


This is the **evidence view**. Different line colors represent the types of evidence for the association.



#### Your Input:

- Abcb4 ATP-binding cassette, sub-family B (MDR/TAP), member 4 Gene; Energy-dependent efflux pump responsible for decreased drug accumulation in multidrug-resistant cells. Mouse MDR2 is not capable of conferring drug resistance (1276 aa)
- Prpsap2 phosphoribosyl pyrophosphate synthetase-associated protein 2 Gene; Seems to play a negative regulatory role in 5- phosphoribose 1-diphosphate synthesis (By similarity) (369 aa)
- Pigl phosphatidylinositol glycan anchor biosynthesis, class L Gene; Involved in the second step of GPI biosynthesis. De-N- acetylation of N-acetylglucosaminy- phosphatidylinositol (By similarity) (252 aa)
- Myh9 myosin, heavy polypeptide 9, non-muscle Gene; Cellular myosin that appears to play a role in cytokinesis, cell shape, and specialized functions such as secretion and capping (1960 aa)
- Pmp22 peripheral myelin protein 22 Gene; Might be involved in growth regulation, and in myelination in the peripheral nervous system (160 aa)
- Gtpbp4 GTP binding protein 4 Gene; Involved in the biogenesis of the 60S ribosomal subunit (By similarity) (634 aa)
- Slc25a17 solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), member 17 Gene; May have transport activity (307 aa)
- Cxadr coxsackie virus and adenovirus receptor Gene; Component of the epithelial apical junction complex that is essential for the tight junction integrity. Proposed to function as a homophilic cell adhesion molecule. Recruits MPDZ to intercellular contact sites. Probably involved in transepithelial migration of polymorphonuclear leukocytes (PMN) through adhesive interactions with AMICA1/JAML located in the plasma membrane of PMN (By similarity) (365 aa)
- Ccrn4l CCR4 carbon catabolite repression 4-like (S. cerevisiae) Gene; Component of the circadian clock or downstream effector of clock function. Exhibits a high amplitude circadian rhythm with maximal levels in early evening. In constant darkness or constant light, the amplitude of the rhythm decreases (By similarity) (429 aa)

