Supplementary Table S2. All proteins detected in EGFP+ cells from the epididymis.

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glutamate oxaloacetate transaminase 2, mitochondrial	Got2	NP_034455	47	156	membrane, mitochondrial inner membrane, mitochondrion, plasma membrane	catalytic activity, L-aspartate:2-oxoglutarate aminotransferase activity, pyridoxal phosphate binding, transaminase activity, transferase activity, transferase activity, transferring nitrogenous groups	aspartate biosynthetic process, biosynthetic process, cellular amino acid metabolic process, glutamate catabolic process to 2-oxoglutarate, glutamate catabolic process to aspartate, lipid transport, oxaloacetate metabolic process, transport
clathrin, heavy polypeptide (Hc)	Cltc	NP_001003908	192	144	clathrin coat of coated pit, clathrin coat of trans-Golgi network vesicle, coated pit, cytoplasmic vesicle, membrane, membrane coat, mitochondrion	binding, protein binding, structural molecule activity	intracellular protein transport, vesicle-mediated transport
histone cluster 1, H4a	Hist1h4a	NP_835499	11	144	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
heat shock protein 5	Hspa5	NP_071705	72	137	cell surface, endoplasmic reticulum, endoplasmic reticulum lumen, extracellular region	ATP binding, nucleotide binding, protein binding, ribosome binding	ER overload response, negative regulation of transforming growth factor beta receptor signaling pathway
tumor rejection antigen gp96	Hsp90b1	NP_035761	92	104	endoplasmic reticulum, plasma membrane part	ATP binding, calcium ion binding, low-density lipoprotein receptor binding, nucleotide binding, unfolded protein binding	protein folding, response to stress
aldehyde dehydrogenase family 1, subfamily A1	Aldh1a1	NP_038495	54	102	cytoplasm	3-chloroallyl aldehyde dehydrogenase activity, oxidoreductase activity, retinal dehydrogenase activity	9-cis-retinoic acid biosynthetic process, embryonic eye morphogenesis, metabolic process, optic cup morphogenesis involved in camera-type eye development, oxidation reduction, positive regulation of apoptosis, response to drug, retinoic acid metabolic process, retinol metabolic process
protein disulfide isomerase associated 3	Pdia3	NP_031978	57	96	endoplasmic reticulum	isomerase activity, protein disulfide isomerase activity	cell redox homeostasis, positive regulation of apoptosis
ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	Atp5b	NP_058054	56	96	membrane, mitochondrial inner membrane, mitochondrion, proton-transporting ATP synthase complex, catalytic core F(1), proton-transporting two-sector ATPase complex, proton-transporting two-sector ATPase complex, catalytic domain	ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, nucleoside-triphosphatase activity, nucleotide binding, proton-transporting ATPase activity, rotational mechanism	ATP biosynthetic process, ATP metabolic process, ATP synthesis coupled proton transport, ion transport, lipid metabolic process, negative regulation of cell adhesion involved in substrate-bound cell migration, proton transport, transport
aldehyde dehydrogenase 2, mitochondrial	Aldh2	NP_033786	57	91	mitochondrion	aldehyde dehydrogenase (NAD) activity, oxidoreductase activity	metabolic process, oxidation reduction
actin, alpha 2, smooth muscle, aorta	Acta2	NP_031418	42	84	actin cytoskeleton, cytoplasm, cytoskeleton, smooth muscle contractile fiber	ATP binding, nucleotide binding, protein binding	regulation of blood pressure, vascular smooth muscle contraction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
myosin, heavy polypeptide 9, non-muscle isoform 1	Myh9	NP_071855	226	84	cell cortex, cell-cell adherens junction, cortical cytoskeleton, cytoplasm, immunological synapse, myosin complex, neuromuscular junction, plasma membrane, spindle, stress fiber, uropod	actin binding, actin filament binding, actin-dependent ATPase activity, ADP binding, ATP binding, calmodulin binding, microfilament motor activity, motor activity, nucleotide binding, protein binding	actin filament-based movement, cell adhesion, cell morphogenesis involved in differentiation, cell motion, cell-cell adhesion, establishment of meiotic spindle localization, establishment of T cell polarity, in utero embryonic development, meiotic metaphase I, meiotic spindle organization, myoblast fusion, regulation of cell shape, uropod organization
ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	Atp5a1	NP_031531	60	80	membrane, mitochondrial inner membrane, mitochondrion, proton-transporting ATP synthase complex, catalytic core F(1), proton-transporting two-sector ATPase complex, proton-transporting two-sector ATPase complex, catalytic domain	ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, nucleotide binding, proton-transporting ATPase activity, rotational mechanism	ATP biosynthetic process, ATP metabolic process, ATP synthesis coupled proton transport, embryonic development, ion transport, lipid metabolic process, proton transport, transport
keratin complex 2, basic, gene 8	Krt8	NP_112447	55	78	intermediate filament, keratin filament, sarcolemma, Z disc	protein binding, structural molecule activity	apoptosis, cell differentiation involved in embryonic placenta development, cell morphogenesis involved in differentiation, multicellular organismal development, response to other organism, tumor necrosis factor-mediated signaling pathway
eukaryotic translation elongation factor 1 alpha 1	Eef1a1	NP_034236	50	77	cytoplasm	GTP binding, nucleotide binding, translation elongation factor activity	not classified
H2A histone family, member X	H2afx	NP_034566	15	77	chromatin, chromosome, male germ cell nucleus, nuclear chromatin, nucleosome, nucleus, replication fork, XY body	damaged DNA binding, DNA binding, protein binding	cell cycle, DNA damage checkpoint, DNA recombination, DNA repair, double-strand break repair via homologous recombination, meiosis, nucleosome assembly, response to DNA damage stimulus, spermatogenesis
heat shock protein 1, beta	Hsp90ab1	NP_032328	83	76	cytoplasm, intracellular, mitochondrion	ATP binding, nucleotide binding, protein binding, unfolded protein binding	placenta development, protein folding, response to stress
calnexin	Canx	NP_001103970	67	70	endoplasmic reticulum, integral to membrane, membrane	calcium ion binding, protein binding, sugar binding, unfolded protein binding	protein folding
aconitase 2, mitochondrial	Aco2	NP_542364	85	70	mitochondrion	4 iron, 4 sulfur cluster binding, aconitate hydratase activity, iron ion binding, iron-sulfur cluster binding, lyase activity, metal ion binding	citrate metabolic process, metabolic process, tricarboxylic acid cycle

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
prolyl 4-hydroxylase, beta polypeptide	P4hb	NP_035162	57	67	endoplasmic reticulum, membrane, microsome, plasma membrane	isomerase activity, procollagen-proline 4-dioxygenase activity, protein disulfide isomerase activity	cell redox homeostasis, peptidyl-proline hydroxylation to 4-hydroxy L-proline
keratin 18	Krt18	NP_034794	48	66	intermediate filament	protein binding, structural molecule activity	apoptosis, tumor necrosis factor-mediated signaling pathway
glycoprotein, synaptic 2	Gpsn2	NP_598879	36	62	cytoplasm, endoplasmic reticulum, integral to membrane, membrane	oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	lipid biosynthetic process, lipid metabolic process, oxidation reduction, steroid biosynthetic process
actin, gamma, cytoplasmic 1	Actg1	NP_033739	42	59	actin cytoskeleton, costamere, cytoplasm, cytoskeleton, myofibril	ATP binding, nucleotide binding, protein binding, structural constituent of cytoskeleton	sarcomere organization
histone cluster 1, H1c	Hist1h1c	NP_056601	21	59	chromosome, nucleosome, nucleus	DNA binding, protein binding	nucleosome assembly, nucleosome positioning
heat shock protein 2	Hspa2	NP_001002012	70	57	mitochondrion	ATP binding, nucleotide binding, protein binding	response to stress
protein disulfide isomerase-associated 6	Pdia6	NP_082235	49	56	endoplasmic reticulum	isomerase activity, protein disulfide isomerase activity	cell redox homeostasis
glyceraldehyde-3-phosphate dehydrogenase	Gapdh	NP_032110	36	55	cytoplasm, mitochondrion	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glyceraldehyde-3-phosphate dehydrogenase activity, NAD or NADH binding, oxidoreductase activity, protein binding	glucose metabolic process, glycolysis, multicellular organismal development, oxidation reduction
malate dehydrogenase 2, NAD (mitochondrial)	Mdh2	NP_032643	36	54	mitochondrial inner membrane, mitochondrion	binding, catalytic activity, L-malate dehydrogenase activity, malate dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, protein binding	carbohydrate metabolic process, cellular carbohydrate metabolic process, glycolysis, malate metabolic process, metabolic process, oxidation reduction, tricarboxylic acid cycle
glutathione S-transferase, mu 1	Gstm1	NP_034488	26	54	cytoplasm	glutathione transferase activity, transferase activity	metabolic process
keratin complex 1, acidic, gene 10	Krt10	NP_034790	57	54	intermediate filament, keratin filament	protein binding, structural molecule activity	not classified
protein disulfide isomerase associated 4	Pdia4	NP_033917	72	53	endoplasmic reticulum, endoplasmic reticulum lumen	isomerase activity, protein binding, protein disulfide isomerase activity	cell redox homeostasis
villin 2	Ezr	NP_033536	69	52	apical part of cell, apical plasma membrane, cell projection, cytoplasm, cytoskeleton, extrinsic to membrane, membrane, microtubule basal body, microvillus, plasma membrane, uropod	binding, cytoskeletal protein binding, protein binding	establishment or maintenance of apical/basal cell polarity, regulation of cell shape
plectin 1 isoform 2	Plec1	NP_958787	516	51	contractile fiber, cytoplasm, cytoskeleton, insoluble fraction	actin binding	not classified
albumin	Alb	NP_033784	69	50	cytoplasm, extracellular region, extracellular space	copper ion binding, lipid binding, metal ion binding	transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
keratin complex 2, basic, gene 1	Krt1	NP_032499	66	48	intermediate filament, keratin filament, membrane, plasma membrane	structural molecule activity	not classified
calreticulin	Calr	NP_031617	48	46	endoplasmic reticulum, external side of plasma membrane, extracellular space, microsome	calcium ion binding, metal ion binding, sugar binding, unfolded protein binding, zinc ion binding	cortical actin cytoskeleton organization, protein folding, regulation of meiosis
ubiquitin B	Ubb	NP_035794	34	46	cytoplasm, nucleus	protein binding	not classified
triosephosphate isomerase 1	Tpi1	NP_033441	27	45	not classified	catalytic activity, isomerase activity, triose-phosphate isomerase activity	embryonic development, fatty acid biosynthetic process, gluconeogenesis, glucose metabolic process, glyceraldehyde-3-phosphate metabolic process, glycolysis, lipid biosynthetic process, metabolic process, multicellular organismal development, pentose-phosphate shunt
solute carrier family 25, member 5	Slc25a5	NP_031477	33	44	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport
glutathione S-transferase, mu 2	Gstm2	NP_032209	26	44	cytoplasm	glutathione transferase activity, protein binding, transferase activity	metabolic process
fatty acid synthase	Fasn	NP_032014	272	41	cytoplasm, glycogen granule	[acyl-carrier-protein] S-acetyltransferase activity, [acyl-carrier-protein] S-malonyltransferase activity, 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase activity, 3-oxoacyl-[acyl-carrier-protein] reductase activity, 3-oxoacyl-[acyl-carrier-protein] synthase activity, acyl carrier activity, acyltransferase activity, binding, catalytic activity, cofactor binding, enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) activity, fatty-acid synthase activity, hydrolase activity, hydrolase activity, acting on ester bonds, lyase activity, oleoyl-[acyl-carrier-protein] hydrolase activity, oxidoreductase activity, phosphopantetheine binding, transferase activity, zinc ion binding	biosynthetic process, fatty acid biosynthetic process, lipid biosynthetic process, metabolic process, oxidation reduction
pyruvate kinase, muscle	Pkm2	NP_035229	58	41	cytoplasm, flagellum, mitochondrion, nucleus	ATP binding, catalytic activity, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, potassium ion binding, protein binding, pyruvate kinase activity, transferase activity	glycolysis

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
dynein, cytoplasmic, heavy chain 1	Dync1h1	NP_084514	532	41	cytoplasm, dynein complex, microtubule	ATP binding, ATPase activity, microtubule motor activity, motor activity, nucleoside-triphosphatase activity, nucleotide binding, protein binding	microtubule-based movement
lamin A isoform A	Lmna	NP_001002011	74	40	intermediate filament, lamin filament, nucleus	protein binding, structural molecule activity	nuclear envelope organization
glutathione S-transferase, mu 4	Gstm4	NP_081040	26	40	cytosol	glutathione transferase activity, transferase activity	nitrobenzene metabolic process, xenobiotic catabolic process
peroxiredoxin 1	Prdx1	NP_035164	22	39	cytoplasm, nucleus	antioxidant activity, oxidoreductase activity, peroxidase activity, peroxiredoxin activity	cell proliferation, cell redox homeostasis, erythrocyte homeostasis, hydrogen peroxide catabolic process, natural killer cell mediated cytotoxicity, oxidation reduction, regulation of NF-kappaB import into nucleus, regulation of stress-activated MAPK cascade, removal of superoxide radicals, response to oxidative stress, response to reactive oxygen species
heat shock protein 8	Hspa8	NP_112442	71	39	cytosol, intracellular	ATP binding, ATPase activity, coupled, nucleotide binding, protein binding, unfolded protein binding	chaperone mediated protein folding requiring cofactor, protein folding, regulation of cell cycle, response to stress
spectrin alpha 2	Spna2	NP_001070022	285	38	cortical cytoskeleton, cytoplasm, cytoskeleton, fascia adherens, membrane, Z disc	actin binding, calcium ion binding, calmodulin binding	actin filament capping
malate dehydrogenase 1, NAD (soluble)	Mdh1	NP_032644	36	36	cytoplasm, cytosol	binding, catalytic activity, L-malate dehydrogenase activity, malate dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	carbohydrate metabolic process, cellular carbohydrate metabolic process, glycolysis, malate metabolic process, metabolic process, oxidation reduction, tricarboxylic acid cycle
acyl-Coenzyme A oxidase 3, pristanoyl	Acox3	NP_109646	78	36	peroxisomal matrix, peroxisome	acyl-CoA dehydrogenase activity, acyl-CoA oxidase activity, electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors, pristanoyl-CoA oxidase activity	fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction
valosin containing protein	Vcp	NP_033529	89	35	cytoplasm, microsome, nucleus	ATP binding, binding, hydrolase activity, lipid binding, nucleoside-triphosphatase activity, nucleotide binding, protein binding	activation of caspase activity, modification-dependent protein catabolic process, transport
glutathione S-transferase, mu 5	Gstm5	NP_034490	27	35	cytoplasm	glutathione transferase activity, transferase activity	metabolic process
hypoxia up-regulated 1	Hyou1	NP_067370	111	35	endoplasmic reticulum	ATP binding, nucleotide binding	response to stress

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	Mthfd1l	NP_758512	106	35	mitochondrion	ATP binding, binding, catalytic activity, formate-tetrahydrofolate ligase activity, ligase activity, nucleotide binding	10-formyltetrahydrofolate biosynthetic process, folic acid and derivative biosynthetic process, metabolic process, one-carbon metabolic process
pyridoxal-dependent decarboxylase domain containing 1 isoform 3	Pdxdc1	NP_001034622	79	34	not classified	carboxy-lyase activity, lyase activity, pyridoxal phosphate binding	carboxylic acid metabolic process
tubulin, beta 3	Tubb3	NP_075768	50	34	axon, intracellular, microtubule, microtubule cytoskeleton, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
ribophorin I	Rpn1	NP_598694	69	34	endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, transferase activity	protein amino acid glycosylation
hemoglobin, beta adult major chain	Hbb-b1	NP_032246	16	32	hemoglobin complex	heme binding, iron ion binding, metal ion binding, oxygen binding, oxygen transporter activity	hemopoiesis, oxygen transport, regulation of eIF2 alpha phosphorylation by heme, transport
Na+/K+ -ATPase alpha 1 subunit	Atp1a1	NP_659149	113	32	basolateral plasma membrane, integral to membrane, membrane, microsome, plasma membrane, sarcolemma	4-nitrophenylphosphatase activity, ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, monovalent inorganic cation transmembrane transporter activity, nucleotide binding, potassium ion binding, protein binding, sodium ion binding, sodium:potassium-exchanging ATPase activity	ATP biosynthetic process, cation transport, ion transport, metabolic process, monovalent inorganic cation transport, negative regulation of glucocorticoid biosynthetic process, negative regulation of heart contraction, positive regulation of heart contraction, positive regulation of striated muscle contraction, potassium ion transport, regulation of blood pressure, regulation of the force of heart contraction, response to drug, sodium ion transport, transport
mitochondrial trifunctional protein, alpha subunit	Hadha	NP_849209	83	32	fatty acid beta-oxidation multienzyme complex, mitochondrial inner membrane, mitochondrion	3-hydroxyacyl-CoA dehydrogenase activity, binding, catalytic activity, coenzyme binding, enoyl-CoA hydratase activity, long-chain-3-hydroxyacyl-CoA dehydrogenase activity, lyase activity, oxidoreductase activity	fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction
tubulin, alpha 4	Tuba4a	NP_033473	50	31	microtubule, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
keratin 7	Krt7	NP_149064	51	31	intermediate filament, keratin filament	protein binding, structural molecule activity	not classified
gelsolin	Gsn	NP_666232	86	31	cytoplasm, cytoskeleton, extracellular region, lamellipodium	actin binding, calcium ion binding	actin filament capping, vesicle-mediated transport
hypothetical protein LOC231293	C130090K23Rik	NP_851840	78	31	integral to membrane, membrane	not classified	GPI anchor biosynthetic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
epididymal secretory protein E1	Npc2	NP_075898	16	30	extracellular region, lysosome	cholesterol binding	cholesterol homeostasis, intracellular cholesterol transport
solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	Slc25a31	NP_848473	35	30	cell projection, cilium, flagellum, integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport
heat shock protein 1, alpha	Hsp90aa1	NP_034610	85	29	cytoplasm, cytosol, intracellular	ATP binding, nitric-oxide synthase regulator activity, nucleotide binding, protein binding, protein homodimerization activity, unfolded protein binding	positive regulation of cytotoxic T cell differentiation, positive regulation of nitric oxide biosynthetic process, protein folding, protein refolding, response to stress, response to unfolded protein
keratin 14	Krt14	NP_058654	53	29	cytoplasm, intermediate filament, keratin filament, nucleus	protein binding, structural molecule activity	not classified
solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	Slc25a3	NP_598429	40	29	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, symporter activity	transport
aldehyde dehydrogenase family 6, subfamily A1	Aldh6a1	NP_598803	58	29	mitochondrion	malonate-semialdehyde dehydrogenase (acetylating) activity, methylmalonate-semialdehyde dehydrogenase (acylating) activity, molecular_function, oxidoreductase activity	brown fat cell differentiation, metabolic process, oxidation reduction, valine metabolic process
UDP-glucose ceramide glucosyltransferase-like 1	Ugcgl1	NP_942602	176	28	endoplasmic reticulum	transferase activity, transferase activity, transferring glycosyl groups, UDP-glucose:glycoprotein glucosyltransferase activity	protein amino acid glycosylation
glutamine synthetase	Glul	NP_032157	42	27	cytoplasm, intracellular, mitochondrion	ATP binding, catalytic activity, glutamate-ammonia ligase activity, ligase activity, nucleotide binding	glutamine biosynthetic process, nitrogen compound metabolic process, response to glucose stimulus
keratin 19	Krt19	NP_032497	45	27	intermediate filament, sarcolemma, Z disc	structural molecule activity	cell differentiation involved in embryonic placenta development
aminolevulinate, delta-, dehydratase	Alad	NP_032551	36	27	not classified	catalytic activity, identical protein binding, lyase activity, metal ion binding, porphobilinogen synthase activity, zinc ion binding	heme biosynthetic process, metabolic process, porphyrin biosynthetic process, tetrapyrrole biosynthetic process
transketolase	Tkt	NP_033414	68	27	not classified	calcium ion binding, catalytic activity, metal ion binding, transferase activity, transketolase activity	metabolic process, regulation of growth
phosphatidylethanolamine binding protein 1	Pebp1	NP_061346	21	27	cell surface, cytoplasm	ATP binding, lipid binding, nucleotide binding, peptidase inhibitor activity, serine-type endopeptidase inhibitor activity	sperm capacitation
histone cluster 1, H1e	Hist1h1e	NP_056602	22	26	chromosome, nucleosome, nucleus	DNA binding, protein binding	nucleosome assembly, nucleosome positioning

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
plasma glutamate carboxypeptidase	Pgcp	NP_061225	52	26	cellular_component, extracellular region	aminopeptidase activity, carboxypeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, molecular_function, peptidase activity, zinc ion binding	biological_process, proteolysis
PREDICTED: hypothetical protein	EG626058	XP_895712	22	26	not classified	not classified	not classified
valyl-tRNA synthetase	Vars	NP_035820	140	25	cytoplasm, mitochondrion	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, valine-tRNA ligase activity	translation, tRNA aminoacylation for protein translation, valyl-tRNA aminoacylation
trypsinogen 7	2210010C04 Rik	NP_075822	26	25	not classified	hydrolase activity, peptidase activity, serine-type peptidase activity	not classified
aldolase A, fructose-bisphosphate	Aldoa	NP_031464	39	24	extracellular region, flagellum, platelet alpha granule lumen	catalytic activity, fructose-bisphosphate aldolase activity, lyase activity	glycolysis, metabolic process
heat shock protein 1 (chaperonin)	Hspd1	NP_034607	61	24	cytoplasm, intracellular membrane-bounded organelle, mitochondrial inner membrane, mitochondrion, plasma membrane part, secretory granule	ATP binding, lipopolysaccharide binding, nucleotide binding, protein binding	cellular protein metabolic process, positive regulation of interferon-alpha production, positive regulation of interferon-gamma production, positive regulation of T cell activation, protein folding, T cell activation
staphylococcal nuclease domain containing 1	Snd1	NP_062750	102	24	cellular_component, cytoplasm, nucleus, RNA-induced silencing complex	hydrolase activity, acting on ester bonds, nuclease activity, nucleic acid binding, protein binding	biological_process, regulation of transcription, RNA interference, transcription
ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform b	Atp5c1	NP_001106209	30	23	membrane, mitochondrial inner membrane, mitochondrion, proton-transporting ATP synthase complex, catalytic core F(1)	hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism	ATP biosynthetic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport
heat shock 70kDa protein 1B	Hspa1b	NP_034608	70	23	intracellular, mitochondrial matrix, mitochondrion	ATP binding, nucleotide binding, protein binding	anti-apoptosis, DNA repair, negative regulation of caspase activity, response to heat, response to stress, telomere maintenance
voltage-dependent anion channel 1	Vdac1	NP_035824	31	23	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion, plasma membrane, pore complex	nucleotide binding, voltage-gated anion channel activity	anion transport, apoptosis, behavioral fear response, ion transport, learning, nerve-nerve synaptic transmission, synaptic transmission, transport
keratin 76	Krt76	NP_001028349	63	22	intermediate filament, keratin filament	structural molecule activity	not classified
tubulin, beta 4	Tubb4	NP_033477	50	22	cell projection, cell soma, cilium, internode region of axon, microtubule, myelin sheath, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	cell projection organization, microtubule-based movement, microtubule-based process, protein polymerization
heat shock protein 9	Hspa9	NP_034611	73	22	cytoplasm, mitochondrion	ATP binding, enzyme binding, nucleotide binding, protein binding, unfolded protein binding	protein export from nucleus, protein folding, response to stress
nucleolin	Ncl	NP_035010	77	22	nucleolus, nucleoplasm, nucleus, ribonucleoprotein complex	DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
peptidylprolyl isomerase B	Ppib	NP_035279	24	22	endoplasmic reticulum	isomerase activity, peptide binding, peptidyl-prolyl cis-trans isomerase activity	protein folding
tubulin, alpha 1	Tuba1a	NP_035783	50	22	cytoplasmic microtubule, microtubule, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization
enolase 1, alpha non-neuron	Eno1	NP_075608	47	22	not classified	lyase activity, magnesium ion binding, phosphopyruvate hydratase activity, protein binding	glycolysis
ribosome binding protein 1 isoform a	Rrbp1	NP_077243	158	22	endoplasmic reticulum, integral to endoplasmic reticulum membrane, integral to membrane, membrane	not classified	protein transport, transmembrane transport, transport
myosin VI	Myo6	NP_001034635	146	21	axon, cell projection, cell soma, coated pit, cytoplasm, cytoplasmic vesicle, Golgi apparatus, membrane, myosin complex, nucleus, perinuclear region of cytoplasm, plasma membrane, synapse, vesicle membrane	actin binding, actin filament binding, ATP binding, calmodulin binding, motor activity, nucleotide binding, protein binding	auditory receptor cell differentiation, dendrite development, endocytosis, glutamate secretion, inner ear development, inner ear morphogenesis, locomotory behavior, protein targeting, protein transport, regulation of synaptic plasticity, sensory perception of sound, synapse assembly, synaptic transmission, transport
annexin A2	Anxa2	NP_031611	39	21	basement membrane, cell junction, cytoplasm, early endosome, extracellular region, membrane fraction, proteinaceous extracellular matrix, sarcolemma, stress fiber	calcium ion binding, calcium-dependent phospholipid binding, cytoskeletal protein binding, phospholipase inhibitor activity, protein binding	angiogenesis, collagen fibril organization, fibrinolysis
voltage-dependent anion channel 2	Vdac2	NP_035825	32	21	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion, pore complex	nucleotide binding, voltage-gated anion channel activity	anion transport, ion transport, transport
IQ motif containing GTPase activating protein 1	Iqgap1	NP_057930	189	21	cell leading edge, cytoplasm, intracellular, membrane, neuron projection, plasma membrane	calmodulin binding, GTPase activator activity, protein binding, Ras GTPase activator activity	regulation of small GTPase mediated signal transduction, small GTPase mediated signal transduction
acetyl-Coenzyme A acetyltransferase 1 precursor	Acat1	NP_659033	45	21	mitochondrial inner membrane, mitochondrion	acetyl-CoA C-acetyltransferase activity, acyltransferase activity, catalytic activity, metal ion binding, potassium ion binding, transferase activity, transferase activity, transferring acyl groups other than amino-acyl groups	metabolic process
keratin complex 2, basic, gene 17	Krt2	NP_034798	71	20	intermediate filament, keratin filament	structural molecule activity	not classified
heterogeneous nuclear ribonucleoprotein K	Hnrnpk	NP_079555	51	20	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	DNA binding, nucleic acid binding, protein binding, RNA binding	mRNA processing, RNA splicing
histone cluster 1, H2ab	Hist1h2ab	NP_783591	14	20	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
histone cluster 2, H2be	Hist2h2be	NP_835586	14	20	chromosome, nucleosome, nucleus	DNA binding, protein binding	nucleosome assembly

