

Up-regulated genes with annotations

Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Related Genes	Mus musculus
BIOCARTA	Multi-Drug Resistance Factors , Nuclear Receptors in Lipid Metabolism and Toxicity ,		
COG_ONTOLOGY	Defense mechanisms , Posttranslational modification , protein turnover , chaperones ,		
GOTERM_BP_FAT	response to inorganic substance , response to metal ion , drug transport , response to drug , response to cadmium ion , transmembrane transport ,		
GOTERM_CC_FAT	Golgi membrane , mitochondrion , Golgi apparatus , plasma membrane , cell-cell junction , endomembrane system , integral to membrane , apical plasma membrane , cell junction , organelle membrane , intrinsic to membrane , Golgi apparatus part , plasma membrane part , apical part of cell , intercellular canaliculus ,		
GOTERM_MF_FAT	nucleotide binding , nucleoside binding , purine nucleoside binding , ATP binding , xenobiotic-transporting ATPase activity , drug transporter activity , multidrug transporter activity , primary active transmembrane transporter activity , P-P-bond-hydrolysis-driven transmembrane transporter activity , hydrolase activity , acting on acid anhydrides , catalyzing transmembrane movement of substances , ATPase activity , purine nucleotide binding , adenyl nucleotide binding , ribonucleotide binding , purine ribonucleotide binding , adenyl ribonucleotide binding , ATPase activity, coupled , ATPase activity, coupled to transmembrane movement of substances , xenobiotic transporter activity , ATPase activity, coupled to movement of substances ,		
INTERPRO	ABC transporter , transmembrane region , ABC transporter-like , ATPase, AAA+ type, core , ABC transporter, conserved site , ABC transporter integral membrane type 1 ,		
KEGG_PATHWAY	ABC transporters ,		
PIR_SUPERFAMILY	PIRSF002773:multidrug resistance protein,		
SMART	AAA ,		
SP_PIR_KEYWORDS	ATP , atp-binding , duplication , glycoprotein , hydrolase , membrane , nucleotide binding , nucleotide-binding , P-loop , phosphoprotein , repeat , transmembrane , transmembrane protein , transport ,		
UP_SEQ_FEATURE	chain:Multidrug resistance protein 1, domain:ABC transmembrane type-1 1, domain:ABC transmembrane type-1 2, domain:ABC transporter 1, domain:ABC transporter 2, glycosylation site:N-linked (GlcNAc...), modified residue, nucleotide phosphate-binding region:ATP 1, nucleotide phosphate-binding region:ATP 2, topological domain:Cytoplasmic, transmembrane region,		
Rab15	RAB15, member RAS oncogene family	Related Genes	Mus musculus
GOTERM_BP_FAT	intracellular signaling cascade , small GTPase mediated signal transduction , protein localization , protein transport , establishment of protein localization ,		
GOTERM_CC_FAT	plasma membrane , internal side of plasma membrane , plasma membrane part ,		
GOTERM_MF_FAT	nucleotide binding , GTP binding , purine nucleotide binding , guanyl nucleotide binding , ribonucleotide		

	binding , purine ribonucleotide binding , guanyl ribonucleotide binding ,		
INTERPRO	Ras GTPase , RNA polymerase sigma factor 54 , interaction , Ras small GTPase , Rab type , Small GTP-binding protein , Ras ,		
SMART	RAB ,		
SP_PIR_KEYWORDS	cell membrane , direct protein sequencing , gtp-binding , lipoprotein , membrane , methylation , nucleotide-binding , prenylation , protein transport , transport ,		
UP_SEQ_FEATURE	chain:Ras-related protein Rab-15, lipid moiety-binding region:S-geranylgeranyl cysteine, modified residue, nucleotide phosphate-binding region:GTP,		
Adam12	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	Related Genes	Mus musculus
BIOCARTA	Role of EGF Receptor Transactivation by GPCRs in Cardiac Hypertrophy ,		
GOTERM_BP_FAT	proteolysis , cell adhesion , biological adhesion ,		
GOTERM_CC_FAT	extracellular region , proteinaceous extracellular matrix , plasma membrane , integral to membrane , extracellular matrix , intrinsic to membrane , extracellular region part ,		
GOTERM_MF_FAT	endopeptidase activity , metalloendopeptidase activity , peptidase activity , metallopeptidase activity , zinc ion binding , SH3 domain binding , protein domain specific binding , ion binding , cation binding , metal ion binding , transition metal ion binding , peptidase activity, acting on L-amino acid peptides ,		
INTERPRO	EGF-like, type 3 , Peptidase M12B , ADAM/reprolysin , Blood coagulation inhibitor , Disintegrin , Peptidase M10A and M12B , matrixin and adamalysin , Peptidase M12B , propeptide , Peptidase M , neutral zinc metallopeptidases , zinc-binding site , ADAM , cysteine-rich , EGF-like region , conserved site , EGF , extracellular , Disintegrin , conserved site ,		
PIR_SUPERFAMILY	PIRSF006749:mouse meltrin alpha,		
SMART	DISIN , ACR ,		
SP_PIR_KEYWORDS	cell adhesion , cleavage on pair of basic residues , disulfide bond , egf-like domain , glycoprotein , hydrolase , membrane , metal-binding , metalloprotease , phosphoprotein , Protease , sh3-binding , signal , transmembrane , zinc , zymogen ,		
UP_SEQ_FEATURE	chain:Disintegrin and metalloproteinase domain- containing protein 12, compositionally biased region:Cys-rich, disulfide bond, domain:Disintegrin, domain:EGF-like, domain:Peptidase M12B, glycosylation site:N-linked (GlcNAc...), metal ion-binding site:Zinc; catalytic, metal ion-binding site:Zinc; in inhibited form, modified residue, short sequence motif:Cysteine switch, short sequence motif:SH3-binding; class I, short sequence motif:SH3-binding; class II, signal peptide, topological domain:Cytoplasmic, topological domain:Extracellular, transmembrane region,		
Csn3	casein kappa	Related Genes	Mus musculus
GOTERM_CC_FAT	extracellular region ,		
INTERPRO	Kappa casein ,		

