydroxy-succinimide	Toplab GmbH
d4-/^{12}C-Nicotinoyl-N-hydroxy-succinimide	Toplab GmbH
deoxynucleotide solution mix, 100 mM	Peqlab
DEPC-treated water	Merck
1,2- dichlorethane	Merck
DIG Easy Hyb (Northern)	Roche Diagnostics
DIG DNA Labeling Mix, PCR (Northern)	Roche Diagnostics
DIG Luminescent Detection Kit, CSPD	Roche Diagnostics
DIG Wash and Block buffer set (Northern)	Roche Diagnostics
dimethylsulfoxide	Fluka
1,4- dithiothreitol	Merck
DNase I	Fluka
DNase kit DNA-free (RTqPCR)	Ambion
DNase RQ1, RNAse-free (RTqPCR)	Promega
EDTA - Na_2	Merck
ethydium bromide	MBL International
elektrospray needle (*on-line/off-line*)	New Objective / Proxeon Biosystems
ethanol absolute	Riedel de Haen
folic acid	Sigma-Aldrich
formaldehyde 37%	Merck
formic acid 98-100%	Merck
fluted filter (Faltenfilter)	Schleicher & Schuell
Gelfiltration Calibration Kit HMW	Amersham Biosciences
Gelfiltration Calibration Kit LMW	Amersham Biosciences
GeLoader-Tips	Eppendorf
glass slides, CMT-GAPS-II coated	Corning
glycerol	Merck
glycine	Merck
guanidine hydrochloride	Sigma-Aldrich
HEPES	Sigma-Aldrich
Hybond N+ nylon membrane	Pharmacia Biotech
hybridization chamber (Northern)	Corning
Hybri-Slip HS 60 mm × 22 mm	Invitrogen
hydrochloric acid (HCl)	Riedel-de-Haen
hydroxylamine hydrochloride	Fluka
iodaacetamide	Fluka
iron chloride	Merck
iron sulfate	Merck
isopropanol	Merck
kerosene	Fluka
L- alanine	Merck
L- arginine	Biomol
L- aspartic acid	Merck
L- cysteine	Merck

L- glutamic acid	Sigma
L- isoleucine	Hoffman- La Roche
L- leucine	Merck
L- lysine · HCl	Acros Organics
L- methionine	Fluka
L- phenylalanine	Fluka
L- proline	Merck
L- serine	Merck
L- threonine	Merck
L- tyrosine	Fluka
L- valine	Fluka
magnesium sulfate	Merck
manganese chloride	Merck
marker, GeneRuler 1kb DNA Ladder	MBI Fermentas
marker, Precision Plus Protein Standards	BioRad
marker, RNA III digoxigenin labeled	Roche Diagnostics
β-mercaptoethanol	Merck
methanol	Merck
1- methylimidazole	Fluka
MicroAmp optical 96-well reaction plates	Applied Biosystems
MicroAmp fast optical 96-well react. plates	Applied Biosystems
MicroAmp 8-tube strip (0.2 μL)	Applied Biosystems
MicroAmp 8 cap strip	Applied Biosystems
MicroCon Ym-30 ultracentrifuge columns	Milipore
MultiScreen MAHV N4550 microtiter plates	Millipore
nickel chloride	Merck
nitrocellulose	BioRad
peptone	Oxoid
peqGold RNAPure extraction solution	Peqlab Biotechnology
Pharmalyte 3-10 (ampholyte, sinulyte)	Amersham Biosciences
phosphoric acid	Merck
potassium chloride	Merck
potassium dihydrophosphate	Merck
potassium ferricyanide (hexacyanoferrateIII)	Fluka
potassium nitrate	Merck
protease inhibitor mixture (COMPLETE without EDTA)	Roche
random hexamer primer (for RTqPCR)	Promega
RNA 6000 Nano LabChip kit	Agilent Technologies
RNaseOUT recombinant RNase inhibitor	Invitrogen
RP-C_{18} material (Reprosil)	Dr. Maisch GmbH
SDS, 2 x cristallized	Serva
silver nitrate	Riedel-de-Haen
sodium acetate	Merck
sodium carbonate	Riedel de Haen
sodium chloride	Merck

(tri)sodium citrate	Merck
sodium dihydrogen phosphate	Merck
sodium-L-glutamate	Merck
(di)sodium hydrogen phosphate	Merck
sodium hydroxide (NaOH)	Merck
(di)sodium molybdate	Merck
sodium thiosulfate	Merck
steritop filter units (0.22 µm)	Millipore
strips, immobiline™dry, pH 3.5-4.5	GE Healthcare
strips, immobiline™dry, pH 4-5	GE Healthcare
strips, readyStrip IPG, pH 3-6	BioRad
succinic anhydride	Sigma
SuperScript III First Strand Kit (RTqPCR)	Invitrogen
SYBR Green PCR Master Mix Kit (RTqPCR)	Applied Biosystems
table salt ("Siedespeisesalz")	Saline Bad Friedrichshall
Taq DNA polymerase	New England BioLabs
taurodeoxycholate	Sigma-Aldrich
TECEP	Sigma-Aldrich
TEMED	BioRad
ThermoPol Reaction Buffer (10×), PCR	New England BioLabs
thiamine	Sigma-Aldrich
thiourea	Sigma-Aldrich
trichlor acedic acid	Riedel-de-Haen
trifluor acetic acid	Perkin Elmer Corporation
tris (hydroxymethyl) aminomethane	Riedel de Haen
trypsin, modified sequencing grade	Promega
urea	Amesham Biosciences
whatman paper	VWR
x-ray film Curix Ultra UV-G	Agfa
yeast extract, bacto	Difco Laboratories
zinc chloride	Merck
zinc sulfate	Merck

2.1.2 Devices

agarosegel-electrophoresis chamber	MPIBC
autoclave, varioklav 500	H+T Labortechnik
autoclave	Webeco
autoclave 23	MELAG
balance HL52, analytical	Mettler-Toledo
balance, precision	A&D
bidestillation system	Fistream Fisons Scientific Equipment
Bioanalyzer 2100	Agilent Technologies
CapLC capillary LC system	Micromass Waters
8-channel pipets (5-50 µL, 25-250 µL)	SL-Pette
centrifuge RC5C	Sorvall
centrifuge Rotixa 120R	Hettich

centrifuge 5417R	Eppendorf
electron microscope	Philips CM12
film processor X-OMAT 1000	Kodak
freezer UF80-450S (-80ºC)	Colora
gel documentation system TFPM / WL	Vilber Lourmat
GeneAmp 5700 Sequence Detection System	Applied Biosystems
GenePix 4000B microarray scanner	Axon Instruments
gradient blender	Bromma
hybridization chamber	Corning
hybridizing oven OV5	Biometra
incubator	Memmert
ice machine AF10	Scotsman
IPG reswelling cassette	Amersham Biosciences
IPG-Phor	Amersham Biosciences
Klett-Summerson photoelectric colorimeter	Klett Manufactoring
magnetic stirrer MR 2000	Heidolph
MALDI 4700 Proteomics Analyzer	Applied Biosystems
MALDI-mass spectrometer Reflex III	Bruker Daltonics
MAP pipetting robot	Bruker Daltonics
microtiter plate shaker	Heidolph MR 2000
microwave NN-5556/5506	Panasonic
Milli-Q and Elix water purification system	Millipore
Multiphor II + IEF equipment	Amersham Biosciences
Multiphor II + IEF equipment	Bromma
pH electrode, micro	Mettler Toledo
pH electrode, Biotrode	Hamilton Bonaduz AG
pH electrode, SenTix 60	Wissenschaftlich-techn. Werkstätten GmbH
pH- meter 522	Wissenschaftlich-techn. Werkstätten GmbH
pH-meter 632	Deutsche Metrohm GmbH
pipets (2, 10, 20, 100, 200, 1000, 5000 µl)	Gilson
power-supply EPS 1000 XL	Amersham Biosciences
power-supply EPS 3500 XL	Amersham Biosciences
Probot micro fraction collector	LC-Packings
Protean II SDS-elektrophoresis tank	BioRad
Q-TOF Ultimate mass spectrometer	Waters
Sephadex G-200 PC 3.2/30 column	Amersham Biosciences
shaker, big	GFL
SMART HPLC system	Amersham Biosciences
Sonifier 250 (cell disrupter)	Branson
Speed Vac	Savant
Speed Vac 150H	Univapo
spotpicking robot spotXress	Bruker Daltonics
Superose 6 HR 10/30 column	Amersham Biosciences
thermal cycler, peltier PT-200	MJ Research
thermal mixer compact	Eppendorf
Ultimat 3000 nanoHPLC system	LC-Packings

ultracentrifuge TL-100	Beckmann Coulter
ultrasonic bath Sonorex RK510	Bandelin
ultrasonic bath 1210	Branson
Ultrospec 3000 photometer	Amersham Biosciences
UV crosslinker Stratalinker 2400	Stratagene
Vortex Genie 2	Bender & Hobein AG
water bath	Julabo C
water bath	GFL

2.1.3 Programs

Program	**Company**
Adobe Photoshop	Adobe
Biotools 2.2	Bruker Daltonics
CorelDraw 11	Microsoft
Data Explorer 4.3 A	Applied Biosystems
EndNote 9	Adept Scientific
Excel OfficeXP	Microsoft
GeneAmp 5700 SDS software 1.1	Perkin Elmer Corporation
Gene Pix Pro 6	Axon Instruments
GPS-Explorer 2.0	Applied Biosystems
GPMAW 6.2	Lighthouse Data
Halolex	https://edman.rzg.mpg.de (external version: http://www.halolex.mpg.de)
Mascot Server (version 1.9.05)	Matrix Science
MassLynx 4.0	Waters
MSQuant (version 1.4.0a12)	Center for Experimental BioInformatics, University of Southern Denmark
Origin 7.0 SR0	OriginLab Corporation
Peakpicker	Applied Biosystems
Peaks-to-Mascot	Applied Biosystems
ProteomWeaver	Definiens
R-2.4.1-win.32	http://www.r-project.org
spControl 3.0	Bruker Daltonics
Spotfire DecisionSite 8.0	Spotfire Inc
TIGR MultiExperiment Viewer MeV 3.0.3	DataNaut Inc
Trans-Proteomic Pipeline v2.9 GALE rev.3	Seattle Proteome Center, Institute for Systems Biology, USA
Word OfficeXP	Microsoft

2.1.4 Oligonucleotides

Primer sequences for RTqPCR:

DnaJ-qRT-for: 5’- GAC CTG CTC GTC GAC GTC -3’,
DnaJ-qRT-rev 5’- AAC ACC GCC TGG GGG AAC -3’,
DnaK-qRT-for 5’-AAG AAG AAC GTC AAC CCC GA -3’,
DnaK-qRT-rev 5’- CGT CCA CCA ACA CGA TGT C -3’,
GrpE-qRT-for 5’- CTG CTT GAC GTT CGT GAC AA -3’,
GrpE-qRT-rev 5’- TCG CGG GTC AGC TCC ACA -3’,
tfbA-qRT-for 5’- AAA GCC GAC TAC AAC CGG AT -3’,
tfbA-qRT-rev 5’- AAC AGC GTG CAG GCC TGG T -3’,
tfbB-qRT-for 5’- CGG AGA AAG ACG AGA AAT CC -3’,
tfbB-qRT-rev 5’- TGT TCC CGT AGG CGT CCT T -3’,
tfbC-qRT-for 5’- TCG ACC AGA AGG AGA TCG G -3’,
tfbC-qRT-rev 5’- ATG ACT TCT TCA GAA AGT TCG A -3’,
tfbD-qRT-for 5’- TTA CGT TCC CCG GTT TTG CT -3’,
tfbD-qRT-rev 5’- GCG ACT TCC CGG ACG TGA -3’,
tfbE-qRT-for 5’- GAA CGA ACG ACT GCT CAA AG -3’,
tfbE-qRT-rev 5’- ATC GGC GCC ACA TCG TCG A -3’,
tfbF-qRT-for 5’- AAC AGT CTC TCC AGC AAC CA -3’,
tfbF-qRT-rev 5’- TGA GGT TGC GCT CTT TGG C -3’,
tfbG-qRT-for 5’- CGG AAA TGG CAG GAA CGA AT -3’,
tfbG-qRT-rev 5’- TGA CTG ATG CGA CTT CCC G -3’,
tfbH-qRT-for 5’- AAT AGA CTC TCC GGA CGG AA -3’,
tfbH-qRT-rev 5’- ATC CGG CGA ACC TCA CCC A -3’,
16SrRNA-qRT-for 5’- TGG TCC GAA GGA ATG AGG ATT -3’,
16SrRNA-qRT-rev 5’- TGT CAC CAA ACC ATC AAG GCT AA -3’.

Primer sequences for Northern blot hybridization:

hsp5-probe-for 5’- ATG CCC CTT CCG ACA GGT TCA A -3’,
hsp5-probe-rev 5’- TCA GGC CTG GAC CTC GAT CTG -3’,
DnaK-probe-for 5’- ATG GCG AGC GAG AAG ATT CTG G -3’,
DnaK-probe-rev 5’- GGT CGA TCC CGT GCT CGT TCT -3’,
tfbB-probe-for 5’- ATG AGT GAC AGT ACA ATC AGA ACA T -3’,
tfbB-probe-rev 5’- GCT GAC CTC GCT TTG GGT GAC -3’,
cctB-probe-for 5’- TGG ACA AGA TGC TCG TCT CCT C -3’,
cctB-probe-rev 5’- CGT CGA GGA CGT TCG TGA GGA -3’.

All oligonucleotides listed have been synthesized by Metabion International AG.

For unspecific cDNA-synthesis, random hexamer primer (Promega) or random nonamer primer (CyScribe-Kit, Amersham Biosciences) have been used for RTqPCR or DNA microarrays, respectively.

2.1.5 Culture media

Synthetic medium for *Halobacterium salinarum*

	Substance:	**MW [g/mol]:**	**Amount in g:**	**Amount in mmol:**	**Final concentration in the medium [mM]:**
Solution 1:	NaCl	58.44	235		4020
	$MgSO_4 \cdot 7\ H_2O$	246.48	20		81.14
	KCl	74.55	2		26.83
	KNO3	101.11	0.1		0.99
	Na_3-citrate $\cdot$ 2 H_2O	294.1	0.5		1.7
The substances were dissolved in a final volume of 750 mL.					
Solution 2:	KH_2PO_4	136.09	0.3		0.42
	$K_2HPO_4 \cdot 3\ H_2O$	228.19	0.3		0.58
Dissolved in 50 mL of water and added to solution 1.					
Solution 3:	$CuSO_4 \cdot 5\ H_2O$	249.68	0.005	0.02	0.0002
	$FeCl_2 \cdot 4\ H_2O$	198.81	0.23	1.16	0.0116
	$MnSO_4 \cdot H_2O$	169	0.03	0.18	0.0018
	$ZnSO_4 \cdot 7\ H_2O$	287.54	0.044	0.15	0.0015
	$Na_2MoO_4 \cdot 2\ H_2O$	241.95	0.024	0.1	0.001
	$CoCl_2 \cdot 6\ H_2O$	237.93	0.024	0.1	0.001
	ascorbic acid	176	2	11.36	0.1136
Trace elements were dissolved consecutively in 100 mL of H_2O. 1 mL (1%) was added to solutions 1 and 2.					
Solution 4:	L-Arg	174.2	2	11.48	2.30
	L-Ile	131.18	2.2	16.77	3.35
	L-Leu	131.18	4	30.49	6.10
	L-Lys · HCl	182.65	1.25	6.84	1.37
	L-Met	149.21	1	6.7	1.34
	L-Thr	119.12	2.5	20.99	4.20
	L-Ser	105.09	3.05	29.02	5.80
	L-Phe	165.19	0.5	3.03	0.61
	L-Ala	89.09	1.11	12.5	2.5
	Gly	75.07	0.38	5	1
	L-Pro	115.13	0.52	4.5	0.9
	L-Asp	133.1	2	15	3
	L-Glu	147.13	6.62	45	9
	L-Val	117.15	1.25	10.67	2.13
Dissolved in 750 mL of water and sterile filtered. 150 mL (20%) were added to the previous three solutions.					
Solution 5:	L-Tyr	181.19	0.2	1.1	1.1
Dissolved in 20 mL of 1M HCl, filled up to 50 mL with water and added to the solutions 1-4. Medium has been adjusted to pH 7.2 with NaOH and sterile filtered (0.22 µm).					
Solution 6:	thiamine	300.81	0.1	0.33	0.0165
	folic acid	441.4	0.1	0.23	0.0115
	biotin	244.31	0.01	0.041	0.0021
Vitamins were dissolved in 10 mL water and stored at -20°C in 0.5 mL portions, of which 17.5 µL were added to 35 mL medium in 100 mL flasks before inoculation.					

Complex medium for *Halobacterium salinarum*

Substance:	MW [g/mol]:	Amount in g:	Final concentration in the medium [mM]:
NaCl	58.44	235	4020
$MgSO_4 \cdot 7\ H_2O$	246.48	20	81.14
KCl	74.55	2	26.83
Na_3-citrate $\cdot\ 2\ H_2O$	294.1	3	10.2
peptone, Oxoid		10	

Dissolved in 1 liter of water. Medium has been adjusted to pH 7.2 with NaOH and sterile filtered (0.22 μm).

modified DSMZ medium 371 for *Natronomonas pharaonis*

Substance:	MW [g/mol]:	Amount in g:	Amount in mmol:	Final concentration in the medium [mM]:
NaCl (“reinst” quality)	58.44	200		3422
KH_2PO_4	136.09	0.3		0.42
KCl	74.55	1		13.41
NH_4Cl	53.41	1		18.72
sodium-L-glutamate	169.11	1		5.91
casamino acids		5		
yeast extract, bacto		5		
Na_2CO_3 (20%)	105.99	variable		

Dissolved in 1 liter of water. Medium has been adjusted to pH 6.5 with NaOH, 1 mL of trace elements SL-10 (see below) added, autoclaved, and pH readjusted to 9.0 with sterile filtered (0.22 μm) Na_2CO_3 (20%) after cooling. No $MgSO_4$ and $CaSO_4$ were added to avoid precipitation of calcium and magnesium carbonates.

H_3BO_3	61.83	6	97.04	0.0097
$FeCl_2 \cdot 4\ H_2O$	198.81	1.5	7.54	0.00754
$MnCl_2 \cdot 4\ H_2O$	197.90	0.1	0.51	0.00051
$ZnCl_2$	136.29	0.07	0.51	0.00051
$Na_2MoO_4 \cdot 2\ H_2O$	241.95	0.036	0.15	0.00015
$CoCl_2 \cdot 6\ H_2O$	237.93	0.19	0.80	0.00080
$NiCl_2 \cdot 2\ H_2O$	165.65	0.024	0.14	0.00014
$CuCl_2 \cdot 2\ H_2O$	170.48	2	11.73	0.01173

$FeCl_2$ was first dissolved in 10 mL HCl (25%) and diluted in 1 liter of water before dissolving the other trace elements. 1 mL (0.1%) was added to the solution above.

2.1.6 Buffers, solutions gels and standards

2.1.6.1 2-DE, silver staining and MS

Sample buffer
7 M urea
2 M thiourea
4% CHAPS
0.6% Pharmalytes 3-10
65 mM DTT
a trace of bromophenol blue

Reswelling solution
7 M urea
2 M thiourea
4% CHAPS
0.6% Pharmalytes 3-10
20 mM DTT
a trace of bromophenol blue

Equilibration solution
50 mM Tris/HC1, pH 8.8
6 M urea
30% (v/v) glycerol
2% (w/v) SDS
a trace of bromophenol blue

Gradient polyacrylamide gels (9% to 16%)
9% fraction:
9% polyacrylamide (30/0.8 acrylamide/bisacrylamide (w/w)); 380 mM Tris/HCl, pH 8.8; 0.015% (v/v) TEMED; 0.015% (w/v) APS.
16% fraction:
16% polyacrylamide (30/0.8 acrylamide/bisacrylamide (w/w)); 380 mM Tris/HCl, pH 8.8; 0.015% (v/v) TEMED; 0.015% (w/v) APS.

Silver staining for 2-D gels (MS compatible)
Fixation solutions:
50/5/45 MeOH/HOAc/H_2O_{dest} (v/v/v) and 50/50 EtOH/H_2O_{dest} (v/v).
Sensitizing solution:
0.02/99.8 sodium thiosulfate/H_2O_{dest} (v/v).
Staining solution:
0.1/0.0375/99.9 silver nitrate/formaldehyde/H_2O_{dest} (v/v/v).
Developing solution:
0.0005/0.025/6/94 sodium thiosulfate/formaldehyde/sodium carbonate/H_2O_{dest} (v/v/w/v).
Stop solution:
5/95 HOAc/H_2O_{dest} (v/v).

Storing solution:
1/99 HOAc/H_2O_{dest} (v/v).

ICPL labeling
Lysis buffer:
6 M guanidine HCl; 0.1 M HEPES; adjusted to pH 8.5 ± 0.1.
Reduction solution:
0.2 M TCEP; 0.1 M HEPES; adjusted to pH 8.5 ± 0.1.
Alkylation reagent:
0.4 M iodacetamide; 0.1 M HEPES
Stop solution I:
0.5 M N-acetyl cysteine, 0.1 M HEPES; adjusted to pH 8.5 ± 0.1.
^{12}C-Nic-reagent solution:
0.15 M d0-/^{12}C-nicotinoyl-N-hydroxy-succinimide (^{12}C-Nic-NHS) in DMSO.
^{13}C-Nic-reagent solution:
0.15 M d0-/^{13}C-nicotinoyl-N-hydroxy-succinimide (^{13}C-Nic-NHS) in DMSO.
d4-Nic-reagent-solution:
0.15 M d4-/^{12}C-nicotinoyl-N-hydroxy-succinimide (d4-Nic-NHS) in DMSO.
Stop solution II:
1.5 M hydroxylamine HCl; adjusted to pH 8.3 ± 0.1.

Peptide standard mix for MS (100 pm/µl)
bradykinin fragment 1-7 (757.3998 g/mol); angiotensin II human acetate (1046.542 g/mol); angiotensin I human acetate (1296.6853 g/mol); substance P (1347.7361 g/mol); bombesin (1619.823 g/mol); ACTH (1-17) (2093.0868 g/mol); ACTH (18-39) (2465.199 g/mol); somatostatin 28 (3147.4714 g/mol); insulin chain B oxidized (3494.651 g/mol)

2.1.6.2 SDS-PAGE and CBB staining

SDS-PAGE (Laemmli)
Stacking gel:
5% polyacrylamide (30/0.8 acrylamide/bisacrylamide (w/w)); 125 mM Tris/HCl, pH 8.8; 0.1% (w/v) SDS; 0.015% (v/v) TEMED; 0.05% (w/v) APS.
Separating gel:
12.5% polyacrylamide (30/0.8 acrylamide/bisacrylamide (w/w)); 375 mM Tris/HCl, pH 8.8; 0.1% (w/v) SDS; 0.015% (v/v) TEMED; 0.05% (w/v) APS.
Running buffer:
25 mM Tris/HCl, pH 8.3; 0.192 M glycin; 0.1% (w/v) SDS.
Sample/Loading buffer (5× concentrated):
50 mM Tris/HCl, pH 6.8; 100 mM DTT; 2% (w/v) SDS; 0.1% bromphenol blue; 10% glycerol.

Tricine-SDS-PAGE (Schaegger)
Gel buffer (3× concentrated):
3 M Tris/HCl, pH 8.45; 0.3% (w/v) SDS.
Anode buffer (10× concentrated):

1 M Tris/HCl, pH 8.9.

Cathode buffer (10× concentrated):

1 M Tris/HCl, pH 8.25; 1 M tricine; 1% (w/v) SDS.

AB-mix S (49.5% T, 3% C)

48/1.5 acrylamide/bisacrylamide (w/w).

Sample/Loading buffer:

150 mM Tris/HCl, pH 7.0; 30% glycerol; 12% (w/v) SDS; 6% mercaptoethanol; 0.05% Serva blue G.

Stacking gel:

1 mL AB-mix S; 3 mL gel buffer (3× conc.); 90 µL APS (10%); 9 µL TEMED; ad 12 mL H_2O_{dest}

Separating gel (10% T, 3% C):

6 mL AB-mix S; 10 mL gel buffer (3× conc.); 3 g glycerol; 150 µL APS (10%); 15 µL TEMED; ad 30 mL H_2O_{dest}.

Coomassie staining for Laemmli gels

Fixation/staining solution:

0.1% (w/v) CBB-R250 dissolved in 45/45/10 MeOH/H_2O_{dest}/HOAc (v/v/v).

Destaining solution:

12.5/77.5/10 *i*-propanol//H_2O_{dest}/HOAc (v/v/v).

Colloidal Coomassie staining for Laemmli gels

Fixation/staining solution:

0.08% (w/v) CBB G-250 dissolved in 1.6/8/20 phosphoric acid/ammonium sulfate/MeOH (v/w/v).

Destaining solution:

H_2O_{dest}

Coomassie staining for tricine gels

Fixation solution:

50/10/40 MeOH/HOAc/ H_2O_{dest} (v/v/v).

Staining solution:

0.025% (w/v) CBB G-250 dissolved in 10/90 HOAc/ H_2O_{dest} (v/v).

Destaining solution:

10/90 HOAc/ H_2O_{dest} (v/v).

Precision Plus Protein standard

The standard contains ten recombinant proteins (10, 15, 20, 25, 37, 50, 75, 100, 150, and 250 kD). Each protein band has been covalently stained with a blue dye, whereas two reference bands are pink (25 and 75 kD).

2.1.6.3Agarose gelelectrophoresis and RTqPCR

Agarose gelelectrophoresis of RNA

RNA loading buffer (6× concentrated):

0.25% bromphenol blue; 0.25% xylene cyanol; 30% glycerol; 1.2% (w/v) SDS in 60 mM Na phosphate buffer, pH 6.8
10× TBE buffer:
1 M Tris; 833.4 mM borate; 100 mM EDTA; adjust with NaOH to pH 8.5; autoclave 2×
agarose gel:
1.5% agarose; 1× TBE buffer; 20 mM guanidine thiocyanate; 15 µL of 10 mg/mL ethidium bromide solution

Agarose gelelectrophoresis for screening of DNA
DNA loading buffer (6× concentrated):
0.25% bromphenol blue; 0.25% xylene cyanol; 30% glycerol; 60 mM EDTA in 10 mM Tris-HCl, pH 7.6
10× TBE buffer:
1 M Tris; 833.4 mM borate; 100 mM EDTA; adjust with NaOH to pH 8.5; autoclaved
agarose gel:
2% agarose; 1× TBE buffer; 15 µL of 10 mg/mL ethidium bromide solution

GeneRule 1kb DNA Ladder
The ladder, dissolved in TE buffer, is composed of fourteen individual DNA fragments: 10000, 8000, 6000, 5000, 4000, 3500, 3000, 2500, 2000, 1500, 1000, 750, 500 and 250 bp, containing three reference bands (6000, 3000 and 1000 bp) for easy orientation.

10× RQ1 DNase reaction buffer
400mM Tris/HCl, pH 8.0
100mM $MgSO_4$
10mM $CaCl_2$.

10× ThermoPol reaction buffer
200 mM Tris/HCl, pH 8.8
100 mM $(NH_4)_2SO_4$
100 mM KCl
20 mM $MgSO_4$
1 % Triton X-100

5× first strand buffer
250 mM Tris/HCl, pH 8.3
375 mM KCl
15 mM $MgCl_2$

2.1.6.4 Northern blot hybridization

DIG-labeled RNA Molecular Weight Marker III

The marker consist of a mixture of the following 5 RNA fragments: 310, 438, 575, 1049 and 1517 bases.

10× DIG DNA Labeling Mix
10 mM ATP, 10 mM CTP, 10 mM GTP,
6.5 mM UTP, 3.5 mM DIG-11-dUTP, pH 7.5

Prehybridization solution
DIG Easy Hyb

Hybridization solution
DIG-labeled probe, diluted in prehybridization solution

20× SSC
3 M NaCl
300 mM sodium citrate, pH 7.0
treated with DMPC

10× SSC
1.5 M NaCl
150 mM sodium citrate, pH 7.0
treated with DMPC

2× wash solution
2× SSC, containing 0.1% SDS

0.5× wash solution
0.5× SSC, containing 0.1% SDS

Anti-Digoxigenin-AP
750 units/mL Anti-Digoxigenin, Fab fragments conjugated to alkaline phosphatase

CSDP
25 mM Disodium 3-(4-methoxyspiro[1,2-dioxetane-3,2'-(5'-chloro)tricyclo[3.3.1.1^{3,7}]decan]-4-yl) phenyl phosphate

Washing buffer* (1× concentrated after 1:10 dilution with H_2O)
100 mM maleic acid
150 mM NaCl, pH 7.5 (20 ºC)
0.3%(v/v) Tween 20

Maleic acid buffer* (1× concentrated after 1:10 dilution with H_2O)
100 mM maleic acid
150 mM NaCl, pH 7.5 (20 ºC)

Blocking solution* (1× concentrated after 1:10 dilution with 1× maleic acid buffer)
1 % (w/v) blocking reagent for nucleic acid hybridization dissolved in maleic acid buffer. Blocking solution is cloudy and should not be filtered. It is stable for at least two weeks when stored at 4 ºC, but must then be brought to room temperature before use.

Detection buffer* (1× concentrated after 1:10 dilution with H_2O)
100 mM Tris/HCl
100 mM NaCl, pH 9.5 (20ºC)
*Available in the DIG Wash and Block Buffer Set (10× conc., Cat. No. 11 585 762 001).

2.1.6.5 Whole genome DNA-microarrays

CyScribe First-Strand cDNA Labeling Kit

Includes the following reagents sufficient for 25 labeling reactions: anchored oligo(dT), random nonamers, 5× CyScript buffer, 0.1 M DTT, nucleotide mix for dUTP, CyScript reverse transcriptase, nuclease-free water, control RNA: 0.24-9.5 kb RNA ladder, microarray hybridization buffer and Cy3-/Cy5-labeled nucleotides of dUTP.

50× Denhardts-solution
2% Ficoll 400
2% (w/v) polyvinylpyrrolidone
2% (w/v) BSA V, pH 7.0

20 x SSC
3 M NaCl
300 mM sodium citrate, pH 7.0

Wash-solution I
0.5× SSC, containing 0.01% SDS

Wash-solution II
0.06× SSC, containing 0.01% SDS

TE-buffer
10mM Tris
1mM EDTA, pH 8.0, autoclaved

PH-buffer
3,5× SSC
0.1% SDS
1% BSA Fraktion V

2.2 Methods

2.2.1 Growth conditions. *Nmn. pharaonis* and *Hbt. salinarum* strain R1 (DSM 671) were grown aerobically to late-log phase at 40ºC in the dark, as described previously [Oesterhelt and Krippahl 1983]. For protein preparation, cells were grown through three successive transfers. For each transfer, 35 mL of fresh medium were inoculated with 1 mL from the previous culture grown to late-log phase (~40 Klett units).

DSMZ medium 371 (see chapter 2.1.5) for *Nmn. pharaonis* (http://www.dsmz.de) was modified as proposed [Balows *et al.* 1992]: due to a sufficient concentration of Ca^{2+} and Mg^{2+} in NaCl ("reinst" quality) no $MgSO_4$ and $CaSO_4$ was added to avoid precipitation of calcium and magnesium carbonates. The pH was adjusted to 6.5 with NaOH before autoclaving and after cooling to pH 9.0 with sterilized Na_2CO_3.

Hbt. salinarum was grown in both complex [Oesterhelt and Stoeckenius 1974] and synthetic medium [Helgerson *et al.* 1992; Oesterhelt and Krippahl 1983] (see chapter 2.1.5).

2.2.2 Protein inventory of *Natronomonas pharaonis*

2.2.2.1 Sample preparation under low ionic strength conditions (water lysis) and protein precipitation by acetone. Cells were harvested by centrifugation at 6500 g for 20 min at 4°C and lysed by exposure to pure water containing a protease inhibitor cocktail ("Complete without EDTA", Roche, Basel, Switzerland) with subsequent tip-sonication (four exposures of 30 sec, Branson Sonifier, cell disruptor B15, Danbury, CT, USA). The cell suspension was ultracentrifuged at 213 000 g for 30 min at 4°C to remove cell debris and cell envelope fragments [Tebbe *et al.* 2005].

Proteins of the supernatant were precipitated by adding a ten-fold excess of acetone (-20°C). After incubation for 30 min at -20°C the proteins were centrifuged at 20 000 g for 15 min at 4°C and the supernatant was carefully removed. The pellet was washed with 80% (v/v) acetone (-20°C) to remove salt, dried and stored at -80°C until use. The amount of protein was estimated on the basis of cell mass (determined by volume and turbidity of the suspension) used for protein preparation [Michel and Oesterhelt 1976]. Optical density of the cell suspension was measured at 578 nm with an Eppendorf spectrophotometer or a Klett-Summerson photoelectric colorimeter with a no. 66 filter [Oesterhelt and Krippahl 1983]. 100 Klett units (Klett MFG. Co. Inc., NY, USA) correspond to an optical density of 1 at 578 nm (Eppendorff spectrophotometer, Netheler and Hinz, Hamburg, Germany) and represent a protein concentration of 0.5 mg/mL. Cytosolic proteins are assumed to amount for about 2/3 of the overall protein.

2.2.2.2 Sample preparation under high ionic strength conditions (native lysis) with subsequent size-exclusion chromatography and protein precipitation by TCA. Cells were harvested, resuspended in basal salt (per liter: 200 g of NaCl, 1 g of sodium L-glutamate monohydrate, 1 g of KH_2PO_4, 1 g of KCl, 1 g of NH_4Cl, pH 9.0) also containing a protease inhibitor cocktail and lysed by tip-sonication with subsequent ultracentrifugation as described for water lysis.

Concentration of native proteins was measured by BCA (bicinchoninic acid) protein assay kit (Pierce, Rockford, IL, USA) and 500 µg were used for size-exclusion chromatography (SEC).

A precision column PC 3.2/30 pre-packed with Superose 6 (GE Healthcare Bio-Sciences AB, Uppsala, Sweden) was used in a SMART system (GE Healthcare Bio-Sciences AB, Uppsala, Sweden) for prefractionation. The optimal range for separation of globular proteins in this column is 5–5000 kDa, with an exclusion limit of 40 000 kDa. The column was calibrated with blue dextran (2000 kDa), ferritin (444 kDa), albumin (67 kDa), ribonuclease A (13.7 kDa), thyroglobulin (669 kDa), catalase (232 kDa) and chymotrypsinogen (25 kDa) (LMW and HMW calibration kits, GE Healthcare Bio-Sciences AB, Uppsala, Sweden, applied in basal salt). (Fig. 10)

Before a chromatographic run the column was first equilibrated with degassed and filtered, distilled H_2O and then with degassed and filtered basal salt. 500 µg (10 µL) of cytoplasmic lysate were injected into the SMART system, the protein profile was monitored at 260 and 280 nm with a column flow rate of 40 µL/min at 4°C and eight fractions (I-VIII) were collected (Fig. 11). The fractions were precipitated by adding 100% (w/v) TCA to a final concentration of 20% (45 min incubation, 15 min centrifugation at 20 000 g, 4°C) and washed with 80% (v/v) acetone (-20°C).

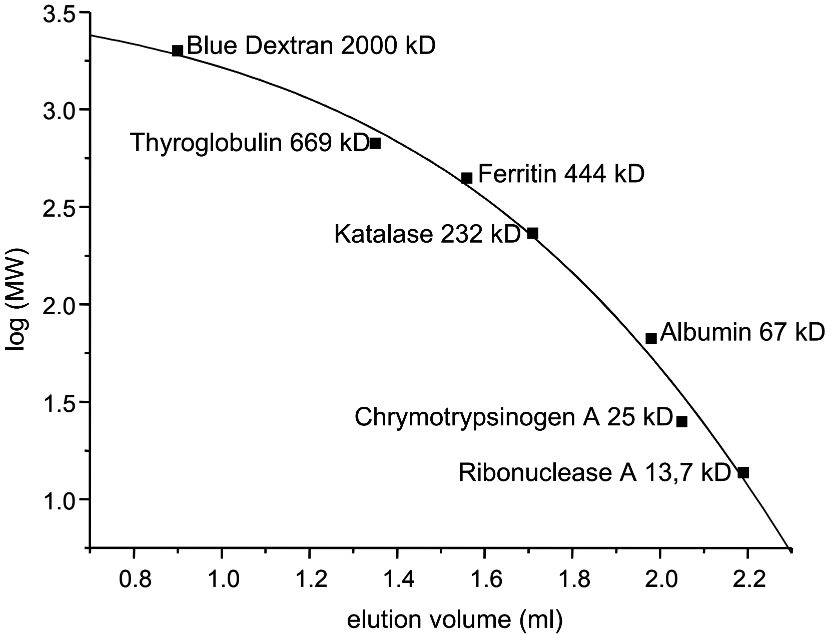


Figure 10. Calibration curve established by SEC using a Superose 6 column.

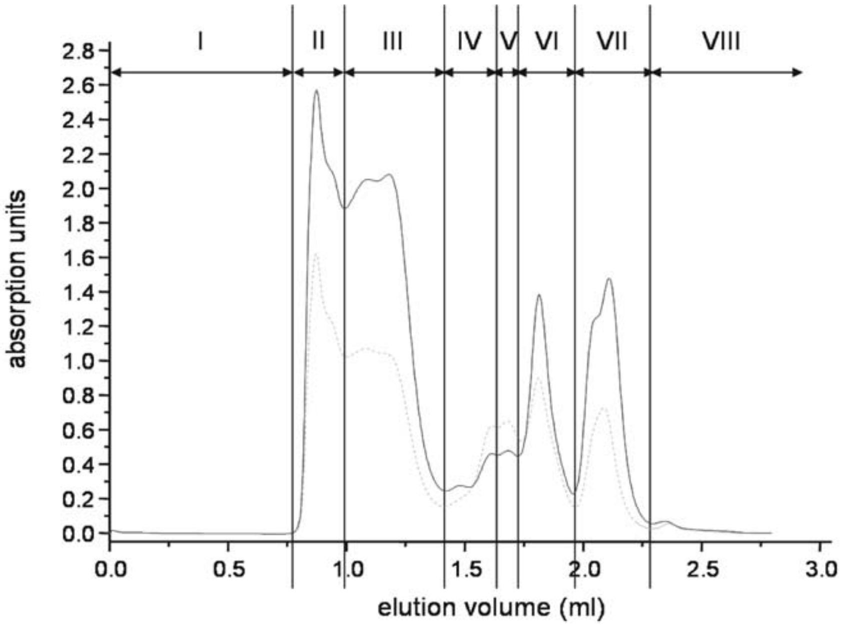


Figure 11. SEC on a Superose 6 column after native lysis of *Nmn. pharaonis* in 3.4 M NaCl. A total of eight fractions (I-VIII) were collected as indicated. Elution of proteins was monitored at 260 nm (—) and 280 nm (---).

2.2.2.3 SDS-PAGE and in-gel digestion. Approximately 250 µg protein from the water-lysed sample (Fig. 12) as well as the eight collected SEC-fractions from one SEC run (Fig. 13) were applied after resuspension in Laemmli sample buffer and denaturation for 5 min at 95ºC onto a 3% *T* stacking / 12.5% *T* separation gel (11 cm long and 1.5 mm thick) for SDS PAGE as described elsewhere [Laemmli 1970]. On each gel also 5 µL of a protein marker (precision plus protein standards, Bio-Rad Laboratories, Munich, Germany) were applied and electrophoresis was carried out at a maximum of 40 mA/gel and 300 V limit setting. Protein staining was done with CBB (0.1% (w/v) CBB-R250 dissolved in 45/45/10 methanol/water/acetic acid (v/v/v)) and destained in 12.5/77.5/10 *i*-propanol/water/acetic acid (v/v/v).

The lane from the water-lysed sample (Fig. 12) and the lanes from the fractions II-VII (Fig. 13) of the native sample were cut into slices and subsequently minced to small pieces before being transferred into reaction vessels. Excised slices of the CBB stained gels were destained by adding 50% (v/v) acetonitrile and 50 mM NH_4HCO_3 for 15 min alternately until complete destaining. Reduction/alkylation [Shevchenko *et al.* 1996] and trypsin digestion/elution [Tebbe *et al.* 2005] of the samples was performed according to published procedures. The eluates were frozen in liquid nitrogen and dried in a vacuum centrifuge.

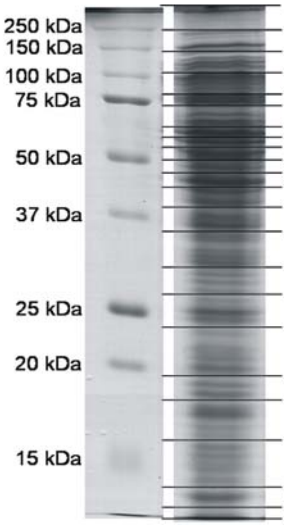


Figure 12. SDS-PAGE of the protein preparation of *Nmn. pharaonis* after lysis in water. After separation, proteins were stained by Coomassie and the lane was cut into 22 slices.

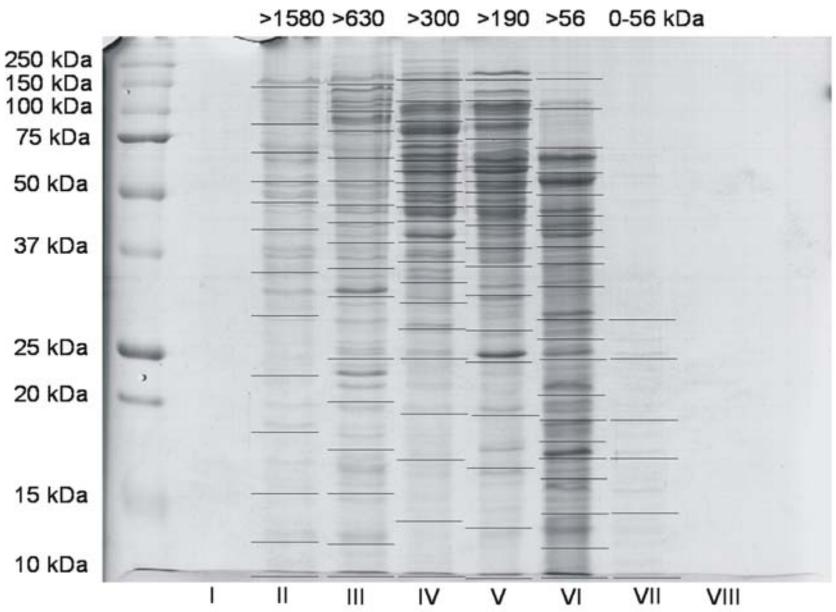


Figure 13. SDS-PAGE of the protein preparation of *Nmn. pharaonis* after native lysis in 3.4 M NaCl. Proteins, prefractionated by SEC to eight fractions (I-VIII), were applied to a SDS-PAGE, and the resulting lanes were cut into a total of 93 slices. The estimated molecular mass ranges (in kDa) of the single fractions deduced from the calibration curve are shown above the gel.

2.2.2.4 NanoLC-MS/MS. For nanoLC-MS/MS our standard protocol [Klein *et al.* 2005] (based on the work of Gevaert *et al*. [Gevaert *et al.* 2002]) was used with minor modifications. In brief, dried protein digests were redissolved in 40 µL 5% (v/v) formic acid of which 10 µL were desalted on a self-prepared micro RP column [Rappsilber *et al.* 2003]. After elution with 10 µL 80/15/5 methanol/water/formic acid (v/v/v), peptide solutions were dried in a vacuum centrifuge, redissolved in 10 µL 5% (v/v) formic acid followed by sonication for 10 s and subjected to nanoflow LC-MS/MS analysis. The column setup was essentially as described by Meiring *et al*. [Meiring *et al.* 2002] RP-C18 material was used for both, the trapping and nanoscale analytical column. The LC-MS/MS system [Klein *et al.* 2005] consisted of a CapLC, a ten-port switching valve, and a Q-TOF Ultimate mass spectrometer (Waters, Milford, MA, USA). Per run, 5 µL were loaded onto a 100 µm X 25 mm trapping column (stationary phase: Reprosil-Pur 300, C18, 5 µm, Dr. Maisch GmbH, Ammerbuch-Entringen, Germany; packed inhouse) at a flow rate of 2 µL/min of solvent A (0.5% v/v formic acid in 2/98 ACN/water). By valve switching, the sample was flushed from the trapping-column onto a nano-scale reversed phase column (75 µm x 150 mm, Reprosil-Pur 300, C18, 3 µm; packed inhouse) and a binary solvent gradient was started. The CapLC system was run at a constant flow of 7 µL/min from which 200 nL/min were directed to the column after flow splitting. Peptides were eluted from the stationary phase using a 90 min gradient from solvent A to solvent B (0.5% v/v formic acid in 80/20 ACN/water). The outlet of the nano-column was in-line connected to a metal-coated fused silica PicoTip needle (PicoTip FS360-20-10-D-20-C7, New Objective, Inc., Woburn, MA, USA) which was placed in front of the MS inlet. Automated data-dependent acquisition with the Q-TOF mass spectrometer was initiated 20 min after the solvent gradient was started. The acquisition parameters were chosen such that at least doubly charged ions were selected for fragmentation. Throughout the analysis 1.5-s MS acquisitions were followed by 6-s MS/MS experiments in information dependent acquisition mode.

2.2.2.5 Protein identification by MS/MS. After nanoLC-MS/MS the obtained CID-spectra were converted to the Mascot (Matrix Science, London, UK) [Perkins *et al.* 1999] acceptable pkl format using ProteinLynx software. These peaklists were used for protein identification in a database of 11 874 potential ORFs from *Nmn. pharaonis,* consisting of the theoretical proteome of 2843 proteins as well as 9031 spurious ORFs, of which more than 99% are longer than 100 codons. Search parameters were used as previously described [Klein *et al.* 2005] which involves application of high stringency to reduce false positive identification. In detail the search parameters were: trypsin as enzyme, max. 1 missed cleavage site, carbamidomethylation as fixed modification, oxidised methionine as variable modification, 0.15 Da peptide tolerance, 0.15 Da MS/MS tolerance. For each identified protein, a score was computed based on the MOWSE scores returned by MASCOT in the following way: (a) only rank 1 results were used (b) for each tryptic peptide, the highest-scoring CID spectrum was chosen and (c) the resulting peptide scores were summed up (d) the Mascot significance level, which was in the range of 17-25, was subtracted once. Proteins are considered as “normal” identified when the summed peptide scores exceed the confidence threshold score for a 95% confidence level by at least 20, which is equivalent to application of a 99.95% confidence level. For “reliable” identification the score must be at least 40 above the confidence threshold score, equivalent to a 99.9995% confidence level. Spectra with a long y- and/or b-series may have very low MOWSE peptide scores. Upon manual inspection, proteins may be considered identified despite a low MASCOT score.

2.2.2.6 Bioinformatic computations. Transmembrane helices were predicted by TMHMM [Krogh *et al.* 2001] and signal sequences by SIGNALP3.0 [Nielsen *et al.* 1997]. N-terminal lipid anchors (as found for halocyanin [Mattar *et al.* 1994]) were characterized by a modified lipobox motif (LAGC) and protein secretion signals were predicted as described [Falb *et al.* 2005]. Proteins are considered membrane-associated when they either have a lipid anchor or are annotated as membrane complex subunits lacking transmembrane domains. Proteins are considered extracellular when they have a secretion signal but are predicted to contain neither transmembrane domains nor a lipid anchor. The GRAVY index (grand average of hydrophobicity) was computed based on the empirical values of Kyte and Doolittle [Kyte and Doolittle 1982]. The codon adaptation index was computed according to previous publications [Carbone *et al.* 2003]. Other statistical data were computed in the framework of HaloLex (www.halolex.mpg.de).

Proteins from *Natronomonas pharaonis* were compared to those from other species using blast [Altschul *et al.* 1997]. Homology searches were made via HaloLex against three other completely sequenced halophiles: *Halobacterium salinarum* (strain R1; www.halolex.mpg.de) [Pfeiffer *et al.* 2008a] which is very closely related to strain NRC-1 [Ng *et al.* 2000]), *Haloarcula marismortui* [Baliga *et al.* 2004b] and *Haloquadratum walsbyi* [Bolhuis *et al.* 2006].

Homology searches against proteins from completely sequenced microbial genomes and public protein sequence databases were performed in the MiGenAS computing environment [Rampp *et al.* 2006].

2.2.3 Quantitative proteomics in *Halobacterium salinarum* after heat shock

2.2.3.1 Heat shock and protein preparation. For heat shock, cells were dipped 2 min in 60 ºC warm water and subsequently shaken for the remaining time (up to 2 h) in an incubator (60 ºC) in the dark. Cell lysis has been performed under high ionic strength conditions as described for *Natronomonas pharaonis* (see chapter 2.2.2.2).

2.2.3.2 BCA protein assay. This assay is based on an analytical method capable of monitoring cuprous cations (Cu^{1+}) in a highly sensitive and selective colorimetric detection by bicinchoninic acid, after reduction of Cu^{2+} to Cu^{1+} by proteins (biuret reaction) in an alkaline medium (Fig. 14). The color produced from this reaction is stable and increases in a proportional fashion over a broad range of increasing protein concentrations[Smith *et al.* 1985].

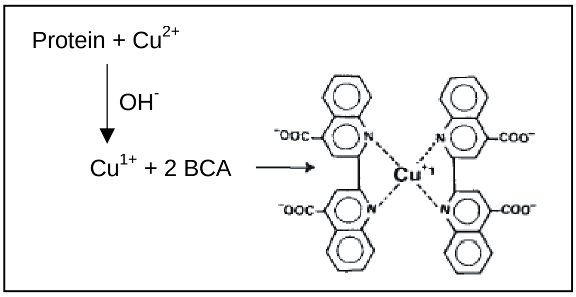


Figure 14. Reaction schematic for the BCA protein assay.

Single amino acids and dipeptides do not give the biuret reaction, but tripeptides and larger polypeptides or proteins will react to produce the light blue to violet complex that absorbs light at 540 nm. One cupric ion forms a colored coordination complex with four to six nearby peptides bonds. The intensity of the color produced is proportional to the number of peptide bonds participating in the reaction.

The BCA reagent, which is approximately 100 times more sensitive than the biuret reagent (NH_2-CO-NH-CO-NH_2), reacts with the cuprous cation (Cu^{1+}) forming a water-soluble complex, that exhibits a strong linear absorbance at 562 nm with increasing protein concentrations. The BCA color formation is strongly influenced by the presence of any of four amino acid residues (cysteine or cystine, tyrosine, and tryptophan) in the amino acid sequence of the protein, even though the peptide backbone must contribute to the reduction of copper as well. The rate of color formation is dependent on the incubation temperature, the types of protein present in the sample and the relative amounts of reactive amino acids contained in the proteins.

50 parts of BCA reagent A (1% BCA-Na_2; 2%$Na_2CO_3 \cdot H_2O$; 0.16% Na_2-tartrat; 0.4% NaOH; 0,95% $NaHCO_3$; adjusted to pH 11.25) were mixed with 1 part of BCA reagent B (4% $CuSO_4 \cdot 5H_2O$) and 1 mL of this working reagent combined with 50 µL of the analysing sample. After incubation at 37°C for 30 min absorption was measured at 562 nm and the protein concentration determined by comparing with absorption data of a BSA standard curve (0.1-1.0 mg/mL).

2.2.3.3 ICPL labeling, 2-DE, MALDI-TOF/TOF and data analysis. Proteins from *Hbt. salinarum*, grown in complex medium (see chapter 2.1.5), were subjected to isotope-coded protein label (ICPL) after cell lysis [Schmidt *et al.* 2005; Tebbe *et al.* 2007]. Cells of three different cell states, labeled by either d0-/^{12}C- (40 ºC; light label), d4-/^{12}C- (1 h at 60 ºC; heavy1 label) or d0-/^{13}C6- (2 h at 60 ºC; heavy2 label) Nicotinoyl-N-hydroxy-succinimide (Nic-NHS) [Schmidt *et al.* 2005; Tebbe *et al.* 2007], were combined, the proteins precipitated, separated by 2-DE and subjected to mass spectrometric analysis (Fig. 15). D0-/^{13}C-Nic-NHS was purchased from Campro Scientific, Berlin, Germany, d0-/^{12}C- and d4-/^{12}C- Nic-NHS were synthesized as described in Hausch *et al.* [Hausch and Jaschke 2000]. Protein labeling (see chapter 2.2.3.3.1), precipitation (see chapter 2.2.3.3.1), separation by 2-DE (see chapter 2.2.3.3.2), digestion with trypsin (see chapter 2.2.3.3.5), purification (see chapter 2.2.3.3.6) and application of peptides on MALDI targets [Tebbe *et al.* 2005] (see chapter 2.2.3.3.7), as well as mass spectrometric analysis on a 4700 Proteomics Analyzer (Applied Biosystems, Framingham, MA) (see chapter 2.2.3.3.8) and data analysis [Tebbe *et al.* 2007], were performed as previously described.

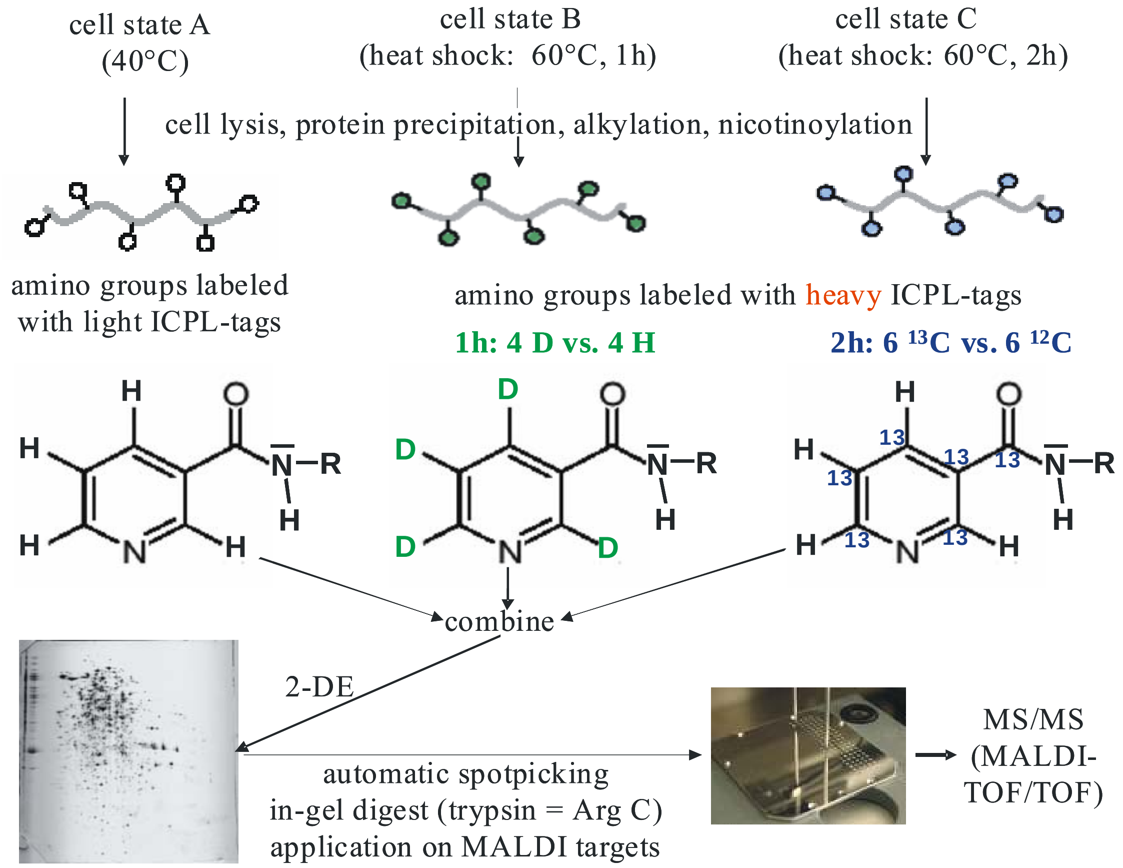


Figure 15. Workflow for protein quantitation using ICPL labeling. After heat shock, cell lysis and alkylation of cysteins, protein amino groups of three different cell states were labeled with three different Nicotinoyl-NHS. The increment of protein mass after label with the light ICPL-tag is 105.09 Da, the mass difference between the light and heavy I tag is 4.1 Da (d0-/^{12}C- and d4-/^{12}C-Nic-NHS) and the mass difference between the light and the heavy II tag is 6.02 Da (d0-/^{12}C- and d0-/^{13}C- Nic-NHS). The samples were combined and applied on 2-D gels spanning different pH ranges (pH 3-6, 3.5-4.5 and 4-5) before staining (silver or colloidal Coomassie), in-gel digest with trypsin and MS/MS analysis on a MALDI TOF/TOF.

Briefly, for the latter all obtained MS/MS-spectra were searched against the *Halobacterium* protein sequence database [Tebbe *et al.* 2005; Pfeiffer *et al.* 2008b], using a locally installed Mascot Server (version 1.9.05) [Perkins *et al.* 1999] in combination with the GPS-Explorer 2.0 software (Applied Biosystems), with carbamidomethylation set as fixed cysteine modification, and methionine oxidation as well as ^{12}C/^{13}C-nicotinoylation of lysine and of the protein N-terminus as variable modifications. Arg-C was selected as enzyme for the Mascot search since lysines are blocked by ICPL tags. For database searches a mass tolerance of 150 ppm in the MS mode and 0.4 Da in the MS/MS mode and the occurrence of one missed cleavage site were allowed. Annotated MS/MS spectra with Mascot scores above the confidence level of 98% in case of singlets or above the confidence level of 93% in case of pairs were considered to be correct calls [Tebbe *et al.* 2007]. Validation of the search results against the database was carried out using the Spotfire DecisionSite Browser 8.0 (Spotfire AB Europe, Göteborg, Sweden), which allows to visualize modified peptides that are considered to be incorrectly identified [Tebbe *et al.* 2007]. If peptide pairs were either wrongly assigned as singlets by the Peak Picker software (Applied Biosystems, Darmstadt, Germany), or showed large deviations among their automatically calculated ratios, or displayed significant regulation factors pointing to possible relevant candidates for being regulated by heat shock, they were manually examined and the ratios confirmed using the Data Explorer software (Applied Biosystems, Darmstadt, Germany). Data are available from two biological replicates, each comprising proteins separated on several 2-D gels spanning different pH-ranges (pH 3-6, 4-5 and 3.5-4.5). The median of the ratios from each of the two sets of quantified peptides was used for computational normalization of the original ratios. The same extent of a positive (2) or negative (0.5) regulation factor was altered, resulting in an identical absolute value of the regulation factor, with ± 1 representing no regulation and ± 2 representing two-fold up- or downregulation, respectively.

2.2.3.3.1 ICPL labeling and protein precipitation by acetone. Prior to labeling, the protein concentration of the samples (light and heavy) has to be determined by BCA protein assay and adjusted to 5 mg/mL by adding lysis buffer. The pH of the sample buffer has to be checked and if necessary, adjusted to 8.5 ± 0.1. The carbamidomethylation protocol is identical for all samples (light and heavy).

-Add 0.5 µl reduction solution to 20 µl sample solution and reduce the disulfide bonds of the proteins for 30 min at 60 °C.

-Cool sample to room temperature and spin down sample to remove condensed solution from the lid.

-Add 0.5 µl of freshly prepared alkylation reagent to each sample, wrap samples quickly in aluminium foil for light protection and leave samples for 30 min at 25 °C for carbamidomethylation of the cystein residues.

-Stop reaction by adding 0.5 µl stop solution I to each sample and incubate for 15 min at 25 °C.

-After carbamidomethylation add 3 µl of ^{12}C-Nic-reagent solution to sample A (light), 3 µl of ^{13}C-Nic-reagent solution to sample B (heavy I) and d4- Nic-reagent solution to sample C (heavy II).

-Overlay both samples with argon to exclude oxidation, vortex (10 sec.) and sonicate for 1 min in ultrasound bath. Spin down samples.

-Incubate samples for 2 h at 25 °C.

-Add 2 µl of stop solution II to each sample and incubate for 20 min at 25 °C to destroy excess reagent.

-Combine all ICPL labeled samples and vortex thoroughly.

-Adjust the pH of the mixture to 11.9 ± 0.1 by adding 2 N NaOH to destroy possible esterification products. After 20 min add the same amount of 2 N HCl to neutralize sample.

-Add the equal amount of H_2O_{dest} to the combined sample and subsequently a 5-fold excess of acetone (-20 ºC) related to the total volume. Vortex and leave at -20 °C overnight.

-Spin down precipitated proteins at 20 000 g for 30 min at 4 °C.

-Discard supernatant and overlay precipitated proteins with 80% acetone (-20 ºC), shake carefully and spin down again at 20 000 g for 5 min at 4 °C.

-Discard supernatant and remove remaining acetone at room temperature by evaporation.

-The samples can be stored at –80 °C or direc tly dissolved in appropriate buffers for protein separation (e.g. 2-DE).

2.2.3.3.2 2-D gel electrophoresis. Protein pellets were resuspended in sample buffer, and the suspension was shaken for 30 min. Prior to use the solution was centrifuged at 213 000 g for 30 min at 18 °C. For isoelectric focusing, 18 cm IPG-strips (pH 3.5-4.5, pH 4-5, GE Healthcare, Uppsala, Sweden; pH 3-6; Bio-Rad, Hercules, CA, USA) were used.

IPG-strips were rehydrated in 350 µL reswelling solution (7 M urea, 2 M thiourea, 4% CHAPS, 0.6% Pharmalytes 3-10, 20 mM DTT). The rehydrated IPG gel strips were blotted between two sheets of wet filter paper to remove excess reswelling solution in order to avoid the formation of urea crystals on the gel surface, held responsible for prolonged focusing time and "empty" vertical lanes in the silver-stained 2-D pattern. The rehydrated IPG gel strips were then positioned onto the cooling plate of the Multiphor II unit (GE Healthcare), with the acidic end of the IPG strips towards the anode. Up to 800 µg of protein were applied on application pieces (GE Healthcare) at the cathodic end of the IPG strips. For improved sample entry, low voltages were applied during the first hours. The following voltage profile was employed: linear increase from 0 to 150 V in 1 min; 150 V for 1h; linear increase from 150 to 300 V in 1 h; 300 V for 1 h; linear increase from 300 to 500 V in 1 h; 500 V for 4 h; linear increase from 500 to 3500 V in 5 h; 3500 V for 11 h. Current and power settings were limited to 0.05 mA and 0.2 W, respectively, per IPG gel strip and focusing temperature was 20 °C. The IPG strips were then equilibrated as decribed earlier [Gorg *et al.* 1995]. Since the focused proteins bind very strong to IPG gels, a long equilibration time to completely load all proteins with SDS is important to improve the protein transfer from the first to the second dimension. The IPG gel strips were equilibrated for 2× 15 min with gentle shaking in 2× 150 mL of equilibration solution. 1% (w/v) DTT was added to the first equilibration step, and 5% (w/v) iodoacetamide to the second to remove excess DTT, held responsible for "point streaking" in silver-stained gels [Gorg *et al.* 1988]. After the equilibration step, the IPG gel strips were slightly blotted on filter paper to remove superfluous equilibration buffer.

Electrophoresis in the second dimension was carried out on 9% to 16% (w/w) gradient polyacrylamide gels in a Protean II apparatus (Bio-Rad). The proteins were transferred onto the polyacrylamide gels by placing the equilibrated IPG gel strips onto the gels. Electrophoresis was performed with maximum setting of 700 V (35 mA and 30 W limiting). When the bromophenol blue front had reached the anodic end of the gels (after approximately 5 h), protein spots were visualised using a mass spectrometric compatible silver stain as described previously [Mortz *et al.* 2001] with minor modifications (see chapter 2.2.3.3.3).

2.2.3.3.3 Silver staining protocol for 2-D gels

-Fix the gel for 2×30 min in 50/5/45 MeOH/HOAc/H_2O_{dest} (v/v/v) and 3×20 min in 50/50 EtOH/H_2O_{dest} (v/v).

-Sensitize the gel by incubating for 1 min in 0.02/99.8 sodium thiosulfate/H_2O_{dest} (v/v).

-Rinse the gel with two changes of H_2O_{dest} for 1 minute each.

-Submerge the gel in 0.1/0.0375/99.9 silver nitrate/formaldehyde/H_2O_{dest} (v/v/v) and incubate for 20 minutes.

-Discard the silver nitrate solution and rinse the gel shortly with H_2O_{dest}.

-Develop the gel using 0.0005/0.025/6/94 sodium thiosulfate/formaldehyde/sodium carbonate/H_2O_{dest} (v/v/w/v) with intensive shaking.

-Terminate staining when the desired staining intensity is reached by discarding the developing solution, rinsing the gel shortly with two changes of H_2O_{dest} and replacing it with 5/95 HOAc/H_2O_{dest} (v/v).

-Store the gel in 1/99 HOAc/H_2O_{dest} (v/v) at 4 ºC.

2.2.3.3.4 Destaining protocol for silver stained 2-D gels

-Presoak the gel in H_2O_{dest} to remove any HOAc.

-Make the destaining solution (1:1 mixture of 30 mM potassium ferricyanide and 100 mM sodium thiosulfate, should be mixed immediately before use).

-Pick out the gel spots by spotpicking robot spotXress (Bruker Daltonics, Bremen, Germany).

-Place the gel piece in a tube and add enough of the destaining solution (~50 µL) to cover the gel pieces in the MicroAmp optical 96-well reaction plates (MultiScreen MAHV N4550, Millipore, Bedford, MA, USA).

-Vortex the samples on a microtiter plate shaker and monitor the stain intensity until the brown color disappears.

-Remove the destaining solution and wash the gel pieces with H_2O_{dest} (3×100 µL) by agitating on a shaker for 5 min each.

2.2.3.3.5 In-gel digestion protocol

-After the last wash, cover the gel pieces or bands with 50% (v/v) acetonitrile (ACN) and 50 mM ammonium bicarbonate (NH_4HCO_3) alternately for 15 min until complete destaining.

-If reduction/alkylation has not been performed, cover the gel pieces or bands with 10 mM DTT and reduce the proteins for 45 min at 56 ºC and subsequently with 100 mM iodoacetamide and alkylate the proteins at room temperature in the dark for 30 min.

-Repeat de- and rehydration steps by alternate application of 50% (v/v) ACN and 50 mM ammonium bicarbonate twice.

-Completely dry the gel pieces at ambient temperature in a vacuum centrifuge for several min after a last dehydration step.

-Prepare the trypsin reagent by adding 50 mM ammonium bicarbonate yielding a concentration of 4-12 ng trypsin/µL solution, depending on the amount of proteins. The trypsin used is a sequencing-grade enzyme that has been modified to inhibit autolysis and to minimize non-tryptic protease activities.

-Cover the gel pieces or bands with trypsin solution and and carry out the digestion overnight on a shaker at 37 °C.

-Extract the peptides produced by successive elution steps using H_2O_{dest}, 50% (v/v) ACN and 50% (v/v) ACN/0.1% (w/v) TFA after mixing for 20 min each. The supernatants are collected.

-Evaporate samples in a vacuum centrifuge at ambient temperature and dissolve in 5% formic acid prior to purification procedure.

2.2.3.3.6 Purification of samples.

-Desalt the peptide mixture solutions using bonded phase octadecyl (C18) self-prepared micro RP columns [Rappsilber *et al.* 2003] or extraction cartridges (C18-HD), respectively.

-Equilibrate each column or cartridge with isopropanol and subsequently with 5% (v/v) formic acid.

-Apply the peptide mixture dissolved in 5% (v/v) formic acid to the column or cartridge wash twice with 5% (v/v) formic acid.

-Elute with 80/15/5 methanol/water/formic acid (v/v/v), dry samples in a vacuum centrifuge and redissolve in 5% (v/v) formic acid prior to LC-MS/MS, or in 33% ACN/0.1% TFA prior to MALDI-TOF/TOF.

2.2.3.3.7 Application on MALDI targets. Mix 0.5 µL of each sample with the same amount of a saturated α-cyano-4-hydroxy-cinnamic acid (CHCA) in 40% ACN/0.1% TFA on a ground steel MALDI target by the use of Bruker`s MAP pipetting robot.

2.2.3.3.8 MALDI-TOF/TOF analysis. Mass-spectrometric analysis was performed on a 4700 Proteomics Analyzer (Applied Biosystems, Framingham, MA) equipped with a 355 nm Nd-YAG laser pulsed at 200 Hz. MS-spectra were acquired by accumulation of 2500 laser shots using the positive reflector mode with a deflection cut-off range of m/z 700. Subsequently, the MS-spectra were automatically analyzed by the Peakpicker software to detect and quantify isotopic peptide pairs and generate a list of precursor ions for MS/MS-analysis. The more intense MS-signal of an isotopically labeled peptide pair was selected for MS/MS-analysis. Precursor selection was achieved using a signal-to-noise threshold of 20 for peptide pairs and of 50 for single MS-peaks. Furthermore, the maximal number of precursors for a single MALDI spot was not allowed to exceed 40. A total of 1500 laser shots were acquired for each high-energy MALDI-TOF/TOF CID spectrum utilizing a collision energy of 1 keV and nitrogen as collision gas.

2.2.3.4 SILAC labeling, SDS-PAGE, nanoLC-Q-TOF and data analysis. For stable isotope labeling by amino acids in cell culture (SILAC) [Ong *et al.* 2002], cells preselected for exposure to heat shock were metabolically labeled by incorporation of ^{13}C6-leucine (Cambridge Isotope Laboratories (Andover, MA)) during growth in synthetic medium [Ong *et al.* 2003] (see chapter 2.1.5). After the heat shock (2 h at 60 ºC) they were combined with unlabeled (40 ºC; ^{12}C6-leucine) cells and subsequently lysed. Protein precipitation (see chapter 2.2.3.3.1), tricine-SDS-PAGE (see chapter 2.2.3.4.1), tryptic digestion (see chapter 2.2.3.3.4) of proteins from 15 gel slices, nanoLC-MS/MS on a ESI Q-TOF Ultima mass spectrometer (Waters, Milford, MA) (see chapter 2.2.2.4) and protein identification (see chapter 2.2.2.5) have been performed as described previously [Konstantinidis *et al.* 2007] (Fig. 16).

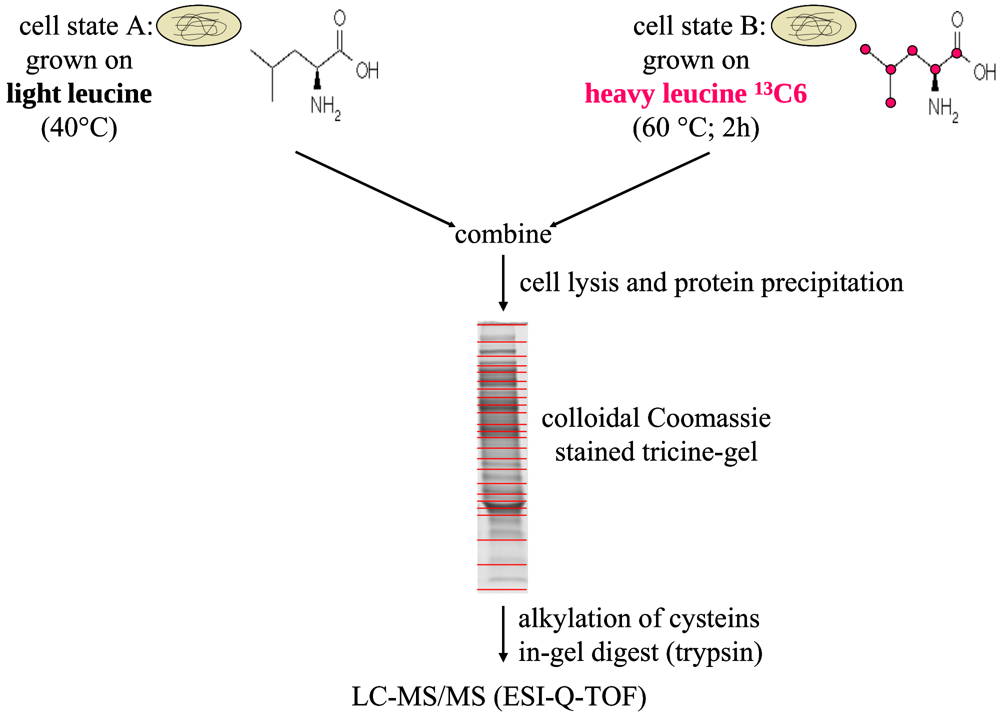


Figure 16. Workflow for protein quantitation using SILAC labeling. The cells were combined directly after heat shock and before cell lysis. The in vivo labeled proteins of two different cell states were combined and separated by tricine-SDS-PAGE. The colloidal Coomassie stained gel was segmented into 15 slices and proteins in each slice alkylated and in-gel digested with trypsin. The resulting peptides were separated by LC using a RP-C_{18} column and subjected to online MS/MS analysis on an ESI-Q/TOF. The mass difference between labeled and unlabeled leucine (^{12}C and ^{13}C) is 6.02 Da.

Labeled and unlabeled peptide pairs were identified using Mascot [Perkins *et al.* 1999], validated by PeptideProphet [Keller *et al.* 2002], their ratios relatively quantified and normalized using ASAPRatio [Li *et al.* 2003], and proteins inferred by ProteinProphet [Nesvizhskii *et al.* 2003] software programs (Trans-Proteomic Pipeline; TPP v2.9 GALE rev.3). Peptides and proteins were considered identified when probability scores were higher than 0.85 or upon manual validation. All chromatograms have been validated manually and inaccurately assigned peptide pairs differing in elution profile were corrected by readjusting the peak or time span selection if feasible, incorrect baseline settings were readjusted and peptide chromatograms overlapped by peaks of contaminants discarded. Data are available from three biological replicates.

2.2.3.4.1 Tricine-SDS-PAGE. Approximately 100 µg protein were applied after resuspension in tricine sample buffer and denaturation for 30 min at 40ºC onto a *49.5% T, 3% C* separation gel (11 cm long and 1.5 mm thick) for SDS PAGE according to Schaegger. On each gel also 5 µL of a protein marker (precision plus protein standards, Bio-Rad Laboratories, Munich, Germany) were applied and electrophoresis was carried out at a maximum of 40 mA/gel and 300 V limit setting.
After fixation in 50/10/40 MeOH/HOAc/ H_2O_{dest} (v/v/v) protein staining was done with CBB (0.025% (w/v) CBB-G250 dissolved in 10/90 HOAc/ H_2O_{dest} (v/v)) and destained in 10/90 HOAc/ H_2O_{dest} (v/v).

2.2.4 Transcriptomic methods in *Halobacterium salinarum* after heat shock

2.2.4.1 RNA isolation. Total RNA was isolated from cells, grown under standard growth conditions (40 ºC) (see chapter 2.2.1), as well as from cells exposed to heat shock (60 ºC) at different time points, by using a standard guanidinium thiocyanate/phenol extraction according to the supplier's instructions for the peqGold RNAPure extraction solution (Peqlab Biotechnology, Erlangen, Germany). After centrifugation of 35 mL cell culture at 5000 g for 5 min at 4 °C the pellet was resuspended in 5 mL RNAPure. 0.2 mL chloroform were added per 1 mL of the homogenate, mixed and incubated for 5 minutes at RT. After centrifugation at 12 000 g for 15 min at RT the colorless upper aqueous phase was transferred in a fresh tube for RNA isolation (the lower organic phase and the interphase contained the DNA and proteins). 1mL of isopropanol per 1mL RNAPure were added, mixed, incubated for 15 min at 4 °C and centrifuged for 15 min at 12 000 g (4 °C). The RNA precipitate was washed twice with 70% $EtOH_{DEPC}$ (8 min at 7500 g and 4 °C). Excess ethanol was removed by air-drying for 5-10 min, and the RNA pellet resuspended in 100 µL H_2O_{DEPC}.

2.2.4.2 DNase treatment, PCR and quality assessment of RNA. Total RNA was treated with 1/10 volume RNAse-free DNase RQ1 (Madison, WI, USA) in 1× RQ1 DNase reaction buffer. After incubation of 45 min at 37 °C, 1/10 volume of stop solution (20mM EGTA, pH 8.0) was added and exposed to 65 °C for 10 min. Absence of DNA was checked by standard PCR using a gradient thermal cycler peltier PT-200 (MJ Research). Amplification was carried out with a final concentration of 200 μM dNTP's, 1.5 μM of the respective primerpairs, 0.7 volume total RNA solution as template and 1.25 units Taq DNA-polymerase (New England BioLabs, Ipswich, MA, USA) in 50 μL 1× ThermoPol reaction buffer. The temperature profile was as follows:

step 1	94 °C	2 min	
step 2	94 °C	30 s	37 cycles
step 3	59 °C	30 s	
step 4	72 °C	30 s	
step 5	72 °C	3 min	
step 6	4 °C	∞	

The quality of the DNA-free total RNA was assessed by capillary electrophoresis using the Bioanalyzer 2100 (Agilent Technologies, Waldbronn, Germany) in association with the RNA6000 Nano LabChip kit (Agilent) according to the supplier's instructions. The criterion for determination of the RNA quality was the integrity of the 16S- and 32S rRNA. Samples were screened for DNA contamination by gelelectrophoretic analyses.

2.2.4.3 Quantitation of nucleic acids. Concentrations of nucleic acids were either assessed by agarose gelelectrophoresis against a marker with known concentration or by use of spectrophotometry. An extinction coefficient of 1 at a weavelength of 260 nm corresponds to 50 μg/mL double-stranded DNA, 33 μg/mL single-stranded DNA or 40 μg/ml RNA, respectively [Sambrook *et al.* 1989]. The relation A260/A280 gives information about the quality of nucleic acid preparations and should be >2 for RNA or >1.8 for DNA.

2.2.4.4 Agarose gelelectrophoresis

2.2.4.4.1 Screening for DNA. Electrophoresis was carried out at 100 V and room temperature in 1× TBE buffer, using 2% agarose gels containing 15 µL of an EtBr solution (10mg/mL). DNA samples and the GeneRuler 1kb DNA Ladder were dissolved in 1× DNA loading buffer and denatured for 5 min at 95 °C before application. For detection of the DNA-fragments, the gel documentation system TFPM / WL (Vilber Lourmat, Marne-la-Vallée, France) was used.

2.2.4.4.2 Separation of RNA. Separation of RNA (10 – 15 µg) before Northern blot hybridization was performed by electrophoresis using 1.2% agarose gels containing 20 mM of the denaturans guanidine thiocyanate and 15 µL of an EtBr solution (10mg/mL). Electrophoresis was carried out at 80 V and room temperature in 1× TBE buffer. Approximately 4 µg of RNA and the DIG-labeled RNA molecular weight marker III, were dissolved in 1× RNA loading buffer and denatured for 5 min at 70 °C before application. All electrophoresis equipment was incubated with 0.1 N NaOH, 1% SDS to destroy RNAses and washed with 2× autoclaved H_2O_{dest}. For detection of the RNA-fragments, the gel documentation system TFPM / WL was used.

2.2.4.5 RTqPCR. Cells grown in complex medium were subjected to heat shock (60 ºC), and the RNA isolated at different time points compared to RNA isolated from cells not exposed to elevated temperatures. Quantitative real-time PCR was performed as previously described [Wende and Oesterhelt 2007].

2 µg total RNA, 2.5 µM random hexamer primer (Promega, Mannheim, Germany) and 0.5 mM dNTPs were incubated 5 min at 65 ºC in a volume of 12 µL, and after 1 min on ice reverse transcribed in a total volume of 20 µL 1× first strand buffer (Invitrogen, Karlsruhe, Germany) with 10 units SuperScript III reverse transcriptase (Invitrogen, Karlsruhe, Germany), 40 units RNaseOUT recombinant RNase inhibitor and 5 mM DTT by incubation of 50 min at 42 ºC and subsequently 15 min at 70 ºC, to produce cDNA templates.

Real-time PCR was performed in a GeneAmp 5700 Sequence Detection System (Applied Biosystems, Darmstadt, Germany) by adding ½ volume SYBR Green PCR Master Mix Kit (Applied Biosystems) to the cDNAs and the selected primers in a total volume of 25 µL. Primers, applied in a final concentration of 0.2 µM, are listed in chapter 2.1.4, and were selected by the use of the „Primer Express“ software (product length ≈ 100bp; Tm ≈ 59-60 °C; primer length >20 bp). The specificity of the primers was inspected before by gelelectrophoretic analyses of their products when applied to genomic DNA. The temperature profile was as follows:

step 1	50 °C	2 min	
step 1	95 °C	10 min	
step 2	95 °C	15 s	40 cycles
step 3	59 °C	1 min	
step 4	4 °C	∞	

Analysis was performed with the GeneAmp 5700 software. Transcript level differences were calculated by a relative quantification approach using the constitutively expressed *16S-rRNA* gene as an internal standard gene [Freeman *et al.* 1999]. For data calculation the mean of three replicate reactions per primer pair was used.

2.2.4.6 Northern blot hybridization. Cells grown in complex medium were subjected to heat shock (60 °C), and the RNA isolated at different time points compared to RNA isolated from cells not exposed to elevated temperatures. Electrophoresis and northern blot hybridization were done as previously described [Tarasov *et al.* 2000] with some modifications. Briefly, total RNA was separated by electrophoresis on 1.2% TBE-Gels containing 20 mM guanidine thiocyanate as described in chapter 2.2.4.4.2. An RNA III digoxigenin labeled marker (Roche Diagnostics) was used as a standard.

RNAs were transferred to Hybond N+ nylon membranes by alkaline downward blotting [Chomczynski 1992]. Therefore the agarose gels were equilibrated 10 min in 50 mM NaOH, 1× SSC and subsequently twice for 15 min in 20× SSC before blotting the RNA from the gel by capillary transfer overnight at room temperature with 20× SSC. Efficiency of the transfer was controlled by EtBr staining of the membrane. The RNA was fixed to the membrane by UV-crosslink (2× 30 sec at 1200× 100µJ).

Amplification of the DNA probes was carried out using a gradient thermal cycler peltier PT-200 (MJ Research) applying a final concentration of 1× DIG DNA Labeling Mix, 3 µM of the respective primerpairs, 0.01 volume genomic DNA solution as template and 1.25 units Taq DNA-polymerase (New England BioLabs) in 50 µL 1× ThermoPol reaction buffer. Primers used for generation of probes are given in chapter 2.1.4. The temperature profile was as follows:

step 1	94 °C	4 min	
step 2	94 °C	30 s	30 cycles
step 3	61-68 °C	30 s	
step 4	72 °C	70 s	
step 5	72 °C	5 min	
step 6	4 °C	∞	

Hybridization and chemiluminescence detection were carried out by use of PCR-generated DIG-dUTP labeled DNA probes according to the supplier’s instructions provided in the “DIG system user’s guide for filter hybridization” (Boehringer, Mannheim, Germany). Briefly, DNA probes were heat-denatured for 5 min at 95 ºC and kept on ice for 5 min before dilution in DIG Easy Hyb prehybridization solution (Boehringer, Mannheim, Germany). The blotted RNAs on the Hybond N+ nylon membranes were also diluted in 20 mL DIG Easy Hyb prehybridization solution for 1 h at 50 ºC. For overnight hybridization at 50 ºC, the prehybridization solution was discarded and replaced by hybridization solution containing the respective DIG-labeled DNA probe. The membranes were finally washed twice, 15 min per wash, in 2× wash solution at room temperature and twice, 15 min per wash, in 0.5 wash solution at 50 ºC. All hybridization and washing steps has been performed by spinning in a flask.

Chemiluminescent detection of the hybridized DNA was performed by the DIG Luminescent Detection Kit using CSPD. The membrane was first equilibrated 1 min in washing buffer, followed by gently agitating for 60 min in blocking solution. Anti-Digoxigenin-alkaline phosphatase (AP) Fab-fragments were diluted 1:10 000 in blocking solution and used for a 30 min incubation of the membran to bind the DIG-labeled DNA-probes, before washing twice, 15 min per wash, in washing buffer. The wet membrane was finally equilibrated for 2 min in detection buffer containing CSPD (1:100), and sealed in a plastic bag. Different exposure times to X-ray films have been conducted for optimal detection of the chemiluminiscent signal.

2.2.4.7 Whole genome DNA microarrays. Cells, grown in either complex or synthetic medium, respectively, were subjected to heat shock (1 h at 60 ºC) and compared to cells not exposed to elevated temperatures. Microarray design and microarray analysis was carried out as previously described [Twellmeyer *et al.* 2007; Wende and Oesterhelt 2007]. Briefly, for the manufacture of the DNA microarrays, DNA probes for 2774 open reading frames (see http://www.halolex.mpg.de) of the *Hbt. salinarum* strain R1 genome were amplified by PCR and all PCR products quality checked by agarose gel electrophoresis and by sequencing of a randomly selected subset of 20%. Five replicate spots of each gene probe were spotted onto γ-amino-silane coated CMT-GAPS-II glass slides (Corning, Schipol-Rijk, Netherlands) using a Virtek ChipWriter Pro system (Bio-Rad Laboratories, Munich, Germany) [Twellmeyer *et al.* 2007].

For cDNA synthesis, 5 µg DNA-free total RNA of the respective cell state was reverse transcribed (90 min, 42°C) into either Cy5- or Cy3-labeled cDNA using the CyScribe First-Strand cDNA Synthesis Kit (GE Healthcare, Freiburg, Germany), with enclosed random nonamer primers and Cy3- and Cy5-dUTP (GE Healthcare, Freiburg, Germany) following the manufacturers instructions. The synthesis was catalyzed by CyScript reverse transcriptase, introducing the Cy3- and Cy5-dUTPs in the cDNAs. For primer annealing, 1 µL of the random nonamer pimer mix was added to the total RNA in a volume of 11 µL, and 5 min incubated at 70ºC. After cooling to room temperature 4 µL 5x CyScript buffer, 2 µL 0.1 M DTT, 1 µL dUTP-nucleotide mix, 1 µL Cy3-/Cy5-dUTPs and 1 µL CyScript reverse transcriptase were added and incubated for 90 min at 42 ºC. Each biological condition was labeled once by Cy3 and once by Cy5 (dye switch) for each experiment. After cDNA synthesis the reaction was stopped by addition of 0.05 M EDTA and the RNA template alkalically hydrolized with 0.2 M NaOH (30min incubation at 65°C). After neutralization (0.3 M Tris/HCl, pH 7.5) the two cell states were combined and the cDNA purified from excessive Cy3-/Cy5-nucleotides, RNA fragments and primers by adding 1 µL yeast-tRNA (4mg/mL) in 420 µL TE-buffer and concentrating the volume to 17 µL using MicroCon Ym-30 ultracentrifuge columns (Milipore, Bedford, MA, USA).

Hybridization was performed as described elsewhere [Zaigler *et al.* 2003]. Briefly, the microarrays were prehybridized for 30 min at 50 ºC in 30 mL prewarmed PH-buffer in a rotating flask, washed for 30 s at room temperature in each H_2O_{dest} and isopropanol, and dried by a 5 min centrifugation step at 600 g in 50 mL centrifuge tubes.

For hybridization, the Cy5- and Cy3-labeled cDNAs were mixed with hybridization buffer (final concentrations: 2.5× SSC, 2× Denhardts reagent, 30 mL final volume) and denatured for 2 min at 98 ºC, applied to the microarrays after cooling to room temperature and addition of 2 µL 1% SDS, and covered with a Hybrislip HS (Sigma-Aldrich, Taufkirchen, Germany). Hybridization of the cDNA was carried out over night at 64 ºC in sealed hybridization chambers (Corning, Schipol-Rijk, NE).

The microarray slides were washed four times to remove un- or not specifically bound cDNA and thus minimizing the background noise in the regions not imprinted by probes. The Hybrislip HS coverslips were removed in wash-solution I, the microarrays rinsed twice for 5 min in each wash-solution I and wash- solution II, and finally dried by centrifugation for 5 min at 600 g in 50 mL centrifuge tubes. Since exposition to light leads to a loss of the signal intensity by bleaching of the fluorescent dyes, the microarray slides were kept in object slide boxes until they were scanned for the Cy5 and Cy3 fluorescence signals using a GenePix 4000B microarray scanner (Axon Instruments, Union City, CA, USA). The images were processed with Gene Pix Pro 6 (Axon Instruments) allowing manual validation of the spots. The fluorescence values of all DNA probes derived from the microarrays were collected in a text file and the data statistically analyzed using the MAANOVA package in the R environment (http://www.r-project.org). Data processing included local background substraction [Yang *et al.* 2001] and pin-wise median normalization [Quackenbush 2002] of the fluorescence ratios, resulting in a median of 1 referring to all probes spotted by the same pin. The R/MAANOVA package (version 0.97-4) provides a complete work flow for microarray data analysis. "Mixed effect ANOVA" models are implemented to estimate variance components and to perform F- and t-tests for differential expressions. The application of formal hypothesis testing provides p-values. These p-values from tests of differential expression summarize the statistical significance of the applied test statistic, based on the variation in gene expression and the error variance. [Twellmeyer *et al.* 2007] For each microarray approach (e.g. heat shock in complex medium or in synthetic medium, respectively) two biological replicates were analyzed, with switching the Cy-dyes for each of the replicates, resulting in data acquisition from four independently analyzed hybridization procedures.

3 Results and Discussion

3.1 Genome-wide proteomics of *Natronomonas pharaonis*

3.1.1 Preparation of proteins. Two different sample preparations, termed “water lysis” and “native lysis”, have been performed in order to achieve maximal identification of soluble proteins and protein complexes.

In the first approach cells were disrupted by osmotic shock, replacing the high molar salt concentration of the growth medium with pure water followed by sonication (“water lysis”). Proteins were collected by acetone precipitation prior to SDS-PAGE (Fig. 12) and MS/MS analysis. The benefit of this method is that all membranes pellet upon ultracentrifugation due to the lower density of water ($\rho = 1.0$ g/cm^3) in comparison to that of membranes ($\rho = 1.05 - 1.18$ g/cm^3) [Klein *et al.* 2005] ensuring a pure cytosolic solution in the supernatant. The drawback is the loss of some soluble proteins, which may become hydrophobic due to denaturation in H_2O, stick to membranes and pellet upon ultracentrifugation.

In the second approach disruption has been made just by sonication retaining high salt molarity (“native lysis”) to allow prefractionation of native protein complexes by SEC (Fig. 11). Fractionated proteins were collected by TCA precipitation, and subjected to SDS-PAGE (Fig. 13) and MS/MS analysis. Here, small membrane vesicles do not pellet by ultracentrifugation due to the high density of the basal salt solution ($\rho \sim 1.13$ g/cm^3). Accordingly a number of integral membrane proteins were identified in the native sample.

3.1.2 Protein inventory of the cytosol. The combination of 1-D SDS-PAGE with nanoLC-MS/MS, performed in both approaches, resulted in the identification of altogether 929 proteins from *Natronomonas pharaonis* (Table I). The vast majority of these, 886, are soluble proteins representing 41% of the theoretical soluble proteome. This is a conservative estimate as we applied stringent search parameters (requesting a 99.95% confidence level). The remaining 43 proteins with predicted transmembrane domains make up less than 5% of the identification and were identified primarily after native lysis. The complete list of identified proteins is provided in Supplemental Table I.

Table I. Number of proteins identified in *Nmn. pharaonis*. The data are given for the two individual experiments as well as the overall data (column "both approaches"). Proteins that lack a predicted transmembrane domain are classified as soluble, more than 90% of these being cytosolic. Only few of the identified proteins are probably extracellular as they carry an export signal. Membrane-associated proteins having an N-terminal lipid anchor were identified mainly upon native lysis. About 5% of the remaining identified soluble proteins are hydrophobic as indicated by a positive GRAVY index.

	both approaches	water lysis	native lysis
total proteins	**929**	698	705
total soluble	**886**	695	662
extracellular	10	2	9
hydrophobic	43	34	34
membrane-associated	40	8	38
transmembrane	**43**	3	43

The classification of the cytosolic proteins by function is shown in Fig. 17. More than 60% of the proteins involved in metabolism (MET) could be identified, thus covering most of the intermediary metabolism. A similar high identification level was reached for proteins involved in genetic information processing (GIP) and for soluble subunits of transport complexes (TP_CP). In contrast, only 15% of the hypothetical proteins and 25% of the conserved hypothetical proteins could be identified. This may indicate persisting errors in gene assignment. Alternatively, these function classes may contain proteins with low expression levels thus having an increased tendency to escape proteomic identification.

The lower identification rates for proteins involved in environmental information processing (ENV, 46%) could be due to their dependence on environmental conditions and thus a subset of the proteins may not be expressed under the applied growth conditions. This functional superclass is also expected to host proteins of low abundance like proteins involved in signal transduction.

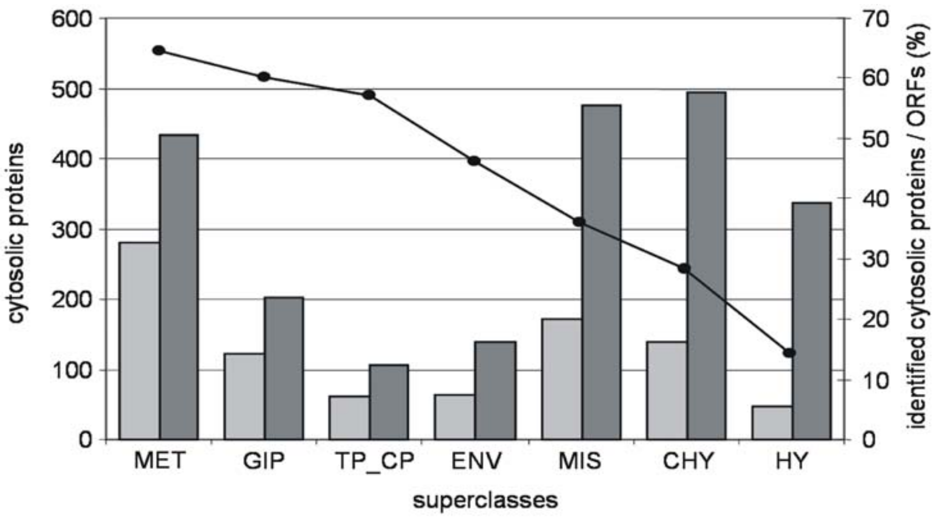


Figure 17. Classification of cytosolic proteins into 7 function superclasses. Columns represent identified cytosolic proteins (light grey) and all non-transmembrane domain proteins from the theoretical proteome (dark grey) (total number, left axis). The percentage of identified proteins for each superclass is also shown (●—●, right axis). Abbreviations for superclasses: MET: metabolism; GIP: genetic information processing; TP_CP: transport and cellular processes; ENV: environmental information processing; MIS: miscellaneous; CHY: conserved hypothetical protein; HY: hypothetical protein.

The improved identification rate of proteins from *Nmn. pharaonis* with a higher codon adaptation index (CAI), which reflects non-random usage of synonymous codons [Sharp and Li 1987], is displayed in Fig. 18. Proteins with a CAI higher than 0.8 could be identified to 60%, while only about 10% of those with a CAI lower than 0.7 were found. The median CAI for the theoretical proteome of *Nmn. pharaonis* is 0.736. Thus, a higher codon adaptation index indicates higher protein abundance which results in preferential identification. A similar correlation has been reported for several species [Sharp and Li 1987]. Proteins involved in genetic information processing and metabolism for which a high proportion has been identified, are likely to be abundant. Correspondingly they have a high average CAI (above 0.76) that exceeds that of the proteins in the other function superclasses with lower identification rates (Fig. 19).

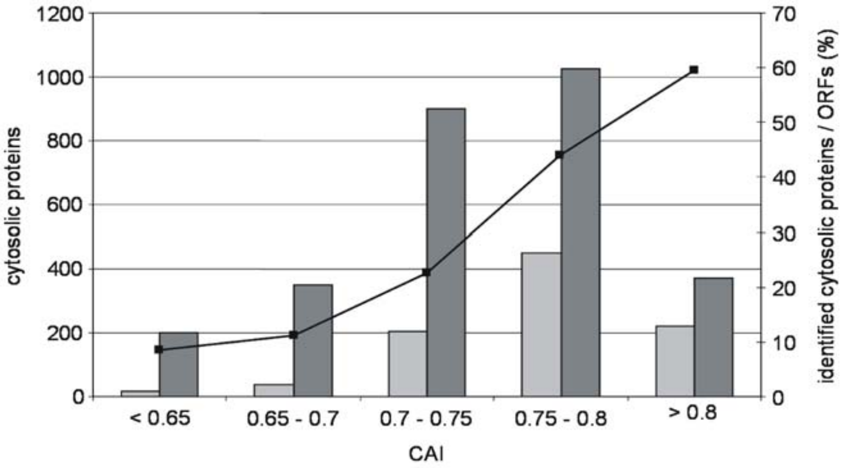


Figure 18. Classification of cytosolic proteins by codon adaptation index (CAI). Columns represent total numbers (left axis) of identified cyotosolic proteins (light grey) and all non-transmembrane domain proteins from the theoretical proteome (dark grey). The percentage of identified proteins (■—■, right axis) is increasing as the CAI increases.

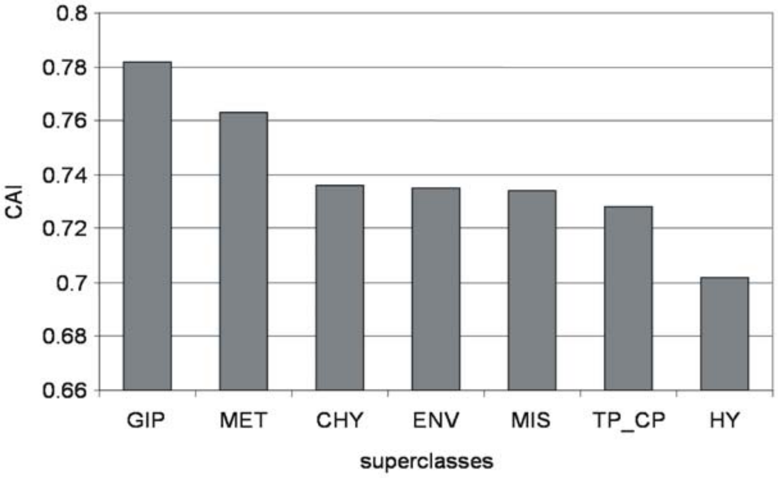


Figure 19. Average CAI values for proteins of different function superclasses. Abbreviations for superclasses: GIP: genetic information processing; MET: metabolism; CHY: conserved hypothetical protein; ENV: environmental information processing; MIS: miscellaneous; TP_CP: transport and cellular processes; HY: hypothetical protein.

3.1.3 Prefractionation by SEC and identification of protein complexes. In the native lysis approach, proteins were fractionated by size using a Superose 6 column and eight fractions (I-VIII) were collected (Fig. 11). The eight SEC fractions were analyzed by

SDS-PAGE, which confirmed that fractions I and VIII are devoid of protein. Fraction VII contains very few proteins as evident from the SDS-PAGE, consistent with the spectroscopic characteristics (comparison of the optical densities at 260 and 280 nm [Warburg and Christian 1942]). As expected, earlier fractions contain larger proteins than later fractions (Fig. 13) but there is a large overlap in protein sizes as SEC is performed under native and SDS-PAGE under denaturing conditions.

Protein identification by nanoLC-MS/MS revealed a similar number of proteins throughout the SEC-fractions II-VI (Fig. 20). The number of proteins identified for each fraction (about 250) is much lower than without prefractionation (about 700). This shows that protein identification is not limited by the capacity of the used mass spectrometer. As expected, only few proteins could be identified in fraction VII having a low protein content. Fig. 21 reveals that most of the proteins occur in only a single SEC fraction or in two adjacent fractions (618 proteins, 88%). Fractions II and III probably contain residual membrane patches as they contained all except 6 integral and membrane-associated proteins identified.

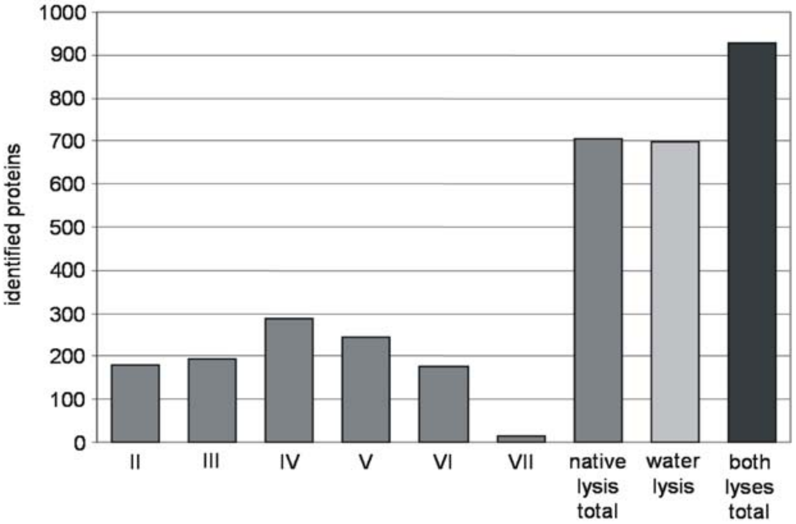


Figure 20. Protein identifications for individual SEC fractions after native lysis (II-VII; dark grey) and total identification for native lysis (dark grey), water lysis (light grey), as well as for both approaches (black).

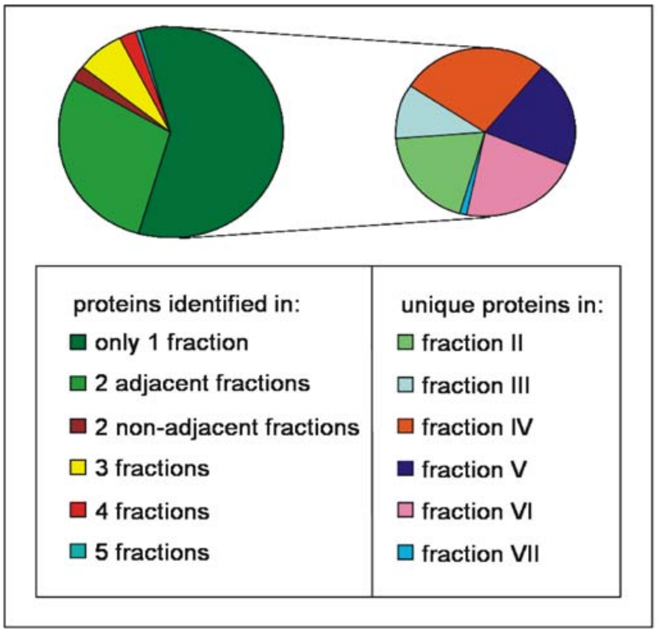


Figure 21. Distribution of identified proteins in different SEC fractions. Left: the majority of the proteins (80%, 618 of 705) is found in only 1 fraction or 2 adjacent fractions. Right: the proteins identified in only one fraction (59%, 415 of 705) are quite evenly distributed over fractions II-VI.

Protein complexes are expected to stay at least partially intact under native SEC. Several subunits from large protein complexes have been identified in our study: (a) RNA polymerase (subunits A', A", B', B", D and N), (b) the thermosome (subunits 1, 2 and 3) and (c) the proteasome (α- and β- subunits as well as the proteasome-activating nucleotidases 1 and 2). We concentrated on fraction IV as fractions II and III seem to contain membrane patches, and thus protein complex formation, co-localization in a membrane patch and unspecific membrane attachment cannot be distinguished. According to our calibration, fraction IV corresponds to 300-630 kDa (Fig. 13), while the identified subunits range in size from 7.3 to 118 kDa and thus are too small to be expected in this fraction IV unless being part of a complex. Five of the six RNA polymerase subunits have been found in fraction IV as well as three of the four proteasome and two of the three thermosome subunits (Fig. 22). This strongly indicates that this fraction contains native protein complexes.

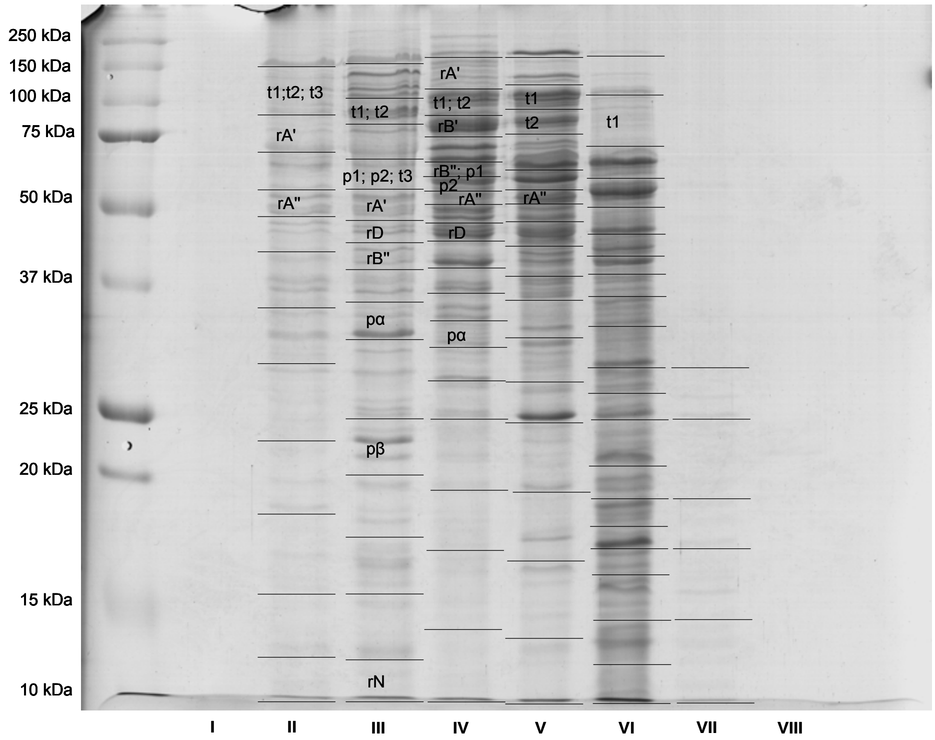


Figure 22. SDS-PAGE of the protein preparation of *Nmn. pharaonis* after native lysis in 3.4 M NaCl. Proteins, prefractionated by SEC to eight fractions (I-VIII), were applied to a SDS-PAGE, and the resulting lanes were cut into a total of 93 slices. The gel shows the distribution of the subunits of three protein complexes through the gel slices. Explanations for the abbreviations used:

rA':	DNA-directed RNA polymerase subunit A'
rA'':	DNA-directed RNA polymerase subunit A''
rB':	DNA-directed RNA polymerase subunit B'
rB'':	DNA-directed RNA polymerase subunit B''
rD:	DNA-directed RNA polymerase subunit D
rN:	DNA-directed RNA polymerase subunit N
t1:	thermosome subunit 1
t2:	thermosome subunit 2
t3:	thermosome subunit 3
p1:	proteasome-activating nucleotidase 1
p2:	proteasome-activating nucleotidase 2
pα:	proteasome alpha subunit
pβ:	proteasome beta subunit

One goal of the native separation by SEC was to reduce the complexity of the sample applied to LC-MS/MS with the expectation of an increased number of protein identifications. However, the total number of identified proteins in this experiment is similar to the sample without prefractionation (Table I, Fig. 20). Up to 300 proteins were identified for each SEC fraction while almost 700 proteins could be identified from a single 1-D gel lane without prefractionation. This proves the high efficiency of the nanoLC-MS/MS approach and excludes instrumental capacity problems. However, about one third of the proteins from each experiment have not been identified by the other approach. This could be due to proteins randomly escaping detection but could also be caused by differences in cell lysis and sample preparation. For example, integral membrane proteins are nearly exclusively found in the native sample.

Although prefractionation did not result in an increased number of identified proteins, it permitted to increase the reliability of the identification. Proteins identified in both experiments were compared concerning the MASCOT score and the number of identified peptides per protein. Both, average score and sequence coverage were higher with prefractionation. The MASCOT score increased on average by 32.5 and the number of identified peptides increased by 0.7. This can be attributed to the reduced complexity of the samples and the higher amount of gel slices measured after prefractionation.

3.1.4 Genetic flexibility of halophilic archaea illustrated by the set of identified proteins. Proteins from *Natronomonas pharaonis* identified in this study were analyzed with respect to specific biological functions with an emphasis on gene conservation and variability within the branch of halophilic archaea, represented by the completely sequenced *Halobacterium salinarum* strain R1[1] (www.halolex.mpg.de), which is very closely related to *Halobacterium* strain NRC-1 [Ng *et al.* 2000]), *Haloarcula marismortui* [Baliga *et al.* 2004b] and *Haloquadratum walsbyi* [Bolhuis *et al.* 2006] (Fig. 1).

For several gene clusters, a high proportion of the encoded proteins have been identified in our proteomic survey of *Nmn. pharaonis*. Examples are gene clusters involved in amino acid and coenzyme biosynthesis, which contribute to the nutritional self-sufficiency of this archaeon.

Arginine biosynthesis: Seven of the nine gene products from an arginine biosynthesis gene cluster were identified. The equivalent clusters occur in *Haloarcula* and *Haloquadratum* with highly conserved gene order. *Halobacterium* contains only two genes involved in the conversion of ornithine to arginine. The latter can be used as energy source by fermenting it to ornithine via the arginine deiminase pathway [Ruepp and Soppa 1996], which does not occur in the other three halophiles. Additional metabolic flexibility with respect to arginine utilization has been described [Falb *et al.* 2005; Falb *et al.* 2008].

Biotin biosynthesis and fatty acid degradation: A gene cluster (Fig. 23) with 12 of 15 gene products identified encodes enzymes involved in biotin biosynthesis (NP4230A-NP4236A) and fatty acid degradation (NP4240A-NP4256A), including the two subunits of a biotin-containing acyl-CoA carboxylase (NP4250A, NP4252A). A highly homologous gene cluster involved in biotin biosynthesis is present on chromosome I of *Haloarcula* (the NP4230A homolog at 763649-764260 has not been annotated). Homologs are encoded neither in *Halobacterium* nor in *Haloquadratum* but in many bacteria. Most of the genes involved in fatty acid degradation have *Haloarcula* homologs clustered on chromosome II. While no homologs for the fatty acid degradation enzymes are found in *Haloquadratum*, *Halobacterium* has some homologs spread throughout the genome. Besides the biotin-dependent carboxylase of *Natronomonas*, the cluster contains three of 12 acyl-CoA synthase homologs (10 identified), one of 13 enoyl-CoA hydratase homologs (7 identified), and one of 12 acyl-CoA dehydrogenase homologs (11 identified). Consistent with the high number of expressed fatty acid degradation enzymes, we could show that *Natronomonas* grows as efficiently on fatty acids as on acetate (L. Koenigsmaier, unpublished observations).

Cobalamin biosynthesis and CO_2 fixation: All halophiles contain several enzymes that are dependent on cobalamin and a large gene cluster in *Natronomonas* (NP1088A-NP1124A, 19 genes) codes for 14 proteins involved in cobalamin biosynthesis (10 of these identified). Genes from this cluster are completely conserved in *Halobacterium*, *Haloarcula* and *Haloquadratum*. Also conserved are the subunits of cobalamin dependent methylmalonyl-CoA mutase (A subunits NP1226A, NP2320A identified) which produce the citric acid cycle intermediate succinyl-CoA from methlymalonyl-CoA. The latter is synthesized from propionate and CO_2 and thus allows CO_2 fixation [Danon and Caplan 1977; Oren 1983]. Another enzyme that is likely to be involved in CO_2 fixation and has been identified in our proteomic survey is ribulose-bisphosphate carboxylase (NP2770A) which occurs in *Natronomonas* but not in any of the other halophiles. The enzyme is highly homologous to that from *Methanococcus* where it was shown to be catalytically active [Finn and Tabita 2004]. In archaea, ribulose-1,5-bisphosphate is generated by oxidation of ribose-1,5-bisphosphate [Finn and Tabita 2004] and the corresponding dehydrogenase is found in all haloarchaea and has been identified (NP5174A). The existence of this additional potential pathway for CO_2 fixation in *Natronomonas* may be explained by the high concentration of carbonates in its natural environment.

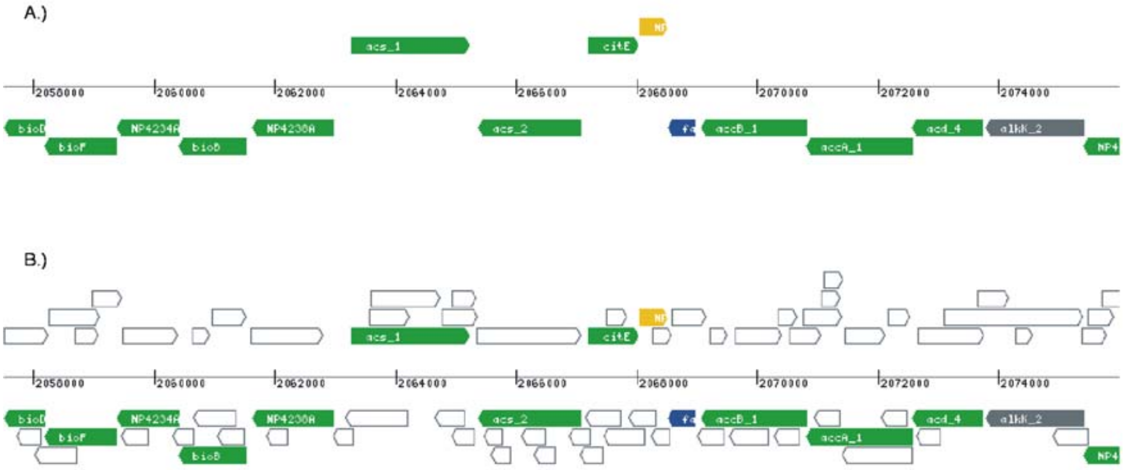


Figure 23. A gene cluster involved in biotin biosynthesis and fatty acid degradation. (A) Only protein-coding genes are shown (filled arrows). (B) All open reading frames are shown, including those that result in spurious ORFs (open arrows). The genome positions (in kbp) are indicated. Arrows pointing right indicate ORFs on the forward strand, those pointing left indicate ORFs on the reverse strand. The colors indicate the level of proteomic identification (based on data from this study and additional data from our group). Green indicates reliable identification (99.9995% confidence level), blue normal identification (99.95% confidence level), grey and yellow indicate not identified.

Ribonucleotide reductase: Another cobalamin-dependent enzyme is the typical haloarchaeal ribonucleotide reductase, which converts ribonucleotides to 2'-deoxyribonucleotides providing the precursors needed for both synthesis and repair of DNA. This type II enzyme is highly conserved (75% sequence identity) and consists only of an alpha-type chain (NP3346A). However, we could not only identify this ribonucleotide reductase but also an additional enzyme consisting of alpha and beta chains (NP6168A and NP6166A, respectively). A second ribonucleotide reductase was also found in *Halobacterium* (classified as type Ia [Borovok *et al.* 2002], consisting of alpha and beta chains) but the additional enzymes from *Halobacterium* and *Natronomonas* are only very distantly related (25% sequence identity). The other two haloarchaea, *Haloarcula* and *Haloquadratum*, do not have an additional ribonucleotide reductase. The second *Natronomonas* enzyme, which is encoded on plasmid PL131, is closely related to an enzyme from *Salinibacter ruber* (70% sequence identity), for which substantial lateral gene transfer to and from haloarchaea has been described [Mongodin *et al.* 2005]. However, the closest homolog for this enzyme is from the haloarchaeal phage AAJ-2005 with 80% sequence identity.

Phage remnants: Consequently, we searched for other proteins with high homology to phage proteins and identified a probable restriction/modification protein (NP3112A, 1258 amino acid residues) with 54% sequence identity to proteins from haloarchaeal phages HF1 and HF2. In order to identify potential phage remnants, we compared all proteins from these three phages against the theoretical *Natronomonas* proteome (using blastP) as well as the genome (using tblastN). Only few phage protein homologs were detected in *Nmn. pharaonis* and all were more closely related to proteins from other halophiles. This excludes phage remnants and thus gene transfer from phages into the *Natronomonas* genome is unlikely for the proteins with suspiciously high homology to phage proteins.

General aspects: In our proteomic analysis, we identified 34% of the chromosomal proteins, 12% of the proteins from PL131 but only 1 of the 36 proteins encoded by PL23 [Falb *et al.* 2005]. However, we identified 4 of the 11 proteins encoded on the 13 kb GC-low region II which is inserted into the chromosomal copy of PL23. One of these (NP3254A) belongs to a small gene family (10 genes) that is distantly related to a protein from *Halobacterium* phage phiH proposed to function as repressor [Ken and Hackett

1991]. The other 3 belong to a long transcription unit (7 genes, NP3262A to NP3274A) which does not occur in other halophiles. However, a highly conserved gene cluster with nearly identical gene order exists in the archaeon *Methanospirillum hungatei*. More distant homologs, also clustered but with different gene order, occur in *Anabaena variabilis*. GC-low region III includes a number of remarkably long proteins, of which five (958-1999 amino acid residues long) have been identified in our proteomic analysis. Three of these proteins (helicase NP3872A, restriction/modification enzyme NP3874A, and helicase NP3876A) are likely to be translated as a transcription unit. Homologous genes with 30% sequence identity are clustered (but with altered gene order) in several bacteria, including *Magnetococcus* and *Deinococcus*. A highly homologous transcription unit with 60-80% sequence identity at the protein level and conserved gene order is found in *Haloquadratum* while *Haloarcula* and *Halobacterium* have no or only distant homologs. In *Natronomonas,* this transcription unit is followed by an ADP-ribosylglycohydrolase homolog (NP3878A) that occurs in many bacteria but not in halophiles. The largest protein in this region (NP3886A, 1999 amino acid residues) is specific for *Natronomonas* as no database homologs could be identified. In conclusion, relatively high proteomic identification ratios have been found for several GC-low regions. This contrasts results from *Halobacterium* where a reduction in GC content correlates with decreased proteomic identification rates [Tebbe *et al.* 2005].

The extreme diversity with respect to metabolic enzymes between halophiles and the occasional extraordinary sequence conservation to proteins from unrelated species is a drastic example for the well-known fact that prokaryotic genomes represent a melting pot for DNA of diverse origin [Doolittle 2005] to an extent that is hard to reconcile with the classical view of vertical inheritance within independent species.

3.1.5 Largely overlapping alternative open reading frames are not used in the GC-rich haloarchaeal genomes. Commonly, neighbouring genes in bacteria and archaea overlap for a few bases, allowing translational coupling [Falb *et al.* 2005; Fukuda *et al.* 2003; Rogozin *et al.* 2002]. Such overlapping genes should be distinguished from usage of alternative and largely overlapping open reading frames so that more than one protein is produced from the same genomic sequence stretch. This phenomenon has been termed "overprinting" [Keese and Gibbs 1992] and is well known for viruses and phages but has been observed in bacteria only in exceptional cases. We searched for protein identification from alternate overlapping reading frames in our proteomic data set in order to find evidences for the eventual occurrence of overprinting in archaea.

Fig. 23 displays the gene cluster involved in biotin biosynthesis and fatty acid degradation (see above). In panel A, only genes considered to code for real proteins are displayed. Panel B also contains the alternative open reading frames which show large-scale overlaps with the protein-coding genes but which we assume to not code for proteins (spurious ORFs) [Falb *et al.* 2005].

In addition to the 15 protein-coding genes, of which 13 have been identified (12 in this study), there are 61 spurious ORFs. Such a high number of spurious ORFs is seen throughout the genome. On average, 3.2 spurious ORFs are found for each protein-containing gene (Table II). In *Natronomonas*, the average protein length is 290 amino acid residues (86% of the proteins longer than 100 codons) while the average length of the spurious ORFs is 173 amino acid residues (99% of the spurious ORFs longer than 100 codons). In all of our proteomic experiments on *Natronomonas* (this report and B. Bisle *et al.*, manuscript in preparation) 1226 proteins were identified under high stringency ("normal" identification, 99.95% confidence), representing 42.9% of the theoretical proteome. Of these, 84% were "reliably" identified (99.9995% confidence). Only 3 spurious ORFs are classified as identified, none of these "reliably". These 3 represent 0.03% of the set of spurious ORFs, which is consistent with the expected false positive rate of 0.05% at the applied 99.95% confidence level for "normal" identification. All three high-scoring spurious ORFs were rated to be false positives upon manual inspection of the MS/MS spectra. Thus, we conclude that not a single case of overprinting could be identified despite the very high incidence of potential alternative and largely overlapping open reading frames in the genome of *Natronomonas*. Reducing the confidence level to 99.5% would increase protein identifications by 114 but would also severely increase doubtful identifications (29 spurious ORFs, representing 0.3% of the spurious ORF set).

The same conclusion is reached for *Halobacterium salinarum* where 70.3% of the theoretical proteome has been identified (1992 of 2831) [Pfeiffer *et al.* 2008a]. For more details see Table II.

The published proteomic data as well as the *Natronomonas pharaonis* genome are accessible through HaloLex (www.halolex.mpg.de).

Table II: Protein identification in *Hbt. salinarum* and *Nmn. pharaonis* in comparison to spurious ORFs. Displayed are the theoretical proteomes of the two organisms, the average lengths of the proteins (in amino acids, “aa”), the percentage of the ORFs coding for proteins which are longer than 100 amino acids, the “normal” (>99.95% confidence) and the “reliable” (>99.9995% confidence) protein identifications as well as proteins with Mascot scores that would be identified (confidence of at least 99.5%) but are excluded (“questionable”) due to our stringent data interpretation (requiring 99.95% confidence).

				identified proteins		
Hbt. salinarum	theoretical proteome (rate of spurious per real ORFs)	average length (aa)	% of ORFs longer than 100 aa	"normal" and "reliable"	"reliable"	questionable
real ORFs	2831	278	84.5	1911	1735	246
spurious ORFs	6511 (2.3)	204	96.0	81	4	860
all ORFs	9342	227	92.5	1992	1739	1106

				identified proteins		
Nmn. pharaonis	theoretical proteome (rate of spurious per real ORFs)	average length (aa)	% of ORFs longer than 100 aa	"normal“ and "reliable"	"reliable"	questionable
real ORFs	2848	290	86.4	1223	1028	114
spurious ORFs	9029 (3.2)	173	99.6	3	0	29
all ORFs	11877	201	96.5	1226	1028	143

3.2 Quantitative analyses of heat shock response in *Halobacterium salinarum*

3.2.1 Experiments and parameter settings. For identification of genes regulated after exposure to elevated temperatures, different approaches have been performed. Changes in protein expression have been elucidated by two different, complementary proteomic analyses (complex *vs.* synthetic medium approach; see chapter 3.2.1.1) to broaden the spectrum of identifications (Fig. 24). Genes coding for regulatory and heat shock proteins that exhibited significant or unexpected regulation factors on the protein level have been selected to investigate their transcriptional profile over a certain time period, employing both RTqPCR and Northern blot hybridization (Fig. 24). The exposure time causing the largest transcriptional regulatory effects has been applied for investigating genome-wide transcriptional regulation by whole genome DNA microarrays (Fig. 24). We mainly focused on genes exhibiting a substantial upregulation and thus on genes with a potential vital function for the survival of the cells under the applied stress conditions. An overview of regulation factors of all relevant genes discussed in this thesis is listed in Table III.

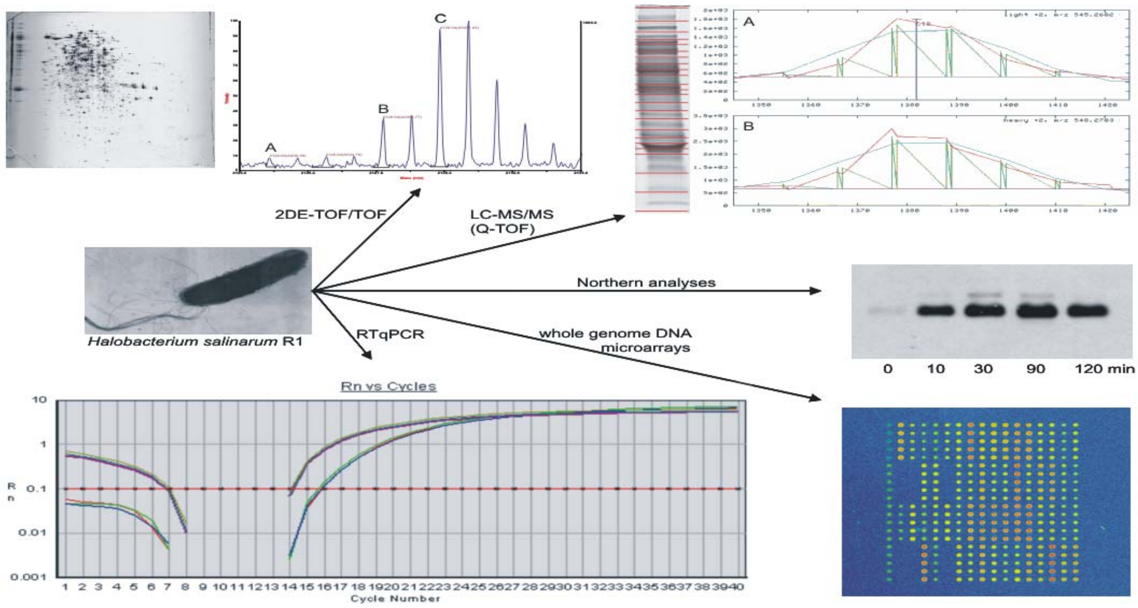


Figure 24. Experimental approaches to study protein and mRNA expression in the halophilic archaeon *Halobacterium salinarum* strain R1 in response to heat shock. Results obtained by two different proteomics approaches were substantiated on the mRNA level by whole genome DNA microarrays, RTqPCR and Northern analysis.

Table III (next page)**.** An overview of the regulation factors of all significantly regulated genes. Regulations of protein (proteomics approaches in complex and synthetic medium after 2 h of heat shock) and mRNA levels (whole genome DNA microarrays of *Hbt. salinarum* wildtyp in complex and synthetic medium, RTqPCR and Northern blots after 1 h of heat shock) are listed. Regulation factors of the different proteomics experiments (Exp) are given in separate columns. Significant regulation factors are highlighted in bold and coloured, induction in green, repression in red.