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Ddx5	NP_031866	69	19	nucleus, ribonucleoprotein complex, spliceosomal complex	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides, nucleic acid binding, nucleotide binding, protein binding, RNA binding, RNA helicase activity, transcription cofactor activity	mRNA processing, positive regulation of transcription, RNA splicing
golgi apparatus protein 1	Glg1	NP_033175	134	19	Golgi apparatus, Golgi membrane, integral to membrane, membrane, plasma membrane	sugar binding	not classified
voltage-dependent anion channel 3	Vdac3	NP_035826	31	19	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion, pore complex	nucleotide binding, voltage-gated anion channel activity	anion transport, behavioral fear response, ion transport, learning, nerve-nerve synaptic transmission, synaptic transmission, transport
heterogeneous nuclear ribonucleoprotein A2/B1 isoform 1	Hnrnpa2b1	NP_058086	36	19	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA processing, RNA splicing
ubiquinol cytochrome c reductase core protein 2	Uqcrc2	NP_080175	48	19	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding	electron transport chain, proteolysis, transport
inner membrane protein, mitochondrial	Immt	NP_083949	84	19	integral to membrane, integral to mitochondrial inner membrane, membrane, mitochondrial inner membrane, mitochondrion	molecular_function	biological_process
lactate dehydrogenase B	Ldhb	NP_032518	37	18	cytoplasm	catalytic activity, L-lactate dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	anaerobic glycolysis, carbohydrate metabolic process, cellular carbohydrate metabolic process, glycolysis, oxidation reduction
lymphocyte cytosolic protein 1	Lcp1	NP_032905	70	18	actin filament, cytoplasm, phagocytic cup, ruffle	actin binding, actin filament binding, calcium ion binding, identical protein binding, protein binding	actin filament bundle formation, response to wounding
spectrin beta 2 isoform 2	Spnb2	NP_033286	251	18	cortical cytoskeleton, cytoplasm, cytoskeleton, membrane, nucleus, plasma membrane, spectrin	actin binding, calmodulin binding, protein binding, structural constituent of cytoskeleton	actin filament capping, common-partner SMAD protein phosphorylation, SMAD protein nuclear translocation
lactate dehydrogenase A	Ldha	NP_034829	36	18	cytoplasm, cytosol, flagellum	catalytic activity, L-lactate dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, protein binding	anaerobic glycolysis, carbohydrate metabolic process, cellular carbohydrate metabolic process, cellular response to extracellular stimulus, glycolysis, oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
oxoglutarate dehydrogenase (lipoamide)	Ogdh	NP_035086	116	18	mitochondrion	oxidoreductase activity, oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, oxoglutarate dehydrogenase (NAD+) activity, oxoglutarate dehydrogenase (succinyl-transferring) activity, thiamin pyrophosphate binding	glycolysis, metabolic process, oxidation reduction
annexin A4	Anxa4	NP_038499	36	18	apical plasma membrane	calcium ion binding, calcium-dependent phospholipid binding	kidney development
carboxylesterase 3	Ces3	NP_444430	62	18	endoplasmic reticulum	carboxylesterase activity, fatty-acyl-ethyl-ester synthase activity, hydrolase activity	acyl-CoA metabolic process, response to toxin
heterogeneous nuclear ribonucleoprotein A3 isoform c	Hnrnpa3	NP_444493	37	18	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
argininosuccinate lyase	Asl	NP_598529	52	18	not classified	argininosuccinate lyase activity, catalytic activity, lyase activity	ammonia assimilation cycle, arginine biosynthetic process, arginine biosynthetic process via ornithine, cellular amino acid biosynthetic process, cellular amino acid metabolic process, locomotory behavior, post-embryonic development, urea cycle
NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	NP_663493	80	18	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	2 iron, 2 sulfur cluster binding, 4 iron, 4 sulfur cluster binding, electron carrier activity, iron ion binding, iron-sulfur cluster binding, metal ion binding, molecular_function, NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on NADH or NADPH	ATP synthesis coupled electron transport, biological_process, electron transport chain, oxidation reduction, transport
mitochondrial trifunctional protein, beta subunit	Hadhb	NP_663533	51	18	mitochondrial inner membrane, mitochondrion	acetyl-CoA C-acyltransferase activity, acyltransferase activity, transferase activity, transferase activity, transferring acyl groups other than amino-acyl groups	fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
myosin heavy chain 10, non-muscle	Myh10	NP_780469	229	18	axon, cell cortex, cell soma, cytoplasm, dendritic spine, growth cone, myosin complex, neuromuscular junction, neuron projection, plasma membrane, spindle, stress fiber	actin binding, actin filament binding, actin-dependent ATPase activity, ADP binding, ATP binding, calmodulin binding, microfilament motor activity, motor activity, nucleotide binding, protein binding	actin cytoskeleton organization, actin filament-based movement, adult heart development, axon guidance, axonogenesis, brain development, cardiac myofibril assembly, cell proliferation, cerebellar Purkinje cell layer development, cytokinesis after mitosis, exocytosis, fourth ventricle development, in utero embryonic development, lateral ventricle development, myofibril assembly, neuromuscular process controlling balance, neuron migration, neuron projection development, nuclear migration, plasma membrane repair, regulation of cell shape, retina development in camera-type eye, substrate-bound cell migration, cell extension, third ventricle development, ventricular cardiac muscle cell development
PREDICTED: similar to vesicle associated protein	Sec31a	XP_912694	144	18	cytoplasm, cytoplasmic vesicle, endoplasmic reticulum, endosome, membrane	not classified	protein transport, transport, vesicle-mediated transport
UbiE-YGHL1 fusion protein	LOC554292	NP_001019843	30	17	not classified	not classified	not classified
ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform a	Atp2a2	NP_001103610	115	17	endoplasmic reticulum, integral to membrane, membrane, membrane fraction, microsome, sarcoplasmic reticulum	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, calcium ion binding, calcium-transporting ATPase activity, catalytic activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, nucleotide binding, protein binding	ATP biosynthetic process, calcium ion transport, cation transport, cellular calcium ion homeostasis, ER-nuclear signaling pathway, ion transport, metabolic process, negative regulation of heart contraction, regulation of muscle contraction, regulation of the force of heart contraction, transport
peroxiredoxin 6	Prdx6	NP_031479	25	17	cytoplasm, cytosol, lysosome	antioxidant activity, catalytic activity, hydrolase activity, oxidoreductase activity, peroxidase activity, peroxiredoxin activity	bleb formation, cell redox homeostasis, lipid catabolic process, oxidation reduction, response to reactive oxygen species
serine (or cysteine) proteinase inhibitor, clade B, member 9	Serpinb9	NP_033282	42	17	not classified	protein binding	anti-apoptosis
ubiquitin-activating enzyme E1	Uba1	NP_033483	118	17	not classified	ATP binding, binding, catalytic activity, ligase activity, nucleotide binding, small protein activating enzyme activity	metabolic process, modification-dependent protein catabolic process, protein modification process
annexin A5	Anxa5	NP_033803	36	17	not classified	calcium ion binding, calcium-dependent phospholipid binding, eukaryotic cell surface binding, protein binding	blood coagulation, negative regulation of coagulation, response to organic substance

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
coatomer protein complex subunit alpha	Copa	NP_034068	139	17	COPI vesicle coat, cytoplasm, cytoplasmic vesicle, extracellular region, extracellular space, Golgi apparatus, membrane, membrane coat, microsome, soluble fraction	hormone activity, protein binding, structural molecule activity	intracellular protein transport, pancreatic juice secretion, protein transport, transport, vesicle-mediated transport
solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	Slc9a3r1	NP_036160	39	17	apical part of cell, apical plasma membrane, membrane	protein binding	cAMP-mediated signaling, cellular phosphate ion homeostasis, Wnt receptor signaling pathway
B-cell receptor-associated protein 37	Phb2	NP_031557	33	16	cytoplasm, membrane, mitochondrial inner membrane, mitochondrion, nucleus	protein binding, receptor activity, specific transcriptional repressor activity	mammary gland alveolus development, mammary gland branching involved in thelarche, negative regulation of estrogen receptor signaling pathway, negative regulation of mammary gland epithelial cell proliferation, regulation of branching involved in mammary gland duct morphogenesis, regulation of transcription, transcription
ribosomal protein SA	Rpsa	NP_035159	33	16	cytoplasm, intracellular, membrane, membrane fraction, nucleus, plasma membrane, ribonucleoprotein complex, ribosome, small ribosomal subunit	laminin binding, receptor activity, structural constituent of ribosome	translation
heterogeneous nuclear ribonucleoprotein U	Hnrnpu	NP_058085	88	16	ribonucleoprotein complex	nucleic acid binding	not classified
keratin 5	Krt5	NP_081287	62	16	intermediate filament, keratin filament	protein binding, structural molecule activity	not classified
actinin, alpha 1	Actn1	NP_598917	103	16	actin cytoskeleton, cortical cytoskeleton, cytoplasm, cytoskeleton, dense core granule membrane, focal adhesion, secretory granule, stress fiber, Z disc	actin binding, actin filament binding, calcium ion binding, protein binding, protein homodimerization activity	actin filament bundle formation, cortical cytoskeleton organization
prominin 2 isoform 1	Prom2	NP_620089	93	16	cell projection, cilium, integral to membrane, membrane, plasma membrane	not classified	not classified
histone cluster 2, H2bb	Hist2h2bb	NP_783597	14	16	chromosome, nucleosome, nucleus	DNA binding	not classified
a disintegrin and metalloprotease domain 7	Adam7	NP_031428	89	15	integral to membrane, membrane, plasma membrane	metalloendopeptidase activity, zinc ion binding	proteolysis
ATPase, H+ transporting, lysosomal V1 subunit A	Atp6v1a	NP_031534	68	15	cytosol, mitochondrion, plasma membrane, proton-transporting two-sector ATPase complex, proton-transporting two-sector ATPase complex, catalytic domain, proton-transporting V-type ATPase, V1 domain	ATP binding, hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, nucleotide binding, proton-transporting ATPase activity, rotational mechanism	ATP metabolic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport
glutathione peroxidase 5	Gpx5	NP_034473	25	15	extracellular region	glutathione peroxidase activity, oxidoreductase activity, peroxidase activity	oxidation reduction, response to oxidative stress