PIR_SUPERFAMILY	PIRSF002374:Casein_kappa, PIRSF002374:kappa-casein,		
SP_PIR_KEYWORDS	milk protein , phosphoprotein , Secreted , signal ,		
UP_SEQ_FEATURE	chain:Kappa-casein, modified residue, signal peptide, site:Cleavage; by chymosin/rennin,		
Copg	coatomer protein complex, subunit gamma	Related Genes	Mus musculus
COG_ONTOLOGY	Intracellular trafficking and secretion ,		
GOTERM_BP_FAT	intracellular protein transport , protein localization , protein transport , vesicle-mediated transport , cellular protein localization , establishment of protein localization , intracellular transport , cellular macromolecule localization ,		
GOTERM_CC_FAT	Golgi membrane , Golgi apparatus , Golgi-associated vesicle , plasma membrane , internal side of plasma membrane , endomembrane system , vesicle membrane , cytoplasmic membrane-bounded vesicle , membrane coat , vesicle coat , COPI vesicle coat , coated vesicle , COPI-coated vesicle , cytoplasmic vesicle membrane , Golgi-associated vesicle membrane , coated vesicle membrane , COPI coated vesicle membrane , organelle membrane , cytoplasmic vesicle , vesicle , membrane-bounded vesicle , Golgi apparatus part , cytoplasmic vesicle part , plasma membrane part , coated membrane ,		
GOTERM_MF_FAT	structural molecule activity ,		
INTERPRO	Clathrin/coatomer adaptor , adaptin-like , N-terminal , Armadillo-like helical , Coatomer , gamma subunit , appendage , Ig-like subdomain , Coatomer , gamma subunit , appendage , Clathrin alpha-adaptin/coatomer adaptor , appendage , C-terminal subdomain , Coatomer , gamma subunit ,		
PIR_SUPERFAMILY	PIRSF037093:coatomer, gamma subunit, PIRSF037093:Coatomer_gamma_subunit,		
SP_PIR_KEYWORDS	cytoplasm , cytoplasmic vesicle , er-golgi transport , golgi apparatus , membrane , protein transport , repeat , transport ,		
UP_SEQ_FEATURE	chain:Coatomer subunit gamma, region of interest:Interaction with ZNF289/ARFGAP2, repeat:HEAT 1, repeat:HEAT 2, repeat:HEAT 3, repeat:HEAT 4, sequence conflict,		
Irak2	interleukin-1 receptor-associated kinase 2	Related Genes	Mus musculus
GOTERM_BP_FAT	protein amino acid phosphorylation , phosphorus metabolic process , phosphate metabolic process , apoptosis , cell surface receptor linked signal transduction , intracellular signaling cascade , protein kinase cascade , I-kappaB kinase/NF-kappaB cascade , activation of NF-kappaB-inducing kinase activity , cell death , regulation of cell death , programmed cell death , death , phosphorylation , regulation of phosphate metabolic process , lipopolysaccharide-mediated signaling pathway , activation of protein kinase activity , positive regulation of kinase activity , regulation of phosphorylation , regulation of apoptosis , regulation of programmed cell death , positive regulation of catalytic activity , positive regulation of DNA binding , negative regulation of DNA binding , negative regulation of transcription factor activity , regulation of kinase activity , negative regulation of molecular function , positive regulation of molecular function , regulation of transcription , regulation of protein kinase activity , positive regulation of protein kinase activity , protein		