ID	protein name	proteomics (2h)					microarrays		RTq	Nor-
		complex		synthetic			comp	synt	PCR	thern
		Exp1	Exp2	Exp1	Exp2	Exp3	(1h)	(1h)	(1h)	(½h)
chaperones and chaperonins										
OE4122R	thermosome alpha subunit	2.76	1.91	1.41	1.52	1.25	5.24	7.72		
OE3925R	thermosome beta subunit	2.38	1.90	1.56	1.85	1.59	4.56	9.09		
OE5083R	heat shock protein homolog hsp5		> 10		3.23	4.00	6.46	3.18		> 10
OE5082R	AAA-type ATPase				2.38	1.79	1.32	1.87		
OE3112R	AAA-type ATPase	2.05		2.08	2.56	1.45	1.68	3.64		
OE3114R	hypothetical protein						2.23	5.23		
dnaK-operon										
OE1736R	chaperone dnaJ						1.18	1.45		
OE1737R	dnaK-type molecular chaperone hsp70		1.04	1.12	1.19	1.08	1.18	1.09	-7.1	~ -5
OE1742R	dnaJ/dnaK ATPase stimulator grpE			1.15	1.30	1.11	1.04	-1.02	-78.8	
transcription initiation factors										
OE4056R	transcription initiation factor tfbA						1.00		2.8	
OE2084R	transcription initiation factor tfbB				3.23	3.45	2.16	2.18	6.2	> 10
OE6026R	transcription initiation factor tfbC						1.14	1.31	-10.2	
OE2281R	transcription initiation factor tfbD						1.30			
OE6071R	transcription initiation factor tfbE						1.09	-1.02	-1.5	
OE1478R	transcription initiation factor tfbF			-1.36	-1.49		1.68	1.86	-71.5	
OE1399R	transcription initiation factor tfbG			-1.01	-1.03	-2.03	1.06	1.19	-2.8	
OE6140R	transcription initiation factor tfbH						1.01			
transcription regulators										
OE2046F	cons. hypot. prot. (prob. transkr. reg.)						1.36	3.47		
OE1797R	transcription regulator sirR						1.66	2.05		
OE3589F	cons. hypot. prot. (phr homologon)						1.00	1.23		
arginine metabolism										
OE5208R	arginine deiminase		1.31	1.11	1.14	-1.04	1.57	2.10		
OE3955F	probable proline dehydrogenase			1.41	1.47	1.43	-1.02	-1.12		
OE3168R	acetylornithine transaminase homolog	1.33	1.52	1.35	1.33	1.19	-1.03			
pyrimidine synthesis										
OE3554F	carbamoyl phosphate synth. (large sub.)			2.50	2.56	2.17	1.06			
OE3556R	carbamoyl phosphate synth. (small sub.)					2.27	1.01	1.04		
OE1672F	orotate phosphorybosyltransferase homol.		1.40	1.67	1.59	1.30	-1.17	1.01		
TCA-cycle										
OE3195F	succinate-CoA ligase (beta subunit)		2.13	1.01	1.00	1.03	1.03	1.12		
OE3196F	succinate-CoA ligase (alpha subunit)		1.97	-1.04	-1.01	1.01	1.05	-1.08		
OE4323F	malate dehydrogenase	1.61		1.10	1.12	1.22	1.01	-1.16		
OE1711R	oxoglutarate-ferredoxin oxidored. α subun.	1.66				1.64	1.03	1.02		
OE1710R	oxoglutarate-ferredoxin oxidored. β subun.	1.46		1.35		1.39	-1.09	1.06		
OE2623R	pyruvate-ferredoxin oxidored. α subunit	1.67	1.48	-1.01	-1.01	1.11	-1.12	-1.20		
OE2622R	pyruvate-ferredoxin oxidored. β subunit	1.28	1.39	1.02	1.15	1.12	-1.06	-1.16		
OE1721R	methylmalonyl-CoA mutase 1A					1.39	1.06	1.02		
miscellaneous										
OE4427R	dps-like ferritin		1.50	1.30	1.67	1.67	2.30	2.09		
OE3467R	deoxyribodipyrimidine photo-lyase				1.59		-1.02	1.04		
OE2397F	flagellin B1 precursor				-2.80	-7.49	-1.90	-1.72		
OE2398F	flagellin B2 precursor				-2.84	-7.07	-1.65	-1.53		
OE2399F	flagellin B3 precursor						-1.81	-1.69		
OE2469F	flagellin A1 precursor						-1.72	-1.71		
OE2470F	flagellin A2 precursor				-3.71	-8.01	-1.72	-1.76		
OE3949R	glutaredoxin homolog						1.53	2.73		
OE4759F	cell surface glycoprotein precursor			1.06	1.09	1.22	-2.95	-2.24		
OE5114R	gas-vesicle operon protein gvpK2						1.69	1.54		
OE7033R	gas-vesicle operon prot. gvpD1 (repressor)							-1.72		
OE1275F	proteasome alpha subunit	1.67	1.35	1.16	1.54	1.20	-1.08	1.32		
OE2296F	proteasome beta subunit	1.35	1.23	1.56	1.85	1.59	1.13	1.57		

Relatively few quantitative DNA microarray analyses [Baliga *et al.* 2004a; Zaigler *et al.* 2003], proteomic analyses [Bisle *et al.* 2006; Tebbe *et al.* 2007], as well as integrated quantitative microarray and proteomic surveys [Baliga *et al.* 2002] have been reported for halophilic archaea, with only two investigating heat shock, both in *Hbt*. NRC-1 [Coker and DasSarma 2007b; Shukla 2006]. In these experiments, cells were exposed to 49 ºC either for 8 h and protein levels analyzed by comparing silver stained 2-D gels [Shukla 2006], or for 1 h for subsequent microarray analyses [Coker and DasSarma 2007b]. Exceeding a temperature of 56 ºC was reported to be lethal for the halobacterial strain NRC-1 [Coker and DasSarma 2007b; Shukla 2006]. In contrast to these findings, this work could prove by comparison of growth curves and viable count that cell lysis does not occur when *Hbt. salinarum* strain R1 is exposed to 60 ºC (Fig. 25).

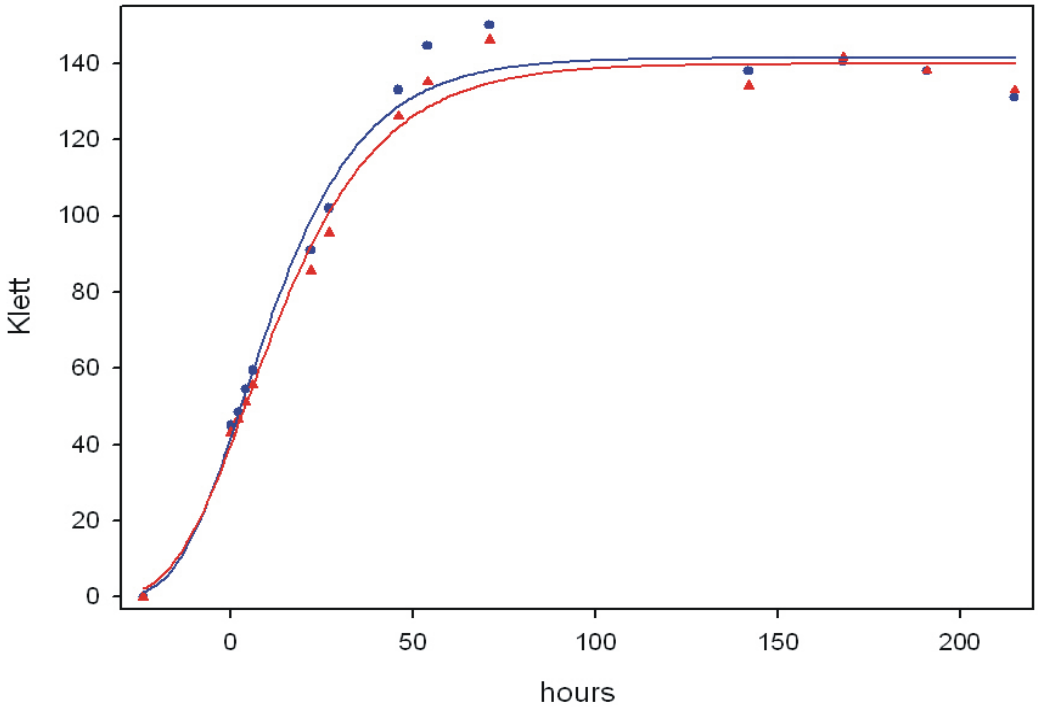


Figure 25. Growth curves of *Hbt. salinarum* strain R1, determined under identical conditions of aeration and preparation of the inoculum (for growth conditions see chapter 2.2.1). The blue line reflects growth rates for cells constantly kept at 40 ºC, the red line for cells exposed from 40 ºC to 60 ºC at the time point zero (x-axis). The y-axis indicates the growth density.

Furthermore, temperature course analysis in *Hfx. volcanii*, that exhibits similar temperature optima and maxima like *Hbt. salinarum*, revealed maximal induction of *cct*-mRNAs [Kuo *et al.* 1997] and heat shock proteins [Daniels *et al.* 1984] at 60 ºC. Induction of cct-proteins did not increase any higher after an exposure time of 2 h at 60 ºC, as determined by Western blotting [Large *et al.* 2002].

In this work, the same parameters (2 h; 60 ºC) were finally chosen for maximal heat shock induction of proteins in *Hbt. salinarum* R1. In addition, Northern analysis demonstrated that exposure to 60 °C induced an expeditious and intense heat shock response in *Hbt. salinarum* R1, as visible in the rapid mRNA induction (10 min) of *hsp5* and *tfbB* (Fig. 30). Time scale experiments performed by both Northern analysis and RTqPCR revealed that as a rule, regulation rates were maximal after approximately 1 h (Fig. 30; Table IV), whereas protein expression after 2 h was slightly more pronounced than after 1 h (Supplemental Table D_manual).

3.2.1.1 Proteome analysis. Protein levels were determined by mass spectrometric analyses. Cells grown in complex medium were exposed to 60 ºC for 1 h or 2 h, respectively, proteins isotopically labeled by ICPL, separated by 2-DE, and tryptic peptides measured by MS/MS on a MALDI-TOF/TOF (Fig. 15; Fig. 26). Due to higher regulation factors we focused on results obtained after 2 h and cells grown in synthetic medium were exposed to 60 ºC for 2 h only. Here, proteins were isotopically labeled in vivo by incorporation of labeled amino acids (SILAC), separated by SDS-PAGE, and tryptic peptides measured by LC-MS/MS on an ESI Q-TOF (Fig. 16; Fig. 26).

A regulation factor of at least ±1.4 or more was considered to indicate significant regulation, yielding only 16 (Supplemental Table D_manual; complex medium approach) or 26 (Supplemental Tables C_regul; synthetic medium approach) significantly upregulated proteins, respectively. All significant regulations have been validaded manually. In previous publications, in which the same ICPL labeling, MS analysis and data processing methods were applied, the cut-off was set to ±1.3 [Bisle *et al.* 2006] or even to ±1.2 [Sarioglu *et al.* 2006]. The relative high cut-off was chosen to restrict the focus on the few most prominent regulation factors only, making sure that a substantial protein regulation is given. Previous quantitative approaches in *Hbt. salinarum* have demonstrated that the regulative response of cells to different living conditions is comparably low [Bisle *et al.* 2006; Tebbe *et al.* 2007]. The reason for the weak response could be the harsh and frequently occurring environmental changes, which may have supplied the cells with a large pool of constitutively expressed molecular chaperones and other proteins important for rapid adaptation.

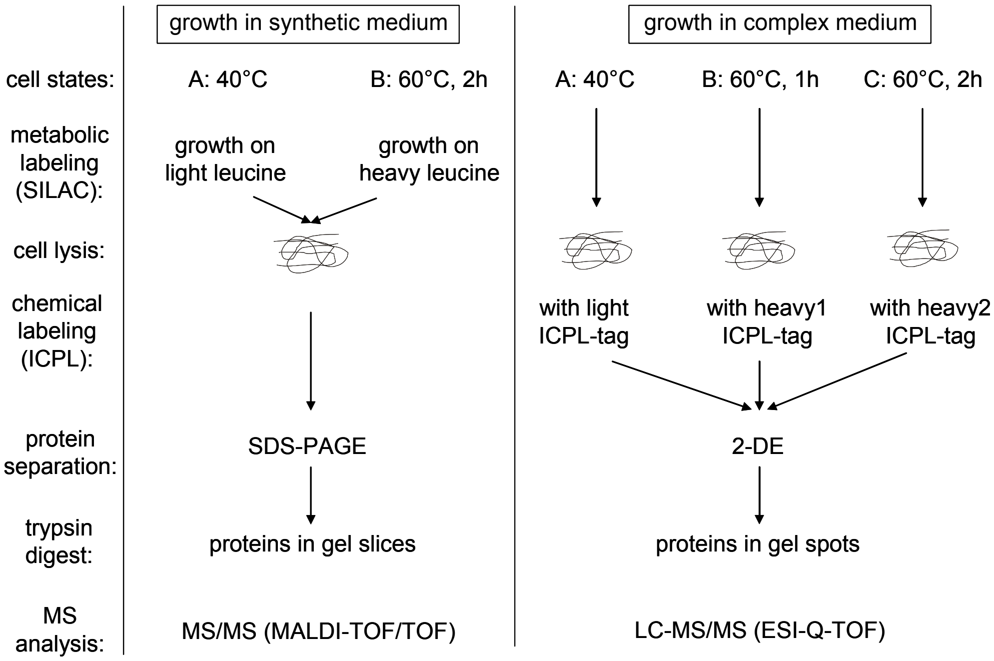


Figure 26. Workflow of the two proteomics approaches. Cells grown in complex medium were exposed to 60 ºC for 1 h or 2 h, respectively, proteins isotopically labeled by ICPL, separated by 2-DE, and tryptic peptides measured by MS/MS on a MALDI-TOF/TOF. Cells grown in synthetic medium were exposed to 60 ºC for 2 h, proteins isotopically labeled in vivo by incorporation of labeled amino acids (SILAC), separated by SDS-PAGE, and tryptic peptides measured by LC-MS/MS on an ESI Q-TOF.

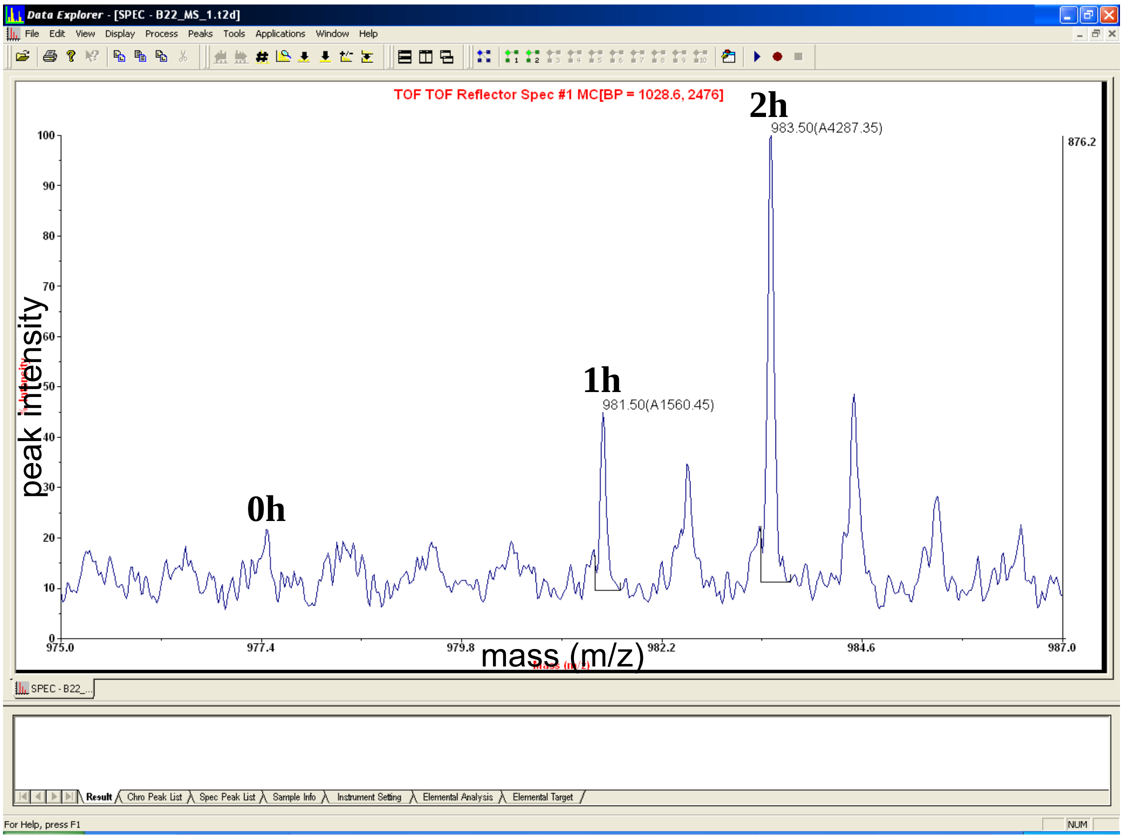


Figure 27. Mass spectrum of the multiplex labeled peptide GKQIEVQA of the heat shock protein homolog hsp5 as determined by MALDI-TOF/TOF. The differentially labeled peaks indicate either no heat shock exposure (0h) or exposure to heat for 1h or 2h, respectively.
Here, the low abundant peak (0h) does not exceed the noise of the mass spectrum due to the relatively low peak intensity. Thus, determination of the level of a regulation factor is always a question of peptide concentration in the sample when applying relative quantification techniques.

At very high ratios in the proteomics approaches, the low abundant peak of a peptide pair or a triplet in case of multiplex labelling, may disappear in the noise of the mass spectrum so that it appears as a singlet, or as a pair, respectively (Fig. 27). Thus, at low peptide concentrations in the sample the ratio is not quantified accurately, but has to be considered as maximally regulated. A regulation factor of 10 was chosen as cut-off value for peptides considered maximally regulated, as applied in the case of hsp5 (Fig 27; complex medium; Supplemental Table D_manual). The whole set of regulation information is given in Supplemental Tables C, D and D2.

It is important to mention that lack of identification by a proteomic method cannot be put on the same level with a potential lack of regulation. Only proteins with a relatively high expression rate can be visualized and picked from the 2-D gels (complex medium; ICPL), or selected after LC-MS by the Q-TOF for MS/MS (synthetic medium). In addition, small proteins are highly underrepresented in proteomics experiments as described by Klein *et al.* [Klein *et al.* 2007]. Further limitations in protein identification for the complex medium-approach were the restricted pH-range (pH 3-6), the precipitation of membrane proteins in 2-DE [Klein *et al.* 2005], and the low abundance of the labeled, lysine-containing tryptic peptides (isotope-coded protein label "ICPL") in *Hbt. salinarum*, being in the detectable mass range of the spectrometer. In contrast, the labeled leucine-containing tryptic peptides (stable isotope labeling by amino acids in cell culture "SILAC") were more abundant in the synthetic medium-approach. This approach is also more beneficial in terms of reliability of generated data, since chemical modification steps for protein labeling could be avoided (in vivo label by incorporation of amino acids). Furthermore, proteins of the two different cell states could be combined before cell lysis, hence diminishing potential protein losses of one of the two cell states during the working up procedure.

3.2.1.2 RTqPCR and Northern blot hybridization. Transcript levels of genes encoding for members of the *dnaK* operon and for transcription initiation factors (*tfb*s) were analyzed by RTqPCR after exposure to 60 ºC for different time periods. The *tfb* genes were selected for transcriptional examination because a high upregulation of tfbB was seen by proteomic approaches, and because of the failure to identify five of the eight TFB proteins. The lack of protein induction of the dnaK operon also led to a transcriptional survey of its genes, to endorse the proteomics findings.

The effects of heat shock on transcription regulation for *tfbB* and *dnaK* were confirmed by Northern blotting. Exposure times were similar to the ones chosen for RTqPCR. Additionally, transcript levels of the heat shock protein homolog *hsp5* were analyzed by Northern blotting. For most genes, maximum regulation was reached after 60 min as determined by RTqPCR. Both approaches were performed with cells grown in complex medium.

3.2.1.3 Transcriptome analysis. The time point showing the highest level of transcriptional regulation by RTqPCR and Northern analysis was chosen to investigate genome wide effects of exposure to elevated temperatures. Thus whole genome DNA microarray analyses on cells, grown in both complex and synthetic medium, have been performed after exposure to heat for 60 min, to additionally investigate a potential impact of nutrients supply. Genes were considered to be significantly upregulated when showing an average regulation factor of at least 1.5 (Supplemental Tables A_regul) or 1.85 (Supplemental Tables B_regul) depending on the background signal. The borders were chosen with respect to the distribution of the regulation factors shown in figures 28 and 29, considering only the outliers as significantly regulated. Thereby only about 20 (Fig. 28; Supplemental Tables A_regul, complex medium; Fig. 29; Supplemental Tables B_regul, synthetic medium) upregulated genes were obtained out of more than 2000 genes. For statistical evaluation a *p*-value of $<10^{-2}$ was chosen. The *p*-value represents the order of evidences for differential expression. In previous microarray analyses, genes were also reported as regulated when exceeding a factor of 1.5 leading to 64 genes regarded as upregulated, even though multiple times genes with a regulation factor of only 1.4 were also referred to as regulated in the discussion [Coker and DasSarma 2007b]. The maximal set of genes we found is included in Supplemental Tables A and B.

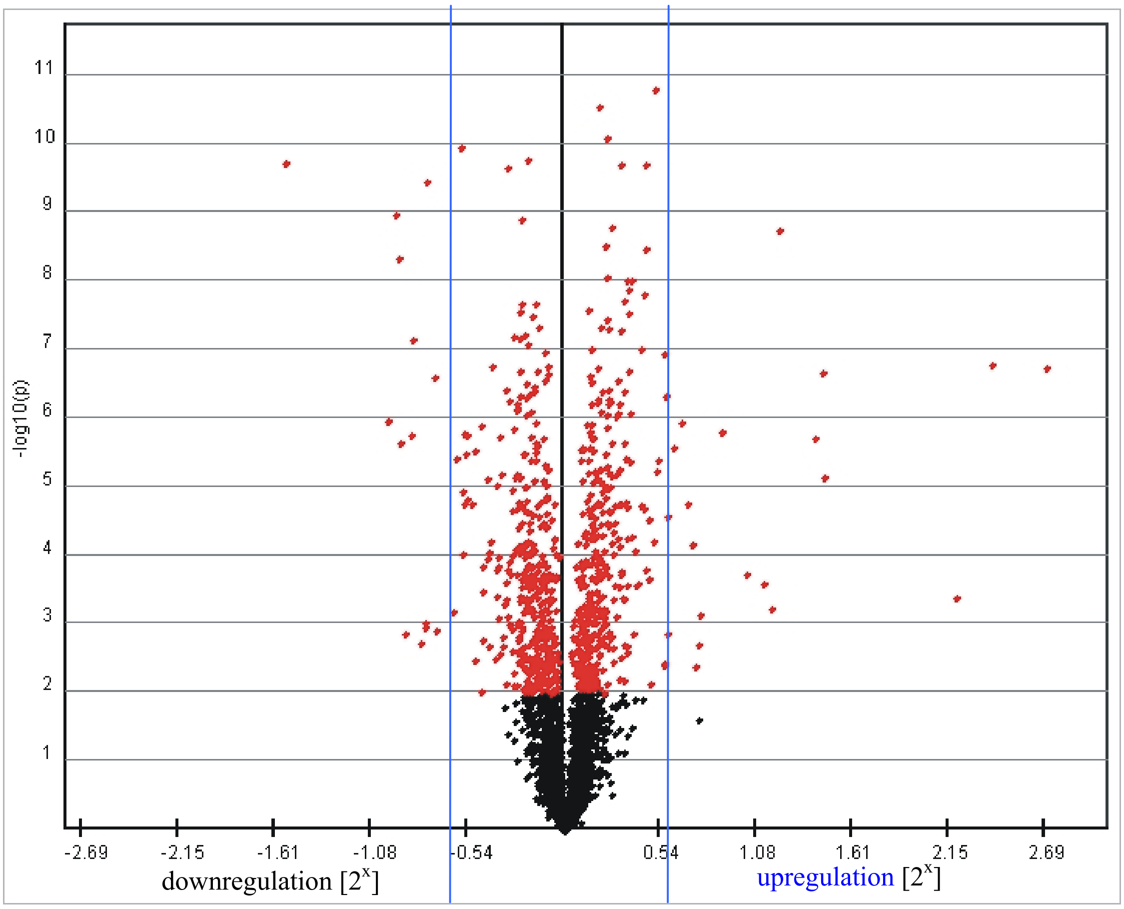


Figure 28. Scatter plot of the mean expression values of the regulation factors derived from the four replicate array formats after whole genome DNA microarray analyses on cells grown in complex medium. Numbers on the x-axis reflect the exponent factors [2^x] of up- (positive numbers, right side) and downregulated (negative numbers, left side) genes, and are plotted against the average *p*-values of the log ratios of the respective genes. Genes with a *p*-value of <10^{-2} are illustrated by black dots; genes with a *p*-value of >10^{-2} are illustrated by red dots. Identification of outlier genes with significant changes in expression level has been performed on a visual basis with cutoffs set to >1.5-fold induction and repression ($2^{\pm 0.59}$), as indicated by the blue vertical lines.

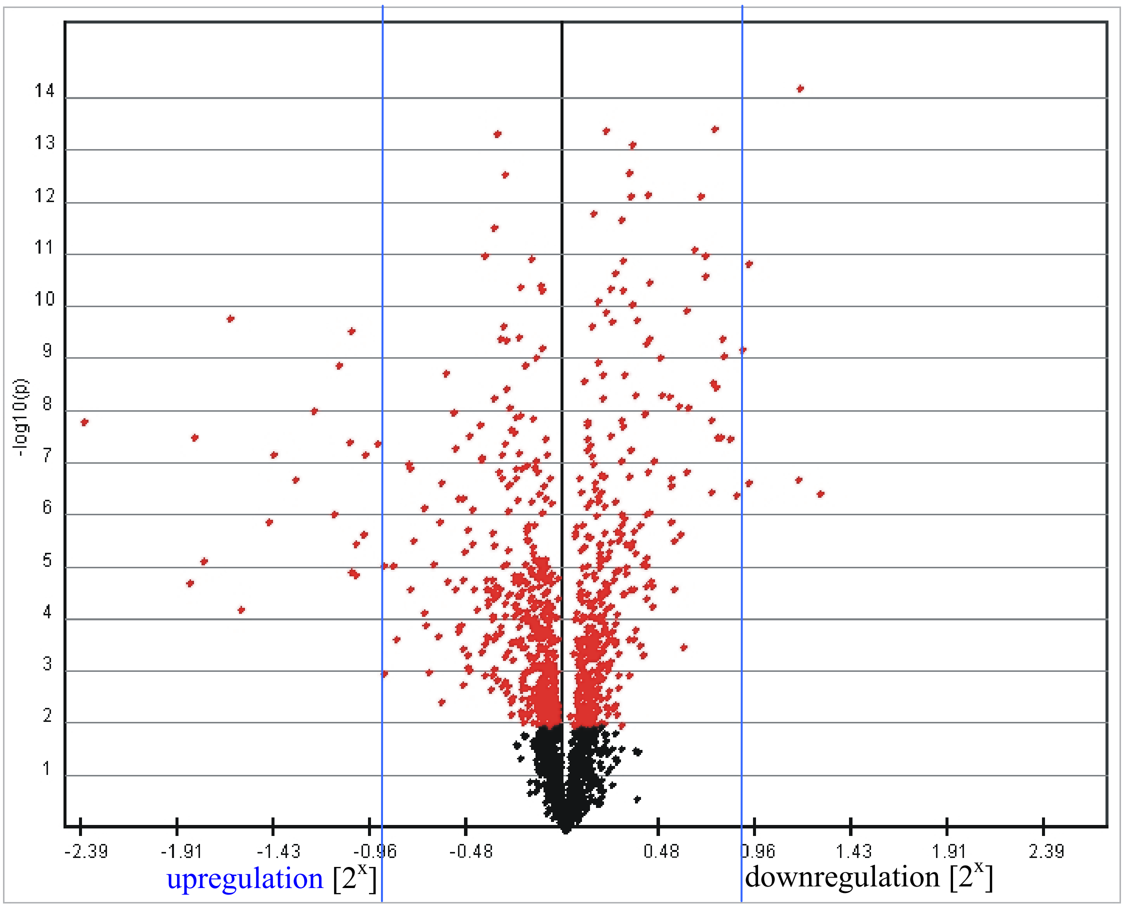


Figure 29. Scatter plot of the mean expression values of the regulation factors derived from the four replicate array formats after whole genome DNA microarray analyses on cells grown in synthetic medium. Numbers on the x-axis reflect the exponent factors [2^x] of up- (negative numbers, left side) and downregulated (positive numbers, right side) genes, and are plotted against the average *p*-values of the log ratios of the respective genes. Genes with a *p*-value of $<10^{-2}$ are illustrated by black dots; genes with a *p*-value of $>10^{-2}$ are illustrated by red dots. Identification of outlier genes with significant changes in expression level has been performed on a visual basis with cutoffs set to >1.85-fold induction and repression ($2^{\pm 0.89}$), as indicated by the blue vertical lines.

3.2.2 Chaperones and chaperonins. In this work, genes encoding for several molecular chaperones like the two thermosome subunits (*cctA* and *cctB*), a heat shock protein homolog (*hsp5*) and the AAA-type ATPases (*aaa3/cdc48b* and *aaa8/cdc48d*) revealed substantial increase in both the protein (Supplemental Table D_manual and Supplemental Tables C_regul) and the transcript (microarrays; Supplemental Tables A_regul and

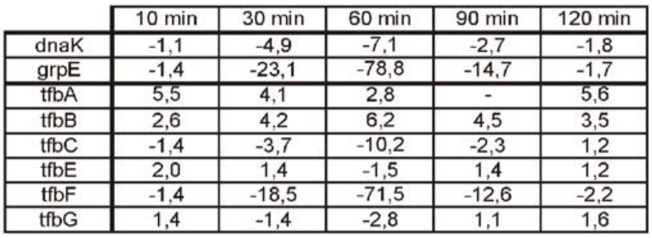
B_regul) level upon heat shock, independent of the growth media chosen (Table III). In *Hbt.* NRC-1, the same molecular chaperones with exception of *cctB* were also found to be highly induced (*cctA*, *cdc48b*, *cdc48d* and *hsp5,* which corresponds to our *hsp5* displaying a blast-result e-value of 3e^{-67}) in microarray experiments [Coker and DasSarma 2007b] emphasizing their inalienability in repairing protein damage and in assisting the cell to recover from denatured states [Morimoto 1998]. Northern blot experiments of *hsp5*, chosen as a typical heat shock protein with one of the highest induction rates, confirmed the strong transcriptional response determined by microarray analyses with maximal regulation being between 30 and 90 min (Fig. 30).

Another highly upregulated gene encoding a small protein, only identified by microarray analyses, is the hypothetical protein *OE3114R* (Supplemental Tables A_regul and B_regul), which forms a transcription unit with the AAA-type ATPase *aaa3/cdc48b* (*OE3112R*), thus bearing a potential heat shock protein function.

The *cct*-TATA motif (5′-TTTATA-3′) and the conserved promoter regions upstream (5′-CGAA-3′) and downstream (5′-GAA-3′) of this TATA box that were found to be important for heat shock expression in *cct*-genes of *Haloferax volcanii* and in other archaea [Thompson and Daniels 1998] are also present in the halobacterial thermosomal genes *cctB* (5′-CAAA…TATATAGAA-3′) and *cctA* (5′-CACA…TAAATAGAA-3′).

3.2.3 Chaperones of the dnaK-operon. In our work it could be undoubtedly disclosed that the *dnaK* operon is not significantly induced after exposure to heat shock, neither on the transcript level performed by whole genome microarrays (Supplemental Tables A and B) nor on the protein level (Supplemental Table D_manual, Supplemental Table C). Furthermore, Northern blot analysis (Fig. 30) and RTqPCR (Table IV) of *dnaK* revealed a significant downregulation after 1 h of heat shock, confirmed by RTqPCR data of its associated *grpE* (Table IV), pointing at a low transcript stability. These findings are in disagreement with results published by Shukla [Shukla 2006]. In that work, an increase in temperature from 42 °C to only 49 °C was sufficient to detect more than a 2-fold induction of DnaJ and GrpE proteins in *Hbt. NRC-1*. The approach was based on a visual comparison of different silver stained 2-D gels, each of them exhibiting protein spots of only one of the two cell states. Proteins were neither labeled nor combined before application to the gels, and normalization of the determined regulation data has not been performed to counterbalance possible longer exposure times of a gel to the staining solution, in comparison to other gels presenting proteins of a different cell state [Shukla 2006]. In addition, previous microarray analyses on *Hbt.* NRC-1 also reported 1.8-fold upregulation of *dnaK*, but no further significant regulation of the other genes of the operon (*dnaJ* and *grpE*) [Coker and DasSarma 2007b]. The lack of substantial regulation of all genes of the *dnaK* operon proven in our work may be either due to an already sufficient pool of mRNA and proteins available in *Hbt. salinarum*, or the operon may not have the same function as in eukaryotes and prokaryotes. The absence of the *dnaK* operon in many archaea would support this theory.

Table IV. RTqPCR of genes of the *dnaK* operon and of *tfb* genes. Exposure times to heat shock (60 ºC) are given in minutes (min). Regulation factors are given in –fold, starting at ±1. Regulation factors are considered significant when exceeding ±5 and were most prominent, with the exception of *tfbA*, after 60 min of heat shock.



	10 min	30 min	60 min	90 min	120 min
dnaK	-1,1	-4,9	-7,1	-2,7	-1,8
grpE	-1,4	-23,1	-78,8	-14,7	-1,7
tfbA	5,5	4,1	2,8	-	5,6
tfbB	2,6	4,2	6,2	4,5	3,5
tfbC	-1,4	-3,7	-10,2	-2,3	1,2
tfbE	2,0	1,4	-1,5	1,4	1,2
tfbF	-1,4	-18,5	-71,5	-12,6	-2,2
tfbG	1,4	-1,4	-2,8	1,1	1,6

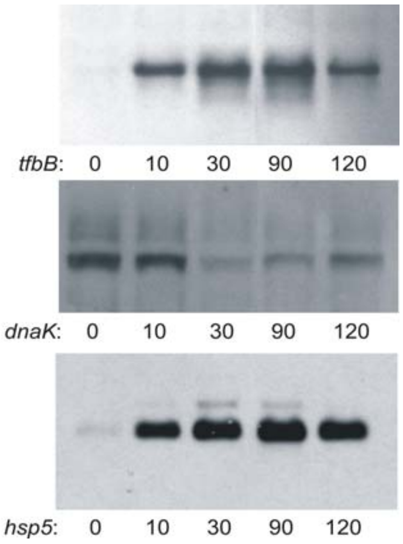


Figure 30. Northern blots of *tfbB* (975 bp), *dnaK* (1890 bp) and *hsp5* (370 bp). Exposure times to heat shock (60 °C) are given in minutes below the respective gels.

3.2.4 Transcription initiation factors. The transcription initiation factor protein tfbB was found to be significantly upregulated when cells were grown in synthetic medium, whereas tfbG and tfbF were not regulated or even downregulated (Supplemental Tables C_regul). RTqPCR (Table IV) and Northern blot (Fig. 30) time series experiments confirmed significant upregulation of *tfbB* mRNA with a maximum between 30 and 90 minutes. A considerable upregulation of *tfb*B has also been found in both microarray approaches (Supplemental Tables A_regul and B_regul) supporting the data derived by proteomics, Northern blot analysis (Fig. 30) and RTqPCR (Table IV).

Congruently with the time series of RTqPCR data (Table IV), *tfb*A, which unveiled considerable upregulation directly after exposure to heat shock (10 min) and at the end of the time scale experiment (120 min), was not found significantly regulated in the microarray approaches, as here cells were exposed to heat for 60 min only (Table III; Supplemental Tables A and B).

The substantial upregulation of *tfb*B on both the transcript and protein level, reaching the highest mRNA levels after 60 min, and of *tfb*A*,* with maximal mRNA upregulation at 10 min and after a decrease, again at 120 min (Table IV), is pointing to a possible reciprocal, regulatory action of *tfb*A and *tfb*B in the induction of heat shock response.

Only two more proteins could be identified in the proteomics approaches (tfbG and tfbF) both not regulated or even downregulated (Table IV; Fig. 30; Supplemental Tables C_regul).

Putative transcription induction of *tfb*F in DNA microarray analyses is opposed to the findings obtained by RTqPCR (Table IV) and proteomics (Supplemental Tables C_regul), both revealing even significant downregulation. The reason for the misleadingly assigned upregulation of *tfb*F, is the very high consensus in the nucleic acid sequence between *tfb*B and *tfb*F (blast-result e-value e^{-136}), leading to unspecific binding of *tfb*B probes to *tfb*F fixed on the glass slides.

Recently, construction of different *tfb* and *tbp* knockouts in *Hbt.* NRC-1 assigned *tfbA* to regulate together with *tbpD* a portion of the heat shock response, whereas *tfbB* was proven to be essential for cell viabily under standard growth conditions and could not be knocked out [Coker and DasSarma 2007b].

Previous microarray analyses on *Hbt.* NRC-1 suggested significant upregulation of only *tfb*G after both heat and cold shock likewise [Coker and DasSarma 2007b]. In our work this could not be confirmed. *tfb*G was neither significantly regulated in our proteomics nor in the microarray approaches and even exhibited a slight decrease in mRNA levels after 60 min upon RTqPCR analysis (Tables III and IV). A temporary descent in mRNA levels after heat shock [Byfield and Scherbaum 1967] may be due to a reduced synthesis of specific mRNAs.. The subsequent recovery of the mRNA levels (Table IV) show how fast the cells get adapted to external hazards and restore their original expression rates.

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3.2.5 Transcription regulators. The transcription regulator *sirR*, a divalent metal cation-dependent transcriptional repressor [Hill *et al.* 1998], revealed significant enhancement in mRNA levels (Supplemental Tables A_regul and B_regul), whereas identification by proteomics approaches failed. Homologues of SirR, like the mycobacterial ideR protein, negatively regulate genes encoding for iron transport systems (siderophores) and protect cells from oxidative stress [Dussurget *et al.* 1996]. The reason for an induction after heat shock is not traceable and may be in the context of a general stress response.

The conserved protein *OE2046F*, with significant transcriptional upregulation only after growth in synthetic medium (Supplemental Tables B_regul), shows homologies to probable transcription factors of other halophilic archaea (highest homology to NP0674A of *Natronomonas pharaonis*; blast-result e-value $9e^{-20}$), indicating a potential role in the expression of enzymes predominantly needed under these nutritional conditions. Enzymes differentially regulated under the growth conditions applied will be discussed later. *OE2046F* could not be identified by proteomics, probably due to its low molecular weight.

In contrast to previous findings in *Pyrococcus furiosus* and *Archaeoglobus fulgidus*, the gene encoding a Phr/AF1298 homologue in *Hbt. salinarum* (OE3589F) did not show fundamental transcription regulation and could not be identified by proteomics.

3.2.6 Arginine and praline metabolism, pyrimidine synthesis and TCA cycle. *Hbt. salinarum* is able to respire aerobically and anaerobically, to grow phototrophically, and to ferment arginine via the ADI (arginine deiminase) pathway [Hartmann *et al.* 1980; Oren and Truper 1990]. It could be proven previously that arginine is consumed extremely fast during cell growth, and that uptake of arginine occurs even under aerobic conditions, finding it nearly depleted in the medium in the beginning log phase [Gonzalez *et al.* 2008] In addition, rapid accumulation of ornithine in the medium was followed by gradual depletion once the arginine supply was exhausted, revealing that ornithine can substitute for arginine without a change in growth quality [Gonzalez *et al.* 2008]. Cells not supplied with either of these two nutrients exhibited limited growth, featuring longer doubling times and a much lower maximum optical density [Gonzalez *et al.* 2008]. These data confirmed that arginine and ornithine are crucial components, but not essential. Significant regulations assigned, and discussed in this chapter, are schematically illustrated in Fig. 31.

Furthermore, the arginine deiminase, one of four genes of the ADI pathway operon [Ruepp and Soppa 1996] (Supplemental Table D_manual and C), was significantly upregulated in both microarray approaches (Table III, Supplemental Tables A_regul and B_regul). This initialization of arginine degradation may lead to the synthesis of pyrimidines (Fig. 31) rather than to fermentative ATP production, which has already been shown to occur also under aerobic conditions [Gonzalez *et al.* 2008], due to the concomitant induction of carbamoyl phosphate synthase. The latter is producing carbamoyl phosphate out of ammonia and CO_2 at the expense of two ATP, and can serve either as a key building block for pyrimidines or for arginine synthesis from ornithine. However, induction of ATP consumptive carbamoyl phosphate synthase for synthesis and subsequent fermentation of arginine, yielding only one ATP molecule, is energetically not reasonable and presumably the reason, why translation of arginine deiminase is hampered after the induced transcription.

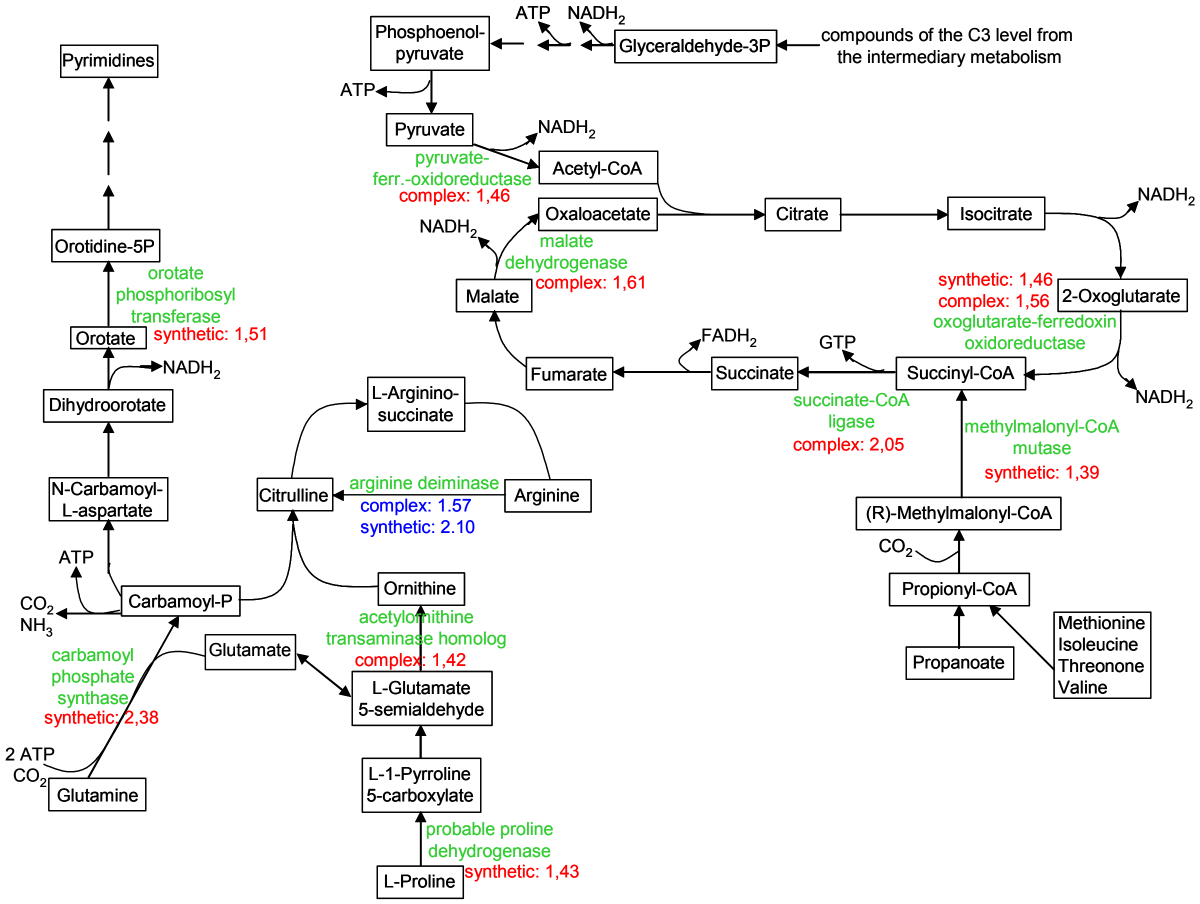

Figure 31. Schematic of significantly regulated heat shock proteins and enzymes (both in green) involved in arginine metabolism, pyrimidine synthesis and TCA cycle. Significant protein (red; proteomic analyses) and transcript (blue; microarray analyses) regulation factors, determined in complex and synthetic medium, are also indicated. Arrows indicate the supposed direction of the regulatory effect.

The carbamoyl phosphate synthase, which could not be proteomically identified in the 2-DE/complex medium approach probably due to its low expression level, showed significant protein upregulation in the SILAC/synthetic medium approach (Supplemental Tables C_regul), whereas transcript levels remained unaffected after heat shock (Table III; Supplemental Tables A and B). Induction of pyrimidine biosynthesis is also supported by the fact that protein levels of orotate phosphoribosyltransferase were enhanced (Supplemental Tables C_regul and D_manual), again in particular after growth in synthetic medium. Both enzymes, the carbamoyl phosphate synthase and the orotate phosphoribosyl-transferase, were already reported to become induced in *Hbt. salinarum* R1 when switching the cells from growth in complex to synthetic medium [Tebbe *et al.* 2007], which has no pyrimidines added. This lack of pyrimidines seems to be an additional challenge for the archaeon when encountering stress conditions.

The heat shock response is an energy consuming process. In *Pyrococcus furiosus*, expression of genes associated with carbohydrate acquisition were relating to the increased demand in ATP during thermal stress [Shockley *et al.* 2003], just as heat shock on *Xenopus laevis* embryos revealed to cause an increase in the demand for ATP [Nickells and Browder 1988]. In the present work, the increased synthesis of carbamoyl phosphate and of diverse molecular chaperones under heat shock conditions are relating to the needs of an additional ATP supply that might be met by translational upregulation of TCA cycle catalysts, as suggested by our data (Fig. 31). Comparing the two approaches, the TCA cycle was suggested to be supplied by different metabolites. In complex medium, the pyruvate-ferredoxin oxidoreductase revealed significant induction (Supplemental Table D_manual), pointing to an introduction of C3-intermediates into the citric acid cycle via Glycerine-3P (Fig. 31), as they are likely to be available in complex medium. In contrast to the composition in the complex medium, synthetic medium contained only specific molecules, amongst others 15 amino acids (see chapter 2.1.5.), being devoid of possible C3-intermediates. Induction of methylmalonyl-CoA mutase (Supplemental Tables C_regul) in the synthetic medium approach, a key enzyme in the carboxylation of propionate to succinate, suggests the conversion of several amino acids to succinate via a part of this pathway, feeding the TCA cycle (Fig. 31).

The importance of ornithine, which can be exported after binding to the arginine:ornithine antiporter, causing arginine uptake into the cell, is demonstrated by the protein upregulation of both a probable proline dehydrogenase (Supplemental Tables C_regul; synthetic medium) and an acetylornithine transaminase homolog (Supplemental Table D_manual; complex medium) that may convert proline into ornithine (Fig. 31; Table III). Proline, explicitly added to synthetic medium and presumably utilized for assembly of ornithine, was apparently also present in complex medium, probably introduced by the bacteriological peptone. Neither the transducer protein car nor the two ornithine synthesizing enzymes (proline dehydrogenase and acetylornithine transaminase homolog) were regulated on the transcript level in each of the microarray approaches (Table III), pointing to the importance of translational regulation.

3.2.7 Miscellaneous.

Dps-like ferritin: The Dps-like ferritin protein DpsA (Dps, DNA-protecting protein during starvation), which exhibits functional similarities to Dps proteins [Zeth *et al.* 2004], also displayed a high upregulation in both, the protein (Supplemental Table D_manual and Supplemental Tables C_regul) and transcript (Supplemental Tables A_regul and B_regul) level upon heat shock, independent of the growth media chosen (Table 1). Dps proteins protect the bacterial cell not only during oxidative stress (exposure to superoxide and peroxide) and from iron toxicity (Fenton reaction) as ferritins are doing, but also from UV, gamma irradiation, thermal stress, as well as acid and base shock [Grant *et al.* 1998; Nair and Finkel 2004]. In *Escherichia coli*, DNA-binding of Dps may recruit repair enzymes or other proteins to the chromosome for increasing the efficiency and accuracy of the repair process [Nair and Finkel 2004]. Furthermore, DNA-binding of Dps may also modulate interactions with proteins involved in maintaining the supercoiled state of the DNA thereby preventing relaxation during heat shock [Adamcik *et al.* 2002; Nair and Finkel 2004], a conclusion correlating with our results of heat shock induction.

Deoxypirimidine photolyase: Heat shock induction of the deoxyribopyrimidine photolyase Phr1 could be assigned only by one peptide (Supplemental Tables C_regul) after growth in synthetic medium (in complex medium not found). Previous findings in *Hbt. NRC-1* proved that only one of the two putative photolyase-like genes, *phr2*, was implicated in photoreactivation [Baliga *et al.* 2004a]. The translational upregulation of the Phr1 protein in *Hbt. salinarum* may be in the wake of a general stress response induced in the cell.

Glutaredoxin homolog: Glutaredoxins utilize the reducing power of glutathione to catalyze disulfide reductions in the presence of NADPH and glutathione reductase, playing a critical role in the protection against oxidative stress. By reducing the ribonucleotide reductase they are also involved in the conversion of ribonucleotides to the corresponding deoxyribonucleotides, providing the precursors needed for DNA synthesis. Transcriptional induction of a glutaredoxin homolog after heat shock may also be explained in the wake of a general stress response [Fernandes and Holmgren 2004].

Gas vesicles: Two genes contributing in gas vesicle formation were found considerably regulated, both being part of the leftward gene clusters *gvpDEFGHIJKLM* of two highly homologous operons located on the plasmids pHS1 and pHS3, respectively. Consistently with an upregulation (Table III and Supplemental Tables A_regul) of *gvpK2* (gas-vesicle operon protein K2) required for gas vesicle synthesis, downregulation (Table III and Supplemental Tables B_regul) of the repressor gene *gvpD1*, which was reported to inhibit synthesis of gas vesicles in the closely related halobacterial strain *Hbt. salinarum* PHH4 [Kruger and Pfeifer 1996], could be detected. Induction of gas vesicle formation by the upregulation of *gvpK2 and* the concomitant downregulation of the repressor gene *gvpD1* are conferring buoyancy to the cells, enabling floatation towards zones with potentially better living conditions. Another consequence of the induction of gas vesicle formation is the removal of water within the cell. With the reduction of the cytosol less energy has to be spent for the import of Cl^- by Halorhodopsin. Cells were grown in the dark, so that the light driven proton pump Bacteriorhodopsin could not be used for light energy-dependent salt import.

Flagellins: Three of the five flagellin precursor proteins (each holding 1 transmembrane domain) could be quantified showing remarkable downregulation after growth in synthetic medium (Supplemental Tables C_regul), whereas none of them could be detected in the 2-DE approach (complex medium), which is not suitable for membrane proteins [Klein *et al.* 2005]. In addition, all five genes encoding flagellin precursors were significantly downregulated in both microarray approaches (Supplemental Tables A_regul and B_regul), confirming the proteomics data (Table III). Reasons for the observed downregulation may be energy saving on the one hand, but also the fact that locomotion seems to be more effective by gas vesicle formation under heat shock conditions.

Cell surface glycoprotein: The gene encoding the cell surface glycoprotein precursor holding 2 transmembrane domains was highly downregulated in both microarray approaches (Supplemental Tables A_regul and B_regul), probably to avoid spending energy for costly glycosylation, whereas proteomic data did not reveal significant regulation or failed to identify the protein by the 2-DE approach. The cell surface glycoproteins are so highly abundand and stable, that a reduced transcription does not affect the protein levels within two hours.

Proteasome: Both proteasome subunits were only slightly upregulated in the approaches performed (Table III, Supplemental Tables A, B, C, C_regul and D_manual), similar to previous findings in the archaea *Archaeoglobus fulgidus* and *Pyrococcus furiosus*, in which the proteasome β-subunits were also slightly heat induced and the α-subunits even decreased [Rohlin *et al.* 2005; Shockley *et al.* 2003]. This is in contrast to *Thermoplasma acidophilum*, where the proteasome plays an essential role for survival under heat shock conditions [Ruepp *et al.* 1998]. Here, the moderate upregulation of the proteasome may be an indication for the good adaptative abilities of *Hbt. salinarum* to extreme conditions, suggesting only few additional protein denaturation after exposure to elevated temperatures.

4 Conclusions

Including membrane proteomic data for *Natronomonas pharaonis* (B. Bisle *et al.*, manuscript in preparation), we have identified a total of 1226 proteins (43% of the theoretical proteome) under high stringency, showing that *Natronomonas pharaonis* has one of the densest coverages with proteome data.

- The shotgun method with analysis of SDS-PAGE slices by nanoLC-MS/MS turned out to be a fast and effective way for examining the protein inventory of a given cell without the need of further prefractionation, whereas a high number of proteins were identified additionally just by a different cell lysis procedure.
- Since not a single case of overprinting could be identified in the genome of both *Natronomonas pharaonis* and *Halobacterium salinarum*, we deduce that in the genome of halophiles large-scale gene overlaps do not occur. Although this does not exclude that such cases will be detected in the future, they may occur only very rarely.
- Many of the identified proteins exemplify the high variability among halophiles on a background of highly conserved and common proteins. This is attributed to the high variability of the environments that share the high salt concentration but may contain additional threats like high pH values. The necessity to cope with several extreme conditions is resolved by genetic exchange between organisms that are evolutionary nearly unrelated. This genetic exchange may affect single genes or larger genome regions and phages or plasmids may participate in transfer of genetic material.
- In addition to the large number of functionally characterized proteins, a total of 200 conserved hypothetical proteins and *Natronomonas*-specific hypothetical proteins have been identified by this proteomic survey, proving their existence.
- Significant transcriptional induction of *tfbB* and *tfbA* in *Halobacterium salinarum* on differing time points suggests these transcription initiation factors to play a role in gene regulation by reciprocal action when challenged by elevated temperatures. Prominent TfbB protein upregulation further confirms that this transcription factor plays an important role in coping with heat shock.
- Genes of the *dnaK*-operon have been confidentially proven by multiple proteome and transcriptome approaches not to be regulated, which is in contrast to findings in *Hbt.* NRC-1 [Coker and DasSarma 2007b; Shukla 2006]. Considering the absence of the

dnaK operon in many archaea, these findings either assume a different function of these genes than in eukaryotes and prokaryotes, or a constitutive high expression level of certain genes, important for rapid adaptation to frequently occurring changes within hostile environments. This may also be the reason for the general low regulative response of *Hbt. salinarum* to different living conditions [Bisle *et al.* 2006; Tebbe *et al.* 2007].

- For most of the genes described in this work, transcriptome and proteome data were consistent, whereas some cases of differential regulation became evident when comparing both datasets, indicating that translational regulation plays an important role in *Hbt. salinarum* [Lange *et al.* 2007]. Examples for translational regulation are visible for some enzymes of the arginine metabolism, pyrimidine synthesis and the TCA cycle, whereas transcript downregulation is not necessarily reflected by proteomics after only two hours, due to the stability of proteins like the cell surface glycoprotein precursor [Byfield and Scherbaum 1967].
- The multiplicity of proteomics and transcriptomics methods are complementing one another, covering a bigger area on the one hand but also confirming unexpected findings.

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6 Appendix

Supplemental Table I. List of all proteins identified and some special features.

Explanations for the abbreviations used:

- Abbreviations for function superclasses:

MET: metabolism; TP_CP: transport and cellular processes; GIP: genetic information processing; ENV: environmental information processing; MIS: miscellaneous; CHY: conserved hypothetical protein; HY: hypothetical protein.

Abbreviations for function classes:

- Function classes are grouped by function superclasses.

MET: metabolism

AA: amino acid metabolism; LIP: lipid metabolism; CIM: central intermediary metabolism;
NUM: nucleotide metabolism; COM: coenzyme metabolism; CHM: carbohydrate metabolism.

TP_CP: transport and cellular processes

TP: small molecule transport; EM: energy metabolism; CP: cellular processes;
SEC: protein secretion; MOT: motility; CE: cell envelope.

GIP: genetic information processing

TL: translation; RRR: replication, repair, recombination; TC: transcription; CHP: chaperones
RMT: RNA maturation

ENV: environmental information processing

SIG: signal transduction; REG: gene regulation

MIS: miscellaneous

GEN: general function; MIS: miscellaneous

- Abbreviations for locations:

transm: proteins with predicted transmembrane domains (not counting TM domains in the first 70 aa, which are likely to be signal sequences)

anchN_lip: proteins which are probably attached to the membrane by an N-terminal lipid anchor (lipobox motif); they are expected to have a ‘periplasmic’ location

extrac: extracellular proteins contain protein export signals for one of the export pathways but are probably not attached to the membrane

cytopl: proteins which are likely to be cytoplasmic and have no indication for a different location

- Other abbreviations:

Score: modified MASCOT protein score (indicating the difference to the confidence threshold score for a 95% confidence level as detailed in Klein *et al*, 2005). The number (#) of distinct identified peptides is given in parenthesis.

id: identification level (“reliable” requires a modified score of at least 39 (equivalent to a confidence level of 99.9995%), “normal” requires a modified score of at least 19 (equivalent to a confidence level of 99.95%)).

Sample: laboratory-internal sample name in which the protein has been identified with the highest Mascot score. This consists of several parts. The first part is the gel number (1dg0001 for water lysis, 1dg0005 for native lysis with SEC). The second part (after the first underscore) is the slice number (22 slices for 1dg0001 (Fig. 12) from top to bottom and 93 slices for 1dg0005 (Fig. 13) from top to bottom and from left to right; slices 1-13 are derived from SEC fraction II, slices 14-29 are derived from SEC fraction III, slices 30-49 are derived from SEC fraction IV, slices 50-67 are derived from SEC fraction V, slices 68-88 are derived from SEC fraction VI and slices 89-93 are derived from SEC fraction VII) . An eventual third secion (after a possible second underscore) is indicative for different MS measurements for the same samples with eventual combination of the peaklists (_ges). These sample names are used in HaloLex (http://halolex.mpg.de).

Code: protein code (corresponds to the ordered locus tag in SwissProt).

- All information provided by the list plus additional information (e.g. the sequences and charge states of the peptides identified) are accessible through HaloLex (http://halolex.mpg.de).

code	sample	id level	score (#peptides)	location	gene	super-classes	classes	protein name
NP0282A	0001_10ges	normal	33.70 (1)	cytopl	metA	MET	AA	homoserine O-acetyltransferase (EC 2.3.1.31)
NP3344A	0001_17ges	normal	33.32 (2)	cytopl	trpG_1	MET	AA	anthranilate synthase (EC 4.1.3.27), component II 1
NP4524A	0001_15ges	normal	33.29 (2)	cytopl	thrB	MET	AA	homoserine kinase (EC 2.7.1.39)
NP2578A	0001_10ges	normal	22.14 (1)	cytopl	agt_1, spt_1	MET	AA	aminotransferase class V (Serine--pyruvate aminotransferase (EC 2.6.1.51) 1; Alanine--glyoxylate aminotransferase (EC 2.6.1.44) 1)
NP5280A	0005_56_2	reliable	910.98 (15)	cytopl	thrC_1	MET	AA	threonine synthase (EC 4.2.3.1) 1
NP2194A	0005_54_2	reliable	629.69 (12)	cytopl	leuC	MET	AA	3-isopropylmalate dehydratase (EC 4.2.1.33), large subunit
NP3342A	0001_06ges	reliable	626.64 (11)	cytopl	trpE_1	MET	AA	anthranilate synthase (EC 4.1.3.27), component I 1
NP0076A	0005_54_2	reliable	600.17 (13)	cytopl	glnA_1	MET	AA	glutamate--ammonia ligase (EC 6.3.1.2) 1
NP5036A	0005_42	reliable	584.71 (13)	cytopl	ilvE_1	MET	AA	branched-chain amino acid aminotransferase (EC 2.6.1.42) 1
NP2954A	0001_04ges	reliable	579.86 (12)	cytopl	hyuA_1	MET	AA	N-methylhydantoinase (ATP-hydrolyzing) (EC 3.5.2.14) A 1
NP0448A	0005_56_2	reliable	556.35 (10)	cytopl	arcB, ocd	MET	AA	ornithine cyclodeaminase (EC 4.3.1.12)
NP3978A	0005_54_2	reliable	548.71 (10)	cytopl	proA	MET	AA	glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41)
NP2952A	0001_05ges	reliable	528.48 (10)	cytopl	hyuB_1	MET	AA	N-methylhydantoinase (ATP-hydrolyzing) (EC 3.5.2.14) B 1
NP5252A	0005_55_2	reliable	477.08 (8)	cytopl	argG	MET	AA	argininosuccinate synthase (EC 6.3.4.5)
NP2050A	0005_54_2	reliable	453.74 (12)	cytopl	glyA	MET	AA	glycine hydroxymethyltransferase (EC 2.1.2.1)
NP0884A	0005_57_2	reliable	447.20 (11)	cytopl	agt_2, spt_2	MET	AA	aminotransferase class V (Serine--pyruvate aminotransferase (EC 2.6.1.51) 2; Alanine--glyoxylate aminotransferase (EC 2.6.1.44) 2)

NP1666A	0005_56_2	reliable	436.07 (9)	cytopl	aspC_2	MET	AA	PLP-dependent aminotransferase (probable aspartate aminotransferase (EC 2.6.1.1) 2)
NP0936A	0005_56_2	reliable	407.42 (11)	cytopl	nifS	MET	AA	cysteine desulfurase (EC 2.8.1.7), class V aminotransferase
NP1806A	0005_36	reliable	389.07 (9)	cytopl	gdhA_1	MET	AA	glutamate dehydrogenase (EC 1.4.1.2 or EC 1.4.1.3 or EC 1.4.1.4) 1
NP4926A	0001_05ges	reliable	373.71 (8)	cytopl	ilvD	MET	AA	dihydroxy-acid dehydratase (EC 4.2.1.9)
NP5254A	0005_34	reliable	343.01 (7)	cytopl	argH	MET	AA	argininosuccinate lyase (EC 4.3.2.1)
NP0280A	0005_36	reliable	339.58 (7)	cytopl	metY_2	MET	AA	O-acetylhomoserine aminocarboxypropyltransferase (EC 2.5.1.49) 2, methionine synthase
NP3164A	0005_56_2	reliable	335.13 (7)	cytopl	trpB_1	MET	AA	tryptophan synthase (EC 4.2.1.20), beta subunit 1
NP2198A	0005_39	reliable	305.60 (8)	cytopl	ilvC	MET	AA	ketol-acid reductoisomerase (EC 1.1.1.86)
NP2190A	0005_39	reliable	299.50 (6)	cytopl	leuB	MET	AA	3-isopropylmalate dehydrogenase (EC 1.1.1.85)
NP1646A	0005_57_2	reliable	298.34 (5)	cytopl	lysA	MET	AA	diaminopimelate decarboxylase (EC 4.1.1.20)
NP0272A	0005_32	reliable	290.37 (9)	cytopl	serA	MET	AA	phosphoglycerate dehydrogenase (EC 1.1.1.95)
NP4506A	0001_05ges	reliable	279.96 (5)	cytopl	carB	MET	AA	carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5), large subunit
NP6188A	0005_37	reliable	265.96 (5)	cytopl	gabT	MET	AA	aminotransferase class III (probable 4-aminobutyrate aminotransferase (EC 2.6.1.19))
NP4410A	0005_56_2	reliable	248.26 (6)	cytopl	aspC_3	MET	AA	PLP-dependent aminotransferase (probable aspartate aminotransferase (EC 2.6.1.1) 3)
NP5266A	0005_55_2	reliable	248.21 (6)	cytopl	argE	MET	AA	acetylornithine deacetylase (EC 3.5.1.16)
NP4570A	0001_12ges	reliable	244.07 (6)	cytopl	cysD	MET	AA	sulfate adenylyltransferase (EC 2.7.7.4), small subunit
NP0302A	0005_39	reliable	236.49 (4)	cytopl	hom	MET	AA	homoserine dehydrogenase (EC 1.1.1.3)
NP1062A	0001_13ges	reliable	230.40 (4)	cytopl	hisG	MET	AA	ATP phosphoribosyltransferase (EC 2.4.2.17)
NP0624A	0001_06ges	reliable	225.05 (5)	cytopl	leuA_2, cimA	MET	AA	2-isopropylmalate synthase (EC 2.3.3.13) 2, (R)-citramalate synthase (EC 2.3.3.-)
NP0274A	0001_14ges	reliable	222.46 (3)	cytopl	serB	MET	AA	phosphoserine phosphatase (EC 3.1.3.3)
NP0106A	0001_15ges	reliable	200.21 (7)	cytopl	pheA2	MET	AA	prephenate dehydratase (EC 4.2.1.51)
NP1582A	0005_36	reliable	195.29 (7)	cytopl	gdhA_2	MET	AA	glutamate dehydrogenase (EC 1.4.1.3 or EC 1.4.1.4) 2
NP0550A	0005_55_2	reliable	186.78 (6)	cytopl	lysC	MET	AA	aspartate kinase (EC 2.7.2.4)
NP4830A	0005_57_2	reliable	186.25 (4)	cytopl	carA	MET	AA	carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5), small subunit
NP2200A	0005_44	reliable	184.31 (6)	cytopl	ilvN	MET	AA	acetolactate synthase (EC 2.2.1.6), small subunit
NP4024A	0001_10ges	reliable	181.03 (3)	cytopl	aspC_1	MET	AA	PLP-dependent aminotransferase (probable aspartate aminotransferase (EC 2.6.1.1) 1)
NP4594A	0005_35	reliable	178.24 (3)	cytopl	gcvP2	MET	AA	glycine dehydrogenase (decarboxylating) (EC 1.4.4.2), subunit 2 of glycin cleavage system P protein
NP3672A	0001_09ges	reliable	174.04 (5)	cytopl	metE_2	MET	AA	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14), methionine synthase II, 2

NP2238A	0001_07ges	reliable	168.07 (3)	cytopl	-	MET	AA	predicted alternative 3-dehydroquinate synthase (EC 4.2.3.4)
NP5264A	0001_12ges	reliable	167.64 (3)	cytopl	argD	MET	AA	acetylornithine aminotransferase (EC 2.6.1.11)
NP5260A	0005_39	reliable	166.80 (5)	cytopl	argC	MET	AA	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)
NP4158A	0005_75_2	reliable	159.15 (5)	cytopl	hisF	MET	AA	imidazoleglycerol-phosphate synthase (EC 2.4.2.-), cyclase subunit HisF
NP4376A	0005_54_2	reliable	158.38 (4)	cytopl	glnA_2	MET	AA	glutamate--ammonia ligase (EC 6.3.1.2) 2
NP3166A	0001_14ges	reliable	157.63 (5)	cytopl	trpC	MET	AA	indole-3-glycerol-phosphate synthase (EC 4.1.1.48)
NP3338A	0001_11ges	reliable	150.74 (3)	cytopl	trpD	MET	AA	anthranilate phosphoribosyltransferase (EC 2.4.2.18)
NP1490A	0001_12ges	reliable	150.37 (3)	cytopl	dapA	MET	AA	dihydrodipicolinate synthase (EC 4.2.1.52)
NP1494A	0005_60_2	reliable	148.96 (5)	cytopl	dapD	MET	AA	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117)
NP5268A	0001_12ges	reliable	138.54 (3)	cytopl	argF	MET	AA	ornithine carbamoyltransferase (EC 2.1.3.3)
NP3082A	0001_09ges	reliable	133.83 (3)	cytopl	aroC	MET	AA	chorismate synthase (EC 4.2.3.5)
NP2140A	0001_12ges	reliable	125.80 (4)	cytopl	hisC	MET	AA	histidinol-phosphate aminotransferase (EC 2.6.1.9) 1
NP3078A	0005_55_2	reliable	124.78 (2)	cytopl	aroA	MET	AA	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
NP2192A	0001_14ges	reliable	122.99 (3)	cytopl	leuD	MET	AA	3-isopropylmalate dehydratase (EC 4.2.1.33), small subunit
NP2202A	0005_32	reliable	122.57 (3)	cytopl	ilvB	MET	AA	acetolactate synthase (EC 2.2.1.6), large subunit
NP3502A	0005_57_2	reliable	117.67 (3)	cytopl	trpB_2	MET	AA	probable tryptophan synthase (EC 4.2.1.20), beta subunit 2
NP3982A	0001_14ges	reliable	109.82 (3)	cytopl	aroK	MET	AA	shikimate kinase (EC 2.7.1.71), archaeal type
NP4464A	0005_55_2	reliable	108.90 (3)	cytopl	thrC_2	MET	AA	threonine synthase (EC 4.2.3.1) 2
NP3162A	0001_14ges	reliable	96.69 (2)	cytopl	trpA	MET	AA	tryptophan synthase (EC 4.2.1.20), alpha subunit
NP4746A	0005_35	reliable	91.23 (2)	cytopl	metB, metC	MET	AA	cystathionine synthase/lyase (cystathionine gamma-synthase (EC 2.5.1.48), cystathionine gamma-lyase (EC 4.4.1.1), cystathionine beta-lyase (EC 4.4.1.8))
NP1076A	0001_10ges	reliable	86.74 (3)	cytopl	ilvA, tdcB	MET	AA	threonine ammonia-lyase (EC 4.3.1.19)
NP3670A	0001_08ges	reliable	81.31 (4)	cytopl	metE_1	MET	AA	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14), methionine synthase II 1
NP3976A	0001_12ges	reliable	73.61 (3)	cytopl	proB	MET	AA	glutamate 5-kinase (EC 2.7.2.11)
NP2876A	0005_55_2	reliable	62.12 (1)	cytopl	hisD	MET	AA	histidinol dehydrogenase (EC 1.1.1.23)
NP0790A	0001_12ges	reliable	55.97 (2)	cytopl	nifS_2	MET	AA	probable cysteine desulfurase (EC 2.8.1.7) 2, class V aminotransferase
NP3974A	0005_60_2	reliable	54.35 (2)	cytopl	proC	MET	AA	pyrroline-5-carboxylate reductase (EC 1.5.1.2)
NP1632A	0001_08ges	reliable	52.84 (2)	cytopl	thrC_3	MET	AA	threonine synthase (EC 4.2.3.1) 3
NP1988A	0005_35	reliable	47.74 (1)	cytopl	asd	MET	AA	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)
NP1492A	0001_15ges	reliable	43.26 (2)	cytopl	dapB	MET	AA	dihydrodipicolinate reductase (EC 1.3.1.26)
NP4596A	0005_36	reliable	41.87 (2)	cytopl	gcvP1	MET	AA	glycine dehydrogenase (decarboxylating) (EC 1.4.4.2), subunit 1 of glycin cleavage system P protein

NP2850A	0001_12ges	normal	35.38 (1)	cytopl	mvk	MET	LIP	mevalonate kinase (EC 2.7.1.36)
NP2852A	0001_15ges	normal	35.08 (1)	cytopl	-	MET	LIP	predicted phosphomevalonate kinase (EC 2.7.4.2)
NP2630A	0001_12ges	normal	25.39 (1)	cytopl	hbd_1	MET	LIP	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 1
NP2858A	0001_04ges	normal	21.34 (1)	cytopl	acdA	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) III (probable acetate--CoA ligase (ADP-forming) (EC 6.2.1.13))
NP4836A	0005_54_2	reliable	948.53 (21)	cytopl	mvaB_2	MET	LIP	hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10) 2
NP5132A	0001_03ges	reliable	842.24 (18)	cytopl	acs_4	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) I 4
NP4242A	0001_05ges	reliable	818.94 (20)	cytopl	acs_2	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) I 2
NP3422A	0005_53_2	reliable	808.61 (16)	cytopl	alkK_3	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) II 3 (probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3))
NP4368A	0001_04ges	reliable	641.53 (12)	cytopl	accA_2	MET	LIP	biotin carboxylase (EC 6.3.4.14) 1, acyl-CoA carboxylase, alpha subunit 2
NP4252A	0001_04ges	reliable	620.26 (16)	cytopl	accA_1	MET	LIP	biotin carboxylase (EC 6.3.4.14) 1, acyl-CoA carboxylase (EC 6.4.1.-), alpha subunit 1
NP3420A	0005_57_2	reliable	579.44 (9)	cytopl	acaB_3	MET	LIP	acetyl-CoA C-acyltransferase (EC 2.3.1.16) 3
NP4364A	0005_18	reliable	579.25 (11)	cytopl	accB_2	MET	LIP	acyl-CoA carboxylase (EC 6.4.1.-) 2, carboxyltransferase component (beta subunit)
NP2934A	0005_33	reliable	535.84 (11)	cytopl	acd_7	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 7
NP1596A	0005_38	reliable	488.19 (14)	cytopl	acd_5	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 5
NP4240A	0005_32	reliable	485.45 (10)	cytopl	acs_1	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) I 1
NP3004A	0005_56_2	reliable	461.76 (9)	cytopl	acd_6	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 6
NP1754A	0005_38	reliable	461.00 (14)	cytopl	acd_11	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 11
NP1226A	0005_53_2	reliable	446.47 (9)	cytopl	mcmA_2	MET	LIP	methylmalonyl-CoA mutase (EC 5.4.99.2), subunit A 2
NP4150A	0005_33	reliable	414.95 (9)	cytopl	alkK_5	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) II 5 (probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3))
NP4250A	0001_05ges	reliable	407.65 (10)	cytopl	accB_1	MET	LIP	acyl-CoA carboxylase (EC 6.4.1.-) 1, carboxyltransferase component (beta subunit)
NP2214A	0005_55_2	reliable	366.50 (8)	cytopl	acaB_8	MET	LIP	acetyl-CoA C-acyltransferase (EC 2.3.1.16) 8
NP4322A	0001_03ges	reliable	365.76 (9)	cytopl	hbd_3, fadA_3	MET	LIP	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 3/ enoyl-CoA hydratase (EC 4.2.1.17) I 3
NP2260A	0005_55_2	reliable	351.61 (6)	cytopl	acaB_6	MET	LIP	acetyl-CoA C-acyltransferase (EC 2.3.1.16) 6
NP1870A	0005_39	reliable	343.09 (7)	cytopl	acd_9	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 9
NP2422A	0005_57_2	reliable	325.47 (6)	cytopl	mvaA_1	MET	LIP	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) 1
NP4254A	0001_11ges	reliable	320.83 (8)	cytopl	acd_4	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 4
NP3438A	0005_55_2	reliable	301.02 (6)	cytopl	acaB_4	MET	LIP	acetyl-CoA C-acyltransferase (EC 2.3.1.16) 4
NP0360A	0001_12ges	reliable	294.96 (7)	cytopl	idiB_1	MET	LIP	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) II 1
NP1630A	0005_5	reliable	291.68 (7)	extrac	crtI_3	MET	LIP	phytoene dehydrogenase (EC 1.14.99.-) 3 (phytoene desaturase)
NP3434A	0005_43	reliable	268.76 (7)	cytopl	fadA_4	MET	LIP	enoyl-CoA hydratase (EC 4.2.1.17) I 4
NP2320A	0005_54_2	reliable	264.51 (7)	cytopl	mcmA_1	MET	LIP	methylmalonyl-CoA mutase (EC 5.4.99.2), subunit A 1

NP6180A	0001_11ges	reliable	255.29 (7)	cytopl	acd_8	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 8
NP3460A	0005_39	reliable	237.39 (6)	cytopl	acd_3	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 3
NP4516A	0001_07ges	reliable	223.16 (4)	cytopl	-	MET	LIP	probable ferredoxin-NAD+ reductase (EC 1.18.1.3) 2
NP1462A	0001_13ges	reliable	217.56 (4)	cytopl	fadA_5	MET	LIP	probable enoyl-CoA hydratase (EC 4.2.1.17) I 5
NP3650A	0005_57_2	reliable	216.78 (4)	cytopl	acaB_7	MET	LIP	acetyl-CoA C-acyltransferase (EC 2.3.1.16) 7
NP4764A	0005_3	reliable	215.13 (5)	anchN_lip	crtI_1	MET	LIP	phytoene dehydrogenase (EC 1.14.99.-) 1 (phytoene desaturase)
NP4174A	0001_04ges	reliable	199.72 (6)	cytopl	lfl	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) IV (probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3))
NP3386A	0005_52_2	reliable	183.52 (5)	cytopl	alkK_4	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) II 4 (probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3))
NP5128A	0005_53_2	reliable	174.57 (4)	cytopl	acs_3	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) I 3
NP2754A	0001_04ges	reliable	170.81 (4)	cytopl	hbd_2, fadA_2	MET	LIP	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 2/ enoyl-CoA hydratase (EC 4.2.1.17) I 2
NP2256A	0001_17ges	reliable	162.21 (3)	cytopl	fadB_3	MET	LIP	probable enoyl-CoA hydratase (EC 4.2.1.17) II 3
NP4580A	0005_57_2	reliable	155.56 (3)	cytopl	acaB_5	MET	LIP	acetyl-CoA C-acyltransferase (EC 2.3.1.16) 5
NP3696A	0001_12ges	reliable	137.09 (5)	cytopl	idsA_3	MET	LIP	probable trifunctional short-chain (E)-prenyl diphosphate synthase (probable dimethylallyltransferase (EC 2.5.1.1) / probable geranyltranstransferase (EC 2.5.1.10) / probable farnesytranstransferase (EC 2.5.1.29))
NP2620A	0005_39	reliable	124.21 (4)	cytopl	acd_1	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 1
NP0164A	0005_53_2	reliable	110.56 (3)	cytopl	acs_5	MET	LIP	acyl-CoA synthetase (EC 6.2.1.-) I 5
NP3830A	0001_15ges	reliable	109.61 (4)	cytopl	fadA_8	MET	LIP	probable enoyl-CoA hydratase (EC 4.2.1.17) I 8
NP1580A	0001_13ges	reliable	94.85 (3)	cytopl	mvaD	MET	LIP	diphosphomevalonate decarboxylase (EC 4.1.1.33)
NP5124A	0005_38	reliable	85.57 (4)	cytopl	idiB_2	MET	LIP	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) II 2
NP2628A	0005_40	reliable	82.01 (2)	cytopl	acd_2	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 2
NP0032A	0001_14ges	reliable	74.83 (3)	cytopl	fadA_6	MET	LIP	probable enoyl-CoA hydratase (EC 4.2.1.17) I 6
NP0368A	0005_3	reliable	70.42 (2)	cytopl	mvaA_2	MET	LIP	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) 1
NP4050A	0005_73_2	reliable	68.13 (3)	cytopl	acd_10	MET	LIP	acyl-CoA dehydrogenase (EC 1.3.99.3) 10
NP1906A	0005_43	reliable	50.87 (4)	cytopl	hbd_4	MET	LIP	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) 4
NP0286A	0005_41	normal	33.97 (2)	cytopl	gnd	MET	CIM	6-phosphogluconate dehydrogenase (EC 1.1.1.44)
NP0606A	0005_41	normal	24.62 (1)	cytopl	prsA	MET	CIM	ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
NP2430A	0005_55_2	reliable	1359.98 (33)	cytopl	icd	MET	CIM	isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)
NP1994A	0005_50	reliable	1228.45 (29)	cytopl	citB_2	MET	CIM	aconitate hydratase (EC 4.2.1.3) 2
NP0404A	0001_04ges	reliable	961.91 (16)	cytopl	citB_1	MET	CIM	aconitate hydratase (EC 4.2.1.3) 1
NP1232A	0001_05ges	reliable	858.81 (18)	cytopl	korA	MET	CIM	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3), alpha subunit
NP3778A	0001_06ges	reliable	834.39 (17)	cytopl	fumC	MET	CIM	fumarate hydratase (EC 4.2.1.2)
NP5174A	0001_11ges	reliable	718.21 (10)	cytopl		MET	CIM	probable ribose-1,5-bisphosphate dehydrogenase

NP4046A	0005_32	reliable	492.68 (12)	cytopl	porA	MET	CIM	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1), alpha subunit
NP4354A	0005_40	reliable	486.10 (10)	cytopl	sucD	MET	CIM	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5), alpha subunit
NP1314A	0001_11ges	reliable	451.17 (12)	cytopl	citZ	MET	CIM	citrate (si)-synthase (EC 2.3.3.1)
NP1196A	0001_03ges	reliable	429.62 (11)	cytopl	ppsA	MET	CIM	pyruvate, water dikinase (EC 2.7.9.2)
NP2770A	0005_57_2	reliable	406.71 (8)	cytopl	rbcL	MET	CIM	ribulose-bisphosphate carboxylase (EC 4.1.1.39), large subunit
NP4266A	0001_13ges	reliable	405.77 (7)	cytopl	sdhB	MET	CIM	succinate dehydrogenase (EC 1.3.99.1), subunit B (iron-sulfur protein)
NP1234A	0005_41	reliable	394.00 (9)	cytopl	korB	MET	CIM	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3), beta subunit
NP4244A	0005_43	reliable	371.67 (7)	cytopl	citE	MET	CIM	citryl-CoA lyase (EC 4.1.3.34) (citrate lyase (EC 4.1.3.6) beta subunit; an ATP citrate synthase (EC 2.3.3.8) subunit)
NP4356A	0005_39	reliable	370.70 (8)	cytopl	sucC	MET	CIM	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5), beta subunit
NP4130A	0001_11ges	reliable	349.14 (7)	cytopl	pgk	MET	CIM	phosphoglycerate kinase (EC 2.7.2.3)
NP4044A	0001_12ges	reliable	317.60 (7)	cytopl	porB	MET	CIM	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1), beta subunit
NP0132A	0001_03ges	reliable	300.99 (7)	cytopl	mdh_1, pta_1	MET	CIM	malate dehydrogenase (oxaloacetate decarboxylating) (EC 1.1.1.40)/ phosphate acetyltransferase (EC 2.3.1.8) 1
NP4264A	0005_4	reliable	282.75 (7)	cytopl	sdhA	MET	CIM	succinate dehydrogenase (EC 1.3.99.1), subunit A (flavoprotein)
NP3160A	0005_43	reliable	275.71 (6)	cytopl	fba_2	MET	CIM	fructose-bisphosphate aldolase (EC 4.1.2.13) 2
NP4992A	0005_37	reliable	272.40 (6)	cytopl	pgi	MET	CIM	glucose-6-phosphate isomerase (EC 5.3.1.9)
NP0012A	0005_55_2	reliable	262.27 (6)	cytopl	gapB	MET	CIM	glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating) (EC 1.2.1.59)
NP1772A	0001_03ges	reliable	238.43 (7)	cytopl	mdh_2, pta_2	MET	CIM	malate dehydrogenase (oxaloacetate decarboxylating) (EC 1.1.1.40)/ phosphate acetyltransferase (EC 2.3.1.8) 2
NP1594A	0001_14ges	reliable	232.15 (8)	cytopl	fba_1	MET	CIM	fructose-bisphosphate aldolase (EC 4.1.2.13) 1
NP2846A	0001_09ges	reliable	217.65 (7)	cytopl	eno	MET	CIM	phosphopyruvate hydratase (EC 4.2.1.11) (enolase)
NP3764A	0005_55_2	reliable	122.57 (2)	cytopl	dld_1	MET	CIM	probable D-lactate dehydrogenase (EC 1.1.1.28) 1
NP3200A	0001_15ges	reliable	115.14 (3)	cytopl	deoC	MET	CIM	deoxyribose-phosphate aldolase (EC 4.1.2.4)
NP0498A	0001_11ges	reliable	102.44 (4)	cytopl	mdhA	MET	CIM	malate dehydrogenase (EC 1.1.1.37)
NP2182A	0005_44	reliable	101.59 (3)	cytopl	tpiA_1	MET	CIM	triosephosphate isomerase (EC 5.3.1.1) 1
NP1592A	0001_13ges	reliable	100.31 (3)	cytopl	fbp	MET	CIM	fructose-bisphosphatase (EC 3.1.3.11)
NP4492A	0001_13ges	reliable	45.33 (2)	cytopl	gldA	MET	CIM	glycerol-1-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261)
NP1452A	0005_1	reliable	43.10 (2)	cytopl	dld_2	MET	CIM	probable D-lactate dehydrogenase (EC 1.1.1.28)/ iron-sulfur protein (probable glycolate oxidase iron-sulfur subunit)
NP1964A	0005_54_2	reliable	41.30 (1)	cytopl	gpmA	MET	CIM	phosphoglycerate mutase (EC 5.4.2.1), 2,3-biphosphateglycerate-independent type

NP2290A	0001_17ges	normal	29.08 (3)	cytopl	purE	MET	NUM	phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21), catalytic subunit
NP1256A	0001_17ges	normal	28.29 (2)	cytopl	pyrE	MET	NUM	orotate phosphoribosyltransferase (EC 2.4.2.10)
NP3346A	0005_31	reliable	839.20 (15)	cytopl	nrdA_2	MET	NUM	ribonucleoside-diphosphate reductase (EC 1.17.4.1), alpha subunit 2
NP1662A	0005_53_2	reliable	483.66 (9)	cytopl	purNH	MET	NUM	phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)/ phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)
NP1530A	0005_54_2	reliable	455.33 (11)	cytopl	purA	MET	NUM	adenylosuccinate synthase (EC 6.3.4.4)
NP3384A	0005_34	reliable	443.52 (10)	cytopl	guaB_1	MET	NUM	IMP dehydrogenase (EC 1.1.1.205) 1/ CBS domain protein
NP1658A	0005_37	reliable	375.06 (8)	cytopl	purB	MET	NUM	adenylosuccinate lyase (EC 4.3.2.2)
NP0732A	0001_16ges	reliable	363.56 (7)	cytopl	purO	MET	NUM	IMP cyclohydrolase (EC 3.5.4.10), archaeal type
NP6168A	0001_06ges	reliable	347.42 (8)	cytopl	nrdA_1	MET	NUM	ribonucleoside-diphosphate reductase (EC 1.17.4.1), alpha subunit 1
NP1968A	0005_33	reliable	283.90 (6)	cytopl	pyrG	MET	NUM	CTP synthase (EC 6.3.4.2)
NP3666A	0001_19ges	reliable	283.75 (8)	cytopl	ndk	MET	NUM	nucleoside-diphosphate kinase (EC 2.7.4.6)
NP4996A	0001_12ges	reliable	271.57 (6)	cytopl	purC	MET	NUM	phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6)
NP0428A	0005_6	reliable	263.54 (6)	cytopl	pyrD	MET	NUM	dihydroorotate oxidase (EC 1.3.3.1)
NP1970A	0001_13ges	reliable	253.60 (6)	cytopl	guaAb	MET	NUM	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2), subunit B
NP3518A	0001_14ges	reliable	251.77 (5)	cytopl	pyrB	MET	NUM	aspartate carbamoyltransferase (EC 2.1.3.2), catalytic subunit
NP4312A	0001_06ges	reliable	238.91 (6)	cytopl	purF	MET	NUM	amidophosphoribosyltransferase (EC 2.4.2.14)
NP2982A	0001_04ges	reliable	227.85 (6)	cytopl	purL	MET	NUM	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3), component II
NP3180A	0005_42	reliable	191.49 (4)	cytopl	udp_2	MET	NUM	uridine phosphorylase (EC 2.4.2.3) 2
NP1706A	0001_07ges	reliable	173.67 (5)	cytopl	pyrC	MET	NUM	dihydroorotase (EC 3.5.2.3)
NP4910A	0001_15ges	reliable	162.63 (4)	cytopl	adk	MET	NUM	adenylate kinase (EC 2.7.4.3)
NP6166A	0001_12ges	reliable	146.94 (5)	cytopl	nrdB_1	MET	NUM	ribonucleoside-diphosphate reductase (EC 1.17.4.1), beta subunit 1
NP3510A	0001_14ges	reliable	124.88 (3)	cytopl	udp_1	MET	NUM	uridine phosphorylase (EC 2.4.2.3) 1
NP4142A	0001_15ges	reliable	119.73 (3)	cytopl	gch3	MET	NUM	GTP cyclohydrolase III (EC 3.5.4.-)
NP5006A	0005_41	reliable	113.42 (3)	cytopl	purU	MET	NUM	formyltetrahydrofolate deformylase (EC 3.5.1.10)
NP5010A	0001_14ges	reliable	113.14 (3)	cytopl	purQ	MET	NUM	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3), component I
NP3972A	0005_70_2	reliable	97.95 (3)	cytopl	purD	MET	NUM	phosphoribosylamine--glycine ligase (EC 6.3.4.13)
NP2272A	0001_16ges	reliable	96.94 (4)	cytopl	pyrH	MET	NUM	uridylate kinase (EC 2.7.4.-)
NP4426A	0001_14ges	reliable	91.47 (1)	cytopl	ham1	MET	NUM	Nucleoside-triphosphatase (EC 3.6.1.15)
NP3940A	0005_57_2	reliable	89.58 (2)	cytopl	purM	MET	NUM	phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)
NP2286A	0001_08ges	reliable	88.55 (4)	cytopl	purK	MET	NUM	phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21), ATPase subunit
NP5008A	0001_22ges	reliable	85.98 (3)	cytopl	purS	MET	NUM	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3), PurS component

NP1408A	0005_62_2	reliable	84.82 (2)	cytopl	upp	MET	NUM	uracil phosphoribosyltransferase (EC 2.4.2.9)
NP1426A	0001_17ges	reliable	71.05 (2)	cytopl	apt_1	MET	NUM	purine phosphoribosyltransferase 1 (adenine phosphoribosyltransferase (EC 2.4.2.7), xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22))
NP1254A	0001_16ges	reliable	68.28 (2)	cytopl	apt_2	MET	NUM	purine phosphoribosyltransferase 2 (adenine phosphoribosyltransferase (EC 2.4.2.7), xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22))
NP3958A	0005_35	reliable	65.13 (2)	cytopl	deoA	MET	NUM	thymidine phosphorylase (EC 2.4.2.4)
NP4914A	0001_17ges	reliable	60.13 (2)	cytopl	cmk	MET	NUM	cytidylate kinase (EC 2.7.4.14)
NP2142A	0001_15ges	reliable	55.77 (2)	cytopl	-	MET	NUM	predicted nucleotide kinase (EC 2.7.4.-)
NP3512A	0001_20ges	reliable	52.77 (2)	cytopl	cdd	MET	NUM	cytidine deaminase (EC 3.5.4.5)
NP5166A	0001_16ges	reliable	42.04 (1)	cytopl	dcd_1	MET	NUM	dCTP deaminase (EC 3.5.4.13) 1
NP4412A	0001_19ges	normal	37.86 (1)	cytopl	ribE	MET	COM	riboflavin synthase (EC 2.5.1.9) beta chain (6,7-dimethyl-8-ribityllumazine synthase)
NP0870A	0005_81_2	normal	32.85 (1)	cytopl	coaE	MET	COM	dephospho-CoA kinase (EC 2.7.1.24)
NP4378A	0005_75_2	normal	32.22 (2)	cytopl	birA2	MET	COM	biotin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15)
NP2138A	0001_16ges	normal	30.59 (2)	cytopl	mobA	MET	COM	molybdopterin-guanine dinucleotide biosynthesis protein A
NP0942A	0005_61_2	normal	28.90 (1)	extrac	apbA	MET	COM	2-dehydropantoate 2-reductase (EC 1.1.1.169)
NP1116A	0001_13ges	normal	21.80 (2)	cytopl	cbiH_1, cobJ_1	MET	COM	precorrin-3B C17-methyltransferase (EC 2.1.1.131) 1
NP1124A	0001_17ges	normal	21.72 (2)	cytopl	cbiT, cobL2	MET	COM	precorrin-8W decarboxylase (EC 1.-.-.-)
NP1092A	0001_02ges	reliable	881.03 (18)	cytopl	cobN	MET	COM	cobalt chelatase (EC 4.99.1.-)
NP1246A	0005_56_2	reliable	560.12 (11)	cytopl	hemL	MET	COM	glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)
NP1440A	0005_56_2	reliable	370.68 (8)	cytopl	moeA_1	MET	COM	molybdenum cofactor biosynthesis protein MoeA 1
NP3770A	0005_55_2	reliable	332.66 (5)	cytopl	folP_2	MET	COM	dihydropteroate synthase (EC 2.5.1.15) 2
NP4528A	0005_42	reliable	308.19 (11)	cytopl	pyroA	MET	COM	pyridoxine biosynthesis enzyme
NP1326A	0001_10ges	reliable	291.27 (7)	cytopl	hemC	MET	COM	hydroxymethylbilane synthase (EC 2.5.1.61) (porphobilinogen deaminase)
NP3828A	0005_41	reliable	239.01 (5)	cytopl	nadE_1	MET	COM	NAD(+) synthase (glutamine-hydrolyzing) (EC 6.3.5.1) 1
NP0968A	0005_35	reliable	200.66 (6)	cytopl	-	MET	COM	adenosylhomocysteinase (EC 3.3.1.1)
NP1088A	0001_14ges	reliable	198.72 (3)	cytopl	cbiE, cobL1	MET	COM	precorrin-6Y C5,15-methyltransferase (decarboxylating) (EC 2.1.1.132)
NP1118A	0001_12ges	reliable	182.08 (5)	cytopl	cbiG	MET	COM	cobalamin biosynthesis protein CbiG
NP1374A	0005_19	reliable	158.22 (3)	cytopl	dfp, coaBC	MET	COM	phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36)/ phosphopantothenate--cysteine ligase (EC 6.3.2.5)
NP2730A	0005_41	reliable	157.36 (5)	cytopl	menB	MET	COM	naphthoate synthase (EC 4.1.3.36)
NP0738A	0001_08ges	reliable	147.89 (4)	cytopl	cbiA, cobB	MET	COM	cobyrinic acid a,c-diamide synthase
NP1442A	0005_52_2	reliable	135.12 (3)	cytopl	moeA_2	MET	COM	molybdenum cofactor biosynthesis protein MoeA 2/ periplasmic molybdate-binding domain
NP0546A	0005_55_2	reliable	130.97 (3)	cytopl	thiD	MET	COM	phosphomethylpyrimidine kinase (EC 2.7.4.7)

NP1478A	0005_31	reliable	106.57 (3)	cytopl	folCP	MET	COM	folylpolyglutamate synthase (EC 6.3.2.17) / dihydropteroate synthase (EC 2.5.1.15)
NP2210A	0001_08ges	reliable	103.55 (4)	cytopl	thiC	MET	COM	thiamin biosynthesis protein ThiC
NP1356A	0001_15ges	reliable	102.96 (2)	anchN_lip	ribC	MET	COM	riboflavin synthase (EC 2.5.1.9), alpha subunit
NP1328A	0001_15ges	reliable	94.20 (3)	cytopl	hemX, cysG2	MET	COM	uroporphyrin-III C-methyltransferase (EC 2.1.1.107)
NP1120A	0001_12ges	reliable	86.79 (3)	cytopl	cbiF, cobM	MET	COM	precorrin-4 C11-methyltransferase (EC 2.1.1.133)
NP1122A	0001_15ges	reliable	85.66 (3)	cytopl	cbiL, cobI	MET	COM	precorrin-2 C20-methyltransferase (EC 2.1.1.130)
NP1174A	0005_40	reliable	85.57 (3)	cytopl	pncB	MET	COM	nicotinate phosphoribosyltransferase (EC 2.4.2.11)
NP2416A	0001_06ges	reliable	83.72 (2)	anchN_lip	nadB	MET	COM	L-aspartate oxidase (EC 1.4.3.16), quinolinate synthetase subunit B
NP4232A	0001_11ges	reliable	82.23 (3)	cytopl	bioF	MET	COM	8-amino-7-oxononanoate synthase (EC 2.3.1.47)
NP4054A	0001_15ges	reliable	78.70 (3)	cytopl	thiE	MET	COM	thiamine-phosphate pyrophosphorylase (EC 2.5.1.3)
NP4334A	0005_41	reliable	78.12 (3)	cytopl	panB	MET	COM	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
NP4814A	0005_43	reliable	67.54 (1)	cytopl	moaB_1	MET	COM	molybdenum cofactor biosynthesis protein B 1
NP0908A	0001_18ges	reliable	60.21 (1)	cytopl	nadM1_1	MET	COM	nicotinamide-nucleotide adenylyltransferase (EC 2.7.7.1) 1
NP1090A	0001_15ges	reliable	55.91 (4)	cytopl	cbiC, cobH	MET	COM	precorrin-8X methylmutase (EC 5.4.1.2)
NP1094A	0001_03ges	reliable	51.31 (3)	cytopl	chlID	MET	COM	magnesium chelatase (EC 6.6.1.1) (protoporphyrin IX magnesium-chelatase), fused subunits ChlI/ChlD
NP0736A	0001_10ges	reliable	50.29 (1)	cytopl	cobT	MET	COM	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase (EC 2.4.2.21)
NP1542A	0001_12ges	reliable	46.34 (1)	cytopl	cmo_2	MET	COM	molybdopterin-based tungsten cofactor biosynthesis protein 2
NP4236A	0001_11ges	reliable	42.68 (2)	cytopl	bioB	MET	COM	biotin synthase (EC 2.8.1.6)
NP2726A	0005_34	reliable	42.25 (2)	cytopl	menD	MET	COM	2-oxoglutarate decarboxylase (EC 4.1.1.71); 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (EC 4.1.3.-)
NP4230A	0001_16ges	reliable	40.93 (2)	cytopl	bioD	MET	COM	dethiobiotin synthase (EC 6.3.3.3)
NP5158A	0005_36	normal	38.58 (3)	cytopl	pmm_4	MET	CHM	phosphohexomutase 4 (phosphoglucomutase (EC 5.4.2.2), phosphomannomutase (EC 5.4.2.8))
NP2386A	0005_38	normal	24.88 (2)	cytopl	graD_5	MET	CHM	sugar nucleotidyltransferase (probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)) 4
NP4112A	0001_13ges	normal	24.05 (1)	cytopl	galE_2	MET	CHM	nucleoside-diphosphate-sugar epimerase 2 (probable UDP-glucose 4-epimerase (EC 5.1.3.2))
NP3366A	0005_8	normal	20.85 (1)	transm	-	MET	CHM	probable glycosyltransferase
NP4658A	0005_8	normal	20.85 (1)	transm	gtl_1	MET	CHM	glycosyltransferase 1 (probable dolichyl-phosphate beta-D-mannosyltransferase (EC 2.4.1.83))
NP4306A	0005_38	reliable	450.62 (12)	cytopl	celM	MET	CHM	probable cellulase (EC 3.2.1.4); probable endo-1,3(4)-beta-glucanase (EC 3.2.1.6)
NP3514A	0005_39	reliable	370.78 (7)	cytopl	pmm_3	MET	CHM	phosphohexomutase 3 (phosphoglucomutase (EC 5.4.2.2), phosphomannomutase (EC 5.4.2.8))

NP4432A	0005_39	reliable	329.68 (9)	cytopl	prpB_2	MET	CHM	probable carboxyvinyl-carboxyphosphonate phosphorylmutase (EC 2.7.8.23) 2 (carboxyphosphonoenolpyruvate phosphonomutase)
NP4674A	0005_43	reliable	212.95 (5)	cytopl	graD_3	MET	CHM	sugar nucleotidyltransferase (probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)) 7
NP4660A	0005_37	reliable	198.69 (3)	cytopl	pmm_1	MET	CHM	phosphohexomutase 1 (phosphoglucomutase (EC 5.4.2.2), phosphomannomutase (EC 5.4.2.8))
NP4652A	0005_40	reliable	191.32 (4)	cytopl	graD_1	MET	CHM	sugar nucleotidyltransferase (probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)) 1
NP4680A	0005_56_2	reliable	167.60 (3)	cytopl	graD_4	MET	CHM	probable sugar nucleotidyltransferase
NP3748A	0005_34	reliable	133.10 (3)	cytopl	-	MET	CHM	predicted sugar kinase (EC 2.7.1.-)
NP4662A	0001_11ges	reliable	132.62 (3)	cytopl	galE_1	MET	CHM	nucleoside-diphosphate-sugar epimerase 1 (probable UDP-glucose 4-epimerase (EC 5.1.3.2))
NP4654A	0005_53_2	reliable	103.94 (2)	cytopl	glmS_1	MET	CHM	glutamine--fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) 1
NP0384A	0001_12ges	reliable	91.27 (3)	cytopl	graD_7	MET	CHM	probable sugar nucleotidyltransferase
NP1922A	0005_6	reliable	83.95 (4)	transm	-	MET	CHM	hexosyltransferase 3
NP4668A	0001_07ges	reliable	54.17 (2)	anchN_lip	ugd_1	MET	CHM	UDP-glucose 6-dehydrogenase (EC 1.1.1.22) 1
NP4276A	0005_44	reliable	50.41 (2)	cytopl	graD_6	MET	CHM	sugar nucleotidyltransferase (probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)) 6
NP2322A	0005_56_2	reliable	47.24 (1)	anchN_lip	ugd_2	MET	CHM	UDP-glucose 6-dehydrogenase (EC 1.1.1.22) 2
NP1916A	0005_7	reliable	46.65 (1)	transm	gtl_2	MET	CHM	glycosyltransferase 2
NP1928A	0005_7	reliable	41.54 (1)	cytopl	-	MET	CHM	hexosyltransferase 4
NP1984A	0005_7	normal	38.76 (3)	cytopl	abc14a, pstB_1	TP_CP	TP	ABC-type transport system ATP-binding protein (probable substrate phosphate) 1
NP4730A	0001_14ges	normal	37.09 (1)	cytopl	abc20a, zurA_2	TP_CP	TP	ABC-type transport system ATP-binding protein (probable substrates zinc/manganese/metal ions) 2
NP1382A	0005_21	normal	37.02 (2)	cytopl	tpa06	TP_CP	TP	transport ATPase (EC 3.6.3.-) 6 (probable substrate arsenite)
NP1978A	0005_6	normal	36.47 (1)	anchN_lip	abc14s, pstS_1	TP_CP	TP	ABC-type transport system periplasmic phosphate-binding protein (probable substrate phosphate) 1
NP1774A	0005_7	normal	35.21 (1)	anchN_lip	abc04p1	TP_CP	TP	ABC-type transport system permease protein I (probable substrates polar amino acids)
NP1470A	0005_8	normal	32.32 (2)	cytopl	abc07a2, livG_3	TP_CP	TP	ABC-type transport system ATP-binding protein II (probable substrates branched-chain/neutral amino acids) 3
NP3044A	0005_8	normal	32.00 (2)	cytopl	abc22a	TP_CP	TP	ABC-type transport system ATP-binding protein
NP1164A	0001_08ges	normal	28.08 (2)	cytopl	tpa07	TP_CP	TP	transport ATPase (EC 3.6.3.-) 7 (probable substrate arsenite)
NP3924A	0005_8	normal	26.66 (1)	cytopl	abc12a, nosF_2	TP_CP	TP	ABC-type transport system ATP-binding protein (probable substrate copper) 2
NP4140A	0005_4	normal	25.64 (1)	anchN_lip	abc05s, livJ_1	TP_CP	TP	ABC-type transport system periplasmic substrate-binding protein (probable substrates branched-chain/neutral amino acids amide) 1

NP3918A	0005_8	normal	21.70 (1)	cytopl	abc11a, nosF_1	TP_CP	TP	ABC-type transport system ATP-binding protein (probable substrate copper) 1
NP1502A	0001_06ges	reliable	474.72 (12)	cytopl	abc31p_1, sufB_1	TP_CP	TP	ABC-type transport system permease protein (probable Fe-S cluster assembly protein) 1
NP1500A	0001_06ges	reliable	403.50 (8)	cytopl	abc31p_2, sufB_2	TP_CP	TP	ABC-type transport system permease protein (probable Fe-S cluster assembly protein) 2
NP3016A	0005_34	reliable	398.24 (11)	cytopl	sufB_3	TP_CP	TP	ABC-type transport system permease protein (probable Fe-S cluster assembly protein) 3
NP1504A	0001_12ges	reliable	351.21 (8)	cytopl	abc31a, sufC	TP_CP	TP	ABC-type transport system ATP-binding protein
NP0758A	0005_2	reliable	348.92 (6)	anchN_lip	abc01s, dppA_1	TP_CP	TP	ABC-type transport system periplasmic substrate-binding protein (probable substrates dipeptide/oligopeptide/nickel) 1
NP3424A	0005_5	reliable	299.47 (7)	anchN_lip	abc08s, livJ_4	TP_CP	TP	ABC-type transport system periplasmic substrate-binding protein (probable substrates branched-chain/neutral amino acids amide) 4
NP3916A	0005_2	reliable	297.55 (7)	extrac	abc11s, nosD_1	TP_CP	TP	ABC-type transport system substrate-binding protein (probable substrate copper) 1
NP1464A	0005_18	reliable	214.25 (5)	anchN_lip	abc07s, livJ_3	TP_CP	TP	ABC-type transport system periplasmic substrate-binding protein (probable substrates branched-chain/neutral amino acids amide) 3
NP2712A	0001_12ges	reliable	165.07 (3)	cytopl	argK	TP_CP	TP	transport ATPase, component for probable LAO/AO transport systems
NP6190A	0005_3	reliable	147.82 (3)	anchN_lip	abc06s, livJ_2	TP_CP	TP	ABC-type transport system periplasmic substrate-binding protein (probable substrates branched-chain/neutral amino acids amide) 2
NP2796A	0001_13ges	reliable	125.80 (4)	cytopl	abc23u	TP_CP	TP	ABC transport system cluster protein (predicted ABC-type transport system substrate-binding protein); predicted oxidoreductase (EC 1.-.-.-) 1
NP3432A	0001_15ges	reliable	119.32 (3)	cytopl	abc08a1, livF_4	TP_CP	TP	ABC-type transport system ATP-binding protein I (probable substrates branched-chain/neutral amino acids) 4
NP0544A	0005_19	reliable	89.43 (2)	anchN_lip	tp53_1	TP_CP	TP	predicted TRAP-type transport system periplasmic protein 1
NP3920A	0005_1	reliable	87.41 (2)	transm	abc11p, nosY_1	TP_CP	TP	ABC-type transport system permease protein (probable substrate copper) 1
NP5000A	0005_3	reliable	84.75 (3)	anchN_lip	abc03s, sfuA	TP_CP	TP	ABC-type transport system periplasmic substrate-binding protein (probable substrate iron(III)) 1
NP0042A	0005_1	reliable	84.57 (2)	transm	tp01_1	TP_CP	TP	transporter system 1 (probable substrates cationic amino acids), subunit 1
NP3040A	0005_8	reliable	83.47 (2)	anchN_lip	abc22s	TP_CP	TP	ABC-type transport system periplasmic substrate-binding protein (probable substrates tungstate/sulfate)
NP3922A	0005_2	reliable	75.74 (4)	extrac	abc12s, nosD_2	TP_CP	TP	ABC-type transport system substrate-binding protein (probable substrate copper) 2
NP3430A	0005_8	reliable	75.43 (2)	cytopl	abc08a2, livG_4	TP_CP	TP	ABC-type transport system ATP-binding protein II (probable substrates branched-chain/neutral amino acids) 4

NP1198A	0005_8	reliable	71.58 (1)	cytopl	abc26a	TP_CP	TP	ABC-type transport system ATP-binding protein (probable substrate copper) 4
NP1778A	0001_14ges	reliable	61.24 (1)	cytopl	abc04a	TP_CP	TP	ABC-type transport system ATP-binding protein (probable substrates glutamine/glutamate/polar amino acids)
NP6196A	0001_15ges	reliable	57.28 (1)	cytopl	abc06a2, livG_2	TP_CP	TP	ABC-type transport system ATP-binding protein II (probable substrates branched-chain/neutral amino acids) 2
NP1818A	0005_21	reliable	48.44 (2)	cytopl	tpa08	TP_CP	TP	transport ATPase (EC 3.6.3.-) 8 (probable substrate arsenite)
NP2442A	0005_7	reliable	46.39 (2)	cytopl	abc28a	TP_CP	TP	ABC-type transport system ATP-binding protein
NP3042A	0005_26	reliable	40.67 (1)	transm	abc22p	TP_CP	TP	ABC-type transport system permease protein (probable substrates tungstate/sulfate)
NP2448A	0005_22	normal	35.48 (1)	transm	coxB_1	TP_CP	EM	cytochrome-c-like terminal oxidase (EC 1.9.3.1), subunit II 1
NP2292A	0005_11	normal	30.46 (1)	transm	nuoA	TP_CP	EM	NADH dehydrogenase-like complex, subunit A
NP3954A	0005_3	normal	28.75 (1)	anchN_lip	hcp_1	TP_CP	EM	halocyanin 1
NP1030A	0005_52_2	reliable	918.06 (22)	cytopl	atpA	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit A.a (A-type ATP synthase)
NP1032A	0001_07ges	reliable	551.40 (12)	cytopl	atpB	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit B.a (A-type ATP synthase)
NP3508A	0001_08ges	reliable	351.43 (8)	cytopl	ndh	TP_CP	EM	probable NADH dehydrogenase (EC 1.6.99.3)
NP1026A	0001_12ges	reliable	332.47 (7)	cytopl	atpC	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit C.a (A-type ATP synthase)
NP3170A	0005_56_2	reliable	319.37 (6)	cytopl	etfB	TP_CP	EM	electron transfer flavoprotein, beta subunit
NP1018A	0001_17ges	reliable	201.10 (7)	cytopl	atpH	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit H.a (A-type ATP synthase)
NP2296A	0005_3	reliable	189.75 (4)	cytopl	nuoCD	TP_CP	EM	NADH dehydrogenase-like complex, subunit CD
NP1020A	0001_08ges	reliable	186.21 (3)	transm	atpI	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit I.a (A-type ATP synthase)
NP1024A	0001_13ges	reliable	183.20 (7)	cytopl	atpE	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit E.a (A-type ATP synthase)
NP1272A	0005_81_2	reliable	152.78 (3)	cytopl	ferA_1	TP_CP	EM	ferredoxin I 1
NP3168A	0005_54_2	reliable	131.56 (5)	cytopl	etfA	TP_CP	EM	electron transfer flavoprotein, alpha subunit
NP0938A	0005_11	reliable	126.01 (3)	anchN_lip	hcp_3	TP_CP	EM	halocyanin 3
NP2294A	0005_9	reliable	107.32 (2)	cytopl	nuoB	TP_CP	EM	NADH dehydrogenase-like complex, subunit B
NP4586A	0005_71_3	reliable	106.98 (6)	cytopl	ferA_3	TP_CP	EM	stress response protein/ ferredoxin I 3
NP0264A	0001_15ges	reliable	94.69 (3)	cytopl	atpD	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit D.a (A-type ATP synthase)
NP0494A	0001_19ges	reliable	87.05 (2)	cytopl	ferC	TP_CP	EM	ferredoxin III
NP2962A	0005_1	reliable	68.88 (2)	transm	cbaA, coxA_2	TP_CP	EM	cytochrome-ba3 oxidase (EC 1.9.3.1), subunit I
NP1022A	0005_29	reliable	63.45 (1)	transm	atpK	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit K.a (A-type ATP synthase)
NP1028A	0001_19ges	reliable	52.94 (2)	cytopl	atpF	TP_CP	EM	H(+)-transporting two-sector ATPase (EC 3.6.3.14) subunit F.a (A-type ATP synthase)
NP4568A	0005_11	reliable	43.36 (1)	cytopl	ferA_2	TP_CP	EM	ferredoxin I 2
NP3462A	0001_14ges	normal	31.02 (1)	cytopl	hchA	TP_CP	CP	probable chaperone protein

NP0944A	0005_54_2	normal	27.03 (1)	cytopl	cxp_1	TP_CP	CP	predicted carboxypeptidase (EC 3.4.17.-)
NP2404A	0005_73_2	reliable	750.36 (17)	cytopl	ftsZ_4	TP_CP	CP	cell division protein
NP0810A	0005_56_2	reliable	532.56 (9)	cytopl	ftsZ_1	TP_CP	CP	cell division protein
NP3738A	0005_23	reliable	449.82 (11)	cytopl	psmA	TP_CP	CP	proteasome alpha subunit
NP5324A	0005_20	reliable	344.94 (8)	cytopl	ftsZ_2	TP_CP	CP	cell division protein
NP0872A	0005_37	reliable	343.75 (9)	cytopl	pepB_2	TP_CP	CP	aminopeptidase (similar to leucyl aminopeptidase, aminopeptidase T) 2
NP3472A	0005_25	reliable	274.35 (6)	cytopl	psmB	TP_CP	CP	proteasome beta subunit
NP2128A	0005_56_2	reliable	203.75 (4)	cytopl	ftsZ_3	TP_CP	CP	cell division protein
NP3076A	0005_55_2	reliable	200.03 (4)	cytopl	pepQ	TP_CP	CP	aminopeptidase (high similarity to Xaa-Pro aminopeptidase (EC 3.4.11.9))
NP1524A	0001_08ges	reliable	180.00 (7)	cytopl	pan_2	TP_CP	CP	proteasome-activating nucleotidase 2
NP1140A	0005_38	reliable	170.28 (4)	cytopl	pepB_3	TP_CP	CP	aminopeptidase (similar to leucyl aminopeptidase, aminopeptidase T) 3
NP5038A	0005_18	reliable	160.46 (4)	cytopl	pan_1	TP_CP	CP	proteasome-activating nucleotidase 1
NP5040A	0005_32	reliable	116.08 (3)	cytopl	pepF	TP_CP	CP	oligoendopeptidase (EC 3.4.24.-)
NP0910A	0005_2	reliable	98.29 (2)	transm	lon	TP_CP	CP	endopeptidase La
NP5372A	0005_55_2	reliable	64.59 (2)	cytopl	cxp_2	TP_CP	CP	carboxypeptidase (similarity to Glutamate carboxypeptidase (EC 3.4.17.11), Carboxypeptidase G2)
NP0316A	0001_19ges	reliable	55.20 (2)	cytopl	hstA	TP_CP	CP	archaeal histone
NP4734A	0005_1	reliable	296.39 (4)	transm	-	TP_CP	CE	probable cell surface glycoprotein
NP4392A	0005_5	reliable	166.66 (3)	anchN_lip	-	TP_CP	CE	probable cell surface glycoprotein
NP0528A	0005_4	reliable	149.80 (4)	anchN_lip	-	TP_CP	CE	probable cell surface glycoprotein
NP4624A	0001_05ges	reliable	95.77 (2)	extrac	-	TP_CP	CE	probable cell surface glycoprotein
NP4616A	0005_3	reliable	81.56 (2)	anchN_lip	-	TP_CP	CE	probable cell surface glycoprotein
NP3390A	0005_2	reliable	76.62 (2)	transm	-	TP_CP	CE	probable cell surface glycoprotein
NP4622A	0005_14	reliable	56.75 (2)	transm	-	TP_CP	CE	probable cell surface glycoprotein
NP4620A	0005_14	reliable	56.42 (2)	transm	-	TP_CP	CE	probable cell surface glycoprotein
NP4348A	0005_10	normal	38.06 (2)	cytopl	tatA_1	TP_CP	SEC	sec-independent protein translocase component TatA 1
NP0182A	0001_06ges	normal	23.40 (1)	cytopl	ftsY	TP_CP	SEC	signal recognition particle receptor SRalpha
NP2524A	0005_22	normal	21.59 (1)	transm	secF	TP_CP	SEC	preprotein translocase subunit secF
NP0096A	0005_19	reliable	79.05 (3)	cytopl	srp54	TP_CP	SEC	signal recognition particle 54K protein
NP0812A	0005_13	reliable	71.77 (2)	transm	secE	TP_CP	SEC	preprotein translocase subunit secE
NP2522A	0005_2	reliable	55.44 (2)	transm	secD	TP_CP	SEC	preprotein translocase subunit secD
NP4350A	0005_11	reliable	39.15 (2)	cytopl	tatA_2	TP_CP	SEC	sec-independent protein translocase component TatA 2
NP2092A	0005_9	normal	19.32 (1)	anchN_lip	flaD	TP_CP	MOT	flagella cluster protein FlaD
NP2154A	0005_18	reliable	84.92 (3)	cytopl	flaCE	TP_CP	MOT	flagella accessory protein FlaCE
NP2156A	0001_16ges	reliable	64.49 (2)	cytopl	flaH	TP_CP	MOT	fla cluster protein FlaH
NP2158A	0005_18	reliable	57.41 (2)	cytopl	flaI	TP_CP	MOT	flagella biogenesis protein FlaI (probable flagellin secretion system protein FlaI)
NP0328A	0005_33	normal	32.02 (1)	cytopl	glyS	GIP	TL	glycine--tRNA ligase (EC 6.1.1.14)
NP4886A	0001_16ges	normal	27.93 (1)	cytopl	rpl6	GIP	TL	ribosomal protein L6
NP0130A	0001_03ges	reliable	1366.66 (26)	cytopl	tef2	GIP	TL	translation elongation factor aEF-2
NP1168A	0005_54_2	reliable	823.75 (18)	cytopl	aspS	GIP	TL	aspartate--tRNA ligase (EC 6.1.1.12)
NP1192A	0005_31	reliable	724.33 (13)	cytopl	metS	GIP	TL	methionine--tRNA ligase (EC 6.1.1.10)
NP0304A	0001_09ges	reliable	676.39 (14)	cytopl	tef1a	GIP	TL	translation elongation factor aEF-1 alpha subunit
NP3774A	0005_31	reliable	640.97 (11)	cytopl	gatE	GIP	TL	glutamyl-tRNA (Gln) amidotransferase (EC 6.3.5.-) subunit E
NP0610A	0005_30	reliable	614.06 (13)	cytopl	ileS	GIP	TL	isoleucine--tRNA ligase (EC 6.1.1.5)

NP4854A	0005_21	reliable	570.76 (11)	cytopl	rpl3	GIP	TL	ribosomal protein L3
NP0066A	0005_54_2	reliable	545.87 (11)	cytopl	argS	GIP	TL	arginine--tRNA ligase (EC 6.1.1.19)
NP0452A	0001_02ges	reliable	496.89 (11)	cytopl	leuS	GIP	TL	leucine--tRNA ligase (EC 6.1.1.4)
NP0710A	0001_02ges	reliable	496.30 (14)	cytopl	alaS	GIP	TL	alanine--tRNA ligase (EC 6.1.1.7)
NP4982A	0005_52_2	reliable	430.37 (8)	cytopl	tif5B	GIP	TL	translation initiation factor aIF-5B (bacterial-type IF2)
NP4452A	0001_14ges	reliable	425.63 (8)	cytopl	rpl1	GIP	TL	ribosomal prot
NP5084A	0005_54_2	reliable	408.78 (7)	cytopl	tif2g	GIP	TL	translation initiation factor aIF-2 gamma subunit
NP3204A	0001_17ges	reliable	395.53 (7)	cytopl	rps15	GIP	TL	ribosomal protein S15
NP4888A	0005_22	reliable	389.32 (6)	cytopl	rpl32R	GIP	TL	ribosomal protein L32.eR
NP0288A	0005_31	reliable	367.60 (8)	cytopl	valS	GIP	TL	valine--tRNA ligase (EC 6.1.1.9)
NP4890A	0001_19ges	reliable	342.34 (5)	cytopl	rpl19R	GIP	TL	ribosomal protein L19.eR
NP3210A	0001_16ges	reliable	335.44 (8)	cytopl	rps3aR	GIP	TL	ribosomal protein S3a.eR
NP4856A	0001_13ges	reliable	331.37 (6)	cytopl	rpl4R	GIP	TL	ribosomal protein L4.eR
NP2848A	0001_13ges	reliable	309.96 (5)	cytopl	rps2	GIP	TL	ribosomal protein S2
NP1692A	0001_06ges	reliable	299.10 (6)	cytopl	serS	GIP	TL	serine--tRNA ligase (EC 6.1.1.11)
NP2410A	0005_32	reliable	291.08 (6)	cytopl	thrS	GIP	TL	threonine--tRNA ligase (EC 6.1.1.3)
NP2830A	0001_18ges	reliable	290.49 (6)	cytopl	rps4	GIP	TL	ribosomal protein S4
NP1618A	0001_13ges	reliable	283.93 (4)	cytopl	tif2a	GIP	TL	translation initiation factor aIF-2 alpha subunit
NP2270A	0005_53_2	reliable	278.88 (8)	cytopl	lysS	GIP	TL	lysine--tRNA ligase (EC 6.1.1.6)
NP4450A	0001_11ges	reliable	278.87 (7)	cytopl	rpl10	GIP	TL	ribosomal protein L10
NP2810A	0005_57_2	reliable	249.91 (4)	cytopl	tyrS	GIP	TL	tyrosine--tRNA ligase (EC 6.1.1.1)
NP2282A	0001_17ges	reliable	247.38 (5)	cytopl	rps19R	GIP	TL	ribosomal protein S19.eR
NP2836A	0005_28	reliable	247.29 (4)	cytopl	rpl18R	GIP	TL	ribosomal protein L18.eR
NP5074A	0001_19ges	reliable	236.40 (5)	cytopl	rps24R	GIP	TL	ribosomal protein S24.eR
NP4866A	0001_12ges	reliable	227.71 (5)	cytopl	rps3	GIP	TL	ribosomal protein S3
NP0306A	0001_21ges	reliable	220.96 (6)	cytopl	rps10	GIP	TL	ribosomal protein S10
NP0694A	0005_33	reliable	219.59 (4)	cytopl	pheY	GIP	TL	phenylalanine--tRNA ligase (EC 6.1.1.20) beta subunit
NP3694A	0001_05ges	reliable	217.44 (6)	cytopl	gltS	GIP	TL	glutamate--tRNA ligase (EC 6.1.1.17)
NP4874A	0001_20ges	reliable	193.14 (5)	cytopl	rpl14	GIP	TL	ribosomal protein L14
NP4752A	0001_18ges	reliable	191.83 (4)	cytopl	tif5A	GIP	TL	translation initiation factor aIF-5A
NP0124A	0001_16ges	reliable	187.36 (5)	cytopl	rps7	GIP	TL	ribosomal protein S7
NP3684A	0001_21ges	reliable	176.18 (6)	cytopl	rpl21R	GIP	TL	ribosomal protein L21.eR
NP1796A	0005_54_2	reliable	174.40 (4)	cytopl	proS	GIP	TL	proline--tRNA ligase (EC 6.1.1.15)
NP1220A	0005_34	reliable	174.12 (5)	cytopl	aatB	GIP	TL	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit B
NP2492A	0001_08ges	reliable	167.95 (4)	cytopl	gatD	GIP	TL	glutamyl-tRNA(Gln) amidotransferase (EC 6.3.5.-), subunit D
NP5044A	0005_56_2	reliable	167.41 (3)	cytopl	hisS	GIP	TL	histidine--tRNA ligase (EC 6.1.1.21)
NP4860A	0001_13ges	reliable	162.43 (5)	cytopl	rpl2	GIP	TL	ribosomal protein L2
NP5232A	0001_20ges	reliable	159.18 (4)	cytopl	rpl37aR	GIP	TL	ribosomal protein L37a.eR
NP4876A	0001_17ges	reliable	158.80 (2)	cytopl	rpl24	GIP	TL	ribosomal protein L24
NP1006A	0001_17ges	reliable	158.12 (4)	cytopl	-	GIP	TL	probable ribosomal RNA assembly protein
NP4872A	0001_18ges	reliable	157.03 (3)	cytopl	rps17	GIP	TL	ribosomal protein S17
NP4864A	0001_19ges	reliable	154.46 (4)	cytopl	rpl22	GIP	TL	ribosomal protein L22
NP2838A	0005_27	reliable	152.00 (4)	cytopl	rpl13	GIP	TL	ribosomal protein L13
NP0442A	0001_07ges	reliable	142.08 (6)	cytopl	trpS	GIP	TL	tryptophan--tRNA ligase (EC 6.1.1.2)
NP4440A	0001_07ges	reliable	140.12 (3)	cytopl	cysS	GIP	TL	cysteine--tRNA ligase (EC 6.1.1.16)
NP0122A	0001_20ges	reliable	136.77 (3)	cytopl	rps12	GIP	TL	ribosomal protein S12
NP1014A	0001_21ges	reliable	136.71 (3)	cytopl	rpl31R	GIP	TL	ribosomal protein L31.eR
NP2832A	0001_21ges	reliable	132.72 (4)	cytopl	rps11	GIP	TL	ribosomal protein S11
NP2828A	0001_17ges	reliable	130.63 (5)	cytopl	rps13	GIP	TL	ribosomal protein S13
NP4896A	0001_17ges	reliable	129.41 (4)	cytopl	rpl30	GIP	TL	ribosomal protein L30
NP0696A	0001_06ges	reliable	114.50 (2)	cytopl	pheS	GIP	TL	phenylalanine--tRNA ligase (EC 6.1.1.20) alpha subunit
NP4878A	0005_77_2	reliable	111.40 (3)	cytopl	rps4R	GIP	TL	ribosomal protein S4.eR
NP2840A	0001_20ges	reliable	106.98 (2)	cytopl	rps9	GIP	TL	ribosomal protein S9
NP4884A	0001_19ges	reliable	92.85 (3)	cytopl	rps8	GIP	TL	ribosomal protein S8