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
lamin B1	Lmnb1	NP_034851	67	15	intermediate filament, lamin filament, membrane, nucleus	structural molecule activity	not classified
ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	Atp5o	NP_613063	23	15	membrane, mitochondrial inner membrane, mitochondrion, plasma membrane, proton-transporting ATP synthase complex, catalytic core F(1)	hydrogen ion transporting ATP synthase activity, rotational mechanism	ATP biosynthetic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport
PREDICTED: similar to aldehyde reductase	LOC100044692	XP_001472913	33	15	not classified	not classified	not classified
aconitase 1	Aco1	NP_031412	98	14	cytoplasm, cytosol, endoplasmic reticulum, Golgi apparatus	4 iron, 4 sulfur cluster binding, aconitate hydratase activity, iron ion binding, iron-responsive element binding, iron-sulfur cluster binding, lyase activity, metal ion binding, RNA binding	cellular iron ion homeostasis, intestinal absorption, metabolic process, post-embryonic development, regulation of gene expression, regulation of translation, tricarboxylic acid cycle
dolichyl-di-phosphooligosaccharide-protein glycotransferase	Ddost	NP_031864	49	14	endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, transferase activity	protein amino acid N-linked glycosylation via asparagine
alpha glucosidase 2 alpha neutral subunit	Ganab	NP_032086	109	14	alpha-glucosidase II complex, endoplasmic reticulum, Golgi apparatus	glucan 1,3-alpha-glucosidase activity, glucosidase activity, hydrolase activity, hydrolase activity, hydrolyzing O-glycosyl compounds, protein binding	carbohydrate metabolic process, N-glycan processing
solute carrier family 16, member 1	Slc16a1	NP_033222	53	14	integral to membrane, membrane, plasma membrane	secondary active monocarboxylate transmembrane transporter activity, symporter activity	organic anion transport, transport
RAN, member RAS oncogene family	Ran	NP_033417	24	14	cytoplasm, nucleus	GTP binding, GTPase activity, nucleotide binding, protein binding	cell cycle, cell division, intracellular protein transport, mitosis, nucleocytoplasmic transport, protein import into nucleus, protein transport, signal transduction, transport
RNA binding motif protein, X-linked	Rbmx	NP_035382	42	14	ribonucleoprotein complex	nucleic acid binding	not classified
ribosomal protein S18	Rps18	NP_035426	18	14	cytoplasm, intracellular, ribonucleoprotein complex, ribosome	RNA binding, rRNA binding, structural constituent of ribosome	translation
tubulin, beta 5	Tubb5	NP_035785	50	14	cytosol, microtubule, protein complex, tubulin complex	GTP binding, GTPase activity, nucleotide binding, structural constituent of cytoskeleton, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization, spindle assembly
peroxiredoxin 5 precursor	Prdx5	NP_036151	22	14	cytoplasm, mitochondrion, peroxisome	antioxidant activity, oxidoreductase activity, peroxidase activity, peroxiredoxin activity	cell redox homeostasis, oxidation reduction
progesterone receptor membrane component	Pgrmc1	NP_058063	22	14	endoplasmic reticulum, integral to membrane, membrane, microsome	heme binding, lipid binding, receptor activity, steroid binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
3-phosphoglycerate dehydrogenase	Phgdh	NP_058662	57	14	not classified	binding, catalytic activity, cofactor binding, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, phosphoglycerate dehydrogenase activity	cell cycle process, cellular amino acid biosynthetic process, gamma-aminobutyric acid metabolic process, glial cell development, glutamine metabolic process, glycine metabolic process, L-serine biosynthetic process, L-serine metabolic process, metabolic process, neural tube development, neurogenesis, neuron projection development, oxidation reduction, regulation of gene expression, spinal cord development, taurine metabolic process, threonine metabolic process
N-acylsphingosine amidohydrolase 1	Asah1	NP_062708	45	14	lysosome	ceramidase activity, hydrolase activity	lipid metabolic process
succinate dehydrogenase Fp subunit	Sdha	NP_075770	73	14	membrane, mitochondrial inner membrane, mitochondrion	electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors, succinate dehydrogenase (ubiquinone) activity	electron transport chain, oxidation reduction, transport, tricarboxylic acid cycle
leucine aminopeptidase 3	Lap3	NP_077754	56	14	cytoplasm, intracellular, mitochondrion	aminopeptidase activity, hydrolase activity, magnesium ion binding, manganese ion binding, metal ion binding, metalloexopeptidase activity, peptidase activity, zinc ion binding	protein metabolic process, proteolysis
diaphorase 1	Cyb5r3	NP_084063	34	14	cytoplasm, endoplasmic reticulum, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion, soluble fraction	cytochrome-b5 reductase activity, electron carrier activity, oxidoreductase activity	cholesterol biosynthetic process, lipid biosynthetic process, oxidation reduction, steroid biosynthetic process, sterol biosynthetic process
ER lipid raft associated 2	Erlin2	NP_705820	38	14	endoplasmic reticulum, integral to membrane, membrane	not classified	not classified
synaptic nuclear envelope 2	Syne2	NP_001005510	783	13	myofibril, nuclear envelope, Z disc	actin binding, molecular_function	establishment or maintenance of cell polarity, fibroblast migration, nuclear envelope organization, protein localization in nucleus
heterogeneous nuclear ribonucleoprotein D isoform b	Hnrnpd	NP_001070734	36	13	chromosome, nucleus, ribonucleoprotein complex	DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding	regulation of mRNA stability, regulation of transcription, transcription
acyl-CoA synthetase long-chain family member 1	Acsl1	NP_032007	78	13	endoplasmic reticulum, integral to membrane, membrane, microsome, mitochondrial outer membrane, mitochondrion, peroxisome	acetate-CoA ligase (ADP-forming) activity, ATP binding, catalytic activity, ligase activity, long-chain-fatty-acid-CoA ligase activity, magnesium ion binding, molecular_function, nucleotide binding	biological_process, fatty acid metabolic process, lipid metabolic process, metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hemoglobin alpha 1 chain	Hba-a1	NP_032244	15	13	hemoglobin complex	heme binding, iron ion binding, metal ion binding, oxygen binding, oxygen transporter activity	erythrocyte development, in utero embryonic development, oxygen transport, transport
AHNAK nucleoprotein isoform 1	Ahnak	NP_033773	604	13	cell-cell junction	not classified	not classified
hexosaminidase B	Hexb	NP_034552	61	13	acrosomal vesicle, lysosome, membrane	beta-N-acetylhexosaminidase activity, catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds, protein heterodimerization activity, protein homodimerization activity	carbohydrate metabolic process, cellular calcium ion homeostasis, cellular protein metabolic process, ganglioside catabolic process, glycosaminoglycan metabolic process, glycosphingolipid metabolic process, lipid storage, locomotory behavior, lysosome organization, male courtship behavior, metabolic process, myelination, neuromuscular process, neuromuscular process controlling balance, oligosaccharide catabolic process, oogenesis, penetration of zona pellucida, phospholipid biosynthetic process, regulation of cellular metabolic process, sensory perception of sound, sexual reproduction, single fertilization, skeletal system development
high mobility group box 1	Hmgb1	NP_034569	25	13	chromosome, cytoplasm, extracellular space, neuron projection, nucleus, soluble fraction	bent DNA binding, calcium-dependent protein kinase regulator activity, crossed form four-way junction DNA binding, cytokine activity, DNA binding, heparin binding, open form four-way junction DNA binding, protein kinase activator activity	DNA geometric change, eye development, induction of positive chemotaxis, lung development, positive regulation of cell migration, positive regulation of gene-specific transcription from RNA polymerase II promoter, positive regulation of glycogen catabolic process, positive regulation of mesenchymal cell proliferation, positive regulation of mitotic cell cycle, positive regulation of myeloid cell differentiation, positive regulation of protein amino acid phosphorylation, response to glucocorticoid stimulus
myosin IB	Myo1b	NP_034993	129	13	myosin complex	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding	not classified
ribosomal protein L6	Rpl6	NP_035420	34	13	cytoplasm, intracellular, nucleolus, nucleus, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
ribosomal protein L7	Rpl7	NP_035421	31	13	cytosolic large ribosomal subunit, intracellular, large ribosomal subunit, ribonucleoprotein complex, ribosome	DNA binding, mRNA binding, protein homodimerization activity, RNA binding, structural constituent of ribosome, transcription regulator activity	translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
sterol carrier protein 2, liver	Scp2	NP_035457	59	13	cytoplasm, mitochondrion, peroxisome	catalytic activity, lipid binding, oxidoreductase activity, propanoyl-CoA C-acyltransferase activity, protein binding, sterol carrier activity, sterol carrier protein X-related thiolase activity, transferase activity, transferase activity, transferring acyl groups other than amino-acyl groups	acyl-CoA metabolic process, lipid transport, metabolic process, peroxisome organization, transport
tryptophanyl-tRNA synthetase	Wars	NP_035840	54	13	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, tryptophan-tRNA ligase activity	translation, tRNA aminoacylation for protein translation, tryptophanyl-tRNA aminoacylation
superoxide dismutase 2, mitochondrial	Sod2	NP_038699	25	13	mitochondrial inner membrane, mitochondrion	manganese ion binding, metal ion binding, oxidoreductase activity, superoxide dismutase activity	age-dependent response to oxidative stress, apoptosis, detection of oxygen, double-strand break repair, erythrophore differentiation, glutathione metabolic process, heart development, hemopoiesis, iron ion homeostasis, liver development, locomotory behavior, mitochondrion organization, negative regulation of apoptosis, negative regulation of fat cell differentiation, negative regulation of fibroblast proliferation, neuron development, oxidation reduction, positive regulation of nitric oxide biosynthetic process, post-embryonic development, regulation of blood pressure, regulation of catalytic activity, regulation of mitochondrial membrane potential, release of cytochrome c from mitochondria, removal of superoxide radicals, respiratory electron transport chain, response to activity, response to axon injury, response to gamma radiation, response to hydrogen peroxide, response to hyperoxia, response to
ribophorin II	Rpn2	NP_062616	69	13	cellular_component, endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane, oligosaccharyltransferase complex	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, molecular_function, transferase activity	biological_process, protein amino acid N-linked glycosylation via asparagine
phosphoglycerate mutase 1	Pgam1	NP_075907	29	13	not classified	2,3-bisphospho-D-glycerate 2-phosphohydrolase activity, bisphosphoglycerate mutase activity, catalytic activity, hydrolase activity, intramolecular transferase activity, phosphotransferases, isomerase activity, phosphoglycerate mutase activity	glycolysis, metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	Sfpq	NP_076092	75	13	cellular_component, nucleus	DNA binding, nucleic acid binding, nucleotide binding, RNA binding	biological_process, DNA repair, mRNA processing, regulation of transcription, response to DNA damage stimulus, RNA splicing, transcription
aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	Akr7a5	NP_079613	41	13	Golgi apparatus, mitochondrion	oxidoreductase activity	oxidation reduction
citrate synthase	Cs	NP_080720	52	13	mitochondrion	citrate (Si)-synthase activity, protein binding, transferase activity, transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	cellular carbohydrate metabolic process, tricarboxylic acid cycle
glutathione S-transferase, mu 7	Gstm7	NP_080948	26	13	cytoplasm	glutathione transferase activity, transferase activity	metabolic process
thioredoxin domain containing 4	Txndc4	NP_083848	47	13	endoplasmic reticulum, endoplasmic reticulum lumen	not classified	cell redox homeostasis, response to unfolded protein
NADH dehydrogenase (ubiquinone) flavoprotein 1	Ndufv1	NP_598427	51	13	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	4 iron, 4 sulfur cluster binding, FMN binding, iron ion binding, iron-sulfur cluster binding, metal ion binding, NAD or NADH binding, NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on NADH or NADPH	electron transport chain, oxidation reduction, transport
high density lipoprotein binding protein	Hdlbp	NP_598569	142	13	cytoplasm, high-density lipoprotein particle, nucleus	RNA binding	cholesterol metabolic process, lipid metabolic process, lipid transport, steroid metabolic process, transport
PREDICTED: hypothetical protein	LOC674419	XP_982574	30	13	not classified	not classified	not classified
aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	NP_031463	54	12	endoplasmic reticulum, integral to membrane, membrane, mitochondrial inner membrane	aldehyde dehydrogenase (NAD) activity, aldehyde dehydrogenase [NAD(P)+] activity, oxidoreductase activity	cellular aldehyde metabolic process, metabolic process, oxidation reduction
carbonyl reductase 1	Cbr1	NP_031646	31	12	cellular_component, cytoplasm	binding, carbonyl reductase (NADPH) activity, catalytic activity, oxidoreductase activity	biological_process, metabolic process, oxidation reduction
protein kinase C substrate 80K-H	Prkcsh	NP_032951	59	12	alpha-glucosidase II complex, endoplasmic reticulum	alpha-glucosidase activity, calcium ion binding, kinase activity, protein binding, RNA binding	N-glycan processing
ribosomal protein L18	Rpl18	NP_033103	22	12	cellular_component, cytoplasm, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
glutathione S-transferase, pi 1	Gstp1	NP_038569	24	12	not classified	glutathione transferase activity, transferase activity	glutathione metabolic process, metabolic process
S-adenosylhomocysteine hydrolase	Ahcy	NP_057870	48	12	cytoplasm, cytosol	adenosylhomocysteinase activity, copper ion binding, hydrolase activity, protein self-association	one-carbon metabolic process, S-adenosylhomocysteine catabolic process
ornithine aminotransferase	Oat	NP_058674	48	12	mitochondrion	catalytic activity, ornithine-oxo-acid transaminase activity, pyridoxal phosphate binding, transaminase activity, transferase activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
RAB11a, member RAS oncogene family	Rab11a	NP_059078	24	12	endosome, membrane, plasma membrane, trans-Golgi network	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
myo-inositol 1-phosphate synthase A1	Isyna1	NP_076116	61	12	cytoplasm	binding, catalytic activity, inositol-3-phosphate synthase activity, isomerase activity	inositol biosynthetic process, metabolic process, phospholipid biosynthetic process
heterogeneous nuclear ribonucleoprotein L	Hnrnpl	NP_796275	60	12	nucleus, pronucleus, ribonucleoprotein complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing
glutathione S-transferase, pi 2	Gstp2	NP_861461	24	12	not classified	glutathione transferase activity, transferase activity	glutathione metabolic process, metabolic process
PREDICTED: similar to desmoplakin	Dsp	XP_001481322	333	12	basolateral plasma membrane, desmosome, mitochondrion	not classified	not classified
PREDICTED: hypothetical protein	LOC640248	XP_922185	22	12	not classified	not classified	not classified
aldo-keto reductase family 1, member C19	Akr1c19	NP_001013807	37	11	cellular_component	molecular_function	biological_process
nucleoside-diphosphate kinase 2	Nme2	NP_001070997	17	11	cytoplasm, membrane, mitochondrion, plasma membrane	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleoside diphosphate kinase activity, nucleotide binding, transferase activity	CTP biosynthetic process, GTP biosynthetic process, nucleotide metabolic process, UTP biosynthetic process
acidic ribosomal phosphoprotein P0	Rplp0	NP_031501	34	11	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	ribosome biogenesis, translational elongation
DEAH (Asp-Glu-Ala-His) box polypeptide 9	Dhx9	NP_031868	150	11	intracellular, nucleolus, nucleus, ribonucleoprotein complex	ATP binding, ATP-dependent helicase activity, DNA binding, double-stranded RNA binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	cellular response to heat
peptidylprolyl isomerase A	Ppia	NP_032933	18	11	cytoplasm, cytosol	isomerase activity, peptide binding, peptidyl-prolyl cis-trans isomerase activity, protein binding	neuron differentiation, protein folding
vinculin	Vcl	NP_033528	117	11	actin cytoskeleton, adherens junction, cell junction, cell-cell junction, costamere, cytoplasm, cytoskeleton, fascia adherens, focal adhesion, membrane, plasma membrane	actin binding, protein binding, structural molecule activity	cell adhesion, lamellipodium assembly, regulation of cell migration
tripeptidyl-peptidase I	Tpp1	NP_034036	61	11	lysosome, mitochondrion	hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	lysosome organization, neuromuscular process controlling balance, proteolysis
heterochromatin protein 1, binding protein 3	Hp1bp3	NP_034600	61	11	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
lamin B2	Lmnb2	NP_034852	67	11	intermediate filament, lamin filament, membrane, nucleus	structural molecule activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
superoxide dismutase 1, soluble	Sod1	NP_035564	16	11	cytoplasm, extracellular space, mitochondrion	antioxidant activity, copper ion binding, metal ion binding, oxidoreductase activity, protein binding, superoxide dismutase activity, zinc ion binding	activation of MAPK activity, aging, auditory receptor cell stereocilium organization, cellular iron ion homeostasis, DNA fragmentation involved in apoptosis, double-strand break repair, embryo implantation, glutathione metabolic process, heart contraction, hydrogen peroxide biosynthetic process, locomotory behavior, muscle homeostasis, myelin maintenance in the peripheral nervous system, myeloid cell homeostasis, negative regulation of apoptosis, negative regulation of neuron apoptosis, neurofilament cytoskeleton organization, ovarian follicle development, oxidation reduction, regulation of blood pressure, regulation of multicellular organism growth, relaxation of vascular smooth muscle, removal of superoxide radicals, response to axon injury, response to drug, response to ethanol, response to heat, response to hydrogen peroxide, response to oxidative stress, response to reactive oxygen
transaldolase 1	Taldo1	NP_035658	37	11	cytoplasm	catalytic activity, transaldolase activity, transferase activity	carbohydrate metabolic process, metabolic process, pentose-phosphate shunt
ubiquitin-activating enzyme E1, Chr Y 1	Ube1y1	NP_035797	118	11	not classified	ATP binding, binding, catalytic activity, ligase activity, nucleotide binding, small protein activating enzyme activity	metabolic process, modification-dependent protein catabolic process, protein modification process
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	Ywhaq	NP_035869	28	11	cellular_component, cytoplasm	monooxygenase activity, protein domain specific binding	protein targeting, signal transduction, small GTPase mediated signal transduction
coatomer protein complex, subunit beta 2 (beta prime)	Copb2	NP_056642	102	11	COPI vesicle coat, cytoplasm, cytoplasmic vesicle, Golgi apparatus, membrane, membrane coat	protein binding, structural molecule activity	intracellular protein transport, protein transport, transport, vesicle-mediated transport
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13	Slc25a13	NP_056644	74	11	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, calcium ion binding, L-glutamate transmembrane transporter activity	aspartate transport, malate-aspartate shuttle, transport
heterogeneous nuclear ribonucleoprotein C	Hnrnpc	NP_058580	34	11	nucleus, pronucleus, ribonucleoprotein complex, spliceosomal complex	mRNA binding, nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
hemoglobin, beta adult minor chain	Hbb-b2	NP_058652	16	11	hemoglobin complex	heme binding, iron ion binding, metal ion binding, oxygen binding, oxygen transporter activity	oxygen transport, transport
acyl-CoA thioesterase 9	Acot9	NP_062710	51	11	mitochondrion	acyl-CoA thioesterase activity, carboxylesterase activity, hydrolase activity, palmitoyl-CoA hydrolase activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
D-lactate dehydrogenase	Ldhd	NP_081846	52	11	mitochondrion	catalytic activity, D-lactate dehydrogenase (cytochrome) activity, D-lactate dehydrogenase activity, FAD binding, oxidoreductase activity, protein binding	ATP biosynthetic process, oxidation reduction
leucine-rich PPR motif-containing protein	Lrpprc	NP_082509	157	11	cytoplasm, membrane, mitochondrion, nucleus	DNA binding, protein binding, RNA binding, single-stranded DNA binding	mRNA transport, regulation of transcription, transcription, transport
FGF receptor activating protein 1	Frag1	NP_663558	29	11	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane, nucleus	protein binding	anti-apoptosis, DNA damage response, signal transduction, GPI anchor biosynthetic process, response to DNA damage stimulus
dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase complex)	Dlat	NP_663589	68	11	mitochondrial pyruvate dehydrogenase complex, mitochondrion, pyruvate dehydrogenase complex	acyltransferase activity, dihydrolipoyllysine-residue acetyltransferase activity, lipoic acid binding, protein binding, transferase activity	acetyl-CoA biosynthetic process from pyruvate, glycolysis, metabolic process, pyruvate metabolic process
adaptor-related protein complex 2, beta 1 subunit isoform a	Ap2b1	NP_001030931	106	10	clathrin adaptor complex, coated pit, membrane, membrane coat, plasma membrane	binding, clathrin binding, protein binding, protein transporter activity	intracellular protein transport, protein transport, vesicle-mediated transport
predicted gene, OTTMUSG00000007855	OTTMUSG00000007855	NP_001074488	15	10	not classified	not classified	not classified
solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4	Slc25a4	NP_031476	33	10	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	binding, transporter activity	transport
ADP-ribosylation factor 5	Arf5	NP_031506	21	10	cytoplasm, Golgi apparatus, intracellular, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
cofilin 1, non-muscle	Cfl1	NP_031713	19	10	cortical actin cytoskeleton, cytoplasm, cytoskeleton, cytosol, extracellular region, intracellular, nucleus	actin binding	actin filament organization, cell motion, cell projection organization, cytokinesis, establishment of cell polarity, negative regulation of cell size, neural crest cell migration, neural fold formation, positive regulation of actin filament depolymerization, protein amino acid phosphorylation, response to amino acid stimulus
cytochrome c oxidase, subunit Va	Cox5a	NP_031773	16	10	membrane, mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity, iron ion binding, metal ion binding	not classified
dihydrolipoamide dehydrogenase	Dld	NP_031887	54	10	acrosomal matrix, cytoplasm, flagellum, mitochondrion	dihydrolipoyl dehydrogenase activity, FAD binding, oxidoreductase activity	cell redox homeostasis, gastrulation, mitochondrial electron transport, NADH to ubiquinone, oxidation reduction, proteolysis, regulation of membrane potential, sperm capacitation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
eukaryotic translation elongation factor 2	Eef2	NP_031933	95	10	cytoplasm, ribonucleoprotein complex	GTP binding, GTPase activity, nucleotide binding, translation elongation factor activity	translation
glutamate dehydrogenase 1	Glud1	NP_032159	61	10	mitochondrial inner membrane, mitochondrion	ATP binding, binding, catalytic activity, glutamate dehydrogenase [NAD(P)+] activity, GTP binding, nucleotide binding, oxidoreductase activity, protein binding	cellular amino acid metabolic process, metabolic process, oxidation reduction, positive regulation of insulin secretion
indolethylamine N-methyltransferase	Inmt	NP_033375	29	10	cytoplasm	amine N-methyltransferase activity, methyltransferase activity, transferase activity	not classified
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	Ywhae	NP_033562	29	10	cytoplasm, mitochondrion	monooxygenase activity, protein binding, protein domain specific binding	cerebral cortex development, hippocampus development, negative regulation of protein amino acid dephosphorylation, neuron migration, protein targeting
filamin, alpha	Flna	NP_034357	281	10	cytoplasm, cytoskeleton, trans-Golgi network	actin binding, protein binding, protein kinase C binding	early endosome to late endosome transport
histone deacetylase 6	Hdac6	NP_034543	126	10	cytoplasm, nucleus	actin binding, histone deacetylase activity, hydrolase activity, metal ion binding, protein binding, zinc ion binding	chromatin modification, negative regulation of microtubule depolymerization, protein amino acid deacetylation, protein polyubiquitination, regulation of transcription, transcription, ubiquitin-dependent protein catabolic process
poly(rC) binding protein 2 isoform 2	Pcbp2	NP_035172	37	10	nucleus, ribonucleoprotein complex	DNA binding, RNA binding	not classified
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Ywhaz	NP_035870	28	10	cytoplasm, mitochondrion, nucleus	protein domain specific binding	protein targeting
aldehyde dehydrogenase family 1, subfamily A7	Aldh1a7	NP_036051	55	10	cellular_component, cytoplasm	aldehyde dehydrogenase (NAD) activity, oxidoreductase activity	metabolic process, oxidation reduction, retinal metabolic process, retinoic acid metabolic process
hexokinase 2	Hk2	NP_038848	103	10	not classified	ATP binding, hexokinase activity, kinase activity, nucleotide binding, phosphotransferase activity, alcohol group as acceptor, transferase activity	carbohydrate metabolic process, carbohydrate phosphorylation, glucose metabolic process, glycolysis
acyl-CoA thioesterase 10	Acot10	NP_073727	51	10	mitochondrion	acyl-CoA thioesterase activity, carboxylesterase activity, hydrolase activity	acyl-CoA metabolic process
abhydrolase domain containing 12	Abhd12	NP_077785	45	10	integral to membrane, membrane	acylglycerol lipase activity, hydrolase activity	not classified
ubiquinol-cytochrome c reductase core protein 1	Uqcrc1	NP_079683	53	10	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	catalytic activity, metal ion binding, metalloendopeptidase activity, zinc ion binding	electron transport chain, mitochondrial electron transport, ubiquinol to cytochrome c, proteolysis, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
myosin, heavy polypeptide 14	Myh14	NP_082297	228	10	axon, cytoplasm, growth cone, myosin complex, stress fiber	actin binding, actin filament binding, actin-dependent ATPase activity, ATP binding, calmodulin binding, microfilament motor activity, motor activity, nucleotide binding	actin filament-based movement, regulation of cell shape
serine hydroxymethyltransferase 2 (mitochondrial)	Shmt2	NP_082506	56	10	mitochondrial inner membrane, mitochondrion	glycine hydroxymethyltransferase activity, methyltransferase activity, transferase activity	one-carbon metabolic process
glutamyl-prolyl-tRNA synthetase	Eprs	NP_084011	170	10	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, catalytic activity, glutamate-tRNA ligase activity, ligase activity, nucleotide binding, proline tRNA ligase activity, RNA binding	glutamyl-tRNA aminoacylation, prolyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
splicing factor 3b, subunit 1	Sf3b1	NP_112456	146	10	nucleus, spliceosomal complex	binding, chromatin binding, protein binding, RNA splicing factor activity, transesterification mechanism	anterior/posterior pattern formation, mRNA processing, nuclear mRNA splicing, via spliceosome, RNA splicing
enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	Echs1	NP_444349	31	10	mitochondrion	catalytic activity, enoyl-CoA hydratase activity, lyase activity	fatty acid metabolic process, lipid metabolic process, metabolic process
plastin 3 precursor	Pls3	NP_663604	71	10	cytoplasm	actin binding, calcium ion binding, molecular_function	biological_process
isocitrate dehydrogenase 2 (NADP+), mitochondrial	Idh2	NP_766599	51	10	mitochondrial inner membrane, mitochondrion	isocitrate dehydrogenase (NADP+) activity, magnesium ion binding, manganese ion binding, metal ion binding, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	glyoxylate cycle, isocitrate metabolic process, oxidation reduction, response to stress, tricarboxylic acid cycle
PREDICTED: similar to Eukaryotic translation elongation factor 2	LOC433776	XP_001475612	46	10	not classified	not classified	not classified
PREDICTED: similar to mKIAA0829 protein isoform 4	Cand1	XP_909201	159	10	nucleus	binding	modification-dependent protein catabolic process, regulation of transcription, transcription
heterogeneous nuclear ribonucleoprotein M isoform b	Hnrnpm	NP_001103383	74	9	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
CD151 antigen	Cd151	NP_001104520	28	9	integral to membrane, membrane	not classified	not classified
cysteine-rich protein 1 (intestinal)	Crip1	NP_031789	9	9	not classified	metal ion binding, zinc ion binding	not classified
cytochrome c, somatic	Cycs	NP_031834	12	9	cytosol, mitochondrion, respiratory chain, soluble fraction	electron carrier activity, heme binding, iron ion binding, metal ion binding	activation of caspase activity by cytochrome c, apoptosis, electron transport chain, hydrogen peroxide metabolic process, positive regulation of apoptosis, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glucose-6-phosphate dehydrogenase X-linked	G6pdx	NP_032088	59	9	not classified	binding, catalytic activity, glucose-6-phosphate dehydrogenase activity, oxidoreductase activity, protein homodimerization activity	angiotensin mediated vasoconstriction involved in regulation of systemic arterial blood pressure, carbohydrate metabolic process, cytokine production, erythrocyte development, glucose metabolic process, glutathione metabolic process, interleukin-10 production, interleukin-12 production, metabolic process, NADP biosynthetic process, oxidation reduction, pentose biosynthetic process, regulation of multicellular organism growth, response to oxidative stress, vasodilation by angiotensin involved in regulation of systemic arterial blood pressure
heat shock protein 4	Hspa4	NP_032326	94	9	cytoplasm	ATP binding, nucleotide binding	response to stress
membrane metallo endopeptidase	Mme	NP_032630	86	9	integral to membrane, membrane, plasma membrane	hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
palmitoyl-protein thioesterase 1	Ppt1	NP_032943	34	9	axon, cell soma, dendrite, extracellular space, lysosome	hydrolase activity, palmitoyl-(protein) hydrolase activity	adult locomotory behavior, associative learning, cellular macromolecule catabolic process, cellular protein catabolic process, grooming behavior, lysosome organization, neurotransmitter secretion, pinocytosis, protein depalmitoylation, protein modification process, receptor-mediated endocytosis, regulation of phospholipase A2 activity, visual perception
prominin 1	Prom1	NP_032961	96	9	apical plasma membrane, brush border, cell projection, cell surface, extracellular space, integral to membrane, integral to plasma membrane, membrane, microvillus, plasma membrane, stereocilium	molecular_function	biological_process
RAB7, member RAS oncogene family	Rab7	NP_033031	23	9	cytoplasmic vesicle, endosome, Golgi apparatus, late endosome, lysosome	GTP binding, nucleotide binding	intracellular protein transport, protein transport, small GTPase mediated signal transduction, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
acetyl-Coenzyme A acetyltransferase 2	Acat2	NP_033364	41	9	cytoplasm	acetyl-CoA C-acetyltransferase activity, acyltransferase activity, catalytic activity, transferase activity, transferase activity, transferring acyl groups other than amino-acyl groups	metabolic process
heterogeneous nuclear ribonucleoprotein A/B isoform 2	Hnrnpab	NP_034578	31	9	cytoplasm, nucleus, ribonucleoprotein complex	DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding, sequence-specific DNA binding, transcription factor activity	epithelial to mesenchymal transition, positive regulation of gene-specific transcription, regulation of transcription, transcription
succinate-Coenzyme A ligase, ADP-forming, beta subunit	Sucla2	NP_035636	50	9	mitochondrion	ATP binding, catalytic activity, ligase activity, nucleotide binding, succinate-CoA ligase (ADP-forming) activity, succinate-CoA ligase activity	metabolic process, tricarboxylic acid cycle
apoptosis-inducing factor, mitochondrion-associated 1	Aifm1	NP_036149	67	9	cytoplasm, cytosol, microsome, mitochondrial intermembrane space, mitochondrial outer membrane, mitochondrion, nucleus, soluble fraction	DNA binding, electron-transferring-flavoprotein dehydrogenase activity, FAD binding, oxidoreductase activity	apoptosis, apoptotic mitochondrial changes, cell redox homeostasis, DNA fragmentation involved in apoptosis, neuron apoptosis, oxidation reduction
aldo-keto reductase family 1, member C13	Akr1c13	NP_038806	37	9	not classified	aldo-keto reductase activity, oxidoreductase activity	oxidation reduction, xenobiotic metabolic process
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Ywhab	NP_061223	28	9	cellular_component, cytoplasm	monooxygenase activity, protein binding, protein domain specific binding	protein targeting
carboxylesterase 1	Ces1	NP_067431	63	9	endoplasmic reticulum	carboxylesterase activity, hydrolase activity	not classified
CNDP dipeptidase 2	Cndp2	NP_075638	53	9	cytosol	carboxypeptidase activity, dipeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, protein dimerization activity, zinc ion binding	proteolysis
chromosome segregation 1-like	Cse1l	NP_076054	110	9	cytoplasm, nucleus	binding, importin-alpha export receptor activity, protein transporter activity	cell proliferation, intracellular protein transport, protein transport, transport
ribosomal protein L4	Rpl4	NP_077174	47	9	intracellular, ribonucleoprotein complex, ribosome	protein binding, structural constituent of ribosome	biological_process, translation
cytochrome b-5	Cyb5	NP_080073	15	9	endoplasmic reticulum, integral to membrane, membrane, microsome, mitochondrion	heme binding, iron ion binding, metal ion binding, stearoyl-CoA 9-desaturase activity	electron transport chain, fatty acid metabolic process, transport
eukaryotic translation elongation factor 1 gamma	Eef1g	NP_080283	50	9	eukaryotic translation elongation factor 1 complex	translation elongation factor activity	translation, translational elongation
acyl-CoA synthetase long-chain family member 5	Acsl5	NP_082252	76	9	endoplasmic reticulum, integral to membrane, membrane, microsome, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion, peroxisome	ATP binding, catalytic activity, ligase activity, long-chain-fatty-acid-CoA ligase activity, magnesium ion binding, molecular_function, nucleotide binding	biological_process, fatty acid metabolic process, lipid metabolic process, metabolic process
phosphoglucomutase 2	Pgm2	NP_082408	62	9	not classified	magnesium ion binding, metal ion binding, phosphoglucomutase activity	glucose metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glutathione S-transferase kappa 1	Gstk1	NP_083831	26	9	mitochondrial inner membrane, mitochondrion, outer membrane-bounded periplasmic space	glutathione peroxidase activity, glutathione transferase activity, protein disulfide oxidoreductase activity, transferase activity	glutathione metabolic process
N-acetylneuraminic acid synthase	Nans	NP_444409	40	9	cytosol	N-acetylneuraminic acid phosphate synthase activity	biological_process
nuclear mitotic apparatus protein 1	Numa1	NP_598708	236	9	nucleus	tubulin binding	not classified
ATPase, H+ transporting, lysosomal V1 subunit B1	Atp6v1b1	NP_598918	57	9	apical plasma membrane, basolateral plasma membrane, membrane fraction	hydrogen ion transmembrane transporter activity	ion transport, proton transport, regulation of pH, sensory perception of sound, transport
pyrroline-5-carboxylate reductase 1	Pycr1	NP_659044	32	9	mitochondrion	binding, catalytic activity, oxidoreductase activity, pyrroline-5-carboxylate reductase activity	cellular amino acid biosynthetic process, metabolic process, oxidation reduction, proline biosynthetic process
epiplakin 1	Eppk1	NP_659097	725	9	cytoplasm, cytoskeleton	not classified	not classified
electron transferring flavoprotein, alpha polypeptide	Etfa	NP_663590	35	9	mitochondrial electron transfer flavoprotein complex, mitochondrion	electron carrier activity, FAD binding	electron transport chain, transport
galactosidase, beta 1-like 2	Glb1l2	NP_722498	74	9	extracellular region	catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds	carbohydrate metabolic process, metabolic process
PREDICTED: similar to S-adenosylhomocysteine hydrolase	LOC677344	XP_001002625	23	9	not classified	not classified	not classified
PREDICTED: similar to Electron transferring flavoprotein, beta polypeptide isoform 2	LOC100045699	XP_001474234	28	9	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L3 isoform 3	LOC100045885	XP_001474762	40	9	not classified	not classified	not classified
PREDICTED: similar to heterogeneous nuclear ribonucleoprotein U-like 2	LOC100046594	XP_001477737	85	9	nucleus	nucleic acid binding, protein binding	not classified
PREDICTED: golgi autoantigen, golgin subfamily b, macrogolgin 1	Golgb1	XP_001481110	369	9	Golgi apparatus	not classified	not classified
alcohol dehydrogenase 5 (class III), chi polypeptide	Adh5	NP_031436	40	8	cytoplasm, mitochondrion	alcohol dehydrogenase (NAD) activity, metal ion binding, oxidoreductase activity, protein homodimerization activity, S-(hydroxymethyl)glutathione dehydrogenase activity, zinc ion binding	ethanol oxidation, formaldehyde catabolic process, oxidation reduction, peptidyl-cysteine S-nitrosylation, positive regulation of blood pressure, respiratory system process, response to lipopolysaccharide, response to nitrosative stress, retinoid metabolic process
ADP-ribosylation factor 3	Arf3	NP_031504	21	8	Golgi apparatus, intracellular	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	Gnb2l1	NP_032169	35	8	cell soma, cytoplasm, membrane, plasma membrane	protein kinase C binding, receptor activity	intracellular signaling cascade, protein localization
kinesin family member 5B	Kif5b	NP_032474	110	8	ciliary rootlet, cytoplasm, cytoskeleton, kinesin complex, membrane-bounded organelle, microtubule, neuron projection	ATP binding, microtubule motor activity, motor activity, nucleotide binding, protein binding	cytoplasm organization, microtubule-based movement, microtubule-based process, mitochondrial transport
cytochrome P450 reductase	Por	NP_032924	77	8	endoplasmic reticulum, membrane, microsome, soluble fraction	electron carrier activity, FMN binding, iron ion binding, NADPH-hemoprotein reductase activity, oxidoreductase activity	oxidation reduction

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
ribosomal protein L13a	Rpl13a	NP_033464	23	8	intracellular, large ribosomal subunit, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
cytochrome c oxidase subunit IV isoform 1	Cox4i1	NP_034071	20	8	membrane, mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity, protein binding	not classified
cytochrome c oxidase, subunit Vb	Cox5b	NP_034072	14	8	membrane, mitochondrial envelope, mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity, metal ion binding, zinc ion binding	not classified
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	Ddx3x	NP_034158	73	8	cytoplasm, nucleus	ATP binding, ATP-dependent helicase activity, DNA binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	not classified
annexin A1	Anxa1	NP_034860	39	8	cell projection, cilium, cytoplasm, membrane, nucleus, plasma membrane, sarcolemma	calcium ion binding, calcium-dependent phospholipid binding, phospholipase A2 inhibitor activity, phospholipase inhibitor activity, protein binding	arachidonic acid secretion, cell cycle, regulation of cell proliferation, signal transduction
NAD(P) dependent steroid dehydrogenase-like	Nsdhl	NP_035071	41	8	integral to membrane, membrane	3-beta-hydroxy-delta5-steroid dehydrogenase activity, binding, catalytic activity, oxidoreductase activity, sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) activity	cholesterol biosynthetic process, cholesterol metabolic process, hair follicle development, labyrinthine layer blood vessel development, lipid biosynthetic process, metabolic process, oxidation reduction, smoothened signaling pathway, steroid biosynthetic process, sterol biosynthetic process
profilin 1	Pfn1	NP_035202	15	8	actin cytoskeleton, cytoplasm, cytoskeleton, cytosol, extracellular region, nucleus	actin binding, protein binding, Rho GTPase binding	actin cytoskeleton organization, cytoskeleton organization, neural tube closure, regulation of actin polymerization or depolymerization, regulation of transcription from RNA polymerase II promoter, sequestering of actin monomers
succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	NP_035637	47	8	mitochondrion	ATP binding, catalytic activity, GTP binding, ligase activity, nucleotide binding, succinate-CoA ligase (GDP-forming) activity, succinate-semialdehyde dehydrogenase activity	metabolic process, tricarboxylic acid cycle