	Hbb-b2	hemoglobin, beta adult minor chain Gene (147 aa)
	Glo1	glyoxalase 1 Gene; Catalyzes the conversion of hemimercaptal, formed from methylglyoxal and glutathione, to S-lactoylglutathione (By similarity) (184 aa)
	Ehd3	EH-domain containing 3 Gene; Plays a role in endocytic transport (By similarity) (535 aa)
	Slc30a6	solute carrier family 30 (zinc transporter), member 6 Gene; Zinc-efflux transporter which allocates the cytoplasmic zinc to the trans-Golgi network (TGN) as well as the vesicular compartment (460 aa)
	Ttc27	tetratricopeptide repeat domain 27 Gene (847 aa)
	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial Gene (589 aa)
	Gnaq	guanine nucleotide binding protein, alpha q polypeptide Gene; Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane signaling systems (359 aa)
	Rgs16	regulator of G-protein signaling 16 Gene; Inhibits signal transduction by increasing the GTPase activity of G protein alpha subunits thereby driving them into their inactive GDP-bound form. Binds to G(i)-alpha and G(o)-alpha, but not to G(s)-alpha. Plays an important role in the phototransduction cascade by regulating the lifetime and effective concentration of activated transducin alpha. May regulate extra and intracellular mitogenic signals (201 aa)
	Map1lc3a	microtubule-associated protein 1 light chain 3 alpha Gene; Probably involved in formation of autophagosomal vacuoles (autophagosomes) (By similarity) (121 aa)
	Ghrh	growth hormone releasing hormone Gene; GRF is released by the hypothalamus and acts on the adenohypophyse to stimulate the secretion of growth hormone (103 aa)
	Ctnnb1	catenin, beta like 1 Gene; Induces apoptosis in CHO cells (By similarity) (563 aa)
	Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae) Gene; Part of ribonuclease P, a protein complex that generates mature tRNA molecules by cleaving their 5'-ends. May function with RPP38 to coordinate the nucleolar targeting and/or assembly of RNase P (By similarity) (221 aa)
	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3 Gene (330 aa)
	Tpp1	tripeptidyl peptidase I Gene; Lysosomal serine protease with tripeptidyl-peptidase I activity. May act as a non-specific lysosomal peptidase which generates tripeptides from the breakdown products produced by lysosomal proteinases. Requires substrates with an unsubstituted N-terminus (By similarity) (562 aa)
	Brf2	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like Gene; General activator of RNA polymerase III transcription. Factor exclusively required for RNA polymerase III transcription of genes with promoter elements upstream of the initiation sites (By similarity) (420 aa)
	Chmp4b	chromatin modifying protein 4B Gene; Probable core component of the endosomal sorting required for transport complex III (ESCRT-III) which is involved in multivesicular bodies (MVBs) formation and sorting of endosomal cargo proteins into MVBs. MVBs contain intraluminal vesicles (ILVs) that are generated by invagination and scission from the limiting membrane of the endosome and mostly are delivered to lysosomes enabling degradation of membrane proteins, such as stimulated growth factor receptors, lysosomal enzymes and lipids. The MVB pathway appears to require the sequential function o [...] (224 aa)
	Kiaa0564	RIKEN cDNA 1300010F03 gene Gene (1038 aa)
	Zfp40	zinc finger protein 40 Gene (796 aa)
	Got11	glutamic-oxaloacetic transaminase 1-like 1 Gene (404 aa)
	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2 Gene; Inhibits the mitochondrial pyruvate dehydrogenase complex by phosphorylation of the E1 alpha subunit, thus contributing to the regulation of glucose metabolism (407 aa)