NP4862A	0001_19ges	reliable	88.26 (4)	cytopl	rps19	GIP	TL	ribosomal protein S19
NP1368A	0005_26	reliable	85.29 (2)	cytopl	rps6R	GIP	TL	ribosomal protein S6.eR
NP1456A	0001_08ges	reliable	84.07 (2)	cytopl	aatA	GIP	TL	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit A
NP4894A	0001_17ges	reliable	83.31 (3)	cytopl	rps5	GIP	TL	ribosomal protein S5
NP4858A	0001_22ges	reliable	82.87 (2)	cytopl	rpl23	GIP	TL	ribosomal protein L23
NP4880A	0005_24_2	reliable	82.04 (2)	cytopl	rpl5	GIP	TL	ribosomal protein L5
NP3202A	0005_40	reliable	80.37 (3)	cytopl	tif2Ba_1	GIP	TL	translation initiation factor 2B alpha chain I
NP4798A	0001_18ges	reliable	80.09 (2)	cytopl	rps8R	GIP	TL	ribosomal protein S8.eR
NP4868A	0001_22ges	reliable	72.73 (2)	cytopl	rpl29	GIP	TL	ribosomal protein L29
NP4892A	0001_17ges	reliable	64.19 (1)	cytopl	rpl18	GIP	TL	ribosomal protein L18
NP4898A	0005_24_2	reliable	61.80 (2)	cytopl	rpl15	GIP	TL	ribosomal protein L15
NP0416A	0005_82_3	reliable	53.89 (3)	cytopl	rpl10R	GIP	TL	ribosomal protein L10.eR
NP4454A	0005_26	reliable	52.44 (2)	cytopl	rpl11	GIP	TL	ribosomal protein L11
NP4314A	0001_18ges	reliable	50.97 (2)	cytopl	tif2b	GIP	TL	translation initiation factor aIF-2 beta subunit
NP3664A	0001_19ges	reliable	49.72 (1)	cytopl	rpl24R	GIP	TL	ribosomal protein L24.eR
NP1258A	0001_20ges	reliable	42.24 (2)	cytopl	tif1A_1	GIP	TL	translation initiation factor aIF-1A I (bacterial-type IF1)
NP0246A	0005_27	reliable	39.14 (1)	cytopl	rpl15R	GIP	TL	ribosomal protein L15.eR
NP0538A	0001_03ges	normal	34.93 (2)	cytopl	mutS_1	GIP	RRR	DNA mismatch repair protein MutS 1
NP4496A	0005_78_2	normal	34.47 (3)	cytopl	-	GIP	RRR	repair DNA N-glycosylase / DNA-(apurinic or apyrimidinic site) lyase
NP0686A	0001_12ges	normal	30.43 (1)	cytopl	priB	GIP	RRR	probable DNA primase large subunit
NP1508A	0001_09ges	normal	26.66 (1)	cytopl	polB1	GIP	RRR	DNA-directed DNA polymerase (family B)
NP0854A	0005_52_2	normal	22.69 (1)	cytopl	-	GIP	RRR	DNA-directed DNA polymerase (EC 2.7.7.7) (family X) / ycdX protein homolog
NP1516A	0005_14	reliable	351.39 (7)	cytopl	rad50	GIP	RRR	DNA double-strand break repair rad50 ATPase
NP3498A	0005_53_2	reliable	347.63 (5)	cytopl	gyrB	GIP	RRR	DNA topoisomerase II subunit B (DNA gyrase)
NP3500A	0005_31	reliable	318.05 (7)	cytopl	gyrA	GIP	RRR	DNA gyrase subunit A
NP0878A	0001_12ges	reliable	271.24 (5)	cytopl	radA	GIP	RRR	DNA repair and recombination protein
NP1222A	0005_31	reliable	232.85 (6)	cytopl	topA	GIP	RRR	DNA topoisomerase I (EC 5.99.1.2)
NP0504A	0005_30	reliable	214.06 (5)	cytopl	uvrA	GIP	RRR	excinuclease ABC chain A
NP3482A	0005_31	reliable	186.01 (5)	cytopl	top6B	GIP	RRR	DNA topoisomerase VI subunit B (type II DNA topoisomerase)
NP0900A	0005_43	reliable	102.00 (5)	cytopl	rfcA	GIP	RRR	replication factor C small subunit I
NP0554A	0001_14ges	reliable	101.79 (3)	cytopl	pcn	GIP	RRR	DNA-directed DNA polymerase sliding clamp
NP4042A	0001_09ges	reliable	87.70 (4)	cytopl	phr_1	GIP	RRR	deoxyribodipyrimidine photolyase
NP3480A	0005_19	reliable	85.68 (2)	cytopl	top6A	GIP	RRR	DNA topoisomerase VI subunit A (type II DNA topoisomerase)
NP3784A	0001_13ges	reliable	83.11 (3)	cytopl	fen	GIP	RRR	flap structure-specific endonuclease
NP5118A	0001_11ges	reliable	69.52 (1)	cytopl	-	GIP	RRR	endonuclease IV
NP0492A	0001_04ges	reliable	46.95 (2)	cytopl	mer3_1	GIP	RRR	ATP-dependent DNA helicase (EC 3.6.1.-) 1
NP4822A	0005_7	normal	35.89 (1)	cytopl	tfbA_6	GIP	TC	transcription initiation factor TFB 6
NP2246A	0001_13ges	normal	35.79 (2)	cytopl	tfbA_3	GIP	TC	transcription initiation factor TFB 3
NP0114A	0005_31	reliable	1009.94 (19)	cytopl	rpoA1, rpoA	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A' (subunit A)
NP0110A	0005_35	reliable	231.92 (8)	cytopl	rpoB2	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B''
NP0112A	0001_05ges	reliable	221.05 (7)	cytopl	rpoB1	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B'
NP0116A	0005_37	reliable	182.46 (3)	cytopl	rpoA2, rpoC	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A'' (subunit C)
NP1064A	0005_26	reliable	138.97 (3)	cytopl	tbpE	GIP	TC	TATA-binding transcription initiation factor

NP2842A	0001_22ges	reliable	131.43 (3)	cytopl	rpoN	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit N
NP2834A	0001_11ges	reliable	121.83 (5)	cytopl	rpoD	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit D
NP3682A	0001_20ges	reliable	106.95 (2)	cytopl	rpoF	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit F
NP4162A	0001_20ges	reliable	86.89 (2)	cytopl	rpoL	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit L
NP1684A	0001_14ges	reliable	62.05 (2)	cytopl	tfbA_1	GIP	TC	transcription initiation factor TFB 1
NP5186A	0005_24_2	reliable	59.99 (2)	cytopl	tfbA_8	GIP	TC	transcription initiation factor TFB 8
NP5080A	0005_79_4	reliable	50.53 (2)	cytopl	rpoE1	GIP	TC	DNA-directed RNA polymerase (EC 2.7.7.6) subunit E'
NP0346A	0001_12ges	normal	37.62 (1)	cytopl	dnaJ	GIP	CHP	chaperone
NP0218A	0001_04ges	reliable	714.28 (14)	cytopl	dnaK	GIP	CHP	dnaK-type molecular chaperone hsp70
NP1008A	0001_04ges	reliable	674.36 (14)	cytopl	ths_1, thsA	GIP	CHP	thermosome subunit 1 (alpha subunit)
NP0570A	0001_04ges	reliable	470.50 (10)	cytopl	ths_2, thsB	GIP	CHP	thermosome subunit 2 (beta subunit)
NP1182A	0005_18	reliable	181.45 (4)	cytopl	ths_3	GIP	CHP	thermosome subunit 3
NP1744A	0005_27	reliable	66.94 (2)	cytopl	hsp20_3	GIP	CHP	hsp20-type chaperone
NP0210A	0005_53_2	reliable	463.39 (10)	cytopl	-	GIP	RMT	predicted mRNA 3'-end processing factor
NP2064A	0005_41	reliable	84.72 (4)	cytopl	nop56	GIP	RMT	probable pre-rRNA-processing protein nop56
NP0320A	0001_09ges	reliable	80.50 (2)	cytopl	cca	GIP	RMT	tRNA adenylyltransferase (EC 2.7.7.25), CCA-adding
NP0444A	0001_13ges	reliable	55.00 (3)	cytopl	endA	GIP	RMT	tRNA-intron endonuclease (EC 3.1.27.9)
NP2516A	0005_37	normal	35.24 (2)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; probable PAS/PAC domain protein
NP5130A	0005_31	normal	31.43 (1)	cytopl	-	ENV	SIG	probable GAF, PAS/PAC domain protein; probable predicted DNA binding protein
NP1756A	0005_3	normal	31.38 (1)	transm	htr22	ENV	SIG	transducer protein htr22
NP1846A	0005_58_3	normal	27.47 (2)	cytopl	-	ENV	SIG	GAF domain protein
NP0144A	0005_32	normal	26.16 (1)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; probable PAS/PAC domain protein
NP0138A	0005_34	normal	25.44 (1)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; response regulator
NP3752A	0001_12ges	normal	25.06 (2)	cytopl	-	ENV	SIG	signal-transducing histidine kinase
NP2560A	0001_16ges	normal	23.32 (1)	cytopl	-	ENV	SIG	probable stress response protein
NP6080A	0005_34	normal	23.12 (1)	cytopl	-	ENV	SIG	signal-transducing histidine kinase
NP0188A	0005_44	normal	23.05 (1)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; response regulator; PAS/PAC domain protein
NP1826A	0005_81_2	normal	22.09 (1)	cytopl	-	ENV	SIG	probable stress response protein
NP2656A	0005_14	reliable	669.51 (16)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; PAS/PAC domain protein
NP3212A	0005_2	reliable	423.27 (8)	cytopl	htr31	ENV	SIG	transducer protein htr31
NP4696A	0005_14	reliable	329.93 (7)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; PAS/PAC domain protein
NP1912A	0005_14	reliable	288.81 (8)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; probable GAF, PAS/PAC domain protein
NP2906A	0001_17ges	reliable	283.53 (6)	cytopl	-	ENV	SIG	response regulator
NP1644A	0005_2	reliable	279.30 (6)	transm	mpcT, htr14	ENV	SIG	transducer protein mpcT
NP1486A	0005_18	reliable	271.57 (6)	cytopl	htr35	ENV	SIG	transducer protein htr35
NP2170A	0005_77_2	reliable	241.08 (6)	cytopl	cheR	ENV	SIG	protein-glutamate O-methyltransferase (EC 2.1.1.80)
NP4146A	0001_16ges	reliable	232.20 (4)	cytopl	cheW	ENV	SIG	purine-binding taxis protein
NP2174A	0005_73_2	reliable	204.94 (3)	cytopl	cheB	ENV	SIG	protein-glutamate methylesterase (EC 3.1.1.61)
NP3638A	0005_2	reliable	203.28 (4)	transm	htr8	ENV	SIG	transducer protein htr8
NP2176A	0005_1	reliable	190.61 (3)	transm	htr21	ENV	SIG	transducer protein htr21

NP4832A	0005_3	reliable	190.59 (4)	transm	htrII, htr2	ENV	SIG	sensory rhodopsin II transducer
NP5274A	0005_35	reliable	184.26 (6)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; probable GAF, PAS/PAC domain protein
NP3374A	0005_33	reliable	168.83 (3)	cytopl	htr33	ENV	SIG	transducer protein htr33
NP2892A	0005_2	reliable	162.52 (4)	cytopl	htr29	ENV	SIG	transducer protein htr28
NP1154A	0005_36	reliable	159.79 (4)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; PAS/PAC domain protein
NP2760A	0005_34	reliable	135.54 (2)	cytopl	htr25	ENV	SIG	transducer protein htr25
NP3458A	0005_56_2	reliable	112.97 (2)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; response regulator
NP5120A	0005_33	reliable	112.78 (3)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; probable PAS/PAC domain protein
NP1860A	0005_2	reliable	105.54 (3)	cytopl	htr26	ENV	SIG	transducer protein htr26
NP3144A	0005_86_2	reliable	91.35 (3)	cytopl	-	ENV	SIG	probable stress response protein
NP0036A	0005_82_2	reliable	90.13 (3)	cytopl	-	ENV	SIG	probable stress response protein
NP0862A	0005_32	reliable	89.43 (3)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; PAS/PAC domain protein
NP2172A	0001_03ges	reliable	82.28 (4)	cytopl	cheA	ENV	SIG	taxis sensor histidine kinase (EC 2.7.3.-)
NP5138A	0001_21ges	reliable	72.88 (2)	cytopl	-	ENV	SIG	probable stress response protein
NP0060A	0005_32	reliable	70.38 (1)	cytopl	hemAT, htr10	ENV	SIG	transducer protein hemAT
NP1322A	0005_32	reliable	70.38 (1)	cytopl	htr27	ENV	SIG	transducer protein htr27
NP0690A	0001_15ges	reliable	70.17 (2)	cytopl	-	ENV	SIG	probable stress response protein
NP3134A	0005_2	reliable	66.67 (2)	transm	htr24	ENV	SIG	transducer protein htr24
NP2698A	0001_17ges	reliable	65.68 (2)	cytopl	-	ENV	SIG	probable stress response protein
NP2742A	0005_32	reliable	64.18 (2)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; PAS/PAC domain protein
NP0090A	0005_30	reliable	56.61 (1)	cytopl	-	ENV	SIG	signal-transducing histidine kinase; probable GAF, PAS/PAC domain protein
NP0056A	0001_17ges	reliable	54.37 (1)	cytopl	-	ENV	SIG	probable stress response protein
NP1642A	0005_32	reliable	52.83 (2)	cytopl	htr34	ENV	SIG	transducer protein htr34
NP2104A	0005_18	reliable	42.63 (2)	cytopl	cheC_1	ENV	SIG	taxis cluster protein CheC 1
NP5024A	0001_20ges	reliable	41.46 (1)	cytopl	-	ENV	SIG	probable stress response protein
NP0682A	0001_21ges	reliable	41.14 (1)	cytopl	-	ENV	SIG	response regulator
NP1678A	0001_22ges	normal	37.23 (2)	cytopl	-	ENV	REG	probable transcription regulator
NP4416A	0001_20ges	normal	34.17 (2)	cytopl	-	ENV	REG	probable DNA binding protein
NP6176A	0001_15ges	normal	24.84 (2)	cytopl	-	ENV	REG	transcription regulator
NP1352A	0001_22ges	normal	21.38 (1)	cytopl	-	ENV	REG	probable transcription regulator
NP5110A	0001_16ges	reliable	286.82 (5)	cytopl	-	ENV	REG	probable KaiC-like transcriptional regulator 3
NP4082A	0001_16ges	reliable	239.67 (5)	cytopl	-	ENV	REG	transcription regulator
NP3002A	0001_21ges	reliable	175.37 (5)	cytopl	-	ENV	REG	probable transcription regulator
NP0078A	0001_18ges	reliable	161.08 (4)	cytopl	-	ENV	REG	transcription regulator
NP5258A	0001_12ges	reliable	155.44 (3)	cytopl	argX	ENV	REG	probable arginine biosynthesis regulator (lysine biosynthesis regulator lysX homolog)
NP3658A	0001_15ges	reliable	117.88 (2)	cytopl	dpsA	ENV	REG	DNA-binding protein, ferretin-like domain protein
NP4258A	0001_15ges	reliable	90.48 (2)	cytopl	-	ENV	REG	transcription regulator
NP0654A	0005_32	reliable	89.90 (2)	cytopl	bat	ENV	REG	bacterioopsin activator
NP4080A	0001_16ges	reliable	80.98 (2)	cytopl	-	ENV	REG	transcription regulator
NP4026A	0001_17ges	reliable	80.08 (3)	cytopl	-	ENV	REG	transcription regulator
NP1386A	0001_12ges	reliable	73.36 (3)	cytopl	phoU_5	ENV	REG	probable transport system regulatory protein (probable substrate phosphate)
NP1496A	0001_20ges	reliable	60.09 (1)	cytopl	-	ENV	REG	probable transcription regulator
NP3058A	0001_19ges	reliable	56.72 (2)	cytopl	-	ENV	REG	probable transcription regulator
NP6106A	0001_13ges	reliable	51.86 (2)	cytopl	tp30u3, trkA_3	ENV	REG	probable transcriptional regulator/ probable TrkA-domain protein (NAD-binding protein)
NP3608A	0005_78_2	reliable	50.25 (3)	cytopl	-	ENV	REG	transcription regulator
NP2878A	0001_14ges	reliable	44.44 (1)	cytopl	-	ENV	REG	transcription regulator
NP5052A	0001_18ges	reliable	44.09 (2)	cytopl	-	ENV	REG	transcription regulator

NP1136A	0001_15ges	normal	38.55 (2)	cytopl	-	MIS	GEN	hydrolase (probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)) 5
NP3688A	0001_22ges	normal	38.47 (1)	cytopl	-	MIS	GEN	probable RNA-binding protein
NP0464A	0001_16ges	normal	37.63 (1)	cytopl	-	MIS	GEN	predicted glutamine amidotransferase
NP2732A	0005_22	normal	36.12 (1)	cytopl	-	MIS	GEN	men cluster protein (homolog 4 to transducer protein)
NP1180A	0005_7	normal	35.82 (1)	cytopl	-	MIS	GEN	glycosyltransferase homolog
NP1228A	0001_20ges	normal	35.58 (1)	cytopl	glo_2	MIS	GEN	lyase / dioxygenase 2 (probable lactoylglutathione lyase (EC 4.4.1.5), aromatic compounds dioxygenase (EC 1.13.11.-))
NP0648A	0005_12	normal	34.38 (1)	cytopl	blp	MIS	GEN	blp-like protein
NP1974A	0005_9	normal	31.88 (1)	cytopl	-	MIS	GEN	hydrolase (probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)) 9
NP2794A	0005_80_2	normal	31.66 (1)	cytopl	-	MIS	GEN	predicted DNA binding protein
NP2162A	0001_14ges	normal	29.85 (1)	cytopl	-	MIS	GEN	conserved fla operon protein
NP0390A	0001_20ges	normal	29.76 (1)	cytopl	-	MIS	GEN	homolog 2 to thiosulfate sulfurtransferase (EC 2.8.1.1)
NP0502A	0001_13ges	normal	29.23 (1)	cytopl	-	MIS	GEN	probable dehydrogenase/ reductase (EC 1.1.1.-) 12
NP2986A	0005_3	normal	26.58 (1)	anchN_lip	-	MIS	GEN	homolog to ABC-type transport system periplasmic substrate-binding protein (probable substrates dipeptide/oligopeptide/nickel)
NP0072A	0001_15ges	normal	25.39 (2)	cytopl	-	MIS	GEN	rib operon protein
NP3098A	0001_19ges	normal	25.18 (1)	cytopl	-	MIS	GEN	homolog to stress response protein
NP4750A	0005_3	normal	24.16 (1)	anchN_lip	-	MIS	GEN	predicted cell surface protein/ lipoprotein
NP2066A	0001_18ges	normal	23.46 (2)	cytopl	-	MIS	GEN	glutaredoxin homolog
NP1230A	0005_77_2	normal	19.47 (1)	cytopl	-	MIS	GEN	homolog to cytochrome-b5 reductase (EC 1.6.2.2)
NP3998A	0005_52_2	reliable	1176.28 (28)	cytopl	-	MIS	GEN	AAA-type ATPase (transitional ATPase homolog)
NP1126A	0005_6	reliable	945.54 (19)	extrac	-	MIS	GEN	stomatin homolog
NP3698A	0005_38	reliable	839.10 (23)	cytopl	-	MIS	GEN	predicted hydrolase
NP0198A	0005_52_2	reliable	783.45 (14)	cytopl	-	MIS	GEN	predicted ATPase
NP0256A	0005_55_2	reliable	770.21 (12)	cytopl	-	MIS	GEN	probable amidase
NP3876A	0005_30	reliable	686.32 (19)	cytopl	-	MIS	GEN	predicted helicase (EC 3.6.1.-)
NP3072A	0001_04ges	reliable	545.74 (15)	cytopl	-	MIS	GEN	AAA-type ATPase (transitional ATPase homolog)
NP3062A	0005_57_2	reliable	487.14 (8)	cytopl	trpD_3	MIS	GEN	homolog to anthranilate phosphoribosyltransferase (EC 2.4.2.18)
NP2252A	0005_56_2	reliable	457.45 (7)	cytopl	-	MIS	GEN	AAA-type ATPase
NP4504A	0005_75_2	reliable	449.84 (14)	cytopl	cbs_1	MIS	GEN	CBS domain protein 1
NP2824A	0005_56_2	reliable	398.58 (7)	cytopl	mrp_1	MIS	GEN	ATP-binding protein Mrp 1
NP1282A	0005_57_2	reliable	376.80 (8)	cytopl	-	MIS	GEN	replication factor A homolog
NP3118A	0005_21	reliable	364.90 (7)	cytopl	cheC_2	MIS	GEN	taxis cluster protein CheC 2
NP2166A	0005_61_2	reliable	364.13 (10)	cytopl	-	MIS	GEN	conserved che operon protein
NP1638A	0001_15ges	reliable	355.75 (5)	cytopl	-	MIS	GEN	protein N-acetyltransferase homolog
NP3228A	0005_4	reliable	326.47 (7)	cytopl	-	MIS	GEN	homolog 2 to phycocyanobilin lyase subunit (EC 4.-.-.-)
NP0930A	0005_53_2	reliable	308.40 (8)	cytopl	-	MIS	GEN	probable helicase
NP0406A	0001_16ges	reliable	305.11 (6)	cytopl	-	MIS	GEN	translation initiation factor aIF-2 beta subunit homolog ; predicted RNA-binding protein
NP4488A	0001_12ges	reliable	303.81 (8)	cytopl	-	MIS	GEN	predicted oxidoreductase (EC 1.-.-.-) 2
NP2894A	0005_19	reliable	282.47 (7)	cytopl	cbs_3	MIS	GEN	CBS domain protein 3
NP3960A	0001_06ges	reliable	259.99 (5)	cytopl	-	MIS	GEN	replication factor A homolog
NP1710A	0001_22ges	reliable	255.47 (5)	cytopl	-	MIS	GEN	homolog to stress response protein

NP4274A	0005_18	reliable	254.11 (5)	cytopl	-	MIS	GEN	homolog 1 to lysine biosynthesis regulator/ribosomal protein S6 modification enzyme (glutaminyl transferase)
NP4166A	0005_60_2	reliable	253.51 (7)	cytopl	-	MIS	GEN	probable dehydrogenase/ reductase (EC 1.1.1.-) 6
NP0326A	0001_13ges	reliable	250.03 (7)	cytopl	cbs_2	MIS	GEN	CBS domain protein 2
NP1518A	0005_18	reliable	248.87 (6)	cytopl	-	MIS	GEN	conserved DNA repair operon protein (probable DNA repair exonuclease)
NP1904A	0001_05ges	reliable	237.08 (5)	cytopl	ilvB_2, mdlC	MIS	GEN	thiamine pyrophosphate-requiring enzyme (Acetolactate synthase (EC 2.2.1.6) 2, large subunit 2; benzoylformate decarboxylase (EC 4.1.1.7))
NP2232A	0005_73_2	reliable	225.87 (4)	cytopl	-	MIS	GEN	homolog 3 to phycocyanobilin lyase subunit (EC 4.-.-.-)
NP1178A	0005_9	reliable	208.94 (5)	cytopl	-	MIS	GEN	homolog 3 to S-adenosylmethionine-dependent methyltransferase (EC 2.1.1.-) 3
NP1110A	0001_16ges	reliable	208.38 (4)	cytopl	-	MIS	GEN	conserved cobalamin operon protein
NP4234A	0001_12ges	reliable	200.21 (5)	cytopl	-	MIS	GEN	biotin operon protein
NP1160A	0005_7	reliable	190.99 (4)	cytopl	-	MIS	GEN	probable dehydrogenase/ reductase (EC 1.1.1.-) 7
NP0532A	0005_57_2	reliable	186.77 (2)	cytopl	trpD_2	MIS	GEN	homolog to anthranilate phosphoribosyltransferase (EC 2.4.2.18)
NP4456A	0001_12ges	reliable	181.73 (4)	cytopl	-	MIS	GEN	GTP-binding protein
NP1948A	0001_03ges	reliable	177.83 (5)	cytopl	-	MIS	GEN	sugar metabolism cluster protein (sugar nucleotidyltransferase homolog)
NP2168A	0005_7	reliable	177.67 (5)	cytopl	-	MIS	GEN	conserved che operon protein (homolog 1 to phycocyanobilin lyase subunit (EC 4.-.-.-))
NP2406A	0005_7	reliable	176.92 (4)	cytopl	nolA_1	MIS	GEN	NADH dehydrogenase 32K chain homolog
NP2178A	0001_07ges	reliable	174.27 (3)	cytopl	rtcB_1	MIS	GEN	RtcB-like protein 1
NP0726A	0005_43	reliable	171.52 (3)	cytopl	-	MIS	GEN	dehydrogenase/ reductase (EC 1.1.1.-) 2
NP1204A	0001_16ges	reliable	168.84 (5)	cytopl	-	MIS	GEN	predicted phosphoribosyltransferase (EC 2.4.2.-)
NP0356A	0005_41	reliable	165.42 (2)	cytopl	-	MIS	GEN	probable methyltransferase
NP4238A	0005_5	reliable	157.78 (4)	anchN_lip	-	MIS	GEN	homolog to ABC-type transport system periplasmic substrate-binding protein (probable substrates branched-chain/neutral amino acids amide) 4
NP4498A	0001_12ges	reliable	152.46 (3)	cytopl	-	MIS	GEN	nirG protein homolog / nirH protein homolog
NP4932A	0005_44	reliable	148.47 (3)	cytopl	-	MIS	GEN	homolog 1 to KaiC-like transcriptional regulator
NP2670A	0005_39	reliable	145.43 (6)	cytopl	-	MIS	GEN	homolog 4 to thiosulfate sulfurtransferase (EC 2.8.1.1)/ hydrolase (probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)) 2
NP4566A	0005_55_2	reliable	145.25 (3)	cytopl	-	MIS	GEN	probable amidase
NP1384A	0001_14ges	reliable	142.29 (4)	cytopl	-	MIS	GEN	thioredoxin reductase homolog
NP2494A	0005_42	reliable	139.70 (3)	cytopl	-	MIS	GEN	protein N-acetyltransferase homolog
NP1294A	0005_43	reliable	137.98 (3)	cytopl	-	MIS	GEN	probable dehydrogenase/ reductase (EC 1.1.1.-) 9
NP3994A	0001_14ges	reliable	133.97 (2)	cytopl	-	MIS	GEN	hydrolase (BioH-like protein)
NP3064A	0001_12ges	reliable	131.95 (3)	cytopl	-	MIS	GEN	nirG protein homolog / nirH protein homolog
NP2994A	0005_75_2	reliable	128.13 (6)	cytopl	leuA_3	MIS	GEN	homolog to 2-isopropylmalate synthase (EC 2.3.3.13), homocitrate synthase (EC 2.3.3.14)

NP0756A	0001_16ges	reliable	127.31 (3)	cytopl	-	MIS	GEN	predicted F420-dependent NADP reductase (EC 1.-.-.-)
NP4940A	0005_55_2	reliable	125.74 (2)	cytopl	mrp_2	MIS	GEN	ATP-binding protein Mrp 2
NP0874A	0001_06ges	reliable	114.52 (4)	cytopl	-	MIS	GEN	ribonuclease R homolog
NP1902A	0001_12ges	reliable	111.40 (3)	cytopl	-	MIS	GEN	monooxygenase (EC 1.14.14.-) (homolog to alkanesulfonate monooxygenase) 2
NP4078A	0005_35	reliable	100.88 (3)	cytopl	-	MIS	GEN	hydrolase (EC 3.5.1.-)/ carboxypeptidase (EC 3.4.-.-)
NP4460A	0001_14ges	reliable	99.84 (3)	cytopl	glo_3	MIS	GEN	lyase/ dioxygenase 3 (probable lactoylglutathione lyase (EC 4.4.1.5), aromatic compounds dioxygenase (EC 1.13.11.-))
NP1688A	0001_12ges	reliable	98.88 (2)	cytopl	-	MIS	GEN	hydrolase (probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)) 4
NP3024A	0005_5	reliable	97.40 (5)	cytopl	-	MIS	GEN	homolog to predicted electron-transferring-flavoprotein dehydrogenase (EC 1.5.5.1)
NP4092A	0001_18ges	reliable	93.87 (3)	cytopl	apa	MIS	GEN	probable bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)
NP4562A	0005_77_2	reliable	90.03 (4)	cytopl	-	MIS	GEN	probable sugar dehydrogenase (EC 1.1.1.-)
NP0594A	0001_16ges	reliable	87.30 (3)	cytopl	-	MIS	GEN	probable GTP-binding protein
NP4218A	0001_19ges	reliable	84.28 (2)	cytopl	-	MIS	GEN	peroxiredoxin homolog
NP0792A	0001_14ges	reliable	82.52 (2)	cytopl	-	MIS	GEN	homolog to hydrolases
NP5076A	0001_16ges	reliable	79.97 (2)	cytopl	-	MIS	GEN	conserved rpo operon protein
NP4330A	0001_19ges	reliable	77.53 (2)	cytopl	cbs_6	MIS	GEN	CBS domain protein 6
NP2900A	0001_17ges	reliable	76.99 (2)	cytopl	-	MIS	GEN	peroxiredoxin homolog
NP3948A	0005_90	reliable	76.17 (2)	cytopl	glo_1	MIS	GEN	lyase/ dioxygenase 1 (probable lactoylglutathione lyase (EC 4.4.1.5), aromatic compounds dioxygenase (EC 1.13.11.-))
NP5144A	0005_53_2	reliable	74.52 (2)	cytopl	-	MIS	GEN	predicted helicase (EC 3.6.1.-)
NP4278A	0001_12ges	reliable	74.30 (2)	cytopl	-	MIS	GEN	probable dehydrogenase/ reductase (EC 1.1.1.-) 8
NP1900A	0001_13ges	reliable	72.88 (2)	cytopl	-	MIS	GEN	probable dehydrogenase/ reductase (EC 1.1.1.-) 5
NP3970A	0005_41	reliable	71.29 (2)	cytopl	-	MIS	GEN	hydrolase (probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)) 3
NP0308A	0001_14ges	reliable	66.89 (1)	cytopl	-	MIS	GEN	sugar epimerase/dehydratase homolog
NP2718A	0001_16ges	reliable	66.09 (2)	cytopl	-	MIS	GEN	reductase (probable nitrate reductase (EC 1.7.99.4)/ sulfite dehydrogenase (EC 1.8.2.1)) 1
NP3878A	0005_78_2	reliable	66.09 (3)	cytopl	-	MIS	GEN	probable ADP-ribosylglycohydrolase
NP1712A	0001_18ges	reliable	64.90 (3)	cytopl	-	MIS	GEN	protein N-acetyltransferase homolog
NP0822A	0005_11	reliable	64.58 (2)	cytopl	cinA_3	MIS	GEN	CinA-like domain protein 3
NP1056A	0001_13ges	reliable	61.15 (2)	cytopl	-	MIS	GEN	monooxygenase (EC 1.14.14.-) (homolog to alkanesulfonate monooxygenase) 1
NP5068A	0001_13ges	reliable	59.72 (2)	cytopl	-	MIS	GEN	protein N-acetyltransferase homolog
NP5026A	0005_34	reliable	57.89 (3)	cytopl	-	MIS	GEN	predicted ATPase
NP5218A	0001_14ges	reliable	57.73 (1)	cytopl	-	MIS	GEN	sugar epimerase/dehydratase homolog
NP0300A	0001_17ges	reliable	57.44 (2)	cytopl	-	MIS	GEN	predicted allosteric regulator of homoserine dehydrogenase
NP4374A	0005_60_2	reliable	56.26 (2)	cytopl	-	MIS	GEN	monooxygenase (EC 1.14.14.-) (homolog to alkanesulfonate monooxygenase) 2
NP1306A	0005_52_2	reliable	53.01 (1)	cytopl	rad3b	MIS	GEN	DNA repair helicase homolog
NP4762A	0001_14ges	reliable	52.68 (1)	cytopl	-	MIS	GEN	probable dehydrogenase/ reductase (EC 1.1.1.-) 14
NP5148A	0001_14ges	reliable	52.61 (1)	cytopl	cinA_2	MIS	GEN	CinA-like domain protein 2
NP3802A	0001_13ges	reliable	52.20 (2)	cytopl	-	MIS	GEN	homolog to ornithine cyclodeaminase (EC 4.3.1.12)

NP4370A	0005_42	reliable	51.94 (1)	cytopl	-	MIS	GEN	dehydrogenase/ reductase (EC 1.1.1.-) 3
NP0092A	0001_14ges	reliable	51.19 (1)	cytopl	-	MIS	GEN	hydrolase (probable hydroxyacylglutathione hydrolase (EC 3.1.2.6)) 8
NP2480A	0001_13ges	reliable	49.10 (3)	cytopl	-	MIS	GEN	mandelate racemase homolog / muconate lactonizing enzyme homolog
NP0940A	0001_20ges	reliable	44.93 (1)	cytopl	-	MIS	GEN	homolog to nitrogen fixation protein NifU
NP3436A	0005_84_2	reliable	43.79 (1)	cytopl	-	MIS	GEN	homolog to stress response protein
NP5312A	0001_06ges	reliable	43.03 (2)	cytopl	-	MIS	GEN	predicted Fe-S oxidoreductase
NP3054A	0001_16ges	reliable	39.40 (2)	cytopl	nudF_2	MIS	GEN	ADP-ribose pyrophosphatase homolog
NP4964A	0005_70_2	normal	38.57 (1)	cytopl	aor_1	MIS	MIS	aldehyde ferredoxin oxidoreductase (EC 1.2.7.5) 1
NP0248A	0005_77_2	normal	38.41 (2)	cytopl	-	MIS	MIS	predicted RIO-like serine/threonine protein kinase I
NP3708A	0005_55_2	normal	37.05 (2)	anchN_lip	-	MIS	MIS	predicted NAD-binding protein 3 (probable Kef-type transporter subunit)
NP2134A	0005_61_2	normal	35.62 (2)	cytopl	hcpE_1	MIS	MIS	probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3.-) 1; probable 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase (EC 4.1.1.68) 1
NP4946A	0005_4	normal	34.35 (1)	cytopl	fdhB_1, dmsB_1	MIS	MIS	conserved anaerobic dehydrogenase subunit/ anaerobic dehydrogenase (probable formate dehydrogenase (EC 1.2.1.2), dimethyl sulfoxide reductase (EC 1.8.-.-)), iron-sulfur binding subunit 1
NP4924A	0001_18ges	normal	31.69 (1)	cytopl	act_1	MIS	MIS	acyl-CoA thioester hydrolase (EC 3.1.2.-) 1
NP5034A	0005_9	normal	29.58 (1)	cytopl	-	MIS	MIS	S-adenosylmethionine-dependent methyltransferase (EC 2.1.1.-) 1
NP2856A	0001_12ges	normal	29.57 (2)	cytopl	-	MIS	MIS	phosphate acetyltransferase domain protein
NP3020A	0005_33	normal	24.83 (1)	cytopl	aldH_2	MIS	MIS	aldehyde dehydrogenase (EC 1.2.1.-) 2
NP4958A	0005_10	normal	22.31 (1)	transm	-	MIS	MIS	anaerobic dehydrogenase transmembrane subunit
NP2540A	0005_5	normal	21.39 (1)	cytopl	cyc	MIS	MIS	unspecific monooxygenase (EC 1.14.14.1) (cytochrome P450)
NP0176A	0005_77_2	normal	20.80 (2)	cytopl	-	MIS	MIS	probable NAD(P)H nitroreductase (EC 1.-.-.-)
NP3444A	0005_52_2	reliable	793.64 (15)	cytopl	prkA_1	MIS	MIS	predicted serine protein kinase (EC 2.7.1.37) 1
NP3874A	0005_30	reliable	585.83 (12)	cytopl	-	MIS	MIS	probable restriction/modification enzyme
NP0104A	0005_54_2	reliable	552.69 (10)	cytopl	lpdA	MIS	MIS	dihydrolipoamide dehydrogenase (EC 1.8.1.4)
NP1432A	0001_05ges	reliable	452.51 (8)	cytopl	aor_2	MIS	MIS	aldehyde ferredoxin oxidoreductase (EC 1.2.7.5) 2
NP4816A	0005_39	reliable	442.54 (11)	cytopl	qor_1	MIS	MIS	NADPH:quinone reductase (EC 1.6.5.5) 1
NP1216A	0005_14	reliable	431.85 (10)	cytopl	smc	MIS	MIS	chromosome partition protein
NP2708A	0005_32	reliable	424.09 (10)	cytopl	perA	MIS	MIS	catalase (EC 1.11.1.6)/ peroxidase (EC 1.11.1.7)
NP3186A	0005_73_2	reliable	396.18 (9)	cytopl	cysA	MIS	MIS	thiosulfate sulfurtransferase (EC 2.8.1.1)
NP3012A	0005_41	reliable	394.00 (9)	cytopl	-	MIS	MIS	probable 2-oxoacid synthase (EC 1.2.7.-), beta subunit
NP0558A	0001_12ges	reliable	391.73 (9)	cytopl	oxdhB	MIS	MIS	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component, beta subunit
NP0678A	0001_05ges	reliable	369.96 (9)	cytopl	-	MIS	MIS	predicted RNase L inhibitor

NP5226A	0001_12ges	reliable	288.56 (6)	cytopl	-	MIS	MIS	NADPH dehydrogenase (EC 1.6.99.1) (old yellow enzyme); 2,4-dienoyl-CoA reductase (NADPH) (EC 1.3.1.34)
NP3090A	0005_35	reliable	266.48 (6)	cytopl	mtfK_2	MIS	MIS	FKBP-type peptidylprolyl isomerase 2
NP3872A	0005_31	reliable	262.18 (6)	cytopl	-	MIS	MIS	ATP-dependent helicase
NP4564A	0005_5	reliable	243.90 (7)	anchN_lip	-	MIS	MIS	predicted electron-transferring-flavoprotein dehydrogenase (EC 1.5.5.1) 2
NP5016A	0005_53_2	reliable	238.31 (4)	cytopl	aor_4	MIS	MIS	aldehyde ferredoxin oxidoreductase (EC 1.2.7.5) 4
NP3100A	0005_72_2	reliable	226.80 (8)	cytopl	mat	MIS	MIS	methionine adenosyltransferase (EC 2.5.1.6)
NP4962A	0005_50	reliable	209.55 (4)	extrac	fdhA_1, dmsA_1	MIS	MIS	anaerobic dehydrogenase (probable formate dehydrogenase (EC 1.2.1.2), probable dimethylsulfoxide reductase (EC 1.8.-.-)), alpha subunit (reductase subunit)
NP1146A	0001_06ges	reliable	206.84 (4)	cytopl	nirA_2	MIS	MIS	probable ferredoxin--nitrite reductase (EC 1.7.7.1) 2
NP0184A	0001_15ges	reliable	192.73 (3)	cytopl	pfdA	MIS	MIS	prefoldin alpha subunit
NP3112A	0005_31	reliable	190.51 (4)	cytopl	-	MIS	MIS	probable restriction/modification enzyme
NP0556A	0001_03ges	reliable	185.65 (6)	cytopl	dsa	MIS	MIS	dihydrolipoamide S-acyltransferase (EC 2.3.1.-)
NP1388A	0005_56_2	reliable	185.22 (4)	cytopl	trxB_2	MIS	MIS	thioredoxin reductase
NP1260A	0005_57_2	reliable	184.63 (4)	cytopl	adh	MIS	MIS	alcohol dehydrogenase (EC 1.1.1.1)
NP5244A	0005_73_2	reliable	174.36 (3)	cytopl	tpc	MIS	MIS	RNA 3'-terminal phosphate cyclase (EC 6.5.1.4)
NP1310A	0001_19ges	reliable	171.95 (5)	cytopl	trxA_1	MIS	MIS	thioredoxin
NP2680A	0005_57_2	reliable	170.65 (4)	cytopl	trxB_1	MIS	MIS	thioredoxin reductase
NP4650A	0005_22	reliable	164.47 (5)	cytopl	-	MIS	MIS	MoxR-like ATPase
NP0424A	0001_19ges	reliable	156.23 (4)	cytopl	-	MIS	MIS	nonhistone chromosomal protein
NP6182A	0005_57_2	reliable	153.31 (3)	cytopl	-	MIS	MIS	predicted crotonobetainyl-CoA:carnitine CoA-transferase (EC 2.8.3.-)/alpha-methylacyl-CoA racemase (EC 5.1.99.4) 1
NP4168A	0001_06ges	reliable	148.39 (4)	anchN_lip	-	MIS	MIS	predicted electron-transferring-flavoprotein dehydrogenase (EC 1.5.5.1) 1
NP1844A	0005_41	reliable	141.26 (4)	cytopl	ggt	MIS	MIS	gamma-glutamyltransferase (EC 2.3.2.2)
NP3190A	0001_10ges	reliable	139.11 (3)	cytopl	map	MIS	MIS	methionyl aminopeptidase (EC 3.4.11.18)
NP3254A	0001_21ges	reliable	131.85 (4)	cytopl	-	MIS	MIS	phage PhiH1 repressor protein homolog
NP5192A	0001_16ges	reliable	121.94 (5)	cytopl	ipp	MIS	MIS	inorganic pyrophosphatase (EC 3.6.1.1)
NP3446A	0005_52_2	reliable	121.66 (2)	cytopl	prkA_2	MIS	MIS	predicted serine protein kinase (EC 2.7.1.37) 2
NP4040A	0001_16ges	reliable	120.01 (2)	cytopl	sod	MIS	MIS	superoxide dismutase (EC 1.15.1.1)
NP2562A	0001_14ges	reliable	119.67 (3)	cytopl	hcpE_3	MIS	MIS	probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3.-) 3; probable 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase (EC 4.1.1.68) 3
NP3766A	0001_12ges	reliable	117.67 (3)	cytopl	qor_2	MIS	MIS	NADPH:quinone reductase (EC 1.6.5.5) 2
NP0560A	0005_20	reliable	112.52 (3)	cytopl	oxdhA_1	MIS	MIS	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component, alpha subunit 1
NP1416A	0001_22ges	reliable	108.79 (2)	cytopl	glx_2	MIS	MIS	probable glutaredoxin
NP5090A	0001_18ges	reliable	85.79 (3)	cytopl	hit_2	MIS	MIS	probable histidine triad (HIT) hydrolase 2 (probable bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17))

NP4384A	0005_3	reliable	81.55 (2)	transm	cpx	MIS	MIS	cytochrome-c peroxidase (EC 1.11.1.5) (CytC-type peroxidase)
NP1722A	0005_2	reliable	74.34 (2)	cytopl	-	MIS	MIS	predicted iron-sulfur protein (probable electron transport protein)/ iron-sulfur protein (probable glycolate oxidase iron-sulfur subunit)
NP0612A	0001_16ges	reliable	59.93 (1)	cytopl	pfdB	MIS	MIS	prefoldin beta subunit
NP3934A	0005_7	reliable	58.35 (1)	anchN_lip	nosL	MIS	MIS	predicted lipoprotein NosL
NP5156A	0005_57_2	reliable	57.27 (1)	cytopl	-	MIS	MIS	homolog to chromosome partition protein
NP4970A	0005_31	reliable	50.20 (2)	cytopl	-	MIS	MIS	iron-sulfur binding protein, ferredoxin-like
NP4578A	0001_13ges	reliable	42.64 (3)	cytopl	dhs	MIS	MIS	deoxyhypusine synthase
NP4144A	0005_12	normal	38.24 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0638A	0005_29	normal	38.00 (1)	transm	-	CHY	CHY	conserved hypothetical protein
NP1420A	0005_82_2	normal	37.90 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4608A	0005_6	normal	36.89 (1)	anchN_lip	-	CHY	CHY	homolog to ABC-type transport system periplasmic substrate-binding protein
NP6074A	0001_09ges	normal	36.47 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1296A	0001_19ges	normal	34.79 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0414A	0005_43	normal	34.56 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5358A	0005_8	normal	34.34 (2)	extrac	-	CHY	CHY	conserved hypothetical protein
NP3680A	0005_77_2	normal	33.91 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0608A	0005_2	normal	33.87 (1)	transm	-	CHY	CHY	homolog to 5'-nucleotidase (EC 3.1.3.5)
NP1574A	0001_16ges	normal	33.31 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4418A	0001_17ges	normal	31.70 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1038A	0001_13ges	normal	30.26 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2970A	0005_10	normal	30.17 (1)	transm	-	CHY	CHY	conserved hypothetical protein
NP6262A	0001_14ges	normal	29.76 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2594A	0005_8	normal	29.42 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3832A	0001_15ges	normal	29.06 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4206A	0005_9	normal	27.91 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3154A	0001_12ges	normal	27.55 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5168A	0001_14ges	normal	26.08 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4934A	0005_7	normal	25.06 (1)	cytopl	-	CHY	CHY	homolog 4 to rad50 ATPase
NP2576A	0001_20ges	normal	24.27 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2764A	0001_15ges	normal	22.26 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1410A	0001_15ges	normal	22.22 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4318A	0001_17ges	normal	21.91 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2490A	0005_23	normal	21.30 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2868A	0001_17ges	normal	21.11 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2030A	0005_73_2	normal	20.87 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0634A	0001_19ges	normal	20.20 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3152A	0001_12ges	normal	19.88 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4986A	0005_83_3	normal	19.55 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3086A	0005_78_2	normal	19.30 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2546A	0005_73_2	reliable	633.29 (12)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2874A	0001_04ges	reliable	576.04 (14)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4430A	0005_34	reliable	551.64 (13)	cytopl	-	CHY	CHY	homolog to citryl-CoA lyase (EC 4.1.3.34)
NP4058A	0001_12ges	reliable	517.83 (12)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3224A	0001_05ges	reliable	474.79 (15)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1910A	0001_13ges	reliable	427.21 (9)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2070A	0005_31	reliable	363.96 (10)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3354A	0001_10ges	reliable	316.73 (7)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2112A	0005_6	reliable	295.20 (6)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2904A	0001_17ges	reliable	269.86 (6)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3030A	0005_4	reliable	244.97 (5)	anchN_lip	-	CHY	CHY	conserved hypothetical protein
NP2028A	0005_57_2	reliable	219.76 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4076A	0001_19ges	reliable	217.21 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3706A	0001_21ges	reliable	209.15 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2072A	0001_17ges	reliable	199.45 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0750A	0005_55_2	reliable	198.32 (5)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4574A	0001_16ges	reliable	184.26 (4)	cytopl	-	CHY	CHY	homolog 9 to S-adenosylmethionine-dependent methyltransferase (EC 2.1.1.-) 3

NP0220A	0001_12ges	reliable	183.64 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3962A	0001_05ges	reliable	178.43 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1280A	0001_17ges	reliable	177.53 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0342A	0001_21ges	reliable	177.14 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0714A	0005_23	reliable	177.06 (5)	cytopl	-	CHY	CHY	homolog 2 to transducer protein
NP0818A	0005_8	reliable	176.85 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4820A	0005_56_2	reliable	175.71 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1590A	0005_56_2	reliable	175.57 (5)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1654A	0005_3	reliable	168.71 (4)	anchN_lip	-	CHY	CHY	conserved hypothetical protein
NP4262A	0001_04ges	reliable	166.00 (5)	cytopl	-	CHY	CHY	homolog 1 to rad50 ATPase
NP1526A	0005_14	reliable	163.19 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1284A	0005_93	reliable	158.93 (5)	cytopl	-	CHY	CHY	homolog to stress response protein
NP1474A	0001_17ges	reliable	157.25 (4)	cytopl	-	CHY	CHY	homolog to acetyltransferases
NP0354A	0001_16ges	reliable	147.32 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3136A	0005_7	reliable	146.44 (5)	anchN_lip	-	CHY	CHY	conserved hypothetical protein
NP4532A	0001_13ges	reliable	143.33 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0430A	0001_19ges	reliable	142.23 (5)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5048A	0001_13ges	reliable	142.01 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1316A	0005_61_2	reliable	140.77 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3468A	0001_20ges	reliable	136.67 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2518A	0005_43	reliable	135.79 (5)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2514A	0005_57_2	reliable	133.89 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4106A	0001_18ges	reliable	133.69 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2902A	0005_42	reliable	127.16 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5198A	0001_08ges	reliable	125.53 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4302A	0005_23	reliable	124.01 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4074A	0005_45	reliable	121.69 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1132A	0001_17ges	reliable	119.96 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4104A	0001_15ges	reliable	119.39 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1428A	0001_09ges	reliable	119.28 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2224A	0001_10ges	reliable	119.24 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3506A	0001_16ges	reliable	114.09 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2262A	0005_18	reliable	112.16 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3528A	0001_19ges	reliable	108.40 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1528A	0001_19ges	reliable	106.20 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4478A	0001_22ges	reliable	104.48 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3966A	0005_52_2	reliable	102.63 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3882A	0005_1	reliable	101.51 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2520A	0001_06ges	reliable	100.74 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4414A	0001_13ges	reliable	100.45 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1690A	0005_22	reliable	98.03 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5370A	0005_79_4	reliable	95.07 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5114A	0001_15ges	reliable	94.56 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5228A	0001_09ges	reliable	92.60 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3418A	0001_20ges	reliable	91.88 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3028A	0005_3	reliable	91.66 (2)	anchN_lip	-	CHY	CHY	conserved hypothetical protein
NP0016A	0001_15ges	reliable	89.86 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4796A	0001_16ges	reliable	88.77 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4610A	0005_6	reliable	88.06 (2)	transm	-	CHY	CHY	conserved hypothetical protein
NP4096A	0001_11ges	reliable	85.12 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1588A	0005_73_2	reliable	84.90 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3936A	0005_26	reliable	84.08 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4070A	0001_19ges	reliable	83.44 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2812A	0001_20ges	reliable	83.32 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1358A	0005_57_2	reliable	81.00 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4844A	0001_15ges	reliable	80.89 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4538A	0005_3	reliable	80.71 (5)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4722A	0005_38	reliable	78.67 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2254A	0001_13ges	reliable	77.57 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4404A	0001_20ges	reliable	77.55 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1036A	0001_07ges	reliable	75.29 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0440A	0001_03ges	reliable	74.19 (2)	cytopl	-	CHY	CHY	homolog 3 to rad50 ATPase
NP4514A	0001_17ges	reliable	73.57 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2482A	0001_12ges	reliable	72.05 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1624A	0001_14ges	reliable	71.96 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1732A	0001_22ges	reliable	70.74 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP6228A	0005_44	reliable	68.30 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein

NP0338A	0005_41	reliable	68.27 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2216A	0001_19ges	reliable	67.76 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4194A	0001_14ges	reliable	66.37 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5224A	0001_21ges	reliable	66.20 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0770A	0001_14ges	reliable	64.31 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2464A	0005_2	reliable	63.90 (2)	transm	-	CHY	CHY	conserved hypothetical protein
NP1248A	0005_12	reliable	62.46 (1)	transm	-	CHY	CHY	conserved hypothetical protein
NP2740A	0001_14ges	reliable	61.80 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1236A	0001_16ges	reliable	60.55 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3408A	0001_16ges	reliable	59.13 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0340A	0005_78_2	reliable	58.07 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2678A	0001_19ges	reliable	56.65 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3402A	0005_64_2	reliable	56.53 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3008A	0005_80_2	reliable	56.48 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2768A	0001_17ges	reliable	55.61 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP1188A	0005_9	reliable	55.28 (1)	transm	-	CHY	CHY	conserved hypothetical protein
NP4388A	0005_75_2	reliable	54.88 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2120A	0005_43	reliable	54.80 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4756A	0005_42	reliable	54.38 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0774A	0001_18ges	reliable	52.87 (3)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2684A	0001_06ges	reliable	52.18 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0382A	0001_15ges	reliable	49.95 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2996A	0001_15ges	reliable	49.91 (4)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3150A	0005_17_2	reliable	47.35 (2)	cytopl	-	CHY	CHY	homolog 3 to transducer protein
NP0850A	0005_1	reliable	46.95 (1)	transm	-	CHY	CHY	conserved hypothetical protein
NP0698A	0001_13ges	reliable	45.82 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP3440A	0001_17ges	reliable	43.38 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2722A	0001_21ges	reliable	43.12 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP2980A	0005_9	reliable	42.96 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP5028A	0005_4	reliable	42.94 (2)	transm	-	CHY	CHY	conserved hypothetical protein
NP0370A	0001_17ges	reliable	41.94 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP4346A	0005_76_2	reliable	41.49 (1)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0572A	0001_16ges	reliable	39.96 (2)	cytopl	-	CHY	CHY	conserved hypothetical protein
NP0094A	0005_88_2	normal	37.49 (1)	cytopl	-	HY	HY	hypothetical protein
NP6258A	0001_12ges	normal	36.76 (2)	cytopl	-	HY	HY	hypothetical protein
NP2930A	0005_4	normal	34.41 (1)	anchN_lip	-	HY	HY	hypothetical protein
NP3902A	0001_22ges	normal	33.89 (2)	cytopl	-	HY	HY	hypothetical protein
NP0914A	0001_15ges	normal	32.79 (1)	cytopl	-	HY	HY	hypothetical protein
NP2570A	0001_22ges	normal	31.13 (2)	cytopl	-	HY	HY	hypothetical protein
NP1364A	0001_17ges	normal	30.42 (1)	cytopl	-	HY	HY	hypothetical protein
NP2124A	0001_15ges	normal	28.89 (1)	cytopl	-	HY	HY	hypothetical protein
NP2592A	0005_12	normal	28.62 (1)	extrac	-	HY	HY	hypothetical protein
NP1798A	0005_12	normal	24.69 (1)	transm	-	HY	HY	hypothetical protein
NP3242A	0005_28	normal	24.46 (1)	cytopl	-	HY	HY	hypothetical protein
NP7066A	0005_28	normal	24.46 (1)	cytopl	-	HY	HY	hypothetical protein
NP2234A	0005_78_2	normal	24.17 (1)	cytopl	-	HY	HY	hypothetical protein
NP2242A	0005_12	normal	21.67 (1)	extrac	-	HY	HY	hypothetical protein
NP0752A	0001_17ges	normal	19.29 (1)	cytopl	-	HY	HY	hypothetical protein
NP3968A	0005_23	normal	19.16 (1)	anchN_lip	-	HY	HY	hypothetical protein
NP3266A	0005_40	reliable	364.02 (7)	cytopl	-	HY	HY	hypothetical protein
NP3886A	0005_14	reliable	222.50 (8)	cytopl	-	HY	HY	hypothetical protein
NP2688A	0005_42	reliable	198.12 (4)	cytopl	-	HY	HY	hypothetical protein
NP1992A	0001_22ges	reliable	186.36 (4)	cytopl	-	HY	HY	hypothetical protein
NP3264A	0001_03ges	reliable	184.58 (5)	cytopl	-	HY	HY	hypothetical protein
NP1152A	0001_16ges	reliable	156.84 (4)	cytopl	-	HY	HY	hypothetical protein
NP1460A	0001_19ges	reliable	156.57 (3)	cytopl	-	HY	HY	hypothetical protein
NP0214A	0001_19ges	reliable	155.74 (5)	cytopl	-	HY	HY	hypothetical protein
NP5172A	0001_14ges	reliable	117.46 (2)	cytopl	-	HY	HY	hypothetical protein
NP0486A	0005_29	reliable	108.63 (2)	cytopl	-	HY	HY	hypothetical protein
NP1446A	0001_22ges	reliable	98.31 (2)	cytopl	-	HY	HY	hypothetical protein
NP5334A	0001_20ges	reliable	94.77 (2)	cytopl	-	HY	HY	hypothetical protein
NP4332A	0005_6	reliable	94.11 (2)	anchN_lip	-	HY	HY	hypothetical protein
NP2896A	0001_20ges	reliable	89.87 (1)	cytopl	-	HY	HY	hypothetical protein
NP5376A	0005_87_2	reliable	88.41 (4)	cytopl	-	HY	HY	hypothetical protein
NP1848A	0001_15ges	reliable	86.71 (2)	cytopl	-	HY	HY	hypothetical protein
NP1660A	0001_18ges	reliable	85.20 (2)	cytopl	-	HY	HY	hypothetical protein
NP4304A	0005_11	reliable	84.93 (2)	transm	-	HY	HY	hypothetical protein
NP1390A	0005_78_2	reliable	81.59 (2)	cytopl	-	HY	HY	hypothetical protein

NP3856A	0005_39	reliable	71.81 (3)	transm	-	HY	HY	hypothetical protein
NP0688A	0001_18ges	reliable	70.43 (2)	cytopl	-	HY	HY	hypothetical protein
NP2596A	0001_20ges	reliable	70.07 (2)	cytopl	-	HY	HY	hypothetical protein
NP2374A	0001_22ges	reliable	69.63 (2)	cytopl	-	HY	HY	hypothetical protein
NP3732A	0005_3	reliable	66.16 (2)	anchN_lip	-	HY	HY	hypothetical protein
NP3268A	0005_42	reliable	63.23 (2)	cytopl	-	HY	HY	hypothetical protein
NP1888A	0005_8	reliable	62.56 (2)	anchN_lip	-	HY	HY	hypothetical protein
NP2360A	0005_70_2	reliable	61.55 (1)	cytopl	-	HY	HY	hypothetical protein
NP1880A	0005_12	reliable	54.42 (2)	transm	-	HY	HY	hypothetical protein
NP6138A	0005_28	reliable	53.28 (1)	cytopl	-	HY	HY	hypothetical protein
NP0450A	0005_12	reliable	50.06 (1)	transm	-	HY	HY	hypothetical protein
NP0044A	0005_86_2	reliable	49.97 (2)	cytopl	-	HY	HY	hypothetical protein
NP1074A	0001_07ges	reliable	47.17 (1)	cytopl	-	HY	HY	hypothetical protein
NP2212A	0005_2	reliable	46.31 (3)	transm	-	HY	HY	hypothetical protein
NP4204A	0005_80_2	reliable	44.27 (3)	cytopl	-	HY	HY	hypothetical protein
NP6254A	0005_6	reliable	41.34 (2)	anchN_lip	-	HY	HY	hypothetical protein
NP1480A	0005_10	reliable	40.58 (2)	anchN_lip	-	HY	HY	hypothetical protein
NP1444A	0001_16ges	reliable	39.28 (1)	cytopl	-	HY	HY	hypothetical protein

Supplemental Table D manual. Proteomic analyses on cells, grown in complex medium. Experiment numbers (Exp.), ID numbers and protein names, number of quantified peptides (Pep), number of peptides from different spots (Sp), regulation factors (Reg) and standard deviations (Std) after 1 h, as well as after 2 h of heat shock are indicated. Data are from proteins separated on different 2-D gels spanning different pH ranges, and subsequently spotted on different targets. Two independent approaches have been performed with proteins spotted on three targets (Exp.1) or on four targets (Exp.2), respectively. Manual validation of MS spectra is implicated in the results given.

Exp	ID	protein name	Reg.		Std.		Pep	Sp
			2h	1h	2h	1h		
2	OE5083R	heat shock protein homolog	>10	5.80	-	0.28	3	2
1	OE4427R	ferritin (Dps-like ferritin DpsA)	3.72	3.95	0.17	0.62	2	2
2			1.50	1.37	0.15	0.08	2	5
1	OE4122R	thermosome alpha chain	2.76	2.31	0.53	0.51	4	5
2			1.91	1.39	0.48	0.25	4	7
1	OE3925R	thermosome beta chain	2.38	2.38	0.38	0.41	3	7
2			1.90	1.58	0.62	0.60	3	7
1	OE3195F	succinate--CoA ligase (ADP-forming) beta chain	-	1.35	-	-	1	1
2			2.13	1.20	0.08	0.04	2	1
1	OE3112R	AAA-type ATPase (transitional ATPase homolog)	2.05	2.95	0.48	0.69	2	2
2	OE3196F	succinate--CoA ligase (ADP-forming) alpha chain	1.97	1.51	0.03	0.15	1	2
1	OE5243F	transducer protein car	1.86	1.07	0.13	0.25	2	1
1	OE1711R	oxoglutarate-ferredoxin oxidoreductase alpha chain	1.66	1.07	-	-	1	1
1	OE4323F	malate dehydrogenase	1.61	1.32	0.26	0.34	2	1
1	OE2623R	pyruvate--ferredoxin oxidoreductase alpha chain	1.67	1.63	0.21	0.14	2	3
2			1.48	1.14	0.09	0.14	1	2
1	OE1275F	proteasome alpha chain	1.67	1.34	0.11	0.12	2	4
2			1.35	1.23	0.10	0.13	2	3
1	OE5205R	ornithine carbamoyltransferase, catabolic	1.70	1.48	0.21	0.24	1	8
2			1.31	1.18	0.08	0.15	1	4
1	OE1710R	oxoglutarate-ferredoxin oxidoreductase beta chain	1.46	1.20	0.18	0.09	1	2
1	OE3168R	pyridoxal phosphate-dependent aminotransferase (acetylornithine transaminase homolog)	1.33	1.26	0.18	0.16	5	9
2			1.52	1.39	0.15	0.20	3	2
2	OE1672F	orotate phosphoribosyltransferase homolog	1.40	1.38	0.38	0.08	2	1
1	OE2935R	fumarate hydratase	1.32	1.18	0.24	0.16	3	2
2			1.42	1.13	0.26	0.14	3	2
1	OE2640F	phosphopyruvate hydratase (enolase)	1.32	1.28	0.09	0.17	2	2
2			1.39	1.19	0.11	0.01	2	1
1	OE2622R	pyruvate--ferredoxin oxidoreductase beta chain	1.28	1.50	0.13	0.14	4	5
2			1.39	1.47	0.12	0.18	3	2
2	OE5208R	arginine deiminase	1.31	1.02	0.17	0.10	2	2
1	OE5201F	aspartate carbamoyltransferase catalytic chain	1.30	1.17	0.16	0.16	3	5
1	OE2019F	fructose-bisphosphate aldolase 1	1.23	0.99	0.10	0.08	2	3
2			1.37	1.15	0.03	0.26	2	1
1	OE2296F	proteasome beta chain	1.35	1.31	0.06	0.21	2	2
2			1.23	1.30	0.11	0.13	2	3
1	OE5206R	carbamate kinase	1.09	1.07	0.00	0.04	1	2
2			1.46	1.13	0.17	0.15	1	4
2	OE3634F	isocitrate dehydrogenase (NADP+)	1.29	1.13	0.06	0.12	2	2
2	OE1737R	dnaK-type molecular chaperone hsp70	1.28	1.21	0.27	0.25	4	2
1	OE4613F	aconitate hydratase	1.11	1.31	0.05	-	1	4
2			1.40	1.30	0.19	0.20	1	2
2	OE2865R	succinate dehydrogenase chain A (flavoprotein)	1.21	1.20	-	-	1	1
1	OE1942F	citryl-CoA lyase beta chain; ATP citrate synthase	1.15	0.84	-	-	1	1
1	OE1270F	glutamate dehydrogenase	1.07	1.09	0.11	0.06	2	4

Supplemental Tables C_regul. Proteomic analyses on cells, grown in synthetic medium. ID numbers, protein names, number of unique peptides identified (Uni Pep), number of unique peptides used for quantification (Qua Pep), regulation factors (Reg.), standard deviations (Std.), *p*-values (p val), gene denotations (gene) and protein molecular weights (MW) of significant up- and downregulated proteins are indicated. Data are from three different experiments (Exp 1-3) after manual validation of all chromatograms has been performed.

Exp	ID	Protein Name	Uni Pep	Qua Pep	Reg.	Std.	p val.	gene	MW
3	OE5083R	heat shock protein homolog	2	1	4.00	0.01	6.67E-08	hsp5	14147
2			2	1	3.23	0.01	0.00E+00		
3	OE2084R	transcription initiat. factor TFB	8	2	3.45	0.07	5.78E-04	tfbB	36134
2			4	2	3.23	0.06	1.11E-05		
2	OE3554F	carbamoyl-phosphate synthase large subunit	17	6	2.56	0.03	4.28E-07	carB	110653
1			14	4	2.50	0.05	1.46E-03		
3			16	8	2.17	0.05	4.71E-03		
3	OE3556R	carbamoyl-phosphate synthase small subunit	2	1	2.27	0.06	3.97E-03	carA	37174
2	OE5082R	AAA-type ATPase (transitional ATPase homolog)	2	1	2.38	0.02	4.78E-07	aaa8 cdc48d	80645
3			5	1	1.79	0.04	2.55E-02		
1	OE1719R	probable oxidoreductase (protochlorophyllide reduct homol)	1	1	2.00	0.07	1.74E-02	-	33706
2	OE3112R	AAA-type ATPase (transitional ATPase homolog)	22	7	2.56	0.09	8.17E-04	aaa3 cdc48b	82104
1			21	9	2.08	0.12	3.97E-02		
3			20	7	1.45	0.1	2.04E-01		
1	OE5162D1F	conserved hypothetical protein	1	1	1.92	0.04	1.28E-02	-	12741
3	OE2474R	transducer protein htrXIII	2	1	2.00	0.12	4.40E-02	htr13	44988
2			5	4	1.89	0.22	1.65E-01		
1			7	2	1.33	0.11	3.16E-01		
2	OE3925R	thermosome beta subunit	23	13	1.85	0.1	1.60E-02	cctB	58753
3			21	10	1.59	0.12	1.41E-01		
1			22	12	1.56	0.09	1.18E-01		
3	OE1711R	oxoglutarate--ferredoxin oxidoreductase alpha subunit	5	2	1.64	0.15	1.60E-01	korA	63456
3	OE4551F	ABC-type transport system periplasmic substrate-bdg prot	5	1	1.61	0.08	9.57E-02	dppD	60487
2			3	1	1.59	0.1	4.88E-02		
2	OE3467R	deoxyribodipyrimidine photo-lyase	1	1	1.59	0.06	1.80E-02	phr1	51399
2	OE2296F	proteasome beta subunit	3	1	1.69	0.1	2.35E-02	psmB	25627
3			4	2	1.67	0.07	6.86E-02		
1			2	1	1.30	0.04	3.09E-01		

2	OE4427R	ferritin	2	2	1.67	0.08	1.86E-02	dpsA	20088
3			2	2	1.67	0.06	6.01E-02		
1			2	2	1.30	0.05	3.14E-01		
1	OE1672F	orotate phosphoribosyltransferase homolog	7	4	1.67	0.16	1.75E-01	pyrE1	22149
2			5	3	1.59	0.16	1.35E-01		
3			7	4	1.30	0.21	4.93E-01		
2	OE1698R	probable oxidoreductase	5	2	1.75	0.09	1.43E-02	oxr4	30405
1			6	2	1.37	0.06	2.48E-01		
2	OE3028R	conserved hypothetical protein	10	6	1.75	0.06	5.70E-03	-	29324
3			10	7	1.43	0.08	2.02E-01		
1			11	7	1.28	0.12	4.04E-01		
1	OE1979R	cytochrome-c oxid. subunit I	1	1	1.45	0.14	2.53E-01	coxA1	65251
1	OE3558F	probable transcription regul.	2	1	1.69	0.1	8.64E-02	trh3	15229
2			3	1	1.28	0.04	1.58E-01		
2	OE3955F	probable proline dehydrogen.	3	2	1.47	0.06	4.24E-02	putA	30987
3			2	2	1.43	0.1	2.30E-01		
1			4	3	1.41	0.08	2.10E-01		
1	OE1081R	probable glycosyltransferase	3	2	1.52	0.07	1.26E-01	rfbU1	44694
2			1	1	1.45	0.06	5.51E-02		
3			2	1	1.33	0.16	3.74E-01		
1	OE2168R	transducer protein htrVI	3	1	1.43	0.15	2.79E-01	htr6	83877
3	OE1730R	conserved hypothetical protein	1	1	1.45	0.19	3.12E-01	-	21049
1			2	1	1.37	0.04	2.27E-01		
2	OE4450R	signal recognition particle 54K	7	3	1.49	0.09	6.57E-02	ffh	50117
3			2	1	1.49	0.07	1.52E-01		
1			6	2	1.28	0.15	4.29E-01		
2	OE3116F	conserved hypothetical protein	2	1	1.45	0.07	6.27E-02	-	57724
1			5	1	1.37	0.1	2.63E-01		
3	OE1721R	methylmalonyl-CoA mutase1A	4	2	1.39	0.1	2.61E-01	mut1A	62025
2	OE4122R	thermosome alpha subunit	27	14	1.52	0.06	3.24E-02	cctA	58632
1			27	12	1.41	0.12	2.67E-01		
3			27	14	1.25	0.1	4.36E-01		

Exp	ID	Protein Name	Uni Pep	Qua Pep	Reg.	Std.	p val.	gene	MW
3	OE2470F	flagellin A2 precursor	6	2	-8.01	2.29	4.98E-08	flgA2	20593
2			6	2	-3.71	1.08	1.03E-04	flgA2	20593
3	OE2397F	flagellin B1 precursor	4	2	-7.49	0.89	0.00E+00	flgB1	20442
2			4	2	-2.80	0.39	2.27E-06	flgB1	20442
3	OE2398F	flagellin B2 precursor	3	1	-7.07	1.01	0.00E+00	flgB2	20669
2			2	1	-2.84	0.22	1.79E-08	flgB2	20669
2	OE1254R	conserved hypothetical protein	3	1	-2.94	0.19	0.00E+00	-	24260
1	OE3017R	UDP-sugar hydrolase	7	2	-2.56	0.38	1.44E-03	ush	71161
3	OE4466R	DNA repair protein	6	4	-2.55	0.28	7.13E-04	radA1	37400
2			7	4	-2.38	0.46	7.29E-04	radA1	37400
1			9	4	-1.38	0.18	2.59E-01	radA1	37400
1	OE3334R	anthranilate phosphoribosyl-transferase	5	5	-2.24	0.37	7.68E-03	trpD1	33494
2			5	2	-2.07	0.31	1.32E-03	trpD1	33494
3			6	3	-1.80	0.14	2.62E-02	trpD1	33494
2	OE2864F	phosphoribosylamine--glycine ligase	8	5	-2.67	0.35	5.02E-06	purD	44672
3			6	4	-1.75	0.45	1.18E-01	purD	44672
1			4	3	-1.46	0.31	2.54E-01	purD	44672
3	OE1500R	pyruvate, water dikinase (phosphoenolpyruvate synthase)	9	3	-2.52	0.41	2.07E-03	ppsA	81124
2			10	2	-1.81	0.13	1.26E-03	ppsA	81124
1			9	2	-1.31	0.14	3.28E-01	ppsA	81124
2	OE2763F	X-Pro dipeptidase	2	1	-1.88	0.17	9.86E-04	pepQ2	42426
1			2	2	-1.48	0.67	4.44E-01	pepQ2	42426
2	OE1319R	cell division protein ftsZ2	5	1	-1.86	0.31	8.22E-03	ftsZ2	41293
1			6	3	-1.50	0.14	1.32E-01	ftsZ2	41293
1	OE1270F	glutamate dehydrogenase	13	5	-1.91	0.27	2.68E-02	gdhA3	45940
2			12	5	-1.77	0.34	2.57E-02	gdhA3	45940
3			12	5	-1.31	0.27	4.13E-01	gdhA3	45940
1	OE4712F	conserved hypothetical protein	4	1	-1.80	0.22	3.65E-02	-	14669
3			3	1	-1.51	0.09	1.15E-01	-	14669
1	OE1470F	tryptophan synthase beta subunit	4	1	-1.74	0.19	4.38E-02	trpB	45423
2			5	4	-1.63	0.22	2.31E-02	trpB	45423
3			4	3	-1.55	0.13	9.86E-02	trpB	45423
3	OE3834R	probable oxidoreductase	4	3	-1.70	0.32	9.39E-02	gsp	38864
2			2	2	-1.47	0.19	7.21E-02	gsp	38864
1			3	2	-1.44	0.45	3.64E-01	gsp	38864
2	OE1478R	transcription initiation factor TFB	5	3	-1.49	0.22	7.64E-02	tfbF	35306
1			3	1	-1.36	0.13	2.50E-01	tfbF	35306
3	OE1471F	tryptophan synthase alpha subunit	4	2	-1.51	0.23	1.66E-01	trpA	28430
1			3	1	-1.43	0.16	2.00E-01	trpA	28430
2			3	1	-1.34	0.18	1.71E-01	trpA	28430

Supplemental Tables A_regul. Whole genome DNA microarray analyses on cells, grown in complex medium. ID numbers, protein names, regulation factors (Reg.), standard deviations (Std.), *t*-values (t val), gene denotations (gene) and protein molecular weights (MW) of significant up- and downregulated genes are indicated. Data from four different experiments were combined to outline statistical conclusions.

ID	protein name	Reg.	Std.	t val.	gene	MW
OE5083R	heat shock protein homolog	6.46	0.60	14.25	hsp5	14147
OE4122R	thermosome alpha subunit	5.24	0.52	14.42	cctA	58632
OE3925R	thermosome beta subunit	4.56	1.27	5.45	cctB	58753
OE3903F	conserved hypothetical protein	2.73	0.50	9.19	-	6693
OE5063R	probable IS200-type transposase (TCE31)	2.71	0.33	13.97	-	14757
OE4727R	IS1341-type transposase (TCE31)	2.63	0.41	10.77	-	50127
OE4427R	ferritin (DNA-binding protein dpsA)	2.30	0.16	24.04	dpsA	20088
OE3114R	hypothetical protein	2.23	0.71	5.18	-	8933
OE2084R	transcription initiation factor TFB	2.16	0.60	5.84	tfbB	36134
OE5048F	conserved hypothetical protein	2.03	0.53	6.10	-	22417
OE1409F	conserved hypothetical protein	1.83	0.25	11.05	-	5539
OE5114R	gas-vesicle operon protein gvpK2	1.69	0.47	5.04	gvpK2	12730
OE3112R	AAA-type ATPase (ATPase homolog)	1.68	0.50	2.05	aaa3	82104
OE1478R	transcription initiation factor TFB	1.68	0.55	4.31	tfbF	35306
OE1107R	conserved hypothetical protein	1.67	0.87	2.72	-	15595
OE1797R	transcription regulator sirR	1.66	0.60	3.83	sirR	24935
OE3815R	conserved hypothetical protein	1.64	0.32	6.97	-	13609
OE7115F	cell division control protein cdc6 homolog	1.61	0.26	8.24	-	51052
OE5208R	arginine deiminase (EC 3.5.3.6)	1.57	0.18	11.50	arcA	54672
OE3949R	glutaredoxin homolog	1.53	0.19	10.40	-	8917

ID	protein name	Reg.	Std.	t val.	gene	MW
OE4759F	cell surface glycoprotein precursor	-2,95	0,16	31,08	csg	89704
OE7056F	hypothetical protein	-1,98	0,27	11,59	-	11142
OE4070R	cytochrome-c oxidase subunit I	-1,92	0,12	25,60	cox1B	61452
OE3062F	ribosomal protein S17.eR	-1,90	0,13	21,72	rps17R	6967
OE2397F	flagellin B1 precursor	-1,90	0,28	10,62	flgB1	20442
OE3989R	H+-transporting 2-sector ATPase sub.K.a	-1,86	0,62	4,59	atpK	8924
OE2399F	flagellin B3 precursor	-1,81	0,25	10,96	flgB3	20508
OE2811F	conserved hypothetical protein	-1,80	0,17	15,91	-	8656
OE4187R	probable DNA-binding protein	-1,75	0,59	4,36	-	6016
OE2469F	flagellin A1 precursor	-1,72	0,51	4,83	flgA1	20610
OE2470F	flagellin A2 precursor	-1,72	0,52	4,73	flgA2	20593
OE1321R	conserved hypothetical protein	-1,70	0,08	28,92	-	6423
OE4071R	cytochrome-c oxidase subunit II	-1,65	0,17	13,72	cox2B	19715
OE2398F	flagellin B2 precursor	-1,65	0,49	4,63	flgB2	20669
OE2577R	conserved hypothetical protein	-1,54	0,39	5,11	-	11536
OE5201F	aspartate carbamoyltransferase catal. sub.	-1,53	0,19	9,97	pyrB	34375

Supplemental Tables B_regul. Whole genome DNA microarray analyses on cells, grown in synthetic medium. ID numbers, protein names, regulation factors (Reg.), standard deviations (Std.), *t*-values (t val), gene denotations (gene) and protein molecular weights (MW) of significant up- and downregulated genes are indicated. Data from four different experiments were combined to outline statistical conclusions.

ID	protein name	Reg.	Std.	t val.	gene	MW
OE3925R	thermosome beta subunit	9.09	0.52	27.55	cctB	58753
OE4122R	thermosome alpha subunit	7.72	0.47	28.11	cctA	58632
OE3114R	hypothetical protein	5.23	1.14	9.38	-	8933
OE3112R	AAA-type ATPase (ATPase homolog)	3.64	1.47	5.67	aaa3	82104
OE5063R	probable IS200-type transposase (TCE31)	3.58	0.92	8.98	-	14757
OE2046F	conserved hypothetical protein	3.47	1.31	6.12	-	10594
OE5083R	heat shock protein homolog	3.18	0.60	12.41	hsp5	14147
OE7090B1	hypothetical protein	3.06	1.41	5.14	-	10934
OE7192F	conserved hypothetical protein	2.77	0.94	6.97	-	23112
OE3949R	glutaredoxin homolog	2.73	0.76	8.56	-	8917
OE2473F	conserved hypothetical protein	2.53	0.75	7.96	-	10068
OE3903F	conserved hypothetical protein	2.38	0.58	9.68	-	6693
OE1023R	hypothetical protein	2.21	0.72	7.16	-	14539
OE2084R	transcription initiation factor TFB	2.18	0.46	10.93	tfbB	36134
OE5208R	arginine deiminase (EC 3.5.3.6)	2.10	0.54	8.84	arcA	54672
OE4427R	ferritin (DNA-binding protein dpsA)	2.09	0.40	12.02	dpsA	20088
OE2527F	conserved hypothetical protein	2.08	0.80	5.91	-	24684
OE1794R	conserved hypothetical protein	2.06	0.72	6.49	-	24278
OE1797R	transcription regulator sirR	2.05	0.80	5.84	sirR	24935
OE1765R	probable proteasome regulatory subunit	2.00	0.67	6.69	pan1	44944
OE4727R	IS1341-type transposase (TCE31)	1.99	0.52	8.55	-	50127
OE1698R	probable oxidoreductase (EC 1.1.1.-)	1.91	0.47	8.81	oxr4	30405
OE5082R	AAA-type ATPase (ATPase homolog)	1.87	1.04	3.90	aaa8	80645
OE1478R	transcription initiation factor TFB	1.86	0.66	6.05	tfbF	35306

ID	protein name	Reg.	Std.	t val.	gene	MW
OE1448R	conserved hypothetical protein	-2.40	0.74	7.60	-	10046
OE4759F	cell surface glycoprotein precursor	-2.24	0.24	21.98	csg	89704
OE1270F	glutamate dehydrogenase (EC 1.4.1.2)	-2.23	0.65	7.95	gdhA3	45940
OE1321R	conserved hypothetical protein	-2.18	0.15	33.35	-	6423
OE1407F	inorganic pyrophosphatase (EC 3.6.1.1)	-1.88	0.52	7.87	ipp	20050
OE4509F	nonhistone chromosomal protein	-1.88	0.29	14.25	-	11691
OE4676F	hypothetical protein	-1.84	0.34	11.43	-	6375
OE3487R	translation initiation factor aIF-5A	-1.80	0.50	7.58	eif5a	14296
OE2470F	flagellin A2 precursor	-1.76	0.41	8.94	flgA2	20593
OE3062F	ribosomal protein S17.eR	-1.76	0.10	35.01	rps17R	6967
OE2397F	flagellin B1 precursor	-1.72	0.31	11.22	flgB1	20442
OE7033R	gas-vesicle operon protein gvpD1	-1.72	0.30	11.75	gvpD1	59306
OE2469F	flagellin A1 precursor	-1.71	0.39	8.96	flgA1	20610
OE2399F	flagellin B3 precursor	-1.69	0.38	8.99	flgB3	20508
OE1187R	hypothetical protein	-1.67	0.32	10.31	-	13834
OE7043R	hypothetical protein	-1.67	0.17	19.91	-	12836
OE3822R	conserved hypothetical protein	-1.66	0.31	10.47	-	9271
OE4070R	cytochrome-c oxidase subunit I	-1.65	0.34	9.44	cox1B	61452
OE5276F	conserved hypothetical protein	-1.65	0.42	7.67	-	43716
OE3989R	H+-transporting 2-sector ATPase sub.K.a	-1.62	0.21	14.57	atpK	8924
OE1319R	cell division protein ftsZ2	-1.61	0.22	13.83	ftsZ2	41293
OE5202F	aspartate carbamoyltransferase regul. sub.	-1.59	0.18	16.88	pyrI	16907
OE7110R	conserved hypothetical protein	-1.56	0.19	14.76	-	25295
OE2398F	flagellin B2 precursor	-1.53	0.28	9.77	flgB2	20669
OE3992R	H+-transporting 2-sector ATPase sub.H.a	-1.52	0.21	12.66	atpH	12196
OE5204R	arginine/ornithine antiporter	-1.52	0.33	8.11	nhaC3	50490

Supplemental Table C. Proteomic analyses on cells, grown in synthetic medium. ID numbers, protein names, number of unique peptides identified (Uni Pep), number of unique peptides used for quantification (Qua Pep), regulation factors (Reg.), standard deviations (Std.), p-values (p val) and gene denotations (gene) are indicated. Data are from three different experiments (E; lanes 1-3) after manual validation of all chromatograms has been performed.

E	ID	Protein Name	Uni Pep	Qua Pep	Reg.	Std.	p val.	gene
1	OE1001F	conserved hypothetical protein	7	4	-1.04	0.21	8.99E-01	-
2	OE1001F	conserved hypothetical protein	6	3	-1.12	0.13	5.66E-01	-
3	OE1001F	conserved hypothetical protein	5	1	-1.16	0.19	6.18E-01	-
2	OE1016R	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	4	1	1.12	0.14	6.24E-01	graD2
3	OE1016R	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	4	1	-1.16	0.11	5.77E-01	graD2
2	OE1077R	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	3	1	1.00	0.1	9.83E-01	ugd
1	OE1077R	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	3	1	-1.03	0.61	9.58E-01	ugd
3	OE1077R	UDP-glucose 6-dehydrogenase	4	1	-1.28	0.21	4.16E-01	ugd

		(EC 1.1.1.22)							
1	OE1079F	conserved hypothetical protein	4	2	-1.05	0.09	8.49E-01	-
2	OE1079F	conserved hypothetical protein	5	1	-1.34	0.12	1.25E-01	-
3	OE1079F	conserved hypothetical protein	4	1	-1.40	0.14	2.13E-01	-
1	OE1081R	probable glycosyltransferase (EC 2.-.-.-)	3	2	1.52	0.07	1.26E-01	rfbU1
2	OE1081R	probable glycosyltransferase (EC 2.-.-.-)	1	1	1.45	0.06	5.51E-02	rfbU1
3	OE1081R	probable glycosyltransferase (EC 2.-.-.-)	2	1	1.33	0.16	3.74E-01	rfbU1
1	OE1109R	probable glycosyltransferase (EC 2.-.-.-) (lipopolysaccharide 1,2-N-acetylglucosaminetransferase homolog/ UDPglucose--starch glucosyltransferase homolog)	1	1	-1.46	0.25	2.16E-01	lpg
2	OE1133F	hypothetical protein	3	1	1.18	0.14	4.89E-01	-
1	OE1133F	hypothetical protein	1	1	1.08	0.12	8.05E-01	-
1	OE1134F	conserved hypothetical protein	3	1	-1.55	0.14	1.03E-01	-
3	OE1151R	aminopeptidase homolog	5	1	1.56	0.06	1.06E-01	-
2	OE1151R	aminopeptidase homolog	5	1	1.30	0.15	3.18E-01	-
1	OE1151R	aminopeptidase homolog	3	1	-1.02	0.1	9.49E-01	-
2	OE1154F	Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating) (EC 1.2.1.59)	9	3	1.12	0.11	5.86E-01	gapB
1	OE1154F	Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating) (EC 1.2.1.59)	7	4	1.02	0.13	9.57E-01	gapB
3	OE1154F	Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating) (EC 1.2.1.59)	7	3	-1.05	0.18	8.77E-01	gapB
3	OE1160R	ribosomal protein L10.eR	8	3	-1.02	0.12	9.40E-01	rpl10R
2	OE1160R	ribosomal protein L10.eR	8	3	-1.13	0.15	5.66E-01	rpl10R
1	OE1160R	ribosomal protein L10.eR	6	2	-1.22	0.14	4.69E-01	rpl10R
3	OE1162R	probable cold shock protein	1	1	-1.27	0.11	3.77E-01	cspD1
2	OE1165R	phosphoglycerate dehydrogenase (EC 1.1.1.95)	3	2	1.28	0.06	1.74E-01	serA3
2	OE1209F	dehydratase homolog	1	1	1.14	0.09	5.28E-01	-
2	OE1220F	archaeal histone	1	1	1.01	0.24	9.67E-01	hstA, hhsA
1	OE1220F	archaeal histone	3	1	-1.21	0.13	4.80E-01	hstA, hhsA
2	OE1254R	conserved hypothetical protein	3	1	-2.94	0.19	0.00E+00	-
2	OE1259R	conserved hypothetical protein	7	2	1.01	0.09	9.49E-01	-
1	OE1259R	conserved hypothetical protein	5	2	-1.09	0.16	7.76E-01	-
3	OE1259R	conserved hypothetical protein	7	2	-2.03	0.26	1.29E-02	-
3	OE1270F	glutamate dehydrogenase (EC 1.4.1.2)	12	5	-1.31	0.27	4.13E-01	gdhA3
2	OE1270F	glutamate dehydrogenase (EC 1.4.1.2)	12	5	-1.77	0.34	2.57E-02	gdhA3
1	OE1270F	glutamate dehydrogenase (EC 1.4.1.2)	13	5	-1.91	0.27	2.68E-02	gdhA3
2	OE1275F	proteasome alpha subunit	12	6	1.54	0.1	5.58E-02	psmA
3	OE1275F	proteasome alpha subunit	11	4	1.20	0.06	4.88E-01	psmA
1	OE1275F	proteasome alpha subunit	12	4	1.16	0.02	5.61E-01	psmA
1	OE1294R	ribosomal protein L15.eR	6	3	-1.06	0.21	8.59E-01	rpl15R
3	OE1294R	ribosomal protein L15.eR	6	3	-1.10	0.13	7.27E-01	rpl15R
2	OE1294R	ribosomal protein L15.eR	6	2	-1.12	0.11	5.51E-01	rpl15R
1	OE1319R	cell division protein ftsZ2	6	3	-1.50	0.14	1.32E-01	ftsZ2
2	OE1319R	cell division protein ftsZ2	5	1	-1.86	0.31	8.22E-03	ftsZ2
2	OE1371R	prefoldin beta subunit	4	4	1.23	0.08	2.85E-01	pfdB

1	OE1371R	prefoldin beta subunit	2	2	1.19	0.09	5.25E-01	pfdB
3	OE1371R	prefoldin beta subunit	4	4	1.00	0.15	9.89E-01	pfdB
2	OE1372R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit P	1	1	1.00	0.05	9.83E-01	rpoP
1	OE1372R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit P	1	1	-1.11	0.09	6.92E-01	rpoP
3	OE1372R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit P	1	1	-1.18	0.13	5.55E-01	rpoP
3	OE1373R	ribosomal protein L37a.eR	3	1	-1.10	0.07	7.08E-01	rpl37aR
1	OE1373R	ribosomal protein L37a.eR	3	1	-1.40	0.15	2.18E-01	rpl37aR
1	OE1385F	conserved hypothetical protein	1	1	1.14	0.13	6.64E-01	-
1	OE1399R	transcription initiation factor TFB	10	4	-1.01	0.09	9.67E-01	tfbG
2	OE1399R	transcription initiation factor TFB	9	2	-1.03	0.1	8.89E-01	tfbG
3	OE1399R	transcription initiation factor TFB	10	3	-2.03	0.17	8.05E-03	tfbG
1	OE1405R	conserved hypothetical protein	3	2	1.37	0.07	2.42E-01	-
3	OE1405R	conserved hypothetical protein	3	2	-1.09	0.11	7.58E-01	-
3	OE1407F	inorganic pyrophosphatase (EC 3.6.1.1)	5	3	1.06	0.1	8.37E-01	ipp
2	OE1407F	inorganic pyrophosphatase (EC 3.6.1.1)	6	3	1.02	0.14	9.25E-01	ipp
1	OE1407F	inorganic pyrophosphatase (EC 3.6.1.1)	6	4	1.00	0.15	9.88E-01	ipp
3	OE1412F	conserved hypothetical protein	5	3	-1.13	0.13	6.67E-01	-
1	OE1414R	cell division protein ftsZ4	4	1	1.11	0.11	7.02E-01	ftsZ4
2	OE1414R	cell division protein ftsZ4	5	2	1.10	0.03	5.74E-01	ftsZ4
3	OE1414R	cell division protein ftsZ4	4	1	-1.09	0.23	7.84E-01	ftsZ4
3	OE1417F	conserved hypothetical protein	3	1	1.05	0.1	8.41E-01	-
1	OE1417F	conserved hypothetical protein	2	1	1.03	0.12	9.28E-01	-
1	OE1442R	conserved hypothetical protein	7	1	1.20	0.08	4.89E-01	-
3	OE1442R	conserved hypothetical protein	7	1	-1.04	0.07	8.85E-01	-
2	OE1451F	probable methyltransferase	6	2	1.08	0.05	6.88E-01	pnm
3	OE1451F	probable methyltransferase	7	2	1.03	0.08	9.14E-01	pnm
1	OE1451F	probable methyltransferase	6	3	-1.06	0.08	8.29E-01	pnm
3	OE1462R	nicotinamide-nucleotide adenylyltransferase (EC 2.7.7.1)	3	2	1.05	0.08	8.46E-01	-
2	OE1465F	endopeptidase La (EC 3.4.21.53)	5	2	1.30	0.06	1.68E-01	lon
1	OE1465F	endopeptidase La (EC 3.4.21.53)	4	1	1.16	0.1	5.95E-01	lon
3	OE1465F	endopeptidase La (EC 3.4.21.53)	2	1	-1.34	0.29	3.74E-01	lon
3	OE1470F	tryptophan synthase (EC 4.2.1.20) beta subunit	4	3	-1.55	0.13	9.86E-02	trpB
2	OE1470F	tryptophan synthase (EC 4.2.1.20) beta subunit	5	4	-1.63	0.22	2.31E-02	trpB
1	OE1470F	tryptophan synthase (EC 4.2.1.20) beta subunit	4	1	-1.74	0.19	4.38E-02	trpB
2	OE1471F	tryptophan synthase (EC 4.2.1.20) alpha subunit	3	1	-1.34	0.18	1.71E-01	trpA
1	OE1471F	tryptophan synthase (EC 4.2.1.20) alpha subunit	3	1	-1.43	0.16	2.00E-01	trpA
3	OE1471F	tryptophan synthase (EC 4.2.1.20) alpha subunit	4	2	-1.51	0.23	1.66E-01	trpA
1	OE1472F	fructose-bisphosphate aldolase (EC 4.1.2.13) 2	6	1	-1.10	0.03	7.00E-01	fba2
3	OE1472F	fructose-bisphosphate aldolase (EC 4.1.2.13) 2	5	1	-1.10	0.13	7.44E-01	fba2
2	OE1472F	fructose-bisphosphate aldolase (EC 4.1.2.13) 2	5	2	-1.13	0.07	4.92E-01	fba2
1	OE1475F	conserved hypothetical protein	2	1	-1.05	0.07	8.60E-01	-
3	OE1475F	conserved hypothetical protein	4	2	-1.12	0.13	6.88E-01	-
1	OE1478R	transcription initiation factor TFB	3	1	-1.36	0.13	2.50E-01	tfbF
2	OE1478R	transcription initiation factor TFB	5	3	-1.49	0.22	7.64E-02	tfbF

1	OE1490R	conserved hypothetical protein	12	6	1.15	0.1	6.25E-01	-
3	OE1490R	conserved hypothetical protein	14	4	1.14	0.25	7.35E-01	-
2	OE1490R	conserved hypothetical protein	12	6	1.09	0.06	6.58E-01	-
2	OE1495R	pyruvate kinase (EC 2.7.1.40)	8	2	1.09	0.14	7.30E-01	pykA
1	OE1495R	pyruvate kinase (EC 2.7.1.40)	12	3	1.02	0.19	9.44E-01	pykA
3	OE1495R	pyruvate kinase (EC 2.7.1.40)	10	4	1.02	0.14	9.40E-01	pykA
2	OE1496R	methionine--tRNA ligase (EC 6.1.1.10)	8	4	1.09	0.12	7.09E-01	metS
1	OE1496R	methionine--tRNA ligase (EC 6.1.1.10)	8	3	1.06	0.09	8.20E-01	metS
3	OE1496R	methionine--tRNA ligase (EC 6.1.1.10)	10	5	-1.02	0.22	9.55E-01	metS
1	OE1500R	pyruvate, water dikinase (EC 2.7.9.2) (phosphoenolpyruvate synthase)	9	2	-1.31	0.14	3.28E-01	ppsA
2	OE1500R	pyruvate, water dikinase (EC 2.7.9.2) (phosphoenolpyruvate synthase)	10	2	-1.81	0.13	1.26E-03	ppsA
3	OE1500R	pyruvate, water dikinase (EC 2.7.9.2) (phosphoenolpyruvate synthase)	9	3	-2.52	0.41	2.07E-03	ppsA
1	OE1501F	hypothetical protein	2	2	1.06	0.05	8.00E-01	-
3	OE1501F	hypothetical protein	2	2	-1.11	0.14	7.26E-01	-
1	OE1515R	structural-maintenance-of-chromosomes protein	7	2	1.14	0.07	6.32E-01	smc
2	OE1515R	structural-maintenance-of-chromosomes protein	3	1	-1.12	0.12	5.59E-01	smc
3	OE1522F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit B	5	2	1.16	0.13	6.18E-01	aatB, gatB
2	OE1522F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit B	4	1	1.14	0.08	5.18E-01	aatB, gatB
1	OE1522F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit B	8	3	1.08	0.14	8.07E-01	aatB, gatB
1	OE1528F	DNA topoisomerase I	5	1	-1.02	0.08	9.48E-01	topA
2	OE1528F	DNA topoisomerase I	4	1	-1.21	0.16	3.70E-01	topA
3	OE1528F	DNA topoisomerase I	6	2	-1.67	0.22	6.97E-02	topA
2	OE1536R	transducer protein htr14	2	1	1.25	0.18	4.42E-01	htr14
1	OE1545F	probable oxidoreductase (EC 1.1.1.-) (cis-retinol dehydrogenase homolog)	7	1	1.02	0.1	9.27E-01	rdh1
2	OE1545F	probable oxidoreductase (EC 1.1.1.-) (cis-retinol dehydrogenase homolog)	4	1	-1.13	0.18	5.97E-01	rdh1
3	OE1545F	probable oxidoreductase (EC 1.1.1.-) (cis-retinol dehydrogenase homolog)	5	1	-1.15	0.13	6.16E-01	rdh1
2	OE1547R	probable anion-transporting ATPase (EC 3.6.1.-)	1	1	1.16	0.11	4.78E-01	arsA1
1	OE1547R	probable anion-transporting ATPase (EC 3.6.1.-)	2	1	1.11	0.15	7.20E-01	arsA1
2	OE1550F	conserved hypothetical protein	1	1	1.32	0.1	2.13E-01	-
1	OE1559R	cell division protein ftsZ1	4	1	1.08	0.16	8.19E-01	ftsZ1
2	OE1559R	cell division protein ftsZ1	4	1	1.04	0.08	8.10E-01	ftsZ1
3	OE1559R	cell division protein ftsZ1	6	4	-1.14	0.51	8.05E-01	ftsZ1
1	OE1565F	shikimate 5-dehydrogenase (EC 1.1.1.25)	3	1	-1.09	0.24	7.88E-01	aroE
1	OE1578F	probable glucose-1-phosphate	4	1	1.10	0.18	7.82E-01	graD1

		thymidylyltransferase (EC 2.7.7.24)						
3	OE1578F	probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	3	1	-1.14	0.11	6.32E-01	graD1
2	OE1578F	probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	2	1	-1.36	0.12	1.10E-01	graD1
2	OE1584R	conserved hypothetical protein	8	6	-1.15	0.08	4.50E-01	-
1	OE1584R	conserved hypothetical protein	6	5	-1.27	0.44	5.84E-01	-
3	OE1584R	conserved hypothetical protein	11	6	-1.40	0.2	2.46E-01	-
2	OE1592R	mRNA 3'-end processing factor homolog	9	2	-1.05	0.11	8.00E-01	epf2
3	OE1592R	mRNA 3'-end processing factor homolog	12	3	-1.10	0.25	7.79E-01	epf2
1	OE1592R	mRNA 3'-end processing factor homolog	7	1	-1.13	0.25	7.22E-01	epf2
1	OE1595F	proline--tRNA ligase (EC 6.1.1.15)	3	2	1.25	0.37	6.78E-01	proS
3	OE1595F	proline--tRNA ligase (EC 6.1.1.15)	7	3	1.25	0.3	6.21E-01	proS
2	OE1595F	proline--tRNA ligase (EC 6.1.1.15)	6	3	-1.05	0.16	8.24E-01	proS
1	OE1602F	glycerol-1 phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261)	2	1	-1.08	0.15	7.98E-01	gldA2
3	OE1615R	folylpolyglutamate synthase (EC 6.3.2.17) / dihydropteroate synthase (EC 2.5.1.15)	6	2	1.00	0.34	9.99E-01	folCP
1	OE1615R	folylpolyglutamate synthase (EC 6.3.2.17) / dihydropteroate synthase (EC 2.5.1.15)	4	2	-1.01	0.14	9.65E-01	folCP
2	OE1615R	folylpolyglutamate synthase (EC 6.3.2.17) / dihydropteroate synthase (EC 2.5.1.15)	2	1	-1.18	0.22	5.15E-01	folCP
1	OE1620R	phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) / phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	14	6	-1.12	0.16	6.86E-01	purH
2	OE1620R	phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) / phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	16	8	-1.26	0.16	2.74E-01	purH
3	OE1620R	phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) / phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3)	12	4	-2.49	0.57	7.73E-03	purH
1	OE1623F	adenylosuccinate lyase (EC 4.3.2.2)	17	13	1.10	0.19	7.81E-01	purB
2	OE1623F	adenylosuccinate lyase (EC 4.3.2.2)	15	13	1.09	0.15	7.10E-01	purB
3	OE1623F	adenylosuccinate lyase (EC 4.3.2.2)	13	11	-1.01	0.15	9.77E-01	purB
3	OE1633F	conserved hypothetical protein	3	2	1.03	0.17	9.13E-01	-
1	OE1633F	conserved hypothetical protein	3	2	-1.11	0.14	7.20E-01	-
3	OE1636F	protein-L-isoaspartate O-methyltransferase homolog	2	1	1.45	0.16	2.71E-01	pimT2
2	OE1636F	protein-L-isoaspartate O-methyltransferase homolog	3	2	1.23	0.02	2.23E-01	pimT2
1	OE1636F	protein-L-isoaspartate O-methyltransferase homolog	2	1	1.02	0.19	9.58E-01	pimT2
2	OE1641R	3-hydroxybutryl-CoA dehydratase (EC 4.2.1.55)	3	2	1.14	0.11	5.58E-01	fad2
1	OE1641R	3-hydroxybutryl-CoA dehydratase	3	2	1.03	0.12	9.24E-01	fad2

		(EC 4.2.1.55)						
3	OE1641R	3-hydroxybutryl-CoA dehydratase (EC 4.2.1.55)	2	2	-1.03	0.32	9.50E-01	fad2
2	OE1651F	ribosomal protein S10 homolog	2	1	1.25	0.08	2.64E-01	-
3	OE1657R	geranylgeranyl hydrogenase homolog	8	1	1.10	0.05	7.16E-01	-
1	OE1661F	conserved hypothetical protein	1	1	-1.17	0.22	6.19E-01	-
1	OE1664R	molecular chaperone P45 (validated)	2	1	1.35	0.05	2.43E-01	rspA
3	OE1665R	dihydrodipicolinate synthase (EC 4.2.1.52)	2	1	1.00	0.18	9.96E-01	dapA
2	OE1665R	dihydrodipicolinate synthase (EC 4.2.1.52)	1	1	-1.09	0.17	7.00E-01	dapA
3	OE1668R	conserved hypothetical protein	2	1	1.00	0.13	9.96E-01	-
2	OE1669F	aldehyde dehydrogenase (glucose 1-dehydrogenase homolog)	4	1	1.05	0.08	7.76E-01	-
1	OE1672F	orotate phosphoribosyltransferase homolog	7	4	1.67	0.16	1.75E-01	pyrE1
2	OE1672F	orotate phosphoribosyltransferase homolog	5	3	1.59	0.16	1.35E-01	pyrE1
3	OE1672F	orotate phosphoribosyltransferase homolog	7	4	1.30	0.21	4.93E-01	pyrE1
3	OE1674R	probable phosphate transport operon protein phoU	4	2	1.23	0.11	4.58E-01	phoU
2	OE1674R	probable phosphate transport operon protein phoU	5	1	1.15	0.17	5.81E-01	phoU
1	OE1674R	probable phosphate transport operon protein phoU	3	2	1.06	0.19	8.60E-01	phoU
1	OE1675R	probable ABC-type phosphate transport system ATP-binding protein	3	1	-1.10	0.14	7.28E-01	pstB2
2	OE1675R	probable ABC-type phosphate transport system ATP-binding protein	4	1	-1.12	0.14	5.81E-01	pstB2
3	OE1675R	probable ABC-type phosphate transport system ATP-binding protein	3	1	-1.33	0.11	2.84E-01	pstB2
2	OE1679R	probable ABC-type phosphate transport system periplasmic phosphate-binding protein	5	4	-1.02	0.14	9.29E-01	phoX2
1	OE1679R	probable ABC-type phosphate transport system periplasmic phosphate-binding protein	6	4	-1.10	0.13	7.39E-01	phoX2
3	OE1679R	probable ABC-type phosphate transport system periplasmic phosphate-binding protein	5	3	-1.17	0.1	5.65E-01	phoX2
1	OE1681F	phoU protein homolog	3	2	-1.20	0.17	5.27E-01	-
2	OE1681F	phoU protein homolog	2	1	-1.21	0.11	3.18E-01	-
1	OE1684F	probable sulfate adenylyltransferase (EC 2.7.7.4) small subunit	8	2	-1.06	0.15	8.29E-01	nodP
2	OE1684F	probable sulfate adenylyltransferase (EC 2.7.7.4) small subunit	7	4	-1.06	0.14	7.84E-01	nodP
3	OE1684F	probable sulfate adenylyltransferase (EC 2.7.7.4) small subunit	9	1	-1.80	0.3	5.25E-02	nodP
3	OE1687F	aspartate--tRNA ligase (EC 6.1.1.12)	15	11	1.02	0.13	9.54E-01	aspS
2	OE1687F	aspartate--tRNA ligase (EC 6.1.1.12)	13	7	-1.01	0.14	9.57E-01	aspS

1	OE1687F	aspartate--tRNA ligase (EC 6.1.1.12)	14	9	-1.09	0.13	7.57E-01	aspS
2	OE1698R	probable oxidoreductase (EC 1.1.1.-) (aldehyde reductase homolog / alcohol dehydrogenase homolog)	5	2	1.75	0.09	1.43E-02	oxr4
1	OE1698R	probable oxidoreductase (EC 1.1.1.-) (aldehyde reductase homolog / alcohol dehydrogenase homolog)	6	2	1.37	0.06	2.48E-01	oxr4
3	OE1710R	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3) beta subunit (alpha-ketoglutarate--ferredoxin oxidoreductase beta chain, oxoglutarate dehydrogenase (ferredoxin) beta chain, oxoglutarate synthase beta chain)	5	1	1.39	0.03	1.97E-01	korB
1	OE1710R	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3) beta subunit (alpha-ketoglutarate--ferredoxin oxidoreductase beta chain, oxoglutarate dehydrogenase (ferredoxin) beta chain, oxoglutarate synthase beta chain)	4	1	1.35	0.11	3.15E-01	korB
3	OE1711R	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3) alpha subunit (alpha-ketoglutarate--ferredoxin oxidoreductase alpha chain, oxoglutarate dehydrogenase (ferredoxin) alpha chain, oxoglutarate synthase alpha chain)	5	2	1.64	0.15	1.60E-01	korA
1	OE1719R	probable oxidoreductase (protochlorophyllide reductase homolog)	1	1	2.00	0.07	1.74E-02	-
3	OE1721R	methylmalonyl-CoA mutase (EC 5.4.99.2) 1A (N-terminal homology)	4	2	1.39	0.1	2.61E-01	mut1A
1	OE1726F	acetate--CoA ligase (EC 6.2.1.1)	1	1	1.52	0.06	1.20E-01	acs1
2	OE1726F	acetate--CoA ligase (EC 6.2.1.1)	2	1	-1.21	0.16	3.70E-01	acs1
3	OE1730R	conserved hypothetical protein	1	1	1.45	0.19	3.12E-01	-
1	OE1730R	conserved hypothetical protein	2	1	1.37	0.04	2.27E-01	-
2	OE1737R	dnaK-type molecular chaperone hsp70	16	7	1.19	0.06	3.58E-01	dnaK
1	OE1737R	dnaK-type molecular chaperone hsp70	15	7	1.12	0.09	6.57E-01	dnaK
3	OE1737R	dnaK-type molecular chaperone hsp70	17	9	1.08	0.09	7.88E-01	dnaK
3	OE1738R	hypothetical protein	4	2	1.19	0.1	5.36E-01	-
2	OE1738R	hypothetical protein	2	1	1.16	0.14	5.25E-01	-
1	OE1738R	hypothetical protein	4	3	1.08	0.09	8.05E-01	-
2	OE1742R	dnaJ/dnaK ATPase stimulator grpE	4	3	1.30	0.1	2.30E-01	grpE
1	OE1742R	dnaJ/dnaK ATPase stimulator grpE	5	2	1.15	0.08	6.18E-01	grpE
3	OE1742R	dnaJ/dnaK ATPase stimulator grpE	3	3	1.11	0.14	7.34E-01	grpE
2	OE1745R	hypothetical protein	2	1	1.09	0.09	6.82E-01	-
3	OE1745R	hypothetical protein	2	1	-1.07	0.06	8.07E-01	-
3	OE1752F	3-isopropylmalate dehydratase homolog	2	1	1.00	0.09	9.95E-01	ppd
1	OE1752F	3-isopropylmalate dehydratase homolog	2	1	-1.14	0.13	6.43E-01	ppd
2	OE1757R	probable GTP-binding protein	3	1	1.09	0.17	7.24E-01	gbp5
2	OE1765R	probable proteasome regulatory subunit (probable proteasome-	6	2	1.04	0.19	8.88E-01	pan1

		activating nucleotidase PAN)						
1	OE1765R	probable proteasome regulatory subunit (probable proteasome-activating nucleotidase PAN)	7	3	-1.31	0.16	3.40E-01	pan1
2	OE1778R	probable oxidoreductase (EC 1.1.1.-) (3-oxoacyl-[acyl-carrier-protein] reductase homolog/ cis-retinol dehydrogenase homolog)	1	1	1.20	0.02	2.69E-01	oxr6
3	OE1778R	probable oxidoreductase (EC 1.1.1.-) (3-oxoacyl-[acyl-carrier-protein] reductase homolog/ cis-retinol dehydrogenase homolog)	2	2	1.10	0.07	7.35E-01	oxr6
1	OE1778R	probable oxidoreductase (EC 1.1.1.-) (3-oxoacyl-[acyl-carrier-protein] reductase homolog/ cis-retinol dehydrogenase homolog)	2	1	1.05	0.1	8.38E-01	oxr6
3	OE1781F	probable ABC-type transport system ATP-binding protein	8	5	1.04	0.27	9.15E-01	-
2	OE1781F	probable ABC-type transport system ATP-binding protein	10	6	1.02	0.12	9.22E-01	-
1	OE1781F	probable ABC-type transport system ATP-binding protein	8	7	1.00	0.19	9.93E-01	-
3	OE1782F	conserved hypothetical protein	13	4	1.10	0.06	7.23E-01	-
1	OE1782F	conserved hypothetical protein	13	6	-1.03	0.15	9.09E-01	-
2	OE1782F	conserved hypothetical protein	11	3	-1.22	0.1	2.93E-01	-
1	OE1783F	conserved hypothetical protein	9	4	-1.06	0.07	8.11E-01	-
2	OE1783F	conserved hypothetical protein	8	4	-1.08	0.14	7.02E-01	-
3	OE1783F	conserved hypothetical protein	7	4	-1.10	0.13	7.43E-01	-
2	OE1792F	conserved hypothetical protein	3	2	1.15	0.18	6.01E-01	-
1	OE1792F	conserved hypothetical protein	3	2	-1.01	0.06	9.66E-01	-
3	OE1792F	conserved hypothetical protein	4	2	-1.02	0.18	9.37E-01	-
2	OE1806R	probable periplasmic protein	4	2	-1.08	0.21	7.53E-01	-
3	OE1806R	probable periplasmic protein	5	2	-1.21	0.15	5.05E-01	-
1	OE1806R	probable periplasmic protein	4	2	-1.31	0.21	3.74E-01	-
2	OE1807R	threonine synthase (EC 4.2.99.2)	2	1	-1.07	0.15	7.66E-01	thrC2
3	OE1816R	3-isopropylmalate dehydratase homolog	6	5	-1.01	0.13	9.63E-01	-
1	OE1816R	3-isopropylmalate dehydratase homolog	6	4	-1.06	0.17	8.40E-01	-
2	OE1816R	3-isopropylmalate dehydratase homolog	5	3	-1.14	0.14	5.34E-01	-
2	OE1818R	translation initiation factor aIF-2 alpha subunit	4	2	-1.17	0.07	3.77E-01	eif2a
1	OE1818R	translation initiation factor aIF-2 alpha subunit	3	2	-1.22	0.14	4.81E-01	eif2a
3	OE1818R	translation initiation factor aIF-2 alpha subunit	3	2	-1.26	0.12	3.95E-01	eif2a
1	OE1838R	conserved hypothetical protein	3	1	1.20	0.2	6.00E-01	-
3	OE1838R	conserved hypothetical protein	3	1	1.06	0.12	8.36E-01	-
3	OE1840R	hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	3	3	1.05	0.06	8.37E-01	hprt, apt
1	OE1840R	hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	2	2	-1.06	0.2	8.63E-01	hprt, apt
2	OE1840R	hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	3	2	-1.06	0.11	7.70E-01	hprt, apt
1	OE1841R	HyfD / HycC / NADH dehydrogenase (ubiquinone)	2	1	-1.07	0.15	8.17E-01	-

		subunit L homolog						
3	OE1854R	conserved hypothetical protein	2	1	1.18	0.06	5.32E-01	-
1	OE1854R	conserved hypothetical protein	5	3	1.08	0.11	7.84E-01	-
2	OE1854R	conserved hypothetical protein	6	3	1.00	0.27	9.89E-01	-
3	OE1856R	probable pantothenate metabolism flavoprotein	3	1	-1.15	0.12	6.22E-01	dfp
2	OE1856R	probable pantothenate metabolism flavoprotein	3	1	-1.16	0.2	5.29E-01	dfp
1	OE1862F	aminopeptidase homolog	1	1	1.02	0.21	9.60E-01	ywaD
1	OE1872R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-) (cytochrome bc complex) cytochrome b/c subunit (plastoquinol--plastocyanin reductase (cytochrome b6-f complex) 17K polypeptide (subunit 4) homolog)	4	2	1.20	0.08	4.97E-01	petD
3	OE1872R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-) (cytochrome bc complex) cytochrome b/c subunit (plastoquinol--plastocyanin reductase (cytochrome b6-f complex) 17K polypeptide (subunit 4) homolog)	4	2	1.10	0.17	7.61E-01	petD
2	OE1872R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-) (cytochrome bc complex) cytochrome b/c subunit (plastoquinol--plastocyanin reductase (cytochrome b6-f complex) 17K polypeptide (subunit 4) homolog)	4	1	1.09	0.02	6.42E-01	petD
3	OE1874R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-) (cytochrome bc complex) cytochrome b subunit (plastoquinol--plastocyanin reductase (cyt. b6-f) cyt. b6 subunit/ ubiquinol--cytochrome-c reductase (cyt. bc1) cyt. b subunit (N-term. domain) homolog)	1	1	-1.02	0.06	9.27E-01	petB
1	OE1876R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-) (cytochrome bc complex) Rieske iron-sulfur protein (ubiquinol--cytochrome-c reductase (cytochrome bc1 complex) Rieske iron-sulfur protein homolog)	5	1	1.08	0.17	8.22E-01	petA
2	OE1876R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-) (cytochrome bc complex) Rieske iron-sulfur protein (ubiquinol--cytochrome-c reductase (cytochrome bc1 complex) Rieske iron-sulfur protein homolog)	6	2	1.00	0.09	9.84E-01	petA
3	OE1876R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-) (cytochrome bc complex) Rieske iron-sulfur protein (ubiquinol--cytochrome-c reductase	6	2	-1.07	0.09	7.89E-01	petA

		(cytochrome bc1 complex) Rieske iron-sulfur protein homolog)						
2	OE1893F	diphosphomevalonate decarboxylase (EC 4.1.1.33)	5	3	1.22	0.1	3.46E-01	mvd
3	OE1893F	diphosphomevalonate decarboxylase (EC 4.1.1.33)	3	1	1.14	0.25	7.39E-01	mvd
1	OE1893F	diphosphomevalonate decarboxylase (EC 4.1.1.33)	4	2	-1.03	0.15	9.11E-01	mvd
1	OE1909F	conserved hypothetical protein	1	1	1.18	0.1	5.51E-01	-
3	OE1909F	conserved hypothetical protein	2	1	1.03	0.04	9.15E-01	-
1	OE1916F	cysteine synthase (EC 4.2.99.8) cysK1	4	3	1.20	0.08	5.00E-01	cysK1
2	OE1916F	cysteine synthase (EC 4.2.99.8) cysK1	2	2	1.20	0.16	4.61E-01	cysK1
3	OE1916F	cysteine synthase (EC 4.2.99.8) cysK1	5	4	1.04	0.09	8.78E-01	cysK1
2	OE1919R	conserved hypothetical protein	2	2	-1.10	0.37	8.00E-01	-
2	OE1934R	proteinase IV (EC 3.4.-.-)	6	1	1.00	0.05	9.81E-01	edp
1	OE1934R	proteinase IV (EC 3.4.-.-)	7	2	-1.04	0.12	8.86E-01	edp
3	OE1942F	citryl-CoA lyase (EC 4.1.3.34) beta subunit; citrate lyase (EC 4.1.3.6) beta subunit; ATP citrate synthase (EC 2.3.3.8) beta subunit	4	1	1.22	0.27	6.32E-01	citE
3	OE1943F	glutamate dehydrogenase (NADP+) (EC 1.4.1.4)	10	3	1.06	0.13	8.27E-01	gdhA1
2	OE1943F	glutamate dehydrogenase (NADP+) (EC 1.4.1.4)	12	5	1.01	0.16	9.58E-01	gdhA1
1	OE1943F	glutamate dehydrogenase (NADP+) (EC 1.4.1.4)	8	3	-1.11	0.11	7.00E-01	gdhA1
1	OE1944R	probable aspartate aminotransferase (EC 2.6.1.1)	5	1	1.37	0.11	2.80E-01	aspB2
3	OE1944R	probable aspartate aminotransferase (EC 2.6.1.1)	9	3	1.09	0.11	7.59E-01	aspB2
2	OE1944R	probable aspartate aminotransferase (EC 2.6.1.1)	7	2	1.06	0.1	7.53E-01	aspB2
2	OE1946R	riboflavin synthase (EC 2.5.1.9) beta subunit (6,7-dimethyl-8-ribityllumazine synthase)	2	1	1.14	0.05	4.85E-01	ribE, risB
1	OE1946R	riboflavin synthase (EC 2.5.1.9) beta subunit (6,7-dimethyl-8-ribityllumazine synthase)	3	2	1.04	0.08	8.69E-01	ribE, risB
1	OE1951F	phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) carbon dioxide-fixation subunit	11	8	-1.07	0.17	8.29E-01	purK
2	OE1951F	phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) carbon dioxide-fixation subunit	12	7	-1.10	0.09	6.10E-01	purK
3	OE1951F	phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) carbon dioxide-fixation subunit	11	9	-1.15	0.13	6.20E-01	purK
2	OE1952F	phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) catalytic subunit	6	2	1.04	0.07	8.06E-01	purE
1	OE1952F	phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) catalytic subunit	5	2	-1.03	0.09	9.17E-01	purE
3	OE1954F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit B	6	3	1.15	0.13	6.32E-01	nuoB
1	OE1954F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit B	6	2	1.14	0.06	6.27E-01	nuoB
2	OE1954F	NADH dehydrogenase	5	3	-1.03	0.05	8.75E-01	nuoB

		(ubiquinone) (EC 1.6.5.3) subunit B						
3	OE1956F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit CD	18	5	1.10	0.11	7.31E-01	nuoCD
1	OE1956F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit CD	14	7	1.06	0.19	8.43E-01	nuoCD
2	OE1956F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit CD	15	8	1.05	0.14	8.13E-01	nuoCD
1	OE1957F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit H	2	1	1.06	0.39	8.99E-01	nuoH
1	OE1969F	CBS domain protein	3	1	1.01	0.1	9.76E-01	-
1	OE1979R	cytochrome-c oxidase (EC 1.9.3.1) subunit I	1	1	1.45	0.14	2.53E-01	cox1A, coxA1
1	OE2007F	conserved hypothetical protein	3	3	-1.09	0.11	7.57E-01	-
2	OE2007F	conserved hypothetical protein	4	2	-1.10	0.09	6.10E-01	-
3	OE2007F	conserved hypothetical protein	3	2	-1.19	0.23	5.90E-01	-
3	OE2011R	probable nonspecific lipid-transfer protein (sterol carrier protein)	3	2	1.04	0.08	8.68E-01	scp
2	OE2011R	probable nonspecific lipid-transfer protein (sterol carrier protein)	3	1	-1.01	0.12	9.55E-01	scp
1	OE2011R	probable nonspecific lipid-transfer protein (sterol carrier protein)	3	1	-1.09	0.1	7.61E-01	scp
2	OE2013R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	8	2	1.32	0.12	2.42E-01	acd4
1	OE2013R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	5	3	1.23	0.08	4.47E-01	acd4
3	OE2013R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	6	2	1.16	0.18	6.55E-01	acd4
2	OE2015R	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	7	2	-1.02	0.18	9.35E-01	hbd1
3	OE2015R	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	7	2	-1.02	0.06	9.43E-01	hbd1
1	OE2015R	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	6	1	-1.05	0.21	8.75E-01	hbd1
1	OE2019F	fructose-bisphosphate aldolase (EC 4.1.2.13) 1	5	2	1.09	0.04	7.42E-01	fba1
2	OE2019F	fructose-bisphosphate aldolase (EC 4.1.2.13) 1	6	3	-1.02	0.08	9.16E-01	fba1
3	OE2019F	fructose-bisphosphate aldolase (EC 4.1.2.13) 1	5	2	-1.02	0.11	9.52E-01	fba1
1	OE2020F	fructose-bisphosphatase (EC 3.1.3.11)	1	1	1.03	0.15	9.31E-01	fbp
1	OE2047R	conserved hypothetical protein	1	1	1.03	0.13	9.29E-01	-
1	OE2055F	conserved hypothetical protein	2	1	1.16	0.04	5.42E-01	-
3	OE2067F	conserved hypothetical protein	2	1	-1.07	0.12	8.20E-01	-
1	OE2081R	RNA 3'-terminal phosphate cyclase (EC 6.5.1.4)	3	2	1.03	0.1	9.11E-01	tpc
2	OE2081R	RNA 3'-terminal phosphate cyclase (EC 6.5.1.4)	3	2	-1.01	0.21	9.65E-01	tpc
3	OE2081R	RNA 3'-terminal phosphate cyclase (EC 6.5.1.4)	4	3	-1.02	0.11	9.53E-01	tpc
3	OE2084R	transcription initiation factor TFB	8	2	3.45	0.07	5.78E-04	tfbB
2	OE2084R	transcription initiation factor TFB	4	2	3.23	0.06	1.11E-05	tfbB

2	OE2097F	conserved hypothetical protein	5	1	1.28	0.08	2.07E-01	-
1	OE2097F	conserved hypothetical protein	3	1	1.20	0.12	5.22E-01	-
3	OE2097F	conserved hypothetical protein	5	1	1.12	0.16	7.04E-01	-
2	OE2110R	UDPglucose 4-epimerase (EC 5.1.3.2)	5	2	1.00	0.16	9.87E-01	galE1
3	OE2110R	UDPglucose 4-epimerase (EC 5.1.3.2)	7	2	-1.03	0.12	9.11E-01	galE1
1	OE2110R	UDPglucose 4-epimerase (EC 5.1.3.2)	9	3	-1.10	0.16	7.56E-01	galE1
2	OE2118F	transcription initiation factor IIE alpha subunit homolog	2	2	1.18	0.18	5.58E-01	tfeA
1	OE2118F	transcription initiation factor IIE alpha subunit homolog	2	1	1.06	0.15	8.37E-01	tfeA
3	OE2118F	transcription initiation factor IIE alpha subunit homolog	3	2	1.05	0.14	8.67E-01	tfeA
2	OE2120F	conserved hypothetical protein	4	2	1.10	0.08	6.11E-01	-
1	OE2120F	conserved hypothetical protein	4	3	1.04	0.07	8.65E-01	-
2	OE2121F	conserved hypothetical protein	4	1	1.06	0.06	7.28E-01	-
1	OE2121F	conserved hypothetical protein	3	1	-1.12	0.13	6.84E-01	-
1	OE2133R	aldehyde dehydrogenase (EC 1.2.1.-) (retinal dehydrogenase homolog)	11	6	1.12	0.06	6.54E-01	aldH2
3	OE2133R	aldehyde dehydrogenase (EC 1.2.1.-) (retinal dehydrogenase homolog)	13	6	1.12	0.06	6.71E-01	aldH2
2	OE2133R	aldehyde dehydrogenase (EC 1.2.1.-) (retinal dehydrogenase homolog)	12	5	-1.02	0.09	9.18E-01	aldH2
2	OE2141F	conserved hypothetical protein	10	4	1.09	0.19	7.44E-01	-
1	OE2141F	conserved hypothetical protein	9	6	1.00	0.14	9.97E-01	-
3	OE2141F	conserved hypothetical protein	11	1	-1.25	0.2	4.60E-01	-
1	OE2149R	conserved hypothetical protein	8	2	1.03	0.09	9.14E-01	-
2	OE2149R	conserved hypothetical protein	10	4	1.00	0.1	9.83E-01	-
3	OE2149R	conserved hypothetical protein	11	5	-1.01	0.13	9.75E-01	-
2	OE2159R	ribosomal protein S3a.eR	8	6	-1.09	0.22	7.41E-01	rps3aR
3	OE2159R	ribosomal protein S3a.eR	10	8	-1.13	0.12	6.59E-01	rps3aR
1	OE2159R	ribosomal protein S3a.eR	8	6	-1.14	0.08	6.12E-01	rps3aR
2	OE2165R	ribosomal protein S15	3	2	-1.04	0.1	8.58E-01	rps15
3	OE2165R	ribosomal protein S15	1	1	-1.16	0.48	7.58E-01	rps15
1	OE2165R	ribosomal protein S15	2	1	-1.24	0.13	4.27E-01	rps15
1	OE2168R	transducer protein htrVI	3	1	1.43	0.15	2.79E-01	htrVI, htr6, htJ
1	OE2170R	probable periplasmic substrate-binding protein (membrane lipoprotein tmpC homolog)	5	1	-1.28	0.1	3.50E-01	tmpC
1	OE2186R	sec-independent protein translocase component tatA	2	1	1.15	0.17	6.70E-01	tatA
1	OE2189R	transducer protein htr4 (htpVI)	8	1	1.33	0.1	3.15E-01	htr4, htpVI, htD
3	OE2189R	transducer protein htr4 (htpVI)	6	1	1.28	0.14	4.34E-01	htr4, htpVI, htD
2	OE2189R	transducer protein htr4 (htpVI)	6	1	1.18	0.08	4.06E-01	htr4, htpVI, htD
2	OE2191F	hypothetical protein	4	1	1.09	0.06	6.24E-01	-
2	OE2197R	conserved hypothetical protein	2	1	1.05	0.02	7.53E-01	-
2	OE2199F	probable alcohol dehydrogenase	2	1	1.28	0.1	2.47E-01	adh5

		(EC 1.1.1.1)						
3	OE2199F	probable alcohol dehydrogenase (EC 1.1.1.1)	3	2	1.01	0.24	9.82E-01	adh5
2	OE2249R	transducer protein weak homolog lacking transduction domain	7	4	1.33	0.19	3.44E-01	-
1	OE2249R	transducer protein weak homolog lacking transduction domain	6	4	1.32	0.2	4.63E-01	-
3	OE2249R	transducer protein weak homolog lacking transduction domain	5	3	1.12	0.2	7.37E-01	-
3	OE2268R	imidazoleglycerol-phosphate synthase (EC 2.4.2.-) subunit hisF	1	1	1.02	0.13	9.33E-01	hisF
2	OE2274R	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) component II	6	3	-1.04	0.16	8.51E-01	purL
1	OE2274R	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) component II	4	4	-1.14	0.33	7.34E-01	purL
3	OE2274R	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) component II	8	2	-1.17	0.14	5.84E-01	purL
1	OE2284F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit A	2	1	-1.10	0.17	7.52E-01	aatA, gatA
3	OE2284F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit A	3	1	-1.11	0.22	7.45E-01	aatA, gatA
2	OE2284F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit A	3	1	-1.17	0.1	4.05E-01	aatA, gatA
3	OE2292F	phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	3	2	1.06	0.08	8.15E-01	purM
1	OE2292F	phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	2	1	1.05	0.11	8.64E-01	purM
3	OE2294R	conserved hypothetical protein	2	1	1.04	0.17	9.00E-01	-
1	OE2294R	conserved hypothetical protein	3	2	1.02	0.13	9.51E-01	-
2	OE2296F	proteasome beta subunit	3	1	1.69	0.1	2.35E-02	psmB
3	OE2296F	proteasome beta subunit	4	2	1.67	0.07	6.86E-02	psmB
1	OE2296F	proteasome beta subunit	2	1	1.30	0.04	3.09E-01	psmB
2	OE2301R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit A	3	1	1.45	0.12	1.28E-01	top6A
3	OE2301R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit A	4	1	-1.32	0.11	2.94E-01	top6A
3	OE2302R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit B	7	1	-1.04	0.19	9.11E-01	top6B
1	OE2302R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit B	11	5	-1.06	0.1	8.25E-01	top6B
2	OE2302R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit B	10	4	-1.33	0.13	1.49E-01	top6B
1	OE2303F	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) subunit B	5	1	1.19	0.16	5.80E-01	gyrB
2	OE2303F	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) subunit B	3	1	-1.18	0.13	4.09E-01	gyrB
2	OE2304F	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) subunit A	9	4	-1.04	0.14	8.41E-01	gyrA
1	OE2304F	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) subunit	10	5	-1.06	0.14	8.50E-01	gyrA