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
peroxiredoxin 2	Prdx2	NP_035693	22	8	cytoplasm	antioxidant activity, oxidoreductase activity, peroxidase activity, peroxiredoxin activity, protein binding, selenium binding, thioredoxin peroxidase activity	activation of MAPK activity, anti-apoptosis, cell redox homeostasis, homeostasis of number of cells, hydrogen peroxide catabolic process, hydrogen peroxide metabolic process, negative regulation of lipopolysaccharide-mediated signaling pathway, negative regulation of NF-kappaB transcription factor activity, negative regulation of oxygen and reactive oxygen species metabolic process, negative regulation of T cell differentiation, oxidation reduction, oxygen and reactive oxygen species metabolic process, regulation of hydrogen peroxide metabolic process, respiratory burst during acute inflammatory response, response to lipopolysaccharide, response to oxidative stress, T cell proliferation, thymus development
alpha isoform of regulatory subunit A, protein phosphatase 2	Ppp2r1a	NP_058587	65	8	cytosol, protein phosphatase type 2A complex	binding, protein binding	not classified
vacuolar protein sorting 35	Vps35	NP_075373	92	8	cytoplasm, integral to membrane, membrane	not classified	protein transport, transport, vacuolar protein processing
DnaJ (Hsp40) homolog, subfamily C, member 10	Dnajc10	NP_077143	91	8	endoplasmic reticulum, extracellular region	heat shock protein binding, unfolded protein binding	cell redox homeostasis, protein folding
source of immunodominant MHC-associated peptides	Stt3b	NP_077184	93	8	cellular_component, endoplasmic reticulum, integral to membrane, membrane, oligosaccharyltransferase complex	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, molecular_function, oligosaccharyl transferase activity, transferase activity	biological_process, protein amino acid glycosylation, protein amino acid N-linked glycosylation via asparagine
cytochrome c oxidase, subunit VIb polypeptide 1	Cox6b1	NP_079904	10	8	mitochondrial inner membrane, mitochondrion	cytochrome-c oxidase activity	not classified
acyl-Coenzyme A dehydrogenase, short/branched chain	Acadsb	NP_080102	48	8	mitochondrion	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors, short-branched-chain-acyl-CoA dehydrogenase activity	fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction
NADH dehydrogenase (ubiquinone) Fe-S protein 3	Ndufs3	NP_080964	30	8	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on NADH or NADPH	biological_process, electron transport chain, oxidation reduction, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
ribosomal protein S27	Rps27	NP_081291	9	8	intracellular, ribonucleoprotein complex, ribosome	metal ion binding, protein binding, structural constituent of ribosome, zinc ion binding	translation
eukaryotic translation initiation factor 4A1	Eif4a1	NP_659207	46	8	not classified	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding, translation initiation factor activity	translation
PREDICTED: similar to hCG1640785	LOC100045659	XP_001474736	12	8	not classified	not classified	not classified
PREDICTED: similar to serine proteinase inhibitor HongrES1	Gm46	XP_001478131	47	8	not classified	not classified	not classified
early endosome antigen 1	Eea1	NP_001001932	161	7	cytoplasm, early endosome, endosome, intracellular, membrane, serine-pyruvate aminotransferase complex	metal ion binding, zinc ion binding	not classified
aminomethyltransferase	Amt	NP_001013836	44	7	cytoplasm, mitochondrion	aminomethyltransferase activity, methyltransferase activity, transaminase activity, transferase activity	glycine catabolic process
NADPH-dependent retinol dehydrogenase/reductase isoform 1	Dhrs4	NP_001033027	30	7	mitochondrion, peroxisome	binding, carbonyl reductase (NADPH) activity, catalytic activity, oxidoreductase activity, retinal dehydrogenase activity	metabolic process, oxidation reduction, retinal metabolic process
ribosomal protein S16-like	LOC100039355	NP_001103687	16	7	not classified	not classified	not classified
vacuolar H+ATPase B2	Atp6v1b2	NP_031535	57	7	cytosol, membrane, plasma membrane, proton-transporting two-sector ATPase complex, proton-transporting two-sector ATPase complex, catalytic domain, proton-transporting V-type ATPase, V1 domain	hydrogen ion transporting ATP synthase activity, rotational mechanism, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, proton-transporting ATPase activity, rotational mechanism	ATP metabolic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport
diaphanous homolog 1	Diap1	NP_031884	139	7	cell projection, cytoplasm, cytoskeleton, membrane, plasma membrane	actin binding, protein binding, Rho GTPase binding	actin cytoskeleton organization, actin filament polymerization, cellular component organization, sensory perception of sound
glutathione S-transferase, mu 6	Gstm6	NP_032210	26	7	cytoplasm	glutathione transferase activity, transferase activity	metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
indoleamine-pyrrole 2,3 dioxygenase	Indo	NP_032350	46	7	cytoplasm	heme binding, indoleamine 2,3-dioxygenase activity, iron ion binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, tryptophan 2,3-dioxygenase activity	behavior, cytokine production during acute inflammatory response, defense response, kynurenic acid biosynthetic process, multicellular organismal response to stress, negative regulation of activated T cell proliferation, negative regulation of interleukin-10 production, negative regulation of T cell apoptosis, negative regulation of T cell proliferation, oxidation reduction, positive regulation of chronic inflammatory response, positive regulation of interleukin-12 production, positive regulation of T cell tolerance induction, positive regulation of T-helper 2 type immune response, response to lipopolysaccharide, tryptophan catabolic process to kynurenine
prohibitin	Phb	NP_032857	30	7	membrane, mitochondrial inner membrane, mitochondrion	not classified	DNA replication
ribosomal protein L12	Rpl12	NP_033102	18	7	cytoplasm, nucleolus, nucleus, ribonucleoprotein complex, ribosome	protein binding, RNA binding, structural constituent of ribosome	biological_process, translation
carbonic anhydrase 2	Car2	NP_033931	29	7	cytoplasm, cytosol	carbonate dehydratase activity, lyase activity, metal ion binding, zinc ion binding	carbon dioxide transport, morphogenesis of an epithelium, one-carbon metabolic process, secretion
creatine kinase, mitochondrial 1, ubiquitous	Ckmt1	NP_034027	47	7	membrane, mitochondrial inner membrane, mitochondrion	ATP binding, catalytic activity, creatine kinase activity, kinase activity, nucleotide binding, transferase activity, transferase activity, transferring phosphorus-containing groups	not classified
fatty acid binding protein 9, testis	Fabp9	NP_035728	15	7	cytoplasm	binding, lipid binding, transporter activity	transport
ribosomal protein S3	Rps3	NP_036182	27	7	cytoplasm, intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, structural constituent of ribosome	translation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hypoxanthine guanine phosphoribosyl transferase 1	Hprt1	NP_038584	25	7	cytoplasm	hypoxanthine phosphoribosyltransferase activity, identical protein binding, magnesium ion binding, metal ion binding, transferase activity, transferase activity, transferring glycosyl groups	adenine metabolic process, adenine salvage, behavior, central nervous system neuron development, cerebral cortex neuron differentiation, cytolysis, dendrite morphogenesis, dopamine metabolic process, grooming behavior, guanine salvage, hypoxanthine metabolic process, lymphocyte proliferation, nucleoside metabolic process, positive regulation of dopamine metabolic process, purine ribonucleoside salvage, response to amphetamine, striatum development
hydroxyacyl-Coenzyme A dehydrogenase type II	Hsd17b10	NP_058043	27	7	endoplasmic reticulum, mitochondrial inner membrane, mitochondrion	3-hydroxy-2-methylbutyryl-CoA dehydrogenase activity, 3-hydroxyacyl-CoA dehydrogenase activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction, tRNA processing
DnaJ (Hsp40) homolog, subfamily C, member 5	Dnajc5	NP_058055	22	7	membrane	heat shock protein binding, unfolded protein binding	negative regulation of neuron apoptosis, protein folding
coatomer protein complex, subunit gamma isoform 1	Copg	NP_059505	98	7	COPI vesicle coat, cytoplasm, cytoplasmic vesicle, Golgi apparatus, Golgi-associated vesicle, membrane, membrane coat	binding, protein binding, structural molecule activity	intracellular protein transport, protein transport, transport, vesicle-mediated transport
histone cluster 1, H1b	Hist1h1b	NP_064418	23	7	chromosome, nucleosome, nucleus	DNA binding, protein binding	muscle organ development, nucleosome assembly
adenylate kinase 3	Ak3	NP_067274	25	7	mitochondrion	adenylate kinase activity, ATP binding, GTP binding, kinase activity, nucleobase, nucleoside, nucleotide kinase activity, nucleoside triphosphate adenylate kinase activity, nucleotide binding, nucleotide kinase activity, phosphotransferase activity, phosphate group as acceptor, transferase activity	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
aspartyl beta-hydroxylase isoform 1	Asph	NP_075553	83	7	endoplasmic reticulum, integral to endoplasmic reticulum membrane, integral to membrane, membrane	binding, iron ion binding, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, peptide-aspartate beta-dioxygenase activity	face morphogenesis, limb morphogenesis, negative regulation of cell proliferation, oxidation reduction, palate development, pattern specification process, peptidyl-amino acid modification, peptidyl-aspartic acid hydroxylation
eukaryotic translation elongation factor 1 delta isoform b	Eef1d	NP_075729	31	7	eukaryotic translation elongation factor 1 complex	translation elongation factor activity	translation, translational elongation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	Mccc1	NP_076133	79	7	mitochondrial inner membrane, mitochondrion	ATP binding, biotin binding, catalytic activity, ligase activity, methylcrotonoyl-CoA carboxylase activity, nucleotide binding	metabolic process
solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	Slc25a11	NP_077173	34	7	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, transporter activity	transport
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	Ndufa9	NP_079634	43	7	mitochondrial inner membrane, mitochondrion, respiratory chain	binding, catalytic activity, coenzyme binding	cellular metabolic process, electron transport chain, metabolic process, transport
signal peptidase complex subunit 2 homolog	Spcs2	NP_079944	25	7	endoplasmic reticulum, integral to membrane, membrane, microsome, signal peptidase complex	hydrolase activity, peptidase activity	signal peptide processing
N-ethylmaleimide sensitive fusion protein attachment protein alpha	Napa	NP_080174	33	7	endoplasmic reticulum, Golgi apparatus, membrane, synaptobrevin 2-SNAP-25-syntaxin-1a complex	binding, SNARE binding, syntaxin binding	apical protein localization, brain development, intracellular protein transport, neuron differentiation, protein transport, transport, vesicle-mediated transport
endoplasmic reticulum protein ERp29 precursor	Erp29	NP_080405	29	7	endoplasmic reticulum, endoplasmic reticulum lumen	not classified	protein secretion
endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	Ergic1	NP_080446	33	7	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane	not classified	transport, vesicle-mediated transport
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	Ndufa8	NP_080979	20	7	mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a	NP_083849	40	7	mitochondrion	isocitrate dehydrogenase (NAD+) activity, magnesium ion binding, manganese ion binding, metal ion binding, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	oxidation reduction, tricarboxylic acid cycle
LPS-responsive beige-like anchor isoform alpha	Lrba	NP_109620	317	7	cytoplasmic membrane-bounded vesicle	protein kinase A binding	endosome transport, protein localization, signal transduction
coatomer protein complex, subunit beta 1	Copb1	NP_203534	107	7	COPI vesicle coat, cytoplasm, cytoplasmic vesicle, Golgi apparatus, membrane, membrane coat	binding, protein binding, structural molecule activity	intracellular protein transport, protein transport, transport, vesicle-mediated transport
MOCO sulphurase C-terminal domain containing 2	Mosc2	NP_598445	38	7	membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	catalytic activity, molybdenum ion binding, oxidoreductase activity, pyridoxal phosphate binding	oxidation reduction
archain 1	Arcn1	NP_666097	57	7	cellular_component, clathrin adaptor complex, cytoplasm, cytoplasmic vesicle, Golgi apparatus, membrane	molecular_function, protein binding	biological_process, intracellular protein transport, protein transport, transport, vesicle-mediated transport
lysophospholipase-like 1	Lyplal1	NP_666218	26	7	cytoplasm	hydrolase activity	not classified
eukaryotic translation initiation factor 3, subunit C	Eif3c	NP_666312	106	7	cytoplasm, eukaryotic translation initiation factor 3 complex	ribosome binding, translation initiation factor activity	translation, translational initiation

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NADH dehydrogenase (ubiquinone) Fe-S protein 2	Ndufs2	NP_694704	53	7	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	4 iron, 4 sulfur cluster binding, electron carrier activity, iron ion binding, iron-sulfur cluster binding, metal ion binding, NAD or NADH binding, NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on NADH or NADPH, quinone binding	biological_process, electron transport chain, oxidation reduction, transport
cytochrome P450, family 4, subfamily a family	Cyp4a12b	NP_758510	58	7	not classified	iron ion binding, metal ion binding, monooxygenase activity, oxidoreductase activity	oxidation reduction
hypothetical protein LOC109154	2410014A08 Rik	NP_780612	32	7	endoplasmic reticulum, integral to membrane, membrane	not classified	carbohydrate metabolic process
ATPase, Na+/K+ transporting, alpha 2 polypeptide	Atp1a2	NP_848492	112	7	integral to membrane, membrane, microsome, sarcolemma	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, monovalent inorganic cation transmembrane transporter activity, nucleotide binding, potassium ion binding, protein binding, sodium ion binding, sodium:potassium-exchanging ATPase activity	adult locomotory behavior, ATP biosynthetic process, cation transport, ion transport, locomotion, metabolic process, monovalent inorganic cation transport, negative regulation of heart contraction, negative regulation of striated muscle contraction, neurotransmitter uptake, potassium ion transport, reduction of cytosolic calcium ion concentration, regulation of blood pressure, regulation of muscle contraction, regulation of respiratory gaseous exchange by neurological system process, regulation of smooth muscle contraction, regulation of striated muscle contraction, regulation of the force of heart contraction, regulation of vasoconstriction, sodium ion transport, transport, visual learning
transgelin 2	Tagln2	NP_848713	22	7	not classified	not classified	muscle organ development
DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	Ddx39	NP_932099	49	7	nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding	mRNA processing, RNA splicing
unc-13 homolog D	Unc13d	NP_001009573	123	6	cytoplasm, endosome, lysosome, membrane	protein binding	defense response to virus, exocytosis, germinal center formation, granuloma formation, natural killer cell degranulation, phagocytosis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
peroxiredoxin 3	Prdx3	NP_031478	28	6	mitochondrion	antioxidant activity, identical protein binding, oxidoreductase activity, peroxidase activity, peroxiredoxin activity	cell redox homeostasis, hydrogen peroxide catabolic process, maternal placenta development, myeloid cell differentiation, oxidation reduction, response to lipopolysaccharide, response to oxidative stress
vacuolar H+ ATPase E1	Atp6v1e1	NP_031536	26	6	apical plasma membrane, cytoplasm, cytosol, endosome, mitochondrion, proton-transporting two-sector ATPase complex, catalytic domain	hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrolase activity, proton-transporting ATPase activity, rotational mechanism	ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport, ion transport, proton transport, transport
glutathione peroxidase 4 isoform 2 precursor	Gpx4	NP_032188	22	6	cytoplasm, cytosol, mitochondrial inner membrane, mitochondrion, nuclear envelope, nucleus	glutathione peroxidase activity, oxidoreductase activity, peroxidase activity, phospholipid-hydroperoxide glutathione peroxidase activity, selenium binding	chromatin organization, multicellular organismal development, oxidation reduction, response to oxidative stress, spermatogenesis
heat-responsive protein 12	Hrsp12	NP_032313	14	6	not classified	endonuclease activity, hydrolase activity, nuclease activity	not classified
hydroxysteroid (17-beta) dehydrogenase 4	Hsd17b4	NP_032318	79	6	mitochondrion, peroxisome	3alpha,7alpha,12alpha-trihydroxy-5beta-cholest-24-enoyl-CoA hydratase activity, 3-hydroxyacyl-CoA dehydrogenase activity, binding, catalytic activity, isomerase activity, lyase activity, oxidoreductase activity, sterol carrier activity	fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction, Sertoli cell development, very-long-chain fatty acid metabolic process
poly A binding protein, cytoplasmic 1	Pabpc1	NP_032800	71	6	cytoplasm, nucleus, spliceosomal complex	nucleic acid binding, nucleotide binding, poly(A) RNA binding, RNA binding	mRNA processing, RNA splicing
SEC23A	Sec23a	NP_033173	86	6	COPII vesicle coat, endoplasmic reticulum, Golgi apparatus, Golgi membrane, membrane, perinuclear region of cytoplasm	protein binding, zinc ion binding	ER to Golgi vesicle-mediated transport, intracellular protein transport, protein transport, transport, vesicle-mediated transport
transglutaminase 2, C polypeptide	Tgm2	NP_033399	77	6	cytoplasm, cytosol, membrane, proteinaceous extracellular matrix	acyltransferase activity, calcium ion binding, GTP binding, metal ion binding, protein-glutamine gamma-glutamyltransferase activity, transferase activity	activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger, branching involved in salivary gland morphogenesis, G-protein coupled receptor protein signaling pathway, peptide cross-linking, positive regulation of cell adhesion, salivary gland cavitation
ubiquitin specific protease 9, X chromosome	Usp9x	NP_033507	290	6	cytoplasm	cysteine-type peptidase activity, hydrolase activity, peptidase activity, protein binding, ubiquitin thiolesterase activity	cell cycle, cell division, chromosome segregation, mitosis, modification-dependent protein catabolic process, ubiquitin-dependent protein catabolic process
cysteine-rich secretory protein 1	Crisp1	NP_033768	28	6	extracellular region	not classified	not classified

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adaptor protein complex AP-1, gamma 1 subunit	Ap1g1	NP_033807	92	6	clathrin adaptor complex, clathrin-coated vesicle, cytoplasmic vesicle, Golgi apparatus, Golgi apparatus part, membrane, membrane coat, perinuclear region of cytoplasm, trans-Golgi network	binding, protein binding, protein transporter activity	endocytosis, intracellular protein transport, protein transport, transport, vesicle-mediated transport
catenin alpha 1	Ctnna1	NP_033948	100	6	actin cytoskeleton, adherens junction, cell junction, cytoplasm, cytoskeleton, lamellipodium, membrane, plasma membrane, zonula adherens	actin filament binding, cadherin binding, protein binding, structural molecule activity	apical junction assembly, cell adhesion, establishment or maintenance of cell polarity, negative regulation of apoptosis, negative regulation of neuroblast proliferation, positive regulation of smoothened signaling pathway, regulation of cell proliferation
chaperonin subunit 8 (theta)	Cct8	NP_033970	60	6	cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
CD2-associated protein	Cd2ap	NP_033977	70	6	cell cortex, cell projection, cytoplasm, cytoskeleton	protein binding, SH3 domain binding	biological_process, cell cycle, cell division, mitosis
dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase)	Dci	NP_034153	32	6	mitochondrial inner membrane, mitochondrion	catalytic activity, dodecenoyl-CoA delta-isomerase activity, isomerase activity	fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, metabolic process
fumarate hydratase 1	Fh1	NP_034339	54	6	cytoplasm, mitochondrion, tricarboxylic acid cycle enzyme complex	catalytic activity, fumarate hydratase activity, lyase activity	fumarate metabolic process, homeostasis of number of cells within a tissue, tricarboxylic acid cycle
t-complex protein 10b	Tcp10b	NP_035683	49	6	not classified	not classified	not classified
nuclease sensitive element binding protein 1	Ybx1	NP_035862	36	6	cytoplasm, nucleus	DNA binding, nucleic acid binding, protein binding, RNA binding, single-stranded DNA binding	in utero embryonic development, mRNA processing, regulation of transcription, regulation of transcription, DNA-dependent, RNA splicing, transcription
poly(rC) binding protein 1	Pcbp1	NP_035995	37	6	nucleus, ribonucleoprotein complex	DNA binding, protein binding, RNA binding, translation activator activity	mRNA processing
myosin, heavy polypeptide 11, smooth muscle	Myh11	NP_038635	223	6	cytoplasm, muscle myosin complex, myosin complex, myosin filament, smooth muscle contractile fiber, stress fiber	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding	smooth muscle contraction
inositol (myo)-1(or 4)-monophosphatase 1	Impa1	NP_061352	30	6	cellular_component, cytoplasm	hydrolase activity, inositol or phosphatidylinositol phosphatase activity, inositol-1(or 4)-monophosphatase activity, lithium ion binding, magnesium ion binding, metal ion binding	inositol metabolic process
cleft lip and palate associated transmembrane protein 1	Clptm1	NP_062623	75	6	external side of plasma membrane, integral to membrane, membrane	not classified	cell differentiation, multicellular organismal development, regulation of T cell differentiation in the thymus
sorting nexin 1	Snx1	NP_062701	59	6	endosome, Golgi apparatus, membrane	phosphoinositide binding, protein binding, protein transporter activity	cell communication, intracellular protein transport, protein transport, transport

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succinate-CoA ligase, GDP-forming, alpha subunit	Suclg1	NP_063932	35	6	mitochondrial inner membrane, mitochondrion	ATP citrate synthase activity, binding, catalytic activity, GTP binding, ligase activity, nucleotide binding, succinate-CoA ligase (ADP-forming) activity, succinate-CoA ligase (GDP-forming) activity	metabolic process, tricarboxylic acid cycle
actinin alpha 4	Actn4	NP_068695	105	6	cortical cytoskeleton, cytoplasm, pseudopodium, stress fiber	actin binding, actin filament binding, calcium ion binding, protein homodimerization activity	actin filament bundle formation, negative regulation of cell motion, positive regulation of cell motion, positive regulation of pinocytosis, protein transport, transport
prostaglandin E synthase	Ptges	NP_071860	17	6	cytoplasm, integral to membrane, membrane, microsome, nuclear envelope lumen, nucleus	isomerase activity, prostaglandin-D synthase activity, prostaglandin-E synthase activity	negative regulation of cell proliferation, prostaglandin metabolic process
ribosomal protein S19	Rps19	NP_075622	16	6	intracellular, nucleolus, ribonucleoprotein complex, ribosome	protein binding, structural constituent of ribosome	translation
L-specific multifunctional beta-oxdiation protein	Ehhadh	NP_076226	78	6	mitochondrion, peroxisome	3-hydroxyacyl-CoA dehydrogenase activity, binding, catalytic activity, coenzyme binding, dodecenoyl-CoA delta-isomerase activity, enoyl-CoA hydratase activity, isomerase activity, lyase activity, oxidoreductase activity	acyl-CoA metabolic process, fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	Ndufa10	NP_077159	41	6	mitochondrion, respiratory chain	ATP binding, phosphotransferase activity, alcohol group as acceptor	electron transport chain, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, transport
pyruvate dehydrogenase (lipoamide) beta	Pdhb	NP_077183	39	6	mitochondrion	catalytic activity, oxidoreductase activity, pyruvate dehydrogenase (acetyl-transferring) activity	glycolysis, metabolic process, oxidation reduction
transmembrane emp24 domain containing 3	Tmed3	NP_079636	25	6	Golgi apparatus, integral to membrane, membrane	not classified	protein transport, transport
electron transferring flavoprotein, dehydrogenase	Etfdh	NP_080070	68	6	integral to membrane, membrane, mitochondrial electron transfer flavoprotein complex, mitochondrial inner membrane, mitochondrion	4 iron, 4 sulfur cluster binding, electron-transferring-flavoprotein dehydrogenase activity, iron ion binding, iron-sulfur cluster binding, metal ion binding, molecular_function, oxidoreductase activity	biological_process, electron transport chain, oxidation reduction, response to oxidative stress, transport
ribosomal protein L14	Rpl14	NP_080250	24	6	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)	Bphl	NP_080788	33	6	cytoplasm, mitochondrion	hydrolase activity	not classified
RAB14, member RAS oncogene family	Rab14	NP_080973	24	6	membrane, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
methyltransferase like 7A1	Mettl7a1	NP_081610	28	6	not classified	methyltransferase activity, transferase activity	not classified