	amino acid autophosphorylation , regulation of transcription factor activity , positive regulation of transcription factor activity , positive regulation of NF-kappaB transcription factor activity , regulation of binding , positive regulation of binding , negative regulation of binding , regulation of DNA binding , regulation of phosphorus metabolic process , regulation of transferase activity , positive regulation of transferase activity ,		
GOTERM_MF_FAT	nucleotide binding , nucleoside binding , purine nucleoside binding , protein kinase activity , protein serine/threonine kinase activity , ATP binding , purine nucleotide binding , adenyl nucleotide binding , ribonucleotide binding , purine ribonucleotide binding , adenyl ribonucleotide binding ,		
INTERPRO	Death , Protein kinase, core , Serine/threonine protein kinase, active site , Protein kinase, ATP binding site , Serine/threonine protein kinase-related ,		
KEGG_PATHWAY	Apoptosis , Neurotrophin signaling pathway ,		
PIR_SUPERFAMILY	PIRSF038190:interleukin-1 receptor associated kinase, IRAK-1/IRAK-2 types,		
SMART	DEATH ,		
SP_PIR_KEYWORDS	alternative splicing ,		
UP_SEQ_FEATURE	chain:Interleukin-1 receptor-associated kinase- like 2, domain:Death, domain:Protein kinase, sequence conflict, splice variant,		
Lrp11	low density lipoprotein receptor-related protein 11	Related Genes	Mus musculus
GOTERM_BP_FAT	endocytosis , membrane invagination , membrane organization , vesicle-mediated transport ,		
GOTERM_CC_FAT	integral to membrane , intrinsic to membrane ,		
INTERPRO	PKD , Low density lipoprotein-receptor, class A, cysteine-rich , Seven cysteines, N-terminal , Seven cysteines ,		
SMART	PKD , LDLa , MANEC ,		
SP_PIR_KEYWORDS	disulfide bond , Endocytosis , glycoprotein , membrane , receptor , signal , transmembrane ,		
UP_SEQ_FEATURE	chain:Low-density lipoprotein receptor-related protein 11, disulfide bond, domain:LDL-receptor class A, domain:MANSC, domain:PKD, glycosylation site:N-linked (GlcNAc...), sequence conflict, signal peptide, topological domain:Cytoplasmic, topological domain:Extracellular, transmembrane region,		
Prkrir	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)	Related Genes	Mus musculus
GOTERM_MF_FAT	DNA binding , zinc ion binding , ion binding , cation binding , metal ion binding , transition metal ion binding , protein dimerization activity ,		
INTERPRO	Zinc finger, C2CH-type , HAT dimerisation ,		
SMART	DM3 ,		
SP_PIR_KEYWORDS	dna-binding , metal-binding , zinc , zinc-finger ,		

UP_SEQ_FEATURE	chain:52 kDa repressor of the inhibitor of the protein kinase, zinc finger region:THAP-type,		
Slc35b4	solute carrier family 35, member B4	Related Genes	Mus musculus
GOTERM_BP_FAT	carbohydrate transport , transmembrane transport ,		
GOTERM_CC_FAT	Golgi apparatus , integral to membrane , intrinsic to membrane ,		
INTERPRO	UAA transporter ,		
PIR_SUPERFAMILY	PIRSF017416:solute carrier family 35, member B type, PIRSF500841:Solute carrier family 35 member B4,		
SP_PIR_KEYWORDS	alternative splicing , golgi apparatus , membrane , sugar transport , transmembrane , transport ,		
UP_SEQ_FEATURE	chain:UDP-xylose and UDP-N-acetylglucosamine transporter, sequence conflict, splice variant, transmembrane region,		
Zfp101	zinc finger protein 101	Related Genes	Mus musculus
COG_ONTOLOGY	General function prediction only ,		
GOTERM_BP_FAT	transcription , regulation of transcription , DNA-dependent , regulation of transcription , regulation of RNA metabolic process ,		
GOTERM_MF_FAT	zinc ion binding , ion binding , cation binding , metal ion binding , transition metal ion binding ,		
INTERPRO	Krueppel-associated box , Zinc finger, C2H2-type , Zinc finger, C2H2-type/integrase , DNA-binding , Zinc finger, C2H2-like ,		
SMART	KRAB , ZnF_C2H2 ,		
SP_PIR_KEYWORDS	metal-binding , nucleus , repeat , Transcription , zinc ,		

Up-regulated genes pathway analysis

Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Related Genes	Mus musculus
KEGG_PATHWAY	ABC transporters ,		
Irak2	interleukin-1 receptor-associated kinase 2	Related Genes	Mus musculus
KEGG_PATHWAY	Apoptosis , Neurotrophin signaling pathway ,		