		A						
2	OE2306F	conserved hypothetical protein	7	1	1.03	0.16	9.03E-01	-
3	OE2306F	conserved hypothetical protein	8	1	-1.07	0.06	7.89E-01	-
1	OE2306F	conserved hypothetical protein	9	2	-1.18	0.1	5.42E-01	-
1	OE2307F	NADH dehydrogenase homolog	7	2	-1.13	0.18	6.72E-01	-
3	OE2307F	NADH dehydrogenase homolog	8	1	-1.26	0.23	4.64E-01	-
2	OE2307F	NADH dehydrogenase homolog	7	2	-1.30	0.39	4.41E-01	-
3	OE2311R	uridine phosphorylase (EC 2.4.2.3)	2	1	-1.09	0.2	7.88E-01	udp2
1	OE2317R	probable ABC-type transport system periplasmic substrate-binding protein (membrane lipoprotein tmpC homolog)	8	6	-1.06	0.11	8.31E-01	-
2	OE2317R	probable ABC-type transport system periplasmic substrate-binding protein (membrane lipoprotein tmpC homolog)	7	5	-1.07	0.09	7.27E-01	-
3	OE2317R	probable ABC-type transport system periplasmic substrate-binding protein (membrane lipoprotein tmpC homolog)	6	3	-2.05	0.33	1.69E-02	-
3	OE2318R	phosphomannomutase (EC 5.4.2.8)	4	2	1.18	0.06	5.39E-01	pmu2
2	OE2318R	phosphomannomutase (EC 5.4.2.8)	7	2	1.02	0.14	9.27E-01	pmu2
1	OE2318R	phosphomannomutase (EC 5.4.2.8)	8	4	-1.02	0.19	9.60E-01	pmu2
3	OE2357F	conserved hypothetical protein	2	1	-1.07	0.13	8.22E-01	-
2	OE2358F	probable nonspecific lipid-transfer protein (sterol carrier protein)	4	2	1.23	0.12	3.52E-01	acaB2
1	OE2358F	probable nonspecific lipid-transfer protein (sterol carrier protein)	4	1	1.12	0.18	7.17E-01	acaB2
3	OE2358F	probable nonspecific lipid-transfer protein (sterol carrier protein)	3	1	-1.01	0.22	9.86E-01	acaB2
2	OE2360R	NADH oxidase homolog	4	2	1.19	0.11	4.28E-01	-
1	OE2360R	NADH oxidase homolog	4	2	1.16	0.11	5.87E-01	-
2	OE2364R	probable NADH oxidase (H2O2-forming) (EC 1.6.99.3)	2	1	1.28	0.25	4.90E-01	noxC
3	OE2364R	probable NADH oxidase (H2O2-forming) (EC 1.6.99.3)	3	1	-1.12	0.64	8.50E-01	noxC
1	OE2367F	aldehyde dehydrogenase (glyceraldehyde-3-phosphate dehydrogenase homolog, succinate-semialdehyde dehydrogenase homolog)	5	1	1.35	0.06	2.49E-01	aldH3
2	OE2367F	aldehyde dehydrogenase (glyceraldehyde-3-phosphate dehydrogenase homolog, succinate-semialdehyde dehydrogenase homolog)	6	2	-1.25	0.17	2.97E-01	aldH3
3	OE2372F	acetate--CoA ligase (ADP-forming) (EC 6.2.1.13) (alpha and beta subunit fusion)	11	4	-1.01	0.15	9.65E-01	acs3
2	OE2372F	acetate--CoA ligase (ADP-forming) (EC 6.2.1.13) (alpha and beta subunit fusion)	11	2	-1.08	0.11	7.12E-01	acs3
1	OE2372F	acetate--CoA ligase (ADP-forming) (EC 6.2.1.13) (alpha and beta subunit fusion)	9	3	-1.22	0.11	4.63E-01	acs3
2	OE2373F	probable phosphate acetyltransferase (EC 2.3.1.8)	9	8	1.12	0.06	5.32E-01	pta
3	OE2373F	probable phosphate	7	5	1.09	0.11	7.56E-01	pta

		acetyltransferase (EC 2.3.1.8)						
1	OE2373F	probable phosphate acetyltransferase (EC 2.3.1.8)	7	6	1.08	0.19	8.26E-01	pta
2	OE2374R	purine-binding chemotaxis protein cheW2	3	2	1.23	0.1	3.11E-01	cheW2
3	OE2374R	purine-binding chemotaxis protein cheW2	3	2	1.18	0.18	6.20E-01	cheW2
2	OE2386R	flagella accessory protein	2	1	-1.03	0.14	9.00E-01	flaCE, flaE
1	OE2392R	transducer protein htr15 (htpIX)	5	3	1.01	0.1	9.81E-01	htr15, htpIX
2	OE2392R	transducer protein htr15 (htpIX)	4	2	-1.07	0.1	7.31E-01	htr15, htpIX
3	OE2392R	transducer protein htr15 (htpIX)	6	3	-1.16	0.35	6.98E-01	htr15, htpIX
1	OE2397F	flagellin B1 precursor	4	2	-1.24	0.1	4.19E-01	flgB1
2	OE2397F	flagellin B1 precursor	4	2	-2.80	0.39	2.27E-06	flgB1
3	OE2397F	flagellin B1 precursor	4	2	-7.49	0.89	0.00E+00	flgB1
1	OE2398F	flagellin B2 precursor	3	1	-1.12	0.15	6.94E-01	flgB2
2	OE2398F	flagellin B2 precursor	2	1	-2.84	0.22	1.79E-08	flgB2
3	OE2398F	flagellin B2 precursor	3	1	-7.07	1.01	0.00E+00	flgB2
2	OE2401F	phycocyanin alpha phycocyanobilin lyase homolog	4	2	1.14	0.15	6.08E-01	cpcE
1	OE2401F	phycocyanin alpha phycocyanobilin lyase homolog	3	1	-1.08	0.18	8.06E-01	cpcE
3	OE2401F	phycocyanin alpha phycocyanobilin lyase homolog	4	3	-1.34	0.15	2.91E-01	cpcE
1	OE2402F	conserved hypothetical protein	2	2	-1.02	0.17	9.41E-01	-
2	OE2404R	conserved hypothetical protein	4	2	1.02	0.14	9.25E-01	-
1	OE2404R	conserved hypothetical protein	6	4	-1.05	0.18	8.63E-01	-
3	OE2404R	conserved hypothetical protein	7	3	-1.23	0.34	5.88E-01	-
1	OE2406R	protein-glutamate O-methyltransferase (EC 2.1.1.80) cheR	8	4	1.02	0.16	9.54E-01	cheR
2	OE2406R	protein-glutamate O-methyltransferase (EC 2.1.1.80) cheR	10	5	-1.02	0.14	9.27E-01	cheR
3	OE2406R	protein-glutamate O-methyltransferase (EC 2.1.1.80) cheR	10	5	-1.27	0.12	3.83E-01	cheR
3	OE2410R	taxis protein cheC3	2	2	1.32	0.04	2.99E-01	cheC3
2	OE2410R	taxis protein cheC3	2	1	1.19	0.12	4.41E-01	cheC3
1	OE2410R	taxis protein cheC3	3	2	-1.09	0.08	7.56E-01	cheC3
1	OE2414R	taxis protein cheC1 (cheJ)	3	2	1.32	0.21	4.69E-01	cheC1, cheJ
2	OE2414R	taxis protein cheC1 (cheJ)	2	1	1.15	0.25	6.69E-01	cheC1, cheJ
3	OE2414R	taxis protein cheC1 (cheJ)	5	3	1.02	0.17	9.59E-01	cheC1, cheJ
2	OE2415R	taxis sensor histidine kinase (EC 2.7.3.-) cheA	7	2	-1.02	0.36	9.60E-01	cheA
1	OE2415R	taxis sensor histidine kinase (EC 2.7.3.-) cheA	7	6	-1.11	0.3	7.72E-01	cheA
3	OE2415R	taxis sensor histidine kinase (EC 2.7.3.-) cheA	8	4	-1.34	0.25	3.43E-01	cheA
2	OE2416R	protein-glutamate methylesterase (EC 3.1.1.61) cheB	3	2	-1.07	0.18	7.81E-01	cheB
1	OE2416R	protein-glutamate methylesterase (EC 3.1.1.61) cheB	4	2	-1.33	0.07	2.75E-01	cheB
3	OE2416R	protein-glutamate methylesterase	3	1	-2.24	0.38	8.45E-03	cheB

		(EC 3.1.1.61) cheB						
1	OE2419R	purine-binding chemotaxis protein cheW1	5	3	1.22	0.12	5.03E-01	cheW1
2	OE2419R	purine-binding chemotaxis protein cheW1	6	1	1.19	0.08	3.55E-01	cheW1
3	OE2419R	purine-binding chemotaxis protein cheW1	5	3	-1.19	0.09	5.19E-01	cheW1
3	OE2425F	probable aminotransferase (EC 2.6.1.-) (histidinol-phosphate transaminase homolog / aspartate transaminase homolog)	1	1	-1.04	0.14	8.84E-01	aat1
1	OE2428R	conserved hypothetical protein	4	1	1.06	0.15	8.39E-01	-
2	OE2450F	acetate--CoA ligase (EC 6.2.1.1)	7	4	-1.02	0.07	9.15E-01	acs2
1	OE2450F	acetate--CoA ligase (EC 6.2.1.1)	7	4	-1.08	0.18	7.96E-01	acs2
3	OE2450F	acetate--CoA ligase (EC 6.2.1.1)	8	3	-1.29	0.16	3.65E-01	acs2
1	OE2451R	probable oxidoreductase	5	2	1.25	0.1	4.35E-01	-
2	OE2451R	probable oxidoreductase	6	1	1.14	0.14	5.63E-01	-
3	OE2451R	probable oxidoreductase	7	2	1.14	0.15	6.75E-01	-
3	OE2458R	IMP dehydrogenase (EC 1.1.1.205)	19	3	1.08	0.13	7.98E-01	guaB
2	OE2458R	IMP dehydrogenase (EC 1.1.1.205)	17	3	-1.05	0.13	8.08E-01	guaB
1	OE2458R	IMP dehydrogenase (EC 1.1.1.205)	17	6	-1.09	0.23	7.98E-01	guaB
1	OE2470F	flagellin A2 precursor	6	1	-1.35	0.09	2.48E-01	flgA2
2	OE2470F	flagellin A2 precursor	6	2	-3.71	1.08	1.03E-04	flgA2
3	OE2470F	flagellin A2 precursor	6	2	-8.01	2.29	4.98E-08	flgA2
3	OE2472F	conserved hypothetical protein	6	1	1.18	0.05	5.32E-01	-
1	OE2472F	conserved hypothetical protein	5	3	1.16	0.06	5.78E-01	-
2	OE2472F	conserved hypothetical protein	3	2	1.15	0.1	4.93E-01	-
3	OE2474R	transducer protein htrXIII	2	1	2.00	0.12	4.40E-02	htrXIII, htr13, htL
2	OE2474R	transducer protein htrXIII	5	4	1.89	0.22	1.65E-01	htrXIII, htr13, htL
1	OE2474R	transducer protein htrXIII	7	2	1.33	0.11	3.16E-01	htrXIII, htr13, htL
1	OE2492F	conserved hypothetical protein	2	1	1.35	0.02	2.37E-01	-
3	OE2492F	conserved hypothetical protein	1	1	1.12	0.05	6.47E-01	-
3	OE2500R	triosephosphate isomerase (EC 5.3.1.1)	2	1	1.15	0.13	6.42E-01	tpiA
2	OE2500R	triosephosphate isomerase (EC 5.3.1.1)	1	1	1.00	0.1	9.83E-01	tpiA
1	OE2500R	triosephosphate isomerase (EC 5.3.1.1)	2	1	-1.09	0.12	7.57E-01	tpiA
2	OE2515F	conserved hypothetical protein	3	2	1.35	0.07	1.21E-01	-
1	OE2515F	conserved hypothetical protein	3	2	1.18	0.08	5.34E-01	-
3	OE2515F	conserved hypothetical protein	3	1	1.05	0.05	8.42E-01	-
1	OE2524R	UDPglucose 6-dehydrogenase (EC 1.1.1.22)	8	2	1.02	0.14	9.36E-01	udg1
2	OE2524R	UDPglucose 6-dehydrogenase (EC 1.1.1.22)	8	2	1.01	0.07	9.47E-01	udg1
3	OE2524R	UDPglucose 6-dehydrogenase (EC 1.1.1.22)	9	3	-1.34	0.31	3.95E-01	udg1
1	OE2527F	conserved hypothetical protein	2	1	-1.05	0.14	8.61E-01	-
3	OE2527F	conserved hypothetical protein	2	2	-1.26	0.08	3.83E-01	-
2	OE2530F	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	4	2	1.09	0.14	7.23E-01	graD4
1	OE2530F	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	6	1	-1.06	0.33	8.83E-01	graD4
3	OE2530F	glucose-1-phosphate	4	2	-1.24	0.13	4.32E-01	graD4

		thymidylyltransferase (EC 2.7.7.24)						
2	OE2548F	probable transmembrane oligosaccharyl transferase	1	1	-1.11	0.22	6.91E-01	tot
1	OE2548F	probable transmembrane oligosaccharyl transferase	1	1	-1.12	0.18	7.05E-01	tot
1	OE2569R	sulfite oxidase homolog	2	1	-1.09	0.17	7.62E-01	-
3	OE2569R	sulfite oxidase homolog	2	2	-1.14	0.17	6.53E-01	-
2	OE2569R	sulfite oxidase homolog	1	1	-1.16	0.16	4.86E-01	-
2	OE2571F	hypothetical protein	1	1	1.12	0.25	7.25E-01	-
3	OE2571F	hypothetical protein	1	1	1.05	0.22	8.92E-01	-
1	OE2577R	conserved hypothetical protein	4	1	-1.03	0.18	9.12E-01	-
3	OE2577R	conserved hypothetical protein	2	1	-1.05	0.17	8.69E-01	-
3	OE2579F	adenylosuccinate synthase (EC 6.3.4.4)	12	7	-1.01	0.16	9.74E-01	purA
1	OE2579F	adenylosuccinate synthase (EC 6.3.4.4)	10	4	-1.04	0.09	8.70E-01	purA
2	OE2579F	adenylosuccinate synthase (EC 6.3.4.4)	11	7	-1.05	0.12	8.04E-01	purA
1	OE2583R	conserved hypothetical protein	5	2	1.11	0.11	6.97E-01	-
2	OE2583R	conserved hypothetical protein	6	3	1.11	0.19	6.98E-01	-
3	OE2601R	ribosomal protein L10	7	4	1.00	0.14	9.94E-01	rpl10
1	OE2601R	ribosomal protein L10	10	6	-1.01	0.09	9.76E-01	rpl10
2	OE2601R	ribosomal protein L10	6	5	-1.03	0.1	8.89E-01	rpl10
3	OE2602R	ribosomal protein L1	7	5	-1.02	0.1	9.52E-01	rpl1
1	OE2602R	ribosomal protein L1	6	4	-1.03	0.09	9.07E-01	rpl1
2	OE2602R	ribosomal protein L1	9	5	-1.12	0.07	5.17E-01	rpl1
2	OE2603R	ribosomal protein L11	4	2	1.05	0.08	7.76E-01	rpl11
1	OE2603R	ribosomal protein L11	1	1	-1.24	0.2	4.73E-01	rpl11
3	OE2603R	ribosomal protein L11	1	1	-1.30	0.26	4.12E-01	rpl11
2	OE2610F	lactoylglutathione lyase (EC 4.4.1.5)	2	1	1.19	0.09	3.67E-01	glo1
1	OE2610F	lactoylglutathione lyase (EC 4.4.1.5)	3	2	1.01	0.08	9.77E-01	glo1
2	OE2622R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta subunit (pyruvate dehydrogenase (ferredoxin) beta chain, pyruvate synthase beta chain)	8	1	1.15	0.19	6.10E-01	porB
3	OE2622R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta subunit (pyruvate dehydrogenase (ferredoxin) beta chain, pyruvate synthase beta chain)	7	2	1.12	0.11	6.85E-01	porB
1	OE2622R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta subunit (pyruvate dehydrogenase (ferredoxin) beta chain, pyruvate synthase beta chain)	10	1	1.02	0.15	9.56E-01	porB
3	OE2623R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) alpha subunit (pyruvate dehydrogenase (ferredoxin) alpha chain, pyruvate synthase alpha chain)	12	6	1.11	0.11	7.08E-01	porA
1	OE2623R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) alpha subunit (pyruvate dehydrogenase (ferredoxin) alpha chain, pyruvate synthase alpha chain)	10	4	-1.01	0.09	9.82E-01	porA
2	OE2623R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) alpha subunit (pyruvate dehydrogenase	13	6	-1.01	0.09	9.51E-01	porA

		(ferredoxin) alpha chain, pyruvate synthase alpha chain)						
2	OE2626R	probable ATP-binding protein mrp	2	1	1.23	0.14	3.80E-01	mrp
3	OE2626R	probable ATP-binding protein mrp	5	3	-1.08	0.24	8.23E-01	mrp
1	OE2626R	probable ATP-binding protein mrp	5	3	-1.09	0.1	7.60E-01	mrp
3	OE2627F	ribosomal protein S13	5	3	1.01	0.16	9.85E-01	rps13
1	OE2627F	ribosomal protein S13	2	1	-1.06	0.16	8.38E-01	rps13
2	OE2627F	ribosomal protein S13	3	1	-1.12	0.15	5.89E-01	rps13
2	OE2628F	ribosomal protein S4	4	3	1.00	0.15	9.85E-01	rps4
3	OE2628F	ribosomal protein S4	6	5	-1.01	0.11	9.75E-01	rps4
1	OE2628F	ribosomal protein S4	4	3	-1.12	0.11	6.74E-01	rps4
1	OE2629F	ribosomal protein S11	3	2	1.01	0.03	9.77E-01	rps11
3	OE2631F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit D	3	2	-1.06	0.2	8.49E-01	rpoD
1	OE2631F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit D	3	2	-1.09	0.17	7.66E-01	rpoD
2	OE2631F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit D	2	1	-1.17	0.14	4.47E-01	rpoD
2	OE2632F	ribosomal protein L18.eR	6	2	-1.10	0.06	5.89E-01	rpl18R
1	OE2632F	ribosomal protein L18.eR	5	2	-1.17	0.11	5.66E-01	rpl18R
3	OE2632F	ribosomal protein L18.eR	5	1	-1.20	0.15	5.22E-01	rpl18R
2	OE2633F	ribosomal protein L13	3	1	-1.01	0.1	9.52E-01	rpl13
3	OE2633F	ribosomal protein L13	6	4	-1.05	0.05	8.61E-01	rpl13
1	OE2633F	ribosomal protein L13	5	3	-1.06	0.09	8.28E-01	rpl13
2	OE2635F	ribosomal protein S9	7	4	-1.06	0.1	7.61E-01	rps9
1	OE2635F	ribosomal protein S9	7	5	-1.08	0.09	7.63E-01	rps9
3	OE2635F	ribosomal protein S9	7	3	-1.10	0.18	7.52E-01	rps9
3	OE2640F	phosphopyruvate hydratase (EC 4.2.1.11) (enolase)	5	3	1.11	0.3	7.94E-01	eno
1	OE2640F	phosphopyruvate hydratase (EC 4.2.1.11) (enolase)	5	3	-1.13	0.2	6.88E-01	eno
2	OE2641F	ribosomal protein S2	4	4	1.01	0.11	9.52E-01	rps2
1	OE2641F	ribosomal protein S2	5	4	-1.02	0.16	9.47E-01	rps2
3	OE2641F	ribosomal protein S2	5	3	-1.07	0.07	7.89E-01	rps2
1	OE2648F	conserved hypothetical protein	13	5	1.10	0.36	8.46E-01	-
2	OE2648F	conserved hypothetical protein	12	7	-1.01	0.13	9.56E-01	-
3	OE2648F	conserved hypothetical protein	10	8	-1.06	0.18	8.56E-01	-
1	OE2650F	probable trifunctional short-chain (E)-prenyl diphosphate synthase (EC 2.5.1.-) (probable dimethylallyltransferase (EC 2.5.1.1) / probable geranyltranstransferase (EC 2.5.1.10) / probable farnesytranstransferase (EC 2.5.1.29))	5	3	-1.17	0.17	5.83E-01	idsA1
2	OE2650F	probable trifunctional short-chain (E)-prenyl diphosphate synthase (EC 2.5.1.-) (probable dimethylallyltransferase (EC 2.5.1.1) / probable geranyltranstransferase (EC 2.5.1.10) / probable farnesytranstransferase (EC 2.5.1.29))	2	1	-1.17	0.16	4.65E-01	idsA1
1	OE2652F	glutamate--tRNA ligase (EC 6.1.1.17)	4	1	-1.16	0.14	5.95E-01	gltS
3	OE2652F	glutamate--tRNA ligase (EC 6.1.1.17)	6	1	-1.18	0.2	5.81E-01	gltS
2	OE2652F	glutamate--tRNA ligase (EC	6	2	-1.21	0.14	3.52E-01	gltS

		6.1.1.17)						
1	OE2662F	ribosomal protein L7a.eR/HS6 (isolated from the small ribosomal subunit)	2	2	-1.09	0.07	7.31E-01	rpl7aR, rpsH6
2	OE2662F	ribosomal protein L7a.eR/HS6 (isolated from the small ribosomal subunit)	2	2	-1.09	0.06	6.23E-01	rpl7aR, rpsH6
3	OE2662F	ribosomal protein L7a.eR/HS6 (isolated from the small ribosomal subunit)	2	2	-1.27	0.04	3.44E-01	rpl7aR, rpsH6
2	OE2667F	nucleoside-diphosphate kinase (EC 2.7.4.6)	3	3	1.06	0.14	7.80E-01	ndk
3	OE2667F	nucleoside-diphosphate kinase (EC 2.7.4.6)	4	3	1.00	0.13	9.97E-01	ndk
1	OE2667F	nucleoside-diphosphate kinase (EC 2.7.4.6)	3	3	-1.03	0.1	9.01E-01	ndk
1	OE2674R	rRNA (adenine-N6,N6-)-dimethyltransferase (EC 2.1.1.-)	3	1	-1.10	0.09	7.12E-01	ksgA
2	OE2676R	conserved hypothetical protein	2	1	1.75	0.1	2.42E-02	-
1	OE2676R	conserved hypothetical protein	3	3	1.30	0.13	3.82E-01	-
3	OE2676R	conserved hypothetical protein	4	3	-2.00	0.29	1.74E-02	-
1	OE2678R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit F	5	2	1.08	0.04	7.74E-01	rpoF
3	OE2678R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit F	5	3	1.06	0.06	7.96E-01	rpoF
3	OE2679R	ribosomal protein L21.eR	2	1	-1.01	0.16	9.65E-01	rpl21R
1	OE2679R	ribosomal protein L21.eR	2	1	-1.08	0.15	7.92E-01	rpl21R
2	OE2681F	probable cystathionine beta-lyase (EC 4.4.1.8)	3	2	1.05	0.11	7.94E-01	metB
1	OE2681F	probable cystathionine beta-lyase (EC 4.4.1.8)	3	2	1.03	0.08	9.24E-01	metB
3	OE2681F	probable cystathionine beta-lyase (EC 4.4.1.8)	2	2	-1.03	0.11	9.17E-01	metB
1	OE2685F	probable pre-rRNA-processing protein nop56	4	1	-1.06	0.09	8.39E-01	nop56
1	OE2697R	probable coenzyme PQQ synthesis protein E	5	1	1.15	0.07	5.93E-01	pqqE2
2	OE2697R	probable coenzyme PQQ synthesis protein E	8	2	-1.13	0.16	5.74E-01	pqqE2
3	OE2697R	probable coenzyme PQQ synthesis protein E	3	1	-1.29	0.26	4.28E-01	pqqE2
2	OE2703F	probable copper-containing oxidoreductase	6	2	-1.11	0.16	6.45E-01	pan1
3	OE2703F	probable copper-containing oxidoreductase	6	1	-1.17	0.15	5.81E-01	pan1
1	OE2703F	probable copper-containing oxidoreductase	5	2	-1.20	0.19	5.31E-01	pan1
1	OE2716R	hypothetical protein	1	1	-1.14	0.06	6.20E-01	-
1	OE2717R	thioredoxin-dependent hydroperoxide peroxidase (EC 1.11.1.-)	1	1	1.04	0.17	8.89E-01	bcp
3	OE2728R	glutamate dehydrogenase (EC 1.4.1.-)	8	5	1.05	0.27	9.03E-01	gdhA2
2	OE2728R	glutamate dehydrogenase (EC 1.4.1.-)	10	4	-1.16	0.14	4.81E-01	gdhA2
1	OE2728R	glutamate dehydrogenase (EC 1.4.1.-)	7	5	-1.20	0.23	5.69E-01	gdhA2
1	OE2750R	conserved hypothetical protein	1	1	1.02	0.06	9.49E-01	-
3	OE2750R	conserved hypothetical protein	1	1	-1.10	0.18	7.63E-01	-
1	OE2755R	conserved hypothetical protein	6	3	1.01	0.15	9.82E-01	-

2	OE2755R	conserved hypothetical protein	7	4	1.01	0.15	9.57E-01	-
3	OE2755R	conserved hypothetical protein	5	1	-1.37	0.15	2.56E-01	-
1	OE2762R	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	1	1	1.03	0.17	9.34E-01	aroA
1	OE2763F	X-Pro dipeptidase (EC 3.4.13.9)	2	2	-1.48	0.67	4.44E-01	pepQ2
2	OE2763F	X-Pro dipeptidase (EC 3.4.13.9)	2	1	-1.88	0.17	9.86E-04	pepQ2
3	OE2791R	hypothetical protein	3	1	-1.06	0.06	8.29E-01	-
1	OE2791R	hypothetical protein	4	3	-1.08	0.15	8.03E-01	-
2	OE2791R	hypothetical protein	4	3	-1.16	0.18	5.12E-01	-
3	OE2800R	conserved hypothetical protein	2	1	1.02	0.05	9.26E-01	-
1	OE2800R	conserved hypothetical protein	4	1	1.01	0.43	9.87E-01	-
2	OE2801R	conserved hypothetical protein	5	3	1.15	0.11	5.04E-01	-
1	OE2801R	conserved hypothetical protein	8	3	1.02	0.23	9.54E-01	-
3	OE2801R	conserved hypothetical protein	7	2	-1.23	0.1	4.40E-01	-
3	OE2809R	translation initiation factor aIF-2 beta subunit	2	1	-1.03	0.07	9.14E-01	-
3	OE2821F	conserved hypothetical protein	5	2	1.05	0.08	8.38E-01	-
1	OE2821F	conserved hypothetical protein	4	1	-1.01	0.38	9.84E-01	-
2	OE2828R	conserved hypothetical protein	5	1	1.09	0.11	6.73E-01	-
1	OE2828R	conserved hypothetical protein	3	2	1.01	0.12	9.72E-01	-
1	OE2838R	trkA domain protein	2	1	-1.05	0.05	8.46E-01	trkA5
2	OE2853R	probable peptidylprolyl isomerase (EC 5.2.1.8)	1	1	-1.02	0.15	9.31E-01	slyD
1	OE2853R	probable peptidylprolyl isomerase (EC 5.2.1.8)	1	1	-1.04	0.08	8.87E-01	slyD
1	OE2857F	S-adenosylmethionine synthetase homolog	5	3	-1.09	0.1	7.47E-01	-
3	OE2857F	S-adenosylmethionine synthetase homolog	5	2	-1.14	0.16	6.43E-01	-
2	OE2857F	S-adenosylmethionine synthetase homolog	4	2	-1.29	0.12	1.83E-01	-
1	OE2864F	phosphoribosylamine--glycine ligase (EC 6.3.4.13)	4	3	-1.46	0.31	2.54E-01	purD
3	OE2864F	phosphoribosylamine--glycine ligase (EC 6.3.4.13)	6	4	-1.75	0.45	1.18E-01	purD
2	OE2864F	phosphoribosylamine--glycine ligase (EC 6.3.4.13)	8	5	-2.67	0.35	5.02E-06	purD
2	OE2865R	succinate dehydrogenase (EC 1.3.99.1) subunit A (flavoprotein)	5	1	1.03	0.06	8.72E-01	sdhA
3	OE2865R	succinate dehydrogenase (EC 1.3.99.1) subunit A (flavoprotein)	7	2	-1.19	0.19	5.62E-01	sdhA
1	OE2865R	succinate dehydrogenase (EC 1.3.99.1) subunit A (flavoprotein)	7	3	-1.33	0.31	4.12E-01	sdhA
3	OE2866R	succinate dehydrogenase (EC 1.3.99.1) subunit B (iron-sulfur protein)	2	2	1.03	0.19	9.34E-01	sdhB
1	OE2871F	probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.157)	6	2	1.33	0.06	2.84E-01	hbd2
2	OE2871F	probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.157)	4	1	1.12	0.13	6.05E-01	hbd2
3	OE2871F	probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.157)	7	2	1.11	0.11	7.12E-01	hbd2
1	OE2898R	conserved hypothetical protein	5	2	-1.09	0.1	7.37E-01	-
2	OE2898R	conserved hypothetical protein	5	2	-1.16	0.15	4.77E-01	-
3	OE2902F	conserved hypothetical protein	2	1	-1.27	0.07	3.53E-01	-
1	OE2908R	conserved hypothetical protein	1	1	1.18	0.04	5.35E-01	-
2	OE2908R	conserved hypothetical protein	1	1	-1.02	0.06	9.12E-01	-
3	OE2908R	conserved hypothetical protein	1	1	-1.13	0.13	6.60E-01	-
1	OE2912F	probable fatty-acid--CoA ligase (EC	8	4	1.49	0.03	1.23E-01	alkK2

		6.2.1.-)						
2	OE2912F	probable fatty-acid--CoA ligase (EC 6.2.1.-)	7	3	1.27	0.08	2.25E-01	alkK2
3	OE2912F	probable fatty-acid--CoA ligase (EC 6.2.1.-)	4	3	1.05	0.13	8.61E-01	alkK2
3	OE2923F	conserved hypothetical protein	1	1	-1.04	0.16	8.85E-01	-
1	OE2923F	conserved hypothetical protein	4	2	-1.11	0.24	7.65E-01	-
3	OE2929R	glutamyl-tRNA (Gln) amidotransferase (EC 6.3.5.-) subunit E	4	1	-1.16	0.24	6.48E-01	gatE
3	OE2935R	fumarate hydratase (EC 4.2.1.2)	9	5	1.15	0.15	6.49E-01	fumC
1	OE2935R	fumarate hydratase (EC 4.2.1.2)	9	2	1.12	0.25	7.47E-01	fumC
2	OE2935R	fumarate hydratase (EC 4.2.1.2)	8	3	1.11	0.1	5.96E-01	fumC
2	OE2945F	probable ornithine cyclodeaminase (EC 4.3.1.12)	4	3	1.39	0.06	8.11E-02	ocd2
1	OE2945F	probable ornithine cyclodeaminase (EC 4.3.1.12)	6	4	1.28	0.08	3.68E-01	ocd2
3	OE2945F	probable ornithine cyclodeaminase (EC 4.3.1.12)	3	2	1.05	0.13	8.59E-01	ocd2
2	OE2969R	probable transcription regulator	1	1	1.10	0.11	6.43E-01	asnC
2	OE2970R	probable myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25) (IMPase/FBPase (dual activity) homolog)	4	1	1.11	0.2	7.05E-01	suhB
3	OE2970R	probable myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25) (IMPase/FBPase (dual activity) homolog)	3	1	1.04	0.44	9.41E-01	suhB
2	OE2989R	conserved hypothetical protein	5	2	1.14	0.06	5.00E-01	-
3	OE2989R	conserved hypothetical protein	4	3	1.00	0.1	9.87E-01	-
1	OE2989R	conserved hypothetical protein	3	3	-1.05	0.15	8.77E-01	-
1	OE3017R	UDP-sugar hydrolase (EC 3.6.1.45) / 5'-nucleotidase (EC 3.1.3.5)	7	2	-2.56	0.38	1.44E-03	ush
2	OE3028R	conserved hypothetical protein	10	6	1.75	0.06	5.70E-03	-
3	OE3028R	conserved hypothetical protein	10	7	1.43	0.08	2.02E-01	-
1	OE3028R	conserved hypothetical protein	11	7	1.28	0.12	4.04E-01	-
1	OE3036F	glycine hydroxymethyltransferase (EC 2.1.2.1)	7	3	1.02	0.2	9.59E-01	glyA
3	OE3036F	glycine hydroxymethyltransferase (EC 2.1.2.1)	7	3	1.00	0.12	9.97E-01	glyA
2	OE3036F	glycine hydroxymethyltransferase (EC 2.1.2.1)	7	4	-1.03	0.09	8.85E-01	glyA
1	OE3038F	methylenetetrahydrofolate dehydrogenase (NAD(P)+) (EC 1.5.1.5) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	11	5	1.22	0.12	4.97E-01	folD
2	OE3038F	methylenetetrahydrofolate dehydrogenase (NAD(P)+) (EC 1.5.1.5) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	10	6	1.16	0.21	6.08E-01	folD
3	OE3038F	methylenetetrahydrofolate dehydrogenase (NAD(P)+) (EC 1.5.1.5) / methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9)	9	5	-1.47	0.27	2.17E-01	folD
1	OE3059F	deoxyhypusine synthase (EC 2.5.1.46)	3	2	1.03	0.07	9.23E-01	dhs
2	OE3059F	deoxyhypusine synthase (EC 2.5.1.46)	4	3	1.00	0.07	9.82E-01	dhs
3	OE3059F	deoxyhypusine synthase (EC 2.5.1.46)	4	3	-1.01	0.19	9.66E-01	dhs
2	OE3062F	ribosomal protein S17.eR	4	2	-1.01	0.06	9.48E-01	rps17R

1	OE3062F	ribosomal protein S17.eR	2	1	-1.10	0.13	7.27E-01	rps17R
3	OE3062F	ribosomal protein S17.eR	2	1	-1.14	0.12	6.35E-01	rps17R
3	OE3063F	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	1	1	-1.02	0.14	9.44E-01	asd
2	OE3063F	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	3	2	-1.03	0.14	8.98E-01	asd
2	OE3065R	probable dehydrogenase (EC 1.-.-.-) (D-3-phosphoglycerate dehydrogenase homolog / 2-ketogluconate reductase homolog)	6	5	1.09	0.09	6.50E-01	serA2
1	OE3065R	probable dehydrogenase (EC 1.-.-.-) (D-3-phosphoglycerate dehydrogenase homolog / 2-ketogluconate reductase homolog)	8	4	1.08	0.12	8.03E-01	serA2
3	OE3065R	probable dehydrogenase (EC 1.-.-.-) (D-3-phosphoglycerate dehydrogenase homolog / 2-ketogluconate reductase homolog)	9	4	1.03	0.11	9.25E-01	serA2
1	OE3071F	histidinol dehydrogenase (EC 1.1.1.23)	4	1	-1.04	0.09	8.77E-01	hisD
2	OE3071F	histidinol dehydrogenase (EC 1.1.1.23)	5	4	-1.08	0.13	7.23E-01	hisD
3	OE3071F	histidinol dehydrogenase (EC 1.1.1.23)	7	2	-1.75	0.17	3.92E-02	hisD
2	OE3081F	conserved hypothetical protein	5	1	1.01	0.16	9.58E-01	-
1	OE3081F	conserved hypothetical protein	7	2	-1.08	0.21	8.04E-01	-
1	OE3092F	probable N-terminal acetyltransferase	1	1	1.10	0.1	7.21E-01	-
3	OE3092F	probable N-terminal acetyltransferase	2	1	-1.09	0.06	7.28E-01	-
2	OE3112R	AAA-type ATPase (transitional ATPase homolog)	22	7	2.56	0.09	8.17E-04	aaa3, cdc48b
1	OE3112R	AAA-type ATPase (transitional ATPase homolog)	21	9	2.08	0.12	3.97E-02	aaa3, cdc48b
3	OE3112R	AAA-type ATPase (transitional ATPase homolog)	20	7	1.45	0.1	2.04E-01	aaa3, cdc48b
2	OE3116F	conserved hypothetical protein	2	1	1.45	0.07	6.27E-02	-
1	OE3116F	conserved hypothetical protein	5	1	1.37	0.1	2.63E-01	-
2	OE3119R	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	1	1	1.04	0.17	8.79E-01	panB
1	OE3119R	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	1	1	1.02	0.14	9.56E-01	panB
3	OE3123R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	11	2	1.03	0.12	9.01E-01	acd5
2	OE3123R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	10	4	1.01	0.04	9.43E-01	acd5
1	OE3123R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	8	2	-1.05	0.11	8.56E-01	acd5
1	OE3139R	amidophosphoribosyltransferase (EC 2.4.2.14)	7	3	1.08	0.06	7.71E-01	purF
2	OE3139R	amidophosphoribosyltransferase (EC 2.4.2.14)	6	2	-1.02	0.1	9.19E-01	purF
3	OE3143R	tetrahedral aminopeptidase	3	1	-1.05	0.06	8.50E-01	-
2	OE3143R	tetrahedral aminopeptidase	4	2	-1.45	0.11	4.43E-02	-
2	OE3153R	conserved hypothetical protein	2	1	-1.03	0.13	8.96E-01	-
2	OE3155R	conserved hypothetical protein	9	7	1.02	0.16	9.31E-01	-
1	OE3155R	conserved hypothetical protein	8	5	-1.01	0.2	9.83E-01	-
3	OE3155R	conserved hypothetical protein	8	4	-1.09	0.27	7.98E-01	-

2	OE3162F	conserved hypothetical protein	2	1	-1.52	0.22	5.95E-02	-
1	OE3168R	pyridoxal phosphate-dependent aminotransferase (acetylornithine transaminase homolog)	9	5	1.35	0.19	4.02E-01	-
2	OE3168R	pyridoxal phosphate-dependent aminotransferase (acetylornithine transaminase homolog)	11	6	1.33	0.12	2.26E-01	-
3	OE3168R	pyridoxal phosphate-dependent aminotransferase (acetylornithine transaminase homolog)	12	8	1.19	0.09	5.30E-01	-
1	OE3175F	propionyl-CoA carboxylase (EC 6.4.1.3)	4	1	-1.14	0.14	6.47E-01	mmdA
3	OE3177F	pyruvate carboxylase (EC 6.4.1.1)	5	3	-1.08	0.14	7.94E-01	pyc
2	OE3177F	pyruvate carboxylase (EC 6.4.1.1)	5	2	-1.21	0.17	3.79E-01	pyc
1	OE3177F	pyruvate carboxylase (EC 6.4.1.1)	9	6	-1.24	0.23	4.90E-01	pyc
1	OE3190F	hypothetical protein	1	1	-1.28	0.16	3.78E-01	-
2	OE3190F	hypothetical protein	2	1	-1.33	0.2	2.04E-01	-
3	OE3195F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta subunit	13	7	1.03	0.09	9.21E-01	sucB
1	OE3195F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta subunit	13	6	1.01	0.06	9.73E-01	sucB
2	OE3195F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta subunit	13	7	1.00	0.06	9.83E-01	sucB
3	OE3196F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha subunit	8	4	1.04	0.15	8.79E-01	sucA
2	OE3196F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha subunit	5	4	-1.01	0.12	9.55E-01	sucA
1	OE3196F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha subunit	7	4	-1.04	0.11	8.91E-01	sucA
3	OE3230F	CobN protein (probable cobalt chelatase) (EC 4.99.1.-) (cobN in PSEDE)	9	2	1.16	0.33	7.42E-01	cobN
2	OE3230F	CobN protein (probable cobalt chelatase) (EC 4.99.1.-) (cobN in PSEDE)	12	3	1.12	0.09	5.57E-01	cobN
1	OE3230F	CobN protein (probable cobalt chelatase) (EC 4.99.1.-) (cobN in PSEDE)	9	3	1.06	0.08	8.23E-01	cobN
1	OE3237F	precorrin-8X methylmutase (EC 5.4.1.2)	3	1	-1.36	0.12	2.48E-01	cbiC, cobH
3	OE3238F	probable precorrin-6Y C5,15-methyltransferase (decarboxylating) (EC 2.1.1.132)	2	1	-1.12	0.07	6.63E-01	cbiE, cobL1
1	OE3238F	probable precorrin-6Y C5,15-methyltransferase (decarboxylating) (EC 2.1.1.132)	1	1	-1.15	0.1	5.94E-01	cbiE, cobL1
1	OE3242F	conserved cobalamin operon protein	2	1	-1.03	0.15	9.08E-01	-
3	OE3242F	conserved cobalamin operon protein	1	1	-1.10	0.27	7.83E-01	-
2	OE3274R	glycine cleavage system protein P-2 (glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) subunit 2)	5	1	1.05	0.1	7.90E-01	gcvP2
1	OE3274R	glycine cleavage system protein P-2 (glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) subunit 2)	4	2	-1.18	0.17	5.74E-01	gcvP2
3	OE3274R	glycine cleavage system protein P-2 (glycine dehydrogenase (decarboxylating) (EC 1.4.4.2)	2	1	-1.19	0.25	5.97E-01	gcvP2

		subunit 2)						
2	OE3275R	glycine cleavage system protein P-1 (glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) subunit 1)	4	2	1.03	0.08	8.79E-01	gcvP1
3	OE3275R	glycine cleavage system protein P-1 (glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) subunit 1)	4	2	-1.03	0.15	9.14E-01	gcvP1
1	OE3275R	glycine cleavage system protein P-1 (glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) subunit 1)	5	1	-1.09	0.13	7.55E-01	gcvP1
1	OE3283F	conserved hypothetical protein	3	1	1.00	0.11	9.93E-01	-
3	OE3283F	conserved hypothetical protein	1	1	-1.24	0.06	4.12E-01	-
2	OE3289F	conserved hypothetical protein	6	4	1.09	0.12	7.09E-01	-
3	OE3289F	conserved hypothetical protein	6	5	-1.02	0.11	9.47E-01	-
1	OE3289F	conserved hypothetical protein	6	4	-1.12	0.1	6.71E-01	-
2	OE3305F	replication factor C large subunit	4	1	-1.09	0.22	7.41E-01	rfcB
1	OE3305F	replication factor C large subunit	4	1	-1.27	0.11	3.67E-01	rfcB
3	OE3308F	malate dehydrogenase (oxaloacetate decarboxylating) (EC 1.1.1.40)	5	2	-1.15	0.17	6.41E-01	mdh
2	OE3308F	malate dehydrogenase (oxaloacetate decarboxylating) (EC 1.1.1.40)	3	2	-1.23	0.26	4.44E-01	mdh
1	OE3308F	malate dehydrogenase (oxaloacetate decarboxylating) (EC 1.1.1.40)	4	1	-1.24	0.21	4.70E-01	mdh
2	OE3322F	conserved hypothetical protein	6	4	1.00	0.08	9.82E-01	-
1	OE3322F	conserved hypothetical protein	4	2	-1.04	0.06	8.75E-01	-
3	OE3322F	conserved hypothetical protein	5	2	-2.76	0.21	1.22E-04	-
1	OE3328R	ribonucleoside-diphosphate reductase (EC 1.17.4.1) alpha subunit	17	13	-1.10	0.16	7.36E-01	nrdA2
3	OE3328R	ribonucleoside-diphosphate reductase (EC 1.17.4.1) alpha subunit	24	2	-1.16	0.12	5.88E-01	nrdA2
2	OE3328R	ribonucleoside-diphosphate reductase (EC 1.17.4.1) alpha subunit	16	12	-1.42	0.23	1.35E-01	nrdA2
1	OE3332R	anthranilate synthase (EC 4.1.3.27) alpha subunit	9	1	-1.36	0.12	2.53E-01	trpE1
3	OE3334R	anthranilate phosphoribosyltransferase (EC 2.4.2.18)	6	3	-1.80	0.14	2.62E-02	trpD1
2	OE3334R	anthranilate phosphoribosyltransferase (EC 2.4.2.18)	5	2	-2.07	0.31	1.32E-03	trpD1
1	OE3334R	anthranilate phosphoribosyltransferase (EC 2.4.2.18)	5	5	-2.24	0.37	7.68E-03	trpD1
2	OE3346R	conserved hypothetical protein	3	2	1.41	0.06	6.32E-02	-
1	OE3346R	conserved hypothetical protein	2	2	1.28	0.09	3.70E-01	-
3	OE3346R	conserved hypothetical protein	3	1	-1.01	0.16	9.64E-01	-
1	OE3347F	transducer protein htrI	7	1	1.56	0.15	1.92E-01	htrI, htr1
3	OE3347F	transducer protein htrI	10	2	1.18	0.09	5.43E-01	htrI, htr1
2	OE3349F	coenzyme F420--quinone oxidoreductase 42K subunit	20	9	1.10	0.09	6.19E-01	-

		homolog						
1	OE3349F	coenzyme F420--quinone oxidoreductase 42K subunit homolog	18	9	1.09	0.07	7.61E-01	-
3	OE3349F	coenzyme F420--quinone oxidoreductase 42K subunit homolog	16	8	-1.62	0.13	6.91E-02	-
2	OE3356F	AAA-type ATPase (transitional ATPase homolog)	8	2	1.25	0.14	3.60E-01	aaa5, cdc48c, cdcH
1	OE3356F	AAA-type ATPase (transitional ATPase homolog)	3	2	1.05	0.16	8.62E-01	aaa5, cdc48c, cdcH
2	OE3357R	ribosomal protein S8.eR	7	2	-1.16	0.09	4.12E-01	rps8R
3	OE3357R	ribosomal protein S8.eR	5	1	-1.17	0.08	5.50E-01	rps8R
1	OE3357R	ribosomal protein S8.eR	6	1	-1.32	0.07	2.85E-01	rps8R
2	OE3374R	hypothetical protein	2	1	1.05	0.07	7.72E-01	-
3	OE3374R	hypothetical protein	2	1	-1.35	0.19	3.03E-01	-
2	OE3383R	methenyltetrahydromethanopterin cyclohydrolase (EC 3.5.4.27)	3	3	1.11	0.14	6.50E-01	mch
1	OE3383R	methenyltetrahydromethanopterin cyclohydrolase (EC 3.5.4.27)	4	2	1.05	0.09	8.46E-01	mch
3	OE3383R	methenyltetrahydromethanopterin cyclohydrolase (EC 3.5.4.27)	2	2	1.03	0.12	9.23E-01	mch
1	OE3386F	conserved hypothetical protein	3	1	1.02	0.11	9.50E-01	-
3	OE3388F	ribosomal protein L3	13	5	1.02	0.14	9.55E-01	rpl3
2	OE3388F	ribosomal protein L3	12	6	-1.08	0.1	7.02E-01	rpl3
1	OE3388F	ribosomal protein L3	14	7	-1.09	0.09	7.58E-01	rpl3
3	OE3389F	ribosomal protein L4.eR	9	8	-1.10	0.13	7.31E-01	rpl4R
2	OE3389F	ribosomal protein L4.eR	10	7	-1.16	0.08	4.27E-01	rpl4R
1	OE3389F	ribosomal protein L4.eR	9	7	-1.17	0.12	5.74E-01	rpl4R
3	OE3390F	ribosomal protein L23	2	2	1.08	0.22	8.28E-01	rpl23
1	OE3390F	ribosomal protein L23	2	2	-1.14	0.09	6.24E-01	rpl23
1	OE3392F	ribosomal protein L2	7	2	-1.14	0.29	7.16E-01	rpl2
3	OE3392F	ribosomal protein L2	8	2	-1.14	0.18	6.51E-01	rpl2
2	OE3392F	ribosomal protein L2	5	1	-1.27	0.08	1.87E-01	rpl2
3	OE3393F	ribosomal protein S19	4	1	1.11	0.04	6.67E-01	rps19
2	OE3393F	ribosomal protein S19	3	1	1.00	0.29	9.91E-01	rps19
2	OE3394F	ribosomal protein L22	3	1	1.18	0.17	5.36E-01	rpl22
3	OE3394F	ribosomal protein L22	4	1	1.00	0.16	9.97E-01	rpl22
1	OE3394F	ribosomal protein L22	2	1	-1.17	0.11	5.71E-01	rpl22
2	OE3395F	ribosomal protein S3	5	3	1.00	0.1	9.83E-01	rps3
1	OE3395F	ribosomal protein S3	5	2	-1.08	0.14	7.84E-01	rps3
3	OE3395F	ribosomal protein S3	7	4	-1.22	0.2	5.06E-01	rps3
3	OE3396F	ribosomal protein L29	2	1	-1.13	0.06	6.32E-01	rpl29
1	OE3396F	ribosomal protein L29	4	3	-1.22	0.22	5.29E-01	rpl29
2	OE3396F	ribosomal protein L29	5	3	-1.25	0.12	2.47E-01	rpl29
1	OE3400F	ribosomal protein S17	4	1	-1.03	0.1	9.03E-01	rps17
3	OE3400F	ribosomal protein S17	4	1	-1.06	0.07	8.19E-01	rps17
2	OE3400F	ribosomal protein S17	3	1	-1.20	0.13	3.70E-01	rps17
3	OE3402F	ribosomal protein L14	7	4	-1.02	0.15	9.48E-01	rpl14
1	OE3402F	ribosomal protein L14	7	5	-1.17	0.15	5.82E-01	rpl14
2	OE3402F	ribosomal protein L14	7	3	-1.20	0.06	3.12E-01	rpl14
1	OE3404F	ribosomal protein L24	2	1	-1.23	0.22	5.04E-01	rpl24
2	OE3404F	ribosomal protein L24	2	1	-1.26	0.16	2.74E-01	rpl24
1	OE3405F	ribosomal protein S4.eR	4	2	-1.06	0.17	8.47E-01	rps4R
3	OE3405F	ribosomal protein S4.eR	3	2	-1.08	0.08	7.65E-01	rps4R
2	OE3405F	ribosomal protein S4.eR	2	1	-1.14	0.11	5.02E-01	rps4R
3	OE3407F	ribosomal protein L5	5	2	1.10	0.09	7.31E-01	rpl5
2	OE3407F	ribosomal protein L5	1	1	1.03	0.1	8.86E-01	rpl5

1	OE3407F	ribosomal protein L5	3	1	-1.14	0.15	6.57E-01	rpl5
2	OE3410F	ribosomal protein S8	4	1	-1.12	0.03	5.22E-01	rps8
3	OE3410F	ribosomal protein S8	5	1	-1.15	0.04	5.92E-01	rps8
3	OE3412F	ribosomal protein L32.eR	5	2	-1.09	0.26	8.12E-01	rpl32R
2	OE3412F	ribosomal protein L32.eR	6	2	-1.25	0.2	3.33E-01	rpl32R
1	OE3412F	ribosomal protein L32.eR	7	2	-1.41	0.17	2.20E-01	rpl32R
2	OE3413F	ribosomal protein L19.eR	5	4	-1.04	0.09	8.20E-01	rpl19R
3	OE3413F	ribosomal protein L19.eR	9	5	-1.06	0.07	8.17E-01	rpl19R
1	OE3413F	ribosomal protein L19.eR	6	5	-1.09	0.15	7.75E-01	rpl19R
3	OE3414F	ribosomal protein L18	1	1	-1.09	0.11	7.58E-01	rpl18
2	OE3414F	ribosomal protein L18	1	1	-1.11	0.19	6.72E-01	rpl18
1	OE3415F	ribosomal protein S5	9	3	-1.07	0.1	7.96E-01	rps5
2	OE3415F	ribosomal protein S5	8	2	-1.10	0.05	5.85E-01	rps5
3	OE3415F	ribosomal protein S5	9	3	-1.14	0.11	6.22E-01	rps5
3	OE3416F	ribosomal protein L30	4	2	-1.10	0.11	7.20E-01	rpl30
2	OE3416F	ribosomal protein L30	2	2	-1.27	0.17	2.68E-01	rpl30
1	OE3416F	ribosomal protein L30	4	2	-1.42	0.34	3.11E-01	rpl30
2	OE3425F	adenylate kinase (EC 2.7.4.3)	6	3	1.06	0.08	7.42E-01	adk
1	OE3425F	adenylate kinase (EC 2.7.4.3)	5	3	-1.03	0.11	9.04E-01	adk
3	OE3425F	adenylate kinase (EC 2.7.4.3)	5	3	-1.39	0.12	2.17E-01	adk
1	OE3427F	conserved hypothetical protein	2	2	1.03	0.29	9.46E-01	-
2	OE3427F	conserved hypothetical protein	1	1	-1.01	0.12	9.55E-01	-
2	OE3430F	tRNA-pseudouridine synthase (EC 5.4.99.12)	2	1	-1.17	0.09	3.90E-01	truB
1	OE3430F	tRNA-pseudouridine synthase (EC 5.4.99.12)	2	1	-1.23	0.24	5.15E-01	truB
3	OE3430F	tRNA-pseudouridine synthase (EC 5.4.99.12)	1	1	-1.43	0.24	2.40E-01	truB
2	OE3456F	conserved hypothetical protein	1	1	-1.01	0.07	9.49E-01	-
1	OE3456F	conserved hypothetical protein	1	1	-1.03	0.11	9.04E-01	-
2	OE3466R	conserved hypothetical protein	5	3	1.19	0.12	4.18E-01	-
1	OE3466R	conserved hypothetical protein	5	4	1.16	0.11	5.85E-01	-
3	OE3466R	conserved hypothetical protein	6	5	-1.21	0.11	4.72E-01	-
2	OE3467R	deoxyribodipyrimidine photo-lyase (EC 4.1.99.3)	1	1	1.59	0.06	1.80E-02	phr1
2	OE3474R	transducer protein cosT	10	3	1.33	0.1	1.83E-01	cosT, htr5, htpIV, htF
3	OE3474R	transducer protein cosT	14	5	1.23	0.12	4.69E-01	cosT, htr5, htpIV, htF
1	OE3474R	transducer protein cosT	11	5	1.20	0.08	4.99E-01	cosT, htr5, htpIV, htF
1	OE3476R	chemotactic signal transduction system periplasmic substrate-binding protein cosB	2	1	1.01	0.17	9.79E-01	cosB, proX
1	OE3482R	conserved hypothetical protein	4	2	-1.13	0.11	6.46E-01	-
3	OE3482R	conserved hypothetical protein	3	3	-1.16	0.17	6.08E-01	-
2	OE3482R	conserved hypothetical protein	2	1	-1.30	0.22	2.77E-01	-
2	OE3487R	translation initiation factor aIF-5A	3	1	-1.07	0.21	7.99E-01	eif5a
3	OE3487R	translation initiation factor aIF-5A	3	1	-1.08	0.14	7.88E-01	eif5a
1	OE3487R	translation initiation factor aIF-5A	3	1	-1.09	0.25	8.01E-01	eif5a
2	OE3498R	probable siroheme synthase (probable precorrin-2 oxidase (EC 1.-.-.-) and/or probable ferrochelatase (EC 4.99.1.-)) (N-	4	1	-1.24	0.06	2.11E-01	cysG1

		terminal domain homology to multifunctional siroheme synthase CysG of Escherichia coli)						
1	OE3498R	probable siroheme synthase (probable precorrin-2 oxidase (EC 1.-.-.-) and/or probable ferrochelatase (EC 4.99.1.-)) (N-terminal domain homology to multifunctional siroheme synthase CysG of Escherichia coli)	6	1	-1.28	0.26	4.41E-01	cysG1
1	OE3517F	conserved hypothetical protein	6	1	-1.01	0.13	9.62E-01	-
2	OE3517F	conserved hypothetical protein	3	1	-1.04	0.21	8.93E-01	-
1	OE3524F	pyridoxine biosynthesis protein	9	4	1.19	0.18	5.94E-01	pyroA
2	OE3524F	pyridoxine biosynthesis protein	8	3	1.15	0.11	5.04E-01	pyroA
3	OE3524F	pyridoxine biosynthesis protein	9	3	1.06	0.11	8.38E-01	pyroA
1	OE3537R	conserved hypothetical protein	2	1	1.12	0.05	6.67E-01	-
2	OE3544F	probable oxidoreductase (ferredoxin reductase homolog)	2	1	1.04	0.07	8.06E-01	noxA
3	OE3544F	probable oxidoreductase (ferredoxin reductase homolog)	2	2	-1.24	0.27	5.29E-01	noxA
2	OE3554F	carbamoyl-phosphate synthase (EC 6.3.-.-) large subunit ((ammonia) (EC6.3.4.16) or (glutamine-hydrolyzing) (EC 6.3.5.5))	17	6	2.56	0.03	4.28E-07	carB
1	OE3554F	carbamoyl-phosphate synthase (EC 6.3.-.-) large subunit ((ammonia) (EC6.3.4.16) or (glutamine-hydrolyzing) (EC 6.3.5.5))	14	4	2.50	0.05	1.46E-03	carB
3	OE3554F	carbamoyl-phosphate synthase (EC 6.3.-.-) large subunit ((ammonia) (EC6.3.4.16) or (glutamine-hydrolyzing) (EC 6.3.5.5))	16	8	2.17	0.05	4.71E-03	carB
3	OE3556R	carbamoyl-phosphate synthase (EC 6.3.-.-) small subunit ((ammonia) (EC 6.3.4.16) or (glutamine-hydrolyzing) (EC 6.3.5.5))	2	1	2.27	0.06	3.97E-03	carA
1	OE3558F	probable transcription regulator	2	1	1.69	0.1	8.64E-02	trh3
2	OE3558F	probable transcription regulator	3	1	1.28	0.04	1.58E-01	trh3
3	OE3560F	probable isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 3	2	1	-1.15	0.05	5.78E-01	idi3
2	OE3560F	probable isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 3	3	1	-1.26	0.08	2.00E-01	idi3
1	OE3563R	alcohol dehydrogenase (EC 1.1.1.1)	1	1	1.25	0.11	4.50E-01	adh4
2	OE3563R	alcohol dehydrogenase (EC 1.1.1.1)	2	1	1.02	0.16	9.31E-01	adh4
3	OE3571R	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2), subunit B	7	2	1.05	0.14	8.49E-01	guaAb
2	OE3571R	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2), subunit B	6	1	1.04	0.18	8.56E-01	guaAb
1	OE3571R	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2), subunit B	6	1	-1.14	0.26	6.96E-01	guaAb
3	OE3572R	CTP synthase (EC 6.3.4.2)	6	3	1.12	0.31	7.79E-01	pyrG
2	OE3572R	CTP synthase (EC 6.3.4.2)	7	4	-1.04	0.14	8.69E-01	pyrG
1	OE3572R	CTP synthase (EC 6.3.4.2)	5	2	-1.10	0.07	7.20E-01	pyrG
1	OE3578R	conserved hypothetical protein	1	1	-1.03	0.09	8.99E-01	-
2	OE3580R	threonine--tRNA ligase (EC 6.1.1.3)	11	4	1.06	0.14	7.85E-01	thrS

1	OE3580R	threonine--tRNA ligase (EC 6.1.1.3)	11	6	-1.11	0.15	7.22E-01	thrS
3	OE3580R	threonine--tRNA ligase (EC 6.1.1.3)	8	5	-1.28	0.2	4.15E-01	thrS
1	OE3591F	glutamyl-tRNA(Gln) amidotransferase (EC 6.3.5.-) subunit D	4	3	-1.03	0.26	9.26E-01	gatD
2	OE3591F	glutamyl-tRNA(Gln) amidotransferase (EC 6.3.5.-) subunit D	3	3	-1.27	0.14	2.43E-01	gatD
3	OE3591F	glutamyl-tRNA(Gln) amidotransferase (EC 6.3.5.-) subunit D	4	1	-1.37	0.25	3.12E-01	gatD
1	OE3592F	conserved hypothetical protein	3	2	-1.07	0.11	8.01E-01	-
3	OE3603R	uridine phosphorylase (EC 2.4.2.3)	5	2	1.08	0.09	7.96E-01	-
2	OE3603R	uridine phosphorylase (EC 2.4.2.3)	4	2	-1.09	0.12	6.62E-01	-
1	OE3603R	uridine phosphorylase (EC 2.4.2.3)	5	2	-1.15	0.13	6.06E-01	-
1	OE3610R	translation initiation factor aIF-2B subunit alpha/delta eif2ba	2	1	1.16	0.1	5.99E-01	eif2ba
3	OE3610R	translation initiation factor aIF-2B subunit alpha/delta eif2ba	3	1	-1.19	0.15	5.35E-01	eif2ba
2	OE3620R	histidine triad family protein	1	1	1.30	0.12	2.59E-01	hit2
1	OE3620R	histidine triad family protein	1	1	1.16	0.12	6.10E-01	hit2
2	OE3629R	ABC-type transport system periplasmic substrate-binding protein	3	1	1.08	0.1	7.21E-01	-
1	OE3629R	ABC-type transport system periplasmic substrate-binding protein	3	1	-1.03	0.08	9.00E-01	-
3	OE3634F	isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	11	6	1.01	0.16	9.84E-01	icd
1	OE3634F	isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	9	5	-1.05	0.17	8.64E-01	icd
2	OE3634F	isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	12	5	-1.11	0.22	6.91E-01	icd
1	OE3637R	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34)	5	1	-1.02	0.14	9.40E-01	hmgR
2	OE3637R	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34)	4	2	-1.02	0.1	9.19E-01	hmgR
3	OE3637R	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34)	6	1	-1.07	0.14	8.05E-01	hmgR
1	OE3644F	quinolinate synthetase A (EC 4.1.99.-) (part of quinolinate synthetase complex)	2	2	1.28	0.08	3.74E-01	nadA
2	OE3644F	quinolinate synthetase A (EC 4.1.99.-) (part of quinolinate synthetase complex)	6	1	1.00	0.12	9.85E-01	nadA
3	OE3644F	quinolinate synthetase A (EC 4.1.99.-) (part of quinolinate synthetase complex)	3	1	-2.04	0.33	1.73E-02	nadA
1	OE3646F	L-aspartate oxidase (EC 1.4.3.16) (quinolinate synthetase B, part of quinolinate synthetase complex)	7	1	-1.01	0.37	9.78E-01	nadB
2	OE3646F	L-aspartate oxidase (EC 1.4.3.16) (quinolinate synthetase B, part of quinolinate synthetase complex)	10	1	-1.46	0.23	9.70E-02	nadB
3	OE3646F	L-aspartate oxidase (EC 1.4.3.16) (quinolinate synthetase B, part of quinolinate synthetase complex)	6	2	-2.29	0.39	6.39E-03	nadB
1	OE3648F	nicotinate-nucleotide pyrophosphorylase (carboxylating) (EC 2.4.2.19)	3	2	-1.01	0.11	9.83E-01	nadC
1	OE3668F	conserved hypothetical protein	3	1	1.15	0.13	6.41E-01	-

2	OE3668F	conserved hypothetical protein	2	1	1.09	0.08	6.43E-01	-
3	OE3668F	conserved hypothetical protein	2	1	-1.35	0.22	3.11E-01	-
2	OE3673F	conserved hypothetical protein	3	3	-1.43	0.21	1.10E-01	-
1	OE3681R	conserved hypothetical protein	3	1	-1.03	0.16	9.31E-01	-
3	OE3681R	conserved hypothetical protein	3	1	-1.29	0.16	3.73E-01	-
2	OE3681R	conserved hypothetical protein	3	1	-1.32	0.25	2.78E-01	-
2	OE3691F	probable anthranilate phosphoribosyltransferase (EC 2.4.2.18)	7	6	-1.06	0.13	7.79E-01	trpD2
3	OE3691F	probable anthranilate phosphoribosyltransferase (EC 2.4.2.18)	10	8	-1.09	0.15	7.52E-01	trpD2
1	OE3691F	probable anthranilate phosphoribosyltransferase (EC 2.4.2.18)	7	6	-1.15	0.19	6.33E-01	trpD2
1	OE3693F	peptidylprolyl isomerase (EC 5.2.1.8)	3	1	-1.01	0.1	9.74E-01	ppiA
2	OE3693F	peptidylprolyl isomerase (EC 5.2.1.8)	1	1	-1.06	0.22	8.30E-01	ppiA
3	OE3699R	conserved hypothetical protein	1	1	-1.01	0.27	9.86E-01	-
2	OE3712R	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component alpha-2 subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	2	1	1.04	0.13	8.34E-01	oxdhA2
1	OE3712R	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component alpha-2 subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	3	1	1.03	0.19	9.14E-01	oxdhA2
3	OE3712R	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component alpha-2 subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	3	1	1.00	0.2	9.96E-01	oxdhA2
2	OE3717F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 32K subunit	4	2	1.33	0.07	1.48E-01	nolA
1	OE3717F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 32K subunit	5	4	1.23	0.06	4.14E-01	nolA
3	OE3717F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 32K subunit	5	3	1.09	0.09	7.68E-01	nolA
1	OE3718F	cell division protein	13	6	1.11	0.27	7.89E-01	ftsZ3
2	OE3718F	cell division protein	10	3	1.02	0.14	9.27E-01	ftsZ3
3	OE3718F	cell division protein	11	6	-1.32	0.14	3.16E-01	ftsZ3
2	OE3724F	phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6)	8	1	1.11	0.02	5.33E-01	purC
1	OE3724F	phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6)	5	2	-1.14	0.06	6.15E-01	purC
3	OE3724F	phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6)	5	1	-1.26	0.13	3.89E-01	purC
2	OE3731R	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) component I	4	2	-1.05	0.31	8.80E-01	purQ
3	OE3731R	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) component I	5	2	-1.17	0.26	6.43E-01	purQ
1	OE3731R	phosphoribosylformylglycinamidine synthase (EC 6.3.5.3) component I	3	2	-1.21	0.12	4.93E-01	purQ
1	OE3732R	conserved hypothetical protein	2	1	-1.08	0.14	7.95E-01	-
2	OE3732R	conserved hypothetical protein	4	3	-1.08	0.19	7.42E-01	-

3	OE3732R	conserved hypothetical protein	4	3	-1.61	0.28	1.20E-01	-
1	OE3735F	formyltetrahydrofolate deformylase (EC 3.5.1.10)	7	2	1.12	0.36	8.11E-01	purU
2	OE3735F	formyltetrahydrofolate deformylase (EC 3.5.1.10)	3	1	-1.27	0.23	3.40E-01	purU
1	OE3762R	glycerol kinase (EC 2.7.1.30)	8	3	-1.04	0.1	8.93E-01	glpK
2	OE3762R	glycerol kinase (EC 2.7.1.30)	7	1	-1.08	0.17	7.25E-01	glpK
3	OE3762R	glycerol kinase (EC 2.7.1.30)	7	2	-1.13	0.11	6.41E-01	glpK
1	OE3763F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit A	2	1	-1.04	0.15	8.87E-01	gpdA2
1	OE3764F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit B	2	1	1.00	0.13	9.99E-01	gpdB
1	OE3784R	preprotein-export translocase subunit secD	6	2	-1.03	0.04	9.19E-01	secD
3	OE3792F	glucose-6-phosphate isomerase (EC 5.3.1.9)	1	1	-1.56	0.19	1.14E-01	pgi
3	OE3798R	conserved hypothetical protein	2	1	1.32	0.07	3.11E-01	-
1	OE3798R	conserved hypothetical protein	1	1	-1.14	0.08	6.24E-01	-
2	OE3800F	translation initiation factor IF2	10	2	1.09	0.35	8.46E-01	infB
3	OE3800F	translation initiation factor IF2	8	2	-1.57	0.44	2.32E-01	infB
1	OE3805R	probable proteasome regulatory subunit (probable proteasome-activating nucleotidase PAN)	6	1	-1.11	0.26	7.58E-01	pan2
1	OE3807R	oligoendopeptidase	6	4	-1.02	0.19	9.43E-01	yjbG
2	OE3807R	oligoendopeptidase	7	5	-1.04	0.09	8.20E-01	yjbG
3	OE3807R	oligoendopeptidase	6	2	-1.10	0.15	7.44E-01	yjbG
2	OE3812R	histidine--tRNA ligase (EC 6.1.1.21)	6	2	1.01	0.15	9.57E-01	hisS
1	OE3812R	histidine--tRNA ligase (EC 6.1.1.21)	4	1	-1.02	0.1	9.50E-01	hisS
3	OE3812R	histidine--tRNA ligase (EC 6.1.1.21)	7	1	-1.26	0.38	5.56E-01	hisS
2	OE3817R	ribosomal protein S19.eR	5	3	-1.10	0.12	6.36E-01	rps19R
3	OE3817R	ribosomal protein S19.eR	3	1	-1.13	0.18	6.73E-01	rps19R
2	OE3826F	lysine--tRNA ligase (EC 6.1.1.6)	5	1	1.04	0.06	8.00E-01	lysS
1	OE3826F	lysine--tRNA ligase (EC 6.1.1.6)	7	4	-1.01	0.11	9.62E-01	lysS
3	OE3826F	lysine--tRNA ligase (EC 6.1.1.6)	5	1	-2.50	0.26	8.42E-04	lysS
2	OE3832F	conserved hypothetical protein	8	2	1.08	0.09	7.14E-01	-
1	OE3832F	conserved hypothetical protein	11	2	-1.16	0.08	5.72E-01	-
3	OE3832F	conserved hypothetical protein	10	2	-1.18	0.12	5.36E-01	-
1	OE3834R	probable oxidoreductase	3	2	-1.44	0.45	3.64E-01	gsp
2	OE3834R	probable oxidoreductase	2	2	-1.47	0.19	7.21E-02	gsp
3	OE3834R	probable oxidoreductase	4	3	-1.70	0.32	9.39E-02	gsp
1	OE3843F	NAD+ synthase (EC 6.3.1.5)	5	2	-1.20	0.15	5.29E-01	nadE
2	OE3843F	NAD+ synthase (EC 6.3.1.5)	5	2	-1.34	0.1	1.10E-01	nadE
1	OE3874R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit E'	2	1	1.00	0.15	9.99E-01	rpoE1
1	OE3876R	translation initiation factor aIF-2 gamma subunit	4	4	1.09	0.16	7.81E-01	aIF2g
2	OE3876R	translation initiation factor aIF-2 gamma subunit	4	4	1.08	0.15	7.63E-01	aIF2g
3	OE3876R	translation initiation factor aIF-2 gamma subunit	4	3	-1.07	0.16	8.12E-01	aIF2g
3	OE3882R	AAA-type ATPase (transitional ATPase homolog)	2	1	1.01	0.09	9.73E-01	aaa7
2	OE3882R	AAA-type ATPase (transitional ATPase homolog)	2	1	-1.08	0.13	6.96E-01	aaa7
2	OE3884F	acetyl-CoA C-ac(et)yltransferase	3	1	1.06	0.14	7.80E-01	aca

		(EC 2.3.1.16) or (EC 2.3.1.9)						
2	OE3889R	probable potassium transport protein kefC	2	1	1.14	0.06	4.92E-01	kefC
1	OE3889R	probable potassium transport protein kefC	1	1	1.03	0.09	9.24E-01	kefC
3	OE3892R	beta-lactamase homolog	1	1	1.01	0.05	9.72E-01	-
2	OE3893F	serine--tRNA ligase (EC 6.1.1.11)	9	4	1.04	0.09	8.47E-01	serS
1	OE3893F	serine--tRNA ligase (EC 6.1.1.11)	8	1	1.03	0.2	9.18E-01	serS
3	OE3893F	serine--tRNA ligase (EC 6.1.1.11)	7	1	-1.02	0.17	9.61E-01	serS
1	OE3910R	probable ABC-type transport system periplasmic substrate-binding protein	6	4	-1.17	0.08	5.47E-01	hpb
2	OE3910R	probable ABC-type transport system periplasmic substrate-binding protein	6	4	-1.77	0.21	5.36E-03	hpb
2	OE3913F	imidazoleglycerol-phosphate synthase (EC 2.4.2.-) (glutamine amidotransferase)	2	1	1.19	0.1	4.03E-01	hisH2
3	OE3913F	imidazoleglycerol-phosphate synthase (EC 2.4.2.-) (glutamine amidotransferase)	2	1	1.05	0.35	9.16E-01	hisH2
2	OE3922R	glutamate--ammonia ligase (EC 6.3.1.2)	13	6	-1.27	0.19	2.95E-01	glnA
3	OE3922R	glutamate--ammonia ligase (EC 6.3.1.2)	15	9	-1.40	0.21	2.48E-01	glnA
1	OE3922R	glutamate--ammonia ligase (EC 6.3.1.2)	12	5	-1.49	0.19	1.57E-01	glnA
2	OE3923F	global transcription regulator	5	3	-1.05	0.14	8.16E-01	lrp
3	OE3923F	global transcription regulator	4	4	-1.12	0.34	7.66E-01	lrp
1	OE3923F	global transcription regulator	4	2	-1.16	0.08	5.77E-01	lrp
2	OE3925R	thermosome beta subunit	23	13	1.85	0.1	1.60E-02	cctB
3	OE3925R	thermosome beta subunit	21	10	1.59	0.12	1.41E-01	cctB
1	OE3925R	thermosome beta subunit	22	12	1.56	0.09	1.18E-01	cctB
2	OE3930R	protein synthesis inhibitor homolog	5	3	1.27	0.12	2.94E-01	-
3	OE3930R	protein synthesis inhibitor homolog	6	3	1.23	0.09	4.55E-01	-
1	OE3930R	protein synthesis inhibitor homolog	5	3	1.15	0.09	6.13E-01	-
2	OE3931R	threonine dehydratase (EC 4.2.1.16)	5	2	-1.04	0.11	8.30E-01	iluA
3	OE3931R	threonine dehydratase (EC 4.2.1.16)	5	1	-1.04	0.3	9.12E-01	iluA
1	OE3931R	threonine dehydratase (EC 4.2.1.16)	5	1	-1.05	0.19	8.70E-01	iluA
3	OE3934R	citrate (si)-synthase (EC 2.3.3.1)	6	4	1.05	0.13	8.48E-01	citZ
2	OE3934R	citrate (si)-synthase (EC 2.3.3.1)	6	3	1.04	0.08	8.10E-01	citZ
1	OE3934R	citrate (si)-synthase (EC 2.3.3.1)	7	4	-1.06	0.23	8.68E-01	citZ
1	OE3936F	potassium channel protein homolog	1	1	1.03	0.11	9.27E-01	pchB
3	OE3940F	conserved hypothetical protein	5	3	-1.02	0.13	9.49E-01	-
2	OE3940F	conserved hypothetical protein	4	3	-1.04	0.1	8.58E-01	-
1	OE3940F	conserved hypothetical protein	3	1	-1.15	0.28	7.00E-01	-
2	OE3951R	conserved hypothetical protein	3	2	1.09	0.05	6.18E-01	-
1	OE3951R	conserved hypothetical protein	4	1	1.03	0.12	9.01E-01	-
3	OE3951R	conserved hypothetical protein	3	2	-1.01	0.07	9.58E-01	-
2	OE3953R	orotate phosphoribosyltransferase (EC 2.4.2.10)	1	1	1.43	0.26	3.76E-01	pyrE2
1	OE3953R	orotate phosphoribosyltransferase (EC 2.4.2.10)	2	1	1.14	0.07	6.32E-01	pyrE2
3	OE3953R	orotate phosphoribosyltransferase (EC 2.4.2.10)	2	1	-1.02	0.2	9.59E-01	pyrE2
2	OE3955F	probable proline dehydrogenase (EC 1.5.99.8)	3	2	1.47	0.06	4.24E-02	putA

3	OE3955F	probable proline dehydrogenase (EC 1.5.99.8)	2	2	1.43	0.1	2.30E-01	putA
1	OE3955F	probable proline dehydrogenase (EC 1.5.99.8)	4	3	1.41	0.08	2.10E-01	putA
1	OE3958F	conserved hypothetical protein	2	1	1.22	0.05	4.50E-01	-
2	OE3959R	branched-chain-amino-acid transaminase (EC 2.6.1.42)	7	5	1.09	0.06	6.63E-01	ilvE
1	OE3959R	branched-chain-amino-acid transaminase (EC 2.6.1.42)	9	6	1.04	0.11	8.78E-01	ilvE
3	OE3959R	branched-chain-amino-acid transaminase (EC 2.6.1.42)	10	4	1.04	0.07	8.81E-01	ilvE
2	OE3964R	conserved hypothetical protein	2	1	1.25	0.08	2.44E-01	-
1	OE3964R	conserved hypothetical protein	2	1	-1.11	0.21	7.38E-01	-
2	OE3973F	peptide chain release factor eRF-1	7	2	1.14	0.07	4.79E-01	erf1
1	OE3973F	peptide chain release factor eRF-1	3	3	-1.08	0.06	7.56E-01	erf1
3	OE3978R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit D.a; A-type ATP synthase subunit D.a	3	2	1.27	0.12	4.23E-01	atpD
1	OE3978R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit D.a; A-type ATP synthase subunit D.a	4	2	1.15	0.1	6.05E-01	atpD
2	OE3978R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit D.a; A-type ATP synthase subunit D.a	5	1	1.11	0.1	5.96E-01	atpD
2	OE3984R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit B.a; A-type ATP synthase subunit B.a	13	9	1.11	0.09	5.88E-01	atpB
1	OE3984R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit B.a; A-type ATP synthase subunit B.a	14	7	1.08	0.09	7.91E-01	atpB
3	OE3984R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit B.a; A-type ATP synthase subunit B.a	14	7	1.01	0.09	9.83E-01	atpB
3	OE3985R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit A.a; A-type ATP synthase subunit A.a	16	11	1.14	0.17	6.92E-01	atpA
2	OE3985R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit A.a; A-type ATP synthase subunit A.a	15	13	1.09	0.15	7.36E-01	atpA
1	OE3985R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit A.a; A-type ATP synthase subunit A.a	15	11	1.06	0.16	8.48E-01	atpA
3	OE3987R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit C.a; A-type ATP synthase subunit C.a	5	2	1.06	0.14	8.24E-01	atpC
2	OE3987R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit C.a; A-type ATP synthase subunit C.a	6	1	1.04	0.2	8.90E-01	atpC
1	OE3987R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit C.a; A-type ATP synthase subunit C.a	7	2	-1.11	0.16	7.27E-01	atpC
1	OE3988R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit E.a; A-type ATP synthase subunit E.a	4	4	-1.07	0.13	8.05E-01	atpE
3	OE3988R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit E.a; A-type ATP synthase subunit E.a	3	2	-1.12	0.14	6.81E-01	atpE
2	OE3988R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit E.a; A-type ATP synthase subunit E.a	2	2	-1.20	0.1	3.27E-01	atpE
2	OE3989R	H+-transporting two-sector ATPase	1	1	1.15	0.03	4.11E-01	atpK

		(EC 3.6.3.14) subunit K.a; A-type ATP synthase subunit K.a							
3	OE3989R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit K.a; A-type ATP synthase subunit K.a	1	1	1.14	0.04	6.21E-01	atpK
1	OE3989R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit K.a; A-type ATP synthase subunit K.a	1	1	1.09	0.05	7.47E-01	atpK
3	OE3991R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit I.a; A-type ATP synthase subunit I.a	7	5	1.14	0.13	6.55E-01	atpI
2	OE3991R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit I.a; A-type ATP synthase subunit I.a	4	4	1.06	0.07	7.37E-01	atpI
1	OE3991R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit I.a; A-type ATP synthase subunit I.a	6	4	1.05	0.09	8.59E-01	atpI
2	OE3992R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit H.a; A-type ATP synthase subunit H.a	2	1	1.02	0.1	9.17E-01	atpH
3	OE3992R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit H.a; A-type ATP synthase subunit H.a	3	1	-1.01	0.1	9.83E-01	atpH
2	OE3994F	menaquinone biosynthesis methyltransferase homolog	5	2	1.16	0.23	6.35E-01	menG
1	OE3994F	menaquinone biosynthesis methyltransferase homolog	4	2	1.14	0.1	6.50E-01	menG
3	OE3994F	menaquinone biosynthesis methyltransferase homolog	4	2	-1.27	0.12	3.80E-01	menG
2	OE4005F	electron transfer flavoprotein beta subunit	3	2	1.09	0.06	6.58E-01	etfB
1	OE4005F	electron transfer flavoprotein beta subunit	3	2	1.04	0.38	9.25E-01	etfB
3	OE4005F	electron transfer flavoprotein beta subunit	3	2	-1.25	0.13	4.08E-01	etfB
1	OE4007F	electron transfer flavoprotein alpha subunit	3	2	1.06	0.12	8.38E-01	etfA
2	OE4007F	electron transfer flavoprotein alpha subunit	4	3	1.04	0.09	8.14E-01	etfA
3	OE4007F	electron transfer flavoprotein alpha subunit	4	3	-1.25	0.1	4.06E-01	etfA
3	OE4021F	probable oxidoreductase (EC 1.1.1.-)	2	1	1.04	0.04	8.87E-01	oxr1, oxrA
2	OE4021F	probable oxidoreductase (EC 1.1.1.-)	3	1	-1.03	0.1	8.87E-01	oxr1, oxrA
1	OE4021F	probable oxidoreductase (EC 1.1.1.-)	4	1	-1.06	0.06	8.26E-01	oxr1, oxrA
3	OE4023F	conserved hypothetical protein	4	3	1.10	0.13	7.31E-01	-
1	OE4023F	conserved hypothetical protein	3	1	1.09	0.16	7.97E-01	-
2	OE4023F	conserved hypothetical protein	5	2	1.03	0.36	9.44E-01	-
3	OE4025F	conserved hypothetical protein	4	1	1.43	0.23	3.83E-01	-
2	OE4025F	conserved hypothetical protein	3	2	1.25	0.21	4.63E-01	-
1	OE4025F	conserved hypothetical protein	3	1	1.11	0.12	7.27E-01	-
2	OE4027F	conserved hypothetical protein	5	1	1.41	0.05	5.69E-02	-
1	OE4027F	conserved hypothetical protein	5	2	1.39	0.05	2.08E-01	-
3	OE4027F	conserved hypothetical protein	3	1	1.23	0.08	4.25E-01	-
2	OE4032R	conserved hypothetical protein	2	1	-1.23	0.18	3.63E-01	-
3	OE4032R	conserved hypothetical protein	2	1	-1.71	0.18	5.09E-02	-
2	OE4068F	isoleucine--tRNA ligase (EC 6.1.1.5)	11	4	-1.01	0.11	9.54E-01	ileS

3	OE4068F	isoleucine--tRNA ligase (EC 6.1.1.5)	12	1	-1.01	0.18	9.66E-01	ileS
1	OE4068F	isoleucine--tRNA ligase (EC 6.1.1.5)	12	5	-1.08	0.1	7.80E-01	ileS
3	OE4085R	ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	4	1	1.00	0.35	9.97E-01	prsA
2	OE4094F	probable phosphomannomutase	6	3	1.04	0.11	8.26E-01	pmu1
1	OE4094F	probable phosphomannomutase	10	5	1.02	0.09	9.32E-01	pmu1
3	OE4094F	probable phosphomannomutase	10	4	-1.05	0.22	8.90E-01	pmu1
3	OE4102R	tRNA-intron endonuclease (EC 3.1.27.9)	7	2	1.35	1.07	8.38E-01	endA
2	OE4102R	tRNA-intron endonuclease (EC 3.1.27.9)	5	1	-1.08	0.16	7.19E-01	endA
1	OE4113F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component alpha-1 subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	7	4	1.11	0.22	7.74E-01	oxdhA1
3	OE4113F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component alpha-1 subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	6	5	-1.04	0.12	8.83E-01	oxdhA1
2	OE4113F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component alpha-1 subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	7	3	-1.08	0.17	7.51E-01	oxdhA1
3	OE4114F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component beta subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	10	7	-1.05	0.09	8.65E-01	oxdhB
1	OE4114F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component beta subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	13	9	-1.09	0.12	7.63E-01	oxdhB
2	OE4114F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component beta subunit (the substrate is NOT pyruvate or 2-oxoglutarate)	12	6	-1.16	0.1	4.27E-01	oxdhB
1	OE4115F	dihydrolipoamide S-acyltransferase (EC 2.3.1.-) (probable E2 component of 2-oxoacid dehydrogenase complex) (the substrate of the complex is NOT pyruvate or 2-oxoglutarate)	17	8	-1.07	0.15	8.25E-01	dsa
2	OE4115F	dihydrolipoamide S-acyltransferase (EC 2.3.1.-) (probable E2 component of 2-oxoacid dehydrogenase complex) (the substrate of the complex is NOT pyruvate or 2-oxoglutarate)	19	6	-1.12	0.1	5.44E-01	dsa
3	OE4115F	dihydrolipoamide S-acyltransferase (EC 2.3.1.-) (probable E2 component of 2-oxoacid dehydrogenase complex) (the substrate of the complex is NOT pyruvate or 2-oxoglutarate)	18	10	-1.12	0.21	7.17E-01	dsa
3	OE4116F	dihydrolipoamide dehydrogenase (EC 1.8.1.4) (probable glycine cleavage system protein L and probable E3 component of the 2-oxoacid dehydrogenase complex) (substrate of 2-oxoacid	7	4	-1.07	0.12	7.98E-01	lpdA

		dehydrogenase complex is NOT pyruvate or 2-oxoglutarate)						
1	OE4116F	dihydrolipoamide dehydrogenase (EC 1.8.1.4) (probable glycine cleavage system protein L and probable E3 component of the 2-oxoacid dehydrogenase complex) (substrate of 2-oxoacid dehydrogenase complex is NOT pyruvate or 2-oxoglutarate)	5	3	-1.11	0.14	7.07E-01	lpdA
2	OE4116F	dihydrolipoamide dehydrogenase (EC 1.8.1.4) (probable glycine cleavage system protein L and probable E3 component of the 2-oxoacid dehydrogenase complex) (substrate of 2-oxoacid dehydrogenase complex is NOT pyruvate or 2-oxoglutarate)	7	3	-1.16	0.14	4.81E-01	lpdA
2	OE4118R	leucine--tRNA ligase (EC 6.1.1.4)	9	3	1.16	0.15	5.36E-01	leuS
3	OE4118R	leucine--tRNA ligase (EC 6.1.1.4)	10	2	1.10	0.17	7.72E-01	leuS
1	OE4118R	leucine--tRNA ligase (EC 6.1.1.4)	10	2	1.06	0.07	8.30E-01	leuS
2	OE4121R	probable ornithine cyclodeaminase (EC 4.3.1.12)	1	1	1.01	0.17	9.59E-01	ocd1
1	OE4121R	probable ornithine cyclodeaminase (EC 4.3.1.12)	1	1	1.00	0.15	9.88E-01	ocd1
3	OE4121R	probable ornithine cyclodeaminase (EC 4.3.1.12)	2	1	-1.07	0.16	8.11E-01	ocd1
2	OE4122R	thermosome alpha subunit	27	14	1.52	0.06	3.24E-02	cctA
1	OE4122R	thermosome alpha subunit	27	12	1.41	0.12	2.67E-01	cctA
3	OE4122R	thermosome alpha subunit	27	14	1.25	0.1	4.36E-01	cctA
1	OE4124R	conserved hypothetical protein	1	1	1.03	0.21	9.38E-01	-
3	OE4124R	conserved hypothetical protein	2	1	1.00	0.37	9.94E-01	-
2	OE4124R	conserved hypothetical protein	2	1	-1.16	0.45	7.18E-01	-
2	OE4139R	tyrosine--tRNA ligase (EC 6.1.1.1)	3	1	1.18	0.04	3.59E-01	tyrS
3	OE4139R	tyrosine--tRNA ligase (EC 6.1.1.1)	4	1	-1.01	0.05	9.82E-01	tyrS
2	OE4142F	replication factor C small subunit	4	1	-1.12	0.09	5.30E-01	rfcC
3	OE4142F	replication factor C small subunit	2	1	-1.52	0.35	2.17E-01	rfcC
2	OE4146F	TATA-binding transcription initiation factor	4	1	1.19	0.04	3.06E-01	tbpE
3	OE4146F	TATA-binding transcription initiation factor	4	3	1.16	0.12	6.14E-01	tbpE
1	OE4146F	TATA-binding transcription initiation factor	4	2	1.09	0.06	7.45E-01	tbpE
2	OE4157F	probable chlorohydrolase	3	1	-1.01	0.23	9.67E-01	trzA
1	OE4157F	probable chlorohydrolase	3	1	-1.06	0.07	8.25E-01	trzA
2	OE4159F	adenosylhomocysteinase (EC 3.3.1.1)	8	2	1.15	0.08	4.60E-01	achY
1	OE4159F	adenosylhomocysteinase (EC 3.3.1.1)	7	1	1.14	0.06	6.29E-01	achY
2	OE4165R	DNA-directed DNA polymerase sliding clamp homolog	5	3	1.25	0.08	2.64E-01	pcn
1	OE4165R	DNA-directed DNA polymerase sliding clamp homolog	3	2	1.09	0.09	7.61E-01	pcn
3	OE4165R	DNA-directed DNA polymerase sliding clamp homolog	5	5	-1.05	0.25	8.93E-01	pcn
2	OE4169F	conserved hypothetical protein	5	1	-1.02	0.4	9.63E-01	-
3	OE4187R	probable DNA-binding protein	1	1	1.03	0.11	9.11E-01	-
1	OE4187R	probable DNA-binding protein	1	1	1.02	0.08	9.47E-01	-
2	OE4190F	probable phosphohexomutase (EC 5.4.2.-)	3	1	1.12	0.14	6.14E-01	pmm

1	OE4190F	probable phosphohexomutase (EC 5.4.2.-)	2	1	1.00	0.05	9.99E-01	pmm
3	OE4190F	probable phosphohexomutase (EC 5.4.2.-)	3	1	-1.03	0.14	9.28E-01	pmm
2	OE4195F	replication factor C small subunit	6	2	-1.03	0.14	9.00E-01	rfcA
1	OE4195F	replication factor C small subunit	5	2	-1.24	0.16	4.48E-01	rfcA
3	OE4195F	replication factor C small subunit	11	4	-1.63	0.4	1.63E-01	rfcA
1	OE4197F	conserved hypothetical protein	4	2	1.08	0.24	8.32E-01	-
2	OE4197F	conserved hypothetical protein	5	1	-1.17	0.18	4.82E-01	-
3	OE4198F	alanine--tRNA ligase (EC 6.1.1.7)	9	2	1.09	0.14	7.85E-01	alaS
1	OE4198F	alanine--tRNA ligase (EC 6.1.1.7)	9	3	1.04	0.16	9.06E-01	alaS
2	OE4198F	alanine--tRNA ligase (EC 6.1.1.7)	11	1	-1.09	0.12	6.62E-01	alaS
2	OE4217R	ferredoxin (2Fe-2S)	2	1	1.10	0.1	6.35E-01	fdx, fer2
3	OE4217R	ferredoxin (2Fe-2S)	3	2	1.09	0.07	7.43E-01	fdx, fer2
1	OE4217R	ferredoxin (2Fe-2S)	3	1	1.08	0.09	7.98E-01	fdx, fer2
1	OE4218F	N-(5'-phospho-D-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	2	1	1.14	0.13	6.64E-01	hisA
3	OE4218F	N-(5'-phospho-D-ribosylformimino)-5-amino-1-(5''-phosphoribosyl)-4-imidazolecarboxamide isomerase (EC 5.3.1.16)	3	2	-1.04	0.13	8.96E-01	hisA
1	OE4221R	hypothetical protein	1	1	1.04	0.1	8.82E-01	-
2	OE4221R	hypothetical protein	1	1	-1.08	0.07	6.87E-01	-
3	OE4221R	hypothetical protein	1	1	-2.09	0.11	4.39E-03	-
2	OE4234R	uracil phosphoribosyltransferase (EC 2.4.2.9) upp	2	1	-1.01	0.13	9.56E-01	upp
1	OE4234R	uracil phosphoribosyltransferase (EC 2.4.2.9) upp	3	1	-1.02	0.18	9.45E-01	upp
3	OE4234R	uracil phosphoribosyltransferase (EC 2.4.2.9) upp	3	2	-1.11	0.14	7.09E-01	upp
3	OE4262F	porphobilinogen synthase (EC 4.2.1.24)	3	1	1.02	0.28	9.50E-01	hemB
2	OE4268F	glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)	4	1	1.18	0.08	4.06E-01	hemL
3	OE4268F	glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)	3	1	-1.24	0.1	4.17E-01	hemL
1	OE4277F	uroporphyrin-III C-methyltransferase (EC 2.1.1.107)	2	2	1.01	0.16	9.77E-01	hemX, sumT, cysG2
1	OE4302R	ABC-type oligopeptide transport system ATP-binding protein	4	2	1.22	0.11	4.84E-01	oppD2
3	OE4305R	ABC-type dipeptide transport system periplasmic dipeptide-binding protein	16	4	1.35	0.12	3.13E-01	dppA
2	OE4305R	ABC-type dipeptide transport system periplasmic dipeptide-binding protein	10	4	1.25	0.06	2.41E-01	dppA
1	OE4305R	ABC-type dipeptide transport system periplasmic dipeptide-binding protein	11	4	1.19	0.16	5.77E-01	dppA
1	OE4306F	conserved hypothetical protein	11	7	-1.05	0.1	8.69E-01	-
2	OE4306F	conserved hypothetical protein	9	4	-1.05	0.18	8.32E-01	-
3	OE4306F	conserved hypothetical protein	8	4	-1.29	0.17	3.69E-01	-
2	OE4307F	glycine--tRNA ligase (EC 6.1.1.14)	4	1	-1.09	0.13	6.69E-01	glyS
1	OE4307F	glycine--tRNA ligase (EC 6.1.1.14)	4	2	-1.15	0.09	6.04E-01	glyS

3	OE4307F	glycine--tRNA ligase (EC 6.1.1.14)	4	2	-1.16	0.15	5.96E-01	glyS
3	OE4323F	malate dehydrogenase (EC 1.1.1.37)	3	1	1.22	0.13	5.08E-01	mdhA
2	OE4323F	malate dehydrogenase (EC 1.1.1.37)	2	1	1.12	0.1	5.67E-01	mdhA
1	OE4323F	malate dehydrogenase (EC 1.1.1.37)	3	1	1.10	0.16	7.74E-01	mdhA
2	OE4329F	conserved hypothetical protein	8	3	-1.01	0.15	9.59E-01	-
1	OE4329F	conserved hypothetical protein	8	2	-1.27	0.09	3.55E-01	-
3	OE4329F	conserved hypothetical protein	8	2	-1.28	0.18	3.92E-01	-
1	OE4330F	probable phosphoesterase (EC 3.1.-.-)	1	1	-1.11	0.15	7.22E-01	-
3	OE4330F	probable phosphoesterase (EC 3.1.-.-)	1	1	-2.19	0.24	4.46E-03	-
3	OE4333R	aspartate kinase (EC 2.7.2.4) II alpha and beta subunit	2	2	-1.12	0.11	6.69E-01	lysC
1	OE4333R	aspartate kinase (EC 2.7.2.4) II alpha and beta subunit	4	1	-1.20	0.13	5.15E-01	lysC
2	OE4339R	ABC-type transport system ATP-binding protein	5	3	-1.15	0.29	6.48E-01	nosF1
1	OE4339R	ABC-type transport system ATP-binding protein	4	2	-1.18	0.23	6.03E-01	nosF1
3	OE4339R	ABC-type transport system ATP-binding protein	3	1	-1.79	0.26	4.49E-02	nosF1
2	OE4355R	thiosulfate sulfurtransferase homolog	4	2	1.09	0.07	6.69E-01	tssA
1	OE4355R	thiosulfate sulfurtransferase homolog	5	3	1.08	0.06	7.68E-01	tssA
3	OE4355R	thiosulfate sulfurtransferase homolog	6	3	-2.62	0.99	3.43E-02	tssA
3	OE4365F	conserved hypothetical protein	1	1	1.05	0.13	8.70E-01	-
3	OE4377R	GTP-binding protein homolog	5	2	1.23	0.05	4.29E-01	gbp3
2	OE4377R	GTP-binding protein homolog	5	3	1.19	0.11	4.28E-01	gbp3
1	OE4377R	GTP-binding protein homolog	6	1	1.18	0.09	5.58E-01	gbp3
1	OE4391F	probable serine--pyruvate aminotransferase (EC 2.6.1.51) (probably including alanine--glyoxylate aminotransferase (EC 2.6.1.44))	3	1	-1.24	0.17	4.57E-01	agxT
1	OE4408F	phosphoglycerate dehydrogenase (EC 1.1.1.95)	13	4	1.06	0.09	8.15E-01	serA1
3	OE4408F	phosphoglycerate dehydrogenase (EC 1.1.1.95)	12	7	-1.04	0.18	9.06E-01	serA1
2	OE4408F	phosphoglycerate dehydrogenase (EC 1.1.1.95)	9	3	-1.14	0.05	4.51E-01	serA1
2	OE4427R	ferritin	2	2	1.67	0.08	1.86E-02	dpsA
3	OE4427R	ferritin	2	2	1.67	0.06	6.01E-02	dpsA
1	OE4427R	ferritin	2	2	1.30	0.05	3.14E-01	dpsA
2	OE4450R	signal recognition particle 54K protein	7	3	1.49	0.09	6.57E-02	srp54, ffh
3	OE4450R	signal recognition particle 54K protein	2	1	1.49	0.07	1.52E-01	srp54, ffh
1	OE4450R	signal recognition particle 54K protein	6	2	1.28	0.15	4.29E-01	srp54, ffh
1	OE4454R	signal recognition particle receptor SRalpha	2	1	-1.11	0.2	7.32E-01	ftsY
1	OE4461F	conserved hypothetical protein	4	1	-1.02	0.2	9.57E-01	-
3	OE4463F	probable cysteine desulfurase	4	1	1.19	0.07	5.21E-01	nifS
1	OE4466R	DNA repair protein	9	4	-1.38	0.18	2.59E-01	radA1
2	OE4466R	DNA repair protein	7	4	-2.38	0.46	7.29E-04	radA1

3	OE4466R	DNA repair protein	6	4	-2.55	0.28	7.13E-04	radA1
1	OE4498F	conserved hypothetical protein	3	1	1.01	0.1	9.76E-01	-
3	OE4500R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	10	2	1.18	0.11	5.78E-01	acd6
1	OE4500R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	10	5	1.03	0.09	8.98E-01	acd6
2	OE4500R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	10	2	-1.04	0.18	8.61E-01	acd6
2	OE4504F	conserved hypothetical protein	6	1	-1.14	0.22	6.06E-01	-
3	OE4505F	phenylalanine--tRNA ligase (EC 6.1.1.20) alpha subunit	3	1	-1.10	0.09	7.27E-01	pheS
2	OE4505F	phenylalanine--tRNA ligase (EC 6.1.1.20) alpha subunit	3	1	-1.20	0.08	3.24E-01	pheS
3	OE4507F	phenylalanine--tRNA ligase (EC 6.1.1.20) beta subunit	8	2	1.01	0.15	9.84E-01	pheY
1	OE4508R	dihydroorotate oxidase (EC 1.3.3.1)	8	3	1.02	0.09	9.48E-01	pyrD
2	OE4508R	dihydroorotate oxidase (EC 1.3.3.1)	7	2	-1.07	0.44	8.83E-01	pyrD
2	OE4529F	aldehyde dehydrogenase (EC 1.2.1.-) (retinal dehydrogenase homolog, glyceraldehyde-3-phosphate dehydrogenase homolog)	11	6	1.33	0.04	1.00E-01	aldH1
1	OE4529F	aldehyde dehydrogenase (EC 1.2.1.-) (retinal dehydrogenase homolog, glyceraldehyde-3-phosphate dehydrogenase homolog)	10	6	1.22	0.07	4.56E-01	aldH1
3	OE4529F	aldehyde dehydrogenase (EC 1.2.1.-) (retinal dehydrogenase homolog, glyceraldehyde-3-phosphate dehydrogenase homolog)	8	6	1.06	0.13	8.41E-01	aldH1
1	OE4539R	hypothetical protein	4	1	-1.02	0.17	9.54E-01	-
3	OE4539R	hypothetical protein	6	1	-1.45	0.25	2.23E-01	-
1	OE4540R	conserved hypothetical protein	6	2	1.41	0.07	2.03E-01	-
3	OE4540R	conserved hypothetical protein	3	1	1.35	0.03	2.41E-01	-
2	OE4540R	conserved hypothetical protein	7	1	1.30	0.06	1.58E-01	-
3	OE4551F	ABC-type transport system periplasmic substrate-binding protein	5	1	1.61	0.08	9.57E-02	dppD
2	OE4551F	ABC-type transport system periplasmic substrate-binding protein	3	1	1.59	0.1	4.88E-02	dppD
1	OE4559R	conserved hypothetical protein	4	1	-1.03	0.07	8.97E-01	-
1	OE4565F	conserved hypothetical protein	4	1	1.01	0.1	9.76E-01	-
1	OE4568R	conserved hypothetical protein	4	1	-1.08	0.12	7.88E-01	-
3	OE4568R	conserved hypothetical protein	5	1	-1.13	0.17	6.75E-01	-
1	OE4571R	probable leucyl aminopeptidase (EC 3.4.11.1)	6	2	1.03	0.13	9.06E-01	pepB3
2	OE4571R	probable leucyl aminopeptidase (EC 3.4.11.1)	7	2	-1.24	0.26	4.12E-01	pepB3
3	OE4571R	probable leucyl aminopeptidase (EC 3.4.11.1)	6	2	-1.25	0.62	6.87E-01	pepB3
2	OE4572R	valine--tRNA ligase (EC 6.1.1.9)	11	4	1.04	0.13	8.63E-01	valS
1	OE4572R	valine--tRNA ligase (EC 6.1.1.9)	9	6	1.03	0.14	9.08E-01	valS
3	OE4572R	valine--tRNA ligase (EC 6.1.1.9)	14	7	1.03	0.1	9.23E-01	valS
1	OE4576F	probable ABC-type transport system substrate-binding protein	2	1	-1.12	0.1	6.71E-01	-
2	OE4581F	probable phosphogluconate dehydrogenase (only N-terminal	3	1	1.25	0.1	2.70E-01	pgd

		domain homology, presumably not functional)						
1	OE4581F	probable phosphogluconate dehydrogenase (only N-terminal domain homology, presumably not functional)	2	1	1.05	0.1	8.50E-01	pgd
3	OE4581F	probable phosphogluconate dehydrogenase (only N-terminal domain homology, presumably not functional)	3	1	-1.15	0.12	6.18E-01	pgd
1	OE4582R	conserved hypothetical protein	1	1	1.09	0.15	7.90E-01	-
3	OE4582R	conserved hypothetical protein	1	1	1.03	0.07	9.10E-01	-
1	OE4613F	aconitate hydratase (EC 4.2.1.3)	19	13	1.18	0.12	5.85E-01	acn
2	OE4613F	aconitate hydratase (EC 4.2.1.3)	18	11	1.08	0.11	7.33E-01	acn
3	OE4613F	aconitate hydratase (EC 4.2.1.3)	17	9	1.06	0.1	8.29E-01	acn
1	OE4626R	probable translation initiation factor SUI1	4	2	-1.03	0.12	9.05E-01	sui1
3	OE4626R	probable translation initiation factor SUI1	3	1	-1.20	0.06	4.85E-01	sui1
2	OE4646R	hypothetical protein	1	1	1.09	0.1	6.57E-01	-
2	OE4648F	thioredoxin	4	1	1.14	0.11	5.31E-01	trxA2
1	OE4648F	thioredoxin	4	1	-1.03	0.19	9.34E-01	trxA2
1	OE4655R	conserved hypothetical protein	5	3	1.37	0.08	2.49E-01	-
3	OE4655R	conserved hypothetical protein	5	2	1.12	0.1	6.87E-01	-
2	OE4655R	conserved hypothetical protein	3	1	1.09	0.12	7.09E-01	-
1	OE4663F	conserved hypothetical protein	2	1	1.25	0.13	4.66E-01	-
2	OE4663F	conserved hypothetical protein	2	1	1.20	0.14	4.35E-01	-
1	OE4667R	AAA domain/ferredoxin domain protein	3	1	1.05	0.09	8.46E-01	-
2	OE4671R	conserved hypothetical protein	6	1	1.03	0.09	8.81E-01	-
3	OE4671R	conserved hypothetical protein	8	2	-1.09	0.21	7.78E-01	-
1	OE4671R	conserved hypothetical protein	7	1	-1.22	0.07	4.39E-01	-
1	OE4673F	carboxypeptidase (EC 3.4.-.-)	4	2	1.25	0.04	3.86E-01	cxp
2	OE4673F	carboxypeptidase (EC 3.4.-.-)	6	3	1.23	0.09	2.98E-01	cxp
3	OE4673F	carboxypeptidase (EC 3.4.-.-)	5	2	-1.30	0.25	4.10E-01	cxp
1	OE4674F	alcohol dehydrogenase (EC 1.1.1.1)	2	1	1.22	0.03	4.40E-01	adh2
3	OE4674F	alcohol dehydrogenase (EC 1.1.1.1)	1	1	1.09	0.19	7.93E-01	adh2
1	OE4677F	DNA helicase II	10	4	-1.04	0.23	9.11E-01	uvrD
2	OE4677F	DNA helicase II	14	2	-1.19	0.11	3.73E-01	uvrD
3	OE4677F	DNA helicase II	18	3	-1.19	0.12	5.13E-01	uvrD
3	OE4688F	conserved hypothetical protein	4	2	1.15	0.09	6.25E-01	-
2	OE4688F	conserved hypothetical protein	4	2	1.14	0.08	5.18E-01	-
1	OE4688F	conserved hypothetical protein	3	1	-1.09	0.44	8.48E-01	-
3	OE4691R	glucokinase (EC 2.7.1.2)	2	2	-1.20	0.09	4.88E-01	glcK
3	OE4699F	excinuclease ABC subunit A	5	2	-1.03	0.25	9.31E-01	uvrA
1	OE4699F	excinuclease ABC subunit A	3	1	-1.08	0.21	8.16E-01	uvrA
3	OE4703R	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	6	2	1.00	0.22	9.93E-01	uae
2	OE4703R	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	3	1	-1.21	0.22	4.42E-01	uae
3	OE4712F	conserved hypothetical protein	3	1	-1.51	0.09	1.15E-01	-
1	OE4712F	conserved hypothetical protein	4	1	-1.80	0.22	3.65E-02	-
1	OE4713R	conserved hypothetical protein	1	1	1.00	0.1	9.99E-01	-
2	OE4713R	conserved hypothetical protein	3	1	-1.08	0.17	7.25E-01	-
1	OE4716R	conserved hypothetical protein	1	1	-1.11	0.19	7.40E-01	-
2	OE4716R	conserved hypothetical protein	2	2	-1.28	0.2	2.76E-01	-
3	OE4716R	conserved hypothetical protein	2	1	-1.48	0.5	3.52E-01	-
1	OE4718F	ribonuclease R homolog	2	1	1.03	0.1	9.26E-01	vacB

2	OE4718F	ribonuclease R homolog	4	2	-1.11	0.12	6.09E-01	vacB
3	OE4718F	ribonuclease R homolog	3	2	-1.30	0.21	3.80E-01	vacB
3	OE4720R	ribosomal protein S10	3	2	-1.01	0.12	9.79E-01	rps10
1	OE4720R	ribosomal protein S10	3	2	-1.15	0.13	6.13E-01	rps10
2	OE4721R	translation elongation factor aEF-1 alpha subunit	13	5	1.05	0.06	7.68E-01	aef1a, tuf
3	OE4721R	translation elongation factor aEF-1 alpha subunit	13	5	1.05	0.14	8.59E-01	aef1a, tuf
1	OE4721R	translation elongation factor aEF-1 alpha subunit	12	5	1.03	0.06	9.12E-01	aef1a, tuf
1	OE4729R	translation elongation factor aEF-2	30	15	-1.02	0.15	9.39E-01	aef2, fus
2	OE4729R	translation elongation factor aEF-2	30	13	-1.04	0.12	8.34E-01	aef2, fus
3	OE4729R	translation elongation factor aEF-2	30	14	-1.34	0.46	4.94E-01	aef2, fus
3	OE4735R	ribosomal protein S7	10	3	-1.04	0.22	8.96E-01	rps7
2	OE4735R	ribosomal protein S7	8	2	-1.11	0.18	6.58E-01	rps7
1	OE4735R	ribosomal protein S7	8	2	-1.16	0.19	6.17E-01	rps7
1	OE4736R	ribosomal protein S12	8	3	-1.02	0.06	9.33E-01	rps12
2	OE4736R	ribosomal protein S12	7	4	-1.07	0.09	7.27E-01	rps12
3	OE4736R	ribosomal protein S12	8	4	-1.17	0.21	6.16E-01	rps12
2	OE4739R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A'' (chain C)	11	5	-1.04	0.2	8.91E-01	rpoA2, rpoC
3	OE4739R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A'' (chain C)	8	5	-1.04	0.11	8.82E-01	rpoA2, rpoC
1	OE4739R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A'' (chain C)	7	4	-1.09	0.23	7.98E-01	rpoA2, rpoC
2	OE4740R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A' (chain A)	16	5	-1.04	0.19	8.88E-01	rpoA1, rpoA
3	OE4740R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A' (chain A)	13	5	-1.10	0.28	7.97E-01	rpoA1, rpoA
1	OE4740R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A' (chain A)	12	6	-1.13	0.14	6.61E-01	rpoA1, rpoA
1	OE4741R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B'	11	7	-1.05	0.22	8.88E-01	rpoB1
3	OE4741R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B'	12	4	-1.07	0.2	8.26E-01	rpoB1
2	OE4741R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B'	8	3	-1.12	0.13	5.66E-01	rpoB1
2	OE4742R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B''	16	9	-1.01	0.11	9.54E-01	rpoB2
3	OE4742R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B''	18	10	-1.08	0.22	8.17E-01	rpoB2
1	OE4742R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B''	19	14	-1.11	0.19	7.36E-01	rpoB2
3	OE4759F	cell surface glycoprotein precursor	16	10	1.22	0.08	4.76E-01	csg
2	OE4759F	cell surface glycoprotein precursor	17	9	1.09	0.11	7.03E-01	csg
1	OE4759F	cell surface glycoprotein precursor	18	9	1.06	0.11	8.33E-01	csg
2	OE5049F	SMC-like protein sph2	2	1	1.09	0.03	6.09E-01	sph2
1	OE5049F	SMC-like protein sph2	1	1	-1.07	0.15	8.17E-01	sph2
2	OE5082R	AAA-type ATPase (transitional ATPase homolog)	2	1	2.38	0.02	4.78E-07	aaa8, cdc48d
3	OE5082R	AAA-type ATPase (transitional ATPase homolog)	5	1	1.79	0.04	2.55E-02	aaa8, cdc48d
3	OE5083R	heat shock protein homolog	2	1	4.00	0.01	6.67E-08	hsp5
2	OE5083R	heat shock protein homolog	2	1	3.23	0.01	0.00E+00	hsp5
1	OE5089F	conserved hypothetical protein	1	1	-1.20	0.09	4.95E-01	-
3	OE5089F	conserved hypothetical protein	1	1	-1.33	0.21	3.37E-01	-
2	OE5089F	conserved hypothetical protein	1	1	-1.49	0.06	2.24E-02	-

3	OE5100R	trkA domain protein	3	1	1.41	0.1	2.38E-01	trkA3
1	OE5100R	trkA domain protein	2	1	1.32	0.21	4.71E-01	trkA3
2	OE5100R	trkA domain protein	3	1	1.30	0.21	4.15E-01	trkA3
1	OE5142F	cell division protein ftsZ5	6	4	-1.02	0.09	9.52E-01	ftsZ5
2	OE5142F	cell division protein ftsZ5	9	4	-1.20	0.13	3.52E-01	ftsZ5
3	OE5142F	cell division protein ftsZ5	7	1	-1.29	0.14	3.62E-01	ftsZ5
1	OE5160F	glycerol dehydrogenase (EC 1.1.1.6)	3	1	1.35	0.08	2.85E-01	gldA1
3	OE5160F	glycerol dehydrogenase (EC 1.1.1.6)	5	1	1.14	0.06	6.27E-01	gldA1
2	OE5160F	glycerol dehydrogenase (EC 1.1.1.6)	2	1	-1.20	0.13	3.52E-01	gldA1
1	OE5162D1F	conserved hypothetical protein	1	1	1.92	0.04	1.28E-02	-
1	OE5186R	catalase (EC 1.11.1.6) (including: peroxidase (EC 1.11.1.7))	16	7	-1.03	0.1	9.06E-01	perA
3	OE5186R	catalase (EC 1.11.1.6) (including: peroxidase (EC 1.11.1.7))	17	8	-1.09	0.15	7.61E-01	perA
2	OE5186R	catalase (EC 1.11.1.6) (including: peroxidase (EC 1.11.1.7))	14	7	-1.12	0.13	5.91E-01	perA
1	OE5187R	probable hydrolase	4	2	1.25	0.06	3.89E-01	-
2	OE5201F	aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	9	6	1.05	0.11	7.94E-01	pyrB
3	OE5201F	aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	10	7	1.05	0.13	8.52E-01	pyrB
1	OE5201F	aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	15	10	-1.02	0.1	9.44E-01	pyrB
2	OE5202F	aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	2	2	1.09	0.1	6.96E-01	pyrI
3	OE5202F	aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	2	1	-1.03	0.18	9.28E-01	pyrI
3	OE5203F	arginine--tRNA ligase (EC 6.1.1.19)	17	8	-1.03	0.13	9.12E-01	argS
2	OE5203F	arginine--tRNA ligase (EC 6.1.1.19)	16	6	-1.04	0.1	8.55E-01	argS
1	OE5203F	arginine--tRNA ligase (EC 6.1.1.19)	16	9	-1.18	0.3	6.34E-01	argS
2	OE5204R	arginine/ornithine antiporter	3	1	1.12	0.08	5.48E-01	nhaC3
1	OE5204R	arginine/ornithine antiporter	3	1	1.10	0.09	7.31E-01	nhaC3
3	OE5204R	arginine/ornithine antiporter	3	1	1.10	0.17	7.53E-01	nhaC3
1	OE5205R	ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	9	3	1.10	0.09	7.23E-01	arcB
2	OE5205R	ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	9	2	1.10	0.05	5.84E-01	arcB
3	OE5205R	ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	9	3	1.10	0.1	7.38E-01	arcB
1	OE5206R	carbamate kinase (EC 2.7.2.2)	9	4	1.18	0.1	5.62E-01	arcC
2	OE5206R	carbamate kinase (EC 2.7.2.2)	7	3	1.16	0.06	4.12E-01	arcC
3	OE5206R	carbamate kinase (EC 2.7.2.2)	11	3	1.03	0.12	9.25E-01	arcC
2	OE5208R	arginine deiminase (EC 3.5.3.6)	11	5	1.14	0.16	6.17E-01	arcA
1	OE5208R	arginine deiminase (EC 3.5.3.6)	14	5	1.11	0.05	6.85E-01	arcA
3	OE5208R	arginine deiminase (EC 3.5.3.6)	15	5	-1.04	0.11	8.74E-01	arcA
2	OE5209R	transcription regulator arcR	1	1	1.28	0.06	1.84E-01	arcR
3	OE5209R	transcription regulator arcR	1	1	1.18	0.03	5.27E-01	arcR
1	OE5209R	transcription regulator arcR	2	1	1.09	0.15	7.78E-01	arcR
2	OE5211F	conserved hypothetical protein	2	1	-1.28	0.11	1.88E-01	-
1	OE5211F	conserved hypothetical protein	2	1	-1.41	0.07	1.82E-01	-
1	OE5212F	SMC-like protein sph1	3	1	-1.21	0.1	4.68E-01	sph1
1	OE5243F	transducer protein car	11	3	1.03	0.06	9.12E-01	car, htr11, htrXI
2	OE5243F	transducer protein car	12	4	-1.02	0.05	9.11E-01	car, htr11,

								htrXI
3	OE5243F	transducer protein car	14	5	-1.13	0.13	6.65E-01	car, htr11, htrXI
1	OE6213R, OE7093R	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 1	7	4	-1.09	0.21	7.77E-01	idi1b
3	OE6213R, OE7093R	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 1	4	2	-1.10	0.26	7.85E-01	idi1b
1	OE6230R, OE7110R	conserved hypothetical protein (nonfunctional, N-terminal part, interrupted by ISH2)	5	2	-1.08	0.12	7.92E-01	-
2	OE6230R, OE7110R	conserved hypothetical protein (nonfunctional, N-terminal part, interrupted by ISH2)	5	3	-1.11	0.07	5.71E-01	-
3	OE6238A1R OE7118A1R	spurious ORF	1	1	-1.29	0.2	3.84E-01	-
2	OE6303F	conserved hypothetical protein	4	1	1.04	0.17	8.79E-01	-
3	OE6303F	conserved hypothetical protein	3	1	-1.19	0.29	6.14E-01	-
1	OE6308F	hypothetical protein	3	1	1.03	0.16	9.10E-01	-
2	OE6308F	hypothetical protein	2	1	-1.09	0.22	7.35E-01	-
1	OE7031R	gas-vesicle operon protein gvpF1	2	1	-1.23	0.14	4.53E-01	gvpF1
3	OE7031R	gas-vesicle operon protein gvpF1	3	2	-1.35	0.22	3.18E-01	gvpF1
2	OE7031R	gas-vesicle operon protein gvpF1	2	1	-1.59	0.27	5.43E-02	gvpF1
3	OE7110R, OE6230R	conserved hypothetical protein (nonfunctional, N-terminal part, interrupted by ISH2)	5	2	-1.17	0.32	6.78E-01	-
1	OE7129F, OE6249F	conserved hypothetical protein	1	1	1.03	0.02	8.93E-01	-
1	OE7189F, OE7166F, OE8006F, OE8020F	conserved hypothetical protein	2	1	1.10	0.04	7.29E-01	-
3	OE7215F, OE8047F	conserved hypothetical protein	6	3	-1.60	0.17	8.99E-02	-
3	OE8006F, OE7166F, OE7189F, OE8020F	conserved hypothetical protein	2	2	-1.10	0.11	7.18E-01	-
3	OE8013F, OE7182F	probable restriction/modification enzyme	8	2	1.16	0.25	7.03E-01	-
1	OE8013F, OE7182F	probable restriction/modification enzyme	6	2	1.03	0.35	9.44E-01	-
2	OE8013F, OE7182F	probable restriction/modification enzyme	8	1	-1.08	0.21	7.76E-01	-
1	OE8023F, OE7192F	conserved hypothetical protein	4	1	-1.32	0.2	3.50E-01	-
3	OE8023F, OE7192F	conserved hypothetical protein	3	2	-2.08	0.7	8.33E-02	-
2	OE8047F, OE7215F	conserved hypothetical protein	2	1	-1.05	0.25	8.62E-01	-
1	OE8047F, OE7215F	conserved hypothetical protein	5	2	-1.11	0.11	7.12E-01	-

Supplemental Table D. Proteomic analyses on cells, grown in complex medium. Experiment numbers (Exp.), ID numbers and protein names, number of quantified peptides (Pep.d), regulation factors (Reg.d) and standard deviations (Std.d) after 1 h, as well as after 2 h (Pep.C, Reg.C and Std.C) of heat shock are indicated. Data are from proteins separated on different 2-D gels spanning different pH ranges, and subsequently spotted on different targets. Two independent approaches have been performed with proteins spotted on three targets (Exp.1) or on four targets (Exp.2), respectively. Manual validation of MS spectra has not been implicated in the results given.