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
protease, serine, 15	Lonp1	NP_083058	106	6	mitochondrion	ATP binding, ATPase activity, ATP-dependent peptidase activity, DNA binding, hydrolase activity, mitochondrial light strand promoter anti-sense binding, nucleoside-triphosphatase activity, nucleotide binding, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity, single-stranded DNA binding	ATP catabolic process, proteolysis
SAC1 (supressor of actin mutations 1, homolog)-like	Sacm1l	NP_109617	67	6	cellular_component, endoplasmic reticulum, integral to membrane, membrane	hydrolase activity, molecular_function	biological_process
chloride intracellular channel 1	Clic1	NP_254279	27	6	chloride channel complex, cytoplasm, integral to membrane, membrane, nuclear envelope, nucleus, plasma membrane	chloride channel activity, chloride ion binding, ion channel activity, protein binding, voltage-gated chloride channel activity, voltage-gated ion channel activity	chloride transport, ion transport, transport
pyrroline-5-carboxylate reductase family, member 2	Pycr2	NP_598466	34	6	not classified	binding, catalytic activity, oxidoreductase activity, pyrroline-5-carboxylate reductase activity	cellular amino acid biosynthetic process, metabolic process, oxidation reduction, proline biosynthetic process
Rho GDP dissociation inhibitor (GDI) alpha	Arhgdia	NP_598557	23	6	cytoplasm, immunological synapse	GTPase activator activity, protein binding, Rho GDP-dissociation inhibitor activity	regulation of protein localization, Rho protein signal transduction
ATPase, H+ transporting, lysosomal V1 subunit H	Atp6v1h	NP_598587	56	6	vacuolar proton-transporting V-type ATPase, V1 domain	binding, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, proton-transporting ATPase activity, rotational mechanism	ATP synthesis coupled proton transport, ion transport, proton transport, transport
glutathione S-transferase, theta 3	Gstt3	NP_598755	27	6	cellular_component	glutathione transferase activity, transferase activity	glutathione metabolic process
CDGSH iron sulfur domain 1	Cisd1	NP_598768	12	6	integral to membrane, intracellular membrane-bounded organelle, membrane, mitochondrial outer membrane, mitochondrion	2 iron, 2 sulfur cluster binding, iron ion binding, iron-sulfur cluster binding, metal ion binding	regulation of cellular respiration
ATP citrate lyase	Acly	NP_598798	120	6	cytoplasm, intracellular	ATP binding, ATP citrate synthase activity, binding, catalytic activity, lyase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein binding, succinate-CoA ligase (ADP-forming) activity, transferase activity, transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	acetyl-CoA biosynthetic process, cellular carbohydrate metabolic process, lipid biosynthetic process, metabolic process
proteasome 26S non-ATPase subunit 2	Psmd2	NP_598862	100	6	proteasome complex	enzyme regulator activity	regulation of protein catabolic process
es1 protein	D10Jhu81e	NP_613067	28	6	centriole, mitochondrion	molecular_function	biological_process
solute carrier organic anion transporter family, member 4a1	Slco4a1	NP_683735	78	6	integral to membrane, integral to plasma membrane, membrane	organic anion transmembrane transporter activity, transporter activity	ion transport, organic anion transport, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
sulfite oxidase	Suox	NP_776094	61	6	mitochondrion	electron carrier activity, heme binding, iron ion binding, metal ion binding, molybdenum ion binding, oxidoreductase activity, sulfite oxidase activity	oxidation reduction
PREDICTED: hypothetical protein	LOC433745	XP_001476854	21	6	not classified	not classified	not classified
PREDICTED: similar to Tubulin, beta 4	LOC100042651	XP_001479082	50	6	not classified	not classified	not classified
PREDICTED: similar to ubiquitin A-52 residue ribosomal protein fusion product 1 isoform 2	LOC629750	XP_899768	15	6	not classified	not classified	not classified
ubiquitin specific protease 14 isoform 2	Usp14	NP_001033678	52	5	soluble fraction, synaptosome	cysteine-type peptidase activity, hydrolase activity, peptidase activity, ubiquitin thiolesterase activity	modification-dependent protein catabolic process, synaptic transmission, ubiquitin-dependent protein catabolic process
WAP four-disulfide core domain 15	Wfdc15b	NP_001039019	9	5	extracellular region	peptidase inhibitor activity	defense response to bacterium
phosphogluconate dehydrogenase	Pgd	NP_001074743	53	5	not classified	binding, catalytic activity, coenzyme binding, NADP or NADPH binding, oxidoreductase activity, phosphogluconate 2-dehydrogenase activity, phosphogluconate dehydrogenase (decarboxylating) activity	metabolic process, oxidation reduction, pentose biosynthetic process, pentose-phosphate shunt
predicted gene, OTTMUSG00000002778	OTTMUSG00000002778	NP_001104805	12	5	not classified	not classified	not classified
alcohol dehydrogenase 1 (class I)	Adh1	NP_031435	40	5	cytoplasm, intracellular, mitochondrion	alcohol dehydrogenase (NAD) activity, metal ion binding, oxidoreductase activity, protein homodimerization activity, zinc ion binding	behavioral response to ethanol, ethanol catabolic process, oxidation reduction, response to retinoic acid, response to steroid hormone stimulus, response to testosterone stimulus, retinoic acid metabolic process, retinoid metabolic process, retinol metabolic process
chaperonin containing Tcp1, subunit 7 (eta)	Cct7	NP_031664	60	5	chaperonin-containing T-complex, cytoplasm	ATP binding, identical protein binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
cathepsin B preproprotein	Ctsb	NP_031824	37	5	lysosome, mitochondrion	cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	proteolysis, regulation of catalytic activity
glioblastoma amplified	Gbas	NP_032121	33	5	mitochondrion	molecular_function	biological_process
guanosine diphosphate (GDP) dissociation inhibitor 2	Gdi2	NP_032138	51	5	cytoplasm, Golgi apparatus, membrane	GTPase activator activity, Rab GDP-dissociation inhibitor activity, Rab GTPase activator activity	protein transport, regulation of GTPase activity, small GTPase mediated signal transduction
glucose phosphate isomerase 1	Gpi1	NP_032181	63	5	cytoplasm, extracellular region, extracellular space	cytokine activity, glucose-6-phosphate isomerase activity, growth factor activity, isomerase activity, protein binding	angiogenesis, gluconeogenesis, glucose metabolic process, glycolysis
L-3-hydroxyacyl-Coenzyme A dehydrogenase	Hadh	NP_032238	34	5	mitochondrial inner membrane, mitochondrion	3-hydroxyacyl-CoA dehydrogenase activity, binding, catalytic activity, coenzyme binding, oxidoreductase activity	fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction

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heat shock protein 1 (chaperonin 10)	Hspe1	NP_032329	11	5	cytoplasm, mitochondrion	ATP binding	protein folding, response to stress
CUB and zona pellucida-like domains 1	Cuzd1	NP_032437	68	5	cytoplasmic vesicle, integral to membrane, membrane, zymogen granule, zymogen granule membrane	protein binding	cell adhesion, cell cycle, cell division
kinectin 1	Ktn1	NP_032503	153	5	endoplasmic reticulum, integral to membrane, membrane	kinesin binding	microtubule-based movement
pyruvate dehydrogenase E1 alpha 1	Pdha1	NP_032836	43	5	intracellular membrane-bounded organelle, mitochondrion	oxidoreductase activity, oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, pyruvate dehydrogenase (acetyl-transferring) activity, pyruvate dehydrogenase activity	glycolysis, metabolic process, oxidation reduction
purine rich element binding protein A	Pura	NP_033015	35	5	cytoplasm, nucleus	DNA binding, double-stranded DNA binding, protein binding, SMAD binding, transcription factor activity	negative regulation of transcription, DNA-dependent, nervous system development, positive regulation of cell proliferation, regulation of transcription, transcription
ribosomal protein L22	Rpl22	NP_033105	15	5	cytoplasm, intracellular, ribonucleoprotein complex, ribosome	heparin binding, RNA binding, structural constituent of ribosome	alpha-beta T cell differentiation, translation
ribosomal protein S5	Rps5	NP_033121	23	5	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	structural constituent of ribosome	translation
adaptor protein complex AP-1, mu 2 subunit isoform 2	Ap1m2	NP_033808	48	5	clathrin adaptor complex, cytoplasmic vesicle, Golgi apparatus, membrane, trans-Golgi network	protein binding	intracellular protein transport, protein transport, transport, vesicle-mediated transport
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	Atp5f1	NP_033855	29	5	membrane, mitochondrial inner membrane, mitochondrial proton-transporting ATP synthase complex, coupling factor F(o), mitochondrion, proton-transporting ATP synthase complex, coupling factor F(o)	hydrogen ion transmembrane transporter activity	ATP synthesis coupled proton transport, ion transport, proton transport, transport
chaperonin containing Tcp1, subunit 3 (gamma)	Cct3	NP_033966	61	5	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
carnitine palmitoyltransferase 2	Cpt2	NP_034079	74	5	membrane, mitochondrial inner membrane, mitochondrion	acyltransferase activity, carnitine O-palmitoyltransferase activity, transferase activity	fatty acid metabolic process, lipid metabolic process, transport
glutathione S-transferase, alpha 4	Gsta4	NP_034487	26	5	cellular_component, cytoplasm	glutathione transferase activity, transferase activity	metabolic process
keratin complex 2, basic, gene 6b	Krt6b	NP_034799	60	5	intermediate filament, keratin filament	structural molecule activity	intermediate filament organization, keratinization, morphogenesis of an epithelium
lysosomal membrane glycoprotein 1	Lamp1	NP_034814	44	5	endosome, external side of plasma membrane, integral to membrane, late endosome, lysosome, melanosome, membrane, multivesicular body, plasma membrane, sarcolemma	protein binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
mannosidase 2, alpha B1	Man2b1	NP_034894	115	5	lysosome	alpha-mannosidase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds, mannosidase activity, metal ion binding, zinc ion binding	carbohydrate metabolic process, learning or memory, mannose metabolic process, metabolic process
myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	Myl6	NP_034990	17	5	myosin complex, unconventional myosin complex	calcium ion binding, motor activity, structural constituent of muscle	muscle filament sliding, skeletal muscle tissue development
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	Ndufa2	NP_035015	11	5	membrane, mitochondrial inner membrane, mitochondrial respiratory chain complex I, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity	electron transport chain, transport
ErbB3-binding protein 1	Pa2g4	NP_035249	44	5	cytoplasm, nucleus, ribonucleoprotein complex	DNA binding, protein binding, RNA binding, transcription factor activity	cellular process, negative regulation of transcription, DNA-dependent, regulation of transcription, regulation of translation, rRNA processing, transcription
prosaposin	Psap	NP_035309	61	5	extracellular region, lysosome, mitochondrion	not classified	developmental growth, epithelial cell differentiation involved in prostate gland development, lipid metabolic process, prostate gland growth, regulation of MAPKKK cascade, sphingolipid metabolic process
serine (or cysteine) proteinase inhibitor, clade B, member 6b	Serpinb6b	NP_035584	43	5	not classified	not classified	not classified
vimentin	Vim	NP_035831	54	5	cell leading edge, cytoplasm, cytoskeleton, intermediate filament, type III intermediate filament	protein binding, structural molecule activity	intermediate filament-based process
stress-induced phosphoprotein 1	Stip1	NP_058017	63	5	cytoplasm, nucleus	binding	not classified
ribosomal protein L13	Rpl13	NP_058018	24	5	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
nucleobindin 2 isoform 2	Nucb2	NP_058053	50	5	cytoplasm, endoplasmic reticulum, nuclear outer membrane, nucleus	calcium ion binding, DNA binding	cellular calcium ion homeostasis
esterase D/formylglutathione hydrolase	Esd	NP_058599	31	5	cytoplasm, cytoplasmic membrane-bounded vesicle, cytoplasmic vesicle	carboxylesterase activity, hydrolase activity, hydrolase activity, acting on ester bonds, S-formylglutathione hydrolase activity	not classified
stratifin	Sfn	NP_061224	28	5	cytoplasm, extracellular region, nucleus	protein domain specific binding	keratinocyte differentiation, keratinocyte proliferation, negative regulation of cell proliferation, positive regulation of cell growth, regulation of cell cycle, regulation of cyclin-dependent protein kinase activity, skin development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hydroxysteroid (17-beta) dehydrogenase 12 protein	Hsd17b12	NP_062631	35	5	endoplasmic reticulum, extracellular matrix, integral to membrane, membrane	binding, catalytic activity, collagen binding, estradiol 17-beta-dehydrogenase activity, fibronectin binding, heparin binding, oxidoreductase activity	extracellular matrix organization, lipid biosynthetic process, metabolic process, oxidation reduction, positive regulation of cell-substrate adhesion, steroid biosynthetic process
leucine zipper-EF-hand containing transmembrane protein 1	Letm1	NP_062668	83	5	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	calcium ion binding	not classified
isovaleryl coenzyme A dehydrogenase	Ivd	NP_062800	46	5	mitochondrion	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, isovaleryl-CoA dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	metabolic process, oxidation reduction
heterogeneous nuclear ribonucleoprotein H2	Hnrnph2	NP_063921	49	5	nucleus, ribonucleoprotein complex	molecular_function, nucleic acid binding, nucleotide binding, RNA binding	biological_process
keratin 71	Krt71	NP_064340	57	5	intermediate filament, keratin filament	structural constituent of cytoskeleton, structural molecule activity	cytoskeleton organization, hair follicle morphogenesis
ribosomal protein S14	Rps14	NP_065625	16	5	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
poly(rC) binding protein 3	Pcbp3	NP_067543	36	5	cytoplasm, ribonucleoprotein complex	DNA binding, RNA binding	not classified
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	Ndufa13	NP_075801	17	5	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, nucleus, respiratory chain	ATP binding	apoptosis, electron transport chain, transport
lectin, mannose-binding 2	Lman2	NP_080104	40	5	Golgi apparatus, integral to membrane, membrane	calcium ion binding, sugar binding	protein transport, transport
acyl-Coenzyme A dehydrogenase family, member 8	Acad8	NP_080138	45	5	mitochondrion	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	branched chain family amino acid catabolic process, metabolic process, oxidation reduction
RAB5A, member RAS oncogene family	Rab5a	NP_080163	24	5	early endosome, endocytic vesicle, endosome, membrane, membrane raft, plasma membrane, ruffle	GTP binding, GTPase activity, guanyl nucleotide binding, nucleotide binding	endocytosis, protein transport, small GTPase mediated signal transduction, transport
ribosomal protein L11	Rpl11	NP_080195	20	5	cellular_component, intracellular, ribonucleoprotein complex, ribosome	protein binding, RNA binding, rRNA binding, structural constituent of ribosome	biological_process, translation
ribosomal protein, large P2	Rplp2	NP_080296	12	5	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translational elongation
2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	NP_080448	36	5	mitochondrion	2,4-dienoyl-CoA reductase (NADPH) activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
transmembrane emp24 protein transport domain containing 9	Tmed9	NP_080487	27	5	endoplasmic reticulum, integral to membrane, membrane	not classified	transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
transmembrane emp24 domain-containing protein 10	Tmed10	NP_081051	25	5	cis-Golgi network, Golgi apparatus, integral to membrane, membrane, zymogen granule membrane	not classified	intracellular protein transport, protein transport, regulated secretory pathway, transport, vesicle targeting, to, from or within Golgi, vesicle-mediated transport
dehydrogenase/reductase (SDR family) member 1	Dhrs1	NP_081095	34	5	mitochondrial inner membrane	binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
chloride intracellular channel 3	Clic3	NP_081361	27	5	chloride channel complex, cytoplasm, integral to membrane, membrane, nucleus	chloride channel activity, chloride ion binding, ion channel activity, voltage-gated chloride channel activity, voltage-gated ion channel activity	chloride transport, ion transport, transport
AFG3(ATPase family gene 3)-like 2	Afg3l2	NP_081406	90	5	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	ATP binding, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, nucleoside-triphosphatase activity, nucleotide binding, peptidase activity, zinc ion binding	axonogenesis, death, muscle fiber development, myelination, nerve development, neuromuscular junction development, protein catabolic process, proteolysis, regulation of multicellular organism growth, righting reflex
annexin A13	Anxa13	NP_081487	36	5	membrane, plasma membrane	calcium ion binding, calcium-dependent phospholipid binding	not classified
brain abundant, membrane attached signal protein 1	Basp1	NP_081671	22	5	cell projection, membrane, plasma membrane	not classified	not classified
RIKEN cDNA 2310001A20	2310001A20 Rik	NP_082253	46	5	integral to membrane, membrane	strictosidine synthase activity	biosynthetic process
sideroflexin 3	Sfxn3	NP_444427	35	5	integral to membrane, membrane, mitochondrion	cation transmembrane transporter activity, iron ion binding	cation transport, ion transport, iron ion transport, transport
transmembrane 9 superfamily member 2	Tm9sf2	NP_542123	75	5	endosome, integral to membrane, membrane	not classified	not classified
transmembrane 9 superfamily protein member 4	Tm9sf4	NP_598608	75	5	integral to membrane, membrane	not classified	not classified
D6Wsu176e protein	D6Wsu176e	NP_613053	25	5	extracellular region	not classified	not classified
eukaryotic translation termination factor 1	Etf1	NP_659115	49	5	cellular_component, cytoplasm	translation release factor activity, translation release factor activity, codon specific	protein amino acid methylation, translation, translational termination
apolipoprotein A-I binding protein	Apoa1bp	NP_659146	31	5	cellular_component, extracellular region	protein binding	biological_process
eukaryotic translation initiation factor 3 subunit 6 interacting protein	Eif3eip	NP_660121	67	5	cytoplasm, eukaryotic translation initiation factor 3 complex, fibrillar center, nucleolus, nucleoplasm	protein binding, translation initiation factor activity	translation, translational initiation
3-hydroxyisobutyrate dehydrogenase precursor	Hibadh	NP_663542	35	5	mitochondrion	3-hydroxyisobutyrate dehydrogenase activity, binding, catalytic activity, coenzyme binding, NAD or NADH binding, oxidoreductase activity, phosphogluconate dehydrogenase (decarboxylating) activity	metabolic process, oxidation reduction, pentose-phosphate shunt, valine metabolic process
Rho GTPase activating protein 1	Arhgap1	NP_666236	50	5	cell leading edge, cytoplasm, intracellular, plasma membrane, ruffle	GTPase activator activity, protein binding, Rac GTPase activator activity, Rho GTPase activator activity, SH3 domain binding	regulation of GTPase activity, signal transduction, small GTPase mediated signal transduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
aspartyl-tRNA synthetase	Dars	NP_803228	57	5	cytoplasm	aminoacyl-tRNA ligase activity, aspartate-tRNA ligase activity, ATP binding, ligase activity, nucleic acid binding, nucleotide binding	aspartyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
cytochrome c oxidase subunit II	COX2	NP_904331	26	5	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	copper ion binding, cytochrome-c oxidase activity, electron carrier activity, metal ion binding, oxidoreductase activity	electron transport chain, oxidation reduction, transport
PREDICTED: similar to AFG3(ATPase family gene 3)-like 2 (yeast)	LOC100048880	XP_001472434	33	5	not classified	not classified	not classified
PREDICTED: similar to Protein disulfide isomerase associated 6	LOC100046302	XP_001476035	43	5	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100047156	XP_001477347	24	5	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100042503	XP_001478493	15	5	not classified	not classified	not classified
PREDICTED: similar to GPI inositol-deacylase	D230012E17Rik	XP_912118	105	5	endoplasmic reticulum, integral to membrane, intrinsic to endoplasmic reticulum membrane, membrane	hydrolase activity, hydrolase activity, acting on ester bonds	anterior/posterior axis specification, embryonic pattern specification, forebrain regionalization, GPI anchor metabolic process, head development, intracellular protein transport, protein transport, sensory perception of sound, transport
reticulon 3 isoform 1	Rtn3	NP_001003934	104	4	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane	molecular_function, protein binding	apoptosis, transport, vesicle-mediated transport
hypothetical protein LOC102502	AI427122	NP_001028382	70	4	cytoplasm	actin binding, calcium ion binding, molecular_function	biological_process
adenylate kinase 2 isoform a	Ak2	NP_001029138	26	4	mitochondrial inner membrane, mitochondrion	adenylate kinase activity, ATP binding, kinase activity, nucleobase, nucleoside, nucleotide kinase activity, nucleotide binding, nucleotide kinase activity, phosphotransferase activity, phosphate group as acceptor, transferase activity	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
hypothetical protein LOC381062 isoform 1	2210404J11Rik	NP_001034641	70	4	not classified	not classified	not classified
hypothetical protein LOC68646 isoform 2	1110020G09Rik	NP_001035485	48	4	mitochondrion	NAD+ kinase activity	metabolic process
myosin IC isoform b	Myo1c	NP_001074243	118	4	brush border, cell projection, cytoplasm, membrane, myosin complex, myosin I complex, nuclear pore, nucleus, plasma membrane, stereocilium	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding, phospholipid binding, protein binding, protein C-terminus binding	mRNA transport, protein transport, transmembrane transport, transport
predicted gene, EG668668	EG668668	NP_001074505	30	4	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
methyl CpG binding protein 2 isoform 1	Mecp2	NP_001075448	54	4	cytoplasm, cytosol, heterochromatin, nucleus	DNA binding, double-stranded methylated DNA binding, methyl-CpG binding, mRNA binding, siRNA binding, transcription factor activity, transcription factor binding, transcription repressor activity	adult locomotory behavior, behavioral fear response, biogenic amine metabolic process, brain development, cardiolipin metabolic process, catecholamine secretion, cerebellum development, chromatin silencing, dendrite development, embryonic development, genetic imprinting, glucocorticoid metabolic process, glutamine metabolic process, histone acetylation, histone methylation, inositol metabolic process, learning, long-term memory, long-term synaptic potentiation, memory, mitochondrial electron transport, ubiquinol to cytochrome c, negative regulation of histone acetylation, negative regulation of histone methylation, negative regulation of neuron apoptosis, negative regulation of transcription, negative regulation of transcription, DNA-dependent, neurological system process involved in regulation of systemic arterial blood pressure, neuromuscular process, neuromuscular process
radixin isoform a	Rdx	NP_001098086	69	4	apical part of cell, cytoplasm, cytoskeleton, extrinsic to membrane, filopodium, lamellipodium, membrane, microvillus, plasma membrane, ruffle, stereocilium	actin binding, binding, cytoskeletal protein binding, protein binding	actin filament capping, apical protein localization, microvillus assembly
annexin A6 isoform b	Anxa6	NP_001103681	75	4	cytoplasm, perinuclear region of cytoplasm	calcium ion binding, calcium-dependent phospholipid binding	calcium ion transport, regulation of muscle contraction
ribosomal protein L27-like	EG621100	NP_001103809	16	4	not classified	not classified	not classified
predicted gene, ENSMUSG00000059775	ENSMUSG00000059775	NP_001104770	13	4	not classified	not classified	not classified
similar to Tu translation elongation factor, mitochondrial	LOC100041265	NP_001104813	50	4	not classified	not classified	not classified
defender against cell death 1	Dad1	NP_001106829	12	4	integral to membrane, membrane	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, transferase activity	anti-apoptosis, apoptosis, blastocyst development
adaptor protein complex AP-2, alpha 2 subunit	Ap2a2	NP_031485	104	4	clathrin adaptor complex, coated pit, membrane, membrane coat, plasma membrane, secretory granule	binding, lipid binding, protein binding, protein transporter activity	endocytosis, intracellular protein transport, protein transport, transport, vesicle-mediated transport
ADP-ribosylation factor 4	Arf4	NP_031505	20	4	cytoplasm, Golgi apparatus, intracellular, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
heterogeneous nuclear ribonucleoprotein D isoform c	Hnrnpd	NP_031542	33	4	chromosome, nucleus, ribonucleoprotein complex	DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding	regulation of mRNA stability, regulation of transcription, transcription
CAP, adenylate cyclase-associated protein 1	Cap1	NP_031624	52	4	cortical actin cytoskeleton, cytoplasm, membrane, plasma membrane	actin binding, binding	actin cytoskeleton organization, ameboidal cell migration, cell morphogenesis, cytoskeleton organization, receptor-mediated endocytosis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
gelsolin-like capping protein	Capg	NP_031625	39	4	cytoplasm, extracellular region, nucleus	actin binding	actin filament capping, cell projection assembly
chaperonin containing Tcp1, subunit 5 (epsilon)	Cct5	NP_031663	60	4	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
cold inducible RNA binding protein	Cirbp	NP_031731	19	4	nucleus	nucleic acid binding, nucleotide binding, RNA binding	response to stress
dynactin 1	Dctn1	NP_031861	142	4	cell leading edge, cytoplasm, cytoskeleton, dynein complex, microtubule	motor activity, protein binding	not classified
histidine triad nucleotide binding protein 1	Hint1	NP_032274	14	4	cytoplasm, nucleus	hydrolase activity	not classified
leukotriene A4 hydrolase	Lta4h	NP_032543	69	4	cytoplasm	catalytic activity, hydrolase activity, leukotriene-A4 hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	leukotriene biosynthetic process, proteolysis
phosphoglycerate kinase 1	Pgk1	NP_032854	45	4	cytoplasm	ATP binding, kinase activity, nucleotide binding, phosphoglycerate kinase activity, transferase activity	glycolysis
lysophospholipase 1	Lypla1	NP_032892	25	4	cytoplasm, mitochondrion	hydrolase activity	fatty acid metabolic process, lipid metabolic process
prostaglandin H2 D-isomerase	Ptgds	NP_032989	21	4	cytoplasm, endoplasmic reticulum, extracellular region, Golgi apparatus, membrane, nucleus	binding, isomerase activity, prostaglandin-D synthase activity, transporter activity	fatty acid biosynthetic process, lipid biosynthetic process, lipid metabolic process, prostaglandin biosynthetic process, regulation of circadian sleep/wake cycle, sleep, transport
prostaglandin-endoperoxide synthase 1	Ptgs1	NP_032995	69	4	cytoplasm, endoplasmic reticulum, membrane, microsome, nucleus	heme binding, iron ion binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, peroxidase activity, prostaglandin-endoperoxide synthase activity	fatty acid biosynthetic process, lipid biosynthetic process, oxidation reduction, prostaglandin biosynthetic process, prostaglandin metabolic process, regulation of blood pressure, regulation of cell proliferation, response to oxidative stress
RAB1, member RAS oncogene family	Rab1	NP_033022	23	4	endoplasmic reticulum, Golgi apparatus	GTP binding, nucleotide binding	ER to Golgi vesicle-mediated transport, intracellular protein transport, protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
RAS-related C3 botulinum substrate 1	Rac1	NP_033033	21	4	cell projection, cytoplasm, cytoplasmic membrane-bounded vesicle, extrinsic to plasma membrane, intracellular, lamellipodium, membrane, membrane fraction, plasma membrane	GTP binding, GTPase activity, nucleotide binding, protein binding	axon guidance, cell adhesion, cell migration, cerebral cortex radially oriented cell migration, cytoskeleton organization, dendrite development, embryonic olfactory bulb interneuron precursor migration, endocytosis, hyperosmotic response, lamellipodium assembly, positive regulation of actin filament polymerization, positive regulation of lamellipodium assembly, positive regulation of phosphoinositide 3-kinase activity, regulation of cell migration, ruffle organization, small GTPase mediated signal transduction
retinoblastoma binding protein 7	Rbbp7	NP_033057	48	4	nucleus, NuRD complex	protein binding, transcription repressor activity	chromatin modification, chromatin remodeling, DNA replication, negative regulation of transcription from RNA polymerase II promoter, regulation of transcription, transcription
reticulocalbin 1	Rcn1	NP_033063	38	4	endoplasmic reticulum	calcium ion binding	not classified
SAR1a gene homolog	Sar1a	NP_033146	22	4	endoplasmic reticulum, Golgi apparatus, intracellular, sarcoplasmic reticulum	GTP binding, nucleotide binding	intracellular protein transport, protein transport, transport, vesicle-mediated transport
signal sequence receptor, delta	Ssr4	NP_033305	19	4	endoplasmic reticulum, integral to membrane, membrane	receptor activity	not classified
topoisomerase (DNA) I	Top1	NP_033434	91	4	chromosome, cytoplasm, nucleus, perikaryon	ATP binding, DNA binding, DNA topoisomerase (ATP-hydrolyzing) activity, DNA topoisomerase activity, DNA topoisomerase type I activity, isomerase activity, nucleotide binding	DNA replication, DNA topological change, embryonic cleavage
aldo-keto reductase family 1, member B3 (aldose reductase)	Akr1b3	NP_033788	36	4	cytoplasm	aldehyde reductase activity, oxidoreductase activity	oxidation reduction
cathepsin D	Ctsd	NP_034113	45	4	lysosome, mitochondrion	aspartic-type endopeptidase activity, hydrolase activity, peptidase activity	autophagic vacuole formation, proteolysis
glutamate oxaloacetate transaminase 1, soluble	Got1	NP_034454	46	4	cytoplasm, cytosol	catalytic activity, L-aspartate:2-oxoglutarate aminotransferase activity, phosphatidylserine decarboxylase activity, pyridoxal phosphate binding, transaminase activity, transferase activity, transferase activity, transferring nitrogenous groups	aspartate biosynthetic process, biosynthetic process, cellular amino acid metabolic process, fatty acid homeostasis, glutamate catabolic process to 2-oxoglutarate, glutamate catabolic process to aspartate, glycerol biosynthetic process, oxaloacetate metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glutathione reductase 1 precursor	Gsr	NP_034474	54	4	cytoplasm, external side of plasma membrane, mitochondrion	FAD binding, glutathione-disulfide reductase activity, NADP or NADPH binding, oxidoreductase activity	cell redox homeostasis, glutathione metabolic process, oxidation reduction
junction plakoglobin	Jup	NP_034723	82	4	cell junction, cell-cell adherens junction, cell-cell junction, cytoplasm, cytoskeleton, cytosol, desmosome, membrane, Z disc	binding, protein binding, RPTP-like protein binding	cell adhesion
lysosomal membrane glycoprotein 2 isoform 2	Lamp2	NP_034815	46	4	endosome, integral to membrane, late endosome, lysosomal membrane, lysosome, membrane, membrane fraction, phagocytic vesicle membrane, plasma membrane, platelet dense granule membrane	not classified	not classified
programmed cell death 6 interacting protein	Pdcd6ip	NP_035182	96	4	cytoplasm, cytosol	protein binding	apoptosis, cell cycle, cell division, protein transport, transport
proline dehydrogenase	Prodh	NP_035302	68	4	mitochondrial inner membrane, mitochondrion	oxidoreductase activity, proline dehydrogenase activity	glutamate biosynthetic process, oxidation reduction, proline catabolic process, proline metabolic process
prostaglandin-endoperoxide synthase 2	Ptgs2	NP_035328	69	4	cytoplasm, endoplasmic reticulum, membrane, microsome, nucleus	heme binding, iron ion binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, peroxidase activity, prostaglandin-endoperoxide synthase activity	anagen, bone mineralization, fatty acid biosynthetic process, lipid biosynthetic process, oxidation reduction, prostaglandin biosynthetic process, regulation of blood pressure, regulation of cell proliferation, response to oxidative stress
proteasome 26S non-ATPase subunit 13	Psmd13	NP_036005	43	4	proteasome complex, proteasome regulatory particle	endopeptidase activity	meiosis I
H2A histone family, member Y	H2afy	NP_036145	40	4	Barr body, centrosome, chromosome, condensed chromosome, nucleosome, nucleus	chromatin binding, DNA binding	chromatin modification, dosage compensation, nucleosome assembly
vesicle amine transport protein 1 homolog (T californica)	Vat1	NP_036167	43	4	not classified	binding, catalytic activity, oxidoreductase activity, zinc ion binding	metabolic process, oxidation reduction
low density lipoprotein receptor-related protein associated protein 1	Lrpap1	NP_038615	42	4	cytoplasm, endoplasmic reticulum, plasma membrane	heparin binding, low-density lipoprotein receptor binding, receptor activity	not classified
vesicle-associated membrane protein, associated protein A	Vapa	NP_038961	28	4	endoplasmic reticulum, integral to membrane, membrane, microtubule, plasma membrane	molecular_function, structural molecule activity	biological_process
RAB10, member RAS oncogene family	Rab10	NP_057885	23	4	Golgi apparatus, membrane, plasma membrane	GTP binding, nucleotide binding, protein binding	intracellular protein transport, protein transport, small GTPase mediated signal transduction, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
acyl-Coenzyme A dehydrogenase, very long chain	Acadvl	NP_059062	71	4	membrane, mitochondrial inner membrane, mitochondrion	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction
caseinolytic protease, ATP-dependent, proteolytic subunit homolog	Clpp	NP_059089	30	4	mitochondrion	ATP binding, hydrolase activity, nucleotide binding, peptidase activity, protein binding, serine-type endopeptidase activity, serine-type peptidase activity	misfolded or incompletely synthesized protein catabolic process, proteolysis
USO1 homolog, vesicle docking protein	Uso1	NP_062363	107	4	cytoplasm, cytosol, Golgi apparatus, Golgi membrane, membrane, microsome, perinuclear region of cytoplasm	binding, protein binding, protein transporter activity	intracellular protein transport, protein transport, transport, vesicle fusion with Golgi apparatus, vesicle-mediated transport
SMC1 structural maintenance of chromosomes 1-like 1	Smc1a	NP_062684	143	4	chromosome, nucleus	ATP binding, nucleotide binding, protein binding	cell cycle, cell division, chromosome organization, DNA repair, meiosis, mitosis, response to DNA damage stimulus
proteolipid protein 2	Plp2	NP_062729	17	4	integral to membrane, membrane	not classified	not classified
mitochondrial carrier homolog 2	Mtch2	NP_062732	33	4	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	transport
destrin	Dstn	NP_062745	19	4	cortical actin cytoskeleton, cytoplasm, intracellular	actin binding	cell motion, cytokinesis, positive regulation of actin filament depolymerization
microsomal glutathione S-transferase 1	Mgst1	NP_064330	18	4	endoplasmic reticulum, membrane, microsome, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	glutathione transferase activity, transferase activity	glutathione metabolic process
Sec11-like 1	Sec11a	NP_064335	21	4	endoplasmic reticulum, integral to membrane, membrane, microsome	hydrolase activity, peptidase activity, serine-type peptidase activity	proteolysis, signal peptide processing
dihydroorotate dehydrogenase	Dhodh	NP_064430	43	4	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	catalytic activity, dihydroorotate dehydrogenase activity, dihydroorotate oxidase activity, oxidoreductase activity	'de novo' pyrimidine base biosynthetic process, metabolic process, oxidation reduction, pyrimidine nucleotide biosynthetic process, UMP biosynthetic process
RAB2A, member RAS oncogene family	Rab2a	NP_067493	24	4	endoplasmic reticulum, Golgi apparatus, membrane	GTP binding, nucleotide binding	intracellular protein transport, protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
ARP3 actin-related protein 3 homolog	Actr3	NP_076224	47	4	cell projection, cytoplasm, cytoskeleton, lamellipodium	actin binding, ATP binding, nucleotide binding, protein binding	regulation of actin filament polymerization
hydroxysteroid dehydrogenase like 2	Hsdl2	NP_077217	54	4	mitochondrion	binding, catalytic activity, oxidoreductase activity, sterol carrier activity	metabolic process, oxidation reduction
glyoxalase 1	Glo1	NP_079650	21	4	not classified	lactoylglutathione lyase activity, lyase activity, metal ion binding, zinc ion binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
hypothetical protein LOC66302	2410005O16 Rik	NP_079752	35	4	cytoplasm, microtubule	binding	not classified
cytochrome c-1	Cyc1	NP_079843	35	4	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	electron carrier activity, heme binding, iron ion binding, metal ion binding	electron transport chain, transport
ribosomal protein L15	Rpl15	NP_079862	24	4	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
nipsnap homolog 3A	Nipsnap3a	NP_079899	28	4	cytoplasm, mitochondrion	not classified	not classified
ribosomal protein S13	Rps13	NP_080809	17	4	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	Ndufa5	NP_080890	13	4	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	oxidoreductase activity, acting on NADH or NADPH	electron transport chain, respiratory electron transport chain, transport
6.8 kDa mitochondrial proteolipid	2010107E04 Rik	NP_081636	7	4	mitochondrion	not classified	not classified
brain protein 44	Brp44	NP_081706	14	4	mitochondrion	not classified	not classified
arginine-rich, mutated in early stage tumors	Armet	NP_083379	20	4	extracellular region	growth factor activity	response to unfolded protein
abhydrolase domain containing 14b	Abhd14b	NP_083907	22	4	cytoplasm, nucleus	hydrolase activity	not classified
ribosomal protein S9-like	Rps9	NP_084043	23	4	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, rRNA binding, structural constituent of ribosome	translation
keratin 82	Krt82	NP_444479	57	4	intermediate filament, keratin filament	structural molecule activity	not classified
ATPase, H+ transporting, lysosomal V0 subunit A isoform 4	Atp6v0a4	NP_536715	96	4	apical part of cell, apical plasma membrane, brush border, endosome, integral to membrane, membrane, plasma membrane, proton-transporting two-sector ATPase complex, proton-transporting domain, vacuolar proton-transporting V-type ATPase complex	hydrogen ion transmembrane transporter activity, hydrogen-exporting ATPase activity, phosphorylative mechanism	ATP hydrolysis coupled proton transport, ATP synthesis coupled proton transport, ion transport, proton transport, transport
acetyl-CoA synthetase 2-like	Acss1	NP_542142	75	4	mitochondrial matrix, mitochondrion	acetate-CoA ligase activity, AMP binding, ATP binding, catalytic activity, ligase activity, nucleotide binding	acetyl-CoA biosynthetic process, metabolic process
U5 snRNP-associated 102 kDa protein	Prpf6	NP_598462	107	4	intracellular, nucleus, spliceosomal complex	androgen receptor binding, binding, transcription coactivator activity	mRNA processing, nuclear mRNA splicing, via spliceosome, positive regulation of transcription from RNA polymerase II promoter, RNA processing, RNA splicing
eukaryotic translation initiation factor 3, subunit 9	Eif3b	NP_598677	91	4	cytoplasm	nucleic acid binding, nucleotide binding, RNA binding, translation initiation factor activity	translation, translational initiation
farnesyl diphosphate synthetase	Fdps	NP_608219	41	4	cytoplasm	dimethylallyltranstransferase activity, geranyltranstransferase activity, transferase activity	cholesterol biosynthetic process, isoprenoid biosynthetic process, lipid biosynthetic process, steroid biosynthetic process, sterol biosynthetic process
protein phosphatase 2A, regulatory subunit B (PR 53)	Ppp2r4	NP_620087	37	4	not classified	phosphatase activator activity	not classified
heterogeneous nuclear ribonucleoprotein L-like	Hnrpll	NP_659051	64	4	nucleus, ribonucleoprotein complex	nucleic acid binding, nucleotide binding, oxidoreductase activity, peroxidase activity, RNA binding, selenium binding	mRNA processing, oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
propionyl-Coenzyme A carboxylase, alpha polypeptide	Pcca	NP_659093	80	4	mitochondrion	ATP binding, biotin binding, catalytic activity, ligase activity, nucleotide binding, propionyl-CoA carboxylase activity	metabolic process
RAS-related protein-1a	Rap1a	NP_663516	21	4	guanyl-nucleotide exchange factor complex, intracellular, membrane, plasma membrane	GTP binding, GTPase activity, nucleotide binding, protein binding, Ras GTPase binding	small GTPase mediated signal transduction
serine proteinase inhibitor member 6C	Serpinb6c	NP_683744	43	4	not classified	not classified	not classified
dynamin 1-like isoform a	Dnm1l	NP_690029	80	4	cytoplasm, membrane	GTP binding, GTPase activity, hydrolase activity, nucleotide binding	not classified
torsin A interacting protein 2	Tor1aip2	NP_766431	54	4	endoplasmic reticulum	protein binding	not classified
choline dehydrogenase	Chdh	NP_780552	66	4	mitochondrial inner membrane, mitochondrion	choline dehydrogenase activity, FAD binding, molecular_function, oxidoreductase activity, oxidoreductase activity, acting on CH-OH group of donors	alcohol metabolic process, biological_process, glycine betaine biosynthetic process from choline, oxidation reduction
bleomycin hydrolase	Blmh	NP_848760	53	4	cytoplasm, soluble fraction	cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	proteolysis, response to drug, response to toxin
ATP synthase F0 subunit 8	ATP8	NP_904332	8	4	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L28	LOC100039731	XP_001473974	16	4	not classified	not classified	not classified
PREDICTED: progesterone receptor membrane component 2 isoform 1	Pgrmc2	XP_130859	23	4	cellular_component, integral to membrane, membrane	heme binding, lipid binding, protein binding, receptor activity, steroid binding	biological_process
PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	EG433184	XP_484732	36	4	not classified	not classified	not classified
PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	LOC675851	XP_990709	14	4	not classified	not classified	not classified
TAR DNA binding protein isoform 5	Tardbp	NP_001003898	34	3	nucleus	DNA binding, nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, regulation of transcription, RNA splicing, transcription
BCL2-associated transcription factor 1 isoform 3	Bclaf1	NP_001020564	100	3	cytoplasm, nucleus	DNA binding, protein binding, transcription repressor activity	negative regulation of transcription, positive regulation of apoptosis, regulation of transcription, transcription
tetratricopeptide repeat domain 38	Ttc38	NP_001028509	52	3	not classified	binding	not classified
hypothetical protein LOC237880	1700071K01Rik	NP_001028937	29	3	not classified	not classified	not classified
heterogeneous nuclear ribonucleoprotein A1 isoform b	Hnrnpa1	NP_001034218	39	3	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding	alternative nuclear mRNA splicing, via spliceosome, mRNA processing, mRNA transport, RNA splicing, transport
zinc finger homeobox 2	Zfhx2	NP_001034287	273	3	cellular_component, nucleus	DNA binding, metal ion binding, molecular_function, zinc ion binding	biological_process
dynamin 2	Dnm2	NP_001034609	98	3	cell junction, cytoplasm, cytoskeleton, membrane, microtubule, plasma membrane, postsynaptic membrane, synapse	GTP binding, GTPase activity, hydrolase activity, motor activity, nucleotide binding, protein binding	endocytosis
lipocalin 5 isoform b	Lcn5	NP_001036095	20	3	extracellular region, extracellular space	binding, retinoid binding, transporter activity	lipid metabolic process, retinoic acid metabolic process, transport