	Elac1	elaC homolog 1 (E. coli) Gene; Zinc phosphodiesterase, which displays some tRNA 3'- processing endonuclease activity. Probably involved in tRNA maturation, by removing a 3'-trailer from precursor tRNA (By similarity) (362 aa)
	Aldh4a1	aldehyde dehydrogenase 4 family, member A1 Gene; Irreversible conversion of delta-1-pyrroline-5-carboxylate (P5C), derived either from proline or ornithine, to glutamate. This is a necessary step in the pathway interconnecting the urea and tricarboxylic acid cycles. The preferred substrate is glutamic gamma-semialdehyde, other substrates include succinic, glutaric and adipic semialdehydes (By similarity) (562 aa)
	Prkcdbp	protein kinase C, delta binding protein Gene; Seems to have an immune potentiation function (By similarity) (260 aa)
	Wdr60	WD repeat domain 60 Gene (999 aa)
	Spag1	sperm associated antigen 1 Gene; Plays a role in fertilization. Binds GTP and has GTPase activity (By similarity) (901 aa)
	Sox5	SRY-box containing gene 5 Gene; Binds specifically to the DNA sequence 5'-AACAAAT-3'. Activates transcription of COL2A1 and AGC1 in vitro (763 aa)
	Fam117a	family with sequence similarity 117, memberA Gene (451 aa)
	Mmgt2	membrane magnesium transporter 2 Gene; Mediates Mg(2+) transport (123 aa)
	Ccdc57	coiled-coil domain containing 57 Gene (1016 aa)
	Morn2	MORN repeat containing 2 Gene (79 aa)
	Syne1	synaptic nuclear envelope 1 Gene (8799 aa)
	Ttc19	tetratricopeptide repeat domain 19 Gene (365 aa)
	Zfp286	zinc finger protein 286 Gene (519 aa)
	Glb1	galactosidase, beta 1 Gene; Cleaves beta-linked terminal galactosyl residues from gangliosides, glycoproteins, and glycosaminoglycans (647 aa)
	Hs3st3a1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 Gene; Transfers a sulfuryl group to an N-unsubstituted glucosamine linked to a 2-O-sulfo iduronic acid unit on heparan sulfate. Catalyzes the O-sulfation of glucosamine in IdoUA2S-GlcNS and also in IdoUA2S-GlcNH2. Unlike 3-OST-1, does not convert non- anticoagulant heparan sulfate to anticoagulant heparan sulfate (By similarity) (393 aa)
	Ric3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans) Gene; Promotes functional expression of homomeric alpha-7 and alpha-8 nicotinic acetylcholine receptors at the cell surface. May also promote functional expression of homomeric serotonergic 5- HT3 receptors, and of heteromeric acetylcholine receptors alpha- 3/beta-2, alpha-3/beta-4, alpha-4/beta-2 and alpha-4/beta-4 (By similarity) (367 aa)
	HnrpII	heterogeneous nuclear ribonucleoprotein L-like Gene; RNA-binding protein that functions as regulator of alternative splicing for multiple target mRNAs, including PTPRC/CD45 and STAT5A. Required for alternative splicing of PTPRC (591 aa)
	Nipbl	Nipped-B homolog (Drosophila) Gene; Probably plays a structural role in chromatin. Involved in sister chromatid cohesion, possibly by interacting with the cohesin complex (By similarity) (2798 aa)
	Rhoj	ras homolog gene family, member J Gene; GTP-binding protein with GTPase activity. Elicits the formation of F-actin-rich structures in fibroblasts and is involved in the regulation of cell morphology (214 aa)
	Mtmr9	myotubularin related protein 9 Gene; Probable pseudophosphatase. Contains a Gly residue instead of a conserved Cys residue in the dsPTPase catalytic loop which renders it catalytically inactive as a phosphatase (Potential) (545 aa)
	Lypd6	LY6/PLAUR domain containing 6 Gene (171 aa)
	Ahcy	S-adenosylhomocysteine hydrolase Gene; Adenosylhomocysteine is a competitive inhibitor of S-adenosyl-L-methionine-dependent methyl transferase reactions; therefore adenosylhomocysteinase may play a key role in the control of methylations via regulation of the intracellular concentration of