Exp	ID and protein name	Pep.d	Reg.d	Std.d	Pep.C	Reg.C	Std.C
1	(OE4420R) argininosuccinate synthase (EC 6.3.4.5)	1	1.63	-	-	-	-
1	(OE2165R) ribosomal protein S15	1	1.47	-	-	-	-
1	(OE1270F) glutamate dehydrogenase (EC 1.4.1.2)	2	1.46	0.55	-	-	-
1	(OE5160F) glycerol dehydrogenase (EC 1.1.1.6)	1	1.39	-	-	-	
1	(OE4115F) dihydrolipoamide S-acyltransferase (EC 2.3.1.-) (probable E2 component of 2-oxoacid dehyd	1	1.31	-	-	-	-
1	(OE3296F) hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5)	2	1.27	0.14	-	-	-
1	(OE3934R) citrate (si)-synthase (EC 2.3.3.1) (formerly EC 4.1.3.7)	1	1.19	-	-	-	-
1	(OE3410F) ribosomal protein S8	2	1.19	0.41	-	-	-
1	(OE2524R) UDPglucose 6-dehydrogenase (EC 1.1.1.22)	3	1.17	0.05	-	-	-
1	(OE3610R) translation initiation factor aIF-2B chain alpha/delta eif2ba	1	1.16	-	-	-	-
1	(OE1687F) aspartate--tRNA ligase (EC 6.1.1.12)	2	1.13	0.16	-	-	-
1	(OE2844R) transcription regulator homolog / trkA C-terminal domain protein	1	1.12	-	-	-	-
1	(OE1951F) phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) carbon dioxide-fixation chain	1	1.08	-	-	-	-
1	(OE2515F) conserved protein	2	1.08	0.08	-	-	-
1	(OE2579F) adenylosuccinate synthase (EC 6.3.4.4)	2	1.07	0.24	-	-	-
1	(OE2005F) methylmalonyl-CoA mutase (EC 5.4.99.2) 2 (C-terminal homology)	1	1.07	-	-	-	-
1	(OE3085R) rtcB protein	1	1.05	-	-	-	-
1	(OE3207F) probable precorrin-8W decarboxylase (EC 1.-.-.-)	4	1.03	0.03	-	-	-
1	(OE2912F) probable fatty-acid--CoA ligase (EC 6.2.1.-)	5	1.02	0.10	-	-	-
1	(OE3082R) translation initiation factor aIF-2B chain alpha/delta eif2bd	1	1.02	-	-	-	-

1	(OE7093R) isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 1	2	1.00	0.23	-	-	-
1	(OE1259R) conserved protein	1	-1.01	-	-	-	-
1	(OE1936R) conserved protein	1	-1.03	-	-	-	-
1	(OE4234R) uracil phosphoribosyltransferase (EC 2.4.2.9) upp	5	-1.03	0.05	-	-	-
1	(OE4613F) aconitate hydratase (EC 4.2.1.3)	2	-1.05	0.95	-	-	-
1	(OE3071F) histidinol dehydrogenase (EC 1.1.1.23)	1	-1.09	-	-	-	-
1	(OE4195F) replication factor C small chain	1	-1.09	-	-	-	-
1	(OE1592R) mRNA 3'-end processing factor homolog	1	-1.10	-	-	-	-
1	(OE4025F) conserved protein	1	-1.11	-	-	-	-
1	(OE2120F) conserved protein	3	-1.11	0.29	-	-	-
1	(OE2627F) ribosomal protein S13	1	-1.14	-	-	-	-
1	(OE3152R) probable peptide chain release factor aRF1	1	-1.19	-	-	-	-
1	(OE1765R) probable proteasome regulatory chain (probable proteasome-activating nucleotidase PAN)	1	-1.26	-	-	-	-
1	(OE2530F) glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1	-1.32	-	-	-	-
1	(OE4571R) probable leucyl aminopeptidase (EC 3.4.11.1)	1	-1.34	-	-	-	-
1	(OE4673F) carboxypeptidase (EC 3.4.-.-)	1	-1.54	-	-	-	-
1	(OE2676R) conserved protein	1	-1.72	-	-	-	-
1	(OE2527F) conserved protein	1	-1.94	-	-	-	-
1	(OE3214F) precorrin-3B C17-methyltransferase (EC 2.1.1.131) 1	4	-2.21	0.03	-	-	-
1	(OE2360R) NADH oxidase homolog	3	-2.72	0.09	-	-	-
1	(OE3209F) probable precorrin-2 C20-methyltransferase (EC 2.1.1.130)	5	-2.73	0.05	-	-	-
1	(OE3547F) conserved protein	2	-3.28	0.06	-	-	-
1	(OE3394F) ribosomal protein L22	1	1.36	-	2	-	-
1	(OE3412F) ribosomal protein L32.eR	-	-	-	1	-	-
1	(OE2602R) ribosomal protein L1	1	1.30	-	1	-	-
1	(OE2632F) ribosomal protein L18.eR	1	-1.10	-	1	-	-
1	(OE3187R) conserved hypothetical protein	1	-2.02	-	1	-	-
1	(OE3402F) ribosomal protein L14	2	-2.01	0.15	2	-	-
1	(OE2628F) ribosomal protein S4	2	1.43	0.13	2	-	-
1	(OE3393F) ribosomal protein S19	3	1.42	0.13	2	-	-
1	(OE3817R) ribosomal protein S19.eR	1	-1.10	-	1	-	-
1	(OE1698R) probable oxidoreductase (EC 1.1.1.-) (aldehyde reductase homolog / alcohol dehydrogenase	2	-1.67	0.01	1	-	-
1	(OE4122R) thermosome alpha chain	5	2.06	0.33	5	2.85	0.27
1	(OE3925R) thermosome beta chain	8	2.20	0.58	7	2.53	0.30
1	(OE4114F) 2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component beta chain (the substrate is NOT pyruva	3	1.23	0.23	2	2.43	0.10

1	(OE3112R) AAA-type ATPase (transitional ATPase homolog)	3	3.64	0.92	5	2.08	0.34
1	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	7	1.54	0.39	7	1.92	0.10
1	(OE4323F) malate dehydrogenase (EC 1.1.1.37)	2	1.50	0.23	2	1.92	0.86
1	(OE5201F) aspartate carbamoyltransferase (EC 2.1.3.2) catalytic chain	3	-1.12	0.27	2	1.76	0.08
1	(OE1275F) proteasome alpha chain	6	1.49	0.55	4	1.74	0.07
1	(OE2623R) pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) alpha chain (pyruvate dehydrogenase (fer	4	1.44	0.09	3	1.72	0.42
1	(OE3931R) threonine dehydratase (EC 4.2.1.16)	1	1.22	-	1	1.65	-
1	(OE4306F) conserved protein	2	1.20	0.13	2	1.62	0.25
1	(OE1710R) oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3) beta chain (alpha-ketoglutarate--fer	2	1.32	0.29	2	1.58	0.11
1	(OE2296F) proteasome beta chain	1	1.64	-	1	1.56	-
1	(OE2622R) pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta chain (pyruvate dehydrogenase (ferr	2	1.59	0.04	1	1.56	-
1	(OE1729R) protein N-acetyltransferase homolog	-		-	1	1.54	-
1	(OE1154F) Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating) (EC 1.2.1.59)	5	1.07	0.15	1	1.40	-
1	(OE2635F) ribosomal protein S9	3	1.09	0.10	1	1.39	-
1	(OE2667F) nucleoside-diphosphate kinase (EC 2.7.4.6)	-		-	1	1.36	-
1	(OE4159F) adenosylhomocysteinase (EC 3.3.1.1)	15	1.12	0.13	13	1.33	0.47
1	(OE3168R) pyridoxal phosphate-dependent aminotransferase (acetylornithine transaminase homolog)	15	1.23	0.17	11	1.33	0.06
1	(OE3308F) malate dehydrogenase (oxaloacetate decarboxylating) (EC 1.1.1.40)	1	1.07	-	1	1.30	-
1	(OE2935R) fumarate hydratase (EC 4.2.1.2)	4	1.18	0.19	1	1.29	-
1	(OE2640F) phosphopyruvate hydratase (EC 4.2.1.11) (enolase)	5	1.26	0.35	5	1.29	0.14
1	(OE2458R) IMP dehydrogenase (EC 1.1.1.205)	3	1.05	0.36	3	1.21	0.13
1	(OE2358F) probable nonspecific lipid-transfer protein (sterol carrier protein)	2	1.19	0.07	1	1.19	-
1	(OE2648F) conserved protein	7	1.07	0.18	6	1.16	0.20
1	(OE3395F) ribosomal protein S3	9	1.24	0.24	8	1.16	0.28
1	(OE3415F) ribosomal protein S5	10	1.23	0.26	7	1.09	0.12
1	(OE4565F) conserved protein	4	1.06	0.05	2	1.08	0.13
1	(OE3571R) GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2), subunit B	4	1.00	0.22	4	1.07	0.29
1	(OE4196R) conserved protein	3	1.05	0.19	3	1.05	0.20

1	(OE2019F) fructose-bisphosphate aldolase (EC 4.1.2.13) 1	2	-1.03	0.01	3	1.05	0.04
1	(OE3874R) DNA-directed RNA polymerase (EC 2.7.7.6) chain E'	6	1.13	0.10	5	1.05	0.36
1	(OE4721R) translation elongation factor aEF-1 alpha chain	27	1.02	0.17	17	1.03	0.02
1	(OE1584R) conserved protein	9	2.31	0.39	7	1.01	0.03
1	(OE2013R) probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	2	1.61	0.04	1	1.01	-
1	(OE3363F) probable orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	2	1.16	0.07	2	-1.01	0.07
1	(OE5206R) carbamate kinase (EC 2.7.2.2)	2	-1.07	0.04	3	-1.01	0.16
1	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	17	1.09	0.32	5	-1.02	0.19
1	(OE2507R) histidinol-phosphate transaminase (EC 2.6.1.9)	1	1.15	-	1	-1.04	-
1	(OE2641F) ribosomal protein S2	1	1.02	-	1	-1.05	-
1	(OE5100R) trkA domain protein	1	1.01	-	1	-1.06	-
1	(OE3195F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta chain	1	1.13	-	1	-1.07	-
1	(OE5208R) arginine deiminase (EC 3.5.3.6)	7	1.06	0.15	6	-1.10	0.14
1	(OE3691F) probable anthranilate phosphoribosyltransferase (EC 2.4.2.18)	6	1.32	0.60	2	-1.10	0.14
1	(OE1412F) conserved protein	-		-	2	-1.11	0.12
1	(OE6008R) parA domain protein	1	1.36	-	2	-1.12	0.11
1	(OE4085R) ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	-		-	1	-1.16	-
1	(OE2451R) probable oxidoreductase	4	1.20	0.28	4	-1.17	0.46
1	(OE4007F) electron transfer flavoprotein alpha chain	2	1.03	0.27	2	-1.19	0.11
1	(OE3748R) probable archaeosine tRNA-ribosyltransferase (EC 2.4.2.-)	2	1.46	0.84	2	-1.19	0.07
1	(OE3710R) trkA domain protein	5	-1.09	0.05	2	-1.20	0.28
1	(OE2374R) purine-binding chemotaxis protein cheW2	2	1.13	0.09	2	-1.21	0.19
1	(OE4500R) probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	9	1.15	0.21	4	-1.25	0.29
1	(OE3063F) aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	1	1.13	-	1	-1.25	0.15
1	(OE2373F) probable phosphate acetyltransferase (EC 2.3.1.8)	10	1.05	0.16	7	-1.28	0.19
1	(OE2419R) purine-binding chemotaxis protein cheW1	1	1.03	-	1	-1.34	-
1	(OE3863R) 6-N-hydroxylaminopurine sensitivity-controlling protein	1	1.37	-	1	-1.34	-
1	(OE2110R) UDPglucose 4-epimerase (EC 5.1.3.2)	3	1.33	0.07	3	-1.43	0.16
1	(OE3807R) oligoendopeptidase	3	-1.02	0.29	1	-1.44	-
1	(OE2871F) probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.157)	7	1.22	0.24	5	-1.44	0.05

1	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	25	1.07	0.11	18	-1.57	0.39
1	(OE1432F) sarcosine oxidase (EC 1.5.3.1) beta chain	1	1.05	-	1	-1.73	-
1	(OE2128F) phoU protein homolog	4	-1.04	0.20	1	-1.75	-
1	(OE2450F) acetate--CoA ligase (EC 6.2.1.1)	3	-1.05	0.18	2	-1.78	0.04
1	(OE3524F) pyridoxine biosynthesis protein	19	-1.31	0.08	16	-1.82	0.08
1	(OE1414R) cell division protein ftsZ4	4	1.15	0.08	2	-1.83	0.05
1	(OE4651F) thiamine biosynthesis protein (thiazole biosynthetic enzyme)	3	1.26	0.20	3	-2.16	0.42
1	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	4	-1.12	0.19	4	-2.24	0.25
1	(OE3487R) translation initiation factor aIF-5A	4	1.03	0.14	4	-2.65	0.11
1	(OE1620R) phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) / phosphoribosylaminoimidazoleca	2	1.02	0.25	1	-2.93	-
1	(OE4729R) translation elongation factor aEF-2	3	1.02	0.15	2	-3.07	0.03
1	(OE2801R) conserved protein	1	-1.38	-	1	-3.29	-
1	(OE4540R) conserved protein	3	-1.22	0.02	3	-3.61	0.23
1	(OE4408F) phosphoglycerate dehydrogenase (EC 1.1.1.95)	2	1.26	0.01	1	-4.37	-
1	(OE4654F) phosphomethylpyrimidine kinase (EC 2.7.4.7)	2	1.07	0.11	1	-4.44	-
1	(OE3718F) cell division protein	1	1.26	-	1	-4.74	-
1	(OE2864F) phosphoribosylamine--glycine ligase (EC 6.3.4.13)	2	-1.49	0.00	1	-5.65	-
1	(OE1613R) probable acylaminoacyl-peptidase (EC 3.4.19.1)	-	-	-	1	-7.94	-
2	(OE2667F) nucleoside-diphosphate kinase (EC 2.7.4.6)	2	1.50	0.11	-	-	-
2	(OE3718F) cell division protein	1	1.43	-	-	-	-
2	(OE2015R) 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	1	1.39	-	-	-	-
2	(OE4720R) ribosomal protein S10	1	1.33	-	-	-	-
2	(OE1160R) ribosomal protein L10.eR	2	1.26	0.33	-	-	-
2	(OE4159F) adenosylhomocysteinase (EC 3.3.1.1)	1	1.25	-	-	-	-
2	(OE2865R) succinate dehydrogenase (EC 1.3.99.1) chain A (flavoprotein)	2	1.24	0.09	-	-	-
2	(OE8020F) conserved protein	1	1.22	-	-	-	-
2	(OE3571R) GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2), subunit B	1	1.20	-	-	-	-
2	(OE4644R) conserved protein	1	1.18	-	-	-	-
2	(OE3209F) probable precorrin-2 C20-methyltransferase (EC 2.1.1.130)	1	1.17	-	-	-	-
2	(OE1559R) cell division protein ftsZ1	2	1.13	0.15	-	-	-
2	(OE1792F) conserved protein	1	1.09	-	-	-	-
2	(OE3168R) pyridoxal phosphate-dependent aminotransferase (acetylornithine transaminase homolog)	1	1.06	-	-	-	-

2	(OE3268F) conserved protein	1	-1.04	-	-	-	-
2	(OE2629F) ribosomal protein S11	1	-1.05	-	-	-	-
2	(OE2450F) acetate--CoA ligase (EC 6.2.1.1)	1	-1.07	-	-	-	-
2	(OE4157F) probable chlorohydrolase	1	-1.19	-	-	-	-
2	(OE5160F) glycerol dehydrogenase (EC 1.1.1.6)	1	-1.26	-	-	-	-
2	(OE4234R) uracil phosphoribosyltransferase (EC 2.4.2.9) upp	3	-1.29	0.03	-	-	-
2	(OE2057F) thiamin biosynthesis protein thiC	2	-1.36	0.45	-	-	-
2	(OE1698R) probable oxidoreductase (EC 1.1.1.-) (aldehyde reductase homolog / alcohol dehydrogenase	1	-1.38	-	-	-	-
2	(OE4116F) dihydrolipoamide dehydrogenase (EC 1.8.1.4) (probable glycine cleavage system protein L a	1	-1.47	-	-	-	-
2	(OE4240F) conserved hypothetical protein	1	-1.49	-	-	-	-
2	(OE1220F) archaeal histone	2	-1.61	0.04	-	-	-
2	(OE2360R) NADH oxidase homolog	1	-1.71	-	-	-	-
2	(OE2197R) conserved protein	4	-1.73	0.08	-	-	-
2	(OE4712F) conserved protein	4	-1.76	0.08	-	-	-
2	(OE4544R) conserved hypothetical protein	1	-1.99	-	-	-	-
2	(OE3038F) methylenetetrahydrofolate dehydrogenase (NAD(P)+) (EC 1.5.1.5) / methenyltetrahydrofolate	1	-2.02	-	-	-	-
2	(OE4509F) nonhistone chromosomal protein	2	-2.26	0.11	-	-	-
2	(OE3547F) conserved protein	1	-2.42	-	-	-	-
2	(OE3195F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta chain	-	-	-	1	2.47	-
2	(OE2579F) adenylosuccinate synthase (EC 6.3.4.4)	1	1.01	-	1	2.07	-
2	(OE2640F) phosphopyruvate hydratase (EC 4.2.1.11) (enolase)	1	1.38	-	1	1.98	-
2	(OE3142R) SM protein	1	2.12	-	1	1.97	-
2	(OE1154F) Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating) (EC 1.2.1.59)	3	1.38	0.84	1	1.93	-
2	(OE3931R) threonine dehydratase (EC 4.2.1.16)	3	1.66	0.11	1	1.73	-
2	(OE2648F) conserved protein	1	1.43	-	2	1.65	0.23
2	(OE3925R) thermosome beta chain	16	1.56	0.54	14	1.61	0.54
2	(OE1270F) glutamate dehydrogenase (EC 1.4.1.2)	1	1.18	-	2	1.61	0.03
2	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	3	1.08	0.29	2	1.57	0.13
2	(OE5208R) arginine deiminase (EC 3.5.3.6)	1	1.14	-	3	1.55	0.36
2	(OE2935R) fumarate hydratase (EC 4.2.1.2)	-	-	-	4	1.49	0.44
2	(OE1672F) orotate phosphoribosyltransferase homolog	4	1.45	0.33	4	1.49	0.32
2	(OE2622R) pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta chain (pyruvate dehydrogenase (ferr	1	1.28	-	2	1.47	0.05

2	(OE4416R) conserved protein	2	1.13	0.04	1	1.45	-
2	(OE4500R) probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	1	-2.20	-	2	1.45	0.31
2	(OE3691F) probable anthranilate phosphoribosyltransferase (EC 2.4.2.18)	1	1.10	-	1	1.44	-
2	(OE3874R) DNA-directed RNA polymerase (EC 2.7.7.6) chain E'	2	1.22	0.14	1	1.44	-
2	(OE2019F) fructose-bisphosphate aldolase (EC 4.1.2.13) 1	2	-1.09	0.06	2	1.40	0.04
2	(OE5206R) carbamate kinase (EC 2.7.2.2)	12	1.21	0.31	11	1.40	0.32
2	(OE4122R) thermosome alpha chain	10	1.21	0.28	9	1.37	0.40
2	(OE4651F) thiamine biosynthesis protein (thiazole biosynthetic enzyme)	8	1.34	0.29	7	1.36	0.51
2	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	3	1.24	0.12	3	1.33	0.10
2	(OE1737R) dnaK-type molecular chaperone hsp70	9	1.04	0.34	3	1.31	0.32
2	(OE4146F) TATA-binding transcription initiation factor	10	1.18	0.08	5	1.28	0.23
2	(OE1903F) glycine-rich protein	4	1.19	0.17	4	1.28	0.05
2	(OE4007F) electron transfer flavoprotein alpha chain	5	1.06	0.10	6	1.28	0.32
2	(OE2641F) ribosomal protein S2	5	1.30	0.22	5	1.26	0.15
2	(OE4721R) translation elongation factor aEF-1 alpha chain	5	1.17	0.18	4	1.26	0.27
2	(OE6177F) conserved hypothetical protein	-	-	-	1	1.24	-
2	(OE4306F) conserved protein	7	1.14	0.11	5	1.23	0.17
2	(OE2374R) purine-binding chemotaxis protein cheW2	4	1.26	0.08	4	1.23	0.07
2	(OE1407F) inorganic pyrophosphatase (EC 3.6.1.1)	2	1.41	0.06	1	1.23	-
2	(OE1275F) proteasome alpha chain	7	1.12	0.06	5	1.23	0.21
2	(OE3196F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain	3	1.03	0.29	4	1.22	0.45
2	(OE2828R) conserved protein	3	1.28	0.69	2	1.20	0.20
2	(OE3425F) adenylate kinase (EC 2.7.4.3)	2	1.19	0.02	2	1.20	0.10
2	(OE2601R) ribosomal protein L10	3	1.05	0.16	2	1.20	0.01
2	(OE3207F) probable precorrin-8W decarboxylase (EC 1.-.-.-)	3	1.22	0.51	1	1.20	-
2	(OE2306F) conserved protein	1	1.12	-	1	1.19	-
2	(OE3219F) conserved cobalamin operon protein	1	-1.20	-	1	1.18	-
2	(OE3415F) ribosomal protein S5	5	1.21	0.07	4	1.17	0.05
2	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	8	1.14	0.48	8	1.17	0.28
2	(OE3394F) ribosomal protein L22	2	-1.04	0.30	1	1.17	-
2	(OE3524F) pyridoxine biosynthesis protein	11	1.15	0.18	10	1.16	0.18
2	(OE4114F) 2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component beta chain (the substrate is NOT pyruva	1	-1.39	-	1	1.16	-
2	(OE2515F) conserved protein	7	1.34	0.15	7	1.15	0.03

2	(OE8006F) conserved protein	1	1.19	-	1	1.14	-
2	(OE3988R) H+-transporting two-sector ATPase (EC 3.6.3.14) chain E.a (A-type ATP synthase) (previous	2	1.30	0.19	1	1.12	-
2	(OE3710R) trkA domain protein	3	1.14	0.10	2	1.12	0.11
2	(OE3395F) ribosomal protein S3	5	1.08	0.31	4	1.11	0.25
2	(OE4027F) conserved protein	-	-	-	1	1.11	-
2	(OE4613F) aconitate hydratase (EC 4.2.1.3)	1	1.46	-	2	1.11	0.44
2	(OE2097F) conserved protein	8	-1.16	0.18	8	1.08	0.10
2	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	4	1.09	0.23	4	1.07	0.22
2	(OE3673F) conserved protein	1	1.22	-	1	1.07	-
2	(OE2602R) ribosomal protein L1	5	1.17	0.08	5	1.07	0.35
2	(OE2633F) ribosomal protein L13	-	-	-	1	1.06	-
2	(OE3565F) molybdenum cofactor biosynthesis protein B	1	1.10	-	1	1.05	-
2	(OE2373F) probable phosphate acetyltransferase (EC 2.3.1.8)	2	1.21	0.24	2	1.04	0.12
2	(OE3884F) acetyl-CoA C-ac(et)yltransferase (EC 2.3.1.16) or (EC 2.3.1.9)	1	1.08	-	1	1.04	-
2	(OE1584R) conserved protein	19	1.07	0.17	15	1.03	0.10
2	(OE3412F) ribosomal protein L32.eR	5	1.10	0.13	4	-1.02	0.14
2	(OE5201F) aspartate carbamoyltransferase (EC 2.1.3.2) catalytic chain	1	-1.03	-	1	-1.04	-
2	(OE3404F) ribosomal protein L24	-	-	-	2	-1.04	0.06
2	(OE2159R) ribosomal protein S3a.eR	2	1.15	0.25	1	-1.04	-
2	(OE1442R) conserved hypothetical protein	1	1.23	-	1	-1.05	-
2	(OE3487R) translation initiation factor aIF-5A	16	1.03	0.19	17	-1.05	0.18
2	(OE3407F) ribosomal protein L5	-	-	-	1	-1.05	-
2	(OE1371R) prefoldin beta chain	2	1.22	0.59	1	-1.06	-
2	(OE4626R) probable translation initiation factor SUI1	1	1.42	-	3	-1.08	0.16
2	(OE2635F) ribosomal protein S9	7	1.13	0.04	5	-1.08	0.07
2	(OE2809R) translation initiation factor aIF-2 beta chain	5	1.83	1.34	4	-1.10	0.23
2	(OE1405R) conserved protein	5	1.34	0.14	3	-1.12	0.28
2	(OE3869R) ribosomal protein S24.eR	6	1.26	0.23	4	-1.14	0.22
2	(OE2632F) ribosomal protein L18.eR	1	1.17	-	2	-1.14	0.02
2	(OE3357R) ribosomal protein S8.eR	1	1.16	-	2	-1.17	0.15
2	(OE4736R) ribosomal protein S12	1	1.10	-	3	-1.17	0.05
2	(OE4459R) ribosomal protein L31.eR	5	1.00	0.27	5	-1.17	0.04
2	(OE3389F) ribosomal protein L4.eR	4	1.19	0.09	3	-1.18	0.21
2	(OE3410F) ribosomal protein S8	8	1.28	0.24	7	-1.20	0.26
2	(OE2628F) ribosomal protein S4	1	1.14	-	1	-1.21	-
2	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	26	1.03	0.30	10	-1.21	0.17
2	(OE2458R) IMP dehydrogenase (EC 1.1.1.205)	1	1.43	-	1	-1.21	-
2	(OE1557R) transcription antitermination protein homolog	1	1.36	-	1	-1.22	-

2	(OE3416F) ribosomal protein L30	-	-	-	1	-1.22	-
2	(OE2165R) ribosomal protein S15	16	1.33	0.38	8	-1.25	0.18
2	(OE2627F) ribosomal protein S13	4	1.31	0.34	4	-1.26	0.16
2	(OE2662F) ribosomal protein L7a.eR/HS6 (isolated from the small ribosomal subunit)	2	1.15	0.08	2	-1.27	0.05
2	(OE3402F) ribosomal protein L14	2	1.19	0.22	1	-1.28	-
2	(OE2664F) ribosomal protein S28.eR	2	1.00	0.31	1	-1.35	-
2	(OE1818R) translation initiation factor aIF-2 alpha chain	-	-	-	1	-1.36	-
2	(OE3798R) conserved hypothetical protein	1	1.26	-	1	-1.37	-
2	(OE5162D1F) conserved protein	1	-1.18	-	1	-1.41	-
2	(OE4735R) ribosomal protein S7	4	1.24	0.09	2	-1.45	0.08
2	(OE3393F) ribosomal protein S19	3	1.10	0.15	2	-1.46	0.00
2	(OE3400F) ribosomal protein S17	1	1.11	-	2	-1.47	0.06
2	(OE3817R) ribosomal protein S19.eR	7	1.08	0.30	5	-1.54	0.18
2	(OE4532F) ribosomal protein S6.eR	2	1.15	0.03	2	-1.64	0.00
2	(OE4540R) conserved protein	2	-1.33	0.06	1	-2.29	-
2	(OE3346R) conserved protein	-	-	-	1	-2.99	-

Supplemental Table D2. Proteomic analyses on cells, grown in complex medium. Target numbers (T), Target Spots (Spot), ID numbers and protein names, initial sequences of peptides quantified (Peptide Seq), label modification status (M) with C = heavy2 (2h heat shock) and d = heavy1 (1h heat shock) label, as well as regulation factors (Reg.) are indicated. Data are from proteins separated on different 2-D gels spanning different pH ranges, and subsequently spotted on different targets. Two independent approaches have been performed with proteins spotted on targets 1-3 (upper table) and targets 4-7 (lower table), respectively. Manual validation of MS spectra has not been implicated in the results given.

T.	Spot	ID and Protein Name	Peptide Seq	M	Reg
1	B2	OE3112R AAA-type ATPase transitional ATPase homolog	DKPLADDVDL	d	4,40
1	D4	OE5243F transducer protein car	APTGDVVGS	C	3,96
1	B2	OE3112R AAA-type ATPase transitional ATPase homolog	KEILQVHTR	d	3,90
2	F2	OE3925R thermosome beta chain	EEVDNVAVDV	d	3,36
1	A2	OE4122R thermosome alpha chain	TSGEDAQSM	d	3,32
2	G9	OE1584R conserved protein	ASERDDLNAK	d	3,21
2	E1	OE4122R thermosome alpha chain	AKSDDFTR	C	3,15
2	E3	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	LNDDGNSVKA	d	3,13
2	F20	OE5201F aspartate carbamoyltransferase EC 2.1.3.2 catalytic chain	ENAGLEDLTIG	d	3,07
1	A2	OE4122R thermosome alpha chain	AKSDDFTR	C	3,06
1	A4	OE3925R thermosome beta chain	DIHPTAIIKGY	C	3,04
1	B2	OE3112R AAA-type ATPase transitional ATPase homolog	EVFEKAR	d	3,01
2	F2	OE3925R thermosome beta chain	VKDRDAQEH	C	3,01

2	F2	OE3925R thermosome beta chain	EEVDNVAVDV	C	2,99
1	C3	OE3925R thermosome beta chain	VKDRDAQEH	d	2,98
1	B3	OE3925R thermosome beta chain	DIHPTAIIKGY	C	2,95
1	A1	OE4122R thermosome alpha chain	AKSDDFTR	C	2,93
1	B3	OE3925R thermosome beta chain	DIHPTAIIKGY	d	2,92
2	G9	OE1584R conserved protein	EKVDEAQEH	d	2,92
1	C3	OE3925R thermosome beta chain	DIHPTAIIKGY	d	2,89
2	F2	OE3925R thermosome beta chain	DIHPTAIIKGY	d	2,88
2	F2	OE3925R thermosome beta chain	VKDRDAQEH	d	2,88
2	E2	OE3925R thermosome beta chain	DIHPTAIIKGY	C	2,86
1	B2	OE3112R AAA-type ATPase transitional ATPase homolog	KEILQVHTR	C	2,81
1	C3	OE3925R thermosome beta chain	DIHPTAIIKGY	C	2,81
2	F2	OE3925R thermosome beta chain	DIHPTAIIKGY	C	2,81
2	B20	OE4122R thermosome alpha chain	AKSDDFTR	C	2,80
2	G9	OE1584R conserved protein	VQEHKEIR	d	2,79
2	F16	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	2,78
1	C3	OE3925R thermosome beta chain	VKDRDAQEH	C	2,74
1	G16	OE3411F ribosomal protein L6	VTDKDTR	d	2,66
2	H2	OE3112R AAA-type ATPase transitional ATPase homolog	KEILQVHTR	d	2,61
1	H17	OE1275F proteasome alpha chain	SPLLEGSSVE	d	2,59
1	B4	OE3925R thermosome beta chain	DIHPTAIIKGY	C	2,55
2	H2	OE3112R AAA-type ATPase transitional ATPase homolog	EVFEKAR	d	2,54
3	A3	OE3925R thermosome beta chain	VKDRDAQEH	C	2,52
1	B3	OE3925R thermosome beta chain	VKDRDAQEH	d	2,50
1	B3	OE3925R thermosome beta chain	VKDRDAQEH	C	2,47
2	E2	OE3925R thermosome beta chain	VKDRDAQEH	C	2,46
1	A4	OE3925R thermosome beta chain	VKDRDAQEH	C	2,45
1	A12	OE1584R conserved protein	KLQKSGHL	d	2,45
1	A2	OE4122R thermosome alpha chain	AKSDDFTR	d	2,44
1	B3	OE3925R thermosome beta chain	EEVDNVAVDV	d	2,43
3	A3	OE3925R thermosome beta chain	DIHPTAIIKGY	d	2,42
2	G9	OE1584R conserved protein	KLQKSGHL	d	2,41
1	B4	OE3925R thermosome beta chain	DIHPTAIIKGY	d	2,40
2	B15	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	d	2,39
1	C3	OE3925R thermosome beta chain	EEVDNVAVDV	d	2,39
1	A4	OE3925R thermosome beta chain	DIHPTAIIKGY	d	2,38
3	A3	OE3925R thermosome beta chain	VKDRDAQEH	d	2,38
2	F16	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	2,35
2	F10	OE1584R conserved protein	EKVDEAQEH	d	2,34
2	E2	OE3925R thermosome beta chain	DIHPTAIIKGY	d	2,32
1	D3	OE4122R thermosome alpha chain	AKSDDFTR	C	2,30
1	C3	OE3925R thermosome beta chain	EEVDNVAVDV	C	2,26
2	G9	OE1584R conserved protein	FKEGETLDTE	d	2,24
2	E1	OE4122R thermosome alpha chain	AKSDDFTR	d	2,24
2	D19	OE1687F aspartate--tRNA ligase EC 6.1.1.12	KPSTKAVFSL	d	2,23
1	A2	OE4122R thermosome alpha chain	RAKSDDFTR	C	2,21
3	A3	OE3925R thermosome beta chain	EEVDNVAVDV	d	2,20
1	A1	OE4122R thermosome alpha chain	AKSDDFTR	d	2,17
1	B2	OE3112R AAA-type ATPase transitional ATPase homolog	DKPLADDVDL	C	2,16

2	E2	OE3925R thermosome beta chain	EEVDNVAVDV	C	2,14
2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	IENVVAKYGD	d	2,13
1	B4	OE3925R thermosome beta chain	EEVDNVAVDV	d	2,09
1	E3	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	2,08
1	B2	OE3112R AAA-type ATPase transitional ATPase homolog	EVFEKAR	C	2,06
2	E12	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GFLVETDRDG	d	2,06
2	A14	OE5201F aspartate carbamoyltransferase EC 2.1.3.2 catalytic chain	LGGDIVDMGS	C	2,04
1	B4	OE3925R thermosome beta chain	VKDRDAQEH	C	2,04
1	B4	OE3925R thermosome beta chain	EEVDNVAVDV	C	2,02
1	A4	OE3925R thermosome beta chain	EEVDNVAVDV	C	2,02
2	C19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	CLAEPVHGSA	d	2,01
1	A12	OE1584R conserved protein	FKEGETLDTE	d	2,00
1	B3	OE3925R thermosome beta chain	EEVDNVAVDV	C	1,99
1	E2	OE2013R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	EVANEGIQIHG	d	1,99
2	F15	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	1,98
1	A4	OE3925R thermosome beta chain	VKDRDAQEH	d	1,97
1	A4	OE3925R thermosome beta chain	EEVDNVAVDV	d	1,94
2	H15	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	1,92
1	C2	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	LNDDGNSVKA	d	1,92
1	F19	OE1275F proteasome alpha chain	TPEGVVLVVD	C	1,91
2	E2	OE3925R thermosome beta chain	EEVDNVAVDV	d	1,88
2	G12	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	SFDVIDRHK	C	1,88
2	F10	OE1584R conserved protein	KLQKSGHL	C	1,87
1	E4	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	1,86
2	E2	OE3925R thermosome beta chain	VKDRDAQEH	d	1,85
2	D15	OE1270F glutamate dehydrogenase EC 1.4.1.2	GPYKGGLR	d	1,84
2	H18	OE1710R oxoglutarate--ferredoxin oxidoreductase EC 1.2.7.3 beta chain	IYGLTKGQAS	C	1,84
1	A12	OE1584R conserved protein	EKVDEAQEH	d	1,83
1	A12	OE1584R conserved protein	VQEHKEIR	d	1,83
2	D17	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	C	1,82
2	G16	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	1,82
1	B4	OE3925R thermosome beta chain	VKDRDAQEH	d	1,82
2	B20	OE4122R thermosome alpha chain	AKSDDFTR	d	1,81
2	H14	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TDTLLVTSTN	d	1,80
3	C14	OE2451R probable oxidoreductase	DDGLTGESKA	d	1,79
2	H2	OE3112R AAA-type ATPase transitional ATPase homolog	EVFEKAR	C	1,78
3	A3	OE3925R thermosome beta chain	EEVDNVAVDV	C	1,76
1	H4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,76
3	A20	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	GLAKEHGR	C	1,75
1	F7	OE4306F conserved protein	AFSAVPVVKA	C	1,75
1	A22	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	GNKTVEAEVT	d	1,74
1	A10	OE3195F succinate--CoA ligase ADP-forming EC 6.2.1.5 beta chain	GDEVAKGINS	d	1,73
2	G15	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	1,73

3	C9	OE1275F proteasome alpha chain	TPEGVVLVVD	C	1,73
1	C2	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	GLAKEHGR	C	1,72
2	E18	OE4323F malate dehydrogenase EC 1.1.1.37	FDVPVQNVDA	d	1,72
3	D6	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	SKLALTDDDH	d	1,71
2	E3	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	GLAKEHGR	C	1,70
1	F3	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	1,69
2	E3	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	NPSEEAVYGD	d	1,68
3	D13	OE3395F ribosomal protein S3	KITTQLEER	d	1,68
1	H17	OE1275F proteasome alpha chain	TPEGVVLVVD	C	1,67
2	B22	OE1275F proteasome alpha chain	TPEGVVLVVD	C	1,66
1	G5	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	YYQDEQRPS	d	1,66
2	G12	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	YYQDEQRPS	d	1,66
2	G2	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	AKEIIFTADR	d	1,66
1	H19	OE2296F proteasome beta chain	VISNKNVQKV	d	1,64
2	E3	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	VAFGPKDPKE	C	1,64
1	C10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	1,64
1	E2	OE2013R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	DAKLNEIYEG	d	1,64
1	F1	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	HTAAPDADPV	d	1,63
1	D3	OE4122R thermosome alpha chain	AKSDDFTR	d	1,63
1	B22	OE4420R argininosuccinate synthase EC 6.3.4.5	LANAAFDGNK	d	1,63
1	E4	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,62
2	G1	OE4613F aconitate hydratase EC 4.2.1.3	TLAAGGKLSL	d	1,62
3	B15	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	SFDVIDRHK	d	1,61
1	B1	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	d	1,61
2	D19	OE1687F aspartate--tRNA ligase EC 6.1.1.12	KFDLLYR	d	1,60
1	H21	OE4655R conserved protein	KLTGFANEMA	d	1,60
1	E2	OE2013R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GESFIKEAAQ	d	1,59
2	H2	OE3112R AAA-type ATPase transitional ATPase homolog	KEILQVHTR	C	1,58
2	G9	OE1584R conserved protein	EKRDELNER	d	1,58
2	D4	OE2165R ribosomal protein S15	GDKLDEEFAY	C	1,58
3	A22	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	GDMPEEPVA	C	1,57
1	H19	OE2296F proteasome beta chain	VISNKNVQKV	C	1,56
3	B15	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	SFDVIDRHK	C	1,56
2	G12	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	SFDVIDRHK	d	1,56
3	A2	OE6008R parA domain protein	AGLKPLVVPL	d	1,55
2	A8	OE3410F ribosomal protein S8	GYIDGFEFVD	C	1,55
2	G4	OE1687F aspartate--tRNA ligase EC 6.1.1.12	EILADEYDHV	d	1,54
2	C8	OE3393F ribosomal protein S19	SSKFVPLK	d	1,54
1	C2	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	VAFGPKDPKE	d	1,54

1	C2	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	LNDDGNSVKA	C	1,53
2	D20	OE3063F aspartate-semialdehyde dehydrogenase EC 1.2.1.11	KLLGEFTGAE	d	1,53
2	D17	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	1,53
3	D19	OE4391F probable serine--pyruvate aminotransferase EC 2.6.1.51	KAESNQTPFT	d	1,53
3	A19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	CLAEPVHGSA	d	1,53
2	H18	OE1710R oxoglutarate--ferredoxin oxidoreductase EC 1.2.7.3 beta chain	IYGLTKGQAS	d	1,52
3	B18	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	C	1,52
1	D11	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	C	1,52
1	B20	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LPGVEGMKG	d	1,51
1	F4	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,51
1	F19	OE1275F proteasome alpha chain	TPEGVVLVVD	d	1,51
2	G15	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	C	1,51
2	B19	OE3308F malate dehydrogenase oxaloacetate decarboxylating EC 1.1	IALGEGGDEK	C	1,50
1	C11	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,50
2	H17	OE4306F conserved protein	AFSAVPVVKA	C	1,50
1	G21	OE2159R ribosomal protein S3a.eR	SVSKQDQEK	d	1,49
2	E20	OE5201F aspartate carbamoyltransferase EC 2.1.3.2 catalytic chain	LGGDIVDMGS	C	1,49
1	C2	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	GLAKEHGR	d	1,49
2	D18	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	1,48
1	B11	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,48
1	E17	OE3717F NADH dehydrogenase ubiquinone EC 1.6.5.3 32K chain	SLKLDNTTSA	d	1,48
1	A12	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,48
1	C13	OE2648F conserved protein	VSSLVEFAKE	d	1,47
1	H3	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,47
3	D13	OE3395F ribosomal protein S3	VEKFNR	d	1,47
2	A8	OE3410F ribosomal protein S8	YSVGADGFEQ	d	1,47
1	D7	OE2458R IMP dehydrogenase EC 1.1.1.205	EIKASVDADV	C	1,47
2	A5	OE2165R ribosomal protein S15	NLLEKAVR	d	1,47
1	D20	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	GNKTVEAEVT	d	1,47
2	F6	OE2458R IMP dehydrogenase EC 1.1.1.205	EIKASVDADV	d	1,46
1	A7	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,46
1	G5	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	GDMPEEPVA	d	1,46
2	B13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,46
1	G7	OE5201F aspartate carbamoyltransferase EC 2.1.3.2 catalytic chain	LGGDIVDMGS	C	1,46
1	F3	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,46
1	E1	OE2358F probable nonspecific lipid-transfer protein sterol carrier protein	KEVDLETVLD	d	1,46
2	B4	OE2667F nucleoside-diphosphate kinase EC 2.7.4.6	TFVMVKPDGV	C	1,45
1	B6	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	C	1,45
3	B2	OE3415F ribosomal protein S5	DDQVGGAIQK	C	1,45
2	G7	OE2579F adenylosuccinate synthase EC 6.3.4.4	GIGPTYEDKIG	C	1,45
1	D1	OE3356F AAA-type ATPase transitional ATPase homolog	EQILKIHTQDT	d	1,45

2	H6	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	C	1,45
2	F7	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,45
2	A22	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	d	1,44
1	E3	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,44
2	C7	OE2632F ribosomal protein L18.eR	YASEDETVIV	d	1,44
1	A22	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	GNKTVEAEVT	C	1,44
1	G6	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain p	YYQDEQRPS	d	1,43
1	C2	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	NPSEEAVYGD	d	1,43
2	G5	OE2935R fumarate hydratase EC 4.2.1.2	TVAGSLNKIA	C	1,43
2	D21	OE1816R 3-isopropylmalate dehydratase homolog	SEEPAGGIVG	d	1,43
1	C8	OE2935R fumarate hydratase EC 4.2.1.2	TVAGSLNKIA	d	1,43
1	F16	OE2019F fructose-bisphosphate aldolase EC 4.1.2.13 1	GQGLKNDKN	d	1,42
1	G8	OE2451R probable oxidoreductase	DDGLTGESKA	d	1,42
3	B18	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,42
2	G1	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	d	1,42
2	D16	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,42
1	H23	OE3415F ribosomal protein S5	TTVNFAKATF	d	1,42
2	C8	OE3393F ribosomal protein S19	GLSEEHHKVL	d	1,42
2	D13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,42
1	E11	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	LSIEKLAALGW	d	1,41
1	D20	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	GNKTVEAEVT	C	1,41
1	B11	OE2579F adenylosuccinate synthase EC 6.3.4.4	ELDGAEEAAK	d	1,41
1	C8	OE2935R fumarate hydratase EC 4.2.1.2	TVAGSLNKIA	C	1,41
1	F5	OE1154F Glyceraldehyde-3-phosphate dehydrogenase NADP	EQYGIEKVR	C	1,41
1	D11	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,41
1	D20	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	TAKLNELIR	C	1,41
2	H15	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,41
2	E3	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	GLAKEHGR	d	1,40
2	G4	OE1687F aspartate--tRNA ligase EC 6.1.1.12	EILADEYDHV	C	1,40
2	F24	OE2159R ribosomal protein S3a.eR	IQPVAYTTKQ	d	1,40
2	B15	OE3395F ribosomal protein S3	KAGHTTIDR	C	1,40
1	F6	OE1154F Glyceraldehyde-3-phosphate dehydrogenase NADP	EQYGIEKVR	C	1,40
2	B24	OE2635F ribosomal protein S9	YQKSYR	C	1,39
3	A2	OE6008R parA domain protein	SLVIPVEPSAK	d	1,39
2	C18	OE5160F glycerol dehydrogenase EC 1.1.1.6	AGHKLAELCY	d	1,39
1	G6	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	GDMPEEPVA	d	1,39
1	C19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	d	1,39
2	D17	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	C	1,39
3	C2	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolo	ENPKGVIVTE	d	1,38
2	G2	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	LKHIVGEGR	d	1,38
2	E15	OE1414R cell division protein ftsZ4	VKGHGVGAD	d	1,38
2	H11	OE2451R probable oxidoreductase	DDGLTGESKA	d	1,38
1	B20	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	d	1,38

3	D13	OE3395F ribosomal protein S3	KAGHTTIDR	d	1,37
2	D1	OE3863R 6-N-hydroxylaminopurine sensitivity-controlling protein	KNALSHR	d	1,37
1	E15	OE3065R probable dehydrogenase EC 1.-.-.- D-3-phosphoglycerate	YTPSKGGPTD	d	1,37
2	C3	OE3487R translation initiation factor aIF-5A	SLSQPVDAKI	d	1,37
2	D16	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,37
2	G12	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	YYQDEQRPS	C	1,37
3	B20	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	d	1,37
2	F7	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,37
1	H24	OE4360R probable methyltransferase EC 2.1.1.- 24-sterol C-methyltransferase	DKGMEDR	C	1,37
1	D11	OE3296F hydroxymethylglutaryl-CoA synthase EC 4.1.3.5	KGLEPADVGR	d	1,37
2	G8	OE2579F adenylosuccinate synthase EC 6.3.4.4	ELDGAEEAAK	d	1,36
1	C12	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	C	1,36
2	D2	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	SKLALTDDDH	d	1,36
2	G24	OE2667F nucleoside-diphosphate kinase EC 2.7.4.6	TFVMVKPDGV	C	1,36
2	G12	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	GDMPEEPVA	d	1,36
1	A1	OE4122R thermosome alpha chain	ATGATPVSNV	d	1,36
1	F17	OE6008R parA domain protein	SLVIPVEPSAK	d	1,36
2	D5	OE3394F ribosomal protein L22	SVPFKQHNSG	d	1,36
1	C16	OE4391F probable serine--pyruvate aminotransferase EC 2.6.1.51	KAESNQTPFT	d	1,35
1	A10	OE3195F succinate--CoA ligase ADP-forming EC 6.2.1.5 beta chain	DVVAADAVM	d	1,35
2	D12	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	GTVVPDFIQK	d	1,35
1	G5	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	YYQDEQRPS	C	1,35
2	G2	OE4613F aconitate hydratase EC 4.2.1.3	TLAAGGKLSL	d	1,35
1	B6	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	d	1,35
2	E3	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	VAFGPKDPKE	d	1,34
2	A13	OE3395F ribosomal protein S3	KAGHTTIDR	d	1,34
2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,34
2	C19	OE1592R mRNA 3'-end processing factor homolog	DPKQFAQDG	d	1,34
3	B17	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,34
1	G21	OE2159R ribosomal protein S3a.eR	IQPVAYTTKQ	d	1,33
2	A13	OE3395F ribosomal protein S3	KAGHTTIDR	C	1,33
2	E7	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	C	1,33
2	E7	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	d	1,33
3	A13	OE3065R probable dehydrogenase EC 1.-.-.- D-3-phosphoglycerate	YTPSKGGPTD	d	1,33
2	H13	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	HTAAPDADPV	d	1,33
1	F10	OE1710R oxoglutarate--ferredoxin oxidoreductase EC 1.2.7.3 beta chain	IYGLTKGQAS	C	1,33
2	H14	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TKDAAVITGG	d	1,33
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,32
1	H4	OE3571R GMP synthase glutamine-hydrolyzing EC 6.3.5.2, subunit B	ATGVKGDNR	d	1,32

3	A16	OE3571R GMP synthase glutamine-hydrolyzing EC 6.3.5.2, subunit B	VIGEVTPEKV	d	1,32
1	F1	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	ILDLKPDQTTL	d	1,32
2	H16	OE3718F cell division protein	KSGESVQGG	d	1,32
1	C6	OE1260R probable oxidoreductase mercuryII reductase homolog	DASSDGVFKT	d	1,32
2	F3	OE2133R aldehyde dehydrogenase EC 1.2.1.- retinal dehydrogenase	LIVHEDLYDE	d	1,32
1	D15	OE4391F probable serine--pyruvate aminotransferase EC 2.6.1.51	KAESNQTPFT	d	1,31
2	G2	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	d	1,31
1	B12	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,31
2	D20	OE3063F aspartate-semialdehyde dehydrogenase EC 1.2.1.11	KMETESR	d	1,31
1	H23	OE3415F ribosomal protein S5	TTVNFAKATF	C	1,31
2	H12	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,31
2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,31
2	F3	OE4115F dihydrolipoamide S-acyltransferase EC 2.3.1.- probable E2 c	EKTLAAPATR	d	1,31
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,30
2	E9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	C	1,30
1	D11	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	1,30
2	F21	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	GTVVPDFIQK	d	1,30
1	H3	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,30
2	F10	OE1584R conserved protein	KLQKSGHL	d	1,30
1	C12	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,30
2	D3	OE2627F ribosomal protein S13	IGGQTDLDGTK	d	1,30
1	F7	OE4306F conserved protein	AFSAVPVVKA	d	1,30
2	B19	OE3308F malate dehydrogenase oxaloacetate decarboxylating	IVINKAKSEQQ	C	1,30
1	A2	OE4122R thermosome alpha chain	ATGATPVSNV	d	1,30
3	C7	OE3415F ribosomal protein S5	TTVNFAKATF	d	1,29
2	F11	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	d	1,29
2	G5	OE2935R fumarate hydratase EC 4.2.1.2	TQVEKGIDR	C	1,29
2	F9	OE4721R translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	d	1,29
3	A7	OE3393F ribosomal protein S19	GLSEEHHKVL	d	1,29
2	A20	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	d	1,29
1	E11	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	GTVVPDFIQK	d	1,28
2	E7	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	C	1,28
3	B2	OE3415F ribosomal protein S5	TTVNFAKATF	d	1,28
2	H13	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	ILDLKPDQTTL	d	1,28
1	D12	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	C	1,28
3	D10	OE6008R parA domain protein	SLVIPVEPSAK	d	1,28
3	B15	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	YYQDEQRPS	C	1,27
3	D13	OE3395F ribosomal protein S3	KITTQLEER	C	1,27
2	F9	OE4721R translation elongation factor aEF-1 alpha chain	DFVKNMITGA	d	1,27
1	H4	OE3571R GMP synthase glutamine-hydrolyzing EC 6.3.5.2, subunit B	VIGEVTPEKV	d	1,27

2	G7	OE2579F adenylosuccinate synthase EC 6.3.4.4	GIGPTYEDKIG	d	1,27
2	D17	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	d	1,27
2	B17	OE3807R oligoendopeptidase	DVKLAEAR	d	1,27
2	D18	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	d	1,27
2	A2	OE3415F ribosomal protein S5	DDQVGGAIQK	d	1,27
2	B1	OE4735R ribosomal protein S7	LKYGGISVPQ	d	1,27
1	C7	OE4408F phosphoglycerate dehydrogenase EC 1.1.1.95	GIAVTETKNH	d	1,27
1	C4	OE3925R thermosome beta chain	VKDRDAQEH	d	1,27
2	A17	OE4268F glutamate-1-semialdehyde 2,1-aminomutase EC 5.4.3.8	HAACPKTGAD	d	1,27
2	G2	OE4613F aconitate hydratase EC 4.2.1.3	IHKANLFNFG	d	1,27
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,26
3	C5	OE2627F ribosomal protein S13	IGQTDLDGTK	C	1,26
2	H16	OE3718F cell division protein	ALLVTAGPPK	d	1,26
3	A19	OE5208R arginine deiminase EC 3.5.3.6	THGGEKPYTL	d	1,26
2	D17	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	C	1,26
2	D18	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,26
3	B16	OE4196R conserved protein	SHGHLNPKR	d	1,26
1	F6	OE1154F Glyceraldehyde-3-phosphate dehydrogenase	EQYGIEKVR	d	1,26
2	E5	OE4408F phosphoglycerate dehydrogenase EC 1.1.1.95	GIAVTETKNH	d	1,26
2	D17	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,25
1	C4	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	d	1,25
1	H1	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TDTLLVTSTN	d	1,25
2	B15	OE3395F ribosomal protein S3	VEKFNR	d	1,25
1	D7	OE2458R IMP dehydrogenase EC 1.1.1.205	FSEKLR	C	1,25
1	B1	OE4613F aconitate hydratase EC 4.2.1.3	IHKANLFNFG	d	1,25
1	H16	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	LKDTIEVPPEY	d	1,24
2	G7	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,24
1	G3	OE1414R cell division protein ftsZ4	KGVEKAR	d	1,24
2	A2	OE3415F ribosomal protein S5	TTVNFAKATF	d	1,24
2	F8	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	C	1,24
2	F10	OE1584R conserved protein	EKVDEAQEH	C	1,24
2	G4	OE1687F aspartate--tRNA ligase EC 6.1.1.12	KFDLLYR	d	1,24
1	E2	OE2013R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LLGEEGDGFK	d	1,24
1	E1	OE2358F probable nonspecific lipid-transfer protein sterol carrier protein	ESLGKVAVKN	d	1,24
2	H6	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,24
3	C2	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	d	1,24
3	D13	OE3395F ribosomal protein S3	KAGHTTIDR	C	1,24
1	C11	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,24
3	C9	OE1275F proteasome alpha chain	TPEGVVLVVD	d	1,23
2	H21	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	IVTKSIDER	d	1,23
1	A17	OE4565F conserved protein	GKLSGTKAVY	C	1,23
3	D7	OE3415F ribosomal protein S5	TTVNFAKATF	d	1,23
2	G15	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,23
2	G15	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,23
1	D11	OE3168R pyridoxal phosphate-dependent aminotransferase acetylorn	EAVVNACVKR	d	1,23

2	C19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	d	1,23
2	E12	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	d	1,22
1	C2	OE2623R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 alpha chain	NPSEEAVYGD	C	1,22
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	KDSPGFVVNR	d	1,22
2	E10	OE4721R translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	d	1,22
2	B22	OE1275F proteasome alpha chain	TPEGVVLVVD	d	1,21
2	G6	OE2524R UDPglucose 6-dehydrogenase EC 1.1.1.22	VAVLGLSFKP	d	1,21
1	B11	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,21
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,21
2	G5	OE2935R fumarate hydratase EC 4.2.1.2	ALGVVKKAAA	d	1,21
2	E12	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GDLRPQHVS	d	1,21
1	A13	OE4688F conserved protein	KGTYLNVCTP	d	1,21
1	D5	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	d	1,21
1	C13	OE2648F conserved protein	VSSLVEFAKE	d	1,21
2	B3	OE2667F nucleoside-diphosphate kinase EC 2.7.4.6	TFVMVKPDGV	C	1,20
1	D18	OE1270F glutamate dehydrogenase EC 1.4.1.2	GPYKGGLR	d	1,20
1	C19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	C	1,20
2	G16	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	1,20
3	C9	OE1275F proteasome alpha chain	SPLLEGSSVE	d	1,20
2	G11	OE3524F pyridoxine biosynthesis protein	MADPASLTGI	d	1,20
1	D10	OE4721R translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	d	1,20
1	D20	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	TAKLNELIR	d	1,20
2	E6	OE2912F probable fatty-acid--CoA ligase EC 6.2.1.-	RVGSIGKPLA	d	1,19
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,19
1	E14	OE4102R tRNA-intron endonuclease EC 3.1.27.9	DGVVKHR	d	1,19
1	A8	OE2524R UDPglucose 6-dehydrogenase EC 1.1.1.22	VAVLGLSFKP	d	1,19
1	F5	OE3934R citrate si-synthase EC 2.3.3.1 formerly EC 4.1.3.7	ITAKLPTIVAA	d	1,19
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,19
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,19
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,19
1	B19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	d	1,19
1	D24	OE3718F cell division protein	KSGESVQGG	d	1,19
1	C9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,19
1	E1	OE2358F probable nonspecific lipid-transfer protein sterol carrier prote	KYLAQYDAPR	C	1,19
2	F10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,19
2	B24	OE2635F ribosomal protein S9	ESKKWGGPG	d	1,19
2	B15	OE3395F ribosomal protein S3	KITTQLEER	d	1,19
2	G2	OE4613F aconitate hydratase EC 4.2.1.3	IHKANLFNFG	C	1,18
2	C2	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KADRLETTR	d	1,18
2	B13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,18
1	E5	OE4007F electron transfer flavoprotein alpha chain	EMYGSKVETT	d	1,18

2	C18	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	1,18
2	D14	OE2451R probable oxidoreductase	DDGLTGESKA	d	1,18
2	C17	OE1943F glutamate dehydrogenase NADP+ EC 1.4.1.4	LKHPER	d	1,18
2	H9	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	GNKTVEAEVT	C	1,18
3	C2	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,18
1	E7	OE4196R conserved protein	SHGHLNPKR	C	1,18
1	H17	OE1275F proteasome alpha chain	TPEGVVLVVD	d	1,17
2	E7	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,17
1	F4	OE1414R cell division protein ftsZ4	KGVEKAR	d	1,17
1	F15	OE2019F fructose-bisphosphate aldolase EC 4.1.2.13 1	GQGLKNDKN	C	1,17
2	D18	OE3296F hydroxymethylglutaryl-CoA synthase EC 4.1.3.5	KGLEPADVGR	d	1,17
1	D1	OE3356F AAA-type ATPase transitional ATPase homolog	EQILKIHTQDT	C	1,17
2	H21	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	LKDTIEVPPEY	d	1,17
2	H12	OE3349F coenzyme F420--quinone oxidoreductase 42K chain	DTEKTTVGDR	d	1,17
1	D19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GDLRPQHVS	d	1,17
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	AKEIIFTADR	d	1,17
2	H4	OE5208R arginine deiminase EC 3.5.3.6	KIINLR	d	1,17
1	D12	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	d	1,16
1	E1	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,16
2	G14	OE1154F Glyceraldehyde-3-phosphate dehydrogenase	VGINGYGTIG	d	1,16
1	E7	OE2128F phoU protein homolog	QANKIFVLLLR	d	1,16
1	E12	OE3610R translation initiation factor aIF-2B chain alpha/delta eif2ba	KQGHITADQL	d	1,16
2	H13	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	LNTEVVASGP	d	1,16
3	D2	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,16
2	B6	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	KDIVKIEGR	d	1,16
2	D23	OE7093R isopentenyl-diphosphate delta-isomerase EC 5.3.3.2.1	TGLDVAKAIA	d	1,16
2	G9	OE1584R conserved protein	VQEHKEIR	C	1,16
2	G9	OE1584R conserved protein	EKVDEAQEH	C	1,16
2	H12	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,16
2	H21	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	IVTKSIDER	C	1,16
2	B13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	IENVVAKYGD	d	1,16
1	D24	OE3718F cell division protein	ALLVTAGPPK	d	1,15
1	G3	OE1414R cell division protein ftsZ4	SLKTLVR	d	1,15
2	C3	OE3487R translation initiation factor aIF-5A	IEAEGVFDGK	d	1,15
3	C7	OE4735R ribosomal protein S7	LKYGGISVPQ	d	1,15
1	H5	OE2507R histidinol-phosphate transaminase EC 2.6.1.9	TFSKAYGLAG	d	1,15
2	H6	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	C	1,15
3	D16	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GDLRPQHVS	d	1,15
1	D22	OE4654F phosphomethylpyrimidine kinase EC 2.7.4.7	VLAADADALT	d	1,15
2	E12	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LPGVEGMKG	d	1,15
2	D19	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	d	1,14
2	E11	OE1270F glutamate dehydrogenase EC 1.4.1.2	AQHDDVRGP	d	1,14

2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	TNKGQIAGTG	d	1,14
1	B11	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,14
1	E1	OE2358F probable nonspecific lipid-transfer protein sterol carrier protein	KYLAQYDAPR	d	1,13
2	C19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	C	1,13
1	H22	OE2515F conserved protein	VGGQKEGFD	d	1,13
1	E1	OE3718F cell division protein	KSGESVQGG	d	1,13
1	A10	OE3195F succinate--CoA ligase ADP-forming EC 6.2.1.5 beta chain	GKAGGIKLAE	d	1,13
1	H4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,13
1	B12	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,13
2	D13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,13
2	A2	OE3415F ribosomal protein S5	DDQVGGAIQK	C	1,13
2	G7	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,13
1	A12	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,13
3	A13	OE3065R phosphoglycerate dehydrogenase EC 1.1.1.95	YTPSKGGPTD	C	1,13
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	LKHIVGEGR	d	1,12
1	F16	OE3045F conserved protein	GEQGAALYVA	d	1,12
3	D24	OE4729R translation elongation factor aEF-2	EGVKPTLFIN	d	1,12
1	E9	OE2844R transcription regulator homolog / trkA C-terminal domain	LSKQVAEIPG	d	1,12
1	G2	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TKDAAVITGG	d	1,12
3	A19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	d	1,12
3	B17	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,12
3	B18	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,12
3	B2	OE3415F ribosomal protein S5	TTVNFAKATF	C	1,12
2	G23	OE3487R translation initiation factor aIF-5A	SLSQPVDAKI	d	1,12
1	F10	OE1710R oxoglutarate--ferredoxin oxidoreductase EC 1.2.7.3 beta chain	IYGLTKGQAS	d	1,12
2	H14	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TVGYMKPKG	d	1,12
2	H14	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	LQSNVGKTLD	d	1,12
1	G6	OE2622R pyruvate--ferredoxin oxidoreductase EC 1.2.7.1 beta chain	YYQDEQRPS	C	1,11
1	D11	OE3296F hydroxymethylglutaryl-CoA synthase EC 4.1.3.5	KAAVLGYR	d	1,11
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,11
1	E7	OE2128F phoU protein homolog	GEAVKALAHG	d	1,11
1	H3	OE3571R GMP synthase glutamine-hydrolyzing EC 6.3.5.2, subunit B	VIGEVTPEKV	d	1,11
2	H17	OE4306F conserved protein	AFSAVPVVKA	d	1,11
3	D16	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	d	1,11
1	C5	OE5208R arginine deiminase EC 3.5.3.6	KIINLR	d	1,11
2	C18	OE2524R UDPglucose 6-dehydrogenase EC 1.1.1.22	VAVLGLSFKP	d	1,11
2	D16	OE2507R histidinol-phosphate transaminase EC 2.6.1.9	VAEAAKR	d	1,11
2	B15	OE3395F ribosomal protein S3	KAGHTTIDR	d	1,11
1	B19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LPGVEGMKG	d	1,11
2	D15	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,11
3	D24	OE4729R translation elongation factor aEF-2	EVLQEAGMD	d	1,11

2	A5	OE2165R ribosomal protein S15	ALQNTQSKIR	d	1,11
3	C7	OE3415F ribosomal protein S5	TTVNFAKATF	C	1,11
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,10
1	A11	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,10
2	G5	OE2935R fumarate hydratase EC 4.2.1.2	TVAGSLNKIA	d	1,10
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	d	1,10
2	H3	OE5208R arginine deiminase EC 3.5.3.6	KIINLR	d	1,10
2	E8	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,10
2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,10
1	C12	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	1,10
1	H16	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	IVTKSIDER	C	1,10
3	D24	OE4729R translation elongation factor aEF-2	KKIVEQCER	d	1,10
1	F17	OE6008R parA domain protein	AGLKPLVVPL	d	1,10
2	D20	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	QRGTVVPDF	d	1,10
2	C18	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,09
2	A13	OE3395F ribosomal protein S3	VEKFNR	d	1,09
2	G3	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	CLAEPVHGSA	C	1,09
2	D19	OE5208R arginine deiminase EC 3.5.3.6	THGGEKPYTL	d	1,09
1	C9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,09
2	D16	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	1,09
2	F9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,08
2	A22	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,08
1	A1	OE4122R thermosome alpha chain	ATGATPVSNV	C	1,08
1	A15	OE1951F phosphoribosylaminoimidazole carboxylase EC 4.1.1.21 car	TIQDKLVQNR	d	1,08
2	H21	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	LLQDKLEGR	d	1,08
1	B22	OE1475F conserved protein	TPDGGTKYLA	d	1,08
1	E7	OE2128F phoU protein homolog	SQDVVKGDE	d	1,08
2	A2	OE3415F ribosomal protein S5	TTVNFAKATF	C	1,08
2	H8	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,08
2	G4	OE1687F aspartate--tRNA ligase EC 6.1.1.12	KFDLLYR	C	1,08
1	F8	OE2006F probable ABC-type transport system ATP-binding protein	AITKIEDR	d	1,08
1	A12	OE1584R conserved protein	KLQKSGHL	C	1,08
1	E9	OE2844R transcription regulator homolog / trkA C-terminal domain	GGISQETLSV	d	1,08
2	E20	OE5201F aspartate carbamoyltransferase EC 2.1.3.2 catalytic chain	LGGDIVDMGS	d	1,08
2	G14	OE1154F Glyceraldehyde-3-phosphate dehydrogenase	EQYGIEKVR	d	1,08
2	G2	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	KDSPGFVVNR	d	1,08
1	H5	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,08
2	B1	OE3415F ribosomal protein S5	TTVNFAKATF	d	1,08
2	F10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,08
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,08
2	C6	OE2005F methylmalonyl-CoA mutase EC 5.4.99.2 2 C-terminal homolog	CLVAKVGLDG	d	1,07

1	A20	OE1270F glutamate dehydrogenase EC 1.4.1.2	GPYKGGLR	d	1,07
2	B3	OE2667F nucleoside-diphosphate kinase EC 2.7.4.6	TFVMVKPDGV	d	1,07
2	D2	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KNLAANGLAD	d	1,07
1	E22	OE2374R purine-binding chemotaxis protein cheW2	VKLGEDGAAD	d	1,07
2	B19	OE3308F malate dehydrogenase oxaloacetate decarboxylating EC 1.1	IVINKAKSEQQ	d	1,07
2	G21	OE3717F NADH dehydrogenase ubiquinone EC 1.6.5.3 32K chain	SLKLDNTTSA	d	1,07
2	H9	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	GNKTVEAEVT	d	1,07
2	B13	OE1668R protein OE1668R	DQAFTALDLY	C	1,07
1	C10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,07
2	B13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,06
2	F12	OE4196R conserved protein	SHGHLNPKR	C	1,06
3	D17	OE2648F conserved protein	VSSLVEFAKE	d	1,06
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	KSGAGFYDYG	d	1,06
2	B1	OE3415F ribosomal protein S5	TTVNFAKATF	C	1,06
1	H16	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	IVTKSIDER	d	1,06
2	C18	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,06
1	C5	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	d	1,06
2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	1,06
2	C11	OE2530F glucose-1-phosphate thymidylyltransferase EC 2.7.7.24	AEYELSDAID	d	1,05
1	C20	OE1432F sarcosine oxidase EC 1.5.3.1 beta chain	VLADAGVPVP	d	1,05
2	G3	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	CLAEPVHGSA	d	1,05
1	F7	OE4306F conserved protein	AFSAVPVVKA	C	1,05
1	C6	OE1260R probable oxidoreductase mercuryII reductase homolog	DASSDGVFKT	C	1,05
1	H16	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	LKDTIEVPPEY	C	1,05
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	1,05
1	A17	OE4565F conserved protein	GKLSGTKAVY	d	1,05
2	C19	OE1592R mRNA 3'-end processing factor homolog	VINETYEDGG	d	1,05
2	E16	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TKDAAVITGG	d	1,05
2	G3	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	C	1,04
1	C10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,04
2	E16	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	LQSNVGKTLD	C	1,04
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,04
1	G18	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,04
1	D5	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	d	1,04
2	E15	OE1414R cell division protein ftsZ4	KGVEKAR	d	1,04
3	A17	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	C	1,04
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,04
1	A19	OE3931R threonine dehydratase EC 4.2.1.16	TGSFKIR	C	1,04
3	D6	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KNLAANGLAD	d	1,04
1	H5	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,03
2	B13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	1,03

1	D14	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	d	1,03
1	G22	OE2419R purine-binding chemotaxis protein cheW1	ADDKQKIGLR	d	1,03
2	D2	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KADRLETTR	d	1,03
2	A13	OE3395F ribosomal protein S3	KITTQLEER	C	1,03
2	E21	OE4234R uracil phosphoribosyltransferase EC 2.4.2.9 upp	AATPFVEGLL	d	1,03
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	LLDLPVSDEM	d	1,03
2	D1	OE3863R 6-N-hydroxylaminopurine sensitivity-controlling protein	FVTTNSGKVQ	d	1,03
1	D11	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	C	1,03
1	G7	OE5201F aspartate carbamoyltransferase EC 2.1.3.2 catalytic chain	LGGDIVDMGS	d	1,03
2	G9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,03
1	F5	OE3934R citrate si-synthase EC 2.3.3.1 formerly EC 4.1.3.7	VYNVKDPR	d	1,03
2	G8	OE2579F adenylosuccinate synthase EC 6.3.4.4	LEYLVDAKR	d	1,02
3	A18	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	LNTEVVASGP	d	1,02
1	D12	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	C	1,02
2	E9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	1,02
2	H5	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,02
2	D19	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	C	1,02
2	F10	OE1584R conserved protein	VQEHKEIR	C	1,02
2	E6	OE2912F probable fatty-acid--CoA ligase EC 6.2.1.-	VGSIGKPLAG	d	1,02
2	F8	OE4159F adenosylhomocysteinase EC 3.3.1.1	GVAKKAAGQ	d	1,02
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,02
1	E1	OE2358F probable nonspecific lipid-transfer protein sterol carrier protein	KEVDLETVLD	C	1,02
1	G9	OE2641F ribosomal protein S2	FPAEKFAEAV	d	1,02
2	G3	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	d	1,02
2	A2	OE4735R ribosomal protein S7	LKYGGISVPQ	C	1,02
1	C13	OE2648F conserved protein	GETPYDIEDG	d	1,02
1	H16	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	LLQDKLEGR	d	1,02
1	H11	OE3082R translation initiation factor aIF-2B chain alpha/delta eif2bd	THSSSVVAVK	d	1,02
1	H1	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	LQSNVGKTLD	d	1,02
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	1,02
2	H8	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,02
1	H14	OE3065R phosphoglycerate dehydrogenase EC 1.1.1.95	YTPSKGGPTD	d	1,01
2	D16	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	1,01
3	D10	OE6008R parA domain protein	SLVIPVEPSAK	C	1,01
3	D17	OE2648F conserved protein	EGEGVLCYIE	d	1,01
2	G4	OE1687F aspartate--tRNA ligase EC 6.1.1.12	KPSTKAVFSL	d	1,01
1	D12	OE3168R pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,01
1	E6	OE3934R citrate si-synthase EC 2.3.3.1 formerly EC 4.1.3.7	VYNVKDPR	d	1,01
2	E21	OE4234R uracil phosphoribosyltransferase EC 2.4.2.9	KGLVKLGR	d	1,01
1	H4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	1,01
1	G23	OE5100R trkA domain protein	VADGAPAAG	d	1,01
3	B4	OE1711R oxoglutarate--ferredoxin oxidoreductase EC 1.2.7.3 alpha ch	HVFTSKDFAS	d	1,01

1	E2	OE2013R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	DAKLNEIYEG	C	1,01
1	D7	OE2458R IMP dehydrogenase EC 1.1.1.205	EAAEAVVDFA	d	1,01
2	B19	OE3308F malate dehydrogenase (oxaloacetate decarboxylating) EC 1.1.1.40	IALGEGGDEK	d	1,00
1	G2	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TVGYMKPKG	d	1,00
2	H1	OE2450F acetate--CoA ligase EC 6.2.1.1	IVASVEDAIGP	d	1,00
3	D7	OE3415F ribosomal protein S5	TTVNFAKATF	C	1,00
2	D15	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	1,00
1	D18	OE1270F glutamate dehydrogenase EC 1.4.1.2	AQHDDVRGP	d	1,00
2	G10	OE1475F conserved protein	TPDGGTKYLA	d	1,00
2	G3	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	C	1,00
1	A7	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,00
2	H24	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KNLAANGLAD	d	1,00
1	H1	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	LQSNVGKTLD	C	1,00
1	A22	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	TAKLNELIR	C	1,00
1	F6	OE1154F Glyceraldehyde-3-phosphate dehydrogenase	VADAVAAQPD	C	-1,01
3	B16	OE2128F phoU protein homolog	SQDVVKGDE	d	-1,01
1	B7	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,01
2	C16	OE1259R conserved protein	SGLPEDEETT	d	-1,01
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	d	-1,01
1	H16	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	LLQDKLEGR	C	-1,01
1	D10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,01
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	-1,01
2	E15	OE1414R cell division protein ftsZ4	SLKTLVR	d	-1,01
1	H5	OE2507R histidinol-phosphate transaminase EC 2.6.1.9	VAEAAKR	d	-1,01
1	A11	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,01
2	C19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	d	-1,01
2	F15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,01
2	E13	OE4654F phosphomethylpyrimidine kinase EC 2.7.4.7	VLAADADALT	d	-1,01
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	-1,02
2	B17	OE3807R oligoendopeptidase	HADLKR	d	-1,02
2	C18	OE5160F glycerol dehydrogenase EC 1.1.1.6	AGHKLAELCY	C	-1,02
2	E4	OE3356F AAA-type ATPase transitional ATPase homolog	EQILKIHTQDT	d	-1,02
2	F11	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GDLRPQHVS	d	-1,02
3	D2	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,02
2	B24	OE2635F ribosomal protein S9	YQKSYR	d	-1,02
1	C8	OE2912F probable fatty-acid--CoA ligase EC 6.2.1.-	KAFTEADGKR	d	-1,02
2	G23	OE3487R translation initiation factor aIF-5A	IEAEGVFDGK	d	-1,02
1	D14	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	CLAEPVHGSA	C	-1,02
2	D5	OE3394F ribosomal protein L22	SISLKHSKAIA	d	-1,02
1	F15	OE2019F fructose-bisphosphate aldolase EC 4.1.2.13 1	GQGLKNDKN	d	-1,02
1	H1	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TKDAAVITGG	d	-1,02
2	G7	OE2579F adenylosuccinate synthase EC 6.3.4.4	ELDGAEEAAK	C	-1,02
3	B20	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	C	-1,03
1	H7	OE1936R conserved protein	EHYDHPASKQ	d	-1,03

2	F9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,03
2	E6	OE2912F probable fatty-acid--CoA ligase EC 6.2.1.-	KAFTEADGKR	d	-1,03
2	E7	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	-1,03
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	d	-1,03
2	F12	OE4196R conserved protein	SHGHLNPKR	d	-1,03
2	G9	OE1584R conserved protein	KLQKSGHL	C	-1,03
2	E22	OE2019F fructose-bisphosphate aldolase EC 4.1.2.13 1	GQGLKNDKN	d	-1,03
2	G2	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	C	-1,03
2	E1	OE4122R thermosome alpha chain	RAKSDDFTR	d	-1,03
2	D15	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,03
2	E10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,03
2	E22	OE2019F fructose-bisphosphate aldolase EC 4.1.2.13 1	GQGLKNDKN	C	-1,04
1	H5	OE2507R histidinol-phosphate transaminase EC 2.6.1.9	VAEAAKR	C	-1,04
1	C8	OE2935R fumarate hydratase EC 4.2.1.2	TQVEKGIDR	d	-1,04
3	B3	OE2451R probable oxidoreductase	DDGLTGESKA	C	-1,04
2	F9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,04
1	B20	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	C	-1,04
2	A20	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	d	-1,04
2	H21	OE3874R DNA-directed RNA polymerase EC 2.7.7.6 chain E'	LLQDKLEGR	C	-1,04
2	G7	OE2579F adenylosuccinate synthase EC 6.3.4.4	ELDGAEEAAK	d	-1,04
2	E9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,04
2	F9	OE4721R translation elongation factor aEF-1 alpha chain	DFVKNMITGA	d	-1,04
1	F6	OE1154F Glyceraldehyde-3-phosphate dehydrogenase	VGINGYGTIG	d	-1,05
1	D12	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	C	-1,05
1	G10	OE4234R uracil phosphoribosyltransferase EC 2.4.2.9 upp	AATPFVEGLL	d	-1,05
1	F6	OE1154F Glyceraldehyde-3-phosphate dehydrogenase	VADAVAAQPD	d	-1,05
2	G9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,05
1	D10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,05
1	G9	OE2641F ribosomal protein S2	FPAEKFAEAV	C	-1,05
1	D8	OE2801R conserved protein	VKAVLDDGTD	d	-1,05
2	A17	OE4268F glutamate-1-semialdehyde 2,1-aminomutase EC 5.4.3.8	HAACPKTGAD	C	-1,06
1	D14	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	d	-1,06
2	H24	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	SKLALTDDDH	d	-1,06
2	D14	OE2451R probable oxidoreductase	DDGLTGESKA	C	-1,06
2	G3	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	d	-1,06
1	G23	OE5100R trkA domain protein	VADGAPAAG	C	-1,06
2	D24	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,06
2	G22	OE3710R trkA domain protein	KYADEVDEIV	C	-1,06
2	H14	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TKDAAVITGG	C	-1,07
1	A10	OE3195F succinate--CoA ligase ADP-forming EC 6.2.1.5 beta chain	GKAGGIKLAE	C	-1,07
3	A4	OE3710R trkA domain protein	KYADEVDEIV	d	-1,07
1	A8	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,07
2	D19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	d	-1,07
2	G5	OE2935R fumarate hydratase EC 4.2.1.2	TQVEKGIDRIE	d	-1,07
2	H3	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	d	-1,07
3	D6	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KADRLETTR	d	-1,07

3	C22	OE3415F ribosomal protein S5	TTVNFAKATF	C	-1,07
2	H24	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KADRLETTR	d	-1,07
1	D9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,07
2	D24	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,07
2	H4	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	d	-1,07
1	D9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,07
3	A19	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	d	-1,07
2	C2	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	SKLALTDDDH	d	-1,08
1	C8	OE2912F probable fatty-acid--CoA ligase EC 6.2.1.-	VGSIGKPLAG	d	-1,08
3	C2	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	-1,08
1	H16	OE3710R trkA domain protein	LLAFGKHDAS	d	-1,08
1	B7	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,08
2	H16	OE3718F cell division protein	AAVAVNTAKA	d	-1,08
1	D10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,08
1	G10	OE4234R uracil phosphoribosyltransferase EC 2.4.2.9 upp	KGLVKLGR	d	-1,08
1	H16	OE3710R trkA domain protein	KYADEVDEIV	d	-1,08
1	B14	OE2648F conserved protein	VSSLVEFAKE	d	-1,08
3	B16	OE4196R conserved protein	SHGHLNPKR	C	-1,09
2	H5	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,09
2	H9	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	TAKLNELIR	d	-1,09
3	B13	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	d	-1,09
3	A16	OE3571R GMP synthase glutamine-hydrolyzing EC 6.3.5.2, subunit B	VIGEVTPEKV	C	-1,09
2	G22	OE3710R trkA domain protein	LLAFGKHDAS	d	-1,09
1	G15	OE4195F replication factor C small chain	IKDFAR	d	-1,09
1	E7	OE4196R conserved protein	SHGHLNPKR	d	-1,09
2	A2	OE4735R ribosomal protein S7	LKYGGISVPQ	d	-1,09
2	D3	OE3817R ribosomal protein S19.eR	KVAIDGPIGVK	d	-1,10
1	G10	OE4234R uracil phosphoribosyltransferase EC 2.4.2.9 upp	GDAHVITHSL	d	-1,10
2	C7	OE2632F ribosomal protein L18.eR	LSSLIAELKSV	d	-1,10
1	F8	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,10
2	E10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,10
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	-1,10
2	A22	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,10
3	A2	OE6008R parA domain protein	SLVIPVEPSAK	C	-1,10
2	C19	OE1592R mRNA 3'-end processing factor homolog	NFLKQER	d	-1,10
1	B11	OE2579F adenylosuccinate synthase EC 6.3.4.4	LEYLVDAKR	d	-1,10
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	d	-1,10
2	H3	OE5208R arginine deiminase EC 3.5.3.6	KIINLR	C	-1,10
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	DLAAGPPIAM	d	-1,10
2	A4	OE4025F conserved protein	DAETPTYVAV	d	-1,11
1	E12	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	d	-1,11
3	C7	OE3415F ribosomal protein S5	DDQVGGAIQK	d	-1,11
2	E12	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	C	-1,11
2	B12	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	KDIVKIEGR	d	-1,11

2	A8	OE3410F ribosomal protein S8	GYIDGFEFVD	d	-1,11
2	D6	OE2969R probable transcription regulator	KPFSEIAR	d	-1,12
2	D15	OE4721R translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	d	-1,12
1	F12	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	d	-1,12
1	D14	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	C	-1,12
1	A8	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,12
3	D16	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	C	-1,12
1	A11	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,12
1	H20	OE3238F probable precorrin-6Y C5,15-methyltransferase	GTAVLMGDP	d	-1,12
2	C17	OE3322F conserved protein	IKAPNDKFR	d	-1,13
1	D7	OE2458R IMP dehydrogenase EC 1.1.1.205	EIKASVDADV	d	-1,13
2	B15	OE1942F citryl-CoA lyase EC 4.1.3.34 citrate lyase EC 4.1.3.6 beta chain	KAPTTGADVV	d	-1,13
1	B19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	C	-1,13
1	F5	OE1154F Glyceraldehyde-3-phosphate dehydrogenase NADP phosph	EQYGIEKVR	d	-1,13
2	F11	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LAGLKER	C	-1,14
3	A19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	d	-1,14
1	A17	OE4565F conserved protein	IALCDTYSDE	d	-1,14
3	C5	OE2627F ribosomal protein S13	IGQTDLDGTK	d	-1,14
1	E12	OE3524F pyridoxine biosynthesis protein	GSELVKR	d	-1,14
1	E22	OE2374R purine-binding chemotaxis protein cheW2	VKLGEDGAAD	C	-1,15
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	d	-1,15
2	G11	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	d	-1,15
1	F17	OE6008R parA domain protein	SLVIPVEPSAK	C	-1,15
3	C22	OE3415F ribosomal protein S5	TTVNFAKATF	d	-1,15
2	H6	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	-1,15
2	E12	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GDLRPQHVS	C	-1,15
1	F11	OE3524F pyridoxine biosynthesis protein	KLEGMDYEE	d	-1,16
1	H9	OE4085R ribose-phosphate pyrophosphokinase EC 2.7.6.1	DAYGTGVTD	C	-1,16
1	H4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	-1,16
1	A19	OE3931R threonine dehydratase EC 4.2.1.16	TGSFKIR	d	-1,16
1	D6	OE3748R probable archaeosine tRNA-ribosyltransferase EC 2.4.2.-	KPYSDSQSH	d	-1,16
1	B1	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	C	-1,16
2	H6	OE3168R pyridoxal phosphate-dependent aminotransferase	EAVVNACVKR	d	-1,17
2	E8	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	-1,17
1	A22	OE2640F phosphopyruvate hydratase EC 4.2.1.11 enolase	TAKLNELIR	d	-1,17
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	IENVVAKYGD	d	-1,17
1	D14	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	CLAEPVHGSA	d	-1,18
2	F16	OE5205R ornithine carbamoyltransferase EC 2.1.3.3, catabolic	MHVQKAIVHT	d	-1,18
3	D24	OE4729R translation elongation factor aEF-2	VFSGTLEKGQ	d	-1,18
2	E16	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	LQSNVGKTLD	d	-1,18
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	IENVVAKYGD	d	-1,18
1	H5	OE3349F coenzyme F420--quinone oxidoreductase 42K chain	DTEKTTVGDR	d	-1,18

		homolo			
1	B13	OE3152R probable peptide chain release factor aRF1	GVHEVLKR	d	-1,19
2	E9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,19
1	D7	OE2458R IMP dehydrogenase EC 1.1.1.205	FSEKLR	d	-1,19
2	A13	OE3395F ribosomal protein S3	KITTQLEER	d	-1,19
1	D5	OE1620R phosphoribosylglycinamide formyltransferase EC 2.1.2.2	VDAVEIAAKK	d	-1,20
2	A20	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	VAIKGPLTTPV	C	-1,20
2	B6	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	DYEVDEKR	d	-1,20
1	F2	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	LNTEVVASGP	C	-1,20
2	F11	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LPGVEGMKG	d	-1,20
2	D23	OE7093R isopentenyl-diphosphate delta-isomerase EC 5.3.3.2.1	QKQIGTLFR	d	-1,20
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	-1,20
2	G22	OE3710R trkA domain protein	KYADEVDEIV	d	-1,20
2	B7	OE4540R conserved protein	GKDAVSAVAD	d	-1,20
2	B18	OE4673F carboxypeptidase EC 3.4.-.-	EEDDFSIFAP	d	-1,21
1	D24	OE3718F cell division protein	AAVAVNTAKA	d	-1,21
3	B5	OE4540R conserved protein	GKDAVSAVAD	d	-1,21
1	C5	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	C	-1,21
2	H12	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	C	-1,21
2	G7	OE2579F adenylosuccinate synthase EC 6.3.4.4	LEYLVDAKR	d	-1,22
2	D17	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,22
2	D15	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	C	-1,22
1	C18	OE2011R probable nonspecific lipid-transfer protein sterol carrier protein	EGVTTKDGR	C	-1,23
1	G8	OE2451R probable oxidoreductase	DDGLTGESKA	C	-1,23
3	B14	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	d	-1,23
2	B4	OE2667F nucleoside-diphosphate kinase EC 2.7.4.6	TFVMVKPDGV	d	-1,23
1	H3	OE3571R GMP synthase glutamine-hydrolyzing EC 6.3.5.2, subunit B	ATGVKGDNR	d	-1,23
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	IENVVAKYGD	d	-1,24
3	B3	OE2451R probable oxidoreductase	DDGLTGESKA	d	-1,24
2	F10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,24
1	C4	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	C	-1,25
2	E10	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,25
1	A17	OE4565F conserved protein	IALCDTYSDE	C	-1,26
1	D12	OE3168R pyridoxal phosphate-dependent aminotransferase	GLLVLGCGHK	d	-1,26
1	B22	OE1765R probable proteasome regulatory chain probable proteasome	EKLDQDSEPA	d	-1,26
1	F11	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	d	-1,26
2	H5	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,26
1	C13	OE2648F conserved protein	EGEGVLCYIE	d	-1,27
1	D10	OE4721R translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	C	-1,27
3	D10	OE6008R parA domain protein	AGLKPLVVPL	d	-1,27
3	B14	OE3524F pyridoxine biosynthesis protein	NIKSAIR	d	-1,28
2	H4	OE5208R arginine deiminase EC 3.5.3.6	KIINLR	C	-1,29

2	H17	OE4306F conserved protein	AFSAVPVVKA	d	-1,29
1	F11	OE3524F pyridoxine biosynthesis protein	GSELVKR	d	-1,29
2	E12	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LPGVEGMKG	C	-1,29
1	E11	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	LSIEKLAALGW	C	-1,30
1	D3	OE4122R thermosome alpha chain	RAKSDDFTR	d	-1,30
1	A10	OE3195F succinate--CoA ligase ADP-forming EC 6.2.1.5 beta chain	GDEVAKGINS	C	-1,30
1	F12	OE3524F pyridoxine biosynthesis protein	NIKSAIR	d	-1,30
1	G2	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	LQSNVGKTLD	d	-1,30
1	H9	OE4085R ribose-phosphate pyrophosphokinase EC 2.7.6.1	DAYGTGVTD	d	-1,31
1	E3	OE2585R conserved protein	NENSAKAIYY	d	-1,31
1	E1	OE2138F probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	ESALAKLDAS	d	-1,31
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,32
1	H12	OE3524F pyridoxine biosynthesis protein	GSELVKR	d	-1,32
1	F12	OE3524F pyridoxine biosynthesis protein	GSELVKR	d	-1,32
3	D2	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,32
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	KDSPGFVVNR	C	-1,32
1	F11	OE3524F pyridoxine biosynthesis protein	NIKSAIR	d	-1,32
1	C4	OE3925R thermosome beta chain	DIHPTAIIKGY	d	-1,32
1	F5	OE3934R citrate si-synthase EC 2.3.3.1 formerly EC 4.1.3.7	VYNVKDPR	C	-1,33
3	A2	OE6008R parA domain protein	AGLKPLVVPL	C	-1,33
1	G22	OE2419R purine-binding chemotaxis protein cheW1	ADDKQKIGLR	C	-1,34
2	D1	OE3863R 6-N-hydroxylaminopurine sensitivity-controlling protein	KNALSHR	C	-1,34
1	G1	OE4571R probable leucyl aminopeptidase EC 3.4.11.1	MANMKTILDE	d	-1,34
1	B21	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,35
1	C13	OE2648F conserved protein	VSSLVEFAKE	C	-1,35
2	G11	OE3524F pyridoxine biosynthesis protein	GSELVKR	d	-1,36
2	G11	OE3524F pyridoxine biosynthesis protein	KLEGMDYEE	d	-1,36
3	B14	OE3524F pyridoxine biosynthesis protein	GSELVKR	d	-1,36
1	H16	OE3710R trkA domain protein	KYADEVDEIV	C	-1,37
3	C7	OE4735R ribosomal protein S7	LKYGGISVPQ	C	-1,37
2	A16	OE1710R oxoglutarate--ferredoxin oxidoreductase EC 1.2.7.3 beta chain	IYGLTKGQAS	C	-1,37
1	D8	OE2801R conserved protein	DGSGLIKR	d	-1,38
3	B14	OE3524F pyridoxine biosynthesis protein	KLEGMDYEE	d	-1,38
1	F17	OE6008R parA domain protein	AGLKPLVVPL	C	-1,39
2	A22	OE4613F aconitate hydratase EC 4.2.1.3	AKAADSGVLV	C	-1,39
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,40
2	H4	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	C	-1,40
2	C19	OE1592R mRNA 3'-end processing factor homolog	TFAPKNLETF	d	-1,41
2	G11	OE3524F pyridoxine biosynthesis protein	NIKSAIR	d	-1,41
2	G2	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	LKHIVGEGR	C	-1,41
3	A4	OE3710R trkA domain protein	LLAFGKHDAS	d	-1,41
2	F6	OE2458R IMP dehydrogenase EC 1.1.1.205	FSEKLR	d	-1,42
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	C	-1,42

1	E24	OE2306F conserved protein	YTQQETAVKG	d	-1,43
3	B13	OE3524F pyridoxine biosynthesis protein	NIKSAIR	d	-1,43
1	D6	OE3748R probable archaeosine tRNA-ribosyltransferase EC 2.4.2.-	KPYSDSQSH	C	-1,43
1	E11	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	GTVVPDFIQK	C	-1,44
2	B17	OE3807R oligoendopeptidase	DVKLAEAR	C	-1,44
3	C14	OE2451R probable oxidoreductase	DDGLTGESKA	C	-1,44
2	B12	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	DYEVDEKR	d	-1,44
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,45
2	D13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,45
2	D15	OE4721R translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	C	-1,46
2	F9	OE2416R protein-glutamate methylesterase EC 3.1.1.61 cheB	AVKDAGGAT	d	-1,46
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	LKHIVGEGR	C	-1,46
2	D16	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,46
1	F12	OE3524F pyridoxine biosynthesis protein	KLEGMDYEE	d	-1,46
3	C4	OE3807R oligoendopeptidase	DVKLAEAR	d	-1,47
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	AKEIIFTADR	C	-1,48
2	A19	OE2864F phosphoribosylamine--glycine ligase EC 6.3.4.13	DIGSKTLLAD	d	-1,49
1	G22	OE2676R conserved protein	ILDEIRDPDLK	d	-1,49
3	D2	OE4721R translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	C	-1,49
1	A19	OE3931R threonine dehydratase EC 4.2.1.16	TVLKDSPGSL	d	-1,49
2	A19	OE2864F phosphoribosylamine--glycine ligase EC 6.3.4.13	VTGDQLSKPA	d	-1,50
3	B16	OE2128F phoU protein homolog	GEAVKALAHG	d	-1,50
3	D17	OE2648F conserved protein	VSSLVEFAKE	d	-1,51
2	H3	OE5208R arginine deiminase EC 3.5.3.6	KPEVDIAR	C	-1,51
2	G2	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	KDSPGFVVNR	C	-1,51
1	E2	OE2013R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LLGEEGDGFK	C	-1,51
3	B13	OE3524F pyridoxine biosynthesis protein	GSELVKR	d	-1,51
1	D9	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,52
1	H4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolo	AVGGILTKTD	C	-1,54
2	B18	OE4673F carboxypeptidase EC 3.4.-.-	STQKSAVSTV	d	-1,54
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,54
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,54
2	H12	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,55
2	G2	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	AKEIIFTADR	C	-1,55
1	F1	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	LNTEVVASGP	C	-1,56
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,56
1	F8	OE2006F probable ABC-type transport system ATP-binding protein	AITKIEDR	C	-1,56
2	D7	OE3402F ribosomal protein L14	VKFEDNAAVI	d	-1,57

2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,57
3	B13	OE3524F pyridoxine biosynthesis protein	NIKSAIR	C	-1,57
3	C13	OE2110R UDPglucose 4-epimerase EC 5.1.3.2	GTVVPDFIQK	C	-1,58
1	E12	OE3524F pyridoxine biosynthesis protein	KLEGMDYEE	C	-1,58
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ERIENVVAKY	d	-1,59
2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,59
1	F12	OE3524F pyridoxine biosynthesis protein	GSELVKR	C	-1,59
1	G10	OE4234R uracil phosphoribosyltransferase EC 2.4.2.9 upp	AKQGVISAGR	d	-1,59
1	F2	OE3691F probable anthranilate phosphoribosyltransferase EC 2.4.2.1	HTAAPDADPV	d	-1,62
2	D1	OE3863R 6-N-hydroxylaminopurine sensitivity-controlling protein	FVTTNSGKVQ	C	-1,62
2	C20	OE3322F conserved protein	IKAPNDKFR	d	-1,62
2	C21	OE1358R methanol dehydrogenase regulatory protein	EYVVPADVKG	d	-1,63
1	F4	OE1414R cell division protein ftsZ4	KGVEKAR	C	-1,63
2	H14	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	LQSNVGKTLD	C	-1,63
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,64
1	E12	OE3524F pyridoxine biosynthesis protein	NIKSAIR	C	-1,64
1	E6	OE3934R citrate si-synthase EC 2.3.3.1 formerly EC 4.1.3.7	VYNVKDPR	C	-1,64
2	D22	OE4355R thiosulfate sulfurtransferase homolog	AYRDDVENA	d	-1,64
2	D7	OE3402F ribosomal protein L14	GTEIKGPISR	d	-1,65
1	H4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-1,66
3	B13	OE3524F pyridoxine biosynthesis protein	GSELVKR	C	-1,68
2	B13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,68
1	H12	OE3524F pyridoxine biosynthesis protein	NIKSAIR	d	-1,68
1	F12	OE3524F pyridoxine biosynthesis protein	NIKSAIR	C	-1,69
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,69
1	B7	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,70
1	G2	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TKDAAVITGG	C	-1,71
1	G22	OE2676R conserved protein	LHQLNLLPGIG	d	-1,72
2	G1	OE4613F aconitate hydratase EC 4.2.1.3	IHKANLFNFG	d	-1,72
2	F20	OE5201F aspartate carbamoyltransferase EC 2.1.3.2 catalytic chain	LGGDIVDMGS	d	-1,72
2	F24	OE2159R ribosomal protein S3a.eR	GSSKVAVTVT	d	-1,73
2	C11	OE2530F glucose-1-phosphate thymidylyltransferase EC 2.7.7.24	KQNIISHYGD	d	-1,73
1	C20	OE1432F sarcosine oxidase EC 1.5.3.1 beta chain	VLADAGVPVP	C	-1,73
1	B19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	LPGVEGMKG	C	-1,74
2	E16	OE2373F probable phosphate acetyltransferase EC 2.3.1.8	TKDAAVITGG	C	-1,74
2	G11	OE3524F pyridoxine biosynthesis protein	NIKSAIR	C	-1,74
2	A22	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIRR	d	-1,74
2	B13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-1,75
1	E7	OE2128F phoU protein homolog	GEAVKALAHG	C	-1,75
1	F11	OE3524F pyridoxine biosynthesis protein	GSELVKR	C	-1,75
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain	DTEKTTVGDR	C	-1,76

		homolog			
2	A4	OE4025F conserved protein	DAETPTYVAV	C	-1,76
2	D17	OE4721R translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	-1,79
1	E12	OE3524F pyridoxine biosynthesis protein	GSELVKR	C	-1,79
2	G11	OE3524F pyridoxine biosynthesis protein	GSELVKR	C	-1,81
1	H5	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,81
3	C2	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,82
1	F11	OE3524F pyridoxine biosynthesis protein	KLEGMDYEE	C	-1,83
2	C2	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	SKLALTDDDH	C	-1,85
1	F11	OE3524F pyridoxine biosynthesis protein	NIKSAIR	C	-1,85
1	F12	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	C	-1,87
2	A5	OE2165R ribosomal protein S15	GDKLDEEFAY	d	-1,88
1	E24	OE2306F conserved protein	YTQQETAVKG	C	-1,89
3	B14	OE3524F pyridoxine biosynthesis protein	GSELVKR	C	-1,90
1	H12	OE3524F pyridoxine biosynthesis protein	GSELVKR	C	-1,92
2	D2	OE3207F probable precorrin-8W decarboxylase EC 1.-.-.-	KADRLETTR	C	-1,94
1	F4	OE1414R cell division protein ftsZ4	SLKTLVR	C	-1,94
2	E15	OE1414R cell division protein ftsZ4	KGVEKAR	C	-1,95
3	A15	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-1,98
3	A8	OE3402F ribosomal protein L14	VKFEDNAAVI	d	-1,98
2	B6	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	KDIVKIEGR	C	-2,00
2	A7	OE3187R conserved hypothetical protein	LLLGSVTEKV	d	-2,02
1	E12	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	C	-2,03
3	B21	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-2,04
2	F22	OE3214F precorrin-3B C17-methyltransferase EC 2.1.1.131 1	QIELAKEAFE	d	-2,04
2	G13	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-2,06
2	G10	OE1475F conserved protein	TPDGGTKYLA	C	-2,08
1	G3	OE1414R cell division protein ftsZ4	KGVEKAR	C	-2,09
2	A21	OE1613R probable acylaminoacyl-peptidase EC 3.4.19.1	ANKQAAYR	d	-2,11
2	D19	OE3634F isocitrate dehydrogenase NADP+ EC 1.1.1.42	AGQDKANPT	d	-2,14
3	D19	OE4391F probable serine--pyruvate aminotransferase EC 2.6.1.51 protein	KAESNQTPFT	C	-2,14
2	B12	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	DYEVDEKR	C	-2,15
1	G4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-2,16
1	H3	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-2,18
1	F11	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	C	-2,18
2	B14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-2,18
1	B19	OE4500R probable acyl/butyryl-CoA dehydrogenase EC 1.3.99.-	GDLRPQHVS	C	-2,19
1	E16	OE3214F precorrin-3B C17-methyltransferase EC 2.1.1.131 1	QIELAKEAFE	d	-2,21
2	G9	OE1584R conserved protein	FKEGETLDTE	C	-2,25
1	D10	OE4721R translation elongation factor aEF-1 alpha chain	DFVKNMITGA	d	-2,25
2	E10	OE2416R protein-glutamate methylesterase EC 3.1.1.61 cheB	AVKDAGGAT	d	-2,26

2	B6	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	DYEVDEKR	C	-2,26
2	D7	OE3402F ribosomal protein L14	ELKITSVMGY	d	-2,27
1	E16	OE3214F precorrin-3B C17-methyltransferase EC 2.1.1.131 1	KHLVTPR	d	-2,27
3	D7	OE3209F probable precorrin-2 C20-methyltransferase EC 2.1.1.130	DTLQKDR	d	-2,29
2	G11	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	C	-2,29
2	D11	OE3214F precorrin-3B C17-methyltransferase EC 2.1.1.131 1	KHLVTPR	d	-2,33
3	B14	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	C	-2,35
2	D11	OE3214F precorrin-3B C17-methyltransferase EC 2.1.1.131 1	QIELAKEAFE	d	-2,39
3	C2	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-2,42
2	F14	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-2,43
2	C3	OE3487R translation initiation factor aIF-5A	IEAEGVFDGK	C	-2,46
1	D15	OE4391F probable serine--pyruvate aminotransferase EC 2.6.1.51 protein	KAESNQTPFT	C	-2,48
3	A8	OE3402F ribosomal protein L14	GTEIKGPISR	d	-2,58
2	G23	OE3487R translation initiation factor aIF-5A	IEAEGVFDGK	C	-2,58
3	C12	OE4330F probable phosphoesterase EC 3.1.-.-	DKYTYPDEFE	d	-2,58
2	C19	OE1592R mRNA 3'-end processing factor homolog	TFAPKNLETF	C	-2,62
2	G1	OE2871F probable 3-hydroxyacyl-CoA dehydrogenase EC 1.1.1.157	KSGAGFYDYG	C	-2,62
2	A16	OE3959R branched-chain-amino-acid transaminase EC 2.6.1.42	GELHTADELF	d	-2,66
2	B12	OE5202F aspartate carbamoyltransferase EC 2.1.3.2 regulatory chain	KDIVKIEGR	C	-2,66
1	B19	OE2360R NADH oxidase homolog	KLSTADIEDVV	d	-2,67
2	B6	OE3547F conserved protein	ADSLQSVKEQ	d	-2,87
3	D24	OE4729R translation elongation factor aEF-2	VFSGTLEKGQ	C	-2,87
1	H18	OE4330F probable phosphoesterase EC 3.1.-.-	DKYTYPDEFE	d	-2,91
1	D5	OE1620R phosphoribosylglycinamide formyltransferase EC 2.1.2.2	VDAVEIAAKK	C	-2,93
2	E9	OE4721R translation elongation factor aEF-1 alpha chain	DFVKNMITGA	d	-2,94
1	H4	OE3349F coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	C	-2,98
1	C16	OE4391F probable serine--pyruvate aminotransferase EC 2.6.1.51 protein	KAESNQTPFT	C	-3,09
2	E13	OE4654F phosphomethylpyrimidine kinase EC 2.7.4.7	VLAADADALT	C	-3,09
1	H23	OE3209F probable precorrin-2 C20-methyltransferase EC 2.1.1.130	DTLQKDR	d	-3,13
1	H23	OE3209F probable precorrin-2 C20-methyltransferase EC 2.1.1.130	IGDLDFPMTS	d	-3,24
3	B13	OE3524F pyridoxine biosynthesis protein	TKGEAGTGD	C	-3,26
1	D8	OE2801R conserved protein	DGSGLIKR	C	-3,29
3	D24	OE4729R translation elongation factor aEF-2	KKIVEQCER	C	-3,31
2	G2	OE4613F aconitate hydratase EC 4.2.1.3	LSVKGGVGKV	d	-3,57
2	B6	OE3547F conserved protein	IRQDFFSGPK	d	-3,83
2	B7	OE4540R conserved protein	GKDAVSAVAD	C	-3,86
3	B5	OE4540R conserved protein	GKDAVSAVAD	C	-4,00
1	C7	OE4408F phosphoglycerate dehydrogenase EC 1.1.1.95	GIAVTETKNH	C	-4,37
1	D22	OE4654F phosphomethylpyrimidine kinase EC 2.7.4.7	VLAADADALT	C	-4,44
2	H16	OE3718F cell division protein	ALLVTAGPPK	C	-4,74
2	A19	OE2864F phosphoribosylamine--glycine ligase EC 6.3.4.13	DIGSKTLLAD	C	-5,65

2	A21	OE1613R probable acylaminoacyl-peptidase EC 3.4.19.1	ANKQAAYR	C	-7,94
6	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	2,99
6	F2	(OE3925R) thermosome beta chain	VKDRDAQEH	C	2,88
5	F6	(OE3196F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain	TAPPGKR	d	2,73
6	G2	(OE3925R) thermosome beta chain	EEVDNVAVDV	d	2,70
6	G2	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	2,54
5	F2	(OE3925R) thermosome beta chain	EEVDNVAVDV	d	2,50
7	C9	(OE3195F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta chain	DVVAADAVM	C	2,47
5	F2	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	2,44
6	F2	(OE3925R) thermosome beta chain	VKDRDAQEH	d	2,29
6	B3	(OE2622R) pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta chain	GDMPEEPVA	d	2,23
6	D4	(OE1154F) Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (pho	VGINGYGTIG	d	2,21
6	D5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	2,19
6	A16	(OE2935R) fumarate hydratase (EC 4.2.1.2)	TQVEKGIDR	C	2,12
5	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	LDTLAFVGDG	d	2,10
6	D14	(OE2579F) adenylosuccinate synthase (EC 6.3.4.4)	GIGPTYEDKIG	C	2,07
4	F15	(OE2828R) conserved protein	VNEVSEGNG	d	2,06
7	H21	(OE4146F) TATA-binding transcription initiation factor	IVFDKLR	C	2,04
6	B7	(OE2640F) phosphopyruvate hydratase (EC 4.2.1.11) (enolase)	GNKTVEAEVT	C	1,98
6	D19	(OE5208R) arginine deiminase (EC 3.5.3.6)	KPEVDIAR	C	1,96
5	H2	(OE3925R) thermosome beta chain	EEVDNVAVDV	d	1,95
6	D4	(OE1154F) Glyceraldehyde-3-phosphate dehydrogenase	EQYGIEKVR	C	1,93
5	F2	(OE3925R) thermosome beta chain	DIHPTAIIKGY	C	1,92
5	F8	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	C	1,88
6	E18	(OE2809R) translation initiation factor aIF-2 beta chain	TQDHVLKFLQ	C	1,81
5	H1	(OE3925R) thermosome beta chain	VKDRDAQEH	C	1,78
7	B4	(OE3207F) probable precorrin-8W decarboxylase (EC 1.-.-.-)	KNLAANGLAD	d	1,78
7	G17	(OE3931R) threonine dehydratase (EC 4.2.1.16)	SLDKGQPQA	d	1,77
5	F8	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	d	1,76
7	C12	(OE4122R) thermosome alpha chain	IFVEDVEEAK	d	1,75
7	G17	(OE3931R) threonine dehydratase (EC 4.2.1.16)	SLDKGQPQA	C	1,73
5	G1	(OE4122R) thermosome alpha chain	AKSDDFTR	C	1,72
6	G2	(OE4122R) thermosome alpha chain	AKSDDFTR	C	1,72
5	H1	(OE3925R) thermosome beta chain	DIHPTAIIKGY	C	1,71
7	B9	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	d	1,70
5	F1	(OE4122R) thermosome alpha chain	AKSDDFTR	C	1,69
5	F2	(OE3925R) thermosome beta chain	DIHPTAIIKGY	d	1,68
7	C12	(OE4122R) thermosome alpha chain	AKSDDFTR	C	1,67
5	F14	(OE2515F) conserved protein	VGGQKEGFD	d	1,67
6	C2	(OE4500R) probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	LAGLKER	C	1,66
5	G9	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase	SPPFSKQFGD	C	1,66
6	D19	(OE5208R) arginine deiminase (EC 3.5.3.6)	KPEVDIAR	d	1,65
7	G17	(OE3931R) threonine dehydratase (EC 4.2.1.16)	TVLKDSPGSL	d	1,65

7	C12	(OE1737R) dnaK-type molecular chaperone hsp70	QATKDAGEIA	C	1,64
5	G2	(OE4122R) thermosome alpha chain	AKSDDFTR	C	1,63
6	C8	(OE1270F) glutamate dehydrogenase (EC 1.4.1.2)	GPYKGGLR	C	1,63
6	H10	(OE2602R) ribosomal protein L1	GKMPTPLQP	C	1,63
7	D6	(OE1371R) prefoldin beta chain	VETLQKQEDR	d	1,63
5	H16	(OE4146F) TATA-binding transcription initiation factor	SGKIVCTGAK	C	1,62
4	D20	(OE2627F) ribosomal protein S13	IGQTDLDGTK	d	1,62
7	D12	(OE3925R) thermosome beta chain	DIHPTAIIKGY	C	1,62
7	B9	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	C	1,61
6	C10	(OE1270F) glutamate dehydrogenase (EC 1.4.1.2)	GPYKGGLR	C	1,59
5	H2	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	1,59
7	C12	(OE1737R) dnaK-type molecular chaperone hsp70	DAEEYLGQDV	C	1,59
4	G8	(OE2667F) nucleoside-diphosphate kinase (EC 2.7.4.6)	TFVMVKPDGV	d	1,58
6	E17	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	d	1,56
6	C7	(OE3931R) threonine dehydratase (EC 4.2.1.16)	TVLKDSPGSL	d	1,56
6	G1	(OE4122R) thermosome alpha chain	AKSDDFTR	C	1,56
5	H1	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	1,54
5	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	EEKLAEFDGF	C	1,53
6	H1	(OE3925R) thermosome beta chain	DIHPTAIIKGY	d	1,53
6	F12	(OE2641F) ribosomal protein S2	FPAEKFAEAV	C	1,51
5	F19	(OE1405R) conserved protein	LYPNLDDLVN	d	1,51
5	G1	(OE4122R) thermosome alpha chain	VKTQAIESAT	d	1,51
7	E17	(OE2622R) pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta chain	GDMPEEPVA	C	1,50
7	D12	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	1,50
7	A21	(OE1160R) ribosomal protein L10.eR	KFPHQIIR	d	1,50
6	H8	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,49
6	G9	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1	SPPFSKQFGD	C	1,48
7	G13	(OE2648F) conserved protein	VSSLVEFAKE	C	1,48
6	B15	(OE2935R) fumarate hydratase (EC 4.2.1.2)	TVAGSLNKIA	C	1,48
4	D13	(OE3869R) ribosomal protein S24.eR	AKVYDSPAQA	d	1,48
5	H8	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,48
6	H1	(OE3925R) thermosome beta chain	EEVDNVAVDV	d	1,48
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,48
6	F19	(OE1405R) conserved protein	YGLAIKR	d	1,46
6	B22	(OE4613F) aconitate hydratase (EC 4.2.1.3)	AKAADSGVLV	d	1,46
7	C12	(OE1737R) dnaK-type molecular chaperone hsp70	QATKDAGEIA	d	1,45
7	C12	(OE1737R) dnaK-type molecular chaperone hsp70	LTEAAEEAKIE	C	1,45
6	B7	(OE2640F) phosphopyruvate hydratase (EC 4.2.1.11)	TAKLNELIR	C	1,45
5	E3	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	VAIKGPLTTPV	C	1,45
4	D13	(OE3869R) ribosomal protein S24.eR	TDVQFKIVHD	d	1,45
5	H1	(OE3925R) thermosome beta chain	VKDRDAQEH	d	1,45
7	E11	(OE1275F) proteasome alpha chain	TPEGVVLVVD	C	1,45
6	C21	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,44
6	B3	(OE2622R) pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta chain	GDMPEEPVA	C	1,44
4	G19	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	d	1,44
4	F13	(OE3874R) DNA-directed RNA polymerase (EC 2.7.7.6) chain	IVTKSIDER	C	1,44

		E'			
6	H16	(OE4146F) TATA-binding transcription initiation factor	IVFDKLR	C	1,43
6	F2	(OE3925R) thermosome beta chain	DIHPTAIIKGY	d	1,43
5	F12	(OE2019F) fructose-bisphosphate aldolase (EC 4.1.2.13) 1	GQGLKNDKN	C	1,43
6	B16	(OE2458R) IMP dehydrogenase (EC 1.1.1.205)	EAAEAVVDFA	d	1,43
6	D21	(OE3718F) cell division protein	KSGESVQGG	d	1,43
5	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	1,43
4	D10	(OE3410F) ribosomal protein S8	FEVELKGAIN	d	1,43
7	A16	(OE4613F) aconitate hydratase (EC 4.2.1.3)	AKAADSGVLV	C	1,42
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	LIEKNTAIPTT	d	1,42
4	F7	(OE2667F) nucleoside-diphosphate kinase (EC 2.7.4.6)	TFVMVKPDGV	d	1,42
4	A22	(OE2627F) ribosomal protein S13	IGQTDLDGTK	d	1,42
6	G1	(OE4122R) thermosome alpha chain	AKSDDFTR	d	1,42
5	G22	(OE4626R) probable translation initiation factor SUI1	NKGFNVA	d	1,42
7	H14	(OE2165R) ribosomal protein S15	GDKLDEEFAY	d	1,41
5	G9	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase	SPPFSKQFGD	d	1,41
5	D19	(OE5208R) arginine deiminase (EC 3.5.3.6)	KPEVDIAR	C	1,40
7	C1	(OE3410F) ribosomal protein S8	GYIDGFEFVD	C	1,39
6	D4	(OE1154F) Glyceraldehyde-3-phosphate dehydrogenase	EQYGIEKVR	d	1,39
7	H8	(OE2015R) 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	YKPAYLLQR	d	1,39
4	C19	(OE2165R) ribosomal protein S15	GDKLDEEFAY	d	1,39
4	G20	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	C	1,38
4	G20	(OE3524F) pyridoxine biosynthesis protein	GSELVKR	C	1,38
4	G19	(OE3524F) pyridoxine biosynthesis protein	GSELVKR	d	1,38
6	B7	(OE2640F) phosphopyruvate hydratase (EC 4.2.1.11)	GNKTVEAEVT	d	1,38
7	H8	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	d	1,38
6	C5	(OE2373F) probable phosphate acetyltransferase (EC 2.3.1.8)	LQSNVGKTLD	d	1,38
6	E9	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase	SPPFSKQFGD	C	1,38
5	H13	(OE2374R) purine-binding chemotaxis protein cheW2	VKLGEDGAAD	d	1,37
7	A8	(OE1407F) inorganic pyrophosphatase (EC 3.6.1.1)	NKYEYDKDIP	d	1,37
6	F12	(OE2019F) fructose-bisphosphate aldolase (EC 4.1.2.13) 1	GQGLKNDKN	C	1,37
7	D12	(OE3925R) thermosome beta chain	VKDRDAQEH	d	1,37
6	F5	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	C	1,37
7	A4	(OE2627F) ribosomal protein S13	IGQTDLDGTK	d	1,37
7	C4	(OE2165R) ribosomal protein S15	VVELAEQGHD	d	1,36
5	H16	(OE4146F) TATA-binding transcription initiation factor	IVFDKLR	C	1,36
6	F17	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	KDIVKIEGR	d	1,36
7	H16	(OE1557R) transcription antitermination protein homolog	IDEGKDQVTV	d	1,36
7	A4	(OE3817R) ribosomal protein S19.eR	KVAIDGPIGVK	d	1,35
7	H13	(OE4735R) ribosomal protein S7	LKYGGISVPQ	d	1,35
5	E3	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	VAIKGPLTTPV	d	1,35
4	G13	(OE1275F) proteasome alpha chain	TPEGVVLVVD	C	1,35
7	H7	(OE3402F) ribosomal protein L14	VKFEDNAAVI	d	1,35
7	B1	(OE1903F) glycine-rich protein	TNNKLDR	C	1,34
6	F1	(OE4122R) thermosome alpha chain	AKSDDFTR	C	1,34
4	F15	(OE2828R) conserved protein	VNEVSEGNG	C	1,34

7	H21	(OE4146F) TATA-binding transcription initiation factor	IVFDKLR	d	1,34
7	B19	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	d	1,34
6	C6	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	1,33
7	G24	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	C	1,33
4	H12	(OE2159R) ribosomal protein S3a.eR	IQPVAYTTKQ	d	1,33
4	C4	(OE4720R) ribosomal protein S10	KSPDGEGTAT	d	1,33
7	C12	(OE1737R) dnaK-type molecular chaperone hsp70	LTEAAEEAKIE	d	1,33
7	H1	(OE3410F) ribosomal protein S8	GYIDGFEFVD	d	1,32
6	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	d	1,32
4	G20	(OE3524F) pyridoxine biosynthesis protein	NIKSAIR	C	1,32
5	F13	(OE1672F) orotate phosphoribosyltransferase homolog	KHQWDEGDM	d	1,32
7	H1	(OE3410F) ribosomal protein S8	YSVGADGFEQ	d	1,32
4	F13	(OE3874R) DNA-directed RNA polymerase (EC 2.7.7.6) chain E'	LLQDKLEGR	d	1,31
7	D12	(OE3925R) thermosome beta chain	EEVDNVAVDV	d	1,31
5	G1	(OE4122R) thermosome alpha chain	AKSDDFTR	d	1,31
6	F17	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	KDIVKIEGR	C	1,31
7	C12	(OE4122R) thermosome alpha chain	VKTQAIESAT	d	1,31
6	G20	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	d	1,31
7	A11	(OE3415F) ribosomal protein S5	DDQVGGAIQK	d	1,31
4	B23	(OE2865R) succinate dehydrogenase (EC 1.3.99.1) chain A (flavoprotein)	TEDGLKQALA	d	1,31
6	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	1,31
6	B7	(OE2640F) phosphopyruvate hydratase (EC 4.2.1.11)	TAKLNELIR	d	1,30
7	D7	(OE3395F) ribosomal protein S3	KAGHTTIDR	d	1,30
5	E18	(OE2809R) translation initiation factor aIF-2 beta chain	KEGNVTVYEN	d	1,30
6	E16	(OE2641F) ribosomal protein S2	FPAEKFAEAV	C	1,30
4	G13	(OE1275F) proteasome alpha chain	SPLLEGSSVE	C	1,30
5	F23	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	d	1,30
6	H1	(OE3925R) thermosome beta chain	VKDRDAQEH	C	1,30
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	QATKDAGEIA	C	1,29
4	G20	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	C	1,29
5	E4	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	VAIKGPLTTPV	C	1,29
7	G6	(OE3389F) ribosomal protein L4.eR	KYQEPTSILFV	d	1,29
7	H1	(OE3410F) ribosomal protein S8	FEVELKGAIN	d	1,29
6	F19	(OE1405R) conserved protein	DLTAFQKNILT	d	1,29
6	D13	(OE3869R) ribosomal protein S24.eR	TDVQFKIVHD	d	1,29
6	D20	(OE5208R) arginine deiminase (EC 3.5.3.6)	KPEVDIAR	C	1,29
7	C2	(OE5162D1F) conserved protein	AAVMPSKTDR	d	1,28
5	H15	(OE2515F) conserved protein	VGGQKEGFD	d	1,28
7	C6	(OE2515F) conserved protein	VGGQKEGFD	d	1,28
7	E2	(OE2165R) ribosomal protein S15	GDKLDEEFAY	d	1,28
5	E22	(OE1903F) glycine-rich protein	TNNKLDR	C	1,28
7	F10	(OE3393F) ribosomal protein S19	GLSEEHHKVL	d	1,28
7	E17	(OE2622R) pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta chain	GDMPEEPVA	d	1,28
6	H10	(OE2602R) ribosomal protein L1	GKMPTPLQP	d	1,28

7	D5	(OE4146F) TATA-binding transcription initiation factor	TQDPKSAALI	C	1,27
4	G17	(OE3412F) ribosomal protein L32.eR	IASKVGAR	C	1,27
5	E4	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	AGQDKANPT	C	1,27
5	F15	(OE3925R) thermosome beta chain	DIHPTAIIKGY	C	1,27
6	H16	(OE4146F) TATA-binding transcription initiation factor	IVFDKLR	d	1,26
4	C19	(OE2165R) ribosomal protein S15	LHEHVEANGQ	d	1,26
6	D5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,26
5	F10	(OE4306F) conserved protein	AFSAVPVVKA	d	1,26
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,26
5	H16	(OE4146F) TATA-binding transcription initiation factor	TQDPKSAALI	C	1,26
7	H8	(OE2015R) 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)	YKPAYLLQR	C	1,26
4	B8	(OE3798R) conserved hypothetical protein	VQAVKDYIVV	d	1,26
6	H16	(OE4146F) TATA-binding transcription initiation factor	TQDPKSAALI	C	1,26
6	E16	(OE2641F) ribosomal protein S2	FPAEKFAEAV	d	1,25
5	E4	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	VAIKGPLTTPV	d	1,25
4	G15	(OE3710R) trkA domain protein	KYADEVDEIV	d	1,25
5	H16	(OE4146F) TATA-binding transcription initiation factor	TQDPKSAALI	d	1,25
7	G2	(OE2097F) conserved protein	KFASDIGR	C	1,25
5	H2	(OE4122R) thermosome alpha chain	TSGEDAQSM	d	1,25
6	D13	(OE4159F) adenosylhomocysteinase (EC 3.3.1.1)	GVAKKAAGQ	d	1,25
5	H13	(OE2374R) purine-binding chemotaxis protein cheW2	VKLGEDGAAD	C	1,25
7	A13	(OE4735R) ribosomal protein S7	LKYGGISVPQ	d	1,25
4	H11	(OE2159R) ribosomal protein S3a.eR	GSSKVAVTVT	d	1,25
6	A11	(OE1584R) conserved protein	FKEGETLDTE	d	1,25
7	B24	(OE4459R) ribosomal protein L31.eR	QHLAKQFAVD	d	1,25
5	F13	(OE1672F) orotate phosphoribosyltransferase homolog	KHQWDEGDM	C	1,25
5	E12	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,25
7	F7	(OE1584R) conserved protein	FKEGETLDTE	d	1,24
5	H16	(OE4146F) TATA-binding transcription initiation factor	SGKIVCTGAK	d	1,24
6	E22	(OE1903F) glycine-rich protein	TNNKLDR	C	1,24
4	B24	(OE4735R) ribosomal protein S7	LKYGGISVPQ	d	1,24
7	H10	(OE1559R) cell division protein ftsZ1	SVKGITELITK	d	1,24
7	F5	(OE2641F) ribosomal protein S2	FPAEKFAEAV	d	1,23
7	B1	(OE4459R) ribosomal protein L31.eR	QHLAKQFAVD	d	1,23
7	H13	(OE3415F) ribosomal protein S5	DDQVGGAIQK	C	1,23
7	D5	(OE4146F) TATA-binding transcription initiation factor	ELSIKVEDDP	d	1,23
7	H13	(OE3415F) ribosomal protein S5	DDQVGGAIQK	d	1,23
7	F6	(OE4306F) conserved protein	AFSAVPVVKA	d	1,23
7	A8	(OE1407F) inorganic pyrophosphatase (EC 3.6.1.1)	NKYEYDKDIP	C	1,23
7	G6	(OE3389F) ribosomal protein L4.eR	VFEEPVRPDL	d	1,23
5	H16	(OE4146F) TATA-binding transcription initiation factor	ELSIKVEDDP	d	1,23
7	E11	(OE1275F) proteasome alpha chain	TPEGVVLVVD	d	1,23
7	F8	(OE1442R) conserved hypothetical protein	YVEIEDIGKQG	d	1,23
5	F19	(OE1405R) conserved protein	DLTAFQKNILT	d	1,22
5	H8	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,22
7	C4	(OE2165R) ribosomal protein S15	GDKLDEEFAY	d	1,22
4	G20	(OE3524F) pyridoxine biosynthesis protein	GSELVKR	d	1,22

7	A13	(OE4735R) ribosomal protein S7	HAQKQFKKS	d	1,22
6	B15	(OE2935R) fumarate hydratase (EC 4.2.1.2)	ALGVVKKAAA	C	1,22
7	H13	(OE3415F) ribosomal protein S5	TTVNFAKATF	d	1,22
6	B4	(OE3673F) conserved protein	KLAELGVGED	d	1,22
4	C20	(OE2165R) ribosomal protein S15	NLLEKAVR	d	1,22
5	G5	(OE4007F) electron transfer flavoprotein alpha chain	EMYGSKVETT	d	1,22
7	C12	(OE4122R) thermosome alpha chain	AKSDDFTR	d	1,22
7	A2	(OE2664F) ribosomal protein S28.eR	VGDVIQLKET	d	1,21
6	A11	(OE1584R) conserved protein	ELIEKIEGKR	d	1,21
7	B10	(OE2601R) ribosomal protein L10	TTEEVPEWKR	C	1,21
7	C4	(OE2165R) ribosomal protein S15	ALQNTQSKIR	d	1,21
6	H15	(OE2515F) conserved protein	VGGQKEGFD	d	1,21
4	G17	(OE3412F) ribosomal protein L32.eR	GLTEKTPDLS	d	1,21
7	B1	(OE1903F) glycine-rich protein	TNNKLDR	d	1,20
7	C21	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	1,20
6	G17	(OE3412F) ribosomal protein L32.eR	GIKGKGDTVE	d	1,20
6	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	d	1,20
7	F6	(OE4306F) conserved protein	AFSAVPVVKA	C	1,20
6	D10	(OE1584R) conserved protein	VQEHKEIR	C	1,20
7	F4	(OE3207F) probable precorrin-8W decarboxylase (EC 1.-.-.-)	KNLAANGLAD	C	1,20
5	F5	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	d	1,20
7	F7	(OE1584R) conserved protein	VQEHKEIR	d	1,20
5	F19	(OE1405R) conserved protein	YGLAIKR	d	1,19
6	H10	(OE2602R) ribosomal protein L1	MKNTVQIR	d	1,19
4	G5	(OE2306F) conserved protein	YTQQETAVKG	C	1,19
5	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	d	1,19
7	B10	(OE2601R) ribosomal protein L10	TAPDLIAKGR	C	1,19
5	E16	(OE2641F) ribosomal protein S2	FPAEKFAEAV	C	1,19
5	E18	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	d	1,19
6	F17	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	DYEVDEKR	d	1,19
7	D5	(OE4146F) TATA-binding transcription initiation factor	TQDPKSAALI	d	1,19
6	C4	(OE3571R) GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2), subun	VIGEVTPEKV	d	1,19
4	C19	(OE2165R) ribosomal protein S15	NLLEKAVR	d	1,19
7	C15	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	d	1,19
7	C6	(OE2515F) conserved protein	VGGQKEGFD	C	1,19
7	D21	(OE2635F) ribosomal protein S9	YQKSYR	d	1,19
6	C8	(OE1270F) glutamate dehydrogenase (EC 1.4.1.2)	GPYKGGLR	d	1,18
7	B2	(OE3219F) conserved cobalamin operon protein	TKETVVGEFD	C	1,18
7	G24	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	d	1,18
6	H17	(OE2097F) conserved protein	KFASDIGR	C	1,18
7	C15	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	C	1,18
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	LTEAAEEAKIE	d	1,18
6	H13	(OE2374R) purine-binding chemotaxis protein cheW2	VKLGEDGAAD	d	1,18
6	H15	(OE2515F) conserved protein	VGGQKEGFD	C	1,18
5	F7	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,18

4	C11	(OE3394F) ribosomal protein L22	EISGETVADA	d	1,18
4	B23	(OE2865R) succinate dehydrogenase (EC 1.3.99.1) chain A (flavoprotein)	YQDVYVADKS	d	1,18
6	F19	(OE1405R) conserved protein	YGLAIKR	C	1,17
4	C20	(OE2165R) ribosomal protein S15	GDKLDEEFAY	d	1,17
4	E2	(OE3415F) ribosomal protein S5	TTVNFAKATF	C	1,17
5	F23	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	C	1,17
5	E16	(OE2641F) ribosomal protein S2	FPAEKFAEAV	d	1,17
6	F10	(OE4306F) conserved protein	AFSAVPVVKA	d	1,17
7	F7	(OE1584R) conserved protein	ASERDDLNAK	C	1,17
7	G10	(OE2635F) ribosomal protein S9	YQKSYR	d	1,17
7	H13	(OE3415F) ribosomal protein S5	TTVNFAKATF	C	1,17
7	B19	(OE3524F) pyridoxine biosynthesis protein	GFAKMQKGG	d	1,17
7	B9	(OE2632F) ribosomal protein L18.eR	YASEDETVIV	d	1,17
5	F12	(OE2641F) ribosomal protein S2	FPAEKFAEAV	d	1,17
4	C11	(OE3394F) ribosomal protein L22	SISLKHSKAIA	C	1,17
7	B9	(OE4122R) thermosome alpha chain	VKTQAIESAT	d	1,17
7	B22	(OE3357R) ribosomal protein S8.eR	NIITKGAIIETD	d	1,16
7	E5	(OE3988R) H+-transporting two-sector ATPase (EC 3.6.3.14) chain E	VNNTFDSILA	d	1,16
7	F5	(OE2641F) ribosomal protein S2	FPAEKFAEAV	C	1,16
7	D7	(OE3395F) ribosomal protein S3	KITTQLEER	C	1,16
5	F10	(OE4306F) conserved protein	EFMTSDVVTV	d	1,16
4	G17	(OE3412F) ribosomal protein L32.eR	IASKVGAR	d	1,16
5	A11	(OE1584R) conserved protein	EKVDEAQEH	d	1,16
5	H1	(OE3925R) thermosome beta chain	DIHPTAIIKGY	d	1,16
5	H2	(OE4122R) thermosome alpha chain	AKSDDFTR	d	1,16
6	A11	(OE1584R) conserved protein	EKVDEAQEH	d	1,16
5	H15	(OE2515F) conserved protein	VGGQKEGFD	C	1,16
4	G19	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	d	1,16
7	F6	(OE4306F) conserved protein	EFMTSDVVTV	d	1,16
6	A16	(OE2935R) fumarate hydratase (EC 4.2.1.2)	TVAGSLNKIA	C	1,16
7	B10	(OE2601R) ribosomal protein L10	TAPDLIAKGR	d	1,16
4	G13	(OE1275F) proteasome alpha chain	TPEGVVLVVD	d	1,15
4	G17	(OE3412F) ribosomal protein L32.eR	GKHPSGFEEV	d	1,15
4	E2	(OE3415F) ribosomal protein S5	TTVNFAKATF	d	1,15
5	H16	(OE4146F) TATA-binding transcription initiation factor	IVFDKLR	d	1,15
4	F19	(OE3389F) ribosomal protein L4.eR	KYQEPTSILFV	d	1,15
7	D5	(OE4146F) TATA-binding transcription initiation factor	SGKIVCTGAK	d	1,15
5	A11	(OE1584R) conserved protein	VQEHKEIR	C	1,15
7	C4	(OE2165R) ribosomal protein S15	NLLEKAVR	d	1,15
7	E2	(OE2165R) ribosomal protein S15	VVELAEQGHD	d	1,15
7	E2	(OE2165R) ribosomal protein S15	ALQNTQSKIR	d	1,15
5	F14	(OE2515F) conserved protein	VGGQKEGFD	C	1,14
6	A11	(OE1584R) conserved protein	VQEHKEIR	d	1,14
6	A11	(OE1584R) conserved protein	ASERDDLNAK	d	1,14
5	F12	(OE2641F) ribosomal protein S2	FPAEKFAEAV	C	1,14
6	D20	(OE5208R) arginine deiminase (EC 3.5.3.6)	KPEVDIAR	d	1,14
5	H8	(OE4721R) translation elongation factor aEF-1 alpha chain	HQNLAVIGHV	d	1,14
7	F7	(OE1584R) conserved protein	EKVDEAQEH	d	1,14