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lysocardiolipin acyltransferase	Lycat	NP_001074540	44	3	endoplasmic reticulum, integral to membrane, membrane	1-acylglycerol-3-phosphate O-acyltransferase activity, acyltransferase activity, transferase activity	metabolic process, multicellular organismal development, phospholipid biosynthetic process
oxoglutarate dehydrogenase-like	Ogdhl	NP_001074599	117	3	not classified	not classified	not classified
myosin IA	Myo1a	NP_001074688	119	3	apical plasma membrane, basal plasma membrane, brush border, lateral plasma membrane, microvillus, myosin complex	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding	cell projection organization, microvillus assembly
transmembrane protein 103	Tmem103	NP_001074850	29	3	cellular_component	molecular_function	biological_process
small nuclear ribonucleoprotein N	Snrpn	NP_001076431	25	3	nucleus, ribonucleoprotein complex	nucleic acid binding, RNA binding	not classified
Bcl-2 inhibitor of transcription isoform b	Ptrh2	NP_001092280	20	3	mitochondrion	aminoacyl-tRNA hydrolase activity, hydrolase activity	translation
adducin 1 (alpha) isoform 3	Add1	NP_001095914	73	3	cytoplasm, cytoskeleton, membrane, plasma membrane	actin binding, calmodulin binding, metal ion binding, structural molecule activity	cell morphogenesis, cell volume homeostasis, erythrocyte differentiation, hemoglobin metabolic process, homeostasis of number of cells within a tissue, in utero embryonic development, multicellular organism growth
transcription factor E3 isoform b	Tcfe3	NP_001098666	58	3	nucleus, transcription factor complex	DNA binding, promoter binding, protein heterodimerization activity, transcription factor activity, transcription regulator activity	humoral immune response, immune response, positive regulation of gene-specific transcription from RNA polymerase II promoter, positive regulation of transcription, DNA-dependent, regulation of osteoclast differentiation, regulation of transcription, transcription
Sjogren syndrome antigen B	Ssb	NP_001103615	48	3	nucleus, ribonucleoprotein complex	nucleic acid binding, nucleotide binding, RNA binding	RNA processing
catechol-O-methyltransferase	Comt	NP_001104533	29	3	cytoplasm, integral to membrane, membrane, plasma membrane	catechol O-methyltransferase activity, magnesium ion binding, metal ion binding, methyltransferase activity, O-methyltransferase activity, transferase activity	catecholamine metabolic process, dopamine catabolic process, neurotransmitter catabolic process
neural precursor cell expressed, developmentally down-regulated gene 9 isoform 1	Nedd9	NP_001104794	93	3	cytoplasm, cytoskeleton, nucleus	protein binding	cell adhesion, cell cycle, cell division, mitosis, regulation of growth
acyl-Coenzyme A dehydrogenase, long-chain	Acadl	NP_031407	48	3	mitochondrion	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, long-chain-acyl-CoA dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	fatty acid metabolic process, lipid metabolic process, metabolic process, oxidation reduction

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acyl-Coenzyme A dehydrogenase, medium chain	Acadm	NP_031408	46	3	mitochondrion	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	cardiac muscle cell differentiation, carnitine metabolic process, fatty acid metabolic process, heart development, lipid metabolic process, liver development, metabolic process, organic acid metabolic process, oxidation reduction, post-embryonic development, response to cold, response to starvation
ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	Atp5k	NP_031533	8	3	membrane, mitochondrial inner membrane, mitochondrial proton-transporting ATP synthase complex, coupling factor F(o), mitochondrion, proton-transporting ATP synthase complex, coupling factor F(o)	hydrogen ion transmembrane transporter activity	ATP biosynthetic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport
complement component 1, q subcomponent binding protein	C1qbp	NP_031599	31	3	mitochondrial matrix, mitochondrion	protein binding	not classified
cathepsin H	Ctsh	NP_031827	37	3	lysosome	cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	proteolysis
fibrillarin	Fbl	NP_032017	34	3	Cajal body, granular component, nucleolus, nucleus, ribonucleoprotein complex	methyltransferase activity, RNA binding, snoRNA binding, transferase activity	rRNA processing, snoRNA metabolic process, tRNA processing
H1 histone family, member 0	H1f0	NP_032223	21	3	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
high mobility group box 3	Hmgb3	NP_032279	23	3	chromosome, nucleus	DNA binding	negative regulation of B cell differentiation, negative regulation of myeloid cell differentiation
isocitrate dehydrogenase 3 (NAD+), gamma	Idh3g	NP_032349	43	3	mitochondrion	ATP binding, isocitrate dehydrogenase (NAD+) activity, magnesium ion binding, manganese ion binding, metal ion binding, NAD or NADH binding, nucleotide binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	oxidation reduction, tricarboxylic acid cycle
intergral membrane protein 1	Stt3a	NP_032434	81	3	endoplasmic reticulum, integral to membrane, membrane, membrane fraction	dolichyl-diphosphooligosaccharide-protein glycotransferase activity, oligosaccharyl transferase activity, transferase activity	protein amino acid glycosylation
integral membrane protein 2B	Itm2b	NP_032436	30	3	Golgi apparatus, integral to membrane, membrane, membrane fraction	ATP binding, protein binding	apoptosis, induction of apoptosis
microtubule-associated protein 4	Mtap4	NP_032659	117	3	microtubule	not classified	negative regulation of microtubule depolymerization
NAD(P)H dehydrogenase, quinone 1	Nqo1	NP_032732	31	3	cytoplasm	coenzyme binding, electron carrier activity, NAD(P)H dehydrogenase (quinone) activity, oxidoreductase activity	negative regulation of catalytic activity, oxidation reduction, response to oxidative stress

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nicotinamide nucleotide transhydrogenase	Nnt	NP_032736	114	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, catalytic activity, electron carrier activity, NAD(P) transhydrogenase activity, NAD(P)+ transhydrogenase (AB-specific) activity, oxidoreductase activity	metabolic process, oxidation reduction, proton transport
N-ethylmaleimide sensitive fusion protein	Nsf	NP_032766	83	3	cytoplasm	ATP binding, ATPase activity, coupled, ATP-dependent peptidase activity, hydrolase activity, magnesium ion binding, metal ion binding, nucleoside-triphosphatase activity, nucleotide binding, protein binding, serine-type endopeptidase activity, syntaxin binding	potassium ion transport, protein transport, proteolysis, transport
outer dense fiber of sperm tails 1	Odf1	NP_032783	28	3	outer dense fiber	not classified	cell differentiation, multicellular organismal development, spermatogenesis
pyruvate dehydrogenase E1 alpha 2	Pdha2	NP_032837	43	3	intracellular membrane-bounded organelle, mitochondrion	oxidoreductase activity, oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, pyruvate dehydrogenase (acetyl-transferring) activity	glycolysis, metabolic process, oxidation reduction
protein kinase, cAMP dependent, catalytic, alpha	Prkaca	NP_032880	41	3	cytoplasm, cytosol, mitochondrion, neuromuscular junction, nucleoplasm, nucleus, plasma membrane	ATP binding, cAMP-dependent protein kinase activity, kinase activity, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	mesoderm formation, positive regulation of protein export from nucleus, protein amino acid autophosphorylation, protein amino acid phosphorylation, regulation of synaptic transmission
pinin	Pnn	NP_032917	83	3	cell junction, cytoplasm, desmosome, nuclear speck, nucleus, spliceosomal complex	DNA binding	cell-cell adhesion, mRNA processing, regulation of transcription, RNA splicing, transcription
periplakin	Ppl	NP_032935	204	3	cell junction, cytoplasm, cytoskeleton, extrinsic to plasma membrane, membrane, mitochondrion, nucleus, plasma membrane	protein binding	keratinization
ribosomal protein L30	Rpl30	NP_033109	13	3	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
ribosomal protein S6	Rps6	NP_033122	29	3	cytoplasm, intracellular, perinuclear region of cytoplasm, polysome, ribonucleoprotein complex, ribosome	structural constituent of ribosome	activation-induced cell death of T cells, erythrocyte development, G1/S transition checkpoint, G1/S transition of mitotic cell cycle, gastrulation, glucose homeostasis, mitosis, negative regulation of apoptosis, oogenesis stage, placenta development, ribosomal small subunit biogenesis, rRNA processing, T cell differentiation in the thymus, T cell proliferation during immune response, translation

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sodium channel, voltage-gated, type X, alpha	Scn10a	NP_033160	220	3	integral to membrane, membrane, voltage-gated sodium channel complex	ion channel activity, sodium channel activity, sodium ion binding, voltage-gated ion channel activity, voltage-gated sodium channel activity	ion transport, sodium ion transport, transport
alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	Adh7	NP_033756	40	3	cytoplasm, intracellular	alcohol dehydrogenase (NAD) activity, metal ion binding, oxidoreductase activity, retinol dehydrogenase activity, zinc ion binding	ethanol catabolic process, oxidation reduction, retinoic acid metabolic process, retinol metabolic process
acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	Anp32a	NP_033802	29	3	cytoplasm, nuclear matrix, nucleus	protein binding	regulation of transcription, transcription
adaptor-related protein complex 3, beta 1 subunit	Ap3b1	NP_033810	123	3	cytoplasmic vesicle, Golgi apparatus, membrane, membrane coat, trans-Golgi network	binding, protein binding, protein transporter activity	antigen processing and presentation, antigen processing and presentation, exogenous lipid antigen via MHC class Ib, blood coagulation, endocytosis, intracellular protein transport, positive regulation of NK T cell differentiation, protein targeting to lysosome, protein transport, transport, vesicle-mediated transport
Na+/K+ -ATPase beta 1 subunit	Atp1b1	NP_033851	35	3	basolateral plasma membrane, integral to membrane, membrane, plasma membrane	potassium ion binding, protein binding, sodium ion binding, sodium:potassium-exchanging ATPase activity	ATP biosynthetic process, ion transport, potassium ion transport, sodium ion transport, transport
D-dopachrome tautomerase	Ddt	NP_034157	13	3	cytoplasm	D-dopachrome decarboxylase activity, lyase activity	melanin biosynthetic process
desmin	Des	NP_034173	53	3	contractile fiber, cytoplasm, cytoskeleton, insoluble fraction, intermediate filament, intracellular, sarcolemma, synapse, Z disc	protein binding, structural constituent of cytoskeleton, structural molecule activity	muscle organ development
epoxide hydrolase 1, microsomal	Ephx1	NP_034275	53	3	endoplasmic reticulum, integral to membrane, membrane, microsome	catalytic activity, cis-stilbene-oxide hydrolase activity, epoxide hydrolase activity, hydrolase activity	aromatic compound catabolic process, cellular aromatic compound metabolic process, response to organic cyclic substance, response to toxin
hexosaminidase A	Hexa	NP_034551	61	3	lysosome, membrane	beta-N-acetylhexosaminidase activity, catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds, protein heterodimerization activity	adult walking behavior, carbohydrate metabolic process, ganglioside catabolic process, glycosaminoglycan metabolic process, lipid storage, locomotory behavior, lysosome organization, metabolic process, myelination, neuromuscular process controlling balance, neuromuscular process controlling posture, sensory perception of sound, sexual reproduction, skeletal system development