	adenosylhomocysteine (432 aa)
● Tmtc2	transmembrane and tetratricopeptide repeat containing 2 Gene (836 aa)
● Samd14	sterile alpha motif domain containing 14 Gene (417 aa)
● BC046404	Leucine-rich repeat-containing protein C17orf76 homolog (339 aa)
● Megf11	multiple EGF-like-domains 11 Gene (1091 aa)
● Tns1	tensin 1 Gene (806 aa)
● Tpr	translocated promoter region Gene (2357 aa)
● LOC632847	RIKEN cDNA 9830001H06 gene Gene (1654 aa)
● Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2 Gene (532 aa)
● Acot11	acyl-CoA thioesterase 11 Gene; Has acyl-CoA thioesterase activity towards medium (C12) and long-chain (C18) fatty acyl-CoA substrates (614 aa)
● Mipep	mitochondrial intermediate peptidase Gene; Cleaves proteins, imported into the mitochondrion, to their mature size (By similarity) (713 aa)
● Ccdc147	coiled-coil domain containing 147 Gene (876 aa)
● Zswim7	zinc finger, SWIM-type containing 7 Gene; Involved in early stages of the homologous recombination repair (HRR) pathway of double-stranded DNA breaks arising during DNA replication or induced by DNA-damaging agents (By similarity) (152 aa)
● H2-T10	histocompatibility 2, T region locus 10 Gene (379 aa)
● Dgkh	diacylglycerol kinase, eta Gene (1156 aa)
● H2-T9	histocompatibility 2, T region locus 10 Gene (379 aa)
● Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1 Gene; Adapter protein that forms a transcriptionally active complex with the gamma-secretase-derived amyloid precursor protein (APP) intracellular domain. Plays a central role in the response to DNA damage by translocating to the nucleus and inducing apoptosis. May act by specifically recognizing and binding histone H2AX phosphorylated on 'Tyr-142' (H2AXY142ph) at double-strand breaks (DSBs), recruiting other pro-apoptosis factors such as MAPK8/JNK1. Required for histone H4 acetylation at double-strand breaks (DSBs). Its A [...] (710 aa)
● Manbal	mannosidase, beta A, lysosomal-like Gene (85 aa)
● Frmd3	FERM domain containing 3 Gene; Putative tumor suppressor gene that may be implicated in the origin and progression of lung cancer (By similarity) (595 aa)
● Alk	anaplastic lymphoma kinase Gene; Orphan receptor with a tyrosine-protein kinase activity. Appears to play an important role in the normal development and function of the nervous system. Phosphorylates almost exclusively at the first tyrosine of the Y-x-x-x-Y-Y motif (By similarity) (1621 aa)
● Shisa3	shisa homolog 3 (Xenopus laevis) Gene; Plays an essential role in the maturation of presomitic mesoderm cells by individual attenuation of both FGF and WNT signaling (By similarity) (238 aa)
● Aebp2	AE binding protein 2 Gene; May interact with and stimulate the activity of the PRC2 complex, which methylates 'Lys-9' and 'Lys-27' residues of histone H3 (By similarity). DNA-binding transcriptional repressor (496 aa)
● Cntn6	contactin 6 Gene; Contactins mediate cell surface interactions during nervous system development. Participates in oligodendrocytes generation by acting as a ligand of NOTCH1. Its association with NOTCH1 promotes NOTCH1 activation through the released notch intracellular domain (NICD) and subsequent translocation to the nucleus (By similarity). Involved in motor coordination (1028 aa)
● Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1 Gene; May play a role as scaffolding protein at cell-cell junctions. May regulate acid-induced ACCN3 currents by modulating its expression at the cell surface (1471 aa)
● Ctnnbp2	cortactin binding protein 2 Gene (1648 aa)
● Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4 Gene; Guanine nucleotide exchange factor (GEF) for RAP1A, RAP1B and RAP2A small GTPases that is activated by binding cAMP. Seems not to activate RAB3A. Involved in cAMP-dependent, PKA- independent exocytosis through interaction with RIMS2 (1011 aa)
● Fcrls	Fc receptor-like 5, scavenger receptor Gene (509 aa)
● Myst2	MYST histone acetyltransferase 2 Gene; Component of the HBO1 complex which has a histone H4-specific acetyltransferase activity, a reduced activity toward histone H3 and is responsible for the bulk of histone H4 acetylation in vivo. Through chromatin acetylation it may regulate DNA replication and act as a coactivator of TP53-dependent transcription. Specifically represses AR-mediated transcription (By similarity) (613 aa)
● Hbb-b1	hemoglobin, beta adult major chain Gene; Involved in oxygen transport from the lung to the various peripheral tissues (147 aa)
● Tbcd	tubulin-specific chaperone d Gene; Tubulin-folding protein; involved in the first step of the tubulin folding pathway. Modulates microtubule dynamics by capturing GTP-bound beta-tubulin (TUBB) (1196 aa)
● H2-T23	histocompatibility 2, T region locus 23 Gene; Involved in the presentation of foreign antigens to the immune system (357 aa)
● Hivep3	human immunodeficiency virus type I enhancer binding protein 3 Gene; Plays a role of transcription factor; binds to recognition signal sequences (Rss heptamer) for somatic recombination of immunoglobulin and T-cell receptor gene segments; Binds also to the kappa-B motif of gene such as S100A4, involved in cell progression and differentiation. Kappa-B motif is a gene regulatory element found in promoters and enhancers of genes involved in immunity, inflammation, and growth and that responds to viral antigens, mitogens, and cytokines. Involvement of HIVEP3 in cell growth is strengthened [...] (2348 aa)
● Cytsb	cytospin B Gene (1067 aa)
● Epn2	epsin 2 Gene; Plays a role in the formation of clathrin-coated invaginations and endocytosis (By similarity) (634 aa)
● Aldh3a1	aldehyde dehydrogenase family 3, subfamily A1 Gene; ALDHs play a major role in the detoxification of alcohol-derived acetaldehyde. They are involved in the metabolism of corticosteroids, biogenic amines, neurotransmitters, and lipid peroxidation. This protein preferentially oxidizes aromatic aldehyde substrates. It may play a role in the oxidation of toxic aldehydes and in preventing corneal damage caused by ultraviolet light (453 aa)
● Mef2c	myocyte enhancer factor 2C Gene; Transcription activator which binds specifically to the MEF2 element present in the regulatory regions of many muscle- specific genes. Controls cardiac morphogenesis and myogenesis, and is also involved in vascular development. May also be involved in neurogenesis and in the development of cortical architecture. Isoform 3 and isoform 4, which lack the repressor domain, are more active than isoform 1, isoform 2 and isoform 5 (By similarity) (442 aa)
● Uqcc	ubiquinol-cytochrome c reductase complex chaperone, CBP3 homolog (yeast) Gene (295 aa)
● Zmynd11	zinc finger, MYND domain containing 11 Gene (618 aa)
● Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2 Gene; Transports L-glutamate and also L- and D-aspartate. Essential for terminating the postsynaptic action of glutamate by rapidly removing released glutamate from the synaptic cleft. Acts as a symport by cotransporting sodium (573 aa)
● Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1) Gene; May regulate the disassembly of focal adhesions. Did not bind receptor-like tyrosine phosphatases type 2A (By similarity) (980 aa)
● Slco1c1	solute carrier organic anion transporter family, member 1c1 Gene; Mediates the Na(+)-independent