7	C15	(OE3524F) pyridoxine biosynthesis protein	GSELVKR	d	1,14
4	F1	(OE4735R) ribosomal protein S7	LKYGGISVPQ	d	1,14
4	F14	(OE1275F) proteasome alpha chain	TPEGVVLVVD	C	1,14
7	B10	(OE2601R) ribosomal protein L10	TTEEVPEWKR	d	1,14
4	G17	(OE3412F) ribosomal protein L32.eR	GIKGKGDTVE	C	1,14
5	F7	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	1,14
4	E2	(OE3415F) ribosomal protein S5	DDQVGGAIQK	d	1,13
7	G10	(OE2635F) ribosomal protein S9	ESKKWGGPG	d	1,13
4	F13	(OE1275F) proteasome alpha chain	TPEGVVLVVD	d	1,13
6	H13	(OE2374R) purine-binding chemotaxis protein cheW2	VKLGEDGAAD	C	1,13
5	E9	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,13
6	C6	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	d	1,13
6	C5	(OE2373F) probable phosphate acetyltransferase (EC 2.3.1.8)	LQSNVGKTLD	C	1,13
6	F17	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	DYEVDEKR	C	1,13
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	KETTVNLPFV	C	1,13
7	E2	(OE2165R) ribosomal protein S15	NLLEKAVR	d	1,13
4	G13	(OE3874R) DNA-directed RNA polymerase (EC 2.7.7.6) chain E'	LLQDKLEGR	d	1,13
5	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	1,12
4	E2	(OE3415F) ribosomal protein S5	DDQVGGAIQK	C	1,12
4	F13	(OE3874R) DNA-directed RNA polymerase (EC 2.7.7.6) chain E'	IVTKSIDER	d	1,12
6	C2	(OE4500R) probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	LPGVEGMKG	C	1,12
6	A11	(OE1584R) conserved protein	KLQKSGHL	C	1,12
4	G5	(OE2306F) conserved protein	YTQQETAVKG	d	1,12
5	E4	(OE3634F) isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	AGQDKANPT	d	1,12
6	A11	(OE1584R) conserved protein	KLQKSGHL	d	1,12
5	E18	(OE2809R) translation initiation factor aIF-2 beta chain	KEGNVTVYEN	C	1,12
6	A11	(OE1584R) conserved protein	VQEHKEIR	C	1,12
7	D21	(OE2635F) ribosomal protein S9	ESKKWGGPG	d	1,12
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	1,12
7	G1	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	d	1,12
4	G13	(OE1275F) proteasome alpha chain	LFETDPSGTS	d	1,11
7	C1	(OE3410F) ribosomal protein S8	FEVELKGAIN	d	1,11
5	E8	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	d	1,11
4	F14	(OE1275F) proteasome alpha chain	TPEGVVLVVD	d	1,11
5	A11	(OE1584R) conserved protein	FKEGETLDTE	C	1,11
7	F7	(OE1584R) conserved protein	ELIEKIEGKR	C	1,11
7	G1	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	C	1,11
6	H8	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	1,11
4	E10	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	C	1,11
6	F23	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	C	1,11
6	E19	(OE4027F) conserved protein	EQLDEQKAYI	C	1,11
5	F10	(OE4306F) conserved protein	AFSAVPVVKA	C	1,11
5	E17	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	C	1,11

6	H16	(OE4146F) TATA-binding transcription initiation factor	ELSIKVEDDP	d	1,11
7	F7	(OE1584R) conserved protein	KLQKSGHL	d	1,11
7	A15	(OE2871F) probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.157	KDSPGFVVNR	d	1,10
7	D7	(OE3395F) ribosomal protein S3	KITTQLEER	d	1,10
7	B1	(OE4459R) ribosomal protein L31.eR	DVTKVPSHER	d	1,10
7	H9	(OE4736R) ribosomal protein S12	GLGKKSDPLE	d	1,10
4	H13	(OE3565F) molybdenum cofactor biosynthesis protein B	SAADIGTKIIG	d	1,10
7	F4	(OE3207F) probable precorrin-8W decarboxylase (EC 1.-.-.-)	KNLAANGLAD	d	1,10
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	QATKDAGEIA	d	1,09
5	F18	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	C	1,09
7	D21	(OE2635F) ribosomal protein S9	LKMLEPFR	d	1,09
6	F23	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	d	1,09
7	D6	(OE2662F) ribosomal protein L7a.eR/HS6 (isolated from the small ribosome)	DTGSVKKGTN	d	1,09
7	B19	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	C	1,09
7	B7	(OE1792F) conserved protein	SAEGGLTGIIK	d	1,09
5	F1	(OE4122R) thermosome alpha chain	AKSDDFTR	d	1,09
6	D17	(OE1584R) conserved protein	FKEGETLDTE	d	1,09
7	G2	(OE2097F) conserved protein	SPTGKAIFGD	C	1,09
5	A11	(OE1584R) conserved protein	ELIEKIEGKR	C	1,09
5	F1	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	1,09
7	G24	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	d	1,09
5	H1	(OE3925R) thermosome beta chain	EEVDNVAVDV	d	1,09
7	A16	(OE3389F) ribosomal protein L4.eR	VFEEPVRPDL	d	1,08
5	F20	(OE1405R) conserved protein	YGLAIKR	d	1,08
4	G15	(OE3710R) trkA domain protein	LLAFGKHDAS	d	1,08
6	G17	(OE3412F) ribosomal protein L32.eR	GLTEKTPDLS	d	1,08
4	G20	(OE3524F) pyridoxine biosynthesis protein	NIKSAIR	d	1,08
6	F10	(OE4306F) conserved protein	AFSAVPVVKA	C	1,08
6	H10	(OE2602R) ribosomal protein L1	MKNTVQIR	C	1,08
5	A11	(OE1584R) conserved protein	EKVDEAQEH	C	1,07
5	H17	(OE2097F) conserved protein	SPTGKAIFGD	C	1,07
5	H17	(OE2097F) conserved protein	KFASDIGR	C	1,07
6	B4	(OE3673F) conserved protein	KLAELGVGED	C	1,07
7	D3	(OE2165R) ribosomal protein S15	NLLEKAVR	d	1,07
7	G2	(OE2097F) conserved protein	VGDKGDEILA	d	1,06
4	D14	(OE2633F) ribosomal protein L13	GMLPYKQDD	C	1,06
7	F7	(OE1584R) conserved protein	KLQKSGHL	C	1,06
5	F23	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	d	1,06
5	G22	(OE4626R) probable translation initiation factor SUI1	NKGFNVA	C	1,06
4	G13	(OE1275F) proteasome alpha chain	SPLLEGSSVE	d	1,06
7	G10	(OE2635F) ribosomal protein S9	LKMLEPFR	C	1,06
6	B13	(OE3168R) pyridoxal phosphate-dependent aminotransferase	HAGTSKVEG	d	1,06
4	G17	(OE3412F) ribosomal protein L32.eR	GKHPSGFEEV	C	1,06
4	G20	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	C	1,06
7	E11	(OE1275F) proteasome alpha chain	LFETDPSGTS	d	1,06
6	C15	(OE2057F) thiamin biosynthesis protein thiC	AQAFHDQTLP	d	1,06
5	G18	(OE2097F) conserved protein	SPTGKAIFGD	C	1,06
7	F3	(OE3817R) ribosomal protein S19.eR	LDEPDWANY	d	1,05

5	G1	(OE4122R) thermosome alpha chain	VKTQAIESAT	C	1,05
5	A11	(OE1584R) conserved protein	KLQKSGHL	d	1,05
4	H13	(OE3565F) molybdenum cofactor biosynthesis protein B	SAADIGTKIIG	C	1,05
5	G5	(OE4007F) electron transfer flavoprotein alpha chain	EMYGSKVETT	C	1,05
5	A11	(OE1584R) conserved protein	KLQKSGHL	C	1,05
7	B19	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	C	1,05
4	E9	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	DYEVDEKR	C	1,05
5	E18	(OE2809R) translation initiation factor aIF-2 beta chain	AMDEKPDVTG	d	1,05
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	1,04
7	H7	(OE3402F) ribosomal protein L14	ELKITSVMGY	d	1,04
4	G15	(OE3710R) trkA domain protein	KYADEVDEIV	C	1,04
4	C20	(OE2165R) ribosomal protein S15	NLLEKAVR	C	1,04
7	G6	(OE3389F) ribosomal protein L4.eR	VFEEPVRPDL	C	1,04
7	C1	(OE3410F) ribosomal protein S8	YSVGADGFEQ	d	1,04
7	F3	(OE3817R) ribosomal protein S19.eR	KVAIDGPIGVK	d	1,04
5	A11	(OE1584R) conserved protein	FKEGETLDTE	d	1,04
6	C5	(OE2373F) probable phosphate acetyltransferase (EC 2.3.1.8)	TKDAAVITGG	d	1,04
7	C15	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	d	1,04
5	E22	(OE1903F) glycine-rich protein	TNNKLDR	d	1,03
7	H7	(OE3402F) ribosomal protein L14	GTEIKGPISR	d	1,03
7	A21	(OE1160R) ribosomal protein L10.eR	KIDKPSYTR	d	1,03
6	A11	(OE1584R) conserved protein	FKEGETLDTE	C	1,03
7	C10	(OE2628F) ribosomal protein S4	YGLKNKEELW	d	1,03
7	H10	(OE1559R) cell division protein ftsZ1	LLDSVGKLPV	d	1,03
7	G1	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	d	1,03
7	G1	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	C	1,02
6	A11	(OE1584R) conserved protein	EKVDEAQEH	C	1,02
7	D22	(OE3393F) ribosomal protein S19	GLSEEHHKVL	d	1,02
7	C21	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	1,02
6	H1	(OE3925R) thermosome beta chain	VKDRDAQEH	d	1,02
7	D21	(OE2635F) ribosomal protein S9	LKMLEPFR	d	1,02
6	H17	(OE2097F) conserved protein	SPTGKAIFGD	C	1,02
5	F13	(OE1672F) orotate phosphoribosyltransferase homolog	KHQWDEGDM	C	1,02
6	H1	(OE3925R) thermosome beta chain	DIHPTAIIKGY	C	1,01
4	B4	(OE4459R) ribosomal protein L31.eR	QHLAKQFAVD	d	1,01
6	D14	(OE2579F) adenylosuccinate synthase (EC 6.3.4.4)	ELDGAEEAAK	d	1,01
7	G24	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	C	1,01
7	F10	(OE3393F) ribosomal protein S19	SSKFVPLK	d	1,00
6	D10	(OE1584R) conserved protein	EKVDEAQEH	d	1,00
6	H16	(OE4146F) TATA-binding transcription initiation factor	TQDPKSAALI	d	1,00
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	LTEAAEEAKIE	C	-1,01
5	E18	(OE2809R) translation initiation factor aIF-2 beta chain	TQDHVLKFLQ	d	-1,01
7	C12	(OE1737R) dnaK-type molecular chaperone hsp70	KETTVNLPFV	d	-1,01
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,01
6	F7	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	d	-1,01
5	H2	(OE4122R) thermosome alpha chain	VKTQAIESAT	d	-1,02

6	E17	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	C	-1,02
7	D1	(OE4626R) probable translation initiation factor SUI1	NKGFNVA	C	-1,02
6	D10	(OE1584R) conserved protein	FKEGETLDTE	d	-1,02
7	D5	(OE4146F) TATA-binding transcription initiation factor	ELSIKVEDDP	C	-1,02
7	F7	(OE1584R) conserved protein	EKVDEAQEH	C	-1,02
4	D10	(OE3410F) ribosomal protein S8	GYIDGFEFVD	d	-1,02
7	D12	(OE3925R) thermosome beta chain	DIHPTAIIKGY	d	-1,03
4	H11	(OE2159R) ribosomal protein S3a.eR	IQPVAYTTKQ	d	-1,03
7	D21	(OE2635F) ribosomal protein S9	ESKKWGGPG	C	-1,03
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	LLDLPVSDEM	d	-1,03
5	F1	(OE3925R) thermosome beta chain	DIHPTAIIKGY	d	-1,03
4	G23	(OE5201F) aspartate carbamoyltransferase (EC 2.1.3.2) catalytic chain	LGGDIVDMGS	d	-1,03
7	G2	(OE2097F) conserved protein	KFASDIGR	d	-1,03
5	F1	(OE4122R) thermosome alpha chain	TSGEDAQSM	C	-1,03
7	G10	(OE2635F) ribosomal protein S9	LKMLEPFR	C	-1,03
7	C21	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,03
5	H8	(OE4721R) translation elongation factor aEF-1 alpha chain	DFVKNMITGA	C	-1,03
7	G10	(OE2635F) ribosomal protein S9	ESKKWGGPG	C	-1,03
7	G10	(OE2635F) ribosomal protein S9	YQKSYR	C	-1,04
4	G23	(OE5201F) aspartate carbamoyltransferase (EC 2.1.3.2) catalytic chain	LGGDIVDMGS	C	-1,04
4	H11	(OE2159R) ribosomal protein S3a.eR	SVSKQDQEK	C	-1,04
7	B22	(OE3357R) ribosomal protein S8.eR	GDAEKVR	C	-1,04
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolo	TNKGQIAGTG	d	-1,04
4	G20	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	d	-1,04
6	F12	(OE2019F) fructose-bisphosphate aldolase (EC 4.1.2.13) 1	GQGLKNDKN	d	-1,04
6	C5	(OE2373F) probable phosphate acetyltransferase (EC 2.3.1.8)	TKDAAVITGG	C	-1,04
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	-1,04
7	F8	(OE1442R) conserved hypothetical protein	YVEIEDIGKQG	C	-1,05
7	G7	(OE2629F) ribosomal protein S11	IEDVTPIPHDG	d	-1,05
6	G9	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase	SPPFSKQFGD	d	-1,05
7	D21	(OE2635F) ribosomal protein S9	LKMLEPFR	C	-1,05
7	H8	(OE5206R) carbamate kinase (EC 2.7.2.2)	IGPFYDEDEA	C	-1,05
6	D10	(OE1584R) conserved protein	VQEHKEIR	d	-1,05
4	A24	(OE3407F) ribosomal protein L5	TKAKSPEPEF	C	-1,05
7	G2	(OE2097F) conserved protein	SPTGKAIFGD	d	-1,05
5	H8	(OE4721R) translation elongation factor aEF-1 alpha chain	DFVKNMITGA	d	-1,06
5	D18	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	-1,06
7	D6	(OE1371R) prefoldin beta chain	VETLQKQEDR	C	-1,06
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,06
6	F2	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	-1,06
6	A11	(OE1584R) conserved protein	DDLNAKTR	d	-1,07
7	H9	(OE4736R) ribosomal protein S12	GNAEKPVR	C	-1,08
7	B24	(OE4459R) ribosomal protein L31.eR	DVTKVPSHER	d	-1,08

7	G2	(OE2097F) conserved protein	VGDKGDEILA	C	-1,08
7	D21	(OE2635F) ribosomal protein S9	YQKSYR	C	-1,08
4	C22	(OE3404F) ribosomal protein L24	ASLHEKQDQV	C	-1,09
4	B4	(OE4459R) ribosomal protein L31.eR	QHLAKQFAVD	C	-1,09
4	D20	(OE2627F) ribosomal protein S13	IGQTDLDGTK	C	-1,09
6	H17	(OE2097F) conserved protein	KFASDIGR	d	-1,09
5	G18	(OE2097F) conserved protein	SPTGKAIFGD	d	-1,09
7	A4	(OE2627F) ribosomal protein S13	IGQTDLDGTK	C	-1,10
7	B19	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	d	-1,10
6	D5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,10
7	E11	(OE1275F) proteasome alpha chain	LFETDPSGTS	C	-1,10
6	B16	(OE2458R) IMP dehydrogenase (EC 1.1.1.205)	EIKASVDADV	d	-1,10
4	A10	(OE2632F) ribosomal protein L18.eR	LSSLIAELKSV	C	-1,10
7	F9	(OE4736R) ribosomal protein S12	GLGKKSDPLE	C	-1,10
5	F19	(OE1405R) conserved protein	YGLAIKR	C	-1,11
6	D10	(OE1584R) conserved protein	FKEGETLDTE	C	-1,11
7	A24	(OE4736R) ribosomal protein S12	GLGKKSDPLE	C	-1,11
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,12
7	B19	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	d	-1,12
4	E9	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	DYEVDEKR	d	-1,12
5	F17	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	KDIVKIEGR	d	-1,12
7	C4	(OE2165R) ribosomal protein S15	NLLEKAVR	C	-1,12
5	E17	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	d	-1,12
6	D10	(OE1584R) conserved protein	EKVDEAQEH	C	-1,12
6	D17	(OE1584R) conserved protein	FKEGETLDTE	C	-1,12
7	B9	(OE2632F) ribosomal protein L18.eR	YASEDETVIV	C	-1,12
4	C19	(OE2165R) ribosomal protein S15	VVELAEQGHD	d	-1,13
6	G17	(OE3412F) ribosomal protein L32.eR	GKHPSGFEEV	d	-1,13
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	C	-1,13
6	B7	(OE2640F) phosphopyruvate hydratase (EC 4.2.1.11)	GIDAGAANSI	C	-1,13
7	G6	(OE3389F) ribosomal protein L4.eR	KYQEPTSILFV	C	-1,14
6	C6	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	-1,14
7	F7	(OE1584R) conserved protein	FKEGETLDTE	C	-1,14
5	F12	(OE2019F) fructose-bisphosphate aldolase (EC 4.1.2.13) 1	GQGLKNDKN	d	-1,14
6	G17	(OE3412F) ribosomal protein L32.eR	GKHPSGFEEV	C	-1,14
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,14
5	G18	(OE2097F) conserved protein	KFASDIGR	d	-1,14
5	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,14
6	E10	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	C	-1,14
5	E17	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	d	-1,14
6	F11	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase	SPPFSKQFGD	d	-1,15
6	H2	(OE4122R) thermosome alpha chain	IFVEDVEEAK	d	-1,15
7	B10	(OE2601R) ribosomal protein L10	GEAKSLGLQA	d	-1,15

7	C4	(OE2165R) ribosomal protein S15	ALQNTQSKIR	C	-1,15
5	H2	(OE3925R) thermosome beta chain	VKDRDAQEH	C	-1,15
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,16
4	D10	(OE3410F) ribosomal protein S8	FEVELKGAIN	C	-1,16
7	B1	(OE4459R) ribosomal protein L31.eR	QHLAKQFAVD	C	-1,16
7	B9	(OE2632F) ribosomal protein L18.eR	LSSLIAELKSV	C	-1,16
7	C21	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	-1,17
5	H10	(OE2602R) ribosomal protein L1	MKNTVQIR	C	-1,17
5	E18	(OE2809R) translation initiation factor aIF-2 beta chain	AMDEKPDVTG	C	-1,17
5	G23	(OE3925R) thermosome beta chain	VKDRDAQEH	C	-1,17
7	H9	(OE4736R) ribosomal protein S12	GLGKKSDPLE	C	-1,17
5	F1	(OE4122R) thermosome alpha chain	VKTQAIESAT	d	-1,17
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-1,18
4	D13	(OE3869R) ribosomal protein S24.eR	NKIGADDADA	d	-1,18
5	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,18
7	C2	(OE5162D1F) conserved protein	AAVMPSKTDR	d	-1,18
6	E10	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	d	-1,18
4	G17	(OE3412F) ribosomal protein L32.eR	GLTEKTPDLS	C	-1,18
6	B8	(OE4157F) probable chlorohydrolase	VGHGVVTVG	d	-1,19
7	F3	(OE2627F) ribosomal protein S13	IGQTDLDGTK	d	-1,20
7	C15	(OE3524F) pyridoxine biosynthesis protein	TKGEAGTGD	C	-1,20
4	D10	(OE3410F) ribosomal protein S8	GYIDGFEFVD	C	-1,20
6	H1	(OE3925R) thermosome beta chain	EEVDNVAVDV	C	-1,20
5	F11	(OE3119R) 3-methyl-2-oxobutanoate hydroxymethyltransferase	SPPFSKQFGD	C	-1,20
7	E2	(OE2165R) ribosomal protein S15	NLLEKAVR	C	-1,20
7	B2	(OE3219F) conserved cobalamin operon protein	TKETVVGEFD	d	-1,20
7	B1	(OE4459R) ribosomal protein L31.eR	DVTKVPSHER	C	-1,20
7	D6	(OE2662F) ribosomal protein L7a.eR/HS6 (isolated from the small ribosome	DTGSVKKGTN	C	-1,21
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	VAAMVTDAPK	d	-1,21
4	C12	(OE3400F) ribosomal protein S17	GQVLEGEVAS	d	-1,21
5	B16	(OE2458R) IMP dehydrogenase (EC 1.1.1.205)	DALELMYEHK	C	-1,21
7	B24	(OE4459R) ribosomal protein L31.eR	QHLAKQFAVD	C	-1,21
6	E17	(OE3487R) translation initiation factor aIF-5A	IEAEGVFDGK	d	-1,21
7	A15	(OE2871F) probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.1.57)	AKEIIFTADR	d	-1,22
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,22
7	H16	(OE1557R) transcription antitermination protein homolog	IDEGKDQVTV	C	-1,22
4	B4	(OE4459R) ribosomal protein L31.eR	DVTKVPSHER	C	-1,22
6	D13	(OE3869R) ribosomal protein S24.eR	TDVQFKIVHD	C	-1,22
7	D3	(OE2165R) ribosomal protein S15	NLLEKAVR	C	-1,23
7	F3	(OE3817R) ribosomal protein S19.eR	KVAIDGPIGVK	C	-1,23
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	d	-1,23
5	F23	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	C	-1,23
6	G10	(OE4234R) uracil phosphoribosyltransferase (EC 2.4.2.9)	KGLVKLGR	d	-1,23

5	F8	(OE5206R) carbamate kinase (EC 2.7.2.2)	EELGETPATV	C	-1,24
7	A24	(OE4736R) ribosomal protein S12	GNAEKPVR	C	-1,24
4	G20	(OE3524F) pyridoxine biosynthesis protein	KLEGMDYEE	d	-1,24
5	F7	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	d	-1,24
5	G11	(OE4234R) uracil phosphoribosyltransferase (EC 2.4.2.9) upp	AATPFVEGLL	d	-1,25
7	D6	(OE1371R) prefoldin beta chain	EVGELLVETE	d	-1,25
4	C19	(OE2165R) ribosomal protein S15	NLLEKAVR	C	-1,25
7	E2	(OE2165R) ribosomal protein S15	ALQNTQSKIR	C	-1,25
6	A11	(OE1584R) conserved protein	LRELDKQEEE	d	-1,26
7	C2	(OE4540R) conserved protein	GKDAVSAVAD	d	-1,26
6	B22	(OE4613F) aconitate hydratase (EC 4.2.1.3)	AKAADSGVLV	C	-1,26
7	F11	(OE5160F) glycerol dehydrogenase (EC 1.1.1.6)	AGHKLAELCY	d	-1,26
4	E9	(OE5202F) aspartate carbamoyltransferase (EC 2.1.3.2) regulatory chain	KDIVKIEGR	C	-1,27
7	F3	(OE2627F) ribosomal protein S13	IGQTDLDGTK	C	-1,28
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	d	-1,28
7	H7	(OE3402F) ribosomal protein L14	ELKITSVMGY	C	-1,28
7	H7	(OE3402F) ribosomal protein L14	VKFEDNAAVI	C	-1,28
6	D5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,28
6	G11	(OE4234R) uracil phosphoribosyltransferase (EC 2.4.2.9) upp	AATPFVEGLL	d	-1,28
7	A13	(OE4735R) ribosomal protein S7	HAQKQFKKS	C	-1,28
4	B3	(OE2664F) ribosomal protein S28.eR	VGDVIQLKET	d	-1,28
7	F4	(OE3207F) probable precorrin-8W decarboxylase (EC 1.-.-.-)	SKLALTDDDH	d	-1,30
6	E12	(OE4721R) translation elongation factor aEF-1 alpha chain	GIGKDDIR	d	-1,30
7	C21	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	-1,30
7	H1	(OE3410F) ribosomal protein S8	YSVGADGFEQ	C	-1,30
4	C19	(OE2165R) ribosomal protein S15	GDKLDEEFAY	C	-1,31
6	D5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	C	-1,31
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolo	ENPKGVIVTE	d	-1,31
5	G16	(OE5205R) ornithine carbamoyltransferase (EC 2.1.3.3), catabolic	MHVQKAIVHT	C	-1,31
6	B5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	d	-1,31
4	C11	(OE3394F) ribosomal protein L22	SVPFKQHNSG	C	-1,32
4	C11	(OE3394F) ribosomal protein L22	SVPFKQHNSG	d	-1,32
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	C	-1,33
7	B22	(OE3357R) ribosomal protein S8.eR	NIITKGAIIETD	C	-1,33
7	H1	(OE3410F) ribosomal protein S8	GYIDGFEFVD	C	-1,33
5	G11	(OE4234R) uracil phosphoribosyltransferase (EC 2.4.2.9) upp	KGLVKLGR	d	-1,33
6	G22	(OE4626R) probable translation initiation factor SUI1	NKGFNVA	C	-1,34
6	E15	(OE2197R) conserved protein	SYLAAKADAD	d	-1,34
7	H13	(OE4735R) ribosomal protein S7	LKYGGISVPQ	C	-1,34
4	B3	(OE2664F) ribosomal protein S28.eR	VGDVIQLKET	C	-1,35
7	E10	(OE1818R) translation initiation factor aIF-2 alpha chain	VQAPNYKTAE	C	-1,36
4	A21	(OE3817R) ribosomal protein S19.eR	KVAIDGPIGVK	C	-1,36
4	B8	(OE3798R) conserved hypothetical protein	VQAVKDYIVV	C	-1,37

6	D21	(OE3718F) cell division protein	ALLVTAGPPK	C	-1,38
6	H17	(OE2097F) conserved protein	SPTGKAIFGD	d	-1,38
4	C12	(OE3400F) ribosomal protein S17	EYDVFVPKYD	C	-1,39
5	F1	(OE4122R) thermosome alpha chain	TSGEDAQSM	d	-1,39
7	B24	(OE4459R) ribosomal protein L31.eR	DVTKVPSHER	C	-1,40
7	A4	(OE3817R) ribosomal protein S19.eR	LDEPDWANY	d	-1,40
4	D10	(OE3410F) ribosomal protein S8	YSVGADGFEQ	C	-1,41
7	C2	(OE5162D1F) conserved protein	AAVMPSKTDR	C	-1,41
5	F5	(OE5206R) carbamate kinase (EC 2.7.2.2)	EELGETPATV	d	-1,43
6	E17	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	C	-1,44
5	H17	(OE2097F) conserved protein	KFASDIGR	d	-1,44
5	F6	(OE3196F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain	LLGPNCPGIIT	d	-1,45
5	E17	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	C	-1,45
7	F10	(OE3393F) ribosomal protein S19	GLSEEHHKVL	C	-1,46
7	D22	(OE3393F) ribosomal protein S19	GLSEEHHKVL	C	-1,46
5	F7	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	AVGGILTKTD	d	-1,47
7	A3	(OE4712F) conserved protein	VSDMLATVEE	d	-1,49
7	A10	(OE3196F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain	LLGPNCPGIIT	d	-1,49
5	F14	(OE4240F) conserved hypothetical protein	AQVVGVSIST	d	-1,49
7	C1	(OE3410F) ribosomal protein S8	FEVELKGAIN	C	-1,50
7	C2	(OE5162D1F) conserved protein	AAVMPSKTDR	C	-1,51
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	KETTVNLPFV	d	-1,52
5	F20	(OE1405R) conserved protein	YGLAIKR	C	-1,54
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	TVGPTEQALE	d	-1,54
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	NVLELKGIEH	C	-1,54
7	E15	(OE1220F) archaeal histone	KTLMASDFEG	d	-1,55
7	C4	(OE2165R) ribosomal protein S15	VVELAEQGHD	C	-1,56
7	D2	(OE3400F) ribosomal protein S17	EYDVFVPKYD	C	-1,57
7	A13	(OE4735R) ribosomal protein S7	LKYGGISVPQ	C	-1,58
7	E2	(OE2165R) ribosomal protein S15	VVELAEQGHD	C	-1,60
4	F19	(OE3389F) ribosomal protein L4.eR	KYQEPTSILFV	C	-1,62
5	E18	(OE2809R) translation initiation factor aIF-2 beta chain	TQDHVLKFLQ	C	-1,62
5	H2	(OE4122R) thermosome alpha chain	ATGATPVSNV	C	-1,63
6	G15	(OE2197R) conserved protein	SYLAAKADAD	d	-1,63
7	F3	(OE3817R) ribosomal protein S19.eR	LDEPDWANY	C	-1,64
4	D13	(OE3869R) ribosomal protein S24.eR	NKIGADDADA	C	-1,64
7	H1	(OE3410F) ribosomal protein S8	FEVELKGAIN	C	-1,64
5	F19	(OE1405R) conserved protein	DLTAFQKNILT	C	-1,65
6	B4	(OE4459R) ribosomal protein L31.eR	QHLAKQFAVD	d	-1,67
6	A6	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	C	-1,69
5	F6	(OE3196F) succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha chain	LLGPNCPGIIT	C	-1,71
5	E21	(OE4712F) conserved protein	VSDMLATVEE	d	-1,74
7	D11	(OE1737R) dnaK-type molecular chaperone hsp70	DAEEYLGQDV	d	-1,75
4	A22	(OE2627F) ribosomal protein S13	IGQTDLDGTK	C	-1,76
6	D5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K	DTEKTTVGDR	d	-1,76

		chain homolog			
6	D14	(OE2579F) adenylosuccinate synthase (EC 6.3.4.4)	ELDGAEEAAK	C	-1,80
7	E18	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	ENPKGVIVTE	C	-1,81
5	E21	(OE4712F) conserved protein	FKDSDLYVVE	d	-1,82
4	E10	(OE3487R) translation initiation factor aIF-5A	SLSQPVDAKI	C	-1,84
5	D4	(OE1154F) Glyceraldehyde-3-phosphate dehydrogenase	VADAVAAQPD	d	-1,87
6	D5	(OE3349F) coenzyme F420--quinone oxidoreductase 42K chain homolog	DTEKTTVGDR	C	-1,87
4	B6	(OE4509F) nonhistone chromosomal protein	QAALKAAR	d	-1,93
6	E11	(OE4234R) uracil phosphoribosyltransferase (EC 2.4.2.9) upp	KGLVKLGR	d	-2,00
7	A3	(OE4712F) conserved protein	FKDSDLYVVE	d	-2,09
6	D10	(OE1584R) conserved protein	KLQKSGHL	d	-2,12
5	H17	(OE2097F) conserved protein	SPTGKAIFGD	d	-2,13
5	G15	(OE2197R) conserved protein	SYLAAKADAD	d	-2,17
6	C15	(OE2057F) thiamin biosynthesis protein thiC	IAAHAGDVAA	d	-2,42
6	F17	(OE3547F) conserved protein	ADSLQSVKEQ	d	-2,42
7	H14	(OE2165R) ribosomal protein S15	GDKLDEEFAY	C	-2,44
7	G22	(OE4540R) conserved protein	GKDAVSAVAD	C	-2,54
4	C13	(OE3346R) conserved protein	VQEAGQKAV	C	-2,99

Supplemental Table A. Whole genome DNA microarray analyses on cells, grown in complex medium. ID numbers, protein names, regulation factors (Reg.), standard deviations (Std.), t-values (t val) and gene denotations (gene) are indicated.

ID	protein name	Reg.	Std.	t val.	gene
OE5083R	heat shock protein homolog	6.46	0.60	14.25	hsp5
OE4122R	thermosome alpha subunit	5.24	0.52	14.42	cctA
OE3925R	thermosome beta subunit	4.56	1.27	5.45	cctB
OE3903F	conserved hypothetical protein	2.73	0.50	9.19	-
OE5063R	probable IS200-type transposase (TCE31)	2.71	0.33	13.97	-
OE4727R	IS1341-type transposase (TCE31)	2.63	0.41	10.77	-
OE4427R	ferritin (former DNA-binding Protein dpsA)	2.30	0.16	24.04	dpsA
OE3114R	hypothetical protein	2.23	0.71	5.18	-
OE2084R	transcription initiation factor TFB	2.16	0.60	5.84	tfbB
OE5048F	conserved hypothetical protein	2.03	0.53	6.10	-
OE1409F	conserved hypothetical protein	1.83	0.25	11.05	-
OE5114R	gas-vesicle operon protein gvpK2	1.69	0.47	5.04	gvpK2
OE3112R	AAA-type ATPase (transitional ATPase homolog)	1.68	0.50	2.05	aaa3
OE1478R	transcription initiation factor TFB	1.68	0.55	4.31	tfbF
OE1107R	conserved hypothetical protein	1.67	0.87	2.72	-
OE1797R	transcription regulator sirR	1.66	0.60	3.83	sirR
OE3815R	conserved hypothetical protein	1.64	0.32	6.97	-
OE7115F	cell division control protein cdc6 homolog	1.61	0.26	8.24	-
OE5208R	arginine deiminase (EC 3.5.3.6)	1.57	0.18	11.50	arcA
OE3949R	glutaredoxin homolog	1.53	0.19	10.40	-
OE7193R	spurious ORF	1.49	0.40	4.59	-
OE1052F	hypothetical protein	1.49	0.23	7.82	-
OE4494R	spurious ORF	1.48	0.14	12.72	-
OE7091F	spurious ORF (OE7090B1R: hypothetical protein)	1.47	0.46	3.87	-
OE5234R	conserved hypothetical protein (nonfunctional	1.47	0.45	3.91	-
OE4626R	probable translation initiation factor SUI1	1.47	0.12	15.06	sui1
OE7192F	conserved hypothetical protein	1.43	0.17	9.91	-
OE3028R	conserved hypothetical protein	1.42	0.17	9.43	-
OE2237F	hypothetical protein	1.42	0.04	40.93	-
OE2473F	conserved hypothetical protein (glutaredoxin homolog)	1.41	0.22	7.05	-
OE7133F	hypothetical protein	1.39	0.43	3.45	-
OE6026R-2 not found in HaloLex		1.39	0.25	5.96	
OE2401F	phycocyanin alpha phycocyanobilin lyase homolog	1.38	0.19	7.73	cpcE
OE7209F	conserved hypothetical protein	1.37	0.06	22.47	-
OE6285F	IS1341-type transposase (TCE31)	1.37	0.23	6.21	-
OE1116F	conserved hypothetical protein	1.37	0.05	30.93	-
OE2046F	conserved hypothetical protein (probable transkription regulator)	1.36	0.07	18.89	-
OE2127R	conserved hypothetical protein	1.36	0.17	8.10	-
OE7159R	probable transposase (ISH7/ISH24)	1.35	0.44	3.13	-
OE1678R	probable ABC-type phosphate transport system permease protein	1.35	0.09	15.31	pstC2
OE1926R	hypothetical protein	1.34	0.16	8.21	-
OE1928R	spurious ORF	1.33	0.22	5.83	-
OE5082R	AAA-type ATPase (transitional ATPase homolog)	1.32	0.22	5.80	aaa8
OE6308F	hypothetical protein	1.31	0.18	6.75	-

OE4262F	porphobilinogen synthase (EC 4.2.1.24)	1.31	0.39	3.13	hemB
OE7154R	hypothetical protein	1.30	0.26	4.57	-
OE2281R	transcription initiation factor TFB	1.30	0.47	2.55	tfbD
OE3067F	hypothetical protein	1.29	0.06	19.89	-
OE1124R	conserved hypothetical protein	1.29	0.16	7.17	-
OE7177F	conserved hypothetical protein	1.29	0.10	11.91	-
OE1470F	tryptophan synthase (EC 4.2.1.20) beta subunit	1.29	0.12	9.80	trpB
OE4555F	ABC-type transport system permease protein	1.28	0.06	17.54	dppC1
OE1279R	DNA-directed RNA polymerase (EC 2.7.7.6) epsilon subunit	1.28	0.06	19.28	rpoeps
OE4641R	phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	1.28	0.08	14.08	hisE
OE1121F	conserved hypothetical protein	1.28	0.27	4.14	-
OE6004F	hypothetical protein	1.27	0.14	8.15	-
OE2302R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit B	1.27	0.06	19.99	top6B
OE2502R	conserved hypothetical protein	1.27	0.46	2.38	-
OE5182R	hypothetical protein	1.27	0.15	7.15	-
OE4552F	ABC-type transport system permease protein	1.27	0.26	4.28	dppB2
OE1120F	conserved hypothetical protein	1.27	0.19	5.79	-
OE1036F	hypothetical protein	1.26	0.13	8.31	-
OE2674R	rRNA (adenine-N6,N6-)-dimethyltransferase (EC 2.1.1.-)	1.26	0.35	3.03	ksgA
OE1765R	probable proteasome regulatory subunit (probable PAN)	1.26	0.11	9.98	pan1
OE2514F	hypothetical protein	1.26	0.30	3.51	-
OE4753R	transcription regulator homolog	1.26	0.10	10.60	-
OE3429F	cytidylate kinase (EC 2.7.4.14)	1.26	0.08	13.02	cmk
OE6051F	restriction system mrr homolog	1.26	0.19	5.42	-
OE7065F	cytochrome d ubiquinol oxidase (EC 1.10.3.-) subunit I	1.26	0.06	18.41	cydA1
OE5212F	SMC-like protein sph1	1.25	0.24	4.33	sph1
OE4307F	glycine--tRNA ligase (EC 6.1.1.14)	1.25	0.31	3.23	glyS
OE1944R	probable aspartate aminotransferase (EC 2.6.1.1)	1.25	0.33	3.10	aspB2
OE5076R	hypothetical protein	1.25	0.19	5.45	-
OE4127R	conserved hypothetical protein	1.24	0.25	4.05	-
OE1078F	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1.24	0.06	16.50	graD6
OE2554R	conserved hypothetical protein	1.24	0.03	30.87	-
OE3927F	conserved hypothetical protein	1.24	0.12	8.27	-
OE2243R	probable carbonate dehydratase (EC 4.2.1.1)	1.24	0.16	6.08	cynT
OE2495F	conserved hypothetical protein	1.24	0.16	6.16	-
OE3994F	menaquinone biosynthesis methyltransferase homolog	1.24	0.10	9.50	menG
OE4644R	conserved hypothetical protein	1.24	0.27	3.56	-
OE2131F	conserved hypothetical protein	1.24	0.12	8.28	-
OE1065R	conserved hypothetical protein	1.23	0.14	6.89	-
OE4376R	conserved hypothetical protein	1.23	0.31	3.07	-
OE2923F	conserved hypothetical protein	1.23	0.17	5.75	-
OE5162R	cell division control protein cdc6 homolog	1.23	0.38	2.53	orc5
OE2071R	transcription regulator homolog	1.23	0.08	12.39	-
OE3923F	global transcription regulator	1.23	0.13	7.12	lrp
OE1698R	probable oxidoreductase (EC 1.1.1.-) (aldehyde reductase homolog)	1.23	0.08	11.90	oxr4
OE3836F	probable acetyltransferase	1.23	0.46	2.02	yyaI
OE1439F	probable IS200-type transposase (TCE31)	1.23	0.07	13.57	-

OE1177F	type I site-specific deoxyribonuclease (EC 3.1.21.3) subunit rmeS	1.22	0.10	9.31	rmeS
OE6085R	conserved hypothetical protein	1.22	0.31	2.97	-
OE1445R	conserved hypothetical protein	1.22	0.18	4.99	-
OE6006R	conserved hypothetical protein	1.22	0.08	11.77	-
OE1379R	conserved hypothetical protein	1.21	0.11	8.22	-
OE2123R	hypothetical protein	1.21	0.12	7.63	-
OE2460F	hypothetical protein	1.21	0.36	2.41	-
OE4685R	conserved hypothetical protein	1.21	0.29	3.01	-
OE5036F	chimaeric conserved hypothetical protein/DNA-directed DNA polymerase	1.21	0.15	5.81	-
OE7006R	probable transposase (ISH7/ISH24)	1.21	0.20	4.25	-
OE2108F	conserved hypothetical protein	1.21	0.22	3.93	-
OE3158R	conserved hypothetical protein	1.21	0.12	7.34	-
OE5326R	hypothetical protein	1.21	0.13	6.67	-
OE2619F	probable aspartate aminotransferase (EC 2.6.1.1)	1.20	0.16	5.40	aspB3
OE2827R	probable GTP-binding protein	1.20	0.03	24.42	hflX2
OE2983F	hypothetical protein	1.20	0.18	4.50	-
OE2427F	conserved hypothetical protein	1.20	0.08	10.57	-
OE8050F	conserved hypothetical protein	1.20	0.09	9.25	-
OE2506R	conserved hypothetical protein	1.20	0.27	2.99	-
OE3637R	hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34)	1.19	0.74	1.09	hmgR
OE1932R	conserved hypothetical protein	1.19	0.12	6.99	-
OE3275R	glycine cleavage system protein P-1 (glycine dehydrogenase subunit 1)	1.19	0.57	1.40	gcvP1
OE1059R	hypothetical protein (nonfunctional	1.19	0.09	8.89	-
OE3273F	DNA-binding protein	1.19	0.10	8.00	tfx
OE5445R	hypothetical protein	1.19	0.30	2.68	-
OE2828R	conserved hypothetical protein	1.19	0.06	12.47	-
OE5209R-2 not found in HaloLex		1.19	0.41	1.93	
OE3270R	conserved hypothetical protein	1.19	0.18	4.48	-
OE5119R	gas-vesicle operon protein gvpH2	1.19	0.13	6.04	gvpH2
OE2268R	imidazoleglycerol-phosphate synthase (EC 2.4.2.-) subunit hisF	1.19	0.09	8.84	hisF
OE3696F	hypothetical protein	1.18	0.06	13.11	-
OE3452F	probable DNA-directed RNA polymerase (EC 2.7.7.6) subunit M	1.18	0.18	4.23	rpoM2
OE6153F	hypothetical protein	1.18	0.31	2.47	-
OE7087F	thioredoxin reductase homolog (nonfunctional	1.18	0.06	12.36	trxB1ba
OE5189F	probable acyl-CoA transferase (3-oxoacid CoA-transferase homolog)	1.18	0.41	1.89	-
OE2283F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit C	1.18	0.08	9.38	aatC
OE1707R	transcription regulator homolog	1.18	0.17	4.63	-
OE1737R	dnaK-type molecular chaperone hsp70	1.18	0.28	2.77	dnaK
OE1964F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit L	1.18	0.09	8.04	nuoL
OE3549F	hypothetical protein	1.18	0.10	7.55	-
OE7042R	probable signal-transducing histidine kinase / response regulator	1.18	0.05	16.55	-
OE1918R	conserved hypothetical protein	1.18	0.06	12.61	-
OE2559R	probable 1	1.18	0.10	7.63	menA
OE1494R	hypothetical protein	1.18	0.08	9.63	-

OE1736R	chaperone dnaJ	1.18	0.04	17.12	dnaJ
OE4496R	ferredoxin (3Fe-4S)(4Fe-4S)	1.18	0.48	1.59	fer4
OE2809R	translation initiation factor aIF-2 beta subunit	1.18	0.02	34.17	-
OE1045F	transposase homolog (TCE39)	1.18	0.22	3.45	-
OE1794R	conserved hypothetical protein	1.18	0.04	20.19	-
OE4283R	probable signal-transducing histidine kinase	1.18	0.06	11.87	-
OE4142F	replication factor C small subunit	1.18	0.07	11.26	rfcC
OE1197R	hypothetical protein	1.18	0.37	2.02	-
OE3547F	conserved hypothetical protein	1.17	0.03	22.71	-
OE1940R	hypothetical protein	1.17	0.14	5.11	-
OE6145R	signal-transducing histidine kinase homolog	1.17	0.08	8.50	-
OE4190F	probable phosphohexomutase (EC 5.4.2.-)	1.17	0.37	1.90	pmm
OE1186F	spurious ORF	1.17	0.11	6.25	-
OE4068F	isoleucine--tRNA ligase (EC 6.1.1.5)	1.17	0.07	10.11	ileS
OE1067R	conserved hypothetical protein	1.17	0.15	4.81	-
OE6070R	conserved hypothetical protein	1.17	0.37	1.89	-
OE3324R	conserved hypothetical protein	1.17	0.28	2.54	-
OE5018R	hypothetical protein	1.17	0.16	4.33	-
OE3603R	uridine phosphorylase (EC 2.4.2.3)	1.17	0.14	4.97	-
OE5267R	conserved hypothetical protein	1.17	0.11	6.35	-
OE4707R	hypothetical protein	1.16	0.14	4.81	-
OE1041R	hypothetical protein	1.16	0.10	6.76	-
OE4167R	Na+/Ca2+-exchanging protein homolog	1.16	0.29	2.41	nce
OE2844R	transcription regulator homolog / trkA C-terminal domain protein	1.16	0.08	8.92	trh2
OE5098F	siderophore biosynthesis protein (probable lysine 6-monooxygenase)	1.16	0.26	2.70	iucD
OE2041R	conserved hypothetical protein	1.16	0.15	4.50	-
OE3165R	probable A/G-specific adenine glycosylase (EC 3.2.2.-)	1.16	0.21	3.22	mutY
OE6276R	transposase homolog (TCE33) (nonfunctional	1.16	0.30	2.30	-
OE5160F	glycerol dehydrogenase (EC 1.1.1.6)	1.16	0.21	3.27	gldA1
OE7116B1R	conserved hypothetical protein	1.16	0.13	5.20	-
OE1658F	ferredoxin (2Fe-2S)	1.16	0.11	6.13	fer3
OE5206R	carbamate kinase (EC 2.7.2.2)	1.16	0.24	2.86	arcC
OE4028R	conserved hypothetical protein	1.16	0.08	7.98	-
OE5437R	arsenical resistance operon repressor (transcription regulator)	1.16	0.32	2.07	arsR
OE5045F	conserved hypothetical protein	1.16	0.15	4.36	-
OE5049F	SMC-like protein sph2	1.16	0.27	2.48	sph2
OE1182F	conserved hypothetical protein	1.16	0.35	1.90	-
OE1539F	conserved hypothetical protein	1.16	0.41	1.62	-
OE7164R	spurious ORF	1.16	0.08	8.68	-
OE4318F	ABC-type transport system ATP-binding protein	1.15	0.26	2.53	appF
OE1713F	electron transfer protein homolog	1.15	0.17	3.77	-
OE2408R	conserved chemotaxis cluster protein cheD	1.15	0.31	2.12	cheD
OE2240F	spurious ORF	1.15	0.09	7.25	-
OE4380F	cell division control protein cdc6 homolog	1.15	0.05	12.99	orc7
OE1565F	shikimate 5-dehydrogenase (EC 1.1.1.25)	1.15	0.12	5.50	aroE
OE7134R	hypothetical protein	1.15	0.07	9.04	-
OE1799R	conserved hypothetical protein	1.15	0.23	2.73	-
OE1702R	conserved hypothetical protein	1.15	0.21	3.09	-
OE4654F	phosphomethylpyrimidine kinase (EC 2.7.4.7)	1.15	0.15	4.38	thiD

OE3153R	conserved hypothetical protein	1.15	0.13	5.01	-
OE2082F	conserved hypothetical protein	1.15	0.11	5.99	-
OE3746R	phage PhiH1 repressor protein homolog	1.15	0.07	9.51	-
OE1374F	conserved hypothetical protein	1.15	0.22	2.93	-
OE6031R	conserved hypothetical protein	1.15	0.05	11.98	-
OE2546F	probable glycosyltransferase (EC 2.-.-.-)	1.15	0.08	7.59	-
OE5406C1F	hypothetical protein (nonfunctional	1.15	0.13	4.67	-
OE2664F	ribosomal protein S28.eR	1.15	0.22	2.89	rps28R
OE8009R	conserved hypothetical protein	1.15	0.13	4.69	-
OE5429R	conserved hypothetical protein	1.15	0.08	8.28	-
OE4345R	ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta subunit	1.15	0.04	16.61	nrdB1
OE1385F	conserved hypothetical protein	1.15	0.10	6.43	-
OE2616F	hypothetical protein	1.15	0.23	2.73	-
OE7105F	cell division control protein cdc6 homolog	1.15	0.10	6.43	-
OE3008F	conserved hypothetical protein	1.14	0.15	4.07	-
OE2465R	hypothetical protein	1.14	0.11	5.51	-
OE2540R-2 not found in HaloLex		1.14	0.38	1.60	
OE3175F	propionyl-CoA carboxylase (EC 6.4.1.3)	1.14	0.09	6.55	mmdA
OE4738R	probable transcription termination factor nusA	1.14	0.23	2.68	nusA
OE3404F	ribosomal protein L24	1.14	0.02	38.27	rpl24
OE4139R	tyrosine--tRNA ligase (EC 6.1.1.1)	1.14	0.07	8.25	tyrS
OE6026R	transcription initiation factor TFB	1.14	0.18	3.36	tfbC
OE2157F	halocyanin hcpH	1.14	0.24	2.50	hcpH
OE2753F	cell division control protein cdc6 homolog	1.14	0.14	4.34	orc8
OE7034F	gas-vesicle protein gvpA1	1.14	0.45	1.33	gvpA1
OE7076R	transcription regulator homolog	1.14	0.35	1.70	-
OE5311R	hypothetical protein	1.14	0.39	1.54	-
OE1113R	probable UDP-glucose 4-epimerase (EC 5.1.3.2)	1.14	0.14	4.43	galE2
OE5298F-2 not found in HaloLex		1.14	0.15	4.10	
OE3376F	geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) (phytoene synthase)	1.14	0.12	5.02	crtB2
OE4289F	hypothetical protein	1.14	0.06	9.54	-
OE1205R	hypothetical protein	1.14	0.11	5.19	-
OE3985R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit A.a	1.14	0.09	6.20	atpA
OE6150R	conserved hypothetical protein	1.14	0.09	6.61	-
OE5438F	transcription regulator arsD	1.14	0.29	2.00	-
OE5447R	spurious ORF	1.14	0.25	2.34	-
OE2206F	probable chitinase (EC 3.2.1.14)	1.14	0.18	3.25	chiA3
OE1365F	conserved hypothetical protein	1.14	0.29	1.97	-
OE5310F	conserved hypothetical protein	1.14	0.09	6.13	-
OE2922F	hypothetical protein	1.14	0.22	2.60	-
OE3206R	conserved hypothetical protein	1.14	0.05	12.60	-
OE2404R	conserved hypothetical protein	1.14	0.23	2.56	-
OE5166F	probable ABC-type transport system periplasmic substrate-binding protein	1.14	0.04	14.27	ugpB
OE7004R	hypothetical protein (nonfunctional	1.13	0.35	1.63	-
OE2186R	sec-independent protein translocase component tatA	1.13	0.19	2.97	tatA
OE1628R	conserved hypothetical protein	1.13	0.17	3.34	-
OE3078R	conserved hypothetical protein	1.13	0.05	12.44	-

OE3541R	probable heat shock protein	1.13	0.12	4.58	hsp1
OE3300F	conserved hypothetical protein	1.13	0.08	7.24	-
OE4189F	conserved hypothetical protein	1.13	0.11	5.37	-
OE2296F	proteasome beta subunit	1.13	0.07	8.31	psmB
OE4012F	conserved hypothetical protein	1.13	0.06	9.14	-
OE4256F	probable ABC-type transport system ATP-binding protein	1.13	0.09	5.94	cbiO2
OE2530F	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1.13	0.21	2.68	graD4
OE1584R	conserved hypothetical protein	1.13	0.26	2.13	-
OE1062F	hypothetical protein	1.13	0.14	3.91	-
OE1761R	conserved hypothetical protein	1.13	0.19	2.92	-
OE3299R	conserved hypothetical protein	1.13	0.11	4.85	-
OE2047R	conserved hypothetical protein	1.13	0.15	3.75	-
OE3432R	conserved hypothetical protein	1.13	0.06	9.19	-
OE2840R	hypothetical protein	1.13	0.09	5.90	-
OE4463F	probable cysteine desulfurase	1.13	0.13	4.24	nifS
OE2676R	conserved hypothetical protein	1.13	0.16	3.46	-
OE3937R	hypothetical protein	1.13	0.35	1.57	-
OE3917F	tRNA (guanine-N2-)-methyltransferase (EC 2.1.1.32)	1.13	0.06	9.39	trm1
OE5116R	gas-vesicle operon protein gvpJ2	1.13	0.19	2.85	gvpJ2
OE3513R	hypothetical protein	1.13	0.11	4.83	-
OE4410F	acyl-CoA thioester hydrolase homolog	1.13	0.20	2.72	-
OE5169F	probable ABC-type transport system permease protein	1.13	0.09	5.96	ugpE
OE1164R	phosphatase homolog	1.13	0.10	5.64	-
OE4677F	DNA helicase II	1.13	0.08	6.41	uvrD
OE2410R	taxis protein cheC3	1.13	0.33	1.64	cheC3
OE2762R	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	1.13	0.17	3.08	aroA
OE1396R	probable kinase (homoserine / mevalonate kinase homolog)	1.12	0.15	3.53	kin2
OE2442R	hypothetical protein	1.12	0.07	7.45	-
OE3902R	conserved hypothetical protein	1.12	0.27	2.00	-
OE7085F	thioredoxin reductase homolog (nonfunctional	1.12	0.09	5.97	trxB1aa
OE1462R	nicotinamide-nucleotide adenylyltransferase (EC 2.7.7.1)	1.12	0.12	4.59	-
OE3473F-2 not found in HaloLex		1.12	0.14	3.88	
OE2121F	conserved hypothetical protein	1.12	0.24	2.18	-
OE3309R	hypothetical protein	1.12	0.07	7.13	-
OE1772F	hypothetical protein	1.12	0.49	1.09	-
OE4459R	ribosomal protein L31.eR	1.12	0.15	3.57	rpl31R
OE3383R	methenyltetrahydromethanopterin cyclohydrolase (EC 3.5.4.27)	1.12	0.06	8.19	mch
OE5158F	hypothetical protein	1.12	0.12	4.25	-
OE5106F	trkA domain protein	1.12	0.15	3.41	trkA7
OE3763F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit A	1.12	0.05	9.49	gpdA2
OE6110R	spurious ORF	1.12	0.14	3.67	-
OE1064R	spurious ORF	1.12	0.07	7.78	-
OE4258F	probable iron-sulfur protein (heterodisulfide reductase homolog)	1.12	0.08	6.78	hdrD
OE1005F	conserved hypothetical protein	1.12	0.10	5.01	-
OE2734F	urocanate hydratase (EC 4.2.1.49)	1.12	0.08	6.61	hutU

OE2464F	hypothetical protein	1.12	0.18	2.76	-
OE1425F	conserved hypothetical protein	1.12	0.17	3.00	-
OE4034R	CBS domain protein	1.12	0.10	5.23	-
OE2314R	ABC-type transport system permease protein	1.12	0.11	4.56	rbsC1
OE3960F	Na+/H+-exchanging protein	1.12	0.18	2.74	nhaC2
OE1676R	probable ABC-type phosphate transport system permease protein	1.12	0.14	3.61	pstA2
OE3551R	erythromycin esterase homolog	1.12	0.17	3.03	ereB
OE5442F	conserved hypothetical protein	1.12	0.14	3.65	-
OE6011R	hypothetical protein	1.12	0.19	2.57	-
OE3946F	conserved hypothetical protein	1.12	0.21	2.38	-
OE4612F	halolysin R4 (EC 3.4.21.-)	1.12	0.17	2.88	hly
OE2509R	oxidoreductase homolog	1.12	0.16	3.14	-
OE2118F	transcription initiation factor IIE alpha subunit homolog	1.12	0.10	4.86	tfeA
OE1540R	hypothetical protein	1.12	0.10	5.12	-
OE5314F	hypothetical protein	1.11	0.08	6.60	-
OE1648R	probable bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)	1.11	0.14	3.67	apa
OE4330F	probable phosphoesterase (EC 3.1.-.-)	1.11	0.31	1.61	-
OE2597R	conserved hypothetical protein	1.11	0.05	9.02	-
OE7152R	hypothetical protein	1.11	0.17	2.83	-
OE2865R	succinate dehydrogenase (EC 1.3.99.1) subunit A (flavoprotein)	1.11	0.10	4.82	sdhA
OE5037R-2 not found in HaloLex		1.11	0.13	3.80	
OE2284F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit A	1.11	0.05	10.78	aatA
OE3534F	hypothetical protein	1.11	0.05	10.27	-
OE3460F	GTP-binding protein	1.11	0.22	2.18	gbp1
OE4377R	GTP-binding protein homolog	1.11	0.19	2.53	gbp3
OE2635F	ribosomal protein S9	1.11	0.31	1.55	rps9
OE3517F	conserved hypothetical protein	1.11	0.13	3.62	-
OE3363F	probable orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	1.11	0.13	3.80	pyrF
OE5432F	spurious ORF	1.11	0.20	2.35	-
OE2866R	succinate dehydrogenase subunit B (iron-sulfur protein)	1.11	0.13	3.75	sdhB
OE2665F	ribosomal protein L24.eR	1.11	0.25	1.89	rpl24R
OE3036F	glycine hydroxymethyltransferase (EC 2.1.2.1)	1.11	0.04	12.35	glyA
OE3355R	carbohydrate reductase homolog	1.11	0.19	2.48	-
OE2579F	adenylosuccinate synthase (EC 6.3.4.4)	1.11	0.36	1.32	purA
OE1133F	hypothetical protein	1.11	0.06	7.58	-
OE1807R	threonine synthase (EC 4.2.99.2)	1.11	0.11	4.23	thrC2
OE8046R	TATA-binding transcription initiation factor	1.11	0.09	5.13	tbpD2
OE6335R	transducer protein htrII weak homolog	1.11	0.16	2.94	-
OE2234F	hypothetical protein	1.11	0.04	10.86	-
OE4630R	probable GTP-binding protein	1.11	0.07	7.15	-
OE3889R	probable potassium transport protein kefC	1.11	0.09	5.33	kefC
OE3950R	conserved hypothetical protein	1.11	0.04	13.47	-
OE4742R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B"	1.11	0.13	3.58	rpoB2
OE2306F	conserved hypothetical protein	1.11	0.27	1.75	-
OE3699R	conserved hypothetical protein	1.11	0.08	6.01	-
OE4110R	conserved hypothetical protein	1.11	0.19	2.51	-
OE2227F	probable dimethylsulfoxide reductase subunit C (membrane anchor subunit)	1.11	0.43	1.08	dmsC

OE2772F	conserved hypothetical protein	1.11	0.08	5.58	-
OE2201F	chitinase (EC 3.2.1.14)	1.11	0.03	15.28	chiA1
OE3159R	thymidine kinase (EC 2.7.1.21)	1.11	0.13	3.56	tdk
OE2132F	conserved hypothetical protein	1.11	0.04	11.39	-
OE3050F	conserved hypothetical protein	1.11	0.26	1.75	-
OE1847R	conserved hypothetical protein	1.11	0.14	3.34	-
OE3842R	hypothetical protein	1.11	0.13	3.43	-
OE1688R	conserved hypothetical protein	1.11	0.09	5.13	-
OE4357F	ABC-type transport system periplasmic substrate-binding protein	1.11	0.07	6.39	-
OE1008F	hypothetical protein	1.11	0.08	5.57	-
OE1664R	molecular chaperone P45 (validated)	1.11	0.14	3.21	rspA
OE4577F	ABC-type transport system permease protein	1.11	0.06	7.27	fhuG
OE2095R	conserved hypothetical protein	1.11	0.04	11.41	-
OE4627F	hypothetical protein	1.10	0.18	2.51	-
OE2059F	hypothetical protein	1.10	0.16	2.86	-
OE2929R	glutamyl-tRNA (Gln) amidotransferase (EC 6.3.5.-) subunit E	1.10	0.20	2.29	gatE
OE1759F	conserved hypothetical protein	1.10	0.21	2.17	-
OE3246F	cobyric acid synthase	1.10	0.27	1.67	cbiP
OE3629R	ABC-type transport system periplasmic substrate-binding protein	1.10	0.12	3.58	-
OE7186F	probable TATA-binding transcription initiation factor	1.10	0.09	5.18	tbpC1
OE2970R	probable myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25)	1.10	0.14	3.14	suhB
OE1114F	probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1.10	0.17	2.62	graD3
OE3814R	conserved hypothetical protein	1.10	0.43	1.02	-
OE3580R	threonine--tRNA ligase (EC 6.1.1.3)	1.10	0.04	10.38	thrS
OE2375F	conserved hypothetical protein	1.10	0.12	3.57	-
OE3214F	precorrin-3B C17-methyltransferase (EC 2.1.1.131) 1	1.10	0.09	4.87	cbiH1
OE3203R	conserved hypothetical protein	1.10	0.03	13.85	-
OE2086F	probable response regulator	1.10	0.04	11.06	hlx2
OE4385F	conserved hypothetical protein	1.10	0.19	2.29	-
OE3973F	peptide chain release factor eRF-1	1.10	0.05	8.06	erf1
OE6147R	conserved hypothetical protein	1.10	0.13	3.36	-
OE2760F	hypothetical protein	1.10	0.08	5.21	-
OE4468F	conserved hypothetical protein	1.10	0.26	1.69	-
OE1752F	3-isopropylmalate dehydratase homolog	1.10	0.18	2.35	ppd
OE3627R	ABC-type transport system permease protein	1.10	0.10	4.26	potB
OE7008F	hypothetical protein (encoded by ISH7/ISH24 subtype 1)	1.10	0.05	7.88	-
OE4648F	thioredoxin	1.10	0.10	4.51	trxA2
OE3007R	conserved hypothetical protein	1.10	0.23	1.87	-
OE2421R	hypothetical protein	1.10	0.14	3.14	-
OE2301R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit A	1.10	0.05	8.57	top6A
OE1074F	IS1341-type transposase (ISH12)	1.10	0.16	2.61	-
OE7089R	conserved hypothetical protein	1.10	0.16	2.71	-
OE7195R	spurious ORF	1.10	0.11	3.85	-
OE2566R	isochorismate synthase (EC 5.4.99.6)	1.10	0.15	2.82	menF
OE4699F	excinuclease ABC subunit A	1.10	0.18	2.40	uvrA
OE3805R	probable proteasome regulatory subunit (probable PAN)	1.10	0.12	3.57	pan2

OE1093R	spurious ORF	1.10	0.24	1.76	-
OE4488F	hypothetical protein	1.10	0.10	4.44	-
OE4214F	spurious ORF	1.10	0.12	3.61	-
OE3765F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit C	1.10	0.12	3.44	gpdC
OE3188R	conserved hypothetical protein	1.10	0.04	9.87	-
OE2618R	conserved hypothetical protein	1.10	0.14	3.13	-
OE2124F	ABC-type transport system permease protein	1.10	0.24	1.73	ybjG
OE2642R	hypothetical protein	1.10	0.15	2.86	-
OE3453R	conserved hypothetical protein	1.10	0.39	1.08	-
OE1909F	conserved hypothetical protein	1.10	0.14	2.98	-
OE2392R	transducer protein htr15 (htpIX)	1.10	0.14	2.91	htr15
OE2916F	probable oxidoreductase (3-oxoacyl-reductase homolog)	1.10	0.16	2.62	oxr5
OE5238R	hypothetical protein	1.10	0.21	2.02	-
OE1842R	NADH dehydrogenase (ubiquinone) subunit L homolog	1.10	0.08	5.37	-
OE3710R	trkA domain protein	1.10	0.15	2.75	trkA6
OE1939F	probable propionyl-CoA carboxylase (EC 6.4.1.3) beta subunit	1.10	0.08	5.46	pccB
OE3177F	pyruvate carboxylase (EC 6.4.1.1)	1.10	0.24	1.76	pyc
OE3787R	preprotein-export translocase subunit secF	1.09	0.30	1.39	secF
OE2868R	succinate dehydrogenase subunit C (cytochrome b-556)	1.09	0.23	1.77	sdhC
OE3953R	orotate phosphoribosyltransferase (EC 2.4.2.10)	1.09	0.22	1.87	pyrE2
OE2594F	cysteine--tRNA ligase (EC 6.1.1.16)	1.09	0.04	9.92	cysS
OE2316R	ABC-type transport system ATP-binding protein	1.09	0.06	6.41	rbsA
OE7049R	conserved hypothetical protein (nonfunctional	1.09	0.17	2.47	-
OE7220F	hypothetical protein	1.09	0.18	2.25	-
OE3389F	ribosomal protein L4.eR	1.09	0.11	3.73	rpl4R
OE3537R	conserved hypothetical protein	1.09	0.08	5.15	-
OE4039F	conserved hypothetical protein	1.09	0.07	5.59	-
OE3749R	queuine tRNA-ribosyltransferase (EC 2.4.2.29)	1.09	0.08	5.19	tgtA1
OE3680R	hypothetical protein	1.09	0.13	3.10	-
OE3829R	conserved hypothetical protein	1.09	0.18	2.34	-
OE2367F	aldehyde dehydrogenase (glyceraldehyde-3-phosphate dehydrogenase homolog	1.09	0.11	3.83	aldH3
OE2244R	probable methyltransferase	1.09	0.28	1.45	-
OE4067R	hypothetical protein	1.09	0.14	2.85	-
OE2595F	conserved hypothetical protein	1.09	0.14	2.99	-
OE5298F	trkA domain protein	1.09	0.02	17.83	trkA8
OE2825F	molybdenum cofactor biosynthesis protein C	1.09	0.08	4.99	moaC
OE2432C1F	hypothetical protein	1.09	0.05	8.12	-
OE3392F	ribosomal protein L2	1.09	0.18	2.29	rpl2
OE1651F	ribosomal protein S10 homolog	1.09	0.15	2.62	-
OE4498F	conserved hypothetical protein	1.09	0.15	2.65	-
OE6071R	transcription initiation factor TFB	1.09	0.10	3.85	tfbE
OE2000R	hypothetical protein	1.09	0.04	9.41	-
OE4388R	probable signal peptidase (EC 3.4.99.-)	1.09	0.13	3.03	sec11
OE1504F	phosphoribosyltransferase homolog	1.09	0.08	4.83	gptA1
OE5268R	ABC-type transport system ATP-binding protein	1.09	0.13	2.99	-
OE3065R	probable dehydrogenase (D-3-phosphoglycerate dehydrogenase homolog)	1.09	0.09	4.29	serA2
OE1978R	hypothetical protein	1.09	0.08	5.06	-

OE1489R	conserved hypothetical protein	1.09	0.26	1.56	-
OE3092F	probable N-terminal acetyltransferase	1.09	0.13	3.10	-
OE5270R	ABC-type transport system permease protein	1.09	0.20	1.97	-
OE1555F	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	1.09	0.17	2.31	acd1
OE1047R	hypothetical protein	1.09	0.09	4.20	-
OE2233F	hypothetical protein	1.09	0.13	3.18	-
OE2288F	pheromone shutdown protein homolog	1.09	0.10	4.03	traB
OE2647F	kinase homolog (acetylglutamate kinase homolog)	1.09	0.09	4.48	-
OE4238R	hemolysin homolog	1.09	0.10	4.08	hlp
OE3826F	lysine--tRNA ligase (EC 6.1.1.6)	1.09	0.10	4.12	lysS
OE2102R	conserved hypothetical protein	1.09	0.17	2.26	-
OE3358F	conserved hypothetical protein	1.09	0.39	1.01	-
OE7106F	hypothetical protein	1.09	0.19	2.08	-
OE2681F	probable cystathionine beta-lyase (EC 4.4.1.8)	1.09	0.05	8.36	metB
OE3936F	potassium channel protein homolog	1.09	0.12	3.21	pchB
OE2985F	O-acetyltransferase homolog	1.09	0.05	7.13	-
OE4235F	hypothetical protein	1.09	0.09	4.53	-
OE1623F	adenylosuccinate lyase (EC 4.3.2.2)	1.09	0.35	1.12	purB
OE3303R	transport system permease protein homolog	1.09	0.07	5.17	-
OE1560R	conserved hypothetical protein	1.09	0.28	1.39	-
OE2293R	CBS domain protein	1.09	0.34	1.12	-
OE2973F	conserved hypothetical protein	1.09	0.03	11.41	-
OE1787F	probable transcription regulator	1.09	0.25	1.54	-
OE2239F	site-specific integrase/recombinase	1.09	0.13	2.83	ssrA
OE7140F	spurious ORF	1.09	0.24	1.56	-
OE4740R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A' (chain A)	1.09	0.15	2.58	rpoA1
OE6105R	conserved hypothetical protein	1.09	0.20	1.88	-
OE2343R	probable ABC-type transport system ATP-binding protein	1.09	0.14	2.70	-
OE3951R	conserved hypothetical protein	1.09	0.13	2.85	-
OE4043R	hypothetical protein	1.09	0.15	2.59	-
OE2175F	conserved hypothetical protein	1.09	0.11	3.47	-
OE1014R	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1.09	0.13	2.96	graD5
OE3335R	hypothetical protein	1.09	0.18	2.07	-
OE3505R	di-trans	1.08	0.08	4.89	uppS2
OE1312R	hypothetical protein	1.08	0.13	2.80	-
OE2285R	probable acyl-CoA thioester hydrolase (EC 3.1.2.-)	1.08	0.12	2.98	act1
OE1557R	transcription antitermination protein homolog	1.08	0.06	5.80	nusG
OE1400F	conserved hypothetical protein	1.08	0.08	4.41	-
OE3304R	conserved hypothetical protein	1.08	0.13	2.90	-
OE7114F-2 not found in HaloLex		1.08	0.20	1.82	
OE1037F	hypothetical protein	1.08	0.11	3.42	-
OE3173F-2 not found in HaloLex		1.08	0.22	1.63	
OE2015R	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	1.08	0.29	1.25	hbd1
OE2105F	hypothetical protein	1.08	0.08	4.55	-
OE4353R	excinuclease ABC subunit B	1.08	0.19	1.88	uvrB
OE7124R	hypothetical protein	1.08	0.05	6.96	-
OE3347F-2 not found in HaloLex		1.08	0.08	4.35	
OE1893F	diphosphomevalonate decarboxylase (EC 4.1.1.33)	1.08	0.25	1.43	mvd
OE6040R	conserved hypothetical protein	1.08	0.11	3.23	-

OE3991R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit I.a	1.08	0.08	4.66	atpI
OE3040R	conserved hypothetical protein	1.08	0.06	6.35	-
OE8010B1F	conserved hypothetical protein	1.08	0.12	2.90	-
OE2223F	probable dimethylsulfoxide reductase subunit A (reductase subunit)	1.08	0.19	1.92	dmsA
OE6357F	conserved hypothetical protein	1.08	0.12	3.01	-
OE4633F	conserved hypothetical protein	1.08	0.20	1.78	-
OE1907F	conserved hypothetical protein	1.08	0.14	2.55	-
OE2600R	ribosomal protein L12	1.08	0.31	1.16	rpl12
OE4739R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A'' (chain C)	1.08	0.07	4.87	rpoA2
OE3138F	conserved hypothetical protein	1.08	0.05	6.48	-
OE4085R	ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	1.08	0.15	2.37	prsA
OE4424R	DNA repair helicase homolog	1.08	0.12	2.98	rad3b
OE6037R	cell division control protein cdc6 homolog	1.08	0.10	3.51	orc4
OE1245F	cadmium-transporting ATPase (EC 3.6.1.-)	1.08	0.08	4.34	cadA
OE3347F	transducer protein htrI	1.08	0.09	3.77	htrI
OE1865F	conserved hypothetical protein	1.08	0.22	1.60	-
OE2481R	hypothetical protein	1.08	0.08	4.14	-
OE3265R	transposase homolog (TCE33) (nonfunctional	1.08	0.05	7.33	-
OE2736F	formiminoglutamase (EC 3.5.3.8)	1.08	0.08	4.10	hutG
OE4416R	conserved hypothetical protein	1.08	0.13	2.77	-
OE1302F	lipoate--protein ligase homolog	1.08	0.08	4.16	lpl
OE3187R	conserved hypothetical protein	1.08	0.10	3.32	-
OE4418R	hypothetical protein	1.08	0.30	1.16	-
OE4032R	conserved hypothetical protein	1.08	0.27	1.27	-
OE1447R	conserved hypothetical protein	1.08	0.19	1.83	-
OE4638F	hypothetical protein	1.08	0.36	0.96	-
OE3380R	conserved hypothetical protein	1.08	0.05	7.23	-
OE1126R	hypothetical protein	1.08	0.42	0.82	-
OE2402F	conserved hypothetical protein	1.08	0.12	2.76	-
OE1547R	probable anion-transporting ATPase (EC 3.6.1.-)	1.08	0.20	1.69	arsA1
OE1488F	conserved hypothetical protein	1.08	0.07	4.56	-
OE1004F	probable ABC-type transport system ATP-binding protein	1.08	0.23	1.49	-
OE5222R	spurious ORF	1.08	0.34	1.00	-
OE3661F	ABC-type transport system ATP-binding protein	1.08	0.16	2.14	trp2
OE1382F	conserved hypothetical protein	1.08	0.13	2.52	-
OE7039F	parA domain protein	1.08	0.10	3.35	parA7
OE7093R	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 1	1.08	0.06	5.27	idi1a
OE1524R	conserved hypothetical protein	1.08	0.07	4.75	-
OE2528R	glycosyltransferase homolog	1.08	0.07	5.07	gtl
OE2671R	HemK protein homolog (protoporphyrinogen oxidase homolog)	1.07	0.08	3.96	hemK
OE2628F	ribosomal protein S4	1.07	0.12	2.76	rps4
OE5295F	hypothetical protein	1.07	0.09	3.58	-
OE4651F	probable ribose-1	1.07	0.37	0.87	-
OE3859F	conserved hypothetical protein	1.07	0.15	2.22	-
OE1887F	hypothetical protein	1.07	0.08	4.09	-
OE2363R	hypothetical protein	1.07	0.03	10.32	-
OE2854R	hypothetical protein	1.07	0.16	2.05	-

OE1127F	conserved hypothetical protein	1.07	0.16	1.97	-
OE3491R	heat shock protein homolog	1.07	0.17	1.82	-
OE6345R	hypothetical protein	1.07	0.24	1.29	-
OE2950R	signal recognition particle 19K protein	1.07	0.07	4.40	srp19
OE1987F	biotin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15) 2	1.07	0.21	1.47	birA2
OE6041R	conserved hypothetical protein	1.07	0.14	2.30	-
OE2385R	fla operon protein flaF	1.07	0.05	6.05	flaF
OE4248R	conserved hypothetical protein	1.07	0.11	2.77	-
OE1384F	dCTP deaminase (EC 3.5.4.13)	1.07	0.18	1.70	dcd
OE1426F	probable carotene dehydrogenase (phytoene dehydrogenase homolog)	1.07	0.15	2.02	pds
OE2776F	probable transcription regulator	1.07	0.07	4.48	lrpA2
OE2103R	protein kinase prkA homolog	1.07	0.13	2.39	prkA2
OE4502R	GMP synthase homolog	1.07	0.05	6.26	-
OE1150R	conserved hypothetical protein	1.07	0.18	1.71	-
OE1418F	conserved hypothetical protein	1.07	0.17	1.83	-
OE1314F	transport protein homolog	1.07	0.08	3.83	-
OE2952F	ABC-type transport system permease protein (iron transport system permease protein homolog)	1.07	0.13	2.31	hemU
OE4716R	conserved hypothetical protein	1.07	0.15	2.07	-
OE5434R	conserved hypothetical protein	1.07	0.12	2.67	-
OE3730R	hypothetical protein	1.07	0.20	1.54	-
OE1211F	heat shock protein homolog	1.07	0.13	2.29	hsp4
OE2712R	signal-transducing histidine kinase weak homolog	1.07	0.09	3.41	-
OE7010R	parA domain protein (nonfunctional	1.07	0.28	1.11	parA10
OE4461F	conserved hypothetical protein	1.07	0.04	7.94	-
OE3563R	alcohol dehydrogenase (EC 1.1.1.1)	1.07	0.03	10.39	adh4
OE1194R	hypothetical protein	1.07	0.03	9.11	-
OE7185F	ATP-dependent helicase	1.07	0.06	4.82	-
OE1770F	DNA double-strand break repair ATPase	1.07	0.15	2.02	rad50
OE3239R	conserved cobalamin cluster protein	1.07	0.06	4.76	-
OE2961F	signal-transducing histidine kinase homolog	1.07	0.26	1.16	kinA1
OE5371R	conserved hypothetical protein	1.07	0.23	1.33	-
OE5276F	conserved hypothetical protein	1.07	0.22	1.34	-
OE3864R	hypothetical protein	1.07	0.19	1.57	-
OE3249F	conserved cobalamin operon protein	1.07	0.09	3.13	-
OE2625R	hypothetical protein	1.07	0.08	3.64	-
OE5365R	conserved hypothetical protein	1.07	0.07	4.14	-
OE5444F	probable methyltransferase (phosphatidylethanolamine N-methyltransferase homolog)	1.07	0.13	2.29	-
OE4199R	phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)	1.07	0.11	2.72	hisI
OE3095R	conserved hypothetical protein	1.07	0.15	1.92	-
OE5069F	cell division control protein cdc6 (nonfunctional	1.07	0.32	0.92	orc3
OE2631F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit D	1.07	0.10	2.85	rpoD
OE2779F	amino acid transport protein (probable phenylalanine transport protein)	1.07	0.28	1.03	pheP
OE3163R	hypothetical protein	1.07	0.09	3.23	-
OE2981F	probable DNA repair helicase	1.07	0.15	1.90	rad3a
OE1823F-2 not found in HaloLex		1.07	0.13	2.30	
OE1526R	conserved hypothetical protein	1.07	0.40	0.73	-
OE3150R-2 not found in HaloLex		1.07	0.18	1.61	
OE2924R	conserved hypothetical protein	1.07	0.12	2.41	-

OE2128F	phoU protein homolog	1.07	0.22	1.30	-
OE3081F	conserved hypothetical protein	1.07	0.03	10.31	-
OE2652F	glutamate--tRNA ligase (EC 6.1.1.17)	1.07	0.22	1.31	gltS
OE7186F-2 not found in HaloLex		1.06	0.09	3.36	
OE2651F	hypothetical protein	1.06	0.19	1.53	-
OE4129R	conserved hypothetical protein	1.06	0.08	3.58	-
OE2750R	conserved hypothetical protein	1.06	0.08	3.71	-
OE3554F	carbamoyl-phosphate synthase (EC 6.3.-.-) large subunit	1.06	0.08	3.67	carB
OE4349F	spurious ORF	1.06	0.30	0.95	-
OE4136R	translation initiation factor aIF-1A	1.06	0.21	1.35	eif1a1
OE7136R	hypothetical protein	1.06	0.40	0.71	-
OE5255R	probable transport protein	1.06	0.19	1.50	-
OE3648F	nicotinate-nucleotide pyrophosphorylase (carboxylating)	1.06	0.06	4.75	nadC
OE3676R	hypothetical protein	1.06	0.30	0.94	-
OE3345F	conserved hypothetical protein	1.06	0.11	2.44	-
OE3490R	conserved hypothetical protein	1.06	0.27	1.03	-
OE1358R	methanol dehydrogenase regulatory protein	1.06	0.12	2.35	moxR
OE1640F	transport protein homolog	1.06	0.19	1.49	-
OE1304F	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18)	1.06	0.11	2.60	xthA
OE2210R	conserved hypothetical protein	1.06	0.09	2.99	-
OE1474R	hypothetical protein	1.06	0.12	2.38	-
OE1399R	transcription initiation factor TFB	1.06	0.13	2.19	tfbG
OE3292F	conserved hypothetical protein	1.06	0.05	5.86	-
OE4544R	conserved hypothetical protein	1.06	0.28	0.98	-
OE5029R	hypothetical protein	1.06	0.12	2.21	-
OE2693F	protein-methionine-S-oxide reductase (EC 1.8.4.6) msrA	1.06	0.05	5.00	msrA
OE2358F	probable nonspecific lipid-transfer protein (sterol carrier protein)	1.06	0.26	1.07	acaB2
OE7155R	conserved hypothetical protein	1.06	0.14	1.94	-
OE1816R	3-isopropylmalate dehydratase homolog	1.06	0.20	1.32	-
OE3866R	probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	1.06	0.28	0.96	gcp
OE2433A1F	probable transposase (ISH3/ISH27)	1.06	0.19	1.43	-
OE2049R	conserved hypothetical protein	1.06	0.04	6.42	-
OE1461R	conserved hypothetical protein	1.06	0.19	1.46	-
OE7129F	conserved hypothetical protein	1.06	0.09	3.10	-
OE1266R	probable 2-keto-3-deoxygluconate kinase (EC 2.7.1.45)	1.06	0.17	1.57	kdgK
OE2524R	UDPglucose 6-dehydrogenase (EC 1.1.1.22)	1.06	0.25	1.07	udg1
OE2037F	endonuclease homolog	1.06	0.07	3.98	-
OE3343R	hypothetical protein	1.06	0.17	1.52	-
OE2784R	probable chorismate mutase (EC 5.4.99.5) (monofunctional)	1.06	0.03	9.90	pheA1
OE2819R	spurious ORF	1.06	0.11	2.38	-
OE5273R	ABC-type transport system periplasmic substrate-binding protein	1.06	0.31	0.86	-
OE2891F	hypothetical protein	1.06	0.34	0.78	-
OE4703R	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	1.06	0.08	3.11	uae
OE2300F	conserved hypothetical protein	1.06	0.10	2.56	-

OE2648F	conserved hypothetical protein	1.06	0.07	4.04	-
OE4209F	maoC protein homolog	1.06	0.09	2.99	maoC1
OE2998R	conserved hypothetical protein	1.06	0.10	2.64	-
OE3038F	methylenetetrahydrofolate dehydrogenase (NAD(P)+) (EC 1.5.1.5)	1.06	0.04	5.94	folD
OE3879F	conserved hypothetical protein	1.06	0.05	5.75	-
OE2322F	Na+/proline symport protein	1.06	0.82	0.32	putP
OE2763F	X-Pro dipeptidase (EC 3.4.13.9)	1.06	0.13	1.97	pepQ2
OE5027R	probable transposase (ISH3/ISH27)	1.06	0.22	1.19	-
OE2650F	probable trifunctional short-chain (E)-prenyl diphosphate synthase	1.06	0.13	2.08	idsA1
OE4317F	ABC-type transport system ATP-binding protein	1.06	0.07	3.76	oppD1
OE4133R	conserved hypothetical protein	1.06	0.10	2.70	-
OE7162R	parA domain protein	1.06	0.06	4.62	parA8
OE6046F	conserved hypothetical protein	1.06	0.24	1.06	-
OE6127F	TATA-binding transcription initiation factor (nonfunctional	1.06	0.04	5.90	tbpFb
OE2870R	DNA-3-methyladenine glycosidase I (EC 3.2.2.20)	1.06	0.08	3.06	alkA
OE2241R	hypothetical protein	1.06	0.27	0.94	-
OE2508F	conserved hypothetical protein	1.06	0.18	1.38	-
OE1782F	conserved hypothetical protein	1.06	0.07	3.74	-
OE4465F	iron-sulfur cofactor synthesis protein	1.06	0.10	2.53	nifU
OE2816F	conserved hypothetical protein	1.06	0.09	2.88	-
OE4508R	dihydroorotate oxidase (EC 1.3.3.1)	1.06	0.05	5.18	pyrD
OE3693F	peptidylprolyl isomerase (EC 5.2.1.8)	1.06	0.26	0.97	ppiA
OE3054R	conserved hypothetical protein	1.06	0.07	3.48	-
OE2758R	conserved hypothetical protein	1.06	0.08	3.00	-
OE1549F	conserved hypothetical protein	1.06	0.16	1.57	-
OE3417F	ribosomal protein L15	1.06	0.08	3.02	rpl15
OE4524F	hypothetical protein	1.06	0.24	1.07	-
OE2780F	hypothetical protein	1.06	0.19	1.29	-
OE4712F	conserved hypothetical protein	1.06	0.23	1.08	-
OE3132F	conserved hypothetical protein	1.06	0.20	1.26	-
OE1721R	methylmalonyl-CoA mutase (EC 5.4.99.2) 1A (N-terminal homology)	1.06	0.21	1.16	mut1A
OE1614F	hexosyltransferase homolog	1.06	0.12	2.03	rfbU2
OE6139F	hypothetical protein	1.06	0.13	1.98	-
OE3639F	conserved hypothetical protein	1.06	0.04	5.86	-
OE1570F	anthranilate synthase (EC 4.1.3.27) component II	1.06	0.15	1.64	trpG2a
OE2573F	hypothetical protein	1.06	0.07	3.44	-
OE7176R	helicase homolog	1.06	0.06	4.10	-
OE2872F	hypothetical protein	1.05	0.19	1.29	-
OE7077F	conserved hypothetical protein	1.05	0.10	2.46	-
OE2996R-2 not found in HaloLex		1.05	0.15	1.66	
OE7159R-2 not found in HaloLex		1.05	0.13	1.90	
OE1919R	conserved hypothetical protein	1.05	0.24	1.01	-
OE4568R	conserved hypothetical protein	1.05	0.05	4.37	-
OE2318R	phosphomannomutase (EC 5.4.2.8)	1.05	0.08	2.93	pmu2
OE4255F	conserved hypothetical protein	1.05	0.16	1.53	-
OE3585A1F	hypothetical protein	1.05	0.18	1.33	-
OE4370R	drug export protein homolog	1.05	0.05	4.93	dip1

OE3967R	conserved hypothetical protein	1.05	0.05	4.60	-
OE2440F	hypothetical protein	1.05	0.08	3.11	-
OE4365F	conserved hypothetical protein	1.05	0.10	2.27	-
OE1959F	NADH dehydrogenase (ubiquinone) subunit J1 (N-terminal homology)	1.05	0.21	1.14	nuoJ1
OE2583R	conserved hypothetical protein	1.05	0.18	1.30	-
OE5205R	ornithine carbamoyltransferase (EC 2.1.3.3)	1.05	0.30	0.78	arcB
OE1097F	hypothetical protein	1.05	0.07	3.46	-
OE6140R-2 not found in HaloLex		1.05	0.12	1.96	
OE2060R	conserved hypothetical protein	1.05	0.08	2.86	-
OE7194F	plasmid replication protein repJ	1.05	0.04	5.94	repJ1
OE5289R	hypothetical protein	1.05	0.06	4.20	-
OE1071F	probable transposase (ISH4/ISH23/ISH50)	1.05	0.17	1.38	-
OE1267R	DNA mismatch repair protein	1.05	0.21	1.11	mutL
OE3843F	NAD+ synthase (EC 6.3.1.5)	1.05	0.07	3.22	nadE
OE1838R	conserved hypothetical protein	1.05	0.16	1.46	-
OE7109R	insertion element protein (ISH2)	1.05	0.16	1.42	-
OE3393F	ribosomal protein S19	1.05	0.10	2.35	rps19
OE1668R	conserved hypothetical protein	1.05	0.21	1.10	-
OE3305F	replication factor C large subunit	1.05	0.07	3.22	rfcB
OE3714F	hypothetical protein	1.05	0.16	1.43	-
OE2182F	conserved hypothetical protein	1.05	0.07	3.04	-
OE2215R	type II secretion system protein homolog	1.05	0.12	1.88	gspE
OE2257F	conserved hypothetical protein	1.05	0.08	2.95	-
OE1989F	protoheme IX farnesyltransferase (EC 2.5.1.-)	1.05	0.14	1.64	ctaB
OE3143R	tetrahedral aminopeptidase	1.05	0.08	2.79	-
OE4709F	hypothetical protein	1.05	0.10	2.22	-
OE5021F	parA domain protein	1.05	0.16	1.43	parA3
OE7012R	hypothetical protein	1.05	0.18	1.22	-
OE2458R	IMP dehydrogenase (EC 1.1.1.205)	1.05	0.12	1.85	guaB
OE1026F	hypothetical protein	1.05	0.03	7.00	-
OE1753R	probable transport protein	1.05	0.16	1.35	yfmO1
OE4680F	conserved hypothetical protein	1.05	0.09	2.32	-
OE1151R	aminopeptidase homolog	1.05	0.06	3.43	-
OE2324F	hypothetical protein	1.05	0.11	2.05	-
OE3662F	conserved hypothetical protein	1.05	0.19	1.13	-
OE7064R	hypothetical protein	1.05	0.20	1.09	-
OE6280R	hypothetical protein	1.05	0.31	0.70	-
OE7020F	hypothetical protein	1.05	0.24	0.91	-
OE5381F-2 not found in HaloLex		1.05	0.06	3.66	
OE3042F	hypothetical protein	1.05	0.04	5.10	-
OE5206R-2 not found in HaloLex		1.05	0.08	2.63	
OE3542R	hypothetical protein	1.05	0.12	1.82	-
OE2503R	conserved hypothetical protein	1.05	0.12	1.80	-
OE1058R-2 not found in HaloLex		1.05	0.16	1.31	
OE3116F	conserved hypothetical protein	1.05	0.09	2.27	-
OE3212F	precorrin-4 C11-methyltransferase (EC 2.1.1.133)	1.05	0.13	1.60	cbiF
OE2785R	probable shikimate kinase (2.7.1.71) (archaeal-type)	1.05	0.08	2.60	aroK
OE4244F	conserved hypothetical protein	1.05	0.15	1.37	-
OE2860R	cysteine synthase (EC 4.2.99.8) cysK2	1.05	0.12	1.76	cysK2
OE6329R-2 not found in HaloLex		1.05	0.21	1.01	
OE7072F	conserved hypothetical protein	1.05	0.12	1.68	-

OE4691R	glucokinase (EC 2.7.1.2)	1.05	0.10	2.07	glcK
OE1532F	hypothetical protein	1.05	0.28	0.75	-
OE1013R	glutamine--fructose-6-phosphate transaminase (isomerizing)	1.05	0.11	1.86	glmS
OE1294R	ribosomal protein L15.eR	1.05	0.05	3.84	rpl15R
OE6088R	hypothetical protein	1.05	0.05	4.40	-
OE2909F	conserved hypothetical protein	1.05	0.08	2.46	-
OE1769F	probable phosphoesterase (EC 3.1.-.-) ppe	1.05	0.17	1.22	ppe
OE3775R	conserved hypothetical protein	1.05	0.10	2.09	-
OE6058F	spurious ORF	1.05	0.09	2.16	-
OE1496R	methionine--tRNA ligase (EC 6.1.1.10)	1.05	0.06	3.70	metS
OE4587R	ABC-type transport system ATP-binding protein	1.05	0.07	2.84	-
OE4414R	salinity-regulated protein homolog	1.05	0.13	1.52	-
OE3318R	cobalt transport protein CbiN	1.05	0.13	1.61	cbiN
OE1906R	probable sugar transferase	1.05	0.10	2.13	-
OE3196F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha subunit	1.05	0.10	2.04	sucA
OE1492R	conserved hypothetical protein	1.05	0.14	1.41	-
OE4533F	hypothetical protein	1.05	0.07	2.72	-
OE2867R	succinate dehydrogenase subunit D (membrane anchor protein)	1.05	0.08	2.58	sdhD
OE1298R	conserved hypothetical protein	1.05	0.14	1.40	-
OE1398R	conserved hypothetical protein	1.04	0.12	1.68	-
OE5094F	diaminobutyrate-pyruvate aminotransferase(siderophore biosynthesis protein)	1.04	0.14	1.39	dat
OE1394R	conserved hypothetical protein	1.04	0.09	2.20	-
OE4590R	spurious ORF	1.04	0.19	1.06	-
OE1207R	conserved hypothetical protein	1.04	0.09	2.20	-
OE4579F	ABC-type transport system ATP-binding protein	1.04	0.09	2.13	yfmF
OE2364R	probable NADH oxidase (H2O2-forming) (EC 1.6.99.3)	1.04	0.09	2.27	noxC
OE2741F	hypothetical protein	1.04	0.05	3.89	-
OE2455F	hypothetical protein	1.04	0.11	1.75	-
OE2360R	NADH oxidase homolog	1.04	0.21	0.96	-
OE6069R	conserved hypothetical protein	1.04	0.21	0.96	-
OE2728R	glutamate dehydrogenase (EC 1.4.1.-)	1.04	0.10	2.06	gdhA2
OE2563R	2-succinyl-6-hydroxy-2	1.04	0.15	1.28	menD
OE3178F	conserved hypothetical protein	1.04	0.15	1.32	-
OE2229F	conserved hypothetical protein	1.04	0.08	2.59	-
OE2014F	farnesyl-diphosphate farnesyltransferase (squalene synthase)	1.04	0.18	1.08	fdfT
OE6289R	conserved hypothetical protein	1.04	0.34	0.58	-
OE4713R	conserved hypothetical protein	1.04	0.08	2.39	-
OE2276F	conserved hypothetical protein	1.04	0.08	2.57	-
OE3642F	conserved hypothetical protein	1.04	0.09	2.12	-
OE4356F	thiosulfate sulfurtransferase (EC 2.8.1.1)	1.04	0.05	3.85	tssB
OE3834R	probable oxidoreductase	1.04	0.15	1.31	gsp
OE6083R	conserved hypothetical protein	1.04	0.12	1.59	-
OE4543R	probable N-terminal acetyltransferase	1.04	0.09	2.07	rimI1
OE2365R	hydrolase homolog	1.04	0.11	1.70	-
OE2716R	hypothetical protein	1.04	0.20	0.96	-
OE1629F	conserved hypothetical protein	1.04	0.21	0.91	-
OE1499R	probable bifunctional CAAX prenyl proteinase/zinc metalloproteinase	1.04	0.14	1.38	caaX

OE1620R	phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	1.04	0.13	1.40	purH
OE4354R	conserved hypothetical protein	1.04	0.12	1.55	-
OE4010F	probable multifunctional long-chain (E)-prenyl diphosphate synthase	1.04	0.21	0.92	idsA2
OE3093R	geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32)	1.04	0.06	3.18	crtB1
OE4391F	probable serine--pyruvate aminotransferase (EC 2.6.1.51)	1.04	0.06	2.93	agxT
OE2027F	conserved hypothetical protein	1.04	0.10	1.95	-
OE7201R	probable transposase (ISH4/ISH23/ISH50)	1.04	0.36	0.52	-
OE1420F	probable ABC-type transport system permease protein	1.04	0.24	0.76	-
OE1772A1R	hypothetical protein	1.04	0.27	0.69	-
OE6098R	conserved hypothetical protein	1.04	0.13	1.38	-
OE1742R	dnaJ/dnaK ATPase stimulator grpE	1.04	0.16	1.15	grpE
OE1641R	3-hydroxybutyryl-CoA dehydratase (EC 4.2.1.55)	1.04	0.21	0.87	fad2
OE2197R	conserved hypothetical protein	1.04	0.10	1.93	-
OE3901R	probable N-acetyltransferase (EC 2.3.1.-)	1.04	0.07	2.55	hat2
OE1968F	conserved hypothetical protein	1.04	0.12	1.48	-
OE1841R	HyfD / HycC / NADH dehydrogenase (ubiquinone) subunit L homolog	1.04	0.11	1.61	-
OE3427F	conserved hypothetical protein	1.04	0.12	1.53	-
OE3892R	beta-lactamase homolog	1.04	0.03	6.30	-
OE3356F	AAA-type ATPase (transitional ATPase homolog)	1.04	0.15	1.16	aaa5
OE3740R	microbial serine proteinase (EC 3.4.21.-)	1.04	0.20	0.89	sub
OE2428R	conserved hypothetical protein	1.04	0.08	2.11	-
OE3934R	citrate (si)-synthase (EC 2.3.3.1)	1.04	0.10	1.82	citZ
OE2537F	sugar transferase homolog	1.04	0.08	2.28	rfbQ
OE1366F	conserved hypothetical protein	1.04	0.07	2.42	-
OE7102R	conserved hypothetical protein	1.04	0.09	1.97	-
OE3722F	conserved hypothetical protein	1.04	0.07	2.52	-
OE2697R	probable coenzyme PQQ synthesis protein E	1.04	0.10	1.77	pqqE2
OE8048F	conserved hypothetical protein	1.04	0.32	0.54	-
OE2939R	probable DNA repair DNAse IV	1.04	0.30	0.58	rad2
OE3466R	conserved hypothetical protein	1.04	0.17	1.01	-
OE6353F	insertion element protein (ISH2)	1.04	0.07	2.61	-
OE7206F	hypothetical protein	1.04	0.15	1.16	-
OE2975F	hypothetical protein	1.04	0.07	2.50	-
OE7001R	conserved hypothetical protein	1.04	0.29	0.58	-
OE5411A1R	conserved hypothetical protein	1.04	0.09	1.93	-
OE3444F	hypothetical protein	1.04	0.09	1.82	-
OE1854R	conserved hypothetical protein	1.04	0.18	0.93	-
OE4622F	conserved hypothetical protein	1.04	0.22	0.76	-
OE3715R	dTMP kinase (EC 2.7.4.9)	1.04	0.06	2.62	tmk
OE3907R	ABC-type transport system permease protein	1.04	0.15	1.09	phnE
OE3047F	conserved hypothetical protein	1.04	0.07	2.44	-
OE2525R	conserved hypothetical protein	1.04	0.11	1.52	-
OE2230F	conserved hypothetical protein	1.04	0.10	1.63	-
OE3712R	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component alpha-2 subunit	1.04	0.04	4.47	oxdhA2
OE3190F	hypothetical protein	1.04	0.07	2.24	-
OE5042R	conserved hypothetical protein	1.04	0.17	0.94	-

OE3386F	conserved hypothetical protein	1.04	0.19	0.87	-
OE4637R	probable GTP-binding protein	1.04	0.21	0.79	gbp4
OE2390R	flagella accessory protein	1.04	0.31	0.53	flaD
OE1931R	potassium channel protein	1.04	0.07	2.15	pchA2
OE1543F	endonuclease V (EC 3.1.-.-)	1.04	0.25	0.63	nfi
OE4160F	holliday-junction resolvase homolog	1.04	0.16	1.01	hjr
OE1102R-2 not found in HaloLex		1.04	0.06	2.62	
OE4367R	conserved hypothetical protein	1.03	0.11	1.41	-
OE1165R	phosphoglycerate dehydrogenase (EC 1.1.1.95)	1.03	0.04	3.69	serA3
OE4222F	conserved hypothetical protein	1.03	0.10	1.63	-
OE1218F	replication protein A homolog	1.03	0.03	4.90	-
OE2245F	hypothetical protein	1.03	0.17	0.89	-
OE4023F	conserved hypothetical protein	1.03	0.09	1.65	-
OE4467F	conserved hypothetical protein	1.03	0.10	1.61	-
OE5110F	conserved hypothetical protein	1.03	0.06	2.39	-
OE2406R	protein-glutamate O-methyltransferase (EC 2.1.1.80) cheR	1.03	0.51	0.30	cheR
OE6080F	conserved hypothetical protein	1.03	0.08	1.79	-
OE3869R	ribosomal protein S24.eR	1.03	0.35	0.43	rps24R
OE4527R	cleavage and polyadenylation specificity factor homolog	1.03	0.05	2.89	epf1
OE1745R	hypothetical protein	1.03	0.06	2.73	-
OE3419F	probable ABC-type transport system substrate-binding protein	1.03	0.08	1.79	-
OE2813R	conserved hypothetical protein	1.03	0.16	0.95	-
OE2205F	chitinase (EC 3.2.1.14)	1.03	0.06	2.59	chiA2
OE4296F	hypothetical protein	1.03	0.12	1.26	-
OE5293F	conserved hypothetical protein	1.03	0.11	1.35	-
OE1718R	conserved hypothetical protein	1.03	0.07	1.99	-
OE1023R	hypothetical protein	1.03	0.18	0.84	-
OE1806R	probable periplasmic protein	1.03	0.06	2.44	-
OE5054F	potassium-transporting ATPase (EC 3.6.3.12) subunit C	1.03	0.10	1.44	kdpC
OE2896R	conserved hypothetical protein	1.03	0.11	1.30	-
OE4435F	hypothetical protein	1.03	0.14	1.02	-
OE1785F	conserved hypothetical protein	1.03	0.06	2.33	-
OE3914R	conserved hypothetical protein	1.03	0.21	0.70	-
OE4025F	conserved hypothetical protein	1.03	0.07	2.01	-
OE3510F	conserved hypothetical protein	1.03	0.17	0.83	-
OE3500R	probable heme biosynthesis protein nirH/G (nirL/nirD homolog)	1.03	0.05	3.13	nirH
OE2668R	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	1.03	0.07	2.02	metE
OE2601R	ribosomal protein L10	1.03	0.07	2.01	rpl10
OE6288R	cell division control protein cdc6 homolog	1.03	0.32	0.45	-
OE4339R	ABC-type transport system ATP-binding protein	1.03	0.06	2.34	nosF1
OE1674R	probable phosphate transport operon protein phoU	1.03	0.10	1.41	phoU
OE4674F	alcohol dehydrogenase (EC 1.1.1.1)	1.03	0.04	3.92	adh2
OE3195F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta subunit	1.03	0.09	1.53	sucB
OE4735R	ribosomal protein S7	1.03	0.50	0.28	rps7
OE2278F	probable asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4)	1.03	0.10	1.33	asnA

OE1626F	conserved hypothetical protein	1.03	0.03	4.49	-
OE4399F	probable oxidoreductase (glycerol-3-phosphate dehydrogenase homolog)	1.03	0.07	1.84	oxr8
OE3893F	serine--tRNA ligase (EC 6.1.1.11)	1.03	0.27	0.52	serS
OE1070R	IS1341-type transposase (TCE32)	1.03	0.12	1.13	-
OE2497F	conserved hypothetical protein	1.03	0.11	1.19	-
OE2222F	hypothetical protein	1.03	0.22	0.61	-
OE2585R	conserved hypothetical protein	1.03	0.13	1.05	-
OE5297F	hypothetical protein	1.03	0.12	1.08	-
OE3654R	hypothetical protein	1.03	0.09	1.50	-
OE1318F	conserved hypothetical protein	1.03	0.24	0.54	-
OE3123R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	1.03	0.19	0.69	acd5
OE5305R	conserved hypothetical protein	1.03	0.18	0.71	-
OE5180F	probable transposase (TCE33)	1.03	0.11	1.16	-
OE3964R	conserved hypothetical protein	1.03	0.16	0.81	-
OE2325F	hypothetical protein	1.03	0.03	4.74	-
OE4300R	hypothetical protein	1.03	0.07	1.87	-
OE3726F	conserved hypothetical protein	1.03	0.10	1.36	-
OE3122F	serine O-acetyltransferase (EC 2.3.1.30) cysE	1.03	0.10	1.25	cysE
OE6345R-2 not found in HaloLex		1.03	0.16	0.82	
OE2527F	conserved hypothetical protein	1.03	0.13	1.01	-
OE5303F	spurious ORF	1.03	0.08	1.63	-
OE2492F	conserved hypothetical protein	1.03	0.07	1.79	-
OE4163R	conserved hypothetical protein	1.03	0.37	0.34	-
OE1711R	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3) alpha subunit	1.03	0.10	1.33	korA
OE3325F	conserved hypothetical protein	1.03	0.09	1.47	-
OE2168R	transducer protein htrVI	1.03	0.19	0.66	htrVI
OE7037F	gas-vesicle operon protein gvpN	1.03	0.20	0.63	gvpN1
OE3200R	probable chloride channel protein	1.03	0.15	0.83	-
OE2803R	hypothetical protein	1.03	0.45	0.28	-
OE5448F	IS1341-type transposase (TCE32) (nonfunctional	1.03	0.05	2.51	-
OE1778R	probable oxidoreductase (3-oxoacyl-reductase homolog)	1.03	0.11	1.08	oxr6
OE4408F	phosphoglycerate dehydrogenase (EC 1.1.1.95)	1.03	0.06	2.10	serA1
OE4140R	conserved hypothetical protein	1.03	0.25	0.49	-
OE1900F	hypothetical protein	1.03	0.03	4.13	-
OE3118F	conserved hypothetical protein	1.03	0.16	0.76	-
OE1615R	folylpolyglutamate synthase / dihydropteroate synthase	1.03	0.22	0.53	folCP
OE4659R	conserved hypothetical protein	1.03	0.14	0.84	-
OE7038F	gas-vesicle operon protein gvpO1	1.03	0.23	0.51	gvpO1
OE3612R	chemotactic signal transduction system periplasmic substrate-bdg. protein basB	1.03	0.12	1.00	basB
OE2260R	rhomboid family protein	1.03	0.07	1.75	-
OE2727R	conserved hypothetical protein	1.03	0.11	1.11	-
OE1599F	dTDPglucose 4	1.03	0.06	2.05	-
OE2627F	ribosomal protein S13	1.03	0.20	0.58	rps13
OE4324R	ferredoxin	1.03	0.22	0.54	-
OE2359F	conserved hypothetical protein	1.03	0.08	1.48	-
OE1899R	conserved hypothetical protein	1.03	0.12	0.97	-
OE2770F	prephenate dehydrogenase (EC 1.3.1.12)	1.03	0.09	1.28	tyrA
OE5100R-	(trkA)	1.03	0.11	1.05	

2 not found in HaloLex					
OE2787R	probable ABC-type transport system ATP-binding protein	1.03	0.05	2.35	-
OE3337F	insertion element protein (ISH2)	1.03	0.25	0.46	-
OE3933F	hypothetical protein	1.03	0.16	0.72	-
OE5043R	conserved hypothetical protein	1.03	0.28	0.41	-
OE4313F	ABC-type transport system permease protein	1.03	0.21	0.55	appB
OE7048F	probable transposase (ISH3/ISH27)	1.03	0.07	1.63	-
OE6303F	conserved hypothetical protein	1.03	0.15	0.76	-
OE3812R	histidine--tRNA ligase (EC 6.1.1.21)	1.03	0.11	1.00	hisS
OE2373F	probable phosphate acetyltransferase (EC 2.3.1.8)	1.02	0.09	1.31	pta
OE2672R	conserved hypothetical protein	1.02	0.08	1.37	-
OE8002F	parA domain protein	1.02	0.22	0.52	parA9
OE2521R	conserved hypothetical protein	1.02	0.20	0.55	-
OE1414R	cell division protein ftsZ4	1.02	0.09	1.19	ftsZ4
OE4277F	uroporphyrin-III C-methyltransferase (EC 2.1.1.107)	1.02	0.11	1.01	hemX
OE5174R	hypothetical protein	1.02	0.03	4.07	-
OE3333R	phosphoribosylanthranilate isomerase (EC 5.3.1.24)	1.02	0.16	0.68	trpF
OE1048F	hypothetical protein	1.02	0.17	0.62	-
OE1309F	aminopeptidase (EC 3.4.11.-)	1.02	0.13	0.81	pepB1
OE1236F	conserved hypothetical protein	1.02	0.19	0.57	-
OE7111F	conserved hypothetical protein	1.02	0.10	1.08	-
OE4183F	DNA mismatch recognition protein homolog	1.02	0.16	0.66	mutS3
OE4617F	hypothetical protein	1.02	0.10	1.05	-
OE2252R	conserved hypothetical protein	1.02	0.10	1.00	-
OE6332R	transducer protein htrII weak homolog	1.02	0.07	1.49	-
OE3644F	quinolinate synthetase A (part of quinolinate synthetase complex)	1.02	0.15	0.67	nadA
OE7172F	hypothetical protein	1.02	0.15	0.70	-
OE6281R	hypothetical protein	1.02	0.08	1.28	-
OE1391R	halocyanin hcpG	1.02	0.04	2.79	hcpG
OE1879R	halocyanin hcpE	1.02	0.06	1.64	hcpE
OE1378R	conserved hypothetical protein	1.02	0.24	0.41	-
OE4728F	probable IS200-type transposase (TCE31)	1.02	0.17	0.57	-
OE2995R	hypothetical protein	1.02	0.04	2.28	-
OE3346R	conserved hypothetical protein	1.02	0.09	1.05	-
OE2304F	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) subunit A	1.02	0.18	0.52	gyrA
OE3481R	transducer protein htrII	1.02	0.14	0.70	htrII
OE5280R	conserved hypothetical protein	1.02	0.09	1.07	-
OE2608F	hypothetical protein	1.02	0.07	1.30	-
OE1693R	probable ABC-type transport system ATP-binding protein	1.02	0.05	1.77	-
OE1602F	glycerol-1 phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261)	1.02	0.08	1.13	gldA2
OE1225F	hypothetical protein	1.02	0.11	0.81	-
OE2357F	conserved hypothetical protein	1.02	0.06	1.61	-
OE1188F	conserved hypothetical protein	1.02	0.06	1.58	-
OE6099F	hypothetical protein	1.02	0.06	1.56	-
OE3264F	hypothetical protein	1.02	0.11	0.80	-
OE1129F	conserved hypothetical protein (nonfunctional	1.02	0.20	0.46	-
OE3204R	conserved hypothetical protein	1.02	0.07	1.37	-

OE4305R	ABC-type dipeptide transport system periplasmic dipeptide-binding protein	1.02	0.07	1.29	dppA
OE2303F	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) subunit B	1.02	0.09	1.04	gyrB
OE4529F	aldehyde dehydrogenase (retinal dehydrogenase homolog	1.02	0.14	0.61	aldH1
OE4206F	methylaspartate mutase (EC 5.4.99.1) large subunit	1.02	0.13	0.69	mamB
OE3522R	conserved hypothetical protein	1.02	0.29	0.30	-
OE2430F	hypothetical protein	1.02	0.17	0.51	-
OE5052F	potassium-transporting ATPase (EC 3.6.3.12) subunit A	1.02	0.14	0.58	kdpA
OE5039R	conserved hypothetical protein	1.02	0.04	2.05	-
OE2032F	conserved hypothetical protein	1.02	0.06	1.31	-
OE5249F	conserved hypothetical protein	1.02	0.07	1.13	-
OE4198F	alanine--tRNA ligase (EC 6.1.1.7)	1.02	0.23	0.35	alaS
OE1438F	conserved hypothetical protein	1.02	0.11	0.77	-
OE2738F	imidazolonepropionase (EC 3.5.2.7)	1.02	0.16	0.50	hutI
OE2379R	fla operon protein flaJ	1.02	0.05	1.57	flaJ
OE4182F	sec-independent protein translocase component tatC1	1.02	0.16	0.52	tatC1
OE1196R	hypothetical protein	1.02	0.09	0.94	-
OE2569R	sulfite oxidase homolog	1.02	0.09	0.92	-
OE4173F	hypothetical protein	1.02	0.35	0.23	-
OE3695F	conserved hypothetical protein	1.02	0.10	0.77	-
OE2859F	conserved hypothetical protein	1.02	0.10	0.83	-
OE2055F	conserved hypothetical protein	1.02	0.11	0.73	-
OE1903F	glycine-rich protein	1.02	0.17	0.47	-
OE4118R	leucine--tRNA ligase (EC 6.1.1.4)	1.02	0.23	0.34	leuS
OE5359R	probable transposase (ISH3/ISH27)	1.02	0.13	0.60	-
OE7081F	conserved hypothetical protein	1.02	0.14	0.57	-
OE3633R	probable N4-(beta-N-acetylglucosaminyl)-L-asparaginase	1.02	0.11	0.71	aga
OE3572R	CTP synthase (EC 6.3.4.2)	1.02	0.18	0.42	pyrG
OE3738F	conserved hypothetical protein	1.02	0.13	0.59	-
OE1984F	cytochrome-c oxidase (EC 1.9.3.1) subunit III	1.02	0.28	0.28	cox3A
OE1376R	conserved hypothetical protein	1.02	0.17	0.43	-
OE1669F	aldehyde dehydrogenase (glucose 1-dehydrogenase homolog)	1.02	0.12	0.60	-
OE3616F	probable deoxyribose-phosphate aldolase (EC 4.1.2.4)	1.02	0.28	0.27	deoC
OE4036R	probable oxidoreductase (maleylacetate reductase homolog)	1.02	0.04	2.03	oxr2
OE4033R	probable DNA helicase (enhancer-binding protein homolog)	1.02	0.08	0.96	dbp
OE3082R	translation initiation factor aIF-2B subunit alpha/delta eif2bd	1.02	0.12	0.60	eif2bd
OE6126R	insertion element protein (ISH2)	1.02	0.07	0.96	-
OE2437F	conserved hypothetical protein	1.02	0.13	0.54	-
OE5265F	conserved hypothetical protein	1.02	0.12	0.58	-
OE3586R	conserved hypothetical protein	1.02	0.29	0.24	-
OE2328F	hypothetical protein	1.02	0.02	2.93	-
OE2259F	conserved hypothetical protein	1.02	0.09	0.75	-
OE5104R	probable IS200-type transposase (ISH12) (nonfunctional	1.02	0.26	0.26	-
OE5308F	conserved hypothetical protein	1.01	0.15	0.46	-
OE3940F	conserved hypothetical protein	1.01	0.11	0.61	-

OE1471F	tryptophan synthase (EC 4.2.1.20) alpha subunit	1.01	0.09	0.77	trpA
OE3621F	hypothetical protein	1.01	0.17	0.39	-
OE5279R	conserved hypothetical protein	1.01	0.12	0.54	-
OE1733R	conserved hypothetical protein	1.01	0.13	0.49	-
OE2607F	probable GTP-binding protein	1.01	0.08	0.77	drg
OE3592F	conserved hypothetical protein	1.01	0.15	0.42	-
OE6016F	cysteine-rich protein	1.01	0.10	0.64	-
OE3125R	conserved hypothetical protein	1.01	0.09	0.67	-
OE1306F	conserved hypothetical protein	1.01	0.17	0.37	-
OE2122F	conserved hypothetical protein	1.01	0.08	0.73	-
OE2745R	phosphoglycerate kinase (EC 2.7.2.3)	1.01	0.10	0.57	pgk
OE1249R	conserved hypothetical protein	1.01	0.18	0.33	-
OE2858F	probable thiamin biosynthesis protein	1.01	0.10	0.60	thiI
OE2453R	conserved hypothetical protein	1.01	0.09	0.68	-
OE1587F	conserved hypothetical protein	1.01	0.02	2.65	-
OE2253F	conserved hypothetical protein	1.01	0.06	1.02	-
OE3796R	conserved hypothetical protein	1.01	0.45	0.13	-
OE3771F	hypothetical protein	1.01	0.06	0.89	-
OE3895F	conserved hypothetical protein (RNase P homolog)	1.01	0.05	1.18	-
OE8006F	conserved hypothetical protein	1.01	0.19	0.30	-
OE4471R	conserved hypothetical protein	1.01	0.07	0.79	-
OE4556F	hypothetical protein	1.01	0.04	1.46	-
OE5337R	probable ATP-dependent helicase (nonfunctional	1.01	0.12	0.46	-
OE5013R	spurious ORF	1.01	0.10	0.55	-
OE1422F	conserved hypothetical protein	1.01	0.10	0.57	-
OE2919R	conserved hypothetical protein	1.01	0.10	0.57	-
OE2092F	hypothetical protein	1.01	0.14	0.39	-
OE2879R	hypothetical protein	1.01	0.15	0.37	-
OE3146R	hypothetical protein	1.01	0.26	0.21	-
OE1226F	conserved hypothetical protein	1.01	0.15	0.37	-
OE1140R	molybdenum cofactor biosynthesis protein moeB	1.01	0.33	0.16	moeB
OE1748R	rRNA methylase homolog	1.01	0.03	1.66	cna
OE5089F	conserved hypothetical protein	1.01	0.22	0.24	-
OE3445F	conserved hypothetical protein	1.01	0.07	0.74	-
OE4282F	single-stranded-DNA-specific exonuclease (EC 3.1.-.-)	1.01	0.11	0.46	recJ
OE2612F	conserved hypothetical protein	1.01	0.17	0.29	-
OE2038R	hypothetical protein	1.01	0.11	0.45	-
OE4476R	phoU protein homolog	1.01	0.07	0.71	-
OE1334R	hypothetical protein	1.01	0.13	0.36	-
OE2761R	chorismate synthase (EC 4.6.1.4)	1.01	0.13	0.38	aroC
OE4649F	probable transport protein	1.01	0.21	0.22	arsB
OE3515F	hypothetical protein	1.01	0.12	0.38	-
OE4355R	thiosulfate sulfurtransferase homolog	1.01	0.19	0.24	tssA
OE1252R	thioredoxin homolog	1.01	0.04	1.05	-
OE1528F	DNA topoisomerase I	1.01	0.25	0.18	topA
OE4204F	methylaspartate mutase (EC 5.4.99.1) small subunit	1.01	0.04	1.07	mamA
OE2377F	conserved hypothetical protein	1.01	0.16	0.28	-
OE4329F	conserved hypothetical protein	1.01	0.10	0.47	-
OE5033R	hypothetical protein	1.01	0.06	0.74	-
OE1512R	segregation and condensation protein scpA	1.01	0.05	0.92	scpA
OE1952F	phosphoribosylaminoimidazole carboxylase catalytic subunit	1.01	0.03	1.74	purE

OE4159F	adenosylhomocysteinase (EC 3.3.1.1)	1.01	0.11	0.41	achY
OE4103R	hypothetical protein	1.01	0.08	0.58	-
OE3145F	conserved hypothetical protein	1.01	0.06	0.76	-
OE3173F	probable transport protein	1.01	0.08	0.58	nac
OE1288F	probable cationic amino acid transport protein	1.01	0.12	0.35	cat1
OE4485R	prob.ABC-type phosph. transport system periplasmic substrate-bdg. protein	1.01	0.13	0.32	phoX1
OE1597F	hypothetical protein	1.01	0.10	0.41	-
OE6140R	transcription initiation factor TFB	1.01	0.22	0.19	tfbH
OE4082F	probable cation-transporting ATPase	1.01	0.09	0.47	cpx
OE1878R	hypothetical protein	1.01	0.31	0.13	-
OE1946R	riboflavin synthase (EC 2.5.1.9) beta subunit	1.01	0.06	0.66	ribE
OE3377R	conserved hypothetical protein	1.01	0.12	0.35	-
OE3407F	ribosomal protein L5	1.01	0.11	0.36	rpl5
OE2149R	conserved hypothetical protein	1.01	0.12	0.33	-
OE3070R-2 not found in HaloLex		1.01	0.21	0.19	
OE3481R-2 not found in HaloLex		1.01	0.11	0.36	
OE7100R-2 not found in HaloLex		1.01	0.18	0.22	
OE3562R	hypothetical protein	1.01	0.10	0.39	-
OE3929R	hypothetical protein	1.01	0.14	0.26	-
OE2878F	hypothetical protein	1.01	0.07	0.53	-
OE1947F	conserved hypothetical protein	1.01	0.09	0.43	-
OE1704R	ABC-type transport system ATP-binding protein	1.01	0.39	0.10	trp3
OE3784R	preprotein-export translocase subunit secD	1.01	0.07	0.51	secD
OE2381R	fla operon protein flaH	1.01	0.06	0.58	flaH
OE3571R	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2)	1.01	0.04	0.96	guaAb
OE2294R	conserved hypothetical protein	1.01	0.04	0.92	-
OE3045F	conserved hypothetical protein	1.01	0.13	0.27	-
OE2698R	hypothetical protein	1.01	0.09	0.37	-
OE4013R	hypothetical protein	1.01	0.19	0.18	-
OE2113R	phosphate permease homolog	1.01	0.06	0.59	-
OE3253F	probable CbiB protein (adenosylcobinamide synthesis)	1.01	0.10	0.34	cbiB
OE7166F	conserved hypothetical protein	1.01	0.17	0.20	-
OE4585R	hypothetical protein	1.01	0.09	0.38	-
OE4323F	malate dehydrogenase (EC 1.1.1.37)	1.01	0.24	0.14	mdhA
OE6059R	iron-sulfur protein homolog / glycerol-3-phosphate dehydrogenase homolog	1.01	0.14	0.23	-
OE1646R	hypothetical protein	1.01	0.06	0.55	-
OE4124R	conserved hypothetical protein	1.01	0.14	0.22	-
OE3155R	conserved hypothetical protein	1.01	0.49	0.06	-
OE2171F	halocyanin hcpC	1.01	0.11	0.28	hcpC
OE4475R	hypothetical protein	1.01	0.08	0.40	-
OE4634F	conserved hypothetical protein	1.01	0.26	0.12	-
OE4007F	electron transfer flavoprotein alpha subunit	1.01	0.21	0.14	etfA
OE2806F	conserved hypothetical protein	1.01	0.18	0.16	-
OE3556R	carbamoyl-phosphate synthase (EC 6.3.-.-) small subunit	1.01	0.18	0.16	carA
OE4093F	hypothetical protein	1.01	0.09	0.34	-
OE1817R	conserved hypothetical protein	1.01	0.19	0.15	-
OE3922R	glutamate--ammonia ligase (EC 6.3.1.2)	1.01	0.28	0.10	glnA
OE5230R	conserved hypothetical protein	1.01	0.13	0.22	-
OE5177F	hypothetical protein	1.01	0.23	0.12	-
OE3678R	conserved hypothetical protein	1.01	0.30	0.09	-

OE3591F	glutamyl-tRNA(Gln) amidotransferase (EC 6.3.5.-) subunit D	1.01	0.12	0.22	gatD
OE2510R	hypothetical protein	1.01	0.05	0.52	-
OE5272R	ABC-type transport system permease protein	1.01	0.10	0.28	-
OE5031R	conserved hypothetical protein	1.01	0.16	0.16	-
OE2315R	ABC-type transport system permease protein	1.01	0.08	0.33	rbsC2
OE1814R	dnaJ N-terminal domain protein	1.01	0.06	0.40	-
OE7068R	conserved hypothetical protein	1.01	0.11	0.23	-
OE5100R	trkA domain protein	1.01	0.16	0.16	trkA3
OE2130F	conserved hypothetical protein	1.01	0.09	0.27	-
OE7035R	spurious ORF	1.01	0.07	0.37	-
OE1016R	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1.01	0.17	0.14	graD2
OE3905F	conserved hypothetical protein	1.00	0.15	0.15	-
OE4118R-2 not found in HaloLex		1.00	0.08	0.29	
OE6288R-2 not found in HaloLex		1.00	0.16	0.13	
OE2749F	uridine kinase (EC 2.7.1.48)	1.00	0.20	0.10	urk
OE2512R	2-hydroxyhepta-2	1.00	0.05	0.35	hpcE
OE2298F	DNA ligase (ATP) (EC 6.5.1.1)	1.00	0.08	0.25	lig
OE4114F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component beta subunit	1.00	0.07	0.27	oxdhB
OE3314R	hypothetical protein	1.00	0.15	0.12	-
OE3108F	probable DNA primase	1.00	0.08	0.22	pri
OE2921R	probable dihydropteroate synthase (EC 2.5.1.15)	1.00	0.03	0.50	dhpS
OE4558R	dihydroorotase (EC 3.5.2.3)	1.00	0.11	0.16	pyrC
OE4276F	hydroxymethylbilane synthase (EC 4.3.1.8)	1.00	0.06	0.26	hemC
OE3462R	hypothetical protein	1.00	0.05	0.32	-
OE2333R	signal-transducing histidine kinase homolog	1.00	0.17	0.09	ark
OE1183F	hypothetical protein	1.00	0.06	0.24	-
OE2219R	probable molybdopterin-guanine dinucleotide biosynthesis protein B	1.00	0.15	0.10	mobB
OE3884F	acetyl-CoA C-ac(et)yltransferase (EC 2.3.1.16) or (EC 2.3.1.9)	1.00	0.08	0.19	aca
OE4398F	O-acetylhomoserine (thiol)-lyase (EC 4.2.99.10)	1.00	0.16	0.08	hal
OE3755R	conserved hypothetical protein	1.00	0.16	0.08	-
OE4220F	imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	1.00	0.05	0.27	hisB
OE4056R	transcription initiation factor TFB	1.00	0.19	0.06	tfbA
OE1898A1F	hypothetical protein	1.00	0.19	0.06	-
OE3154R	histone acetyltransferase homolog	1.00	0.13	0.09	-
OE3245F	cob(I)alamin adenosyltransferase (EC 2.5.1.17) (cobO in PSEDE)	1.00	0.10	0.11	cobO
OE2319R	conserved hypothetical protein	1.00	0.05	0.19	-
OE4002F	hypothetical protein	1.00	0.08	0.12	-
OE2280R	hypothetical protein	1.00	0.24	0.04	-
OE3610R	translation initiation factor aIF-2B subunit alpha/delta eif2ba	1.00	0.09	0.10	eif2ba
OE7135R	hypothetical protein	1.00	0.07	0.13	-
OE1687F	aspartate--tRNA ligase (EC 6.1.1.12)	1.00	0.16	0.06	aspS
OE4609F	hypothetical protein	1.00	0.05	0.18	-
OE3496R	glutamyl-tRNA reductase (EC 1.2.1.-)	1.00	0.03	0.22	hemA
OE4559R	conserved hypothetical protein	1.00	0.13	0.06	-
OE7105F-2 not found in HaloLex		1.00	0.20	0.03	

OE2986R	hypothetical protein	1.00	0.07	0.10	-
OE3768F	hypothetical protein	1.00	0.16	0.04	-
OE1691R	conserved hypothetical protein	1.00	0.12	0.05	-
OE5143F	probable transport protein	1.00	0.18	0.04	-
OE3876R	translation initiation factor aIF-2 gamma subunit	1.00	0.06	0.10	aIF2g
OE1942F	citryl-CoA lyase (EC 4.1.3.34) beta subunit	1.00	0.14	0.04	citE
OE3589F	conserved hypothetical protein	1.00	0.09	0.04	-
OE3634F	isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	1.00	0.14	0.02	icd
OE2007F	conserved hypothetical protein	1.00	0.03	0.10	-
OE3439F	conserved hypothetical protein	1.00	0.18	0.01	-
OE5294R	hypothetical protein	1.00	0.13	0.01	-
OE1924F	hypothetical protein	1.00	0.14	0.01	-
OE2979F	conserved hypothetical protein	1.00	0.08	0.01	-
OE4615F	N-terminal acetyltransferase	1.00	0.17	0.01	rimI2
OE6170R	hypothetical protein	1.00	0.10	0.00	-
OE3394F	ribosomal protein L22	-1.00	0.14	0.01	rpl22
OE1911R	conserved hypothetical protein	-1.00	0.14	0.01	-
OE4143F	hypothetical protein	-1.00	0.17	0.01	-
OE4449R	hypothetical protein	-1.00	0.13	0.01	-
OE5219F	hypothetical protein	-1.00	0.26	0.01	-
OE4360R	probable methyltransferase (24-sterol C-methyltransferase homolog)	-1.00	0.06	0.03	scm
OE2955F	ABC-type transport system ATP-binding protein	-1.00	0.06	0.03	hemV2
OE3322F	conserved hypothetical protein	-1.00	0.09	0.03	-
OE3739R	CBS domain protein	-1.00	0.13	0.03	-
OE3983R	lycopene cyclase (EC 1.14.-.-)	-1.00	0.17	0.02	crtY
OE2159R	ribosomal protein S3a.eR	-1.00	0.10	0.04	rps3aR
OE2478R	conserved hypothetical protein	-1.00	0.18	0.03	-
OE3906F	bacteriophage-type DNA polymerase homolog	-1.00	0.18	0.03	-
OE3169R	conserved hypothetical protein	-1.00	0.06	0.09	-
OE1457R	conserved hypothetical protein	-1.00	0.11	0.06	-
OE7148F	hypothetical protein (nonfunctional	-1.00	0.15	0.04	-
OE1272R	DNA mismatch recognition protein	-1.00	0.03	0.29	mutS1
OE1853R	Na+/cholate efflux system protein mrpF homolog	-1.00	0.20	0.04	-
OE1888R	conserved hypothetical protein	-1.00	0.24	0.04	-
OE1490R	conserved hypothetical protein	-1.00	0.09	0.10	-
OE5125F	gas-vesicle protein gvpA2	-1.00	0.04	0.23	gvpA2
OE1100F	hypothetical protein	-1.00	0.05	0.20	-
OE5416A1R	hypothetical protein	-1.00	0.07	0.13	-
OE3849F	conserved hypothetical protein	-1.00	0.17	0.06	-
OE7007F	hypothetical protein (encoded by ISH7/ISH24 subtype 1)	-1.00	0.18	0.06	-
OE3039F	conserved hypothetical protein	-1.00	0.08	0.15	-
OE4267F	conserved hem operon protein	-1.00	0.06	0.20	-
OE3119R	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	-1.00	0.05	0.26	panB
OE3731R	phosphoribosylformylglycinamidine synthase component I	-1.00	0.17	0.07	purQ
OE1424F	hypothetical protein	-1.00	0.25	0.05	-
OE1963F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit K	-1.00	0.11	0.13	nuoK
OE3655R	hypothetical protein	-1.00	0.14	0.09	-