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hexokinase 1	Hk1	NP_034568	106	3	cytosol, membrane, mitochondrial outer membrane, mitochondrion	ATP binding, hexokinase activity, kinase activity, nucleotide binding, phosphotransferase activity, alcohol group as acceptor, transferase activity	carbohydrate metabolic process, glycolysis
keratin 86	Krt86	NP_034797	53	3	intermediate filament, keratin filament	structural molecule activity	not classified
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	Ndufa4	NP_035016	9	3	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
proteasome (prosome, macropain) 28 subunit, alpha	Psme1	NP_035319	29	3	proteasome activator complex, proteasome complex	proteasome activator activity, protein binding	antigen processing and presentation of exogenous antigen
purine rich element binding protein B	Purb	NP_035351	34	3	DNA replication factor A complex, nucleus	DNA binding, double-stranded DNA binding, mRNA binding, protein binding, single-stranded DNA binding, SMAD binding, transcription factor activity, transcription factor binding	apoptosis, cell differentiation, cell proliferation, negative regulation of transcription, DNA-dependent, regulation of transcription, transcription
muscle glycogen phosphorylase	Pygm	NP_035354	97	3	Z disc	glycogen phosphorylase activity, nucleotide binding, phosphorylase activity, pyridoxal phosphate binding, transferase activity, transferase activity, transferring glycosyl groups	carbohydrate metabolic process, glycogen catabolic process, glycogen metabolic process
retinol binding protein 1, cellular	Rbp1	NP_035384	16	3	cytoplasm	binding, lipid binding, retinal binding, retinoid binding, retinol binding, transporter activity	retinoic acid metabolic process, retinol metabolic process, transport
WD repeat domain 1	Wdr1	NP_035845	66	3	actin cytoskeleton, cytoplasm, cytoskeleton	actin binding	sensory perception of sound
bisphosphate 3'-nucleotidase 1	Bpnt1	NP_035924	33	3	not classified	3'(2'),5'-bisphosphate nucleotidase activity, hydrolase activity, inositol or phosphatidylinositol phosphatase activity, lithium ion binding, magnesium ion binding, metal ion binding	not classified
proteasome (prosome, macropain) subunit, alpha type 1	Psma1	NP_036095	30	3	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, protein binding, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process, ubiquitin-dependent protein catabolic process
proteasome (prosome, macropain) subunit, alpha type 6	Psma6	NP_036098	27	3	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process, ubiquitin-dependent protein catabolic process
acyl-CoA thioesterase 1	Acot1	NP_036136	46	3	cytoplasm	acyl-CoA thioesterase activity, carboxylesterase activity, hydrolase activity, palmitoyl-CoA hydrolase activity, thiolester hydrolase activity	acyl-CoA metabolic process, lipid metabolic process, long-chain fatty acid metabolic process
annexin A11	Anxa11	NP_038497	54	3	nucleus	calcium ion binding, calcium-dependent phospholipid binding, phosphatidylethanolamine binding	not classified
guanine nucleotide-binding protein, beta-4 subunit	Gnb4	NP_038559	37	3	heterotrimeric G-protein complex	GTPase activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction

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splicing factor, arginine/serine-rich 3 (SRp20)	Sfrs3	NP_038691	19	3	nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
ras-GTPase-activating protein SH3-domain binding protein	G3bp1	NP_038744	52	3	cytoplasm, intracellular, membrane, nucleus, plasma membrane	ATP binding, DNA binding, endonuclease activity, helicase activity, hydrolase activity, nuclease activity, nucleic acid binding, nucleotide binding, RNA binding	transport
ribosomal protein S11	Rps11	NP_038753	18	3	intracellular, ribonucleoprotein complex, ribosome	RNA binding, rRNA binding, structural constituent of ribosome	translation
solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	Slc25a10	NP_038798	32	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, secondary active transmembrane transporter activity	mitochondrial transport, transport
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	Atp5l	NP_038823	11	3	membrane, mitochondrial inner membrane, mitochondrial proton-transporting ATP synthase complex, mitochondrial proton-transporting ATP synthase complex, coupling factor F(o), mitochondrion, proton-transporting ATP synthase complex, coupling factor F(o)	hydrogen ion transmembrane transporter activity, hydrogen-exporting ATPase activity, phosphorylative mechanism	ATP biosynthetic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport
FK506 binding protein 3	Fkbp3	NP_038930	25	3	nucleus	isomerase activity, peptidyl-prolyl cis-trans isomerase activity	protein folding
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	Galnt3	NP_056551	73	3	Golgi apparatus, integral to membrane, membrane	calcium ion binding, manganese ion binding, polypeptide N-acetylgalactosaminyltransferase activity, sugar binding, transferase activity, transferase activity, transferring glycosyl groups	not classified
ERO1-like	Ero1l	NP_056589	54	3	endoplasmic reticulum, endoplasmic reticulum membrane, integral to endoplasmic reticulum membrane, membrane	electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on sulfur group of donors, disulfide as acceptor, protein binding	brown fat cell differentiation, electron transport chain, endoplasmic reticulum unfolded protein response, oxidation reduction, protein folding, protein thiol-disulfide exchange, transport
heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	NP_057899	46	3	cytoplasm, nucleus	DNA binding, nucleic acid binding, nucleotide binding, RNA binding	mRNA metabolic process, regulation of transcription, transcription
AU RNA-binding enoyl-coenzyme A hydratase	Auh	NP_057918	33	3	mitochondrion	catalytic activity, enoyl-CoA hydratase activity, lyase activity, methylglutaconyl-CoA hydratase activity, RNA binding	branched chain family amino acid catabolic process, metabolic process, nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay
enoyl coenzyme A hydratase 1, peroxisomal	Ech1	NP_058052	36	3	mitochondrion, peroxisome	catalytic activity, isomerase activity	fatty acid metabolic process, lipid metabolic process, metabolic process
ribosomal protein L5	Rpl5	NP_058676	34	3	cytoplasm, intracellular, nucleus, ribonucleoprotein complex, ribosome	5S rRNA binding, protein binding, RNA binding, rRNA binding, structural constituent of ribosome	biological_process, translation
ribosomal protein L36	Rpl36	NP_061200	12	3	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation

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ribosomal protein, large, P1	Rplp1	NP_061341	11	3	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translational elongation
protein phosphatase 2a, catalytic subunit, alpha isoform	Ppp2ca	NP_062284	36	3	chromosome, centromeric region, cytoplasm, cytosol, nucleus, plasma membrane, protein phosphatase type 2A complex	hydrolase activity, iron ion binding, manganese ion binding, metal ion binding, phosphoprotein phosphatase activity, protein binding, protein serine/threonine phosphatase activity	mesoderm development, protein amino acid dephosphorylation, regulation of cell cycle
HLA-B-associated transcript 1A	Bat1a	NP_062667	49	3	nucleus, spliceosomal complex	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
cytochrome P450, family 51	Cyp51	NP_064394	57	3	endoplasmic reticulum, integral to membrane, membrane, microsome	electron carrier activity, heme binding, iron ion binding, metal ion binding, monooxygenase activity, oxidoreductase activity, sterol 14-demethylase activity	cholesterol biosynthetic process, lipid biosynthetic process, oxidation reduction, steroid biosynthetic process, sterol biosynthetic process
cell line NK14 derived transforming oncogene	Rab8a	NP_075615	24	3	membrane, plasma membrane	GTP binding, nucleotide binding, protein binding	protein transport, small GTPase mediated signal transduction, transport
NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	Ndufa7	NP_075691	13	3	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity	ATP synthesis coupled electron transport, electron transport chain, transport
upregulated during skeletal muscle growth 5	Usmg5	NP_075700	6	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	not classified
succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	Sdhb	NP_075863	32	3	membrane, mitochondrial inner membrane, mitochondrion	2 iron, 2 sulfur cluster binding, 3 iron, 4 sulfur cluster binding, 4 iron, 4 sulfur cluster binding, electron carrier activity, iron ion binding, iron-sulfur cluster binding, metal ion binding, oxidoreductase activity, succinate dehydrogenase (ubiquinone) activity	electron transport chain, oxidation reduction, transport, tricarboxylic acid cycle
SET translocation	Set	NP_076360	33	3	cytoplasm, endoplasmic reticulum, nucleus	not classified	nucleosome assembly
ribosomal protein S23	Rps23	NP_077137	16	3	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	structural constituent of ribosome	translation
haloacid dehalogenase-like hydrolase domain containing 3	Hdhd3	NP_077219	28	3	mitochondrion	catalytic activity, hydrolase activity, phosphoglycolate phosphatase activity	metabolic process
tetratricopeptide repeat domain 11	Fis1	NP_079838	17	3	integral to membrane, membrane, mitochondrial outer membrane, mitochondrion, peroxisome	binding	apoptosis

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ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	Uqcrfs1	NP_079986	29	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	2 iron, 2 sulfur cluster binding, electron carrier activity, iron ion binding, iron-sulfur cluster binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on diphenols and related substances as donors, ubiquinol-cytochrome-c reductase activity	electron transport chain, oxidation reduction, transport
ADP-ribosylation factor-like 1	Arl1	NP_080135	20	3	cytoplasm, Golgi apparatus, intracellular, membrane	GTP binding, magnesium ion binding, metal ion binding, nucleotide binding	small GTPase mediated signal transduction
signal sequence receptor, alpha	Ssr1	NP_080241	32	3	endoplasmic reticulum, integral to membrane, membrane	calcium ion binding	not classified
ribosomal protein S20	Rps20	NP_080423	13	3	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, structural constituent of ribosome	translation
ubiquinol-cytochrome c reductase binding protein	Uqcrb	NP_080495	14	3	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	ubiquinol-cytochrome-c reductase activity	electron transport chain, mitochondrial electron transport, ubiquinol to cytochrome c, transport
diacetyl/L-xylulose reductase	Dcxr	NP_080704	26	3	brush border, membrane, microvillus, plasma membrane	binding, catalytic activity, L-xylulose reductase (NADP+) activity, oxidoreductase activity, oxidoreductase activity, acting on CH-OH group of donors, protein binding	carbohydrate metabolic process, D-xylose metabolic process, glucose metabolic process, metabolic process, NADP metabolic process, oxidation reduction, xylulose metabolic process
arginine/serine-rich splicing factor 6	Sfrs6	NP_080775	39	3	not classified	not classified	not classified
actin related protein 2/3 complex, subunit 4	Arpc4	NP_080828	20	3	Arp2/3 protein complex, cell projection, cytoplasm, cytoskeleton	actin binding, molecular_function	actin filament polymerization, biological_process
apolipoprotein O-like	Apool	NP_080841	29	3	extracellular region, mitochondrial inner membrane, mitochondrion	not classified	not classified
CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	Cdipt	NP_080914	24	3	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane, plasma membrane	CDP-diacylglycerol-inositol 3-phosphatidyltransferase activity, manganese ion binding, phosphotransferase activity, for other substituted phosphate groups, transferase activity	phospholipid biosynthetic process
epsin	Serpina1f	NP_080963	46	3	extracellular region	peptidase inhibitor activity, serine-type endopeptidase inhibitor activity	not classified
lectin, mannose-binding, 1	Lman1	NP_081676	58	3	endoplasmic reticulum, ER-Golgi intermediate compartment, Golgi apparatus, integral to membrane, membrane, sarcomere	sugar binding	ER to Golgi vesicle-mediated transport, protein transport, transport, vesicle-mediated transport
katanin p60 subunit A-like 2	Katnal2	NP_081997	46	3	microtubule	ATP binding, hydrolase activity, microtubule-severing ATPase activity, nucleotide binding	not classified
solute carrier family 25, member 35	Slc25a35	NP_082324	33	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	transport
protein disulfide isomerase associated 5	Pdia5	NP_082571	59	3	endoplasmic reticulum	isomerase activity, protein disulfide isomerase activity	cell redox homeostasis, response to stress

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N-acetylneuraminate pyruvate lyase	Npl	NP_083025	35	3	cellular_component, cytoplasm	catalytic activity, lyase activity, N-acetylneuraminate lyase activity	biological_process, carbohydrate metabolic process, metabolic process
mitochondrial phosphoenolpyruvate carboxykinase 2	Pck2	NP_083270	73	3	mitochondrion	carboxy-lyase activity, GTP binding, lyase activity, manganese ion binding, metal ion binding, nucleotide binding, phosphoenolpyruvate carboxykinase (GTP) activity, phosphoenolpyruvate carboxykinase activity, purine nucleotide binding	gluconeogenesis
NADH dehydrogenase (ubiquinone) Fe-S protein 7	Ndufs7	NP_083548	25	3	mitochondrial inner membrane, mitochondrion, respiratory chain	4 iron, 4 sulfur cluster binding, iron ion binding, iron-sulfur cluster binding, metal ion binding, NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on NADH or NADPH, quinone binding	biological_process, electron transport chain, oxidation reduction, transport
Sec1 family domain containing 1	Scfd1	NP_084101	72	3	cellular_component, cytoplasm, endoplasmic reticulum, Golgi apparatus, membrane	molecular_function	biological_process, protein transport, transport, vesicle docking during exocytosis, vesicle-mediated transport
dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	Dlst	NP_084501	49	3	mitochondrion, oxoglutarate dehydrogenase complex	acyltransferase activity, dihydrolipoyllysine-residue succinyltransferase activity, lipoic acid binding, transferase activity	metabolic process, tricarboxylic acid cycle
ribosomal protein 10	Rpl10	NP_443067	25	3	cytoplasm, cytosolic large ribosomal subunit, intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
isocitrate dehydrogenase 3, beta subunit	Idh3b	NP_570954	42	3	mitochondrion	oxidoreductase activity	oxidation reduction
acidic nuclear phosphoprotein 32 family, member B	Anp32b	NP_570959	31	3	nucleus	molecular_function, protein binding	S phase of mitotic cell cycle
acyl-Coenzyme A binding domain containing 3	Acbd3	NP_573488	60	3	Golgi apparatus, membrane, mitochondrion	acyl-CoA binding, binding	lipid biosynthetic process, steroid biosynthetic process
hypothetical protein LOC70984	4931406C07 Rik	NP_598493	35	3	nucleus	hydrolase activity, hydrolase activity, acting on ester bonds, metal ion binding, zinc ion binding	not classified
phosphoserine phosphatase	Psph	NP_598661	25	3	cellular_component	catalytic activity, hydrolase activity, magnesium ion binding, molecular_function, phosphatase activity, phosphoserine phosphatase activity	biological_process, cellular amino acid biosynthetic process, L-serine biosynthetic process, metabolic process
splicing factor 3b, subunit 3	Sf3b3	NP_598714	136	3	nucleus, spliceosomal complex	nucleic acid binding	mRNA processing, RNA splicing
transmembrane emp24 protein transport domain containing 4	Tmed4	NP_598781	26	3	endoplasmic reticulum, integral to membrane, membrane	not classified	transport
DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	Ddx1	NP_598801	83	3	ribonucleoprotein complex	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, molecular_function, nucleic acid binding, nucleotide binding, RNA binding	biological_process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
otubain 1	Otub1	NP_598911	31	3	not classified	cysteine-type peptidase activity, hydrolase activity, peptidase activity	immune response, modification-dependent protein catabolic process
NADH dehydrogenase (ubiquinone) Fe-S protein 8	Ndufs8	NP_659119	24	3	membrane, mitochondrion, respiratory chain	4 iron, 4 sulfur cluster binding, electron carrier activity, iron ion binding, iron-sulfur cluster binding, metal ion binding, NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on NADH or NADPH	electron transport chain, oxidation reduction, transport
ribonuclease/angiogenin inhibitor 1	Rnh1	NP_660117	50	3	cytoplasm	protein binding	not classified
thioredoxin domain containing 5	Txndc5	NP_663342	46	3	endoplasmic reticulum, endoplasmic reticulum lumen	isomerase activity	cell redox homeostasis
solute carrier family 25, member 1	Slc25a1	NP_694790	34	3	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	not classified	transport
pyrroline-5-carboxylate synthetase isoform 2	Aldh18a1	NP_705782	87	3	cytoplasm, membrane, mitochondrial inner membrane, mitochondrion	ATP binding, catalytic activity, glutamate 5-kinase activity, glutamate-5-semialdehyde dehydrogenase activity, kinase activity, nucleotide binding, oxidoreductase activity, transferase activity	cellular amino acid biosynthetic process, metabolic process, oxidation reduction, proline biosynthetic process
ciliary rootlet coiled-coil, rootletin	Crocc	NP_742120	227	3	centriole, ciliary rootlet	kinesin binding, structural molecule activity	cell cycle, cell projection organization
phospholipase C, gamma 2	Plcg2	NP_758489	148	3	not classified	calcium ion binding, hydrolase activity, phosphoinositide phospholipase C activity, phospholipase C activity, phosphoric diester hydrolase activity, protein binding, signal transducer activity	activation of store-operated calcium channel activity, follicular B cell differentiation, inositol trisphosphate biosynthetic process, intracellular signaling cascade, lipid catabolic process, lipid metabolic process, negative regulation of programmed cell death, phospholipid catabolic process, regulation of gene expression, response to lipopolysaccharide, signal transduction, T cell receptor signaling pathway
cytoskeleton-associated protein 4	Ckap4	NP_780660	64	3	cell surface, endoplasmic reticulum, integral to membrane, membrane	protein binding	biological_process
U5 snRNP-specific protein, 200 kDa	Ascc3l1	NP_796188	245	3	ribonucleoprotein complex	ATP binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding	not classified
acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	Acaa2	NP_803421	42	3	mitochondrial inner membrane, mitochondrion	acetyl-CoA C-acyltransferase activity, acyltransferase activity, catalytic activity, transferase activity, transferase activity, transferring acyl groups other than amino-acyl groups	fatty acid metabolic process, lipid metabolic process, metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
prominin 2 isoform 2	Prom2	NP_835148	55	3	cell projection, cilium, integral to membrane, membrane, plasma membrane	not classified	not classified
importin 7	Ipo7	NP_852658	119	3	cytoplasm, nucleus	binding, histone binding, protein binding, protein transporter activity	intracellular protein transport, protein import into nucleus, protein transport, transport
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform 3	Smarcc2	NP_937803	121	3	chromatin, nucleus	chromatin binding, DNA binding	chromatin assembly or disassembly, chromatin modification, regulation of transcription, transcription
RAB35, member RAS oncogene family	Rab35	NP_937806	23	3	membrane, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport
pantophysin isoform 2	Sypl	NP_942003	27	3	cytoplasmic vesicle, integral to membrane, membrane, secretory granule, synaptic vesicle	transporter activity	transport
ring finger protein 138 isoform 1	Rnf138	NP_997506	28	3	cellular_component, intracellular	ligase activity, metal ion binding, molecular_function, protein binding, zinc ion binding	biological_process, modification-dependent protein catabolic process, Wnt receptor signaling pathway
glycerol kinase isoform 2	Gyk	NP_997609	61	3	cytoplasm, membrane, mitochondrial outer membrane, mitochondrion	ATP binding, glycerol kinase activity, kinase activity, nucleotide binding, phosphotransferase activity, alcohol group as acceptor, transferase activity	carbohydrate metabolic process, glycerol metabolic process, glycerol-3-phosphate metabolic process
hypothetical protein LOC270156	AU019823	NP_997614	31	3	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100039525	XP_001473106	18	3	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG621837	XP_001473932	9	3	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100046199	XP_001475883	21	3	not classified	not classified	not classified
PREDICTED: similar to Phosphoserine aminotransferase 1 isoform 2	LOC100047252	XP_001478041	36	3	not classified	not classified	not classified
PREDICTED: similar to proteasome (prosome, macropain) subunit, alpha type, 8 isoform 4	Psma8	XP_911847	24	3	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process, ubiquitin-dependent protein catabolic process
PREDICTED: hypothetical protein	LOC634429	XP_914246	282	3	not classified	not classified	not classified
eukaryotic translation initiation factor 4, gamma 1 isoform b	Eif4g1	NP_001005331	175	2	cytoplasm	protein binding, RNA binding, translation initiation factor activity	regulation of translation, RNA metabolic process, translation
aspartylglucosaminidase	Aga	NP_001005847	37	2	lysosome	hydrolase activity, N4-(beta-N-acetylglucosaminyl)-L-asparaginase activity	protein maturation
ribonuclease, RNase A family, 12 (non-active)	Rnase12	NP_001011875	17	2	extracellular region	nucleic acid binding, pancreatic ribonuclease activity	not classified
proteasome activator subunit 2 isoform 2	Psme2	NP_001025026	26	2	proteasome activator complex, proteasome complex	proteasome activator activity, protein binding	antigen processing and presentation of exogenous antigen
NADH dehydrogenase (ubiquinone) Fe-S protein 5	Ndufs5	NP_001025445	13	2	mitochondrion	not classified	not classified
glycogen synthase kinase 3 alpha	Gsk3a	NP_001026837	52	2	not classified	ATP binding, kinase activity, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, tau-protein kinase activity, transferase activity	insulin receptor signaling pathway, protein amino acid phosphorylation
nuclear cap binding protein subunit 1, 80kDa	AU014645	NP_001028373	92	2	cellular_component, nucleus	molecular_function, protein binding, RNA binding	biological_process, mRNA transport, RNA metabolic process, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	Ndufb6	NP_001028477	16	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
hypothetical protein LOC328099	AU021838	NP_001032835	28	2	not classified	not classified	not classified
milk fat globule-EGF factor 8 protein isoform 2	Mfge8	NP_001038954	47	2	external side of plasma membrane, extracellular space, extrinsic to plasma membrane, membrane	integrin binding, phosphatidylethanolamine binding, phosphatidylserine binding, protein binding	cell adhesion, phagocytosis, engulfment, phagocytosis, recognition, positive regulation of phagocytosis, single fertilization
ribosomal protein L38	Rpl38	NP_001041522	8	2	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
glutathione S-transferase, alpha 3	Gsta3	NP_001070821	25	2	cytoplasm	glutathione transferase activity, transferase activity	metabolic process
enhancer trap locus 4	Etl4	NP_001074475	218	2	cytoplasm	not classified	embryonic skeletal system development, multicellular organismal development
apoptotic chromatin condensation inducer 1 isoform 4	Acin1	NP_001078942	65	2	nucleolus, nucleus	nucleic acid binding, nucleotide binding	apoptosis
ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	Arfgef1	NP_001095900	208	2	cellular_component	molecular_function	biological_process
catenin (cadherin associated protein), alpha 2 isoform 2	Ctnna2	NP_001103234	105	2	actin cytoskeleton, adherens junction, axon, basolateral plasma membrane, cell junction, cell-cell adherens junction, cytoplasm, cytoskeleton, lamellipodium, membrane, plasma membrane	cadherin binding, protein binding, structural molecule activity	axonogenesis, brain morphogenesis, cell adhesion, dendrite morphogenesis, prepulse inhibition, radial glia guided migration of Purkinje cell, regulation of synapse structural plasticity
arsenate resistance protein 2 isoform 3	Ars2	NP_001103380	99	2	cellular_component	molecular_function	not classified
elongation factor Tu GTP binding domain containing 2 isoform b	Eftud2	NP_001103465	109	2	nucleus, spliceosomal complex	GTP binding, GTPase activity, nucleotide binding, protein binding, translation elongation factor activity	mRNA processing, RNA splicing
peptidylprolyl isomerase H isoform 1	Ppih	NP_001103599	19	2	cytoplasm, nucleus, spliceosomal complex	isomerase activity, peptidyl-prolyl cis-trans isomerase activity	mRNA processing, protein folding, RNA splicing
hypothetical protein LOC209550	EG209550	NP_001104588	112	2	not classified	not classified	not classified
isocitrate dehydrogenase 1 (NADP+), soluble	Idh1	NP_001104790	47	2	cytoplasm, cytosol	isocitrate dehydrogenase (NADP+) activity, magnesium ion binding, manganese ion binding, metal ion binding, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	glutathione metabolic process, glyoxylate cycle, isocitrate metabolic process, oxidation reduction, response to oxidative stress, tricarboxylic acid cycle
adaptor protein complex AP-1, beta 1 subunit	Ap1b1	NP_031480	104	2	clathrin adaptor complex, cytoplasmic vesicle, Golgi apparatus, membrane, membrane coat, trans-Golgi network	binding, protein binding, protein transporter activity	endocytosis, intracellular protein transport, protein transport, transport, vesicle-mediated transport
capping protein (actin filament) muscle Z-line, alpha 2	Capza2	NP_031630	33	2	cortical cytoskeleton, F-actin capping protein complex, membrane	actin binding	actin cytoskeleton organization, actin filament capping
chaperonin subunit 2 (beta)	Cct2	NP_031662	57	2	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
chondroitin sulfate proteoglycan 6	Smc3	NP_031816	142	2	chromosome, lateral element, nucleus	ATP binding, nucleotide binding, protein binding	cell cycle, cell division, chromosome organization, DNA repair, meiosis, mitosis, response to DNA damage stimulus
cysteine and glycine-rich protein 1	Csrp1	NP_031817	21	2	actin cytoskeleton, nucleus	metal ion binding, protein binding, zinc ion binding	actin cytoskeleton organization
microtubule-associated protein, RP/EB family, member 1	Mapre1	NP_031922	30	2	cell projection, cell projection membrane, cytoplasm, cytoplasmic microtubule, cytoskeleton, Golgi apparatus, microtubule	microtubule binding, microtubule plus-end binding, protein binding	cell cycle, cell division, mitosis
enolase 3, beta muscle	Eno3	NP_031959	47	2	cytoplasm, phosphopyruvate hydratase complex	lyase activity, magnesium ion binding, metal ion binding, phosphopyruvate hydratase activity	glycolysis
enhancer of rudimentary homolog	Erh	NP_031977	12	2	not classified	molecular_function	cell cycle
ferredoxin 1	Fdx1	NP_032022	20	2	mitochondrion	2 iron, 2 sulfur cluster binding, electron carrier activity, iron ion binding, iron-sulfur cluster binding, metal ion binding	electron transport chain, transport
ferrochelatase	Fech	NP_032024	47	2	membrane, mitochondrial inner membrane, mitochondrion	2 iron, 2 sulfur cluster binding, ferrochelatase activity, heme binding, iron ion binding, iron-responsive element binding, iron-sulfur cluster binding, lyase activity, metal ion binding, tetrapyrrole binding	cholesterol metabolic process, detection of UV, erythrocyte differentiation, heme biosynthetic process, iron ion homeostasis, porphyrin biosynthetic process, protoporphyrinogen IX metabolic process, regulation of eIF2 alpha phosphorylation by heme, regulation of hemoglobin biosynthetic process, response to light stimulus, very-low-density lipoprotein particle assembly
glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	Gapdhs	NP_032111	47	2	cytoplasm, flagellum, microtubule-based flagellum	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) activity, glyceraldehyde-3-phosphate dehydrogenase activity, NAD or NADH binding, oxidoreductase activity	glucose metabolic process, glycolysis, oxidation reduction, positive regulation of glycolysis, sperm motility