	high affinity transport of organic anions such as the thyroid hormones thyroxine (T4) and triiodothyronine (T3). Other potential substrates, such as triiodothyronine (T3), estradiol-17-beta-glucuronide, estrone-3-sulfate and sulfobromophthalein (BSP) are transported with much lower efficiency (By similarity) (716 aa)
BC003331	Protein odr-4 homolog (mODR-4); May play a role in the trafficking of a subset of G- protein coupled receptors (By similarity) (447 aa)
Map4k3	mitogen-activated protein kinase kinase kinase kinase 3 Gene; May play a role in the response to environmental stress. Appears to act upstream of the JUN N-terminal pathway (By similarity) (896 aa)
Rpl15	ribosomal protein L15 Gene (204 aa)
Stx3	syntaxin 3 Gene; Potentially involved in docking of synaptic vesicles at presynaptic active zones (289 aa)
Etl4	enhancer trap locus 4 Gene; Required for normal development of intervertebral disks (1997 aa)
Fgfr2	fibroblast growth factor receptor 2 Gene; Receptor for acidic and basic fibroblast growth factors. Possesses a higher affinity for acidic than for basic FGF's (840 aa)
Pde4d	phosphodiesterase 4D, cAMP specific Gene; Regulates the levels of cAMP in the cell (By similarity) (803 aa)
Jakmip1	janus kinase and microtubule interacting protein 1 Gene; Associates with microtubules and may play a role in the microtubule-dependent transport of the GABA-B receptor. May play a role in JAK1 signaling and regulate microtubule cytoskeleton rearrangements (831 aa)
EG329541	RIKEN cDNA D430041D05 gene Gene (1678 aa)
Usp10	UDP-N-acetyl-alpha-D-galactosamine-polypeptide N-acetylgalactosaminyltransferase 2 Gene; Catalyzes the initial reaction in O-linked oligosaccharide biosynthesis, the transfer of an N-acetyl-D-galactosamine residue to a serine or threonine residue on the protein receptor. Has a broad spectrum of substrates for peptides such as EA2, Muc5AC, Muc1a, Muc1b. Probably involved in O-linked glycosylation of the immunoglobulin A1 (IgA1) hinge region (By similarity) (793 aa) ( <i>Mus musculus</i> )

Neighborhood  
Gene Fusion  
Cooccurrence  
Coexpression  
Experiments  
Databases  
Textmining  
[Homology]  
Score

### Predicted Functional Partners:

Views:        

Neighborhood Fusion Occurrence Coexpression Experiments Database Textmining Summary Network

### Info & Parameters ...

Network Display - Nodes are either colored (if they are directly linked to the input - as in the table) or white (nodes of a higher iteration/depth). Edges, i.e. predicted functional links, consist of up to eight lines: one color for each type of evidence. Hover or click to reveal more information about the node/edge.

#### Active Prediction Methods:

- ☒ Neighborhood ☒ Gene Fusion ☒ Co-occurrence  
☒ Co-expression ☒ Experiments ☒ Databases ☒ Textmining

required confidence (score):

interactors shown:

or custom value:

custom limit:

additional (white) nodes