OE6130F	conserved hypothetical protein	-1.00	0.18	0.07	-
OE4505F	phenylalanine--tRNA ligase (EC 6.1.1.20) alpha subunit	-1.00	0.07	0.21	pheS
OE1895B1F	hypothetical protein	-1.00	0.19	0.07	-
OE2090R	hypothetical protein	-1.00	0.02	0.75	-
OE4132R	tryptophan--tRNA ligase (EC 6.1.1.2)	-1.00	0.13	0.11	trpS2
OE3330F	conserved hypothetical protein	-1.00	0.16	0.09	-
OE1568F	anthranilate synthase (EC 4.1.3.27) component I	-1.00	0.14	0.11	trpE2
OE8007F	hypothetical protein	-1.00	0.08	0.20	-
OE1178F	type I site-specific deoxyribonuclease (EC 3.1.21.3) subunit rmeR	-1.00	0.05	0.28	rmeR
OE2863R	conserved hypothetical protein	-1.00	0.13	0.12	-
OE2179F	ABC-type transport system ATP-binding protein	-1.00	0.24	0.07	-
OE2988R	conserved hypothetical protein	-1.00	0.21	0.09	-
OE3319R	CbiM protein (prob.ABC-type cobalt transport system permease prot. 2)	-1.00	0.23	0.08	cbiM
OE1259R	conserved hypothetical protein	-1.00	0.08	0.24	-
OE1775R	hypothetical protein	-1.00	0.12	0.16	-
OE1856R	probable pantothenate metabolism flavoprotein	-1.00	0.16	0.12	dfp
OE1722R	conserved hypothetical protein	-1.00	0.15	0.13	-
OE4550F	ABC-type transport system ATP-binding protein	-1.00	0.17	0.11	dppF
OE4294R	conserved hypothetical protein	-1.00	0.11	0.17	-
OE1147R	protein-L-isoaspartate O-methyltransferase pimT1	-1.00	0.09	0.23	pimT1
OE6034F	IS1341-type transposase (TCE32)	-1.00	0.31	0.07	-
OE4335F	conserved hypothetical protein	-1.00	0.16	0.13	-
OE1708R	hypothetical protein	-1.00	0.09	0.23	-
OE6329R	hypothetical protein	-1.00	0.16	0.14	-
OE7216F	conserved hypothetical protein	-1.00	0.26	0.08	-
OE1915F	hypothetical protein	-1.01	0.09	0.25	-
OE3828F	conserved hypothetical protein	-1.01	0.21	0.11	-
OE4308F	hypothetical protein	-1.01	0.15	0.16	-
OE3817R	ribosomal protein S19.eR	-1.01	0.10	0.22	rps19R
OE5144R	ABC-type transport system permease protein	-1.01	0.12	0.20	-
OE4331R	tryptophanase (EC 4.1.99.1)	-1.01	0.08	0.28	tnaA
OE1440F	IS1341-type transposase (TCE31)	-1.01	0.27	0.09	-
OE7011R	hypothetical protein	-1.01	0.08	0.32	-
OE4230F	probable acylaminoacyl-peptidase (EC 3.4.19.1)	-1.01	0.14	0.18	yuxL
OE2640F	phosphopyruvate hydratase (EC 4.2.1.11) (enolase)	-1.01	0.11	0.23	eno
OE1957F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit H	-1.01	0.19	0.13	nuoH
OE2026F	ABC-type transport system ATP-binding protein	-1.01	0.05	0.55	trp5
OE1979R	cytochrome-c oxidase (EC 1.9.3.1) subunit I	-1.01	0.04	0.70	cox1A
OE2269F	hypothetical protein	-1.01	0.11	0.24	-
OE1231R-2 not found in HaloLex		-1.01	0.13	0.20	
OE5417R	conserved hypothetical protein	-1.01	0.17	0.16	-
OE7171F	hypothetical protein	-1.01	0.07	0.38	-
OE3221F	conserved cobalamin operon protein	-1.01	0.10	0.28	-
OE3121R	probable phosphoglycolate phosphatase (EC 3.1.3.18)	-1.01	0.07	0.41	-
OE7027R	gas-vesicle operon protein gvpI1	-1.01	0.44	0.07	gvpI1
OE2747R	conserved hypothetical protein	-1.01	0.13	0.22	-
OE3762R	glycerol kinase (EC 2.7.1.30)	-1.01	0.08	0.35	glpK

OE5296F	hypothetical protein	-1.01	0.30	0.10	-
OE7161R	conserved hypothetical protein	-1.01	0.05	0.58	-
OE4040R	conserved hypothetical protein	-1.01	0.23	0.13	-
OE4487F	conserved hypothetical protein	-1.01	0.02	1.41	-
OE2725R	L-fuculose-phosphate aldolase (EC 4.1.2.17)	-1.01	0.11	0.30	fucA
OE3070R	transducer protein htrXII	-1.01	0.15	0.22	htrXII
OE3625R	ABC-type transport system permease protein	-1.01	0.04	0.93	potC
OE5291F	hypothetical protein	-1.01	0.05	0.62	-
OE2414R	taxis protein cheC1 (cheJ)	-1.01	0.17	0.20	cheC1
OE6012F	probable transposase (ISH6/ISHS1)	-1.01	0.12	0.28	-
OE2900F	conserved hypothetical protein	-1.01	0.17	0.20	-
OE3790R	hypothetical protein	-1.01	0.14	0.25	-
OE2311R	uridine phosphorylase (EC 2.4.2.3)	-1.01	0.05	0.67	udp2
OE2739F	histidine ammonia-lyase (EC 4.3.1.3)	-1.01	0.08	0.42	hutH
OE1849R	conserved hypothetical protein	-1.01	0.16	0.23	-
OE5209R	transcription regulator arcR	-1.01	0.08	0.50	arcR
OE7147F	probable transposase (ISH8/ISH26)	-1.01	0.46	0.08	-
OE7092F	hypothetical protein	-1.01	0.12	0.33	-
OE2519F	hypothetical protein	-1.01	0.24	0.16	-
OE1254R	conserved hypothetical protein	-1.01	0.08	0.49	-
OE3261F	conserved cobalamin operon protein	-1.01	0.07	0.56	-
OE3686F	hypothetical protein	-1.01	0.09	0.45	-
OE3152R	probable peptide chain release factor aRF1	-1.01	0.07	0.57	pelA
OE7217F	conserved hypothetical protein	-1.01	0.14	0.30	-
OE2743F	hypothetical protein	-1.01	0.05	0.84	-
OE3308F	malate dehydrogenase (oxaloacetate decarboxylating) (EC 1.1.1.40)	-1.01	0.08	0.52	mdh
OE1699R	oxidoreductase (EC 1.-.-.-) (geranylgeranyl hydrogenase homolog)	-1.01	0.10	0.43	-
OE2730R	probable guanine deaminase (EC 3.5.4.3)	-1.01	0.08	0.60	hac
OE3706F	hypothetical protein	-1.01	0.06	0.77	-
OE3090R	conserved hypothetical protein	-1.01	0.11	0.42	-
OE1500R	pyruvate	-1.01	0.09	0.48	ppsA
OE1283R	conserved hypothetical protein	-1.01	0.06	0.71	-
OE2447F	hypothetical protein	-1.01	0.27	0.17	-
OE1727R	hypothetical protein	-1.01	0.30	0.15	-
OE3665R	conserved hypothetical protein	-1.01	0.09	0.49	-
OE1079F	conserved hypothetical protein	-1.01	0.08	0.62	-
OE5078F	sodium-dependent phosphate transport protein homolog	-1.01	0.10	0.45	phoT2
OE1820R	ribosomal protein S27.eR	-1.01	0.16	0.29	rps27R
OE2435F	hypothetical protein	-1.01	0.12	0.38	-
OE5363R	insertion element protein (ISH2)	-1.01	0.02	2.30	-
OE5128F	gas-vesicle operon protein gvpN2	-1.01	0.07	0.74	gvpN2
OE4479R	probable ABC-type phosphate transport system ATP-binding protein	-1.01	0.17	0.30	pstB1
OE3274R	glycine cleavage system protein P-2 (glycine dehydrogenase subunit 2)	-1.01	0.17	0.29	gcvP2
OE4018F	conserved hypothetical protein	-1.01	0.07	0.70	-
OE3597R	hypothetical protein	-1.01	0.10	0.53	-
OE4526R	hypothetical protein	-1.01	0.23	0.22	-
OE6055R	conserved hypothetical protein	-1.01	0.15	0.34	-

OE7026R	gas-vesicle operon protein gvpJ1	-1.01	0.13	0.38	gvpJ1
OE3243F	cobyrinic acid a	-1.01	0.14	0.37	cbiA
OE1034R	spurious ORF	-1.01	0.09	0.59	-
OE6053F	phage PhiH1 repressor protein homolog	-1.01	0.32	0.17	-
OE1579R	conserved hypothetical protein	-1.01	0.14	0.38	-
OE3205A1 R	hypothetical protein	-1.01	0.10	0.55	-
OE2946R	conserved hypothetical protein	-1.01	0.34	0.16	-
OE6032F	conserved hypothetical protein	-1.01	0.13	0.44	-
OE2231R	probable transcription regulator	-1.01	0.06	0.87	idr2
OE3980R	brp protein homolog	-1.01	0.13	0.44	blh
OE1054F	hypothetical protein	-1.01	0.05	1.24	-
OE1595F	proline--tRNA ligase (EC 6.1.1.15)	-1.01	0.16	0.35	proS
OE5197R	conserved hypothetical protein	-1.01	0.37	0.15	-
OE1060F	hypothetical protein	-1.01	0.09	0.62	-
OE2065R	probable X-Pro dipeptidase (EC 3.4.13.9)	-1.01	0.21	0.28	pepQ1
OE2217R	probable molybdopterin-guanine dinucleotide biosynthesis protein A	-1.01	0.06	1.03	mobA
OE5325F	conserved hypothetical protein	-1.01	0.13	0.45	-
OE5424R	conserved hypothetical protein	-1.01	0.13	0.48	-
OE2596F	conserved hypothetical protein	-1.01	0.15	0.40	-
OE1554R	hypothetical protein	-1.01	0.07	0.92	-
OE3511F	probable sodium/pantothenate symporter	-1.01	0.32	0.20	panF
OE1372R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit P	-1.01	0.16	0.40	rpoP
OE5383F	probable transposase (ISH3/ISH27)	-1.01	0.08	0.82	-
OE2626R	probable ATP-binding protein mrp	-1.01	0.09	0.70	mrp
OE3456F	conserved hypothetical protein	-1.01	0.21	0.30	-
OE4462F	conserved hypothetical protein	-1.01	0.28	0.23	-
OE3224F	conserved cobalamin operon protein	-1.01	0.16	0.40	-
OE5037R	cell division control protein cdc6 (nonfunctional	-1.01	0.05	1.41	orc2
OE3468R	phytoene dehydrogenase (EC 1.14.99.-) (phytoene desaturase) 2	-1.01	0.11	0.57	crtI2
OE4446R	hypothetical protein	-1.01	0.09	0.69	-
OE7214R-2 not found in HaloLex		-1.01	0.15	0.43	
OE4661R	conserved hypothetical protein	-1.01	0.15	0.44	-
OE3472F	conserved hypothetical protein	-1.01	0.08	0.88	-
OE4382R	hypothetical protein	-1.01	0.14	0.48	-
OE4683F	riboflavin synthase (EC 2.5.1.9) alpha subunit	-1.01	0.07	0.89	ribC
OE2845R	conserved hypothetical protein	-1.01	0.04	1.77	-
OE4041F	helicase homolog	-1.01	0.22	0.30	-
OE5162R-2 not found in HaloLex		-1.01	0.09	0.76	
OE2905F	hypothetical protein	-1.01	0.07	0.99	-
OE1203F	probable creatininase (EC 3.5.2.10)	-1.02	0.05	1.35	-
OE2744R	conserved hypothetical protein	-1.02	0.12	0.56	-
OE3955F	probable proline dehydrogenase (EC 1.5.99.8)	-1.02	0.10	0.67	putA
OE3988R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit E.a	-1.02	0.07	1.06	atpE
OE7222R	hypothetical protein	-1.02	0.07	1.05	-
OE6096A1 R	hypothetical protein	-1.02	0.32	0.22	-
OE3384R	conserved hypothetical protein	-1.02	0.03	2.33	-
OE2187F	conserved hypothetical protein	-1.02	0.19	0.38	-
OE2080F	hypothetical protein	-1.02	0.04	1.92	-

OE2645F	mevalonate kinase (EC 2.7.1.36)	-1.02	0.10	0.70	mvk
OE4281F	uroporphyrinogen-III synthase (EC 4.2.1.75)	-1.02	0.29	0.26	hemD
OE5001R	DNA primase homolog	-1.02	0.15	0.50	-
OE3467R	deoxyribodipyrimidine photo-lyase (EC 4.1.99.3)	-1.02	0.14	0.52	phr1
OE1448R	conserved hypothetical protein	-1.02	0.05	1.56	-
OE3807R	oligoendopeptidase	-1.02	0.11	0.70	yjbG
OE2066F	hypothetical protein	-1.02	0.06	1.22	-
OE1044F	hypothetical protein	-1.02	0.39	0.20	-
OE2499F	hypothetical protein	-1.02	0.15	0.53	-
OE5071F	protein kinase weak homolog	-1.02	0.22	0.36	-
OE3899R	probable ADP-ribose pyrophosphatase (EC 3.6.1.13)	-1.02	0.11	0.67	mutT
OE5030R	hypothetical protein	-1.02	0.05	1.51	-
OE3002R	conserved hypothetical protein	-1.02	0.08	0.99	-
OE2724F	hypothetical protein	-1.02	0.10	0.79	-
OE4743R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit H	-1.02	0.16	0.50	rpoH
OE1730R	conserved hypothetical protein	-1.02	0.24	0.33	-
OE7070R	conserved hypothetical protein	-1.02	0.35	0.23	-
OE2189R	transducer protein htr4 (htpVI)	-1.02	0.15	0.53	htr4
OE6277R	transposase homolog (TCE33) (nonfunctional	-1.02	0.17	0.47	-
OE6113F	conserved hypothetical protein	-1.02	0.09	0.91	-
OE3405F	ribosomal protein S4.eR	-1.02	0.22	0.38	rps4R
OE6114R	hypothetical protein	-1.02	0.41	0.20	-
OE1591R	hypothetical protein	-1.02	0.11	0.78	-
OE1550F	conserved hypothetical protein	-1.02	0.29	0.29	-
OE5343R	probable ATP-dependent helicase (nonfunctional	-1.02	0.10	0.83	-
OE4005F	electron transfer flavoprotein beta subunit	-1.02	0.10	0.88	etfB
OE4621F	ADP-ribose pyrophosphatase homolog	-1.02	0.17	0.49	-
OE2969R	probable transcription regulator	-1.02	0.21	0.41	asnC
OE1143R	probable molybdenum cofactor biosynthesis protein moeA2	-1.02	0.22	0.39	moeA2
OE1804R	conserved hypothetical protein	-1.02	0.03	2.56	-
OE1656F	indole-3-acetyl-L-aspartic acid hydrolase (EC 3.5.1.-)	-1.02	0.06	1.37	-
OE7114F	probable DNA-directed DNA polymerase (EC 2.7.7.7) type II	-1.02	0.25	0.35	polB3a
OE2063R	conserved hypothetical protein	-1.02	0.14	0.62	-
OE1475F	conserved hypothetical protein	-1.02	0.10	0.84	-
OE1453F	conserved hypothetical protein	-1.02	0.08	1.10	-
OE6165R	probable transposase (ISH3/ISH27)	-1.02	0.09	1.00	-
OE2381R-2 not found in HaloLex		-1.02	0.08	1.14	
OE2679R	ribosomal protein L21.eR	-1.02	0.18	0.49	rpl21R
OE6154F	hypothetical protein	-1.02	0.03	2.80	-
OE2886R	probable transposase (ISH1)	-1.02	0.19	0.47	-
OE2937R	conserved hypothetical protein	-1.02	0.03	2.64	-
OE4436R	L-allo-threonine aldolase (EC 4.2.1.-)	-1.02	0.07	1.35	lta
OE3186F	biotin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15) 1	-1.02	0.04	2.05	birA1
OE1373R	ribosomal protein L37a.eR	-1.02	0.05	1.69	rpl37aR
OE3579F	thiol-specific antioxidant protein	-1.02	0.17	0.54	hyrA
OE3320F	halocyanin hcpA	-1.02	0.04	2.45	hcpA
OE3451A1F	hypothetical protein	-1.02	0.12	0.78	-
OE3669R	conserved hypothetical protein	-1.02	0.13	0.74	-
OE5055F	cationic amino acid transport protein homolog	-1.02	0.25	0.37	cat3

OE2232F	conserved hypothetical protein	-1.02	0.10	0.98	-
OE1545F	probable oxidoreductase (cis-retinol dehydrogenase homolog)	-1.02	0.20	0.48	rdh1
OE1436R	spurious ORF	-1.02	0.08	1.15	-
OE1974R	conserved hypothetical protein	-1.02	0.07	1.43	-
OE3725F	hypothetical protein	-1.02	0.29	0.33	-
OE3131F	hypothetical protein	-1.02	0.14	0.71	-
OE4614F	hypothetical protein	-1.02	0.06	1.50	-
OE3721F	conserved hypothetical protein	-1.02	0.28	0.34	-
OE4411F	ABC-type transport system permease protein homolog	-1.02	0.10	0.94	-
OE2380R	flagella biogenesis protein flaI (prob. flagellin secretion system prot. flaI)	-1.02	0.08	1.19	flaI
OE3150R	transducer protein hemAT	-1.02	0.10	0.97	hemAT
OE4240F	conserved hypothetical protein	-1.02	0.07	1.35	-
OE6356F	conserved hypothetical protein	-1.02	0.08	1.27	-
OE4448R	hypothetical protein	-1.02	0.18	0.53	-
OE2764R	signal-transducing histidine kinase homolog	-1.02	0.28	0.35	-
OE2805R	thioredoxin reductase (NADPH) (EC 1.6.4.5)	-1.02	0.11	0.89	trxB2
OE5192R	alkaline phosphatase (EC 3.1.3.1)	-1.02	0.09	1.11	aph
OE4341R	hypothetical protein	-1.02	0.22	0.45	-
OE2989R	conserved hypothetical protein	-1.02	0.24	0.43	-
OE2945F	probable ornithine cyclodeaminase (EC 4.3.1.12)	-1.02	0.08	1.28	ocd2
OE1541F	rhomboid family protein	-1.02	0.02	6.58	-
OE2024F	conserved hypothetical protein	-1.02	0.05	2.24	-
OE3349F	coenzyme F420--quinone oxidoreductase 42K subunit homolog	-1.02	0.03	3.95	-
OE4610R	dCTP deaminase homolog	-1.02	0.15	0.69	-
OE5080F	conserved hypothetical protein	-1.02	0.11	0.96	-
OE2948R	conserved hypothetical protein	-1.02	0.09	1.09	-
OE7224R	insertion element protein (ISH2)	-1.02	0.06	1.72	-
OE1905R	probable hexosyltransferase	-1.02	0.17	0.61	-
OE1190F	probable oxidoreductase (cis-retinol dehydrogenase homolog)	-1.02	0.18	0.56	rdh2
OE5130F-2 not found in HaloLex		-1.02	0.19	0.55	
OE6120F	hypothetical protein	-1.02	0.18	0.59	-
OE2076F	conserved hypothetical protein	-1.02	0.15	0.73	-
OE5141R	conserved hypothetical protein	-1.02	0.12	0.92	-
OE3371F	translation elongation factor aEF-1 alpha subunit homolog	-1.02	0.11	1.00	-
OE2956F	hypothetical protein	-1.02	0.08	1.33	-
OE5190R	hydrogenase expression/formation protein homolog	-1.02	0.08	1.30	hypE1
OE4689R	conserved hypothetical protein	-1.02	0.18	0.59	-
OE2591R	conserved hypothetical protein	-1.02	0.15	0.73	-
OE3575R	hypothetical protein	-1.02	0.08	1.43	-
OE3176F	hypothetical protein	-1.02	0.23	0.48	-
OE1876R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-)	-1.02	0.10	1.11	petA
OE1965F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit M	-1.02	0.34	0.32	nuoM
OE3974R	dnaJ N-terminal domain / ferredoxin fusion protein	-1.02	0.21	0.54	fer1
OE1882R	hypothetical protein	-1.02	0.14	0.81	-
OE3691F	probable anthranilate phosphoribosyltransferase (EC 2.4.2.18)	-1.02	0.25	0.45	trpD2

OE1134F	conserved hypothetical protein	-1.02	0.22	0.51	-
OE4697R	hypothetical protein	-1.02	0.20	0.57	-
OE3810R	tRNA-pseudouridine synthase (EC 5.4.99.12)	-1.03	0.04	2.58	truA
OE6298B1F	hypothetical protein (nonfunctional	-1.03	0.23	0.50	-
OE1451F	probable methyltransferase	-1.03	0.05	2.23	pnm
OE7094F	conserved hypothetical protein	-1.03	0.05	2.38	-
OE1719R	probable oxidoreductase (protochlorophyllide reductase homolog)	-1.03	0.08	1.51	-
OE1953F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit A	-1.03	0.21	0.54	nuoA
OE4599F	potassium transport system protein trkH3	-1.03	0.32	0.36	trkH3
OE3017R	UDP-sugar hydrolase (EC 3.6.1.45) / 5'-nucleotidase (EC 3.1.3.5)	-1.03	0.05	2.10	ush
OE2874F	hypothetical protein	-1.03	0.29	0.40	-
OE3000R	conserved hypothetical protein	-1.03	0.14	0.82	-
OE2690R	hypothetical protein	-1.03	0.12	0.97	-
OE7174R	conserved hypothetical protein	-1.03	0.34	0.34	-
OE3764F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit B	-1.03	0.19	0.60	gpdB
OE3792F	glucose-6-phosphate isomerase (EC 5.3.1.9)	-1.03	0.19	0.61	pgi
OE4301R	ABC-type transport system ATP-binding protein	-1.03	0.15	0.80	ykfD
OE1852R	conserved hypothetical protein	-1.03	0.13	0.89	-
OE3606R	sugar kinase (EC 2.7.1.-)	-1.03	0.07	1.75	suk
OE5184F	conserved hypothetical protein	-1.03	0.42	0.28	-
OE2133R	aldehyde dehydrogenase (EC 1.2.1.-) (retinal dehydrogenase homol.)	-1.03	0.11	1.12	aldH2
OE4044R	hypothetical protein	-1.03	0.06	2.14	-
OE3524F	pyridoxine biosynthesis protein	-1.03	0.19	0.62	pyroA
OE2330R	hypothetical protein	-1.03	0.21	0.59	-
OE1755F	probable aspartate aminotransferase (EC 2.6.1.1)	-1.03	0.23	0.53	aspB1
OE2142R	conserved hypothetical protein	-1.03	0.07	1.69	-
OE6279R	hypothetical protein	-1.03	0.06	2.14	-
OE2450F	acetate--CoA ligase (EC 6.2.1.1)	-1.03	0.06	2.11	acs2
OE2717R	thioredoxin-dependent hydroperoxide peroxidase (EC 1.11.1.-)	-1.03	0.09	1.38	bcp
OE3942R	hypothetical protein	-1.03	0.10	1.23	-
OE7060R	insertion element protein (ISH2)	-1.03	0.08	1.52	-
OE1495R	pyruvate kinase (EC 2.7.1.40)	-1.03	0.46	0.27	pykA
OE4052F	DNA helicase (EC 3.6.1.-) mcm (intein-containing)	-1.03	0.12	1.05	mcm
OE3863R	6-N-hydroxylaminopurine sensitivity-controlling protein	-1.03	0.08	1.52	ham1
OE6315F	conserved hypothetical protein	-1.03	0.05	2.32	-
OE7144R	conserved hypothetical protein	-1.03	0.06	2.06	-
OE1934R	proteinase IV (EC 3.4.-.-)	-1.03	0.06	2.07	edp
OE3585R	conserved hypothetical protein	-1.03	0.06	2.29	-
OE5149R	hypothetical protein	-1.03	0.06	2.17	-
OE4227F	thioredoxin reductase (NADPH) (EC 1.6.4.5)	-1.03	0.03	3.72	txrB3
OE3688F	hypothetical protein	-1.03	0.14	0.92	-
OE5430F	spurious ORF	-1.03	0.04	3.40	-
OE3874R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit E'	-1.03	0.07	1.85	rpoE1
OE6321R	hypothetical protein	-1.03	0.06	2.20	-
OE4117F	probable prephenate dehydratase (EC 4.2.1.51) (monofunctional)	-1.03	0.16	0.80	pheA2
OE1101R	hypothetical protein	-1.03	0.03	4.15	-

OE1146R-2 not found in HaloLex		-1.03	0.15	0.85	
OE4065R	histidine triad family protein	-1.03	0.04	2.96	hit1
OE1342R	hypothetical protein	-1.03	0.10	1.25	-
OE4596R	conserved hypothetical protein	-1.03	0.15	0.90	-
OE1874R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-)	-1.03	0.18	0.73	petB
OE3971R	parA domain protein	-1.03	0.16	0.82	parA2
OE4343R	hypothetical protein	-1.03	0.11	1.24	-
OE3168R	pyridoxal phosphate-dependent aminotransferase	-1.03	0.19	0.72	-
OE1777F	DNA-directed DNA polymerase (EC 2.7.7.7) type II	-1.03	0.29	0.47	polB1
OE7150R	conserved hypothetical protein	-1.03	0.15	0.88	-
OE4049R	hypothetical protein	-1.03	0.10	1.32	-
OE3569R	hypothetical protein	-1.03	0.04	3.19	-
OE1362R	hypothetical protein	-1.03	0.16	0.86	-
OE2386R	flagella accessory protein	-1.03	0.06	2.23	flaCE
OE1929R-2 not found in HaloLex		-1.03	0.07	2.02	
OE4741R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B'	-1.03	0.12	1.17	rpoB1
OE4022R	mannose-1-phosphate guanylyltransferase (EC 2.7.7.13)	-1.03	0.11	1.22	manC
OE1829R	conserved hypothetical protein	-1.03	0.19	0.74	-
OE2857F	S-adenosylmethionine synthetase homolog	-1.03	0.17	0.79	-
OE1659R	conserved hypothetical protein	-1.03	0.31	0.44	-
OE4442F	conserved hypothetical protein	-1.03	0.12	1.11	-
OE8001F	conserved hypothetical protein	-1.03	0.26	0.54	-
OE4263F	conserved hem operon protein	-1.03	0.09	1.52	-
OE5282R	conserved hypothetical protein	-1.03	0.25	0.57	-
OE8010R	helicase N-terminal region homolog	-1.03	0.12	1.22	-
OE1277F	probable thioredoxin	-1.03	0.06	2.42	trxA3
OE4511R	hypothetical protein	-1.03	0.08	1.66	-
OE3010F	probable DNA repair helicase	-1.03	0.10	1.43	rhl
OE1625F	hypothetical protein	-1.03	0.10	1.45	-
OE2547R	probable glycosyltransferase (EC 2.-.-.-)	-1.03	0.09	1.52	exoM
OE5286R	ATP-dependent RNA helicase homolog	-1.03	0.14	1.00	-
OE4545F	hypothetical protein	-1.03	0.14	1.03	-
OE4619R	iron-dependent transcription repressor homolog	-1.03	0.14	1.03	idr1
OE3503F	di-trans	-1.03	0.13	1.12	uppS1
OE3495R	4a-hydroxytetrahydrobiopterin dehydratase homolog	-1.03	0.07	1.91	cad
OE1202F	probable ABC-type transport system ATP-binding/permease protein	-1.03	0.13	1.11	trp1
OE3194R	probable oxidoreductase (glucose 1-dehydrogenase homolog)	-1.03	0.06	2.30	-
OE5440F	probable arsenical pump-driving ATPase (EC 3.6.1.-)	-1.03	0.04	3.52	arsA
OE2558R	probable O-succinylbenzoate-CoA synthase (OSB synthase)	-1.03	0.11	1.34	menC
OE3986R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit F.a	-1.03	0.15	0.94	atpF
OE1193F	hypothetical protein	-1.03	0.09	1.70	-
OE6062R	conserved hypothetical protein	-1.03	0.17	0.86	-
OE7066F	cytochrome d ubiquinol oxidase (EC 1.10.3.-) subunit II	-1.03	0.19	0.76	cydB1
OE5183R	IS240-type transposase (ISH103)	-1.03	0.09	1.66	-
OE3954R	conserved hypothetical protein	-1.03	0.07	2.00	-
OE2249R	transducer protein weak homolog lacking transduction domain	-1.03	0.18	0.80	-
OE5233F	probable transposase (ISH5)	-1.03	0.18	0.81	-

OE3838F	hypothetical protein	-1.03	0.15	0.99	-
OE5205R-2 not found in HaloLex		-1.03	0.27	0.56	
OE1221F	acetylpolyamine aminohydrolase	-1.03	0.05	2.85	aup
OE5443F	probable transcription regulator	-1.03	0.22	0.67	-
OE2136R	conserved hypothetical protein	-1.03	0.19	0.77	-
OE3947R	conserved hypothetical protein	-1.03	0.06	2.70	-
OE1482R	probable dolichyl-phosphate beta-glucosyltransferase (N-terminal homol.)	-1.03	0.30	0.50	dpg
OE1055R	hypothetical protein	-1.03	0.07	2.08	-
OE5318F	hypothetical protein	-1.03	0.13	1.13	-
OE4270R	spurious ORF	-1.03	0.04	4.36	-
OE5061F	hypothetical protein	-1.03	0.11	1.44	-
OE4736R	ribosomal protein S12	-1.03	0.30	0.51	rps12
OE3659F	hypothetical protein	-1.03	0.13	1.16	-
OE2533F	hypothetical protein	-1.03	0.16	0.96	-
OE7057F	conserved hypothetical protein	-1.03	0.20	0.78	-
OE2056F	probable methyltransferase (caffeoyl-CoA O-methyltransferase homol.)	-1.03	0.13	1.23	-
OE4234R	uracil phosphoribosyltransferase (EC 2.4.2.9) upp	-1.03	0.19	0.84	upp
OE4571R	probable leucyl aminopeptidase (EC 3.4.11.1)	-1.03	0.03	6.04	pepB3
OE1956F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit CD	-1.03	0.09	1.66	nuoCD
OE5053F	potassium-transporting ATPase (EC 3.6.3.12) subunit B	-1.04	0.03	5.14	kdpB
OE1119F	dTDPglucose 4	-1.04	0.09	1.73	-
OE4169F	conserved hypothetical protein	-1.04	0.11	1.39	-
OE4105R	RNA helicase homolog	-1.04	0.26	0.61	brr2
OE3413F	ribosomal protein L19.eR	-1.04	0.26	0.62	rpl19R
OE3908R	ABC-type transport system ATP-binding protein	-1.04	0.32	0.51	phnC
OE3388F	ribosomal protein L3	-1.04	0.04	4.03	rpl3
OE3891R	long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	-1.04	0.21	0.76	lfl2
OE7178F	plasmid replication protein repI	-1.04	0.18	0.90	repI1
OE6337R	cell division protein homolog	-1.04	0.19	0.84	-
OE7214R	TATA-binding transcription initiation factor	-1.04	0.10	1.57	tbpD1
OE4141R	RNAse Z	-1.04	0.25	0.66	-
OE1636F	protein-L-isoaspartate O-methyltransferase homolog	-1.04	0.06	2.81	pimT2
OE2560R	probable glycine betaine transport protein	-1.04	0.11	1.49	opuD
OE3823F	uridine 5'-monophosphate kinase (EC 2.7.4.-)	-1.04	0.07	2.46	-
OE1268F	probable transcription regulator boa1	-1.04	0.19	0.85	boa1
OE3336R	spurious ORF	-1.04	0.04	4.02	-
OE2590R	hypothetical protein	-1.04	0.05	3.27	-
OE3126F	hypothetical protein	-1.04	0.05	3.60	-
OE5127F	gas-vesicle protein gvpC2	-1.04	0.07	2.32	gvpC2
OE2678R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit F	-1.04	0.34	0.50	rpoF
OE1890R	DNA-(apurinic or apyrimidinic site) lyase endonuclease III	-1.04	0.23	0.72	nthA2
OE2486F	probable alcohol dehydrogenase (NADP+) (EC 1.1.1.2)	-1.04	0.34	0.49	adh3
OE4197F	conserved hypothetical protein	-1.04	0.06	2.86	-
OE2808F	hypothetical protein	-1.04	0.35	0.48	-
OE7063R	spurious ORF	-1.04	0.08	2.00	-
OE1538F	spurious ORF	-1.04	0.06	2.94	-
OE3030R	conserved hypothetical protein	-1.04	0.11	1.50	-

OE3458R	probable oxidoreductase (versicolorin reductase homolog)	-1.04	0.07	2.52	-
OE1477R	3-dehydroquinate dehydratase (EC 4.2.1.10)	-1.04	0.16	1.05	aroD
OE3520F	conserved hypothetical protein	-1.04	0.03	5.97	-
OE1936R	conserved hypothetical protein	-1.04	0.08	2.08	-
OE4693R	conserved hypothetical protein	-1.04	0.23	0.73	-
OE2907R	deoxyribodipyrimidine photo-lyase (EC 4.1.99.3)	-1.04	0.03	6.69	phr2
OE5198R	conserved hypothetical protein	-1.04	0.17	1.02	-
OE3479R	hypothetical protein	-1.04	0.13	1.34	-
OE2967R	hypothetical protein	-1.04	0.06	3.09	-
OE4732F	hypothetical protein	-1.04	0.21	0.83	-
OE4249F	spurious ORF	-1.04	0.10	1.71	-
OE1515R	structural-maintenance-of-chromosomes protein	-1.04	0.07	2.45	smc
OE6323R	hypothetical protein	-1.04	0.08	2.28	-
OE5433F	probable transposase (ISH3/ISH27)	-1.04	0.08	2.24	-
OE5068F	DNA-directed DNA polymerase (nonfunctional	-1.04	0.13	1.42	-
OE3473F	transducer protein htrVII	-1.04	0.13	1.42	htrVII
OE5093F	hypothetical protein	-1.04	0.05	3.57	-
OE5275R	hypothetical protein	-1.04	0.20	0.90	-
OE2789R	hypothetical protein	-1.04	0.12	1.52	-
OE4700F	hypothetical protein	-1.04	0.18	1.02	-
OE4176R	hypothetical protein	-1.04	0.18	1.03	-
OE3438R	conserved hypothetical protein	-1.04	0.08	2.26	-
OE4623F	conserved hypothetical protein	-1.04	0.14	1.36	-
OE2856F	conserved hypothetical protein	-1.04	0.05	3.76	-
OE3987R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit C.a	-1.04	0.15	1.21	atpC
OE2935R	fumarate hydratase (EC 4.2.1.2)	-1.04	0.12	1.60	fumC
OE2475F	DNA damage-inducible protein homolog	-1.04	0.19	0.96	yqjH
OE2448F	transcription regulator bat homolog	-1.04	0.02	8.24	boa4
OE6142R	conserved hypothetical protein	-1.04	0.11	1.69	-
OE1222R	tRNA adenylyltransferase (EC 2.7.7.25)	-1.04	0.25	0.73	cca
OE4636F	conserved hypothetical protein	-1.04	0.26	0.72	-
OE2603R	ribosomal protein L11	-1.04	0.11	1.68	rpl11
OE3374R	hypothetical protein	-1.04	0.17	1.11	-
OE4178R	conserved hypothetical protein	-1.04	0.05	3.74	-
OE4422R	spurious ORF	-1.04	0.04	4.45	-
OE6161R	conserved hypothetical protein (nonfunctional	-1.04	0.11	1.77	-
OE1783F	conserved hypothetical protein	-1.04	0.11	1.67	-
OE6102R	conserved hypothetical protein	-1.04	0.05	3.62	-
OE4582R	conserved hypothetical protein	-1.04	0.21	0.90	-
OE3474R-2 not found in HaloLex		-1.04	0.09	2.25	
OE3846R	probable enoyl/3-hydroxybutryl-CoA dehydratase (EC 4.2.1.-)	-1.04	0.14	1.41	fad1
OE3560F	probable isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 3	-1.04	0.16	1.19	idi3
OE2582F	hypothetical protein	-1.04	0.12	1.64	-
OE2392R-2 not found in HaloLex		-1.04	0.12	1.63	
OE3921F	conserved hypothetical protein	-1.04	0.20	0.97	-
OE2370R	gufA protein	-1.04	0.07	2.80	gufA
OE5067R	hypothetical protein	-1.04	0.04	4.51	-
OE2941R	hypothetical protein	-1.04	0.21	0.91	-
OE3910R	probable ABC-type transport system periplasmic	-1.04	0.16	1.24	hpb

	substrate-bdg prot.				
OE3852F	hypothetical protein	-1.04	0.18	1.07	-
OE3868R	ribosomal protein S27a.eR	-1.04	0.18	1.07	rps27aR
OE4302R	ABC-type oligopeptide transport system ATP-binding protein	-1.04	0.05	4.33	oppD2
OE5017R	probable transposase (ISH5)	-1.04	0.07	2.94	-
OE4363F	hypothetical protein	-1.04	0.15	1.35	-
OE6283R	IS200-type transposase homolog (TCE31) (nonfunctional	-1.04	0.03	7.14	-
OE5074R	conserved hypothetical protein	-1.04	0.11	1.74	-
OE6156F	conserved hypothetical protein	-1.04	0.33	0.61	-
OE7207F	hypothetical protein	-1.04	0.06	3.26	-
OE5413F	restriction system mrr homolog	-1.04	0.03	7.09	-
OE4062F	spurious ORF	-1.04	0.17	1.18	-
OE1637R	probable DNA-directed RNA polymerase (EC 2.7.7.6) subunit M	-1.05	0.22	0.93	rpoM1
OE4231R	hypothetical protein	-1.05	0.25	0.81	-
OE1293F	spurious ORF	-1.05	0.10	2.03	-
OE2415R	taxis sensor histidine kinase (EC 2.7.3.-) cheA	-1.05	0.13	1.55	cheA
OE4444F	conserved hypothetical protein	-1.05	0.12	1.71	-
OE1653R	Na+/H+ antiporter homolog	-1.05	0.11	1.91	nhaC1
OE1613R	probable acylaminoacyl-peptidase (EC 3.4.19.1)	-1.05	0.13	1.59	-
OE7180F	hypothetical protein	-1.05	0.13	1.59	-
OE5124R	gas-vesicle operon protein gvpD2 (probable repressor protein)	-1.05	0.20	1.00	gvpD2
OE1158R	ribosomal protein S6 modification protein rimK	-1.05	0.15	1.36	rimK
OE1566F	hypothetical protein	-1.05	0.07	2.90	-
OE4601F	conserved hypothetical protein	-1.05	0.09	2.24	-
OE2513F	conserved hypothetical protein	-1.05	0.19	1.09	-
OE5165R	hypothetical protein	-1.05	0.15	1.39	-
OE6018R	hypothetical protein	-1.05	0.14	1.48	-
OE4655R	conserved hypothetical protein	-1.05	0.22	0.93	-
OE6127F-2 not found in HaloLex		-1.05	0.10	2.18	
OE7118R	hypothetical protein	-1.05	0.14	1.52	-
OE4499F	conserved hypothetical protein	-1.05	0.25	0.85	-
OE3257F	conserved cobalamin operon protein	-1.05	0.06	3.56	-
OE3594R	probable glycerophosphoryl diester phosphodiesterase	-1.05	0.07	2.99	ugpQ
OE1171F	type I restriction-modification system DNA-methyltransferase rmeM	-1.05	0.17	1.26	rmeMa
OE1260R	probable oxidoreductase (mercury(II) reductase homolog)	-1.05	0.21	1.00	merA
OE2139R	glycerol-3-phosphate cytidyltransferase homolog	-1.05	0.11	1.86	taqD
OE4162F	hypothetical protein	-1.05	0.05	4.04	-
OE3087R	conserved hypothetical protein	-1.05	0.10	2.15	-
OE4101R	tryptophan--tRNA ligase (EC 6.1.1.2)	-1.05	0.25	0.85	trpS1
OE4714F	hypothetical protein	-1.05	0.18	1.20	-
OE5112R	gas-vesicle operon protein gvpM2	-1.05	0.08	2.59	gvpM2
OE1972F	methylmalonyl-CoA mutase (EC 5.4.99.2) 1B (N-terminal homology)	-1.05	0.04	5.43	mut1B
OE4027F	conserved hypothetical protein	-1.05	0.20	1.09	-
OE4565F	conserved hypothetical protein	-1.05	0.17	1.30	-
OE5124R-2 not found in HaloLex		-1.05	0.18	1.20	
OE7050F	probable transposase (ISH9/ISH28)	-1.05	0.11	2.01	-

OE4184F	cell division control protein cdc6 homolog	-1.05	0.14	1.61	orc6
OE6063F	probable L-lactate permease	-1.05	0.22	0.99	lctP
OE2097F	conserved hypothetical protein	-1.05	0.10	2.15	-
OE4504F	conserved hypothetical protein	-1.05	0.05	4.33	-
OE3766R	hypothetical protein	-1.05	0.28	0.80	-
OE1073F	probable IS200-type transposase (ISH12)	-1.05	0.12	1.79	-
OE3861F	conserved hypothetical protein	-1.05	0.13	1.77	-
OE6107R	probable transposase (ISH11)	-1.05	0.15	1.50	-
OE5415R	hypothetical protein	-1.05	0.14	1.57	-
OE5223R	ABC-type transport system ATP-binding protein (nonfunctional	-1.05	0.14	1.59	trp7b
OE3544F	probable oxidoreductase (ferredoxin reductase homolog)	-1.05	0.15	1.48	noxA
OE4359F	ABC-type transport system ATP-binding protein	-1.05	0.11	2.08	cysA
OE2274R	phosphoribosylformylglycinamidine synthase component II	-1.05	0.11	2.03	purL
OE1442R	conserved hypothetical protein	-1.05	0.08	2.87	-
OE3501R	hypothetical protein	-1.05	0.20	1.13	-
OE5065R	conserved hypothetical protein	-1.05	0.09	2.38	-
OE1077R	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	-1.05	0.24	0.94	ugd
OE1994F	probable ABC-type transport system ATP-binding protein	-1.05	0.08	2.81	-
OE2140R	conserved hypothetical protein	-1.05	0.04	6.02	-
OE7127R	hypothetical protein	-1.05	0.27	0.86	-
OE3361F	conserved hypothetical protein	-1.05	0.07	3.34	-
OE2964F	signal-transducing histidine kinase homolog	-1.05	0.11	2.15	-
OE3139R	amidophosphoribosyltransferase (EC 2.4.2.14)	-1.05	0.05	4.46	purF
OE3783F	conserved hypothetical protein	-1.05	0.03	6.87	-
OE2019F	fructose-bisphosphate aldolase (EC 4.1.2.13) 1	-1.05	0.20	1.18	fba1
OE7170R	probable transposase (ISH4/ISH23/ISH50)	-1.05	0.05	4.73	-
OE7145R	hypothetical protein	-1.05	0.14	1.71	-
OE1469F	indole-3-glycerol-phosphate synthase (EC 4.1.1.48)	-1.05	0.08	3.02	trpC
OE4054F	hypothetical protein	-1.05	0.10	2.26	-
OE4412R	threonine synthase (EC 4.2.99.2)	-1.05	0.06	4.14	thrC1
OE3641F	ABC-type transport system periplasmic substrate-binding protein	-1.05	0.12	1.91	thb
OE2500R	triosephosphate isomerase (EC 5.3.1.1)	-1.05	0.14	1.68	tpiA
OE3728R	hypothetical protein	-1.05	0.27	0.89	-
OE2168R-2 not found in HaloLex		-1.05	0.21	1.14	
OE1467R	conserved hypothetical protein	-1.05	0.03	7.74	-
OE2572F	conserved hypothetical protein	-1.05	0.16	1.48	-
OE5020F	hypothetical protein	-1.05	0.29	0.83	-
OE2926R	conserved hypothetical protein	-1.05	0.05	4.58	-
OE2944F	conserved hypothetical protein	-1.05	0.11	2.22	-
OE1291R	conserved hypothetical protein	-1.05	0.10	2.34	-
OE4152R	ATP phosphoribosyltransferase (EC 2.4.2.17)	-1.05	0.08	2.90	hisG
OE3780F	ribonuclease HII (EC 3.1.26.-)	-1.05	0.16	1.55	rnh
OE2254R	hypothetical protein	-1.05	0.07	3.49	-
OE2951R	ABC-type transport system periplasmic substrate-binding protein	-1.05	0.13	1.94	-
OE2423F	hypothetical protein	-1.05	0.13	1.94	-
OE1323R	conserved hypothetical protein	-1.06	0.25	0.97	-
OE7131R	conserved hypothetical protein	-1.06	0.15	1.64	-

OE2052F	conserved hypothetical protein	-1.06	0.32	0.78	-
OE3744R	probable cell surface glycoprotein	-1.06	0.42	0.59	-
OE4171R	conserved hypothetical protein	-1.06	0.08	3.28	-
OE2126F	conserved hypothetical protein	-1.06	0.16	1.53	-
OE2850R	hypothetical protein	-1.06	0.17	1.49	-
OE2720R	geranylgeranyl hydrogenase homolog	-1.06	0.12	2.16	-
OE3961R	probable Na+/H+-exchanging protein	-1.06	0.06	3.88	-
OE2190R	aldehyde dehydrogenase (succinate-semialdehyde dehydrogenase homolog)	-1.06	0.15	1.70	aldH4
OE4050F	conserved hypothetical protein	-1.06	0.17	1.49	-
OE2436A1F	hypothetical protein	-1.06	0.21	1.17	-
OE5301F-2 not found in HaloLex		-1.06	0.06	4.05	
OE3578R	conserved hypothetical protein	-1.06	0.18	1.43	-
OE4500R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	-1.06	0.09	2.95	acd6
OE6045R	transposase homolog (ISH3/ISH27) (nonfunctional	-1.06	0.24	1.04	-
OE5123R	gas-vesicle operon protein gvpE2 (probable activator protein)	-1.06	0.35	0.71	gvpE2
OE3719F	conserved hypothetical protein	-1.06	0.07	3.82	-
OE2120F	conserved hypothetical protein	-1.06	0.21	1.22	-
OE3611R-2 not found in HaloLex		-1.06	0.09	2.72	
OE3315R	ABC-type cobalt transport system ATP-binding protein	-1.06	0.04	5.68	cbiO1
OE5335R	nuclease subunit B homolog	-1.06	0.07	3.80	-
OE6079F	conserved hypothetical protein	-1.06	0.17	1.49	-
OE4393R	transport protein homolog	-1.06	0.12	2.14	-
OE3084F	hypothetical protein	-1.06	0.23	1.12	-
OE1679R	prob.ABC-type phosph. transport system periplasmic phosphate-bdg. protein	-1.06	0.30	0.86	phoX2
OE3289F	conserved hypothetical protein	-1.06	0.24	1.05	-
OE1480F	probable ABC-type transport system periplasmic substrate-bdg. protein	-1.06	0.10	2.57	-
OE7166F-2 not found in HaloLex		-1.06	0.20	1.30	
OE6128R	hypothetical protein	-1.06	0.25	1.01	-
OE3297R	NADH-dependent FMN reductase	-1.06	0.14	1.87	msuE
OE3488R	probable creatininase (EC 3.5.2.10)	-1.06	0.06	4.30	cre
OE4671R	conserved hypothetical protein	-1.06	0.11	2.35	-
OE7084F	thioredoxin	-1.06	0.11	2.25	trxA1a
OE4729R	translation elongation factor aEF-2	-1.06	0.15	1.78	aef2
OE2077F	hypothetical protein	-1.06	0.08	3.18	-
OE3958F	conserved hypothetical protein	-1.06	0.09	2.94	-
OE3875R	conserved hypothetical protein	-1.06	0.08	3.15	-
OE3348F	sensory rhodopsin I	-1.06	0.05	5.35	sopI
OE4541F	conserved hypothetical protein	-1.06	0.08	3.45	-
OE4181R	sec-independent protein translocase component tatC2	-1.06	0.05	5.47	tatC2
OE1168R	hypothetical protein	-1.06	0.05	5.36	-
OE2386R-2 not found in HaloLex		-1.06	0.09	2.90	
OE5058F	hypothetical protein	-1.06	0.10	2.71	-
OE7009F	conserved hypothetical protein (encoded by ISH7/ISH24 subtype 1)	-1.06	0.09	2.86	-
OE4316F	ABC-type transport system permease protein	-1.06	0.21	1.29	appC
OE4320R	conserved hypothetical protein	-1.06	0.11	2.42	-
OE3492R	probable phosphatase (phosphoglycolate phosphatase homolog)	-1.06	0.10	2.79	pgp

OE3717F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 32K subunit	-1.06	0.08	3.15	nolA
OE2622R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) beta subunit	-1.06	0.32	0.84	porB
OE1347R	type II secretion system protein gspE1	-1.06	0.13	2.07	gspE1
OE2289F	conserved hypothetical protein	-1.06	0.19	1.45	-
OE1286R	DNA mismatch repair protein	-1.06	0.13	2.13	mutS
OE3238F	probable precorrin-6Y C5	-1.06	0.08	3.53	cbiE
OE2653R	hypothetical protein	-1.06	0.23	1.19	-
OE1929R	transducer protein htr16	-1.06	0.07	4.12	htr16
OE3400F	ribosomal protein S17	-1.06	0.10	2.66	rps17
OE6020R	hypothetical protein	-1.06	0.24	1.15	-
OE3668F	conserved hypothetical protein	-1.06	0.10	2.83	-
OE1417F	conserved hypothetical protein	-1.06	0.22	1.22	-
OE1592R	mRNA 3'-end processing factor homolog	-1.06	0.23	1.19	epf2
OE3101R	bacterioopsin activator	-1.06	0.06	4.90	bat
OE2116R	glutamate-rich protein	-1.06	0.20	1.42	-
OE3262R	conserved hypothetical protein	-1.06	0.06	4.55	-
OE1559R-2 not found in HaloLex		-1.06	0.10	2.85	
OE2438R	hypothetical protein	-1.06	0.21	1.31	-
OE2058R	signal-transducing histidine kinase homolog	-1.06	0.05	5.99	afsQ2
OE3269R	probable ABC-type transport system permease protein	-1.06	0.23	1.22	-
OE2903R	hypothetical protein	-1.06	0.23	1.21	-
OE4111F	lipoic acid synthase (EC 2.8.1.-)	-1.06	0.13	2.21	lip
OE3681R	conserved hypothetical protein	-1.06	0.11	2.62	-
OE6166R	conserved hypothetical protein (nonfunctional	-1.06	0.11	2.49	-
OE1501F	hypothetical protein	-1.06	0.05	6.08	-
OE1898R	spurious ORF	-1.06	0.24	1.17	-
OE2350R	conserved hypothetical protein	-1.07	0.11	2.59	-
OE3531R	homoserine kinase (EC 2.7.1.39)	-1.07	0.10	2.86	thrB
OE7204F	hypothetical protein	-1.07	0.14	2.11	-
OE4755F	probable cell surface glycoprotein	-1.07	0.08	3.57	-
OE2220F	conserved hypothetical protein	-1.07	0.24	1.21	-
OE4077F	hypothetical protein	-1.07	0.19	1.52	-
OE2930R	conserved hypothetical protein	-1.07	0.10	2.99	-
OE1652R	hypothetical protein	-1.07	0.10	2.86	-
OE3798R	conserved hypothetical protein	-1.07	0.15	1.88	-
OE1695R	hypothetical protein	-1.07	0.29	1.00	-
OE5163R	spurious ORF	-1.07	0.09	3.11	-
OE1675R	probable ABC-type phosphate transport system ATP-binding protein	-1.07	0.21	1.42	pstB2
OE1328F	spurious ORF	-1.07	0.06	5.09	-
OE7143R	conserved hypothetical protein	-1.07	0.11	2.70	-
OE4696R	hypothetical protein	-1.07	0.13	2.26	-
OE3970R	hypothetical protein	-1.07	0.23	1.31	-
OE3650R	conserved hypothetical protein	-1.07	0.21	1.41	-
OE4731R	spurious ORF	-1.07	0.05	6.09	-
OE2700F	probable coenzyme PQQ synthesis protein E	-1.07	0.09	3.52	pqqE1
OE4236F	phosphate transport protein homolog	-1.07	0.32	0.95	-
OE1356F	conserved hypothetical protein	-1.07	0.11	2.85	-
OE2093R	conserved hypothetical protein	-1.07	0.03	9.50	-
OE2332F	probable kynureninase (EC 3.7.1.3)	-1.07	0.18	1.70	hakA
OE1038R	conserved hypothetical protein	-1.07	0.60	0.50	-

OE6043R	transposase homolog (ISH3/ISH27) (nonfunctional	-1.07	0.06	5.42	-
OE2195F-2 not found in HaloLex		-1.07	0.09	3.43	
OE3998R	hypothetical protein	-1.07	0.12	2.60	-
OE5339R	probable transposase (ISH1)	-1.07	0.11	2.75	-
OE5019F	cell division control protein cdc6 homolog	-1.07	0.14	2.12	orc1
OE2683R	translation elongation factor aEF-1 beta subunit	-1.07	0.07	4.15	aef1b
OE5428R	conserved hypothetical protein	-1.07	0.08	3.71	-
OE7189F	conserved hypothetical protein	-1.07	0.28	1.11	-
OE4695F	probable acetoacetyl-CoA reductase (EC 1.1.1.36)	-1.07	0.32	0.96	phbB
OE3748R	probable archaeosine tRNA-ribosyltransferase (EC 2.4.2.-)	-1.07	0.16	1.96	tgtA2
OE1793F	conserved hypothetical protein	-1.07	0.08	3.93	-
OE2871F	probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.157)	-1.07	0.14	2.28	hbd2
OE1352F	hypothetical protein	-1.07	0.17	1.79	-
OE3708R	probable transcription regulator trh5	-1.07	0.28	1.10	trh5
OE4157F	probable chlorohydrolase	-1.07	0.12	2.68	trzA
OE4572R	valine--tRNA ligase (EC 6.1.1.9)	-1.07	0.07	4.50	valS
OE1738R	hypothetical protein	-1.07	0.02	14.34	-
OE5095F	L-2	-1.07	0.05	6.04	bdb
OE3277R	glycine cleavage system protein H	-1.07	0.46	0.69	gcvH
OE6337R-2 not found in HaloLex		-1.07	0.02	13.92	
OE3263R	transposase homolog (TCE33) (nonfunctional	-1.07	0.20	1.55	-
OE3794F	conserved hypothetical protein	-1.07	0.10	3.08	-
OE1632R	unspecific monooxygenase (EC 1.14.14.1) (cytochrome P450)	-1.07	0.18	1.77	cyc
OE6311F-2 not found in HaloLex		-1.07	0.11	2.97	
OE2798R	phosphoesterase homolog	-1.07	0.13	2.39	yhcR
OE7054R	conserved hypothetical protein	-1.07	0.07	4.65	-
OE5203F	arginine--tRNA ligase (EC 6.1.1.19)	-1.07	0.06	5.66	argS
OE2637F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit N	-1.07	0.28	1.13	rpoN
OE3498R	probable siroheme synthase (probable precorrin-2 oxidase	-1.07	0.15	2.16	cysG1
OE1982R	conserved hypothetical protein	-1.07	0.11	2.97	-
OE4451F	hypothetical protein	-1.07	0.04	7.50	-
OE5070R	conserved hypothetical protein	-1.07	0.21	1.55	-
OE2299F	p-nitrophenylphosphatase homolog	-1.07	0.08	3.86	pho2
OE2782F	probable stationary-phase survival protein	-1.07	0.04	8.94	surE
OE1840R	hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	-1.07	0.10	3.29	hprt
OE7210R	conserved hypothetical protein	-1.07	0.16	1.97	-
OE3219F	conserved cobalamin operon protein	-1.07	0.18	1.78	-
OE2791R	hypothetical protein	-1.07	0.21	1.53	-
OE2529F	polysaccharide biosynthesis protein homolog	-1.07	0.08	4.08	-
OE4643R	conserved hypothetical protein	-1.07	0.08	4.19	-
OE4717F	hypothetical protein	-1.07	0.13	2.45	-
OE1215R	hypothetical protein	-1.07	0.23	1.46	-
OE2898R	conserved hypothetical protein	-1.07	0.25	1.29	-
OE4196R	conserved hypothetical protein	-1.08	0.23	1.42	-
OE3486R	agmatinase (EC 3.5.3.11)	-1.08	0.12	2.78	speB
OE3584R	probable muconate cycloisomerase (EC 5.5.1.1)	-1.08	0.28	1.17	catB
OE4151F	hypothetical protein	-1.08	0.13	2.58	-
OE2417R	response regulator cheY	-1.08	0.21	1.59	cheY
OE5022F	conserved hypothetical protein	-1.08	0.07	4.52	-

OE3777R	conserved hypothetical protein	-1.08	0.12	2.86	-
OE3883R	conserved hypothetical protein	-1.08	0.04	7.97	-
OE1606R	conserved hypothetical protein	-1.08	0.15	2.23	-
OE1285F	conserved hypothetical protein	-1.08	0.19	1.73	-
OE1128F	conserved hypothetical protein (nonfunctional	-1.08	0.08	4.28	-
OE2451R	probable oxidoreductase	-1.08	0.05	6.32	-
OE7059R	TATA-binding transcription initiation factor (nonfunctional	-1.08	0.23	1.45	tbpB1b
OE3820R	conserved hypothetical protein	-1.08	0.30	1.11	-
OE3106F	bacteriorhodopsin precursor	-1.08	0.25	1.37	bop
OE5200R	glutamate/aspartate transport protein	-1.08	0.10	3.54	gltP
OE4724R	conserved hypothetical protein	-1.08	0.04	8.44	-
OE2067F	conserved hypothetical protein	-1.08	0.04	8.52	-
OE4673F	carboxypeptidase (EC 3.4.-.-)	-1.08	0.13	2.59	cxp
OE1102R	probable transposase (ISH8/ISH26)	-1.08	0.07	4.73	-
OE1432F	sarcosine oxidase (EC 1.5.3.1) beta subunit	-1.08	0.17	1.98	soxB
OE3425F	adenylate kinase (EC 2.7.4.3)	-1.08	0.20	1.75	adk
OE7120R	conserved hypothetical protein	-1.08	0.27	1.30	-
OE1275F	proteasome alpha subunit	-1.08	0.13	2.66	psmA
OE1263F	conserved hypothetical protein	-1.08	0.16	2.21	-
OE4374R	conserved hypothetical protein	-1.08	0.08	4.44	-
OE3167F-2 not found in HaloLex		-1.08	0.20	1.74	
OE2695F	flagellin flgXXX precursor	-1.08	0.11	3.16	flgXXX
OE7208F	hypothetical protein	-1.08	0.11	3.23	-
OE3414F	ribosomal protein L18	-1.08	0.08	4.69	rpl18
OE6111R	spurious ORF	-1.08	0.07	5.19	-
OE4298R	hypothetical protein	-1.08	0.12	2.94	-
OE3197F	site-specific DNA-methyltransferase (EC 2.1.1.-)	-1.08	0.02	15.15	zim
OE4419R	argininosuccinate lyase (EC 4.3.2.1)	-1.08	0.06	5.89	argH
OE4272F	conserved hem operon protein	-1.08	0.19	1.93	-
OE4148F	hypothetical protein	-1.08	0.24	1.47	-
OE7191F	spurious ORF	-1.08	0.25	1.42	-
OE3565F	molybdenum cofactor biosynthesis protein B	-1.08	0.03	13.60	moaB
OE3237F	precorrin-8X methylmutase (EC 5.4.1.2)	-1.08	0.08	4.71	cbiC
OE2710F	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	-1.08	0.04	9.72	acd3
OE3888F	conserved hypothetical protein	-1.08	0.30	1.22	-
OE1967F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit N	-1.08	0.12	2.94	nuoN
OE3941F	threonine synthase (EC 4.2.99.2)	-1.08	0.04	8.43	thrC3
OE1582R	conserved hypothetical protein	-1.08	0.08	4.68	-
OE4153F	conserved hypothetical protein	-1.08	0.16	2.22	-
OE2834R	hypothetical protein	-1.08	0.14	2.59	-
OE1997F	conserved hypothetical protein	-1.08	0.05	7.51	-
OE1112R	probable glycosyltransferase (EC 2.-.-.-)	-1.08	0.10	3.74	lpb
OE7074F	conserved hypothetical protein	-1.08	0.12	3.03	-
OE7149F	hypothetical protein	-1.08	0.18	1.99	-
OE4245R	hypothetical protein	-1.08	0.07	5.39	-
OE2633F	ribosomal protein L13	-1.08	0.08	4.71	rpl13
OE2832R	hypothetical protein	-1.08	0.11	3.24	-
OE5173R	hypothetical protein	-1.08	0.10	3.69	-
OE2934R	conserved hypothetical protein	-1.08	0.06	6.41	-
OE5118R	gas-vesicle operon protein gvpI2	-1.09	0.21	1.74	gvpI2

OE4722R	homoserine dehydrogenase (EC 1.1.1.3)	-1.09	0.03	10.82	hom
OE4115F	dihydrolipoamide S-acyltransferase (EC 2.3.1.-)	-1.09	0.06	5.79	dsa
OE2443R	hypothetical protein	-1.09	0.05	7.61	-
OE5146R	ABC-type transport system ATP-binding protein	-1.09	0.10	3.87	zurA
OE4164F	conserved hypothetical protein	-1.09	0.21	1.80	-
OE5187R	probable hydrolase	-1.09	0.17	2.23	-
OE2088F	signal-transducing histidine kinase homolog	-1.09	0.16	2.36	kinA2
OE2173F	cystathionine gamma-lyase (EC 4.4.1.1)	-1.09	0.08	4.62	cgs
OE3006R	conserved hypothetical protein	-1.09	0.10	3.69	-
OE5090F	hypothetical protein	-1.09	0.27	1.38	-
OE1559R	cell division protein ftsZ1	-1.09	0.08	4.58	ftsZ1
OE1756F	conserved hypothetical protein	-1.09	0.13	2.91	-
OE6352F	IS1341-type transposase (TCE32) (nonfunctional	-1.09	0.05	7.61	-
OE1960F	NADH dehydrogenase (ubiquinone) subunit J2 (C-terminal homology)	-1.09	0.08	4.77	nuoJ2
OE1136F	conserved hypothetical protein	-1.09	0.08	4.70	-
OE2847R	conserved hypothetical protein	-1.09	0.26	1.47	-
OE7131A1R	hypothetical protein	-1.09	0.04	9.12	-
OE2696F	hypothetical protein	-1.09	0.26	1.44	-
OE1018F	sugar transferase	-1.09	0.10	3.91	-
OE1434R	conserved hypothetical protein	-1.09	0.18	2.13	-
OE5097F	siderophore biosynthesis protein (malonyl-CoA decarboxylase hom.)	-1.09	0.43	0.90	iucB
OE2656R	conserved hypothetical protein	-1.09	0.10	3.80	-
OE5096F	siderophore biosynthesis protein	-1.09	0.08	4.69	iucA
OE7036F	gas-vesicle protein gvpC1	-1.09	0.12	3.10	gvpC1
OE4450R	signal recognition particle 54K protein	-1.09	0.16	2.39	srp54
OE1665R	dihydrodipicolinate synthase (EC 4.2.1.52)	-1.09	0.09	4.49	dapA
OE3782R	conserved hypothetical protein	-1.09	0.11	3.68	-
OE5243F	transducer protein car	-1.09	0.30	1.29	car
OE7190R	hypothetical protein	-1.09	0.16	2.37	-
OE3689R	probable heme biosynthesis protein nirD/L (nirH/nirG homolog)	-1.09	0.15	2.57	nirD
OE3332R	anthranilate synthase (EC 4.1.3.27) alpha subunit	-1.09	0.06	6.09	trpE1
OE7146R	transcription initiation factor TFB (nonfunctional	-1.09	0.06	6.43	tfbl1b
OE3506F	conserved hypothetical protein	-1.09	0.21	1.86	-
OE1743R	hypothetical protein	-1.09	0.16	2.49	-
OE3802R	hypothetical protein	-1.09	0.11	3.57	-
OE4059F	hypothetical protein	-1.09	0.16	2.42	-
OE4271F	conserved hem operon protein	-1.09	0.27	1.47	-
OE3595R	molybdopterin (MPT) converting factor	-1.09	0.07	6.01	moaD
OE4454R	signal recognition particle receptor SRalpha	-1.09	0.17	2.39	ftsY
OE1710R	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3) beta subunit	-1.09	0.24	1.65	korB
OE2561R	naphthoate synthase (EC 4.1.3.36)	-1.09	0.23	1.75	menB
OE1812R	conserved hypothetical protein	-1.09	0.15	2.65	-
OE3617F	conserved hypothetical protein	-1.09	0.20	2.00	-
OE3487R	translation initiation factor aIF-5A	-1.09	0.26	1.55	eif5a
OE4195F	replication factor C small subunit	-1.09	0.39	1.04	rfcA
OE4333R	aspartate kinase (EC 2.7.2.4) II alpha and beta subunit	-1.09	0.10	4.24	lysC
OE1326R	conserved hypothetical protein	-1.09	0.07	5.82	-
OE3411F	ribosomal protein L6	-1.09	0.06	6.60	rpl6

OE3818F	probable thiamin-phosphate kinase (EC 2.7.4.16)	-1.09	0.08	5.34	thiL
OE4405R	phosphoserine phosphatase (EC 3.1.3.3)	-1.09	0.14	2.97	serB
OE2383R	fla operon protein flaG	-1.09	0.12	3.45	flaG
OE5211F-2 not found in HaloLex		-1.09	0.10	3.92	
OE2536F	hypothetical protein	-1.09	0.08	4.92	-
OE5132F	probable phosphate transport protein	-1.09	0.20	2.03	phoT3
OE3283F	conserved hypothetical protein	-1.09	0.07	5.69	-
OE5102R	IS1341-type transposase (ISH12)	-1.09	0.11	3.64	-
OE4055F	hypothetical protein	-1.09	0.11	3.65	-
OE7223F	conserved hypothetical protein (nonfunctional	-1.09	0.08	5.00	-
OE5366R	conserved hypothetical protein	-1.09	0.14	2.87	-
OE3312R	probable oxidoreductase (aryl-alcohol dehydrogenase homolog)	-1.10	0.27	1.55	oxr3
OE2338R	hypothetical protein	-1.10	0.12	3.34	-
OE3164F	hypothetical protein	-1.10	0.13	3.14	-
OE1790R	hypothetical protein	-1.10	0.29	1.44	-
OE1872R	probable menaquinol--cytochrome-c reductase (EC 1.10.2.-)	-1.10	0.09	4.53	petD
OE7059R-2 not found in HaloLex		-1.10	0.09	4.90	
OE1344R	hypothetical protein	-1.10	0.27	1.56	-
OE4665R	GTP-binding protein	-1.10	0.09	4.63	hflX1
OE4021F	probable oxidoreductase (EC 1.1.1.-)	-1.10	0.10	4.30	oxr1
OE1576F	conserved hypothetical protein	-1.10	0.20	2.13	-
OE4099R	hypothetical protein	-1.10	0.08	5.10	-
OE7036F-2 not found in HaloLex		-1.10	0.21	2.00	
OE3147F	probable DNA helicase	-1.10	0.12	3.54	hel
OE4551F	ABC-type transport system periplasmic substrate-binding protein	-1.10	0.35	1.22	dppD
OE7062R	TATA-binding transcription initiation factor (nonfunctional	-1.10	0.16	2.72	tbpB1a
OE1844R	NADH dehydrogenase (ubiquinone) subunit N homolog	-1.10	0.10	4.30	-
OE3723R	conserved hypothetical protein	-1.10	0.05	8.31	-
OE2918F	N5	-1.10	0.25	1.70	mer
OE2545F	conserved hypothetical protein	-1.10	0.23	1.88	-
OE3913F	imidazoleglycerol-phosphate synthase (glutamine amidotransferase)	-1.10	0.21	2.09	hisH2
OE3881R	phnP protein	-1.10	0.09	5.09	phnP
OE3567F	hypothetical protein	-1.10	0.16	2.69	-
OE4628R	conserved hypothetical protein	-1.10	0.14	3.16	-
OE2053F	hypothetical protein	-1.10	0.14	3.05	-
OE5322R	conserved hypothetical protein	-1.10	0.28	1.57	-
OE2396R	hypothetical protein	-1.10	0.08	5.29	-
OE3341F	hypothetical protein	-1.10	0.07	5.90	-
OE4223R	conserved hypothetical protein	-1.10	0.41	1.08	-
OE7075F	conserved hypothetical protein	-1.10	0.14	3.16	-
OE5051R	trkA domain protein	-1.10	0.06	7.52	trkA2
OE3369F	conserved hypothetical protein	-1.10	0.14	3.16	-
OE2641F	ribosomal protein S2	-1.10	0.28	1.59	rps2
OE6325R	hypothetical protein	-1.10	0.11	3.91	-
OE8010G1F	replication protein repI2	-1.10	0.31	1.46	repI2
OE1921R	protoheme IX farnesyltransferase homolog	-1.10	0.10	4.51	hhoA
OE5091F	conserved hypothetical protein	-1.10	0.15	3.04	-

OE3227F	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase homolog	-1.10	0.08	5.65	cobT
OE3053F	hypothetical protein	-1.10	0.13	3.53	-
OE1388R	hypothetical protein	-1.10	0.16	2.88	-
OE4702F	geranylgeranyl hydrogenase homolog	-1.10	0.12	3.71	-
OE1724R	conserved hypothetical protein	-1.11	0.08	5.68	-
OE4089R	conserved hypothetical protein	-1.11	0.15	2.97	-
OE3631F	ABC-type transport system ATP-binding protein	-1.11	0.07	6.38	potA
OE4051R	probable signal-transducing histidine kinase	-1.11	0.13	3.40	-
OE4177F	23S rRNA methyltransferase (EC 2.1.1.-)	-1.11	0.10	4.79	ftsJ
OE4094F	probable phosphomannomutase	-1.11	0.16	2.97	pmu1
OE4549R	conserved hypothetical protein	-1.11	0.48	0.96	-
OE3620R	histidine triad family protein	-1.11	0.07	6.35	hit2
OE1578F	probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	-1.11	0.27	1.70	graD1
OE4069R	hypothetical protein	-1.11	0.13	3.47	-
OE2110R	UDPglucose 4-epimerase (EC 5.1.3.2)	-1.11	0.12	3.98	galE1
OE1295R	hypothetical protein	-1.11	0.28	1.70	-
OE2908R	conserved hypothetical protein	-1.11	0.12	3.82	-
OE1410F	conserved hypothetical protein	-1.11	0.12	4.01	-
OE5431A1R	conserved hypothetical protein	-1.11	0.15	3.18	-
OE4358F	ABC-type transport system permease protein	-1.11	0.13	3.62	cysT1
OE3334R	anthranilate phosphoribosyltransferase (EC 2.4.2.18)	-1.11	0.03	16.64	trpD1
OE4045R	hypothetical protein	-1.11	0.18	2.71	-
OE5122R	gas-vesicle operon protein gvpF2	-1.11	0.18	2.67	gvpF2
OE6030R	conserved hypothetical protein	-1.11	0.06	7.82	-
OE3372F	hypothetical protein	-1.11	0.20	2.42	-
OE2094F	hypothetical protein	-1.11	0.11	4.53	-
OE3259F	cobC protein (adenosylcobinamide synthesis)	-1.11	0.09	5.48	cobC
OE5136R	conserved hypothetical protein	-1.11	0.14	3.56	-
OE3474R	transducer protein cosT	-1.11	0.11	4.50	cosT
OE4344F	excinuclease ABC subunit C	-1.11	0.12	4.11	uvrC
OE2586F	hypothetical protein	-1.11	0.05	10.44	-
OE1498R	glutamate decarboxylase homolog	-1.11	0.12	4.25	gadD
OE3015F	conserved hypothetical protein	-1.11	0.03	14.10	-
OE1039R	conserved hypothetical protein	-1.11	0.27	1.86	-
OE2551F	conserved hypothetical protein	-1.11	0.11	4.65	-
OE3476R	chemotactic signal transduction system periplasmic substrate-bdg. protein cosB	-1.11	0.37	1.33	cosB
OE4201R	probable preflagellin peptidase	-1.11	0.08	6.16	flaK
OE1556F	hypothetical protein	-1.12	0.16	3.14	-
OE4144R	conserved hypothetical protein	-1.12	0.23	2.18	-
OE2851R	hypothetical protein	-1.12	0.14	3.51	-
OE1340R	hypothetical protein	-1.12	0.12	4.28	-
OE2010R	conserved hypothetical protein	-1.12	0.12	4.00	-
OE2623R	pyruvate--ferredoxin oxidoreductase (EC 1.2.7.1) alpha subunit	-1.12	0.19	2.59	porA
OE5009R	transfer complex protein homolog	-1.12	0.36	1.39	trsE
OE5307F	ABC-type transport system ATP-binding protein	-1.12	0.11	4.42	-
OE5147R	probable ABC-type transport system periplasmic substrate-bdg. protein	-1.12	0.09	5.70	ycdH
OE2553R	glycerol-3-phosphate dehydrogenase subunit A homologue	-1.12	0.06	8.21	gpdA1

OE2853R	probable peptidylprolyl isomerase (EC 5.2.1.8)	-1.12	0.05	9.87	slyD
OE1943F	glutamate dehydrogenase (NADP+) (EC 1.4.1.4)	-1.12	0.11	4.54	gdhA1
OE4748F	conserved hypothetical protein	-1.12	0.14	3.75	-
OE1290F	trkA domain protein	-1.12	0.11	4.64	trkA1
OE3390F	ribosomal protein L23	-1.12	0.50	1.04	rpl23
OE6089R	IS1341-type transposase (TCE32)	-1.12	0.18	2.85	-
OE3454F	spurious ORF	-1.12	0.12	4.25	-
OE5142F	cell division protein ftsZ5	-1.12	0.33	1.60	ftsZ5
OE6036F-2 not found in HaloLex		-1.12	0.33	1.60	
OE5195R	conserved hypothetical protein	-1.12	0.05	10.40	-
OE1870R	hypothetical protein	-1.12	0.15	3.59	-
OE2042F	probable copper-transporting ATPase (EC 3.6.1.-)	-1.12	0.09	6.15	yvgX
OE1860F	conserved hypothetical protein	-1.12	0.25	2.14	-
OE3671F	conserved hypothetical protein	-1.12	0.25	2.08	-
OE1001F	conserved hypothetical protein	-1.12	0.03	18.21	-
OE1502R	conserved hypothetical protein	-1.12	0.05	10.22	-
OE1589F	DNA-(apurinic or apyrimidinic site) lyase endonuclease III	-1.12	0.14	3.85	nthA1
OE2757F	hypothetical protein	-1.12	0.09	5.95	-
OE4576F	probable ABC-type transport system substrate-binding protein	-1.12	0.05	11.52	-
OE8005F	conserved hypothetical protein	-1.12	0.05	10.58	-
OE4535F	sugar kinase (EC 2.7.1.-)	-1.12	0.20	2.63	-
OE2708R	superoxide dismutase (EC 1.15.1.1) 1 (Mn containing)	-1.12	0.15	3.47	sod1
OE1577R	conserved hypothetical protein	-1.13	0.19	2.83	-
OE3255F	probable cobalamin (5'-phosphate) synthase (EC 2.7.8.-)	-1.13	0.04	13.26	cobS
OE1781F	probable ABC-type transport system ATP-binding protein	-1.13	0.10	5.55	-
OE5170F	probable ABC-type transport system ATP-binding protein	-1.13	0.04	13.01	ugpC
OE3134F	transcription regulator bat homolog	-1.13	0.17	3.12	boa2
OE6311F	AAA-type ATPase (transitional ATPase homolog)	-1.13	0.20	2.66	aaa10
OE1951F	phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation subunit	-1.13	0.13	4.05	purK
OE3759R	hypothetical protein	-1.13	0.15	3.76	-
OE4224F	conserved hypothetical protein	-1.13	0.13	4.40	-
OE2078R	2-dehydropantoate 2-reductase (EC 1.1.1.169)	-1.13	0.22	2.48	apbA
OE7052F	probable transposase (ISH5)	-1.13	0.30	1.83	-
OE3752R	mutT domain protein	-1.13	0.08	6.78	-
OE4165R	DNA-directed DNA polymerase sliding clamp homolog	-1.13	0.23	2.38	pcn
OE4239F	conserved hypothetical protein	-1.13	0.17	3.35	-
OE4483R	probable ABC-type phosphate transport system permease protein	-1.13	0.11	4.99	pstC1
OE2003R	conserved hypothetical protein	-1.13	0.13	4.40	-
OE3230F	CobN protein (probable cobalt chelatase) (EC 4.99.1.-)	-1.13	0.06	9.10	cobN
OE5414R	conserved hypothetical protein	-1.13	0.28	2.04	-
OE1916F	cysteine synthase (EC 4.2.99.8) cysK1	-1.13	0.17	3.28	cysK1
OE2532R	conserved hypothetical protein	-1.13	0.09	6.30	-
OE3209F	probable precorrin-2 C20-methyltransferase (EC 2.1.1.130)	-1.13	0.13	4.44	cbiL
OE4311F	ABC-type transport system periplasmic substrate-binding protein	-1.13	0.10	6.00	appA
OE1148R	hypothetical protein	-1.13	0.10	5.48	-

OE5260F	probable transposase (ISH10)	-1.13	0.11	5.12	-
OE2902F	conserved hypothetical protein	-1.13	0.15	3.82	-
OE2522F	hypothetical protein	-1.13	0.08	6.96	-
OE2706R	hypothetical protein	-1.13	0.17	3.43	-
OE2456F	hypothetical protein	-1.13	0.07	7.91	-
OE3800F	translation initiation factor IF2	-1.14	0.21	2.77	infB
OE6008R	parA domain protein	-1.14	0.23	2.57	parA5
OE3732R	conserved hypothetical protein	-1.14	0.31	1.91	-
OE1610R	hypothetical protein	-1.14	0.32	1.81	-
OE2996R	transducer protein htr9 (htpIII)	-1.14	0.09	6.82	htr9
OE3872R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit E"	-1.14	0.10	5.74	rpoE2
OE2199F	probable alcohol dehydrogenase (EC 1.1.1.1)	-1.14	0.31	1.88	adh5
OE4008R	conserved hypothetical protein	-1.14	0.10	5.80	-
OE4221R	hypothetical protein	-1.14	0.21	2.81	-
OE2155R	CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)	-1.14	0.03	17.41	pssA
OE3894R	conserved hypothetical protein	-1.14	0.10	6.08	-
OE4581F	probable phosphogluconate dehydrogenase (N-term. domain homology)	-1.14	0.21	2.85	pgd
OE1403F	hypothetical protein	-1.14	0.06	10.85	-
OE1661F	conserved hypothetical protein	-1.14	0.22	2.73	-
OE2684R	signal-transducing histidine kinase homolog	-1.14	0.27	2.23	phoR
OE4670F	conserved hypothetical protein	-1.14	0.20	3.03	-
OE4326F	conserved hypothetical protein	-1.14	0.25	2.44	-
OE1416F	hypothetical protein	-1.14	0.20	3.07	-
OE1087R	probable transposase (ISH8/ISH26)	-1.14	0.15	3.92	-
OE5142F-2 not found in HaloLex		-1.14	0.18	3.46	
OE3412F	ribosomal protein L32.eR	-1.14	0.05	11.97	rpl32R
OE4561F	conserved hypothetical protein	-1.14	0.06	9.92	-
OE4667R	AAA domain/ferredoxin domain protein	-1.14	0.12	5.18	-
OE3704R	camphor resistance protein homolog	-1.14	0.16	3.83	crcB
OE5130F	trkA domain protein	-1.14	0.28	2.16	trkA4
OE4397F	homoserine O-acetyltransferase (EC 2.3.1.31)	-1.14	0.18	3.47	metA
OE2821F	conserved hypothetical protein	-1.14	0.22	2.82	-
OE1553F	hypothetical protein	-1.14	0.20	3.14	-
OE4429F	conserved hypothetical protein	-1.14	0.09	6.68	-
OE1083R	probable transposase (ISH3/ISH27)	-1.14	0.09	6.74	-
OE7141R	multidrug resistance transport protein homolog	-1.15	0.23	2.70	-
OE1353F	hypothetical protein	-1.15	0.12	5.24	-
OE5246R	permease protein homolog	-1.15	0.21	2.94	-
OE5108F	parA domain protein	-1.15	0.10	6.35	parA4
OE3789R	hypothetical protein	-1.15	0.11	5.92	-
OE3057F	conserved hypothetical protein	-1.15	0.39	1.58	-
OE4336R	probable ABC-type transport system permease protein	-1.15	0.08	7.40	nosY
OE2928F	probable transcription regulator	-1.15	0.16	4.01	trh6
OE4304R	ABC-type transport system permease protein	-1.15	0.11	5.71	dppB1
OE2689F	fibrillarin	-1.15	0.08	7.62	fib
OE1808F	probable phytoene dehydrogenase (EC 1.14.99.-) 3	-1.15	0.12	5.16	crtI3
OE4583F	ferredoxin (2Fe-2S)	-1.15	0.05	12.86	fer5
OE3977R	hypothetical protein	-1.15	0.17	3.66	-
OE1858F	hypothetical protein	-1.15	0.29	2.18	-
OE3822R	conserved hypothetical protein	-1.15	0.20	3.21	-

OE2020F	fructose-bisphosphatase (EC 3.1.3.11)	-1.15	0.19	3.30	fbp
OE1368R	hypothetical protein	-1.15	0.31	2.08	-
OE4192R	conserved hypothetical protein	-1.15	0.16	4.03	-
OE7079F	tetracyclin resistance protein homolog	-1.15	0.12	5.39	-
OE1792F	conserved hypothetical protein	-1.15	0.21	2.98	-
OE1726F	acetate--CoA ligase (EC 6.2.1.1)	-1.15	0.15	4.34	acs1
OE2548F	probable transmembrane oligosaccharyl transferase	-1.15	0.20	3.16	tot
OE3073R	dodecin	-1.15	0.17	3.74	-
OE1090F	conserved hypothetical protein (nonfunctional	-1.15	0.12	5.16	-
OE1209F	dehydratase homolog	-1.15	0.10	6.34	-
OE4646R	hypothetical protein	-1.15	0.27	2.41	-
OE1371R	prefoldin beta subunit	-1.15	0.23	2.84	pfdB
OE3963R	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 5.4.99.-)	-1.15	0.24	2.66	ribB
OE1657R	geranylgeranyl hydrogenase homolog	-1.15	0.04	15.61	-
OE3311F	conserved hypothetical protein	-1.15	0.21	3.04	-
OE1019R	IS1341-type transposase (TCE32)	-1.15	0.08	7.99	-
OE6027R	hypothetical protein	-1.15	0.02	31.35	-
OE3919F	conserved hypothetical protein	-1.15	0.25	2.63	-
OE3436R	transducer protein htr17	-1.16	0.16	4.02	htr17
OE3317R	probable cobalt transport protein CbiQ	-1.16	0.12	5.41	cbiQ
OE2012R	hypothetical protein	-1.16	0.12	5.34	-
OE1465F	endopeptidase La (EC 3.4.21.53)	-1.16	0.24	2.72	lon
OE3069R	conserved hypothetical protein	-1.16	0.10	7.02	-
OE1520R	hypothetical protein	-1.16	0.05	13.41	-
OE5211F	conserved hypothetical protein	-1.16	0.18	3.76	-
OE7101R	conserved hypothetical protein	-1.16	0.11	6.21	-
OE7187F	conserved hypothetical protein	-1.16	0.12	5.91	-
OE2307F	NADH dehydrogenase homolog	-1.16	0.11	5.99	-
OE6104R	conserved hypothetical protein	-1.16	0.33	2.05	-
OE7160R	hypothetical protein (encoded by ISH7/ISH24 subtype 2)	-1.16	0.06	11.82	-
OE4720R	ribosomal protein S10	-1.16	0.33	2.10	rps10
OE3596F	potassium channel protein pchA1	-1.16	0.11	6.25	pchA1
OE1299R	halorhodopsin	-1.16	0.13	5.45	hop
OE2189R-2 not found in HaloLex		-1.16	0.13	5.34	
OE3167F	transducer protein htrVIII	-1.16	0.12	5.78	htrVIII
OE4303R	ABC-type transport system permease protein	-1.16	0.13	5.23	dppC2
OE2491F	conserved hypothetical protein	-1.16	0.10	6.94	-
OE5202F	aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	-1.16	0.22	3.18	pyrI
OE7003R	conserved hypothetical protein	-1.16	0.46	1.52	-
OE1821R	ribosomal protein L36a.eR (HLA)	-1.16	0.23	3.07	rpl36aR
OE3832F	conserved hypothetical protein	-1.16	0.20	3.52	-
OE1505F	probable 5'-methylthioadenosine phosphorylase (nonfunctional	-1.16	0.25	2.83	-
OE1536R	transducer protein htr14	-1.16	0.08	8.38	htr14
OE4613F	aconitate hydratase (EC 4.2.1.3)	-1.17	0.08	8.87	acn
OE2346R	probable ABC-type transport system permease protein	-1.17	0.06	12.66	-
OE4387F	hypothetical protein	-1.17	0.20	3.41	-
OE3395F	ribosomal protein S3	-1.17	0.11	6.58	rps3
OE4523F	hypothetical protein	-1.17	0.16	4.29	-

OE7071F	conserved hypothetical protein	-1.17	0.04	16.14	-
OE1476R	hypothetical protein	-1.17	0.19	3.80	-
OE3735F	formyltetrahydrofolate deformylase (EC 3.5.1.10)	-1.17	0.21	3.34	purU
OE4193R	hypothetical protein	-1.17	0.09	8.03	-
OE6340R	conserved hypothetical protein	-1.17	0.17	4.28	-
OE4688F	conserved hypothetical protein	-1.17	0.26	2.78	-
OE3619R	probable cation efflux system membrane protein (zinc/cadmium)	-1.17	0.25	2.85	cef
OE1672F	orotate phosphoribosyltransferase homolog	-1.17	0.08	8.87	pyrE1
OE4137F	hypothetical protein	-1.17	0.14	5.11	-
OE4225F	hypothetical protein	-1.17	0.22	3.30	-
OE2194R	hypothetical protein	-1.17	0.10	6.99	-
OE4456R	prefoldin alpha subunit	-1.17	0.11	6.73	gimC
OE6347R	transducer protein htrII weak homolog	-1.17	0.07	10.16	-
OE2906R	superoxide dismutase (EC 1.15.1.1) 2	-1.17	0.19	3.84	sod2
OE2571F	hypothetical protein	-1.18	0.23	3.20	-
OE3839F	hypothetical protein	-1.18	0.18	4.10	-
OE7104R	conserved hypothetical protein	-1.18	0.07	10.15	-
OE4563F	hypothetical protein	-1.18	0.13	5.94	-
OE2472F	conserved hypothetical protein	-1.18	0.22	3.37	-
OE1094R	probable transposase (ISH10)	-1.18	0.15	5.10	-
OE2336F	glycosyltransferase homolog	-1.18	0.18	4.07	gst
OE3582F	probable cold shock protein	-1.18	0.12	6.14	cspD2
OE4458R	ribosome anti-association protein (initiation factor aIF6)	-1.18	0.11	6.84	-
OE3984R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit B.a	-1.18	0.24	3.14	atpB
OE4113F	2-oxoacid dehydrogenase E1 component alpha-1 subunit	-1.18	0.18	4.12	oxdhA1
OE2740F	conserved hypothetical protein	-1.18	0.09	8.21	-
OE1862F	aminopeptidase homolog	-1.18	0.13	5.95	ywaD
OE4607R	flaG protein homolog	-1.18	0.18	4.24	flaG2
OE6093F	probable phenazine biosynthesis protein	-1.18	0.10	7.62	phzF
OE2862F	thioredoxin homolog	-1.18	0.16	4.71	-
OE2247R	conserved hypothetical protein	-1.18	0.30	2.52	-
OE5193F	hemolysin homolog	-1.18	0.11	6.77	-
OE1643F	conserved hypothetical protein	-1.18	0.13	5.77	-
OE3351F	hypothetical protein	-1.18	0.20	3.95	-
OE7024R	gas-vesicle operon protein gvpK1	-1.18	0.03	25.08	gvpK1
OE2474R	transducer protein htrXIII	-1.19	0.27	2.89	htrXIII
OE3149F	conserved hypothetical protein	-1.19	0.04	18.24	-
OE1173F	probable transposase (ISH8/ISH26)	-1.19	0.17	4.66	-
OE7031R	gas-vesicle operon protein gvpF1	-1.19	0.19	4.21	gvpF1
OE3367F	dnaJ N-terminal domain protein	-1.19	0.05	16.01	-
OE4532F	ribosomal protein S6.eR	-1.19	0.04	17.64	rps6R
OE6036F	probable DNA-directed DNA polymerase (EC 2.7.7.7) type II	-1.19	0.06	14.05	polB2
OE3854R	probable response regulator	-1.19	0.06	12.74	hlx1
OE5328R	probable helicase	-1.19	0.15	5.39	-
OE3229R	probable chelatase (EC 4.99.1.-) (cobalamin cluster)	-1.19	0.19	4.13	hmcA
OE3943R	conserved hypothetical protein	-1.19	0.12	6.71	-
OE1835F	hypothetical protein	-1.19	0.15	5.48	-
OE7019F	probable transposase (ISH8/ISH26)	-1.19	0.09	9.20	-
OE1789R	conserved hypothetical protein	-1.19	0.17	4.82	-

OE3268F	conserved hypothetical protein	-1.19	0.12	6.90	-
OE2310F	conserved hypothetical protein	-1.19	0.20	3.94	-
OE7215F	conserved hypothetical protein	-1.20	0.17	4.87	-
OE3808F	probable aminopeptidase (EC 3.4.11.-)	-1.20	0.21	3.92	-
OE3416F	ribosomal protein L30	-1.20	0.20	4.14	rpl30
OE1154F	Glyceraldehyde-3-phosphate dehydrogenase (NAD(P))	-1.20	0.18	4.51	gapB
OE4560F	conserved hypothetical protein	-1.20	0.12	6.89	-
OE5157F	conserved hypothetical protein	-1.20	0.10	8.30	-
OE4083F	conserved hypothetical protein	-1.20	0.11	7.50	-
OE3075R	hypothetical protein	-1.20	0.19	4.43	-
OE3959R	branched-chain-amino-acid transaminase (EC 2.6.1.42)	-1.20	0.17	4.87	ilvE
OE2348R	probable ABC-type transport system periplasmic substrate-bdg. prot.	-1.20	0.45	1.87	-
OE3526R	nuclease homolog	-1.20	0.07	12.07	-
OE2703F	probable copper-containing oxidoreductase	-1.20	0.14	6.08	pan1
OE1031F	probable transposase (ISH10)	-1.20	0.10	8.12	-
OE4073R	halocyanin hcpB	-1.20	0.07	12.15	hcpB
OE5285R	hypothetical protein	-1.20	0.07	12.35	-
OE2864F	phosphoribosylamine--glycine ligase (EC 6.3.4.13)	-1.21	0.09	9.33	purD
OE7198F	probable transposase (ISH8/ISH26)	-1.21	0.18	4.79	-
OE3022R	conserved hypothetical protein	-1.21	0.25	3.44	-
OE3682F	fsxA protein	-1.21	0.13	6.80	fsxA
OE2662F	ribosomal protein L7a.eR/HS6 (isol. from the small ribosomal subunit)	-1.21	0.33	2.67	rpl7aR
OE2474R-2 not found in HaloLex		-1.21	0.29	3.08	
OE3396F	ribosomal protein L29	-1.21	0.10	9.22	rpl29
OE4650R	hypothetical protein	-1.22	0.06	16.05	-
OE5431R	conserved hypothetical protein	-1.22	0.08	11.22	-
OE3398F	conserved hypothetical protein	-1.22	0.39	2.29	-
OE3141R	ribosomal protein L37.eR	-1.22	0.26	3.43	rpl37R
OE2515F	conserved hypothetical protein	-1.22	0.25	3.69	-
OE3855R	probable signal-transducing histidine kinase	-1.22	0.22	4.16	-
OE1270F	glutamate dehydrogenase (EC 1.4.1.2)	-1.23	0.14	6.60	gdhA3
OE3342R	hypothetical protein	-1.23	0.11	8.78	-
OE3424R	hypothetical protein	-1.23	0.20	4.70	-
OE5225R	probable transposase (ISH3/ISH27)	-1.23	0.12	8.03	-
OE5171R	hypothetical protein	-1.24	0.16	6.07	-
OE3097R	hypothetical protein	-1.24	0.15	6.44	-
OE3352R	DNA repair protein	-1.24	0.08	12.50	radA2
OE1160R	ribosomal protein L10.eR	-1.24	0.21	4.79	rpl10R
OE7110R	conserved hypothetical protein (nonfunctional	-1.25	0.20	4.97	-
OE5134F	conserved hypothetical protein	-1.25	0.03	30.49	-
OE3216F	precorrin-3B C17-methyltransferase (EC 2.1.1.131) 2	-1.25	0.16	6.21	cbiH2
OE4346R	ribonucleoside-diphosphate reductase (EC 1.17.4.1) alpha subunit	-1.25	0.42	2.43	nrdA1
OE3157R	hypothetical protein	-1.25	0.19	5.43	-
OE7014F	plasmid replication protein repH	-1.26	0.18	5.87	repH
OE3207F	probable precorrin-8W decarboxylase (EC 1.-.-.-)	-1.26	0.08	13.10	cbiT
OE3142R	SM protein	-1.26	0.31	3.44	snp
OE1081R	probable glycosyltransferase (EC 2.-.-.-)	-1.26	0.20	5.30	rfbU1
OE1941R	maoC protein homolog	-1.26	0.36	2.96	maoC

					2
OE4384R	conserved hypothetical protein	-1.27	0.24	4.50	-
OE1405R	conserved hypothetical protein	-1.27	0.26	4.28	-
OE2195F	transducer protein htr18	-1.28	0.12	9.31	htr18
OE1506R	probable transposase (ISH8/ISH26)	-1.28	0.11	10.88	-
OE3718F	cell division protein	-1.29	0.28	4.12	ftsZ3
OE7017R	probable transposase (ISH3/ISH27)	-1.29	0.18	6.59	-
OE7139R	hypothetical protein	-1.29	0.24	4.97	-
OE2638F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit K	-1.30	0.19	6.33	rpoK
OE4080F	conserved hypothetical protein	-1.30	0.13	8.96	-
OE2602R	ribosomal protein L1	-1.30	0.22	5.49	rpl1
OE3410F	ribosomal protein S8	-1.31	0.20	6.23	rps8
OE4121R	probable ornithine cyclodeaminase (EC 4.3.1.12)	-1.31	0.31	3.99	ocd1
OE1958F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit I	-1.32	0.09	14.36	nuoI
OE4509F	nonhistone chromosomal protein	-1.34	0.19	7.04	-
OE7028R	gas-vesicle operon protein gvpH1	-1.34	0.31	4.29	gvpH1
OE6001R	probable transposase (ISH8/ISH26)	-1.34	0.20	6.72	-
OE3652F	small multidrug export protein	-1.35	0.21	6.54	-
OE3136F	conserved hypothetical protein	-1.35	0.15	9.16	-
OE3402F	ribosomal protein L14	-1.37	0.26	5.62	rpl14
OE5015F	probable transposase (ISH8/ISH26)	-1.37	0.23	6.32	-
OE3930R	protein synthesis inhibitor homolog	-1.38	0.33	4.45	-
OE1162R	probable cold shock protein	-1.39	0.45	3.30	cspD1
OE6296R	probable transposase (ISH8/ISH26)	-1.39	0.13	11.35	-
OE1407F	inorganic pyrophosphatase (EC 3.6.1.1)	-1.42	0.40	3.97	ipp
OE4217R	ferredoxin (2Fe-2S)	-1.42	0.16	10.25	fdx
OE3357R	ribosomal protein S8.eR	-1.43	0.20	8.25	rps8R
OE3992R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit H.a	-1.46	0.21	8.44	atpH
OE6133R	probable transposase (ISH10)	-1.46	0.16	10.94	-
OE5204R	arginine/ornithine antiporter	-1.47	0.17	10.13	nhaC3
OE5407F	probable transposase (ISH8/ISH26)	-1.48	0.22	8.26	-
OE1102R-3 not found in HaloLex		-1.48	0.16	11.02	
OE1110F	sulfatase homolog	-1.49	0.21	8.68	-
OE1187R	spurious ORF	-1.49	0.27	6.69	-
OE5340R	transposase homolog (ISH8/ISH26) (nonfunctional	-1.50	0.06	32.94	-
OE5201F	aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	-1.53	0.19	9.97	pyrB
OE2577R	conserved hypothetical protein	-1.54	0.39	5.11	-
OE2398F	flagellin B2 precursor	-1.65	0.49	4.63	flgB2
OE4071R	cytochrome-c oxidase (EC 1.9.3.1) subunit II	-1.65	0.17	13.72	cox2B
OE1321R	conserved hypothetical protein	-1.70	0.08	28.92	-
OE2470F	flagellin A2 precursor	-1.72	0.52	4.73	flgA2
OE2469F	flagellin A1 precursor	-1.72	0.51	4.83	flgA1
OE4187R	probable DNA-binding protein	-1.75	0.59	4.36	-
OE2811F	conserved hypothetical protein	-1.80	0.17	15.91	-
OE2399F	flagellin B3 precursor	-1.81	0.25	10.96	flgB3
OE3989R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit K.a	-1.86	0.62	4.59	atpK
OE2397F	flagellin B1 precursor	-1.90	0.28	10.62	flgB1
OE3062F	ribosomal protein S17.eR	-1.90	0.13	21.72	rps17R

OE4070R	cytochrome-c oxidase (EC 1.9.3.1) subunit I	-1.92	0.12	25.60	cox1B
OE7056F	hypothetical protein	-1.98	0.27	11.59	-
OE4759F	cell surface glycoprotein precursor	-2.95	0.16	31.08	csg

Supplemental Table B. Whole genome DNA microarray analyses on cells, grown in synthetic medium. ID numbers, protein names, regulation factors (Reg.), standard deviations (Std.), t-values (t val) and gene denotations (gene) are indicated.

ID	protein name	Reg.	Std.	t val.	gene
OE3925R	thermosome beta subunit	9.09	0.52	27.55	cctB
OE4122R	thermosome alpha subunit	7.72	0.47	28.11	cctA
OE3114R	hypothetical protein	5.23	1.14	9.38	-
OE3112R	AAA-type ATPase (transitional ATPase homolog)	3.64	1.47	5.67	aaa3
OE5063R	probable IS200-type transposase (TCE31)	3.58	0.92	8.98	-
OE2046F	conserved hypothetical protein (probable transkription regulator)	3.47	1.31	6.12	-
OE5083R	heat shock protein homolog	3.18	0.60	12.41	hsp5
OE7091F	spurious ORF (OE7090B1R: hypothetical protein)	3.06	1.41	5.14	-
OE7192F	conserved hypothetical protein	2.77	0.94	6.97	-
OE3949R	glutaredoxin homolog	2.73	0.76	8.56	-
OE2473F	conserved hypothetical protein (glutaredoxin homolog)	2.53	0.75	7.96	-
OE3903F	conserved hypothetical protein	2.38	0.58	9.68	-
OE1023R	hypothetical protein	2.21	0.72	7.16	-
OE2084R	transcription initiation factor TFB	2.18	0.46	10.93	tfbB
OE5208R	arginine deiminase (EC 3.5.3.6)	2.10	0.54	8.84	arcA
OE4427R	ferritin (former DNA-binding Protein dpsA)	2.09	0.40	12.02	dpsA
OE2527F	conserved hypothetical protein	2.08	0.80	5.91	-
OE1794R	conserved hypothetical protein	2.06	0.72	6.49	-
OE1797R	transcription regulator sirR	2.05	0.80	5.84	sirR
OE1765R	probable proteasome regulatory subunit (probable PAN)	2.00	0.67	6.69	pan1
OE4727R	IS1341-type transposase (TCE31)	1.99	0.52	8.55	-
OE1698R	probable oxidoreductase (EC 1.1.1.-) (aldehyde reductase homolog)	1.91	0.47	8.81	oxr4
OE5082R	AAA-type ATPase (transitional ATPase homolog)	1.87	1.04	3.90	aaa8
OE1478R	transcription initiation factor TFB	1.86	0.66	6.05	tfbF
OE1838R	conserved hypothetical protein	1.81	0.64	6.04	-
OE2077F	hypothetical protein	1.79	0.82	4.57	-
OE3028R	conserved hypothetical protein	1.71	0.42	8.31	-
OE3834R	probable oxidoreductase	1.71	0.42	8.21	gsp
OE3680R	hypothetical protein	1.70	0.62	5.56	-
OE5208R-2 not found in HaloLex		1.69	0.52	6.55	
OE2127R	conserved hypothetical protein	1.63	0.43	7.29	-
OE6046F	conserved hypothetical protein	1.62	0.61	5.08	-
OE4494R	spurious ORF	1.62	0.65	4.82	-
OE3964R	conserved hypothetical protein	1.60	0.77	3.91	-
OE2296F	proteasome beta subunit	1.57	0.48	6.07	psmB
OE2946R	conserved hypothetical protein	1.55	0.61	4.61	-
OE3537R	conserved hypothetical protein	1.54	0.40	6.98	-
OE5114R	gas-vesicle operon protein gvpK2	1.54	0.35	7.86	gvpK2
OE3963R	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 5.4.99.-)	1.53	0.83	3.33	ribB
OE5163R	spur ORF;OE5162D1F_cons hyp prot	1.51	0.25	10.73	-
OE5101R	probable cationic amino acid transport protein	1.50	0.46	5.70	cat2

OE3815R	conserved hypothetical protein	1.47	0.26	9.64	-
OE7133F	hypothetical protein	1.46	0.28	8.69	-
OE2364R	probable NADH oxidase (H2O2-forming) (EC 1.6.99.3)	1.46	0.44	5.55	noxC
OE1410F	conserved hypothetical protein	1.45	0.51	4.70	-
OE1736R	chaperone dnaJ	1.45	0.50	4.79	dnaJ
OE6074R	hypothetical protein	1.45	0.32	7.49	-
OE7193R	spurious ORF	1.43	0.48	4.84	-
OE4626R	probable translation initiation factor SUI1	1.42	0.30	7.50	sui1
OE4683F	riboflavin synthase (EC 2.5.1.9) alpha subunit	1.42	0.62	3.68	ribC
OE2082F	conserved hypothetical protein	1.42	0.52	4.39	-
OE4641R	phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)	1.42	0.39	5.75	hisE
OE2254R	hypothetical protein	1.41	0.35	6.33	-
OE2175F	conserved hypothetical protein	1.40	0.51	4.25	-
OE4465F	iron-sulfur cofactor synthesis protein	1.40	0.32	6.79	nifU
OE7220F	hypothetical protein	1.40	0.54	4.02	-
OE1425F	conserved hypothetical protein	1.39	0.24	9.02	-
OE4622F	conserved hypothetical protein	1.39	0.54	3.95	-
OE4529F	aldehyde dehydrogenase (retinal dehydrogenase homolog)	1.38	0.29	7.27	aldH1
OE4648F	thioredoxin	1.37	0.32	6.51	trxA2
OE4345R	ribonucleoside-diphosphate reductase (EC 1.17.4.1) beta subunit	1.37	0.37	5.53	nrdB1
OE2865R	succinate dehydrogenase (EC 1.3.99.1) subunit A (flavoprotein)	1.35	0.38	5.15	sdhA
OE3923F	global transcription regulator	1.34	0.21	9.29	lrp
OE2515F	conserved hypothetical protein	1.33	0.22	8.48	-
OE1070R	IS1341-type transposase (TCE32)	1.33	0.22	8.42	-
OE2945F	probable ornithine cyclodeaminase (EC 4.3.1.12)	1.33	0.43	4.32	ocd2
OE1275F	proteasome alpha subunit	1.32	0.47	3.86	psmA
OE1903F	glycine-rich protein	1.32	0.40	4.47	-
OE6006R	conserved hypothetical protein	1.32	0.12	14.57	-
OE2519F	hypothetical protein	1.32	0.31	5.73	-
OE4028R	conserved hypothetical protein	1.31	0.38	4.62	-
OE6026R	transcription initiation factor TFB	1.31	0.32	5.54	tfbC
OE2585R	conserved hypothetical protein	1.31	0.33	5.25	-
OE5234R	conserved hypothetical protein (nonfunctional	1.31	0.31	5.56	-
OE2753F	cell division control protein cdc6 homolog	1.31	0.32	5.32	orc8
OE2199F	probable alcohol dehydrogenase (EC 1.1.1.1)	1.31	0.38	4.59	adh5
OE3985R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit A.a	1.29	0.46	3.58	atpA
OE2621R	transcription regulator	1.29	0.28	5.73	lrpA1
OE5178F	conserved hypothetical protein	1.29	0.30	5.48	-
OE8048F	conserved hypothetical protein	1.29	0.33	4.95	-
OE2401F	phycocyanin alpha phycocyanobilin lyase homolog	1.29	0.24	6.73	cpcE
OE5206R	carbamate kinase (EC 2.7.2.2)	1.28	0.42	3.86	arcC
OE1439F	probable IS200-type transposase (TCE31)	1.28	0.32	5.03	-
OE2597R	conserved hypothetical protein	1.28	0.35	4.54	-
OE5113R	gas-vesicle operon protein gvpL2	1.28	0.40	3.99	gvpL2
OE3572R	CTP synthase (EC 6.3.4.2)	1.28	0.30	5.36	pyrG
OE5205R	ornithine carbamoyltransferase (EC 2.1.3.3)	1.28	0.10	15.59	arcB

OE5212F	SMC-like protein sph1	1.28	0.25	6.47	sph1
OE5205R-2 not found in HaloLex		1.28	0.16	10.03	
OE2186R	sec-independent protein translocase component tatA	1.27	0.28	5.60	tatA
OE1120F	conserved hypothetical protein	1.27	0.33	4.63	-
OE3974R	dnaJ N-terminal domain / ferredoxin fusion protein	1.27	0.28	5.41	fer1
OE6276R	transposase homolog (TCE33) (nonfunctional	1.26	0.40	3.76	-
OE4552F	ABC-type transport system permease protein	1.26	0.08	19.69	dppB2
OE6285F	IS1341-type transposase (TCE31)	1.26	0.18	8.15	-
OE1279R	DNA-directed RNA polymerase (EC 2.7.7.6) epsilon subunit	1.25	0.26	5.55	rpoeps
OE4623F	conserved hypothetical protein	1.25	0.30	4.81	-
OE4217R	ferredoxin (2Fe-2S)	1.25	0.12	11.75	fdx
OE3481R	transducer protein htrII	1.25	0.31	4.68	htrII
OE7154R	hypothetical protein	1.25	0.39	3.64	-
OE2086F	probable response regulator	1.25	0.17	8.56	hlx2
OE1713F	electron transfer protein homolog	1.24	0.18	7.98	-
OE2827R	probable GTP-binding protein	1.24	0.11	12.12	hflX2
OE3937R	hypothetical protein	1.24	0.23	6.04	-
OE7173F	conserved hypothetical protein	1.23	0.36	3.73	-
OE5248F	conserved hypothetical protein	1.23	0.32	4.22	-
OE3452F	probable DNA-directed RNA polymerase (EC 2.7.7.6) subunit M	1.23	0.15	8.81	rpoM2
OE4140R	conserved hypothetical protein	1.23	0.27	5.01	-
OE3589F	conserved hypothetical protein	1.23	0.25	5.26	-
OE3696F	hypothetical protein	1.23	0.07	17.78	-
OE3805R	probable proteasome regulatory subunit (probable PAN)	1.23	0.11	11.68	pan2
OE2042F	probable copper-transporting ATPase (EC 3.6.1.-)	1.23	0.37	3.53	yvgX
OE2360R	NADH oxidase homolog	1.22	0.22	6.07	-
OE6105R	conserved hypothetical protein	1.22	0.13	10.29	-
OE4283R	probable signal-transducing histidine kinase	1.22	0.18	7.23	-
OE7085F	thioredoxin reductase homolog (nonfunctional	1.22	0.17	7.78	trxB1aa
OE2805R	thioredoxin reductase (NADPH) (EC 1.6.4.5)	1.22	0.35	3.64	trxB2
OE5022F	conserved hypothetical protein	1.22	0.24	5.42	-
OE4159F	adenosylhomocysteinase (EC 3.3.1.1)	1.22	0.29	4.32	achY
OE2717R	thioredoxin-dependent hydroperoxide peroxidase (EC 1.11.1.-)	1.22	0.20	6.36	bcp
OE6004F	hypothetical protein	1.21	0.13	9.74	-
OE6308F	hypothetical protein	1.21	0.23	5.45	-
OE2059F	hypothetical protein	1.21	0.16	7.83	-
OE2582F	hypothetical protein	1.21	0.36	3.35	-
OE4326F	conserved hypothetical protein	1.21	0.39	3.10	-
OE3580R	threonine--tRNA ligase (EC 6.1.1.3)	1.21	0.13	9.19	thrS
OE4124R	conserved hypothetical protein	1.21	0.27	4.49	-
OE3739R	CBS domain protein	1.20	0.35	3.41	-
OE5187R	probable hydrolase	1.20	0.26	4.50	-
OE2253F	conserved hypothetical protein	1.20	0.34	3.44	-
OE2052F	conserved hypothetical protein	1.20	0.28	4.16	-
OE5062R	IS1341-type transposase (TCE31)	1.19	0.23	5.03	-
OE5132F	probable phosphate transport protein	1.19	0.20	5.71	phoT3

OE3407F	ribosomal protein L5	1.19	0.22	5.24	rpl5
OE2182F	conserved hypothetical protein	1.19	0.19	5.85	-
OE1151R	aminopeptidase homolog	1.19	0.12	9.09	-
OE5238R	hypothetical protein	1.19	0.14	8.20	-
OE1291R	conserved hypothetical protein	1.19	0.14	7.99	-
OE2474R	transducer protein htrXIII	1.19	0.44	2.49	htrXIII
OE1399R	transcription initiation factor TFB	1.19	0.21	5.24	tfbG
OE5431R	conserved hypothetical protein	1.18	0.24	4.53	-
OE4753R	transcription regulator homolog	1.18	0.11	9.52	-
OE4011R	conserved hypothetical protein	1.18	0.14	7.46	-
OE6315F	conserved hypothetical protein	1.18	0.20	5.42	-
OE3389F	ribosomal protein L4.eR	1.18	0.21	5.14	rpl4R
OE2618R	conserved hypothetical protein	1.18	0.43	2.46	-
OE3376F	geranylgeranyl-diphosphate geranylgeranyltransferase	1.18	0.09	11.82	crtB2
OE3309R	hypothetical protein	1.18	0.23	4.46	-
OE4463F	probable cysteine desulfurase	1.18	0.12	8.60	nifS
OE2559R	probable 1	1.17	0.18	5.67	menA
OE4240F	conserved hypothetical protein	1.17	0.22	4.79	-
OE1469F	indole-3-glycerol-phosphate synthase (EC 4.1.1.48)	1.17	0.23	4.47	trpC
OE2071R	transcription regulator homolog	1.17	0.18	5.77	-
OE1782F	conserved hypothetical protein	1.17	0.23	4.48	-
OE4160F	holliday-junction resolvase homolog	1.17	0.20	5.10	hjr
OE5174R	hypothetical protein	1.17	0.18	5.72	-
OE2502R	conserved hypothetical protein	1.17	0.32	3.16	-
OE4043R	hypothetical protein	1.17	0.10	9.56	-
OE2131F	conserved hypothetical protein	1.17	0.18	5.41	-
OE4628R	conserved hypothetical protein	1.17	0.46	2.18	-
OE2860R	cysteine synthase (EC 4.2.99.8) cysK2	1.17	0.22	4.54	cysK2
OE3346R	conserved hypothetical protein	1.17	0.17	5.84	-
OE3158R	conserved hypothetical protein	1.17	0.07	13.42	-
OE3947R	conserved hypothetical protein	1.16	0.29	3.40	-
OE1907F	conserved hypothetical protein	1.16	0.17	5.74	-
OE7178F	plasmid replication protein repI	1.16	0.20	4.96	repI1
OE2500R	triosephosphate isomerase (EC 5.3.1.1)	1.16	0.26	3.73	tpiA
OE2740F	conserved hypothetical protein	1.16	0.31	3.06	-
OE3689R	probable heme biosynthesis protein nirD/L (nirH/nirG homolog)	1.16	0.22	4.41	nirD
OE3917F	tRNA (guanine-N2-)-methyltransferase (EC 2.1.1.32)	1.16	0.12	8.21	trm1
OE1036F	hypothetical protein	1.16	0.17	5.53	-
OE3629R	ABC-type transport system periplasmic substrate-binding protein	1.16	0.25	3.80	-
OE3931R	threonine dehydratase (EC 4.2.1.16)	1.16	0.27	3.58	iluA
OE1916F	cysteine synthase (EC 4.2.99.8) cysK1	1.16	0.32	2.95	cysK1
OE5184F	conserved hypothetical protein	1.15	0.25	3.66	-
OE1465F	endopeptidase La (EC 3.4.21.53)	1.15	0.34	2.69	lon
OE5430F	spurious ORF	1.15	0.24	3.89	-
OE2124F	ABC-type transport system permease protein	1.15	0.18	4.99	ybjG
OE2467R	conserved hypothetical protein	1.15	0.15	6.06	-
OE1870R	hypothetical protein	1.15	0.34	2.65	-
OE2157F	halocyanin hcpH	1.15	0.08	10.94	hcpH

OE7216F	conserved hypothetical protein	1.15	0.20	4.39	-
OE4292F	conserved hypothetical protein	1.15	0.11	8.26	-
OE1974R	conserved hypothetical protein	1.15	0.18	5.00	-
OE7164R	spurious ORF	1.15	0.24	3.60	-
OE3578R	conserved hypothetical protein	1.14	0.17	5.10	-
OE4136R	translation initiation factor aIF-1A	1.14	0.13	6.78	eif1a1
OE1471F	tryptophan synthase (EC 4.2.1.20) alpha subunit	1.14	0.13	6.61	trpA
OE2179F	ABC-type transport system ATP-binding protein	1.14	0.13	6.83	-
OE1783F	conserved hypothetical protein	1.14	0.15	5.69	-
OE4411F	ABC-type transport system permease protein homolog	1.14	0.27	3.13	-
OE6118F	hypothetical protein	1.14	0.22	3.92	-
OE3914R	conserved hypothetical protein	1.14	0.22	3.95	-
OE3333R	phosphoribosylanthranilate isomerase (EC 5.3.1.24)	1.14	0.17	4.93	trpF
OE5136R	conserved hypothetical protein	1.14	0.28	3.05	-
OE1121F	conserved hypothetical protein	1.14	0.26	3.26	-
OE3203R	conserved hypothetical protein	1.14	0.25	3.40	-
OE3820R	conserved hypothetical protein	1.14	0.13	6.55	-
OE6026R-2 not found in HaloLex		1.14	0.12	6.90	
OE3905F	conserved hypothetical protein	1.13	0.19	4.25	-
OE5160F	glycerol dehydrogenase (EC 1.1.1.6)	1.13	0.15	5.54	gldA1
OE5270R	ABC-type transport system permease protein	1.13	0.19	4.18	-
OE2078R	2-dehydropantoate 2-reductase (EC 1.1.1.169)	1.13	0.49	1.64	apbA
OE5121R	gas-vesicle operon protein gvpG2	1.13	0.20	3.96	gvpG2
OE1673F	glutaredoxin homolog	1.13	0.19	4.22	-
OE4262F	porphobilinogen synthase (EC 4.2.1.24)	1.13	0.16	4.92	hemB
OE3257F	conserved cobalamin operon protein	1.13	0.20	3.95	-
OE4353R	excinuclease ABC subunit B	1.13	0.17	4.62	uvrB
OE4732F	hypothetical protein	1.13	0.20	3.96	-
OE1576F	conserved hypothetical protein	1.13	0.17	4.63	-
OE1211F	heat shock protein homolog	1.13	0.16	4.96	hsp4
OE3460F	GTP-binding protein	1.13	0.58	1.35	gbp1
OE5078F	sodium-dependent phosphate transport protein homolog	1.13	0.13	5.96	phoT2
OE4630R	probable GTP-binding protein	1.13	0.15	5.31	-
OE4502R	GMP synthase homolog	1.13	0.17	4.60	-
OE5413F	restriction system mrr homolog	1.13	0.14	5.40	-
OE3070R	transducer protein htrXII	1.13	0.19	3.99	htrXII
OE4559R	conserved hypothetical protein	1.13	0.24	3.15	-
OE2497F	conserved hypothetical protein	1.12	0.13	5.96	-
OE3195F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) beta subunit	1.12	0.17	4.58	sucB
OE1606R	conserved hypothetical protein	1.12	0.15	4.86	-
OE2509R	oxidoreductase homolog	1.12	0.10	7.44	-
OE4543R	probable N-terminal acetyltransferase	1.12	0.05	14.43	rimI1
OE4196R	conserved hypothetical protein	1.12	0.13	5.86	-
OE1134F	conserved hypothetical protein	1.12	0.13	5.59	-
OE7155R	conserved hypothetical protein	1.12	0.30	2.47	-
OE3927F	conserved hypothetical protein	1.12	0.08	9.48	-
OE7084F	thioredoxin	1.12	0.22	3.38	trxA1a
OE5190R	hydrogenase expression/formation protein homolog	1.12	0.12	6.30	hypE1

OE7159R	probable transposase (ISH7/ISH24)	1.12	0.15	4.76	-
OE4358F	ABC-type transport system permease protein	1.12	0.20	3.58	cysT1
OE3369F	conserved hypothetical protein	1.12	0.15	4.80	-
OE1213F	hypothetical protein	1.12	0.25	2.93	-
OE2653R	hypothetical protein	1.12	0.21	3.45	-
OE6345R	hypothetical protein	1.12	0.11	6.43	-
OE4716R	conserved hypothetical protein	1.12	0.18	4.06	-
OE3619R	probable cation efflux system membrane protein (zinc/cadmium)	1.12	0.14	5.22	cef
OE4581F	probable phosphogluconate dehydrogenase (N-term. domain homol)	1.12	0.16	4.59	pgd
OE3631F	ABC-type transport system ATP-binding protein	1.12	0.28	2.57	potA
OE7152R	hypothetical protein	1.12	0.18	3.97	-
OE5209R-2 not found in HaloLex		1.11	0.17	4.20	
OE3513R	hypothetical protein	1.11	0.13	5.17	-
OE7063R	spurious ORF	1.11	0.14	4.82	-
OE4651F	probable ribose-1	1.11	0.08	8.23	-
OE1597F	hypothetical protein	1.11	0.11	6.17	-
OE5162R	cell division control protein cdc6 homolog	1.11	0.10	6.91	orc5
OE5200R	glutamate/aspartate transport protein	1.11	0.14	4.97	gltP
OE2486F	probable alcohol dehydrogenase (NADP+) (EC 1.1.1.2)	1.11	0.14	4.78	adh3
OE1778R	probable oxidoreductase (3-oxoacyl-reductase homolog)	1.11	0.27	2.46	oxr6
OE5108F	parA domain protein	1.11	0.40	1.65	parA4
OE3332R	anthranilate synthase (EC 4.1.3.27) alpha subunit	1.11	0.26	2.53	trpE1
OE3125R	conserved hypothetical protein	1.11	0.14	4.65	-
OE1528F	DNA topoisomerase I	1.11	0.28	2.37	topA
OE3620R	histidine triad family protein	1.11	0.25	2.58	hit2
OE5141R	conserved hypothetical protein	1.11	0.11	5.80	-
OE5021F	parA domain protein	1.11	0.06	11.17	parA3
OE1236F	conserved hypothetical protein	1.11	0.30	2.14	-
OE1022R	hypothetical protein	1.11	0.12	5.29	-
OE5144R	ABC-type transport system permease protein	1.11	0.19	3.33	-
OE1823F-2 not found in HaloLex		1.11	0.13	4.89	
OE7191F	spurious ORF	1.11	0.46	1.41	-
OE1055R	hypothetical protein	1.11	0.25	2.55	-
OE4654F	phosphomethylpyrimidine kinase (EC 2.7.4.7)	1.10	0.18	3.61	thiD
OE4408F	phosphoglycerate dehydrogenase (EC 1.1.1.95)	1.10	0.08	8.38	serA1
OE4555F	ABC-type transport system permease protein	1.10	0.16	4.00	dppC1
OE2551F	conserved hypothetical protein	1.10	0.15	4.21	-
OE3755R	conserved hypothetical protein	1.10	0.10	6.14	-
OE3652F	small multidrug export protein	1.10	0.31	2.05	-
OE4613F	aconitate hydratase (EC 4.2.1.3)	1.10	0.26	2.37	acn
OE2458R	IMP dehydrogenase (EC 1.1.1.205)	1.10	0.18	3.55	guaB
OE3345F	conserved hypothetical protein	1.10	0.11	5.84	-
OE1887F	hypothetical protein	1.10	0.19	3.24	-
OE1695R	hypothetical protein	1.10	0.19	3.19	-
OE4005F	electron transfer flavoprotein beta subunit	1.10	0.27	2.32	etfB
OE4738R	probable transcription termination factor nusA	1.10	0.32	1.93	nusA
OE5093F	hypothetical protein	1.10	0.19	3.22	-
OE2212R	conserved hypothetical protein	1.10	0.13	4.57	-

OE1059R	hypothetical protein (nonfunctional	1.10	0.07	8.12	-
OE1951F	phosphoribosylaminoimidazole carboxylasecarbon dioxide-fixation subunit	1.10	0.28	2.18	purK
OE4354R	conserved hypothetical protein	1.10	0.13	4.80	-
OE1893F	diphosphomevalonate decarboxylase (EC 4.1.1.33)	1.10	0.21	2.91	mvd
OE4308F	hypothetical protein	1.10	0.15	4.03	-
OE4218F	N-5-amino-1-4-imidazolecarboxamide isomerase	1.10	0.18	3.40	hisA
OE2141F	conserved hypothetical protein	1.10	0.12	4.81	-
OE1124R	conserved hypothetical protein	1.10	0.19	3.06	-
OE4448R	hypothetical protein	1.10	0.18	3.28	-
OE1378R	conserved hypothetical protein	1.10	0.10	6.17	-
OE1436R	spurious ORF	1.10	0.10	6.13	-
OE7072F	conserved hypothetical protein	1.10	0.10	5.86	-
OE5139F	lipoate--protein ligase (EC 6.3.4.-) lipB	1.10	0.16	3.67	lipB
OE4590R	spurious ORF	1.10	0.13	4.43	-
OE7089R	conserved hypothetical protein	1.10	0.08	7.60	-
OE4121R	probable ornithine cyclodeaminase (EC 4.3.1.12)	1.10	0.17	3.42	ocd1
OE2276F	conserved hypothetical protein	1.09	0.18	3.16	-
OE3843F	NAD+ synthase (EC 6.3.1.5)	1.09	0.17	3.36	nadE
OE1932R	conserved hypothetical protein	1.09	0.13	4.43	-
OE1737R	dnaK-type molecular chaperone hsp70	1.09	0.25	2.31	dnaK
OE2319R	conserved hypothetical protein	1.09	0.21	2.76	-
OE1295R	hypothetical protein	1.09	0.38	1.53	-
OE1899R	conserved hypothetical protein	1.09	0.17	3.36	-
OE7209F	conserved hypothetical protein	1.09	0.10	5.78	-
OE6110R	spurious ORF	1.09	0.29	1.98	-
OE1952F	phosphoribosylaminoimidazole carboxylase catalytic subunit	1.09	0.12	4.65	purE
OE7129F	conserved hypothetical protein	1.09	0.15	3.74	-
OE1669F	aldehyde dehydrogenase (glucose 1-dehydrogenase homolog)	1.09	0.21	2.72	-
OE1738R	hypothetical protein	1.09	0.21	2.76	-
OE1659R	conserved hypothetical protein	1.09	0.14	4.06	-
OE3167F	transducer protein htrVIII	1.09	0.25	2.34	htrVIII
OE3084F	hypothetical protein	1.09	0.13	4.35	-
OE6012F	probable transposase (ISH6/ISHS1)	1.09	0.10	5.60	-
OE4320R	conserved hypothetical protein	1.09	0.21	2.67	-
OE7066F	cytochrome d ubiquinol oxidase (EC 1.10.3.-) subunit II	1.09	0.09	6.05	cydB1
OE4480R	probable ABC-type phosphate transport system permease protein	1.09	0.24	2.38	pstA1
OE4601F	conserved hypothetical protein	1.09	0.12	4.75	-
OE2676R	conserved hypothetical protein	1.09	0.10	5.93	-
OE1148R	hypothetical protein	1.09	0.12	4.71	-
OE3300F	conserved hypothetical protein	1.09	0.18	3.15	-
OE3356F	AAA-type ATPase (transitional ATPase homolog)	1.09	0.18	3.17	aaa5
OE1268F	probable transcription regulator boa1	1.09	0.18	3.11	boa1
OE4410F	acyl-CoA thioester hydrolase homolog	1.09	0.21	2.63	-
OE4248R	conserved hypothetical protein	1.09	0.12	4.59	-
OE2136R	conserved hypothetical protein	1.09	0.22	2.43	-
OE4615F	N-terminal acetyltransferase	1.09	0.30	1.82	rimI2

OE4644R	conserved hypothetical protein	1.09	0.22	2.51	-
OE1510F	conserved hypothetical protein	1.09	0.24	2.26	-
OE5267R	conserved hypothetical protein	1.09	0.20	2.65	-
OE2259F	conserved hypothetical protein	1.09	0.14	3.76	-
OE2922F	hypothetical protein	1.09	0.10	5.26	-
OE1549F	conserved hypothetical protein	1.09	0.21	2.57	-
OE4214F	spurious ORF	1.09	0.04	13.51	-
OE3336R	spurious ORF	1.09	0.13	4.02	-
OE1400F	conserved hypothetical protein	1.09	0.09	6.13	-
OE1190F	probable oxidoreductase (cis-retinol dehydrogenase homolog)	1.09	0.23	2.34	rdh2
OE4561F	conserved hypothetical protein	1.09	0.15	3.52	-
OE2626R	probable ATP-binding protein mrp	1.08	0.07	7.19	mrp
OE2513F	conserved hypothetical protein	1.08	0.19	2.81	-
OE1073F	probable IS200-type transposase (ISH12)	1.08	0.18	2.89	-
OE4446R	hypothetical protein	1.08	0.18	2.85	-
OE7150R	conserved hypothetical protein	1.08	0.09	5.86	-
OE2293R	CBS domain protein	1.08	0.05	11.47	-
OE3515F	hypothetical protein	1.08	0.10	5.05	-
OE5162R-2 not found in HaloLex		1.08	0.15	3.43	
OE1865F	conserved hypothetical protein	1.08	0.16	3.12	-
OE5146R	ABC-type transport system ATP-binding protein	1.08	0.24	2.16	zurA
OE8050F	conserved hypothetical protein	1.08	0.13	4.07	-
OE2521R	conserved hypothetical protein	1.08	0.13	3.83	-
OE7194F	plasmid replication protein repJ	1.08	0.17	2.99	repJ1
OE3303R	transport system permease protein homolog	1.08	0.04	13.33	-
OE5297F	hypothetical protein	1.08	0.15	3.28	-
OE3808F	probable aminopeptidase (EC 3.4.11.-)	1.08	0.17	2.95	-
OE1347R	type II secretion system protein gspE1	1.08	0.19	2.62	gspE1
OE1648R	probable bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)	1.08	0.24	2.05	apa
OE3149F	conserved hypothetical protein	1.08	0.24	2.08	-
OE4731R	spurious ORF	1.08	0.26	1.90	-
OE4129R	conserved hypothetical protein	1.08	0.08	6.08	-
OE7118R	hypothetical protein	1.08	0.09	5.81	-
OE1799R	conserved hypothetical protein	1.08	0.10	5.16	-
OE6104R	conserved hypothetical protein	1.08	0.12	3.94	-
OE5431B1R	conserved hypothetical protein	1.08	0.13	3.62	-
OE1218F	replication protein A homolog	1.08	0.14	3.60	-
OE4300R	hypothetical protein	1.08	0.09	5.45	-
OE5429R	conserved hypothetical protein	1.08	0.12	3.98	-
OE4424R	DNA repair helicase homolog	1.08	0.11	4.37	rad3b
OE4163R	conserved hypothetical protein	1.08	0.11	4.36	-
OE5104R	probable IS200-type transposase (ISH12) (nonfunctional	1.08	0.11	4.38	-
OE1379R	conserved hypothetical protein	1.08	0.11	4.59	-
OE4485R	probable ABC-type phosphate transport system periplasmic substrate-binding protein	1.08	0.06	7.80	phoX1
OE3549F	hypothetical protein	1.08	0.15	3.15	-
OE4638F	hypothetical protein	1.08	0.13	3.75	-

OE6150R	conserved hypothetical protein	1.08	0.16	3.08	-
OE7172F	hypothetical protein	1.08	0.30	1.61	-
OE1759F	conserved hypothetical protein	1.08	0.13	3.66	-
OE2495F	conserved hypothetical protein	1.08	0.18	2.70	-
OE3686F	hypothetical protein	1.08	0.25	1.91	-
OE1026F	hypothetical protein	1.08	0.13	3.74	-
OE3075R	hypothetical protein	1.08	0.22	2.16	-
OE7068R	conserved hypothetical protein	1.08	0.15	3.09	-
OE1541F	rhomboid family protein	1.08	0.18	2.66	-
OE1661F	conserved hypothetical protein	1.08	0.18	2.58	-
OE3150R	transducer protein hemAT	1.07	0.14	3.44	hemAT
OE3197F	site-specific DNA-methyltransferase (EC 2.1.1.-)	1.07	0.08	6.18	zim
OE5025F	conserved hypothetical protein	1.07	0.18	2.59	-
OE7001R	conserved hypothetical protein	1.07	0.14	3.23	-
OE2448F	transcription regulator bat homolog	1.07	0.22	2.14	boa4
OE2859F	conserved hypothetical protein	1.07	0.16	2.91	-
OE4549R	conserved hypothetical protein	1.07	0.42	1.10	-
OE2280R	hypothetical protein	1.07	0.14	3.22	-
OE1756F	conserved hypothetical protein	1.07	0.12	3.84	-
OE4661R	conserved hypothetical protein	1.07	0.12	3.86	-
OE2314R	ABC-type transport system permease protein	1.07	0.15	3.13	rbsC1
OE3586R	conserved hypothetical protein	1.07	0.05	8.95	-
OE7100R	parA domain protein	1.07	0.17	2.62	parA6a
OE7009F	conserved hypothetical protein (encoded by ISH7/ISH24 subtype 1)	1.07	0.25	1.82	-
OE1418F	conserved hypothetical protein	1.07	0.12	3.89	-
OE1215R	hypothetical protein	1.07	0.19	2.41	-
OE2105F	hypothetical protein	1.07	0.09	4.94	-
OE3646F	L-aspartate oxidase (EC 1.4.3.16) (quinolinate synthetase B	1.07	0.18	2.53	nadB
OE1203F	probable creatininase (EC 3.5.2.10)	1.07	0.12	3.74	-
OE3607R	conserved hypothetical protein	1.07	0.09	4.74	-
OE5282R	conserved hypothetical protein	1.07	0.29	1.56	-
OE4492F	conserved hypothetical protein	1.07	0.14	3.31	-
OE3058F	conserved hypothetical protein	1.07	0.21	2.17	-
OE3188R	conserved hypothetical protein	1.07	0.06	7.49	-
OE3270R	conserved hypothetical protein	1.07	0.11	3.93	-
OE2985F	O-acetyltransferase homolog	1.07	0.08	5.70	-
OE2553R	glycerol-3-phosphate dehydrogenase subunit A homologue	1.07	0.14	3.10	gpdA1
OE1545F	probable oxidoreductase (cis-retinol dehydrogenase homolog)	1.07	0.14	3.12	rdh1
OE3118F	conserved hypothetical protein	1.07	0.16	2.69	-
OE4498F	conserved hypothetical protein	1.07	0.10	4.39	-
OE2529F	polysaccharide biosynthesis protein homolog	1.07	0.29	1.51	-
OE5298F-2 not found in HaloLex		1.07	0.16	2.80	
OE4527R	cleavage and polyadenylation specificity factor homolog	1.07	0.19	2.27	epf1
OE2301R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit A	1.07	0.07	5.98	top6A

OE6093F	probable phenazine biosynthesis protein	1.07	0.21	2.02	phzF
OE3239R	conserved cobalamin cluster protein	1.07	0.18	2.39	-
OE1911R	conserved hypothetical protein	1.07	0.28	1.53	-
OE3585R	conserved hypothetical protein	1.07	0.05	8.57	-
OE5432F	spurious ORF	1.07	0.08	5.48	-
OE3906F	bacteriophage-type DNA polymerase homolog	1.07	0.08	5.31	-
OE1396R	probable kinase (homoserine / mevalonate kinase homolog)	1.07	0.10	4.17	kin2
OE5168F	probable ABC-type transport system permease protein	1.07	0.28	1.52	ugpA
OE2645F	mevalonate kinase (EC 2.7.1.36)	1.07	0.11	3.71	mvk
OE1610R	hypothetical protein	1.07	0.10	4.26	-
OE5118R	gas-vesicle operon protein gvpI2	1.07	0.21	2.00	gvpI2
OE4577F	ABC-type transport system permease protein	1.07	0.07	6.00	fhuG
OE4169F	conserved hypothetical protein	1.07	0.15	2.76	-
OE1142F	probable molybdenum cofactor biosynthesis protein A	1.07	0.55	0.75	moaA
OE6032F	conserved hypothetical protein	1.07	0.10	4.32	-
OE4568R	conserved hypothetical protein	1.07	0.10	4.17	-
OE1637R	probable DNA-directed RNA polymerase (EC 2.7.7.6) subunit M	1.07	0.13	3.10	rpoM1
OE6087R	conserved hypothetical protein	1.07	0.10	3.95	-
OE4055F	hypothetical protein	1.07	0.13	3.05	-
OE2631F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit D	1.07	0.33	1.26	rpoD
OE7174R	conserved hypothetical protein	1.07	0.16	2.50	-
OE4420R	argininosuccinate synthase (EC 6.3.4.5)	1.07	0.29	1.42	argG
OE7036F	gas-vesicle protein gvpC1	1.06	0.15	2.65	gvpC1
OE4171R	conserved hypothetical protein	1.06	0.07	5.52	-
OE4541F	conserved hypothetical protein	1.06	0.18	2.28	-
OE4153F	conserved hypothetical protein	1.06	0.10	4.01	-
OE1249R	conserved hypothetical protein	1.06	0.16	2.51	-
OE2546F	probable glycosyltransferase (EC 2.-.-.-)	1.06	0.08	4.78	-
OE6036F	probable DNA-directed DNA polymerase (EC 2.7.7.7) type II	1.06	0.08	5.18	polB2
OE1710R	oxoglutarate--ferredoxin oxidoreductase (EC 1.2.7.3) beta subunit	1.06	0.13	3.15	korB
OE1969F	CBS domain protein	1.06	0.24	1.64	-
OE6057R	conserved hypothetical protein	1.06	0.11	3.52	-
OE1453F	conserved hypothetical protein	1.06	0.15	2.65	-
OE7037F	gas-vesicle operon protein gvpN	1.06	0.12	3.17	gvpN1
OE4451F	hypothetical protein	1.06	0.16	2.35	-
OE1730R	conserved hypothetical protein	1.06	0.09	4.09	-
OE6357F	conserved hypothetical protein	1.06	0.13	3.05	-
OE5099F	siderophore biosynthesis protein	1.06	0.19	1.98	iucC
OE2260R	rhomboid family protein	1.06	0.12	3.34	-
OE5345R	hypothetical protein	1.06	0.18	2.20	-
OE2991F	transcription factor TFB homolog	1.06	0.22	1.79	-
OE3768F	hypothetical protein	1.06	0.11	3.50	-
OE6059R	iron-sulfur protein homol./glycerol-3-phosphate dehydrogenase hom.	1.06	0.07	5.78	-
OE3644F	quinolinate synthetase A (part of quinolinate synthetase complex)	1.06	0.07	5.18	nadA
OE3861F	conserved hypothetical protein	1.06	0.12	3.19	-

OE4059F	hypothetical protein	1.06	0.08	4.65	-
OE4012F	conserved hypothetical protein	1.06	0.12	3.29	-
OE4272F	conserved hem operon protein	1.06	0.29	1.31	-
OE1045F	transposase homolog (TCE39)	1.06	0.25	1.51	-
OE3764F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit B	1.06	0.08	4.89	gpdB
OE5102R	IS1341-type transposase (ISH12)	1.06	0.43	0.88	-
OE5097F	siderophore biosynthesis protein (malonyl-CoA decarboxylase hom)	1.06	0.12	3.23	iucB
OE6332R	transducer protein htrII weak homolog	1.06	0.18	2.12	-
OE2693F	protein-methionine-S-oxide reductase (EC 1.8.4.6) msrA	1.06	0.08	4.93	msrA
OE4346R	ribonucleoside-diphosphate reductase (EC 1.17.4.1) alpha subunit	1.06	0.26	1.43	nrdA1
OE4685R	conserved hypothetical protein	1.06	0.16	2.28	-
OE2896R	conserved hypothetical protein	1.06	0.18	2.10	-
OE1547R	probable anion-transporting ATPase (EC 3.6.1.-)	1.06	0.07	5.15	arsA1
OE1482R	probable dolichyl-phosphate beta-glucosyltransferase(N-term. hom.)	1.06	0.14	2.63	dpg
OE3582F	probable cold shock protein	1.06	0.23	1.59	cspD2
OE3951R	conserved hypothetical protein	1.06	0.08	4.81	-
OE3659F	hypothetical protein	1.06	0.15	2.48	-
OE6311F	AAA-type ATPase (transitional ATPase homolog)	1.06	0.17	2.13	aaa10
OE4144R	conserved hypothetical protein	1.06	0.16	2.26	-
OE2126F	conserved hypothetical protein	1.06	0.06	5.81	-
OE2563R	2-succinyl-6-hydroxy-2	1.06	0.13	2.80	menD
OE3738F	conserved hypothetical protein	1.06	0.08	4.52	-
OE2998R	conserved hypothetical protein	1.06	0.07	5.05	-
OE1936R	conserved hypothetical protein	1.06	0.04	7.98	-
OE3269R	probable ABC-type transport system permease protein	1.06	0.08	4.51	-
OE3392F	ribosomal protein L2	1.06	0.12	3.04	rpl2
OE3022R	conserved hypothetical protein	1.06	0.10	3.51	-
OE4380F	cell division control protein cdc6 homolog	1.06	0.25	1.42	orc7
OE2656R	conserved hypothetical protein	1.06	0.07	4.71	-
OE1474R	hypothetical protein	1.06	0.18	1.96	-
OE4370R	drug export protein homolog	1.06	0.27	1.31	dip1
OE2935R	fumarate hydratase (EC 4.2.1.2)	1.06	0.07	4.72	fumC
OE4041F	helicase homolog	1.06	0.14	2.45	-
OE3169R	conserved hypothetical protein	1.06	0.10	3.58	-
OE2353R	hypothetical protein	1.06	0.21	1.68	-
OE2625R	hypothetical protein	1.06	0.08	4.10	-
OE4281F	uroporphyrinogen-III synthase (EC 4.2.1.75)	1.06	0.07	5.20	hemD
OE4418R	hypothetical protein	1.06	0.19	1.86	-
OE3065R	probable dehydrogenase(D-3-phosphoglycerate dehydrogenase hom)	1.05	0.07	5.23	serA2
OE3146R	hypothetical protein	1.05	0.09	3.89	-
OE2336F	glycosyltransferase homolog	1.05	0.11	3.16	gst
OE5017R	probable transposase (ISH5)	1.05	0.15	2.30	-
OE3940F	conserved hypothetical protein	1.05	0.09	3.59	-
OE3547F	conserved hypothetical protein	1.05	0.14	2.50	-
OE2961F	signal-transducing histidine kinase homolog	1.05	0.12	2.71	kinA1
OE3648F	nicotinate-nucleotide pyrophosphorylase (carboxylating)	1.05	0.12	2.88	nadC

OE2934R	conserved hypothetical protein	1.05	0.25	1.34	-
OE2816F	conserved hypothetical protein	1.05	0.14	2.48	-
OE1164R	phosphatase homolog	1.05	0.10	3.41	-
OE1100F	hypothetical protein	1.05	0.16	2.13	-
OE1054F	hypothetical protein	1.05	0.24	1.39	-
OE6347R	transducer protein htrII weak homolog	1.05	0.15	2.27	-
OE3849F	conserved hypothetical protein	1.05	0.18	1.89	-
OE1587F	conserved hypothetical protein	1.05	0.12	2.73	-
OE4117F	probable prephenate dehydratase (EC 4.2.1.51) (monofunctional)	1.05	0.09	3.54	pheA2
OE1534F	conserved hypothetical protein	1.05	0.23	1.42	-
OE2205F	chitinase (EC 3.2.1.14)	1.05	0.13	2.54	chiA2
OE4065R	histidine triad family protein	1.05	0.15	2.24	hit1
OE3575R	hypothetical protein	1.05	0.12	2.63	-
OE2758R	conserved hypothetical protein	1.05	0.08	3.89	-
OE4036R	probable oxidoreductase (maleylacetate reductase homolog)	1.05	0.09	3.76	oxr2
OE1543F	endonuclease V (EC 3.1.-.-)	1.05	0.07	4.50	nfi
OE4663F	conserved hypothetical protein	1.05	0.28	1.17	-
OE7186F	probable TATA-binding transcription initiation factor	1.05	0.16	2.04	tbpC1
OE1905R	probable hexosyltransferase	1.05	0.18	1.81	-
OE3221F	conserved cobalamin operon protein	1.05	0.15	2.09	-
OE6311F-2 not found in HaloLex		1.05	0.05	5.86	
OE2453R	conserved hypothetical protein	1.05	0.16	1.96	-
OE4054F	hypothetical protein	1.05	0.10	3.13	-
OE5337R	probable ATP-dependent helicase (nonfunctional	1.05	0.14	2.26	-
OE3456F	conserved hypothetical protein	1.05	0.06	5.67	-
OE5039R	conserved hypothetical protein	1.05	0.11	2.90	-
OE1753R	probable transport protein	1.05	0.18	1.72	yfmO1
OE3584R	probable muconate cycloisomerase (EC 5.5.1.1)	1.05	0.19	1.63	catB
OE3988R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit E.a	1.05	0.06	5.17	atpE
OE7111F	conserved hypothetical protein	1.05	0.10	3.04	-
OE1829R	conserved hypothetical protein	1.05	0.13	2.48	-
OE3899R	probable ADP-ribose pyrophosphatase (EC 3.6.1.13)	1.05	0.08	4.00	mutT
OE1416F	hypothetical protein	1.05	0.20	1.59	-
OE2858F	probable thiamin biosynthesis protein	1.05	0.10	3.24	thiI
OE3723R	conserved hypothetical protein	1.05	0.17	1.79	-
OE1488F	conserved hypothetical protein	1.05	0.17	1.82	-
OE7206F	hypothetical protein	1.05	0.09	3.42	-
OE2359F	conserved hypothetical protein	1.05	0.22	1.37	-
OE2952F	ABC-type transport system permease protein	1.05	0.07	4.49	hemU
OE3829R	conserved hypothetical protein	1.05	0.09	3.39	-
OE1882R	hypothetical protein	1.05	0.14	2.14	-
OE2825F	molybdenum cofactor biosynthesis protein C	1.05	0.14	2.15	moaC
OE4224F	conserved hypothetical protein	1.05	0.12	2.54	-
OE4724R	conserved hypothetical protein	1.05	0.10	2.95	-
OE5096F	siderophore biosynthesis protein	1.05	0.14	2.15	iucA
OE2227F	probable dimethylsulfoxide reductase subunit C	1.05	0.09	3.19	dmsC
OE2996R	transducer protein htr9 (htpIII)	1.05	0.16	1.92	htr9

OE4245R	hypothetical protein	1.05	0.15	1.97	-
OE4294R	conserved hypothetical protein	1.05	0.07	4.60	-
OE2217R	probable molybdopterin-guanine dinucleotide biosynthesis proteinA	1.05	0.13	2.35	mobA
OE2948R	conserved hypothetical protein	1.05	0.14	2.12	-
OE2819R	spurious ORF	1.05	0.13	2.22	-
OE1906R	probable sugar transferase	1.05	0.06	5.01	-
OE7131A1R	hypothetical protein	1.05	0.12	2.54	-
OE4099R	hypothetical protein	1.05	0.04	7.40	-
OE1641R	3-hydroxybutryl-CoA dehydratase (EC 4.2.1.55)	1.05	0.11	2.54	fad2
OE4449R	hypothetical protein	1.05	0.10	2.85	-
OE6340R	conserved hypothetical protein	1.05	0.30	0.97	-
OE5219F	hypothetical protein	1.05	0.16	1.82	-
OE4607R	flaG protein homolog	1.05	0.17	1.67	flaG2
OE1318F	conserved hypothetical protein	1.04	0.08	3.77	-
OE4039F	conserved hypothetical protein	1.04	0.07	3.99	-
OE3556R	carbamoyl-phosphate synthase small subunit	1.04	0.07	4.06	carA
OE6147R	conserved hypothetical protein	1.04	0.08	3.40	-
OE2540R-2 not found in HaloLex		1.04	0.07	3.80	
OE1566F	hypothetical protein	1.04	0.16	1.79	-
OE1928R	spurious ORF	1.04	0.16	1.76	-
OE7094F	conserved hypothetical protein	1.04	0.18	1.53	-
OE3491R	heat shock protein homolog	1.04	0.10	2.88	-
OE4677F	DNA helicase II	1.04	0.31	0.89	uvrD
OE1405R	conserved hypothetical protein	1.04	0.06	4.32	-
OE1285F	conserved hypothetical protein	1.04	0.23	1.20	-
OE3699R	conserved hypothetical protein	1.04	0.13	2.14	-
OE7075F	conserved hypothetical protein	1.04	0.16	1.75	-
OE3054R	conserved hypothetical protein	1.04	0.14	1.88	-
OE3246F	cobyric acid synthase	1.04	0.15	1.85	cbiP
OE4110R	conserved hypothetical protein	1.04	0.22	1.22	-
OE3384R	conserved hypothetical protein	1.04	0.13	2.07	-
OE2642R	hypothetical protein	1.04	0.09	3.06	-
OE4184F	cell division control protein cdc6 homolog	1.04	0.14	1.87	orc6
OE2189R	transducer protein htr4 (htpVI)	1.04	0.15	1.81	htr4
OE2325F	hypothetical protein	1.04	0.16	1.63	-
OE2252R	conserved hypothetical protein	1.04	0.08	3.34	-
OE6283R	IS200-type transposase homolog (TCE31) (nonfunctional	1.04	0.10	2.78	-
OE3355R	carbohydrate reductase homolog	1.04	0.22	1.23	-
OE2421R	hypothetical protein	1.04	0.10	2.69	-
OE1915F	hypothetical protein	1.04	0.07	3.66	-
OE3954R	conserved hypothetical protein	1.04	0.09	2.80	-
OE1357F	hypothetical protein	1.04	0.13	1.99	-
OE2548F	probable transmembrane oligosaccharyl transferase	1.04	0.14	1.80	tot
OE7162R	parA domain protein	1.04	0.09	2.77	parA8
OE1231R-2 not found in HaloLex		1.04	0.45	0.57	
OE5434R	conserved hypothetical protein	1.04	0.24	1.06	-
OE4349F	spurious ORF	1.04	0.31	0.83	-
OE1849R	conserved hypothetical protein	1.04	0.11	2.26	-

OE3488R	probable creatininase (EC 3.5.2.10)	1.04	0.13	1.95	cre
OE2918F	N5	1.04	0.15	1.66	mer
OE4139R	tyrosine--tRNA ligase (EC 6.1.1.1)	1.04	0.12	2.12	tyrS
OE1808F	probable phytoene dehydrogenase (EC 1.14.99.-) 3	1.04	0.13	2.01	crtI3
OE1989F	protoheme IX farnesyltransferase (EC 2.5.1.-)	1.04	0.08	3.11	ctaB
OE2027F	conserved hypothetical protein	1.04	0.06	4.23	-
OE1385F	conserved hypothetical protein	1.04	0.24	1.04	-
OE1182F	conserved hypothetical protein	1.04	0.29	0.85	-
OE3363F	probable orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	1.04	0.07	3.70	pyrF
OE1221F	acetylpolyamine aminohydrolase	1.04	0.08	3.21	aup
OE3814R	conserved hypothetical protein	1.04	0.26	0.96	-
OE2608F	hypothetical protein	1.04	0.05	4.52	-
OE6153F	hypothetical protein	1.04	0.07	3.38	-
OE5195R	conserved hypothetical protein	1.04	0.19	1.29	-
OE2245F	hypothetical protein	1.04	0.20	1.24	-
OE1467R	conserved hypothetical protein	1.04	0.07	3.43	-
OE2380R-2 not found in HaloLex		1.04	0.13	1.91	
OE5423R	hypothetical protein	1.04	0.09	2.67	-
OE1391R	halocyanin hcpG	1.04	0.13	1.92	hcpG
OE2941R	hypothetical protein	1.04	0.08	3.14	-
OE2929R	glutamyl-tRNA (Gln) amidotransferase (EC 6.3.5.-) subunit E	1.04	0.11	2.14	gatE
OE2596F	conserved hypothetical protein	1.04	0.06	3.74	-
OE5129F	gas-vesicle operon protein gvpO2	1.04	0.18	1.34	gvpO2
OE3571R	GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2)	1.04	0.07	3.22	guaAb
OE1653R	Na+/H+ antiporter homolog	1.04	0.11	2.12	nhaC1
OE1147R	protein-L-isoaspartate O-methyltransferase pimT1	1.04	0.07	3.21	pimT1
OE2191F	hypothetical protein	1.04	0.17	1.37	-
OE7127R	hypothetical protein	1.04	0.16	1.43	-
OE3008F	conserved hypothetical protein	1.04	0.17	1.39	-
OE3467R	deoxyribodipyrimidine photo-lyase (EC 4.1.99.3)	1.04	0.13	1.85	phr1
OE1283R	conserved hypothetical protein	1.04	0.14	1.70	-
OE5293F	conserved hypothetical protein	1.04	0.13	1.81	-
OE2834R	hypothetical protein	1.04	0.10	2.39	-
OE5166F	probable ABC-type transport system periplasmic substrate-binding protein (sugar-binding protein / sn-glycerol-3-phosphate-binding protein)	1.04	0.08	2.87	ugpB
OE6062R	conserved hypothetical protein	1.04	0.06	3.53	-
OE4695F	probable acetoacetyl-CoA reductase (EC 1.1.1.36)	1.04	0.15	1.55	phbB
OE2465R	hypothetical protein	1.04	0.10	2.23	-
OE4143F	hypothetical protein	1.04	0.16	1.42	-
OE1774R	hypothetical protein	1.04	0.22	1.02	-
OE1676R	probable ABC-type phosphate transport system permease protein	1.04	0.06	3.58	pstA2
OE3594R	probable glycerophosphoryl diester phosphodiesterase	1.04	0.10	2.25	ugpQ
OE2874F	hypothetical protein	1.04	0.11	2.14	-
OE4220F	imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)	1.04	0.06	3.91	hisB
OE5414R	conserved hypothetical protein	1.04	0.15	1.53	-
OE4276F	hydroxymethylbilane synthase (EC 4.3.1.8)	1.04	0.07	2.99	hemC
OE2798R	phosphoesterase homolog	1.04	0.10	2.13	yhcR

OE6329R	hypothetical protein	1.04	0.21	1.07	-
OE3143R	tetrahedral aminopeptidase	1.04	0.06	3.93	-
OE1625F	hypothetical protein	1.04	0.12	1.82	-
OE2379R	fla operon protein flaJ	1.04	0.13	1.71	flaJ
OE1008F	hypothetical protein	1.03	0.09	2.38	-
OE2019F	fructose-bisphosphate aldolase (EC 4.1.2.13) 1	1.03	0.13	1.73	fba1
OE2628F	ribosomal protein S4	1.03	0.22	1.02	rps4
OE4450R	signal recognition particle 54K protein	1.03	0.11	1.95	srp54
OE4193R	hypothetical protein	1.03	0.22	0.98	-
OE3079F	UDP-sugar hydrolase homolog/ 5'-nucleotidase homolog	1.03	0.07	3.07	-
OE3505R	di-trans	1.03	0.08	2.74	uppS2
OE4720R	ribosomal protein S10	1.03	0.18	1.22	rps10
OE1940R	hypothetical protein	1.03	0.17	1.28	-
OE2328F	hypothetical protein	1.03	0.07	2.98	-
OE2838R	trkA domain protein	1.03	0.13	1.70	trkA5
OE4282F	single-stranded-DNA-specific exonuclease (EC 3.1.-.-)	1.03	0.10	2.03	recJ
OE3319R	CbiM protein (unassigned function)	1.03	0.14	1.52	cbiM
OE1708R	hypothetical protein	1.03	0.04	4.98	-
OE3436R	transducer protein htr17	1.03	0.12	1.69	htr17
OE2284F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit A	1.03	0.33	0.63	aatA
OE4227F	thioredoxin reductase (NADPH) (EC 1.6.4.5)	1.03	0.07	3.17	txrB3
OE2057F	thiamin biosynthesis protein thiC	1.03	0.13	1.52	thiC
OE5230R	conserved hypothetical protein	1.03	0.06	3.30	-
OE4436R	L-allo-threonine aldolase (EC 4.2.1.-)	1.03	0.19	1.08	lta
OE4018F	conserved hypothetical protein	1.03	0.09	2.15	-
OE4343R	hypothetical protein	1.03	0.12	1.73	-
OE4524F	hypothetical protein	1.03	0.15	1.37	-
OE3998R	hypothetical protein	1.03	0.14	1.48	-
OE3498R	probable siroheme synthase	1.03	0.14	1.42	cysG1
OE3462R	hypothetical protein	1.03	0.09	2.10	-
OE5424R	conserved hypothetical protein	1.03	0.10	2.09	-
OE2794R	ATP-dependent helicase homolog	1.03	0.11	1.75	helA
OE6099F	hypothetical protein	1.03	0.09	2.25	-
OE4341R	hypothetical protein	1.03	0.15	1.31	-
OE1165R	phosphoglycerate dehydrogenase (EC 1.1.1.95)	1.03	0.16	1.21	serA3
OE4080F	conserved hypothetical protein	1.03	0.13	1.48	-
OE7045F	TATA-binding transcription initiation factor homolog	1.03	0.12	1.54	tbpA
OE3305F	replication factor C large subunit	1.03	0.03	5.77	rfcB
OE2560R	probable glycine betaine transport protein	1.03	0.12	1.62	opuD
OE4230F	probable acylaminoacyl-peptidase (EC 3.4.19.1)	1.03	0.11	1.68	yuxL
OE2080F	hypothetical protein	1.03	0.07	2.64	-
OE1127F	conserved hypothetical protein	1.03	0.14	1.36	-
OE4558R	dihydroorotase (EC 3.5.2.3)	1.03	0.13	1.38	pyrC
OE4398F	O-acetylhomoserine (thiol)-lyase (EC 4.2.99.10)	1.03	0.06	3.25	hal
OE3314R	hypothetical protein	1.03	0.06	3.14	-
OE4700F	hypothetical protein	1.03	0.03	5.35	-
OE1312R	hypothetical protein	1.03	0.20	0.91	-
OE1277F	probable thioredoxin	1.03	0.16	1.14	trxA3

OE1620R	phosphoribosylglycinamide formyltransferase	1.03	0.07	2.57	purH
OE3800F	translation initiation factor IF2	1.03	0.16	1.15	infB
OE5110F	conserved hypothetical protein	1.03	0.12	1.50	-
OE2278F	probable asparagine synthase (glutamine-hydrolyzing)	1.03	0.10	1.69	asnA
OE3439F	conserved hypothetical protein	1.03	0.27	0.65	-
OE5186R	catalase (EC 1.11.1.6) (including: peroxidase (EC 1.11.1.7))	1.03	0.17	1.05	perA
OE2357F	conserved hypothetical protein	1.03	0.12	1.47	-
OE1888R	conserved hypothetical protein	1.03	0.10	1.67	-
OE4157F	probable chlorohydrolase	1.03	0.14	1.27	trzA
OE5037R	cell division control protein cdc6 (nonfunctional	1.03	0.09	1.82	orc2
OE5042R	conserved hypothetical protein	1.03	0.06	2.72	-
OE4504F	conserved hypothetical protein	1.03	0.04	4.54	-
OE3921F	conserved hypothetical protein	1.03	0.16	1.07	-
OE3854R	probable response regulator	1.03	0.16	1.02	hlx1
OE2302R	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) VI subunit B	1.03	0.17	0.96	top6B
OE1769F	probable phosphoesterase (EC 3.1.-.-) ppe	1.02	0.05	2.96	ppe
OE3474R	transducer protein cosT	1.02	0.13	1.18	cosT
OE2015R	3-hydroxyacyl-CoA dehydrogenase	1.02	0.06	2.78	hbd1
OE2725R	L-fuculose-phosphate aldolase (EC 4.1.2.17)	1.02	0.09	1.64	fucA
OE1058R	probable transposase (ISH1)	1.02	0.42	0.36	-
OE1721R	methylmalonyl-CoA mutase 1A (N-terminal homology)	1.02	0.16	0.93	mut1A
OE2706R	hypothetical protein	1.02	0.13	1.20	-
OE2508F	conserved hypothetical protein	1.02	0.11	1.41	-
OE4458R	ribosome anti-association protein (initiation factor aIF6)	1.02	0.10	1.55	-
OE6126R	insertion element protein (ISH2)	1.02	0.17	0.88	-
OE4722R	homoserine dehydrogenase (EC 1.1.1.3)	1.02	0.06	2.64	hom
OE7079F	tetracyclin resistance protein homolog	1.02	0.09	1.60	-
OE1947F	conserved hypothetical protein	1.02	0.08	1.84	-
OE4419R	argininosuccinate lyase (EC 4.3.2.1)	1.02	0.05	2.83	argH
OE7007F	hypothetical protein (encoded by ISH7/ISH24 subtype 1)	1.02	0.14	1.05	-
OE4545F	hypothetical protein	1.02	0.16	0.90	-
OE3771F	hypothetical protein	1.02	0.13	1.10	-
OE4040R	conserved hypothetical protein	1.02	0.07	2.08	-
OE5215R	conserved hypothetical protein	1.02	0.20	0.72	-
OE2100R	spore cortext formation protein homolog	1.02	0.10	1.48	spoVR
OE1711R	oxoglutarate--ferredoxin oxidoreductase alpha subunit	1.02	0.08	1.76	korA
OE4027F	conserved hypothetical protein	1.02	0.19	0.75	-
OE6018R	hypothetical protein	1.02	0.12	1.13	-
OE3894R	conserved hypothetical protein	1.02	0.16	0.86	-
OE2650F	probable trifunctional short-chain (E)-prenyl diphosphate synthase	1.02	0.07	1.98	idsA1
OE4593R	probable ABC-type transport system substrate-binding protein	1.02	0.08	1.72	-
OE1447R	conserved hypothetical protein	1.02	0.08	1.70	-
OE1866F	hypothetical protein	1.02	0.11	1.26	-
OE2088F	signal-transducing histidine kinase homolog	1.02	0.17	0.80	kinA2
OE2616F	hypothetical protein	1.02	0.13	1.01	-
OE3454F	spurious ORF	1.02	0.10	1.37	-

OE2561R	naphthoate synthase (EC 4.1.3.36)	1.02	0.18	0.74	menB
OE6063F	probable L-lactate permease	1.02	0.08	1.63	lctP
OE4691R	glucokinase (EC 2.7.1.2)	1.02	0.06	2.19	glcK
OE1076F	cell division control protein cdc6 homolog	1.02	0.11	1.25	-
OE3347F-2 not found in HaloLex	(OE3347F: transd. prot. htr1)	1.02	0.08	1.74	
OE4360R	probable methyltransferase(24-sterol C-methyltransferase homolog)	1.02	0.26	0.51	scm
OE3676R	hypothetical protein	1.02	0.14	0.96	-
OE5142F	cell division protein ftsZ5	1.02	0.09	1.42	ftsZ5
OE1286R	DNA mismatch repair protein	1.02	0.08	1.65	mutS
OE5197R	conserved hypothetical protein	1.02	0.11	1.22	-
OE3735F	formyltetrahydrofolate deformylase (EC 3.5.1.10)	1.02	0.11	1.21	purU
OE5074R	conserved hypothetical protein	1.02	0.11	1.14	-
OE3892R	beta-lactamase homolog	1.02	0.15	0.84	-
OE1568F	anthranilate synthase (EC 4.1.3.27) component I	1.02	0.14	0.87	trpE2
OE3715R	dTMP kinase (EC 2.7.4.9)	1.02	0.15	0.86	tmk
OE4333R	aspartate kinase (EC 2.7.2.4) II alpha and beta subunit	1.02	0.16	0.75	lysC
OE2785R	probable shikimate kinase (2.7.1.71) (archaeal-type)	1.02	0.10	1.26	aroK
OE4550F	ABC-type transport system ATP-binding protein	1.02	0.09	1.32	dppF
OE5359R	probable transposase (ISH3/ISH27)	1.02	0.34	0.36	-
OE4062F	spurious ORF	1.02	0.20	0.60	-
OE2063R	conserved hypothetical protein	1.02	0.14	0.82	-
OE2832R	hypothetical protein	1.02	0.18	0.64	-
OE4668R	conserved hypothetical protein	1.02	0.10	1.19	-
OE6034F	IS1341-type transposase (TCE32)	1.02	0.13	0.89	-
OE3522R	conserved hypothetical protein	1.02	0.17	0.66	-
OE3492R	probable phosphatase (phosphoglycolate phosphatase homolog)	1.02	0.05	2.08	pgp
OE1665R	dihydrodipicolinate synthase (EC 4.2.1.52)	1.02	0.12	0.98	dapA
OE2747R	conserved hypothetical protein	1.02	0.11	1.01	-
OE7139R	hypothetical protein	1.02	0.21	0.53	-
OE1929R	transducer protein htr16	1.02	0.06	1.98	htr16
OE1136F	conserved hypothetical protein	1.02	0.24	0.47	-
OE5091F	conserved hypothetical protein	1.02	0.09	1.27	-
OE2545F	conserved hypothetical protein	1.02	0.09	1.16	-
OE7071F	conserved hypothetical protein	1.02	0.13	0.85	-
OE2332F	probable kynureninase (EC 3.7.1.3)	1.02	0.12	0.89	hakA
OE7065F	cytochrome d ubiquinol oxidase (EC 1.10.3.-) subunit I	1.02	0.14	0.75	cydA1
OE1168R	hypothetical protein	1.02	0.05	2.26	-
OE4385F	conserved hypothetical protein	1.02	0.15	0.73	-
OE1582R	conserved hypothetical protein	1.02	0.08	1.33	-
OE1842R	NADH dehydrogenase (ubiquinone) subunit L homolog	1.02	0.14	0.75	-
OE3535A1R	hypothetical protein	1.02	0.07	1.42	-
OE2346R	probable ABC-type transport system permease protein	1.02	0.18	0.60	-
OE2924R	conserved hypothetical protein	1.02	0.10	1.02	-
OE1112R	probable glycosyltransferase (EC 2.-.-.-)	1.02	0.07	1.45	lpb
OE1557R	transcription antitermination protein homolog	1.02	0.31	0.33	nusG
OE4560F	conserved hypothetical protein	1.02	0.18	0.55	-

OE4483R	probable ABC-type phosphate transport system permease protein	1.02	0.12	0.84	pstC1
OE3603R	uridine phosphorylase (EC 2.4.2.3)	1.02	0.20	0.48	-
OE3731R	phosphoribosylformylglycinamidine synthase component I	1.02	0.13	0.74	purQ
OE2386R	flagella accessory protein	1.01	0.07	1.33	flaCE
OE3759R	hypothetical protein	1.01	0.15	0.62	-
OE1081R	probable glycosyltransferase (EC 2.-.-.-)	1.01	0.28	0.33	rfbU1
OE4488F	hypothetical protein	1.01	0.15	0.63	-
OE2898R	conserved hypothetical protein	1.01	0.07	1.28	-
OE1209F	dehydratase homolog	1.01	0.11	0.85	-
OE2432B1R	hypothetical protein	1.01	0.08	1.10	-
OE7095F	conserved hypothetical protein	1.01	0.20	0.45	-
OE4416R	conserved hypothetical protein	1.01	0.10	0.89	-
OE3224F	conserved cobalamin operon protein	1.01	0.07	1.29	-
OE4195F	replication factor C small subunit	1.01	0.23	0.39	rfcA
OE3633R	probable N4-(beta-N-acetylglucosaminyl)-L-asparaginase	1.01	0.23	0.39	aga
OE1334R	hypothetical protein	1.01	0.10	0.86	-
OE3320F	halocyanin hcpA	1.01	0.09	1.00	hcpA
OE5009R	transfer complex protein homolog	1.01	0.17	0.51	trsE
OE4585R	hypothetical protein	1.01	0.09	0.96	-
OE2330R	hypothetical protein	1.01	0.06	1.42	-
OE1629F	conserved hypothetical protein	1.01	0.14	0.60	-
OE3832F	conserved hypothetical protein	1.01	0.12	0.67	-
OE5004R	conserved hypothetical protein	1.01	0.16	0.50	-
OE1060F	hypothetical protein	1.01	0.06	1.26	-
OE1982R	conserved hypothetical protein	1.01	0.10	0.83	-
OE3866R	probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	1.01	0.07	1.07	gcp
OE3526R	nuclease homolog	1.01	0.13	0.58	-
OE3000R	conserved hypothetical protein	1.01	0.05	1.54	-
OE6080F	conserved hypothetical protein	1.01	0.05	1.55	-
OE4008R	conserved hypothetical protein	1.01	0.13	0.53	-
OE1293F	spurious ORF	1.01	0.13	0.54	-
OE2392R	transducer protein htr15 (htpIX)	1.01	0.17	0.38	htr15
OE1651F	ribosomal protein S10 homolog	1.01	0.07	0.92	-
OE4649F	probable transport protein	1.01	0.10	0.68	arsB
OE4192R	conserved hypothetical protein	1.01	0.13	0.47	-
OE1426F	probable carotene dehydrogenase (phytoene dehydrogenase homol)	1.01	0.10	0.65	pds
OE1781F	probable ABC-type transport system ATP-binding protein	1.01	0.16	0.38	-
OE3087R	conserved hypothetical protein	1.01	0.15	0.39	-
OE3116F	conserved hypothetical protein	1.01	0.14	0.44	-
OE8001F	conserved hypothetical protein	1.01	0.06	1.00	-
OE1909F	conserved hypothetical protein	1.01	0.23	0.26	-
OE1559R-2 not found in HaloLex		1.01	0.10	0.56	
OE3953R	orotate phosphoribosyltransferase (EC 2.4.2.10)	1.01	0.06	1.01	pyrE2
OE2879R	hypothetical protein	1.01	0.11	0.52	-
OE2303F	DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) subunit B	1.01	0.11	0.53	gyrB

OE3871R	conserved hypothetical protein	1.01	0.11	0.51	-
OE6329R-2 not found in HaloLex		1.01	0.07	0.73	
OE3794F	conserved hypothetical protein	1.01	0.14	0.39	-
OE3177F	pyruvate carboxylase (EC 6.4.1.1)	1.01	0.10	0.50	pyc
OE5123R	gas-vesicle operon protein gvpE2 (probable activator protein)	1.01	0.17	0.28	gvpE2
OE7104R	conserved hypothetical protein	1.01	0.10	0.49	-
OE3913F	imidazoleglycerol-phosphate synthase(glutamine amidotransferase)	1.01	0.07	0.63	hisH2
OE4467F	conserved hypothetical protein	1.01	0.10	0.47	-
OE1964F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit L	1.01	0.27	0.17	nuoL
OE3325F	conserved hypothetical protein	1.01	0.10	0.46	-
OE3922R	glutamate--ammonia ligase (EC 6.3.1.2)	1.01	0.08	0.55	glnA
OE4239F	conserved hypothetical protein	1.01	0.30	0.14	-
OE2142R	conserved hypothetical protein	1.01	0.22	0.19	-
OE4699F	excinuclease ABC subunit A	1.01	0.16	0.24	uvrA
OE4260R	probable N-acetyltransferase (EC 2.3.1.-)	1.01	0.10	0.36	-
OE3312R	probable oxidoreductase (aryl-alcohol dehydrogenase homolog)	1.01	0.10	0.37	oxr3
OE1672F	orotate phosphoribosyltransferase homolog	1.01	0.12	0.30	pyrE1
OE5157F	conserved hypothetical protein	1.01	0.13	0.27	-
OE2863R	conserved hypothetical protein	1.01	0.09	0.36	-
OE7140F	spurious ORF	1.01	0.14	0.24	-
OE1876R	probable menaquinol--cytochrome-c reductase	1.01	0.17	0.19	petA
OE1554R	hypothetical protein	1.01	0.14	0.24	-
OE2095R	conserved hypothetical protein	1.01	0.11	0.31	-
OE3967R	conserved hypothetical protein	1.00	0.11	0.27	-
OE5444F	probable methyltransferase	1.00	0.13	0.23	-
OE7207F	hypothetical protein	1.00	0.12	0.24	-
OE3121R	probable phosphoglycolate phosphatase (EC 3.1.3.18)	1.00	0.14	0.20	-
OE3164F	hypothetical protein	1.00	0.05	0.51	-
OE3238F	probable precorrin-6Y C5	1.00	0.11	0.24	cbiE
OE2140R	conserved hypothetical protein	1.00	0.10	0.25	-
OE4148F	hypothetical protein	1.00	0.11	0.21	-
OE5106F	trkA domain protein	1.00	0.09	0.27	trkA7
OE7214R	TATA-binding transcription initiation factor	1.00	0.06	0.36	tbpD1
OE2118F	transcription initiation factor IIE alpha subunit homolog	1.00	0.15	0.16	tfeA
OE3324R	conserved hypothetical protein	1.00	0.14	0.16	-
OE3842R	hypothetical protein	1.00	0.13	0.16	-
OE8009R	conserved hypothetical protein	1.00	0.17	0.13	-
OE4167R	Na+/Ca2+-exchanging protein homolog	1.00	0.24	0.08	nce
OE3681R	conserved hypothetical protein	1.00	0.06	0.35	-
OE1499R	probable bifunctional CAAX prenyl proteinase/zinc metalloproteinase	1.00	0.23	0.08	caaX
OE2499F	hypothetical protein	1.00	0.10	0.18	-
OE4579F	ABC-type transport system ATP-binding protein	1.00	0.12	0.15	yfmF
OE6098R	conserved hypothetical protein	1.00	0.16	0.10	-
OE2579F	adenylosuccinate synthase (EC 6.3.4.4)	1.00	0.16	0.10	purA
OE2377F	conserved hypothetical protein	1.00	0.07	0.21	-
OE3777R	conserved hypothetical protein	1.00	0.11	0.13	-

OE3424R	hypothetical protein	1.00	0.14	0.11	-
OE3352R	DNA repair protein	1.00	0.16	0.09	radA2
OE2318R	phosphomannomutase (EC 5.4.2.8)	1.00	0.11	0.10	pmu2
OE1823F	hypothetical protein	1.00	0.03	0.30	-
OE2916F	probable oxidoreductase (3-oxoacyl-reductase homolog)	1.00	0.13	0.08	oxr5
OE6089R	IS1341-type transposase (TCE32)	1.00	0.12	0.09	-
OE3566F	conserved hypothetical protein	1.00	0.22	0.04	-
OE2637F	DNA-directed RNA polymerase (EC 2.7.7.6) subunit N	1.00	0.10	0.08	rpoN
OE2764R	signal-transducing histidine kinase homolog	1.00	0.12	0.06	-
OE6037R	cell division control protein cdc6 homolog	1.00	0.18	0.03	orc4
OE6053F	phage PhiH1 repressor protein homolog	1.00	0.27	0.02	-
OE4537R	photosystem I biogenesis protein homolog	1.00	0.13	0.02	-
OE3318R	cobalt transport protein CbiN	1.00	0.28	0.01	cbiN
OE1726F	acetate--CoA ligase (EC 6.2.1.1)	1.00	0.11	0.01	acs1
OE4342F	spurious ORF	1.00	0.11	0.01	-
OE7180F	hypothetical protein	1.00	0.12	0.01	-
OE1872R	probable menaquinol--cytochrome-c reductase	1.00	0.09	0.01	petD
OE3823F	uridine 5'-monophosphate kinase (EC 2.7.4.-)	1.00	0.09	0.01	-
OE2930R	conserved hypothetical protein	-1.00	0.11	0.01	-
OE1924F	hypothetical protein	-1.00	0.11	0.01	-
OE5418F	insertion element protein (ISH2)	-1.00	0.20	0.01	-
OE4412R	threonine synthase (EC 4.2.99.2)	-1.00	0.08	0.04	thrC1
OE3427F	conserved hypothetical protein	-1.00	0.10	0.05	-
OE4621F	ADP-ribose pyrophosphatase homolog	-1.00	0.09	0.06	-
OE4258F	probable iron-sulfur protein (heterodisulfide reductase homolog)	-1.00	0.22	0.03	hdrD
OE3941F	threonine synthase (EC 4.2.99.2)	-1.00	0.10	0.06	thrC3
OE1414R	cell division protein ftsZ4	-1.00	0.09	0.07	ftsZ4
OE3721F	conserved hypothetical protein	-1.00	0.20	0.03	-
OE7217F	conserved hypothetical protein	-1.00	0.13	0.05	-
OE6356F	conserved hypothetical protein	-1.00	0.09	0.13	-
OE2668R	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	-1.00	0.46	0.03	metE
OE3789R	hypothetical protein	-1.00	0.19	0.06	-
OE2443R	hypothetical protein	-1.00	0.10	0.15	-
OE5415R	hypothetical protein	-1.00	0.04	0.35	-
OE4688F	conserved hypothetical protein	-1.00	0.09	0.17	-
OE5100R-2 not found in HaloLex	(OE5100: trkA domain)	-1.00	0.05	0.28	
OE1814R	dnaJ N-terminal domain protein	-1.00	0.12	0.14	-
OE4610R	dCTP deaminase homolog	-1.00	0.10	0.17	-
OE4177F	23S rRNA methyltransferase (EC 2.1.1.-)	-1.00	0.05	0.37	ftsJ
OE2243R	probable carbonate dehydratase (EC 4.2.1.1)	-1.00	0.10	0.17	cynT
OE3790R	hypothetical protein	-1.00	0.08	0.24	-
OE1207R	conserved hypothetical protein	-1.00	0.11	0.17	-
OE4671R	conserved hypothetical protein	-1.00	0.07	0.26	-
OE1785F	conserved hypothetical protein	-1.00	0.15	0.12	-
OE3889R	probable potassium transport protein kefC	-1.00	0.69	0.03	kefC
OE3826F	lysine--tRNA ligase (EC 6.1.1.6)	-1.00	0.26	0.07	lysS

OE3606R	sugar kinase (EC 2.7.1.-)	-1.00	0.12	0.18	suk
OE2011R	probable nonspecific lipid-transfer protein (sterol carrier protein)	-1.00	0.07	0.30	scp
OE1064R	spurious ORF	-1.00	0.15	0.15	-
OE3960F	Na+/H+-exchanging protein	-1.00	0.07	0.32	nhaC2
OE4249F	spurious ORF	-1.00	0.21	0.11	-
OE5068F	DNA-directed DNA polymerase (nonfunctional	-1.00	0.09	0.26	-
OE1376R	conserved hypothetical protein	-1.00	0.06	0.41	-
OE6154F	hypothetical protein	-1.00	0.04	0.63	-
OE5193F	hemolysin homolog	-1.00	0.22	0.11	-
OE2612F	conserved hypothetical protein	-1.00	0.06	0.44	-
OE4739R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A'' (chain C)	-1.00	0.14	0.20	rpoA2
OE3297R	NADH-dependent FMN reductase	-1.00	0.13	0.22	msuE
OE2780F	hypothetical protein	-1.00	0.36	0.08	-
OE3315R	ABC-type cobalt transport system ATP-binding protein	-1.00	0.10	0.29	cbiO1
OE4740R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit A' (chain A)	-1.00	0.12	0.24	rpoA1
OE3859F	conserved hypothetical protein	-1.00	0.14	0.19	-
OE4103R	hypothetical protein	-1.00	0.06	0.46	-
OE7144R	conserved hypothetical protein	-1.00	0.15	0.20	-
OE3253F	probable CbiB protein (adenosylcobinamide synthesis)	-1.00	0.05	0.58	cbiB
OE5203F	arginine--tRNA ligase (EC 6.1.1.19)	-1.00	0.10	0.30	argS
OE4022R	mannose-1-phosphate guanylyltransferase (EC 2.7.7.13)	-1.00	0.09	0.34	manC
OE3227F	nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase homolog	-1.00	0.07	0.45	cobT
OE7204F	hypothetical protein	-1.00	0.07	0.48	-
OE3946F	conserved hypothetical protein	-1.00	0.13	0.26	-
OE5442F	conserved hypothetical protein	-1.01	0.08	0.40	-
OE3782R	conserved hypothetical protein	-1.01	0.08	0.42	-
OE1578F	probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	-1.01	0.20	0.18	graD1
OE3895F	conserved hypothetical protein (RNase P homolog)	-1.01	0.11	0.33	-
OE5211F	conserved hypothetical protein	-1.01	0.19	0.19	-
OE2923F	conserved hypothetical protein	-1.01	0.25	0.15	-
OE3147F	probable DNA helicase	-1.01	0.10	0.39	hel
OE3828F	conserved hypothetical protein	-1.01	0.17	0.23	-
OE2921R	probable dihydropteroate synthase (EC 2.5.1.15)	-1.01	0.05	0.74	dhpS
OE2734F	urocanate hydratase (EC 4.2.1.49)	-1.01	0.22	0.18	hutU
OE3910R	probable ABC-type transport system periplasmic substrate-binding protein	-1.01	0.14	0.29	hpb
OE4544R	conserved hypothetical protein	-1.01	0.10	0.40	-
OE1577R	conserved hypothetical protein	-1.01	0.11	0.38	-
OE1288F	probable cationic amino acid transport protein	-1.01	0.10	0.42	cat1
OE2436A1F	hypothetical protein	-1.01	0.06	0.71	-
OE4238R	hemolysin homolog	-1.01	0.11	0.39	hlp
OE6166R	conserved hypothetical protein (nonfunctional	-1.01	0.19	0.24	-
OE3569R	hypothetical protein	-1.01	0.05	0.95	-
OE4118R-2 not found in HaloLex		-1.01	0.08	0.62	
OE5149R	hypothetical protein	-1.01	0.08	0.58	-

OE3517F	conserved hypothetical protein	-1.01	0.10	0.51	-
OE1640F	transport protein homolog	-1.01	0.05	1.05	-
OE3846R	probable enoyl/3-hydroxybutryl-CoA dehydratase (EC 4.2.1.-)	-1.01	0.11	0.50	fad1
OE7059R	TATA-binding transcription initiation factor (nonfunctional	-1.01	0.12	0.46	tbpB1b
OE2547R	probable glycosyltransferase (EC 2.-.-.-)	-1.01	0.10	0.52	exoM
OE1678R	probable ABC-type phosphate transport system permease protein	-1.01	0.22	0.25	pstC2
OE5198R	conserved hypothetical protein	-1.01	0.07	0.83	-
OE3710R	trkA domain protein	-1.01	0.06	0.94	trkA6
OE2447F	hypothetical protein	-1.01	0.39	0.15	-
OE2365R	hydrolase homolog	-1.01	0.10	0.60	-
OE2988R	conserved hypothetical protein	-1.01	0.06	0.91	-
OE1929R-2 not found in HaloLex		-1.01	0.08	0.77	
OE2828R	conserved hypothetical protein	-1.01	0.07	0.84	-
OE7120R	conserved hypothetical protein	-1.01	0.12	0.52	-
OE3263R	transposase homolog (TCE33) (nonfunctional	-1.01	0.08	0.78	-
OE2762R	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	-1.01	0.14	0.43	aroA
OE2956F	hypothetical protein	-1.01	0.09	0.67	-
OE4307F	glycine--tRNA ligase (EC 6.1.1.14)	-1.01	0.12	0.55	glyS
OE4479R	probable ABC-type phosphate transport system ATP-binding prot.	-1.01	0.13	0.51	pstB1
OE3273F	DNA-binding protein	-1.01	0.06	1.18	tfx
OE6325R	hypothetical protein	-1.01	0.10	0.63	-
OE3334R	anthranilate phosphoribosyltransferase (EC 2.4.2.18)	-1.01	0.12	0.55	trpD1
OE1745R	hypothetical protein	-1.01	0.05	1.45	-
OE3039F	conserved hypothetical protein	-1.01	0.13	0.53	-
OE4271F	conserved hem operon protein	-1.01	0.04	1.64	-
OE2524R	UDPglucose 6-dehydrogenase (EC 1.1.1.22)	-1.01	0.19	0.36	udg1
OE1879R	halocyanin hcpE	-1.01	0.13	0.54	hcpE
OE2770F	prephenate dehydrogenase (EC 1.3.1.12)	-1.01	0.12	0.61	tyrA
OE4032R	conserved hypothetical protein	-1.01	0.17	0.42	-
OE3341F	hypothetical protein	-1.01	0.09	0.78	-
OE1793F	conserved hypothetical protein	-1.01	0.11	0.69	-
OE3693F	peptidylprolyl isomerase (EC 5.2.1.8)	-1.01	0.16	0.48	ppiA
OE4118R	leucine--tRNA ligase (EC 6.1.1.4)	-1.01	0.09	0.89	leuS
OE5049F	SMC-like protein sph2	-1.01	0.18	0.42	sph2
OE5310F	conserved hypothetical protein	-1.01	0.15	0.52	-
OE4127R	conserved hypothetical protein	-1.01	0.15	0.52	-
OE6298A1R	insertion element protein (ISH2)	-1.01	0.19	0.42	-
OE4356F	thiosulfate sulfurtransferase (EC 2.8.1.1)	-1.01	0.16	0.51	tssB
OE1016R	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	-1.01	0.08	1.01	graD2
OE3706F	hypothetical protein	-1.01	0.10	0.81	-
OE6142R	conserved hypothetical protein	-1.01	0.22	0.37	-
OE1538F	spurious ORF	-1.01	0.13	0.66	-
OE2110R	UDPglucose 4-epimerase (EC 5.1.3.2)	-1.01	0.06	1.33	galE1
OE1492R	conserved hypothetical protein	-1.01	0.08	1.08	-
OE4113F	2-oxoacid dehydrogenase E1 component alpha-1 subunit	-1.01	0.16	0.53	oxdhA1

OE3741R	hypothetical protein	-1.01	0.18	0.47	-
OE2886R	probable transposase (ISH1)	-1.01	0.11	0.82	-
OE3259F	cobC protein (adenosylcobinamide synthesis)	-1.01	0.15	0.59	cobC
OE1743R	hypothetical protein	-1.01	0.16	0.55	-
OE3474R-2 not found in HaloLex		-1.01	0.12	0.74	
OE5308F	conserved hypothetical protein	-1.01	0.23	0.40	-
OE3473F-2 not found in HaloLex		-1.01	0.08	1.11	
OE1860F	conserved hypothetical protein	-1.01	0.16	0.57	-
OE4263F	conserved hem operon protein	-1.01	0.13	0.71	-
OE5094F	diaminobutyrate--pyruvate aminotransferase	-1.01	0.13	0.70	dat
OE1080F	probable polysaccharide export protein	-1.01	0.14	0.67	-
OE2635F	ribosomal protein S9	-1.01	0.19	0.49	rps9
OE1222R	tRNA adenylyltransferase (EC 2.7.7.25)	-1.01	0.17	0.57	cca
OE1900F	hypothetical protein	-1.02	0.13	0.75	-
OE2383R	fla operon protein flaG	-1.02	0.09	1.06	flaG
OE2093R	conserved hypothetical protein	-1.02	0.07	1.31	-
OE4235F	hypothetical protein	-1.02	0.25	0.39	-
OE3682F	fsxA protein	-1.02	0.07	1.45	fsxA
OE6114R	hypothetical protein	-1.02	0.30	0.33	-
OE2402F	conserved hypothetical protein	-1.02	0.13	0.74	-
OE7070R	conserved hypothetical protein	-1.02	0.19	0.52	-
OE4010F	probable multifunctional long-chain (E)-prenyl diphosphate synthase	-1.02	0.11	0.90	idsA2
OE1294R	ribosomal protein L15.eR	-1.02	0.09	1.13	rpl15R
OE2586F	hypothetical protein	-1.02	0.17	0.59	-
OE2569R	sulfite oxidase homolog	-1.02	0.09	1.08	-
OE1422F	conserved hypothetical protein	-1.02	0.20	0.50	-
OE3038F	methylenetetrahydrofolate dehydrogenase (NAD(P)+)	-1.02	0.06	1.81	folD
OE4614F	hypothetical protein	-1.02	0.11	0.90	-
OE4697R	hypothetical protein	-1.02	0.21	0.50	-
OE5222R	spurious ORF	-1.02	0.18	0.58	-
OE5233F	probable transposase (ISH5)	-1.02	0.11	1.01	-
OE6128R	hypothetical protein	-1.02	0.10	1.05	-
OE1613R	probable acylaminoacyl-peptidase (EC 3.4.19.1)	-1.02	0.11	0.98	-
OE6071R	transcription initiation factor TFB	-1.02	0.05	2.21	tfbE
OE4705R	aminomethyltransferase homolog	-1.02	0.10	1.15	-
OE4367R	conserved hypothetical protein	-1.02	0.17	0.65	-
OE1807R	threonine synthase (EC 4.2.99.2)	-1.02	0.27	0.42	thrC2
OE3348F	sensory rhodopsin I	-1.02	0.19	0.59	sopI
OE1353F	hypothetical protein	-1.02	0.10	1.19	-
OE1742R	dnaJ/dnaK ATPase stimulator grpE	-1.02	0.13	0.85	grpE
OE5177F	hypothetical protein	-1.02	0.06	1.98	-
OE2299F	p-nitrophenylphosphatase homolog	-1.02	0.12	0.96	pho2
OE3167F-2 not found in HaloLex		-1.02	0.09	1.34	
OE2381R	fla operon protein flaH	-1.02	0.13	0.92	flaH
OE4376R	conserved hypothetical protein	-1.02	0.04	3.06	-
OE5295F	hypothetical protein	-1.02	0.10	1.24	-
OE2139R	glycerol-3-phosphate cytidyltransferase homolog	-1.02	0.15	0.82	taqD
OE7077F	conserved hypothetical protein	-1.02	0.09	1.35	-

OE3961R	probable Na+/H+-exchanging protein	-1.02	0.12	0.99	-
OE3380R	conserved hypothetical protein	-1.02	0.15	0.80	-
OE4523F	hypothetical protein	-1.02	0.08	1.53	-
OE1018F	sugar transferase	-1.02	0.14	0.92	-
OE4655R	conserved hypothetical protein	-1.02	0.07	1.83	-
OE3473F	transducer protein htrVII	-1.02	0.06	1.99	htrVII
OE6085R	conserved hypothetical protein	-1.02	0.13	0.98	-
OE4133R	conserved hypothetical protein	-1.02	0.18	0.71	-
OE7011R	hypothetical protein	-1.02	0.16	0.79	-
OE2149R	conserved hypothetical protein	-1.02	0.08	1.55	-
OE6345R-2 not found in HaloLex		-1.02	0.10	1.26	
OE4582R	conserved hypothetical protein	-1.02	0.07	1.84	-
OE7093R	isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 1	-1.02	0.17	0.79	idi1a
OE4052F	DNA helicase (EC 3.6.1.-) mcm (intein-containing)	-1.02	0.13	1.01	mcm
OE2315R	ABC-type transport system permease protein	-1.02	0.07	1.98	rbsC2
OE4236F	phosphate transport protein homolog	-1.02	0.12	1.18	-
OE2871F	probable 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.157)	-1.02	0.07	2.08	hbd2
OE3714F	hypothetical protein	-1.02	0.19	0.73	-
OE1477R	3-dehydroquinate dehydratase (EC 4.2.1.10)	-1.02	0.13	1.06	aroD
OE1761R	conserved hypothetical protein	-1.02	0.13	1.07	-
OE5065R	conserved hypothetical protein	-1.02	0.05	2.55	-
OE4359F	ABC-type transport system ATP-binding protein	-1.02	0.14	0.99	cysA
OE7105F	cell division control protein cdc6 homolog	-1.02	0.14	1.03	-
OE1186F	spurious ORF	-1.02	0.11	1.28	-
OE6301F	hypothetical protein	-1.02	0.06	2.28	-
OE5171R	hypothetical protein	-1.02	0.07	2.19	-
OE1848R	conserved hypothetical protein	-1.02	0.17	0.86	-
OE6279R	hypothetical protein	-1.02	0.12	1.20	-
OE7020F	hypothetical protein	-1.02	0.24	0.61	-
OE5322R	conserved hypothetical protein	-1.02	0.19	0.79	-
OE1047R	hypothetical protein	-1.02	0.06	2.53	-
OE5169F	probable ABC-type transport system permease protein	-1.02	0.15	0.98	ugpE
OE1536R	transducer protein htr14	-1.02	0.07	2.26	htr14
OE2289F	conserved hypothetical protein	-1.02	0.08	1.97	-
OE3405F	ribosomal protein S4.eR	-1.02	0.13	1.22	rps4R
OE5328R	probable helicase	-1.02	0.11	1.39	-
OE3592F	conserved hypothetical protein	-1.02	0.17	0.95	-
OE1252R	thioredoxin homolog	-1.02	0.15	1.08	-
OE2373F	probable phosphate acetyltransferase (EC 2.3.1.8)	-1.02	0.07	2.34	pta
OE1595F	proline--tRNA ligase (EC 6.1.1.15)	-1.02	0.10	1.57	proS
OE4162F	hypothetical protein	-1.02	0.09	1.71	-
OE4329F	conserved hypothetical protein	-1.02	0.13	1.25	-
OE7208F	hypothetical protein	-1.03	0.08	2.05	-
OE2651F	hypothetical protein	-1.03	0.17	0.93	-
OE4132R	tryptophan--tRNA ligase (EC 6.1.1.2)	-1.03	0.12	1.38	trpS2
OE3237F	precorrin-8X methylmutase (EC 5.4.1.2)	-1.03	0.08	2.07	cbiC
OE7171F	hypothetical protein	-1.03	0.19	0.84	-
OE5067R	hypothetical protein	-1.03	0.06	2.90	-

OE2802F	5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)	-1.03	0.09	1.88	ribG
OE4397F	homoserine O-acetyltransferase (EC 2.3.1.31)	-1.03	0.10	1.74	metA
OE3775R	conserved hypothetical protein	-1.03	0.11	1.53	-
OE2044F	conserved hypothetical protein	-1.03	0.13	1.23	-
OE3725F	hypothetical protein	-1.03	0.33	0.51	-
OE3506F	conserved hypothetical protein	-1.03	0.29	0.59	-
OE2292F	phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	-1.03	0.24	0.70	purM
OE1440F	IS1341-type transposase (TCE31)	-1.03	0.14	1.25	-
OE3134F	transcription regulator bat homolog	-1.03	0.09	1.83	boa2
OE4049R	hypothetical protein	-1.03	0.12	1.44	-
OE2187F	conserved hypothetical protein	-1.03	0.14	1.26	-
OE3155R	conserved hypothetical protein	-1.03	0.14	1.23	-
OE3343R	hypothetical protein	-1.03	0.27	0.65	-
OE2268R	imidazoleglycerol-phosphate synthase (EC 2.4.2.-) subunit hisF	-1.03	0.21	0.85	hisF
OE4256F	probable ABC-type transport system ATP-binding protein	-1.03	0.12	1.44	cbiO2
OE4633F	conserved hypothetical protein	-1.03	0.15	1.20	-
OE1146R-2 not found in HaloLex		-1.03	0.09	1.90	
OE1498R	glutamate decarboxylase homolog	-1.03	0.09	1.97	gadD
OE3634F	isocitrate dehydrogenase (NADP+) (EC 1.1.1.42)	-1.03	0.18	1.04	icd
OE5013R	spurious ORF	-1.03	0.11	1.75	-
OE4289F	hypothetical protein	-1.03	0.04	4.29	-
OE4152R	ATP phosphoribosyltransferase (EC 2.4.2.17)	-1.03	0.09	1.96	hisG
OE1858F	hypothetical protein	-1.03	0.09	2.04	-
OE4025F	conserved hypothetical protein	-1.03	0.16	1.20	-
OE3173F-2 not found in HaloLex		-1.03	0.14	1.35	
OE4511R	hypothetical protein	-1.03	0.07	2.75	-
OE7176R	helicase homolog	-1.03	0.26	0.74	-
OE4073R	halocyanin hcpB	-1.03	0.10	2.00	hcpB
OE3836F	probable acetyltransferase	-1.03	0.17	1.12	yyaI
OE4442F	conserved hypothetical protein	-1.03	0.10	1.91	-
OE3585A1F	hypothetical protein	-1.03	0.07	2.68	-
OE3855R	probable signal-transducing histidine kinase	-1.03	0.14	1.40	-
OE3595R	molybdopterin (MPT) converting factor	-1.03	0.04	4.95	moaD
OE7039F-2 not found in HaloLex		-1.03	0.10	2.07	
OE3987R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit C.a	-1.03	0.19	1.04	atpC
OE5116R	gas-vesicle operon protein gvpJ2	-1.03	0.19	1.05	gvpJ2
OE5286R	ATP-dependent RNA helicase homolog	-1.03	0.12	1.61	-
OE3040R	conserved hypothetical protein	-1.03	0.16	1.26	-
OE2120F	conserved hypothetical protein	-1.03	0.14	1.38	-
OE5142F-2 not found in HaloLex		-1.03	0.14	1.41	
OE4476R	phoU protein homolog	-1.03	0.11	1.80	-
OE4667R	AAA domain/ferredoxin domain protein	-1.03	0.09	2.26	-
OE2294R	conserved hypothetical protein	-1.03	0.15	1.38	-
OE3796R	conserved hypothetical protein	-1.03	0.14	1.49	-
OE5052F	potassium-transporting ATPase (EC 3.6.3.12) subunit A	-1.03	0.11	1.94	kdpA
OE1191R	spurious ORF	-1.03	0.17	1.21	-

OE3229R	probable chelatase (EC 4.99.1.-) (cobalamin cluster)	-1.03	0.15	1.36	hmcA
OE1462R	nicotinamide-nucleotide adenylyltransferase (EC 2.7.7.1)	-1.03	0.20	1.01	-
OE3361F	conserved hypothetical protein	-1.03	0.03	6.75	-
OE1787F	probable transcription regulator	-1.03	0.07	2.86	-
OE1941R	maoC protein homolog	-1.03	0.15	1.37	maoC2
OE3311F	conserved hypothetical protein	-1.03	0.10	2.03	-
OE1835F	hypothetical protein	-1.03	0.16	1.34	-
OE5071F	protein kinase weak homolog	-1.03	0.03	6.68	-
OE3090R	conserved hypothetical protein	-1.03	0.20	1.04	-
OE1757R	probable GTP-binding protein	-1.03	0.19	1.13	gbp5
OE8010G1F	replication protein repI2	-1.03	0.21	1.03	repI2
OE3216F	precorrin-3B C17-methyltransferase (EC 2.1.1.131) 2	-1.03	0.08	2.75	cbiH2
OE3881R	phnP protein	-1.03	0.12	1.81	phnP
OE3377R	conserved hypothetical protein	-1.03	0.20	1.08	-
OE1719R	probable oxidoreductase (protochlorophyllide reductase homolog)	-1.03	0.25	0.85	-
OE3919F	conserved hypothetical protein	-1.03	0.09	2.32	-
OE3425F	adenylate kinase (EC 2.7.4.3)	-1.03	0.13	1.71	adk
OE1555F	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	-1.03	0.13	1.65	acd1
OE4535F	sugar kinase (EC 2.7.1.-)	-1.03	0.14	1.56	-
OE2478R	conserved hypothetical protein	-1.03	0.10	2.16	-
OE3395F	ribosomal protein S3	-1.03	0.11	2.07	rps3
OE7003R	conserved hypothetical protein	-1.03	0.38	0.58	-
OE4013R	hypothetical protein	-1.03	0.13	1.76	-
OE4313F	ABC-type transport system permease protein	-1.03	0.17	1.31	appB
OE1495R	pyruvate kinase (EC 2.7.1.40)	-1.03	0.13	1.65	pykA
OE7185F	ATP-dependent helicase	-1.04	0.23	0.98	-
OE2907R	deoxyribodipyrimidine photo-lyase (EC 4.1.99.3)	-1.04	0.16	1.38	phr2
OE3567F	hypothetical protein	-1.04	0.32	0.70	-
OE3520F	conserved hypothetical protein	-1.04	0.19	1.21	-
OE2522F	hypothetical protein	-1.04	0.14	1.62	-
OE3740R	microbial serine proteinase (EC 3.4.21.-)	-1.04	0.10	2.23	sub
OE1097F	hypothetical protein	-1.04	0.10	2.19	-
OE6016F	cysteine-rich protein	-1.04	0.03	6.87	-
OE1358R	methanol dehydrogenase regulatory protein	-1.04	0.21	1.10	moxR
OE1939F	probable propionyl-CoA carboxylase beta subunit	-1.04	0.09	2.66	pccB
OE2338R	hypothetical protein	-1.04	0.14	1.71	-
OE4082F	probable cation-transporting ATPase	-1.04	0.09	2.69	cpx
OE1480F	probable ABC-type transport system periplasmic substrate-binding protein	-1.04	0.07	3.51	-
OE4689R	conserved hypothetical protein	-1.04	0.12	2.04	-
OE1727R	hypothetical protein	-1.04	0.11	2.27	-
OE2757F	hypothetical protein	-1.04	0.12	2.05	-
OE2981F	probable DNA repair helicase	-1.04	0.24	1.03	rad3a
OE7177F	conserved hypothetical protein	-1.04	0.11	2.20	-
OE5089F	conserved hypothetical protein	-1.04	0.08	2.92	-
OE2989R	conserved hypothetical protein	-1.04	0.05	5.07	-
OE1748R	rRNA methylase homolog	-1.04	0.13	1.92	cna

OE2662F	ribosomal protein L7a.eR/HS6 (isol. from the small ribosomal subunit)	-1.04	0.08	3.31	rpl7aR
OE2324F	hypothetical protein	-1.04	0.07	3.44	-
OE1704R	ABC-type transport system ATP-binding protein	-1.04	0.27	0.93	trp3
OE4045R	hypothetical protein	-1.04	0.06	4.55	-
OE3864R	hypothetical protein	-1.04	0.26	1.00	-
OE1038R	conserved hypothetical protein	-1.04	0.18	1.39	-
OE2414R	taxis protein cheC1 (cheJ)	-1.04	0.12	2.18	cheC1
OE3304R	conserved hypothetical protein	-1.04	0.11	2.42	-
OE1306F	conserved hypothetical protein	-1.04	0.13	1.96	-
OE3317R	probable cobalt transport protein CbiQ	-1.04	0.08	3.06	cbiQ
OE1114F	probable glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	-1.04	0.15	1.71	graD3
OE3347F	transducer protein htrI	-1.04	0.18	1.44	htrI
OE1342R	hypothetical protein	-1.04	0.25	1.03	-
OE2850R	hypothetical protein	-1.04	0.11	2.41	-
OE1646R	hypothetical protein	-1.04	0.14	1.83	-
OE2772F	conserved hypothetical protein	-1.04	0.22	1.17	-
OE5437R	arsenical resistance operon repressor (transcription regulator)	-1.04	0.16	1.65	arsR
OE2041R	conserved hypothetical protein	-1.04	0.19	1.39	-
OE5001R	DNA primase homolog	-1.04	0.17	1.53	-
OE7222R	hypothetical protein	-1.04	0.08	3.36	-
OE2288F	pheromone shutdown protein homolog	-1.04	0.09	3.00	traB
OE7169F	transposase homolog (ISH3/ISH27) (nonfunctional	-1.04	0.06	4.07	-
OE3490R	conserved hypothetical protein	-1.04	0.32	0.82	-
OE7187F	conserved hypothetical protein	-1.04	0.09	2.99	-
OE2641F	ribosomal protein S2	-1.04	0.16	1.64	rps2
OE1078F	glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	-1.04	0.38	0.70	graD6
OE3186F	biotin--[acetyl-CoA-carboxylase] ligase (EC 6.3.4.15) 1	-1.04	0.09	2.90	birA1
OE1898R	spurious ORF	-1.04	0.20	1.31	-
OE2020F	fructose-bisphosphatase (EC 3.1.3.11)	-1.04	0.15	1.83	fbp
OE4304R	ABC-type transport system permease protein	-1.04	0.17	1.56	dppB1
OE4500R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	-1.04	0.21	1.29	acd6
OE4429F	conserved hypothetical protein	-1.04	0.13	2.10	-
OE2273F	hypothetical protein	-1.04	0.62	0.44	-
OE2060R	conserved hypothetical protein	-1.04	0.26	1.04	-
OE2872F	hypothetical protein	-1.04	0.13	2.12	-
OE3081F	conserved hypothetical protein	-1.04	0.12	2.23	-
OE2475F	DNA damage-inducible protein homolog	-1.04	0.13	2.12	yqjH
OE5054F	potassium-transporting ATPase (EC 3.6.3.12) subunit C	-1.04	0.14	1.91	kdpC
OE4377R	GTP-binding protein homolog	-1.04	0.27	1.03	gbp3
OE4702F	geranylgeranyl hydrogenase homolog	-1.04	0.14	2.00	-
OE3891R	long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	-1.04	0.09	3.25	lfl2
OE3732R	conserved hypothetical protein	-1.04	0.14	1.97	-
OE2195F	transducer protein htr18	-1.04	0.15	1.93	htr18
OE1158R	ribosomal protein S6 modification protein rimK	-1.04	0.06	4.43	rimK
OE7170R	probable transposase (ISH4/ISH23/ISH50)	-1.04	0.10	2.84	-
OE1997F	conserved hypothetical protein	-1.04	0.30	0.93	-
OE3274R	glycine cleavage system protein P-2 (glycine	-1.05	0.07	3.80	gcvP2

	dehydrogenase subunit 2)				
OE3744R	probable cell surface glycoprotein	-1.05	0.11	2.48	-
OE4316F	ABC-type transport system permease protein	-1.05	0.07	3.85	appC
OE5173R	hypothetical protein	-1.05	0.07	4.15	-
OE1702R	conserved hypothetical protein	-1.05	0.30	0.94	-
OE3466R	conserved hypothetical protein	-1.05	0.20	1.44	-
OE5325F	conserved hypothetical protein	-1.05	0.09	3.45	-
OE8005F	conserved hypothetical protein	-1.05	0.09	3.16	-
OE6027R	hypothetical protein	-1.05	0.07	4.24	-
OE1960F	NADH dehydrogenase (ubiquinone) subunit J2(C-terminal homology)	-1.05	0.21	1.40	nuoJ2
OE4311F	ABC-type transport system periplasmic substrate-binding protein	-1.05	0.08	3.62	appA
OE6088R	hypothetical protein	-1.05	0.44	0.68	-
OE5134F	conserved hypothetical protein	-1.05	0.20	1.51	-
OE3936F	potassium channel protein homolog	-1.05	0.15	2.00	pchB
OE1852R	conserved hypothetical protein	-1.05	0.27	1.12	-
OE3322F	conserved hypothetical protein	-1.05	0.10	2.97	-
OE2607F	probable GTP-binding protein	-1.05	0.44	0.69	drg
OE1512R	segregation and condensation protein scpA	-1.05	0.14	2.12	scpA
OE2844R	transcription regulator homolog / trkA C-terminal domain protein	-1.05	0.20	1.50	trh2
OE5307F	ABC-type transport system ATP-binding protein	-1.05	0.05	5.67	-
OE1314F	transport protein homolog	-1.05	0.10	3.15	-
OE5246R	permease protein homolog	-1.05	0.10	2.99	-
OE1505F	probable 5'-methylthioadenosine phosphorylase (nonfunctional	-1.05	0.07	4.17	-
OE2472F	conserved hypothetical protein	-1.05	0.12	2.61	-
OE1589F	DNA-(apurinic or apyrimidinic site) lyase endonuclease III	-1.05	0.10	3.23	nthA1
OE2423F	hypothetical protein	-1.05	0.07	4.42	-
OE5210F	hypothetical protein	-1.05	0.07	4.48	-
OE2944F	conserved hypothetical protein	-1.05	0.09	3.56	-
OE6353F	insertion element protein (ISH2)	-1.05	0.16	1.97	-
OE3802R	hypothetical protein	-1.05	0.12	2.53	-
OE4234R	uracil phosphoribosyltransferase (EC 2.4.2.9) upp	-1.05	0.06	5.46	upp
OE1668R	conserved hypothetical protein	-1.05	0.09	3.47	-
OE2010R	conserved hypothetical protein	-1.05	0.16	1.97	-
OE2803R	hypothetical protein	-1.05	0.17	1.90	-
OE5296F	hypothetical protein	-1.05	0.31	1.03	-
OE4137F	hypothetical protein	-1.05	0.09	3.70	-
OE1602F	glycerol-1 phosphate dehydrogenase [NAD(P)] (EC 1.1.1.261)	-1.05	0.14	2.25	gldA2
OE4587R	ABC-type transport system ATP-binding protein	-1.05	0.06	5.39	-
OE4599F	potassium transport system protein trkH3	-1.05	0.12	2.73	trkH3
OE4454R	signal recognition particle receptor SRalpha	-1.05	0.10	3.08	ftsY
OE1352F	hypothetical protein	-1.05	0.04	7.99	-
OE1290F	trkA domain protein	-1.05	0.14	2.38	trkA1
OE3763F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit A	-1.05	0.29	1.12	gpdA2
OE2491F	conserved hypothetical protein	-1.05	0.35	0.94	-
OE2558R	probable O-succinylbenzoate-CoA synthase (OSB	-1.05	0.08	4.02	menC

	synthase)				
OE2225F	dimethylsulfoxide reductase subunit B (electron transfer protein)	-1.05	0.50	0.67	dmsB
OE2102R	conserved hypothetical protein	-1.05	0.31	1.08	-
OE3752R	mutT domain protein	-1.05	0.13	2.51	-
OE5130F	trkA domain protein	-1.05	0.12	2.81	trkA4
OE1102R-2 not found in HaloLex		-1.05	0.13	2.62	
OE2506R	conserved hypothetical protein	-1.05	0.31	1.08	-
OE2951R	ABC-type transport system periplasmic substrate-binding protein	-1.05	0.05	6.38	-
OE3579F	thiol-specific antioxidant protein	-1.05	0.17	2.06	hyrA
OE2919R	conserved hypothetical protein	-1.05	0.21	1.60	-
OE2566R	isochorismate synthase (EC 5.4.99.6)	-1.05	0.15	2.25	menF
OE7143R	conserved hypothetical protein	-1.05	0.10	3.62	-
OE2595F	conserved hypothetical protein	-1.06	0.31	1.10	-
OE1496R	methionine--tRNA ligase (EC 6.1.1.10)	-1.06	0.08	4.57	metS
OE1461R	conserved hypothetical protein	-1.06	0.30	1.18	-
OE4277F	uroporphyrin-III C-methyltransferase (EC 2.1.1.107)	-1.06	0.18	1.94	hemX
OE3596F	potassium channel protein pchA1	-1.06	0.08	4.29	pchA1
OE3719F	conserved hypothetical protein	-1.06	0.09	4.08	-
OE5011F	spurious ORF	-1.06	0.05	7.66	-
OE5045F	conserved hypothetical protein	-1.06	0.13	2.68	-
OE5268R	ABC-type transport system ATP-binding protein	-1.06	0.10	3.66	-
OE4165R	DNA-directed DNA polymerase sliding clamp homolog	-1.06	0.08	4.27	pcn
OE2720R	geranylgeranyl hydrogenase homolog	-1.06	0.09	4.11	-
OE5183R	IS240-type transposase (ISH103)	-1.06	0.07	4.91	-
OE1718R	conserved hypothetical protein	-1.06	0.07	5.44	-
OE3213F	CbiG protein (unassigned function)	-1.06	0.07	5.52	cbiG
OE2741F	hypothetical protein	-1.06	0.10	3.66	-
OE3209F	probable precorrin-2 C20-methyltransferase (EC 2.1.1.130)	-1.06	0.07	5.01	cbiL
OE2379R-2 not found in HaloLex		-1.06	0.08	4.53	
OE5051R	trkA domain protein	-1.06	0.06	5.99	trkA2
OE2902F	conserved hypothetical protein	-1.06	0.08	4.33	-
OE3444F	hypothetical protein	-1.06	0.17	2.18	-
OE4270R	spurious ORF	-1.06	0.06	6.01	-
OE3416F	ribosomal protein L30	-1.06	0.07	5.30	rpl30
OE1770F	DNA double-strand break repair ATPase	-1.06	0.09	3.96	rad50
OE7038F	gas-vesicle operon protein gvpO1	-1.06	0.13	2.89	gvpO1
OE3565F	molybdenum cofactor biosynthesis protein B	-1.06	0.12	3.03	moaB
OE6303F	conserved hypothetical protein	-1.06	0.27	1.35	-
OE3798R	conserved hypothetical protein	-1.06	0.11	3.28	-
OE4305R	ABC-type dipeptide transport system periplasmic dipeptide-binding protein	-1.06	0.18	2.12	dppA
OE3812R	histidine--tRNA ligase (EC 6.1.1.21)	-1.06	0.12	2.98	hisS
OE7190R	hypothetical protein	-1.06	0.05	6.91	-
OE5095F	L-2	-1.06	0.10	3.86	bdb
OE3007R	conserved hypothetical protein	-1.06	0.20	1.86	-
OE2862F	thioredoxin homolog	-1.06	0.14	2.62	-
OE4209F	maoC protein homolog	-1.06	0.15	2.47	maoC 1

OE5124R-2 not found in HaloLex		-1.06	0.15	2.60	
OE4405R	phosphoserine phosphatase (EC 3.1.3.3)	-1.06	0.08	4.56	serB
OE1956F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit CD	-1.06	0.17	2.33	nuoCD
OE4714F	hypothetical protein	-1.06	0.21	1.86	-
OE3876R	translation initiation factor aIF-2 gamma subunit	-1.06	0.15	2.58	aIF2g
OE5053F	potassium-transporting ATPase (EC 3.6.3.12) subunit B	-1.06	0.11	3.69	kdpB
OE3413F	ribosomal protein L19.eR	-1.06	0.19	2.04	rpl19R
OE4729R	translation elongation factor aEF-2	-1.06	0.12	3.14	aef2
OE4068F	isoleucine--tRNA ligase (EC 6.1.1.5)	-1.06	0.19	2.07	ileS
OE1344R	hypothetical protein	-1.06	0.20	1.96	-
OE2782F	probable stationary-phase survival protein	-1.06	0.10	3.85	surE
OE7131R	conserved hypothetical protein	-1.06	0.12	3.19	-
OE5291F	hypothetical protein	-1.06	0.06	6.41	-
OE1841R	HyfD / HycC / NADH dehydrogenase (ubiquinone) subunit L homol.	-1.06	0.17	2.37	-
OE1994F	probable ABC-type transport system ATP-binding protein	-1.06	0.21	1.92	-
OE3152R	probable peptide chain release factor aRF1	-1.06	0.15	2.78	pelA
OE3765F	glycerol-3-phosphate dehydrogenase (EC 1.1.99.5) subunit C	-1.06	0.33	1.21	gpdC
OE1171F	type I restriction-modification system DNA-methyltransferase rmeM	-1.07	0.12	3.47	rmeMa
OE3511F	probable sodium/pantothenate symporter	-1.07	0.17	2.39	panF
OE2014F	farnesyl-diphosphate farnesyltransferase (squalene synthase)	-1.07	0.04	10.48	fdfT
OE4422R	spurious ORF	-1.07	0.12	3.47	-
OE2417R	response regulator cheY	-1.07	0.10	4.29	cheY
OE4336R	probable ABC-type transport system permease protein	-1.07	0.13	3.29	nosY
OE1615R	folylpolyglutamate synthase / dihydropteroate synthase	-1.07	0.17	2.53	folCP
OE1844R	NADH dehydrogenase (ubiquinone) subunit N homolog	-1.07	0.09	5.00	-
OE2438R	hypothetical protein	-1.07	0.13	3.23	-
OE1374F	conserved hypothetical protein	-1.07	0.14	3.15	-
OE4399F	probable oxidoreductase (glycerol-3-phosphate dehydrogenase hom)	-1.07	0.24	1.76	oxr8
OE2190R	aldehyde dehydrogenase (succinate-semialdehyde dehydrogenase homolog)	-1.07	0.12	3.74	aldH4
OE6043R	transposase homolog (ISH3/ISH27)	-1.07	0.10	4.13	-
OE2573F	hypothetical protein	-1.07	0.18	2.36	-
OE3414F	ribosomal protein L18	-1.07	0.13	3.44	rpl18
OE1041R	hypothetical protein	-1.07	0.21	2.03	-
OE4583F	ferredoxin (2Fe-2S)	-1.07	0.08	5.84	fer5
OE3139R	amidophosphoribosyltransferase (EC 2.4.2.14)	-1.07	0.11	3.89	purF
OE4365F	conserved hypothetical protein	-1.07	0.17	2.56	-
OE2249R	transducer protein weak homolog lacking transduction domain	-1.07	0.51	0.87	-
OE3748R	probable archaeosine tRNA-ribosyltransferase (EC 2.4.2.-)	-1.07	0.14	3.14	tgtA2
OE2806F	conserved hypothetical protein	-1.07	0.12	3.76	-
OE3874R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit E'	-1.07	0.13	3.43	rpoE1
OE3165R	probable A/G-specific adenine glycosylase (EC 3.2.2.-)	-1.07	0.41	1.10	mutY
OE7105F-2 not found in HaloLex		-1.07	0.13	3.59	
OE2168R-2 not found	(OE2168R: transd. prot. htr 6)	-1.07	0.10	4.60	

in HaloLex					
OE1037F	hypothetical protein	-1.07	0.13	3.62	-
OE7048F	probable transposase (ISH3/ISH27)	-1.07	0.49	0.93	-
OE4713R	conserved hypothetical protein	-1.07	0.26	1.77	-
OE2350R	conserved hypothetical protein	-1.07	0.17	2.73	-
OE4267F	conserved hem operon protein	-1.07	0.11	4.16	-
OE4146F	TATA-binding transcription initiation factor	-1.08	0.06	7.33	tbpE
OE1263F	conserved hypothetical protein	-1.08	0.30	1.58	-
OE1957F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit H	-1.08	0.16	2.86	nuoH
OE1004F	probable ABC-type transport system ATP-binding protein	-1.08	0.17	2.79	-
OE7074F	conserved hypothetical protein	-1.08	0.19	2.45	-
OE4021F	probable oxidoreductase (EC 1.1.1.-)	-1.08	0.14	3.51	oxr1
OE4344F	excinuclease ABC subunit C	-1.08	0.08	6.02	uvrC
OE3187R	conserved hypothetical protein	-1.08	0.27	1.78	-
OE4231R	hypothetical protein	-1.08	0.13	3.56	-
OE1299R	halorhodopsin	-1.08	0.13	3.79	hop
OE4067R	hypothetical protein	-1.08	0.11	4.47	-
OE2878F	hypothetical protein	-1.08	0.07	6.65	-
OE3136F	conserved hypothetical protein	-1.08	0.09	5.44	-
OE2864F	phosphoribosylamine--glycine ligase (EC 6.3.4.13)	-1.08	0.05	9.32	purD
OE2316R	ABC-type transport system ATP-binding protein	-1.08	0.23	2.11	rbsA
OE4432R	conserved hypothetical protein	-1.08	0.17	2.93	-
OE4617F	hypothetical protein	-1.08	0.10	4.71	-
OE3402F	ribosomal protein L14	-1.08	0.07	6.66	rpl14
OE1107R	conserved hypothetical protein	-1.08	0.11	4.32	-
OE7210R	conserved hypothetical protein	-1.08	0.08	6.04	-
OE3299R	conserved hypothetical protein	-1.08	0.22	2.20	-
OE2671R	HemK protein homolog (protoporphyrinogen oxidase homolog)	-1.08	0.20	2.43	hemK
OE3138F	conserved hypothetical protein	-1.08	0.06	8.67	-
OE4105R	RNA helicase homolog	-1.08	0.23	2.14	brr2
OE4301R	ABC-type transport system ATP-binding protein	-1.08	0.06	8.95	ykfD
OE4114F	2-oxoacid dehydrogenase (EC 1.2.4.-) E1 component beta subunit	-1.08	0.21	2.38	oxdhB
OE3283F	conserved hypothetical protein	-1.08	0.10	4.79	-
OE2727R	conserved hypothetical protein	-1.08	0.16	3.00	-
OE4222F	conserved hypothetical protein	-1.08	0.21	2.41	-
OE3817R	ribosomal protein S19.eR	-1.08	0.27	1.84	rps19R
OE5448F	IS1341-type transposase (TCE32) (nonfunctional	-1.08	0.35	1.44	-
OE4201R	probable preflagellin peptidase	-1.08	0.13	3.81	flaK
OE5314F	hypothetical protein	-1.08	0.05	9.40	-
OE7049R	conserved hypothetical protein (nonfunctional	-1.08	0.35	1.44	-
OE4572R	valine--tRNA ligase (EC 6.1.1.9)	-1.08	0.16	3.13	valS
OE3367F	dnaJ N-terminal domain protein	-1.08	0.27	1.82	-
OE1592R	mRNA 3'-end processing factor homolog	-1.08	0.10	5.23	epf2
OE3196F	succinate--CoA ligase (ADP-forming) (EC 6.2.1.5) alpha subunit	-1.08	0.16	3.22	sucA
OE1202F	probable ABC-type transport system ATP-binding/permease protein	-1.08	0.12	4.29	trp1

OE2536F	hypothetical protein	-1.08	0.10	5.30	-
OE4066F	hypothetical protein	-1.08	0.24	2.10	-
OE1178F	type I site-specific deoxyribonuclease (EC 3.1.21.3) subunit rmeR	-1.08	0.16	3.16	rmeR
OE7014F	plasmid replication protein repH	-1.08	0.20	2.61	repH
OE3108F	probable DNA primase	-1.08	0.10	5.25	pri
OE6156F	conserved hypothetical protein	-1.08	0.15	3.42	-
OE5335R	nuclease subunit B homolog	-1.08	0.16	3.14	-
OE4223R	conserved hypothetical protein	-1.08	0.15	3.55	-
OE3728R	hypothetical protein	-1.08	0.12	4.37	-
OE4459R	ribosomal protein L31.eR	-1.08	0.16	3.31	rpl31R
OE2870R	DNA-3-methyladenine glycosidase I (EC 3.2.2.20)	-1.08	0.15	3.59	alkA
OE3036F	glycine hydroxymethyltransferase (EC 2.1.2.1)	-1.09	0.30	1.75	glyA
OE3888F	conserved hypothetical protein	-1.09	0.20	2.58	-
OE4206F	methylaspartate mutase (EC 5.4.99.1) large subunit	-1.09	0.27	1.96	mamB
OE3541R	probable heat shock protein	-1.09	0.14	3.70	hsp1
OE1470F	tryptophan synthase (EC 4.2.1.20) beta subunit	-1.09	0.27	1.98	trpB
OE4199R	phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19)	-1.09	0.23	2.32	hisI
OE5383F	probable transposase (ISH3/ISH27)	-1.09	0.32	1.66	-
OE3042F	hypothetical protein	-1.09	0.16	3.33	-
OE1921R	protoheme IX farnesyltransferase homolog	-1.09	0.15	3.64	hhoA
OE3159R	thymidine kinase (EC 2.7.1.21)	-1.09	0.47	1.15	tdk
OE2909F	conserved hypothetical protein	-1.09	0.15	3.67	-
OE1840R	hypoxanthine phosphoribosyltransferase (EC 2.4.2.8)	-1.09	0.11	5.02	hprt
OE1958F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit I	-1.09	0.20	2.71	nuoI
OE2194R	hypothetical protein	-1.09	0.12	4.46	-
OE2437F	conserved hypothetical protein	-1.09	0.13	4.18	-
OE3342R	hypothetical protein	-1.09	0.16	3.48	-
OE2219R	probable molybdopterin-guanine dinucleotide biosynthesis protein B	-1.09	0.37	1.49	mobB
OE5127F	gas-vesicle protein gvpC2	-1.09	0.19	2.96	gvpC2
OE3704R	camphor resistance protein homolog	-1.09	0.06	8.79	crcB
OE2247R	conserved hypothetical protein	-1.09	0.15	3.58	-
OE2779F	amino acid transport protein (probable phenylalanine transport prot.)	-1.09	0.12	4.57	pheP
OE2577R	conserved hypothetical protein	-1.09	0.21	2.65	-
OE3119R	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	-1.09	0.08	6.64	panB
OE3544F	probable oxidoreductase (ferredoxin reductase homolog)	-1.09	0.12	4.76	noxA
OE2274R	phosphoribosylformylglycinamidine synthase component II	-1.09	0.08	7.43	purL
OE5027R	probable transposase (ISH3/ISH27)	-1.09	0.44	1.27	-
OE2026F	ABC-type transport system ATP-binding protein	-1.09	0.19	2.95	trp5
OE7050A1R	conserved hypothetical protein (nonfunctional	-1.09	0.31	1.80	-
OE2716R	hypothetical protein	-1.09	0.19	3.04	-
OE1931R	potassium channel protein	-1.09	0.17	3.30	pchA2
OE3908R	ABC-type transport system ATP-binding protein	-1.09	0.20	2.87	phnC
OE1394R	conserved hypothetical protein	-1.09	0.18	3.12	-
OE2708R	superoxide dismutase (EC 1.15.1.1) 1 (Mn containing)	-1.09	0.20	2.89	sod1

OE3214F	precorrin-3B C17-methyltransferase (EC 2.1.1.131) 1	-1.09	0.29	1.96	cbiH1
OE3933F	hypothetical protein	-1.09	0.22	2.58	-
OE1664R	molecular chaperone P45 (validated)	-1.09	0.22	2.57	rspA
OE1001F	conserved hypothetical protein	-1.09	0.14	4.28	-
OE1699R	oxidoreductase (EC 1.-.-.-) (geranylgeranyl hydrogenase homolog)	-1.09	0.14	4.27	-
OE1475F	conserved hypothetical protein	-1.09	0.13	4.39	-
OE3175F	propionyl-CoA carboxylase (EC 6.4.1.3)	-1.09	0.20	2.93	mmdA
OE4755F	probable cell surface glycoprotein	-1.09	0.16	3.68	-
OE1328F	spurious ORF	-1.09	0.34	1.74	-
OE4335F	conserved hypothetical protein	-1.09	0.20	2.86	-
OE3991R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit I.a	-1.10	0.25	2.34	atpI
OE2310F	conserved hypothetical protein	-1.10	0.12	4.80	-
OE5170F	probable ABC-type transport system ATP-binding protein	-1.10	0.05	12.15	ugpC
OE4508R	dihydroorotate oxidase (EC 1.3.3.1)	-1.10	0.12	5.03	pyrD
OE3994F	menaquinone biosynthesis methyltransferase homolog	-1.10	0.28	2.13	menG
OE7136R	hypothetical protein	-1.10	0.23	2.57	-
OE1816R	3-isopropylmalate dehydratase homolog	-1.10	0.15	3.94	-
OE1356F	conserved hypothetical protein	-1.10	0.07	8.50	-
OE3712R	2-oxoacid dehydrogenase E1 component alpha-2 subunit	-1.10	0.20	3.06	oxdhA2
OE1853R	Na+/cholate efflux system protein mrpF homolog	-1.10	0.22	2.81	-
OE1752F	3-isopropylmalate dehydratase homolog	-1.10	0.12	5.17	ppd
OE2168R	transducer protein htrVI	-1.10	0.17	3.59	htrVI
OE3510F	conserved hypothetical protein	-1.10	0.17	3.71	-
OE3558F	probable transcription regulator	-1.10	0.34	1.80	trh3
OE3219F	conserved cobalamin operon protein	-1.10	0.16	3.77	-
OE1591R	hypothetical protein	-1.10	0.07	8.31	-
OE3292F	conserved hypothetical protein	-1.10	0.40	1.55	-
OE1972F	methylmalonyl-CoA mutase (EC 5.4.99.2) 1B (N-terminal homology)	-1.10	0.04	16.20	mut1B
OE4563F	hypothetical protein	-1.10	0.14	4.58	-
OE7054R	conserved hypothetical protein	-1.10	0.13	4.72	-
OE2600R	ribosomal protein L12	-1.10	0.14	4.54	rpl12
OE1309F	aminopeptidase (EC 3.4.11.-)	-1.10	0.21	3.00	pepB1
OE4183F	DNA mismatch recognition protein homolog	-1.10	0.24	2.59	mutS3
OE7166F-2 not found in HaloLex		-1.10	0.11	5.85	
OE2975F	hypothetical protein	-1.10	0.15	4.32	-
OE2222F	hypothetical protein	-1.10	0.15	4.20	-
OE4111F	lipoic acid synthase (EC 2.8.1.-)	-1.10	0.08	7.74	lip
OE2097F	conserved hypothetical protein	-1.10	0.22	2.84	-
OE1451F	probable methyltransferase	-1.10	0.13	4.99	pnm
OE4703R	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)	-1.11	0.38	1.72	uae
OE2979F	conserved hypothetical protein	-1.11	0.20	3.29	-
OE2903R	hypothetical protein	-1.11	0.15	4.28	-
OE1524R	conserved hypothetical protein	-1.11	0.11	5.76	-
OE1417F	conserved hypothetical protein	-1.11	0.08	7.88	-
OE1143R	probable molybdenum cofactor biosynthesis protein moeA2	-1.11	0.57	1.15	moeA2
OE2683R	translation elongation factor aEF-1 beta subunit	-1.11	0.12	5.32	aef1b

OE1812R	conserved hypothetical protein	-1.11	0.15	4.40	-
OE1205R	hypothetical protein	-1.11	0.26	2.53	-
OE4255F	conserved hypothetical protein	-1.11	0.19	3.51	-
OE2012R	hypothetical protein	-1.11	0.25	2.66	-
OE4002F	hypothetical protein	-1.11	0.16	4.19	-
OE2370R	gufA protein	-1.11	0.42	1.59	gufA
OE5124R	gas-vesicle operon protein gvpD2 (probable repressor protein)	-1.11	0.25	2.75	gvpD2
OE1094R	probable transposase (ISH10)	-1.11	0.10	7.10	-
OE1772F	hypothetical protein	-1.11	0.25	2.76	-
OE1384F	dCTP deaminase (EC 3.5.4.13)	-1.11	0.19	3.57	dcd
OE1584R	conserved hypothetical protein	-1.11	0.22	3.20	-
OE4357F	ABC-type transport system periplasmic substrate-binding protein	-1.11	0.22	3.11	-
OE1229R	hypothetical protein	-1.11	0.20	3.44	-
OE1890R	DNA-(apurinic or apyrimidinic site) lyase endonuclease III	-1.12	0.16	4.31	nthA2
OE3955F	probable proline dehydrogenase (EC 1.5.99.8)	-1.12	0.29	2.39	putA
OE2667F	nucleoside-diphosphate kinase (EC 2.7.4.6)	-1.12	0.18	3.92	ndk
OE3277R	glycine cleavage system protein H	-1.12	0.30	2.32	gcvH
OE3132F	conserved hypothetical protein	-1.12	0.16	4.49	-
OE7161R	conserved hypothetical protein	-1.12	0.16	4.61	-
OE3875R	conserved hypothetical protein	-1.12	0.10	7.54	-
OE5417R	conserved hypothetical protein	-1.12	0.68	1.05	-
OE2367F	aldehyde dehydrogenase (glyceraldehyde-3-phosphate dehydrogen. homolog	-1.12	0.10	7.43	aldH3
OE3942R	hypothetical protein	-1.12	0.20	3.60	-
OE4374R	conserved hypothetical protein	-1.12	0.07	11.05	-
OE1856R	probable pantothenate metabolism flavoprotein	-1.12	0.18	3.97	dfp
OE3230F	CobN protein (probable cobalt chelatase) (cobN in PSEDE)	-1.12	0.19	3.87	cobN
OE5443F	probable transcription regulator	-1.12	0.25	2.88	-
OE4083F	conserved hypothetical protein	-1.12	0.16	4.64	-
OE1087R	probable transposase (ISH8/ISH26)	-1.12	0.06	12.95	-
OE7101R	conserved hypothetical protein	-1.12	0.21	3.47	-
OE2432C1F	hypothetical protein	-1.12	0.23	3.16	-
OE2697R	probable coenzyme PQQ synthesis protein E	-1.12	0.26	2.83	pqqE2
OE2590R	hypothetical protein	-1.12	0.15	5.02	-
OE7052F	probable transposase (ISH5)	-1.12	0.11	6.46	-
OE1476R	hypothetical protein	-1.12	0.12	6.20	-
OE1388R	hypothetical protein	-1.12	0.18	4.08	-
OE2108F	conserved hypothetical protein	-1.12	0.49	1.52	-
OE7028R	gas-vesicle operon protein gvpH1	-1.12	0.12	6.11	gvpH1
OE1724R	conserved hypothetical protein	-1.12	0.36	2.08	-
OE7189F	conserved hypothetical protein	-1.12	0.12	6.09	-
OE4741R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit B'	-1.12	0.12	6.50	rpoB1
OE2983F	hypothetical protein	-1.12	0.72	1.05	-
OE4211F	probable succinal-CoA transferase (EC 2.8.3.-)	-1.12	0.18	4.27	cat
OE4693R	conserved hypothetical protein	-1.12	0.20	3.77	-
OE2433A1F	probable transposase (ISH3/ISH27)	-1.13	0.53	1.44	-

OE2283F	aspartyl-tRNA(Asn) amidotransferase (EC 6.3.5.-) subunit C	-1.13	0.19	3.98	aatC
OE8006F	conserved hypothetical protein	-1.13	0.16	4.91	-
OE2679R	ribosomal protein L21.eR	-1.13	0.13	6.01	rpl21R
OE2171F	halocyanin hcpC	-1.13	0.12	6.29	hcpC
OE3069R	conserved hypothetical protein	-1.13	0.14	5.49	-
OE5260F	probable transposase (ISH10)	-1.13	0.13	6.12	-
OE2307F	NADH dehydrogenase homolog	-1.13	0.47	1.67	-
OE4331R	tryptophanase (EC 4.1.99.1)	-1.13	0.63	1.25	tnaA
OE3390F	ribosomal protein L23	-1.13	0.18	4.31	rpl23
OE1722R	conserved hypothetical protein	-1.13	0.15	5.40	-
OE2133R	aldehyde dehydrogenase (retinal dehydrogenase homolog)	-1.13	0.23	3.42	aldH2
OE7026R	gas-vesicle operon protein gvpJ1	-1.13	0.10	7.66	gvpJ1
OE3394F	ribosomal protein L22	-1.13	0.40	1.97	rpl22
OE3162F	conserved hypothetical protein	-1.13	0.35	2.30	-
OE4339R	ABC-type transport system ATP-binding protein	-1.13	0.27	2.95	nosF1
OE1862F	aminopeptidase homolog	-1.13	0.10	8.06	ywaD
OE3524F	pyridoxine biosynthesis protein	-1.13	0.28	2.84	pyroA
OE3612R	chemotactic signal transduction system periplasmic substrate-bdg protein basB	-1.13	0.15	5.25	basB
OE4444F	conserved hypothetical protein	-1.13	0.19	4.30	-
OE1614F	hexosyltransferase homolog	-1.13	0.33	2.44	rfbU2
OE1101R	hypothetical protein	-1.14	0.18	4.67	-
OE1570F	anthranilate synthase (EC 4.1.3.27) component II	-1.14	0.22	3.81	trpG2a
OE3787R	preprotein-export translocase subunit secF	-1.14	0.08	10.01	secF
OE2392R-2 not found in HaloLex		-1.14	0.16	5.01	
OE2554R	conserved hypothetical protein	-1.14	0.34	2.40	-
OE1040R	IS1341-type transposase (TCE32)	-1.14	0.20	4.08	-
OE1633F	conserved hypothetical protein	-1.14	0.19	4.40	-
OE1116F	conserved hypothetical protein	-1.14	0.15	5.50	-
OE3560F	probable isopentenyl-diphosphate delta-isomerase (EC 5.3.3.2) 3	-1.14	0.08	10.67	idi3
OE2503R	conserved hypothetical protein	-1.14	0.59	1.42	-
OE4318F	ABC-type transport system ATP-binding protein	-1.14	0.35	2.40	appF
OE5192R	alkaline phosphatase (EC 3.1.3.1)	-1.14	0.18	4.77	aph
OE3883R	conserved hypothetical protein	-1.14	0.18	4.75	-
OE3863R	6-N-hydroxylaminopurine sensitivity-controlling protein	-1.14	0.15	5.67	ham1
OE3145F	conserved hypothetical protein	-1.14	0.30	2.91	-
OE5294R	hypothetical protein	-1.14	0.12	7.33	-
OE1919R	conserved hypothetical protein	-1.14	0.13	6.73	-
OE3017R	UDP-sugar hydrolase (EC 3.6.1.45) / 5'-nucleotidase (EC 3.1.3.5)	-1.14	0.18	4.87	ush
OE2664F	ribosomal protein S28.eR	-1.14	0.33	2.67	rps28R
OE3261F	conserved cobalamin operon protein	-1.14	0.32	2.70	-
OE1031F	probable transposase (ISH10)	-1.15	0.11	8.00	-
OE1965F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit M	-1.15	0.07	12.60	nuoM
OE4034R	CBS domain protein	-1.15	0.33	2.67	-
OE2710F	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	-1.15	0.04	19.81	acd3

OE6133R	probable transposase (ISH10)	-1.15	0.22	4.08	-
OE3501R	hypothetical protein	-1.15	0.16	5.56	-
OE3762R	glycerol kinase (EC 2.7.1.30)	-1.15	0.20	4.45	glpK
OE1196R	hypothetical protein	-1.15	0.18	5.13	-
OE1083R	probable transposase (ISH3/ISH27)	-1.15	0.28	3.25	-
OE1806R	probable periplasmic protein	-1.15	0.35	2.57	-
OE3063F	aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	-1.15	0.23	4.01	asd
OE1520R	hypothetical protein	-1.15	0.27	3.42	-
OE1365F	conserved hypothetical protein	-1.15	0.40	2.29	-
OE1188F	conserved hypothetical protein	-1.15	0.20	4.68	-
OE1967F	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) subunit N	-1.15	0.15	6.20	nuoN
OE1675R	probable ABC-type phosphate transport system ATP-binding protein	-1.15	0.23	3.96	pstB2
OE3770F	hypothetical protein	-1.15	0.17	5.50	-
OE2973F	conserved hypothetical protein	-1.16	0.16	5.65	-
OE4302R	ABC-type oligopeptide transport system ATP-binding protein	-1.16	0.30	3.08	oppD2
OE2306F	conserved hypothetical protein	-1.16	0.50	1.88	-
OE4612F	halolysin R4 (EC 3.4.21.-)	-1.16	0.42	2.27	hly
OE2358F	probable nonspecific lipid-transfer protein (sterol carrier protein)	-1.16	0.41	2.31	acaB2
OE2622R	pyruvate--ferredoxin oxidoreductase beta subunit	-1.16	0.15	6.34	porB
OE2165R	ribosomal protein S15	-1.16	0.30	3.21	rps15
OE4323F	malate dehydrogenase (EC 1.1.1.37)	-1.16	0.21	4.55	mdhA
OE3123R	probable acyl/butyryl-CoA dehydrogenase (EC 1.3.99.-)	-1.16	0.27	3.55	acd5
OE3331R	anthranilate synthase (EC 4.1.3.27) beta subunit	-1.16	0.24	4.05	trpG1
OE2532R	conserved hypothetical protein	-1.16	0.19	5.20	-
OE3073R	dodecin	-1.16	0.11	9.00	-
OE3943R	conserved hypothetical protein	-1.17	0.07	13.40	-
OE1323R	conserved hypothetical protein	-1.17	0.24	4.14	-
OE4735R	ribosomal protein S7	-1.17	0.15	6.54	rps7
OE2640F	phosphopyruvate hydratase (EC 4.2.1.11) (enolase)	-1.17	0.50	1.99	eno
OE5301F-2 not found in HaloLex		-1.17	0.22	4.57	
OE5245F	ABC-type transport system ATP-binding protein	-1.18	0.08	12.30	-
OE4325F	probable DNA helicase	-1.18	0.44	2.38	rad24b
OE2763F	X-Pro dipeptidase (EC 3.4.13.9)	-1.18	0.67	1.55	pepQ2
OE3708R	probable transcription regulator trh5	-1.18	0.22	4.71	trh5
OE3400F	ribosomal protein S17	-1.18	0.33	3.22	rps17
OE3393F	ribosomal protein S19	-1.18	0.19	5.73	rps19
OE3093R	geranylgeranyl-diphosphate geranylgeranyltransferase	-1.18	0.34	3.24	crtB1
OE3243F	cobyrinic acid a	-1.18	0.50	2.19	cbiA
OE7198F	probable transposase (ISH8/ISH26)	-1.18	0.19	5.90	-
OE3730R	hypothetical protein	-1.18	0.08	13.90	-
OE3176F	hypothetical protein	-1.18	0.40	2.70	-
OE2445R	phage PhiH1 repressor protein homolog	-1.19	0.24	4.51	-
OE2789R	hypothetical protein	-1.19	0.23	4.87	-
OE7215F	conserved hypothetical protein	-1.19	0.15	7.45	-
OE5243F	transducer protein car	-1.19	0.34	3.28	car
OE3984R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit B.a	-1.19	0.25	4.45	atpB

OE2442R	hypothetical protein	-1.19	0.22	5.04	-
OE2906R	superoxide dismutase (EC 1.15.1.1) 2	-1.19	0.37	3.08	sod2
OE1490R	conserved hypothetical protein	-1.19	0.17	6.78	-
OE2230F	conserved hypothetical protein	-1.20	0.54	2.13	-
OE4244F	conserved hypothetical protein	-1.20	0.32	3.62	-
OE3265R	transposase homolog (TCE33) (nonfunctional	-1.20	0.27	4.28	-
OE2647F	kinase homolog (acetylglutamate kinase homolog)	-1.20	0.30	3.84	-
OE2623R	pyruvate--ferredoxin oxidoreductase alpha subunit	-1.20	0.20	5.93	porA
OE2704F	halocyanin hcpD	-1.20	0.18	6.57	hcpD
OE1162R	probable cold shock protein	-1.21	0.13	9.43	cspD1
OE2215R	type II secretion system protein homolog	-1.21	0.43	2.87	gspE
OE4414R	salinity-regulated protein homolog	-1.21	0.18	6.69	-
OE2309F	hypothetical protein	-1.21	0.52	2.38	-
OE2698R	hypothetical protein	-1.21	0.18	6.89	-
OE7027R	gas-vesicle operon protein gvpI1	-1.21	0.08	15.90	gvpI1
OE3057F	conserved hypothetical protein	-1.21	0.15	8.40	-
OE1173F	probable transposase (ISH8/ISH26)	-1.21	0.17	7.16	-
OE2003R	conserved hypothetical protein	-1.22	0.09	13.30	-
OE3106F	bacteriorhodopsin precursor	-1.22	0.23	5.46	bop
OE4736R	ribosomal protein S12	-1.22	0.14	9.26	rps12
OE1110F	sulfatase homolog	-1.22	0.09	14.38	-
OE2602R	ribosomal protein L1	-1.22	0.12	10.68	rpl1
OE1934R	proteinase IV (EC 3.4.-.-)	-1.23	0.24	5.46	edp
OE2619F	probable aspartate aminotransferase (EC 2.6.1.1)	-1.23	0.19	7.03	aspB3
OE2847R	conserved hypothetical protein	-1.23	0.22	6.00	-
OE3986R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit F.a	-1.23	0.21	6.50	atpF
OE5015F	probable transposase (ISH8/ISH26)	-1.23	0.23	5.88	-
OE8047F	conserved hypothetical protein	-1.24	0.08	17.88	-
OE3930R	protein synthesis inhibitor homolog	-1.24	0.17	8.03	-
OE3030R	conserved hypothetical protein	-1.24	0.31	4.55	-
OE4197F	conserved hypothetical protein	-1.25	0.37	3.85	-
OE1373R	ribosomal protein L37a.eR	-1.25	0.17	8.67	rpl37aR
OE3262R	conserved hypothetical protein	-1.25	0.26	5.56	-
OE7032R	gas-vesicle operon protein gvpE1 (probable activator protein)	-1.25	0.09	16.90	gvpE1
OE3268F	conserved hypothetical protein	-1.25	0.23	6.41	-
OE7023R	gas-vesicle operon protein gvpL1	-1.25	0.08	19.15	gvpL1
OE2808F	hypothetical protein	-1.26	0.23	6.54	-
OE3357R	ribosomal protein S8.eR	-1.26	0.12	12.84	rps8R
OE1792F	conserved hypothetical protein	-1.26	0.22	6.76	-
OE7031R	gas-vesicle operon protein gvpF1	-1.27	0.27	5.55	gvpF1
OE3668F	conserved hypothetical protein	-1.27	0.34	4.54	-
OE1183F	hypothetical protein	-1.27	0.15	10.09	-
OE2285R	probable acyl-CoA thioester hydrolase (EC 3.1.2.-)	-1.27	0.66	2.35	act1
OE4636F	conserved hypothetical protein	-1.27	0.25	6.30	-
OE4187R	probable DNA-binding protein	-1.27	0.33	4.75	-
OE2410R	taxis protein cheC3	-1.28	1.34	1.18	cheC3
OE1119F	dTDPglucose 4	-1.28	0.13	12.35	-

OE2745R	phosphoglycerate kinase (EC 2.7.2.3)	-1.29	0.69	2.34	pgk
OE3542R	hypothetical protein	-1.29	0.24	6.91	-
OE2900F	conserved hypothetical protein	-1.29	0.37	4.45	-
OE5225R	probable transposase (ISH3/ISH27)	-1.31	0.41	4.25	-
OE2853R	probable peptidylprolyl isomerase (EC 5.2.1.8)	-1.31	0.29	6.06	slyD
OE1160R	ribosomal protein L10.eR	-1.31	0.18	9.61	rpl10R
OE4712F	conserved hypothetical protein	-1.32	0.29	6.19	-
OE1102R-3 not found in HaloLex		-1.32	0.15	11.62	
OE2603R	ribosomal protein L11	-1.32	0.30	6.03	rpl11
OE1943F	glutamate dehydrogenase (NADP+) (EC 1.4.1.4)	-1.32	0.33	5.35	gdhA1
OE4456R	prefoldin alpha subunit	-1.32	0.32	5.61	gimC
OE2381R-2 not found in HaloLex		-1.32	0.25	7.14	
OE2678R	DNA-directed RNA polymerase (EC 2.7.7.6) subunit F	-1.33	0.22	8.13	rpoF
OE2912F	probable fatty-acid--CoA ligase (EC 6.2.1.-)	-1.33	0.11	16.92	alkK2
OE1090F	conserved hypothetical protein (nonfunctional	-1.33	0.14	13.60	-
OE5201F	aspartate carbamoyltransferase (EC 2.1.3.2) catalytic subunit	-1.34	0.26	7.17	pyrB
OE2571F	hypothetical protein	-1.34	0.16	11.76	-
OE4748F	conserved hypothetical protein	-1.34	0.33	5.72	-
OE7017R	probable transposase (ISH3/ISH27)	-1.35	0.37	5.22	-
OE1371R	prefoldin beta subunit	-1.35	0.34	5.62	pfdB
OE3718F	cell division protein	-1.36	0.24	8.39	ftsZ3
OE4460R	ribosomal protein L39.eR	-1.38	0.19	11.17	rpl39R
OE2572F	conserved hypothetical protein	-1.39	0.21	10.12	-
OE3107F	conserved hypothetical protein	-1.43	0.23	10.08	-
OE3545F	hypothetical protein	-1.44	0.34	6.97	-
OE7056F	spurious ORF	-1.44	0.30	7.78	-
OE2811F	conserved hypothetical protein	-1.44	0.29	7.98	-
OE4071R	cytochrome-c oxidase (EC 1.9.3.1) subunit II	-1.45	0.37	6.56	cox2B
OE4296F	hypothetical protein	-1.45	0.43	5.54	-
OE2053F	hypothetical protein	-1.48	0.26	9.79	-
OE4650R	hypothetical protein	-1.48	0.38	6.70	-
OE2450F	acetate--CoA ligase (EC 6.2.1.1)	-1.50	0.59	4.40	acs2
OE5204R	arginine/ornithine antiporter	-1.52	0.33	8.11	nhaC3
OE3992R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit H.a	-1.52	0.21	12.66	atpH
OE2398F	flagellin B2 precursor	-1.53	0.28	9.77	flgB2
OE7110R	conserved hypothetical protein (nonfunctional	-1.56	0.19	14.76	-
OE5202F	aspartate carbamoyltransferase (EC 2.1.3.2) regulatory subunit	-1.59	0.18	16.88	pyrI
OE1319R	cell division protein ftsZ2	-1.61	0.22	13.83	ftsZ2
OE3989R	H+-transporting two-sector ATPase (EC 3.6.3.14) subunit K.a	-1.62	0.21	14.57	atpK
OE5276F	conserved hypothetical protein	-1.65	0.42	7.67	-
OE4070R	cytochrome-c oxidase (EC 1.9.3.1) subunit I	-1.65	0.34	9.44	cox1B
OE3822R	conserved hypothetical protein	-1.66	0.31	10.47	-
OE7043R	hypothetical protein	-1.67	0.17	19.91	-
OE1187R	hypothetical protein	-1.67	0.32	10.31	-
OE2399F	flagellin B3 precursor	-1.69	0.38	8.99	flgB3
OE2469F	flagellin A1 precursor	-1.71	0.39	8.96	flgA1

OE7033R	gas-vesicle operon protein gvpD1 (probable repressor protein)	-1.72	0.30	11.75	gvpD1
OE2397F	flagellin B1 precursor	-1.72	0.31	11.22	flgB1
OE3062F	ribosomal protein S17.eR	-1.76	0.10	35.01	rps17R
OE2470F	flagellin A2 precursor	-1.76	0.41	8.94	flgA2
OE3487R	translation initiation factor aIF-5A	-1.80	0.50	7.58	eif5a
OE4676F	hypothetical protein	-1.84	0.34	11.43	-
OE4509F	nonhistone chromosomal protein	-1.88	0.29	14.25	-
OE1407F	inorganic pyrophosphatase (EC 3.6.1.1)	-1.88	0.52	7.87	ipp
OE1321R	conserved hypothetical protein	-2.18	0.15	33.35	-
OE1270F	glutamate dehydrogenase (EC 1.4.1.2)	-2.23	0.65	7.95	gdhA3
OE4759F	cell surface glycoprotein precursor	-2.24	0.24	21.98	csg
OE1448R	conserved hypothetical protein	-2.40	0.74	7.60	-

7 Acknowledgement

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Finally, Dr. Karina Valer has always had an open ear and was a reliable pillar to lean on when dealing with difficulties.

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8 Curriculum vitae

PERSONAL DETAILS

Name:	Konstantinos Konstantinidis
Date of Birth:	September 3, 1970
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Address:	Tegernseer Landstr. 129; 81539 München; Germany
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ACADEMIC TRAINING

02/2004-12/2008	PhD thesis at the Max Planck Institute of Biochemistry in Martinsried, Germany. Department of Membrane Biochemistry (supervisor: Prof. Dr. Dieter Oesterhelt). Subject: Genome-Wide Proteomics and Quantitative Analyses on Halophilic Archaea. Grade of PhD thesis: 1.0. Final grade of dissertation: 1.2
02/2003-10/2003	Master thesis at the Ludwig-Maximilians University in Munich, Germany. Department Biology I (supervisor: Private Lecturer Dr. Axel Mithöfer). Subject: Spezifische Bindung von 6-Azido-1-oxo-indanoyl-isoleucin-Methylester an Membranfraktionen von Sojabohne (*Glycine max* L.). Grade of master's thesis: 1.0
10/1999-10/2003	Student at the Ludwig-Maximilians University in Munich, Germany. Final examinations in one major subject (physiological botany) and three subsidiary subjects (pharmacology/toxicology, systematic botany and biochemistry). Final grade of master's degree: 1.5
09/1998-05/1999	Overseas studies at the University of Guelph, Ontario, Canada.

09/1996-07/1998	Pre-degree at the Eberhard-Karls University in Tübingen, Germany.

EDUCATION & OCCUPATION

09/1993-06/1996	High school degree (A-level) at the Kolleg am Stiftsgymnasium in Sindelfingen, Germany. Grade: 2.0
07/1990-06/1993	Occupation as industrial mechanic at the Robert Bosch GmbH in Rutesheim, Germany.
09/1987-07/1990	Professional training as industrial mechanic at the Robert Bosch GmbH in Rutesheim, Germany. Grade 2.2
09/1977-06/1987	Secondary school certificate (O-level) at the Realschule in Renningen, Germany.

LABORATORY AND SUPERVISING EXPERIENCE

02/2004-12/2008	PhD thesis at the Max Planck Institute of Biochemistry in Martinsried, Germany. Department of Membrane Biochemistry. Good expertise in several proteomics methods, cell cultures, size exclusion chromatography, SDS-PAGE, 2-dimensional gel electrophoresis, agarose gel electrophoresis, protein- and RNA-extraction, quantitative RT-PCR, Northern blot analysis and whole genome DNA microarrays. Student supervisor in several laboratory courses in biochemistry.
02/2003-10/2003	Master thesis at the Ludwig-Maximilians University in Munich, Germany. Department Biology I. Good expertise in enzyme kinetics, Western blot analysis, adsorption chromatography, protein assays and analysis of substances by HPLC. Student supervisor in several laboratory courses in physiological botany.
09/1996–10/2003	Diverse laboratory experience as student of the Eberhard-Karls University in Tübingen, the University of Guelph, and the Ludwig-Maximilians University in Munich.