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glutathione peroxidase 1	Gpx1	NP_032186	22	2	cytoplasm, mitochondrion	glutathione peroxidase activity, oxidoreductase activity, peroxidase activity, selenium binding	angiogenesis involved in wound healing, apoptosis, blood vessel endothelial cell migration, cell proliferation, endothelial cell development, fat cell differentiation, heart contraction, hydrogen peroxide catabolic process, induction of apoptosis, induction of apoptosis by oxidative stress, interaction with symbiont, lipid metabolic process, myoblast proliferation, myotube differentiation, negative regulation of apoptosis, negative regulation of inflammatory response to antigenic stimulus, oxidation reduction, positive regulation of protein kinase B signaling cascade, protein amino acid oxidation, regulation of neuron apoptosis, response to gamma radiation, response to hydrogen peroxide, response to hydroperoxide, response to oxidative stress, response to reactive oxygen species, response to symbiotic bacterium, response to toxin, response to wounding, response to xenobiotic stimulus, sensory
glutathione S-transferase, alpha 1 (Ya)	Gsta1	NP_032207	26	2	not classified	glutathione transferase activity, transferase activity	glutathione metabolic process, metabolic process
histidyl-tRNA synthetase	Hars	NP_032240	58	2	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, histidine-tRNA ligase activity, ligase activity, nucleotide binding	histidyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
high mobility group box 2	Hmgb2	NP_032278	24	2	chromosome, nucleus	DNA binding	male gonad development, positive regulation of gene-specific transcription from RNA polymerase II promoter, response to steroid hormone stimulus, spermatogenesis
Harvey rat sarcoma virus oncogene 1	Hras1	NP_032310	21	2	Golgi apparatus, intracellular, membrane, plasma membrane	GTP binding, nucleotide binding, protein binding	cell aging, cell proliferation, endocytosis, negative regulation of neuron apoptosis, positive regulation of cell proliferation, Ras protein signal transduction, regulation of long-term neuronal synaptic plasticity, small GTPase mediated signal transduction
karyopherin (importin) beta 1	Kpnb1	NP_032405	97	2	cytoplasm, nucleus	binding, protein binding, protein transporter activity	intracellular protein transport, protein import into nucleus, protein transport, ribosomal protein import into nucleus, transport
napsin A aspartic peptidase	Napsa	NP_032463	46	2	not classified	aspartic-type endopeptidase activity, hydrolase activity, peptidase activity	proteolysis
keratin 15	Krt15	NP_032495	49	2	intermediate filament	structural molecule activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
tumor-associated calcium signal transducer 1	Tacstd1	NP_032558	35	2	apical plasma membrane, basolateral plasma membrane, integral to membrane, membrane	not classified	not classified
ATP-binding cassette, sub-family C, member 1	Abcc1	NP_032602	171	2	integral to membrane, integral to plasma membrane, membrane, plasma membrane	ATP binding, ATPase activity, ATPase activity, coupled to transmembrane movement of substances, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding, transporter activity	transport
solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Slc3a2	NP_032603	58	2	integral to membrane, membrane, plasma membrane	catalytic activity, cation binding, protein binding	amino acid transport, carbohydrate metabolic process, transport
4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1	Nipsnap1	NP_032724	33	2	mitochondrial inner membrane, mitochondrion	molecular_function	biological_process
nucleobindin 1	Nucb1	NP_032775	53	2	cytoplasm, Golgi apparatus, membrane	calcium ion binding, DNA binding	not classified
platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	Pafah1b3	NP_032802	26	2	cytoplasm	1-alkyl-2-acetylglycerophosphocholine esterase activity, hydrolase activity, hydrolase activity, acting on ester bonds, lipase activity, protein binding	lipid catabolic process, lipid metabolic process, spermatogenesis
protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	Pcmt1	NP_032812	25	2	cytoplasm	methyltransferase activity, protein-L-isoaspartate (D-aspartate) O-methyltransferase activity, transferase activity	protein amino acid methylation, protein modification process
peptidase D	Pepd	NP_032846	55	2	not classified	aminopeptidase activity, dipeptidase activity, hydrolase activity, manganese ion binding, metal ion binding, metalloexopeptidase activity, metallopeptidase activity, peptidase activity	cellular process, collagen catabolic process, proteolysis
phosphofructokinase, liver, B-type	Pfkl	NP_032852	85	2	6-phosphofructokinase complex, cytoplasm, cytosol	6-phosphofructokinase activity, ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, transferase activity	fructose 6-phosphate metabolic process, glycolysis, negative regulation of insulin secretion, response to glucose stimulus
proteasome (prosome, macropain) subunit, alpha type 2	Psma2	NP_032970	26	2	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process, ubiquitin-dependent protein catabolic process
protease (prosome, macropain) 26S subunit, ATPase 1	Psmc1	NP_032973	49	2	cytoplasm, nucleus, proteasome complex	ATP binding, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding	protein catabolic process
polypyrimidine tract binding protein 1 isoform 2	Ptbp1	NP_032982	57	2	nucleus	nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA processing, RNA splicing
retinoblastoma binding protein 4	Rbbp4	NP_033056	48	2	nucleus, NuRD complex	protein binding	cell cycle, chromatin modification, chromatin remodeling, DNA replication, regulation of transcription, transcription
regucalcin	Rgn	NP_033086	33	2	cytoplasm, nucleus	calcium ion binding, enzyme regulator activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
serine hydroxymethyltransferase 1 (soluble)	Shmt1	NP_033197	53	2	cytoplasm, mitochondrion	catalytic activity, glycine hydroxymethyltransferase activity, methyltransferase activity, pyridoxal phosphate binding, transferase activity	glycine metabolic process, L-serine metabolic process, one-carbon metabolic process
small nuclear ribonucleoprotein D1	Snrpd1	NP_033252	13	2	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	not classified	mRNA processing, RNA splicing
small nuclear ribonucleoprotein E	Snrpe	NP_033253	11	2	nucleus, ribonucleoprotein complex, spliceosomal complex	RNA binding	mRNA processing, RNA splicing
serine (or cysteine) proteinase inhibitor, clade A, member 1c	Serpina1c	NP_033271	46	2	extracellular region	peptidase inhibitor activity, protein binding, serine-type endopeptidase inhibitor activity	protein amino acid N-linked glycosylation, response to cytokine stimulus, response to peptide hormone stimulus
syntaxin 4A (placental)	Stx4a	NP_033320	34	2	cytoplasm, integral to membrane, membrane, perinuclear region of cytoplasm, plasma membrane, trans-Golgi network	protein binding, SNAP receptor activity	intracellular protein transport, neurotransmitter transport, synaptic vesicle exocytosis, transport
TAP binding protein isoform 2	Tapbp	NP_033344	50	2	endoplasmic reticulum, integral to membrane, integral to plasma membrane, membrane, microsome	not classified	antigen processing and presentation of endogenous peptide antigen via MHC class I, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, defense response, peptide antigen stabilization
transcription factor A, mitochondrial	Tfam	NP_033386	28	2	mitochondrion, nucleus, transcription factor complex	DNA binding, transcription factor activity	mitochondrial respiratory chain complex assembly, regulation of transcription, transcription
proteasome 26S non-ATPase subunit 3	Psmd3	NP_033465	61	2	proteasome complex	enzyme regulator activity	regulation of protein catabolic process
Wiskott-Aldrich syndrome homolog	Was	NP_033541	54	2	cytoplasm, cytoskeleton, vesicle membrane	identical protein binding, protein binding	actin filament polymerization, actin filament-based movement, actin polymerization or depolymerization, endosome transport, T cell activation
aldolase C, fructose-bisphosphate	Aldoc	NP_033787	39	2	mitochondrion	catalytic activity, fructose-bisphosphate aldolase activity, lyase activity, protein binding	glycolysis, metabolic process
branched chain aminotransferase 2, mitochondrial	Bcat2	NP_033867	44	2	mitochondrion	branched-chain-amino-acid transaminase activity, catalytic activity, transaminase activity, transferase activity	branched chain family amino acid biosynthetic process, branched chain family amino acid catabolic process, branched chain family amino acid metabolic process, cellular amino acid biosynthetic process, metabolic process
cyclin K	Ccnk	NP_033962	64	2	not classified	not classified	cell cycle, cell division, mitosis, regulation of transcription, transcription
chaperonin containing Tcp1, subunit 6a (zeta)	Cct6a	NP_033968	58	2	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
cell division cycle 10 homolog	7-Sep	NP_033989	51	2	cytoplasm, septin complex, synaptosome	GTP binding, nucleotide binding, protein binding	cell cycle, cell division, mitosis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cell division cycle 42	Cdc42	NP_033991	21	2	apical part of cell, cell projection, intracellular, membrane, plasma membrane	GTP binding, GTPase activity, GTP-dependent protein binding, nucleotide binding, protein binding	adherens junction organization, cell division, cell-cell adhesion, cellular protein localization, endosome transport, establishment or maintenance of apical/basal cell polarity, filopodium assembly, neuron fate determination, nuclear migration, nucleus localization, positive regulation of phosphoinositide 3-kinase activity, regulation of mitosis, Rho protein signal transduction, small GTPase mediated signal transduction
claudin 3	Cldn3	NP_034032	23	2	cell junction, integral to membrane, membrane, plasma membrane, tight junction	identical protein binding, structural molecule activity	calcium-independent cell-cell adhesion
dihydropyrimidinase-like 2	Dpysl2	NP_034085	62	2	axon, cell soma, cytoplasm, dendrite, mitochondrion	hydrolase activity	cell differentiation, multicellular organismal development, nervous system development
dynein cytoplasmic 1 intermediate chain 2	Dync1i2	NP_034194	68	2	dynein complex, microtubule	motor activity	not classified
FK506 binding protein 4	Fkbp4	NP_034349	52	2	cytoplasm, nucleus	ATP binding, binding, glucocorticoid receptor binding, GTP binding, heat shock protein binding, isomerase activity, peptidyl-prolyl cis-trans isomerase activity, phosphoprotein binding	androgen receptor signaling pathway, embryo implantation, male sex differentiation, prostate gland development, protein complex localization, protein folding, reproductive structure development, steroid hormone receptor complex assembly
ferritin heavy chain 1	Fth1	NP_034369	21	2	not classified	binding, ferric iron binding, ferroxidase activity, iron ion binding, metal ion binding, oxidoreductase activity	cellular iron ion homeostasis, iron ion transport, oxidation reduction
guanine deaminase	Gda	NP_034396	51	2	not classified	guanine deaminase activity, hydrolase activity, metal ion binding, protein binding, zinc ion binding	not classified
gamma-glutamyl hydrolase	Ggh	NP_034411	35	2	extracellular region, lysosome	catalytic activity, gamma-glutamyl-peptidase activity, hydrolase activity, omega peptidase activity, peptidase activity	glutamine metabolic process
glutathione S-transferase, theta 2	Gstt2	NP_034491	28	2	cytoplasm, nucleus	glutathione transferase activity, transferase activity	glutathione metabolic process
glutathione transferase zeta 1 (maleylacetoacetate isomerase)	Gstz1	NP_034493	24	2	cytoplasm, mitochondrion	catalytic activity, glutathione transferase activity, isomerase activity, maleylacetoacetate isomerase activity, transferase activity	aromatic amino acid family metabolic process, L-phenylalanine catabolic process, tyrosine catabolic process
histocompatibility 13	H13	NP_034506	42	2	endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane	aspartic-type endopeptidase activity, hydrolase activity, peptidase activity	not classified

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mago-nashi homolog, proliferation-associated	Magoh	NP_034890	17	2	cytoplasm, nucleus, spliceosomal complex	RNA binding	female gamete generation, mRNA processing, mRNA transport, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, regulation of translation, RNA splicing, transport
matrin 3	Matr3	NP_034901	95	2	intracellular, nucleus	metal ion binding, nucleic acid binding, nucleotide binding, RNA binding, zinc ion binding	not classified
macrophage migration inhibitory factor	Mif	NP_034928	13	2	cytoplasm, extracellular region, extracellular space	cytokine activity, dopachrome isomerase activity, isomerase activity, phenylpyruvate tautomerase activity	cell aging, DNA damage response, signal transduction by p53 class mediator, immune response, inflammatory response, innate immune response, regulation of cell proliferation
proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	Psmd7	NP_034947	37	2	proteasome complex	not classified	not classified
COX4 neighbor	Cox4nb	NP_035056	23	2	mitochondrion	not classified	not classified
proteasome (prosome, macropain) subunit, alpha type 3	Psma3	NP_035314	28	2	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, protein binding, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process, ubiquitin-dependent protein catabolic process
proteasome (prosome, macropain) 26S subunit, ATPase 2	Psmc2	NP_035318	53	2	cytoplasm, nucleus, proteasome complex	ATP binding, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding, protein binding	protein catabolic process
RAB geranylgeranyl transferase, b subunit	Rabggtb	NP_035361	38	2	not classified	catalytic activity, metal ion binding, prenyltransferase activity, Rab geranylgeranyltransferase activity, transferase activity, zinc ion binding	not classified
ribosomal protein L10A	Rpl10a	NP_035417	25	2	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, RNA binding, structural constituent of ribosome	biological_process, RNA processing, translation
SEC22 vesicle trafficking protein-like 1	Sec22b	NP_035472	25	2	endoplasmic reticulum, endoplasmic reticulum membrane, Golgi apparatus, Golgi membrane, integral to membrane, membrane	not classified	ER to Golgi vesicle-mediated transport, protein transport, transport, vesicle-mediated transport
transgelin	Tagln	NP_035656	23	2	cytoplasm	not classified	cytoskeleton organization, muscle organ development
tripartite motif protein 28	Trim28	NP_035718	89	2	chromatin, intracellular, nuclear euchromatin, nuclear heterochromatin, nucleolus, nucleoplasm, nucleus	metal ion binding, protein binding, protein kinase activity, sequence-specific DNA binding, transcription coactivator activity, transcription factor activity, transcription repressor activity, zinc ion binding	epithelial to mesenchymal transition, negative regulation of transcription from RNA polymerase II promoter, negative regulation of transcription, DNA-dependent, positive regulation of gene-specific transcription, positive regulation of transcription, DNA-dependent, protein amino acid autophosphorylation, protein amino acid phosphorylation, regulation of transcription, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
translin	Tsn	NP_035780	26	2	cytoplasm, nucleus	DNA binding, mRNA binding, protein binding, RNA binding, sequence-specific DNA binding	not classified
thioredoxin 1	Txn1	NP_035790	12	2	cytoplasm, cytosol, mitochondrion, nucleus	peptide disulfide oxidoreductase activity, protein binding	cell redox homeostasis, electron transport chain, negative regulation of protein export from nucleus, negative regulation of transcription from RNA polymerase II promoter, transport
ubiquitin-conjugating enzyme E2I	Ube2i	NP_035795	18	2	cytoplasm, nucleus	ATP binding, HLH domain binding, ligase activity, nucleotide binding, protein binding, small conjugating protein ligase activity	cell cycle, cell division, chromosome segregation, interspecies interaction between organisms, mitosis, modification-dependent protein catabolic process, multicellular organismal development, post-translational protein modification, regulation of protein metabolic process
tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Ywhah	NP_035868	28	2	cytoplasm	actin binding, protein binding, protein domain specific binding	cytoskeleton organization, intracellular protein transport, negative regulation of apoptosis, negative regulation of dendrite morphogenesis, regulation of mitosis
solute carrier family 27 (fatty acid transporter), member 2	Slc27a2	NP_036108	70	2	endoplasmic reticulum, integral to membrane, membrane, mitochondrion, peroxisome	ATP binding, catalytic activity, fatty acid transporter activity, ligase activity, long-chain-fatty-acid-CoA ligase activity, nucleotide binding, very-long-chain-fatty-acid-CoA ligase activity	fatty acid metabolic process, fatty acid transport, lipid metabolic process, long-chain fatty acid metabolic process, metabolic process, very-long-chain fatty acid metabolic process
dihydropyrimidinase-related protein 4	Dpysl4	NP_036123	62	2	cytoplasm	hydrolase activity, protein binding	not classified
clusterin	Clu	NP_038520	52	2	extracellular region	not classified	cell death
proprotein convertase subtilisin/kexin type 1	Pcsk1	NP_038656	84	2	cytoplasmic vesicle, extracellular space	calcium ion binding, hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	peptide biosynthetic process, peptide hormone processing, protein maturation by peptide bond cleavage, proteolysis
t-complex protein 1	Tcp1	NP_038714	60	2	chaperonin-containing T-complex, cytoplasm, microtubule organizing center, nuclear heterochromatin, pericentriolar material	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
transducin (beta)-like 2	Tbl2	NP_038791	50	2	cellular_component	molecular_function	biological_process
tight junction protein 3	Tjp3	NP_038797	99	2	cell junction, membrane, plasma membrane, tight junction	protein binding	not classified
drebrin-like	Dbnl	NP_038838	48	2	cell cortex, cell projection, cytoplasm, cytoskeleton, intracellular, lamellipodium, ruffle	actin binding, actin filament binding, protein binding	actin filament bundle formation, actin filament severing, barbed-end actin filament capping, endocytosis, immune response, Rac protein signal transduction

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
chloride intracellular channel 4 (mitochondrial)	Clic4	NP_038913	29	2	chloride channel complex, cytoplasm, cytoplasmic vesicle, integral to membrane, membrane, mitochondrion, nucleus, plasma membrane	chloride channel activity, chloride ion binding, ion channel activity, protein binding, voltage-gated chloride channel activity, voltage-gated ion channel activity	chloride transport, ion transport, transport
galactosamine (N-acetyl)-6-sulfate sulfatase	Galns	NP_057931	58	2	lysosome	calcium ion binding, catalytic activity, hydrolase activity, metal ion binding, N-acetylgalactosamine-6-sulfatase activity, sulfuric ester hydrolase activity	metabolic process
Nedd8 ultimate buster-1	Nub1	NP_058016	70	2	nucleus	not classified	not classified
MYB binding protein (P160) 1a	Mybbp1a	NP_058056	152	2	cytoplasm, NLS-dependent protein nuclear import complex, nucleolus, nucleus	DNA binding, DNA-directed DNA polymerase activity, protein binding, transcription factor binding, transcription repressor activity, zinc ion binding	negative regulation of transcription, nucleocytoplasmic transport, regulation of transcription, respiratory electron transport chain, transcription
thiopurine methyltransferase	Tpmt	NP_058065	28	2	cytoplasm	methyltransferase activity, thiopurine S-methyltransferase activity, transferase activity	metabolic process
ubiquitin-conjugating enzyme E2-25K	Ube2k	NP_058066	22	2	cellular_component, cytoplasm	ATP binding, ligase activity, nucleotide binding, small conjugating protein ligase activity, ubiquitin-protein ligase activity	modification-dependent protein catabolic process, post-translational protein modification, regulation of protein metabolic process
syntaxin 7	Stx7	NP_058077	30	2	endosome, integral to membrane, membrane	iron ion binding, protein binding, SNAP receptor activity	intracellular protein transport
ras homolog gene family, member A	Rhoa	NP_058082	22	2	cytoplasm, cytoskeleton, cytosol, intracellular, membrane, nucleus, plasma membrane	GTP binding, GTPase activity, nucleotide binding, protein binding	actin cytoskeleton organization, androgen receptor signaling pathway, cell adhesion, cell differentiation, cell morphogenesis, cell-matrix adhesion, integrin-mediated signaling pathway, negative regulation of neuron apoptosis, negative regulation of steroid hormone receptor signaling pathway, positive regulation of neuron differentiation, positive regulation of stress fiber formation, regulation of transcription from RNA polymerase II promoter, Rho protein signal transduction, skeletal muscle tissue development, small GTPase mediated signal transduction, stress fiber formation
RNA binding motif protein 3	Rbm3	NP_058089	17	2	not classified	nucleic acid binding, nucleotide binding, ribosomal large subunit binding, RNA binding	production of miRNAs involved in gene silencing by miRNA, response to cold, translation
ARP1 actin-related protein 1 homolog A	Actr1a	NP_058556	43	2	cytoplasm, cytoskeleton	ATP binding, nucleotide binding, protein binding	not classified
keratin complex 2, basic gene 18	Krt85	NP_058575	56	2	intermediate filament, keratin filament	structural molecule activity	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
Sec61 alpha subunit homolog	Sec61a1	NP_058602	52	2	endoplasmic reticulum, integral to membrane, membrane	P-P-bond-hydrolysis-driven protein transmembrane transporter activity, ribosome binding	protein transport, transmembrane transport, transport
ribosomal protein S3a	Rps3a	NP_058655	30	2	cytosol, intracellular, nucleus, ribonucleoprotein complex, ribosome	protein binding, structural constituent of ribosome	translation
eukaryotic translation elongation factor 1 beta 2	Eef1b2	NP_061266	25	2	eukaryotic translation elongation factor 1 complex	translation elongation factor activity	translation, translational elongation
nucleoporin 210	Nup210	NP_061285	204	2	endoplasmic reticulum, integral to membrane, membrane, nuclear envelope, nuclear pore, nucleus	not classified	mRNA transport, protein transport, transmembrane transport, transport
nucleolar protein 5	Nol5	NP_061356	60	2	nucleolus, nucleus	snoRNP binding	ribosome biogenesis
profilin 2	Pfn2	NP_062283	15	2	actin cytoskeleton, cytoplasm, cytoskeleton	actin binding, protein binding	actin cytoskeleton organization, cytoskeleton organization
arsA arsenite transporter, ATP-binding, homolog 1	Asna1	NP_062626	39	2	not classified	arsenite transmembrane-transporting ATPase activity, ATP binding, hydrolase activity, nucleotide binding	cellular metal ion homeostasis, response to arsenic
soc-2 (suppressor of clear) homolog	Shoc2	NP_062632	65	2	not classified	protein binding	not classified
NS1-associated protein 1 isoform 1	Syncrip	NP_062640	70	2	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, poly(A) RNA binding, RNA binding	mRNA processing, RNA splicing
RuvB-like protein 1	Ruvbl1	NP_062659	50	2	nucleus, ribonucleoprotein complex	ATP binding, DNA helicase activity, helicase activity, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding, protein binding	cell cycle, cell division, chromatin modification, DNA recombination, mitosis, regulation of growth, regulation of transcription, transcription
ADP-ribosylation factor-like 3	Arl3	NP_062692	20	2	Golgi apparatus, intracellular, membrane, nucleus	GTP binding, magnesium ion binding, metal ion binding, nucleotide binding	cell cycle, cell division, small GTPase mediated signal transduction
non-metastatic cells 3, protein expressed in	Nme3	NP_062704	19	2	not classified	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleoside diphosphate kinase activity, nucleotide binding, transferase activity	CTP biosynthetic process, GTP biosynthetic process, nucleotide metabolic process, UTP biosynthetic process
SUMO1 activating enzyme subunit 1	Sae1	NP_062722	39	2	nucleus	binding, catalytic activity, ligase activity, small protein activating enzyme activity	metabolic process, modification-dependent protein catabolic process, protein modification process
prostaglandin E synthase 3 (cytosolic)	Ptges3	NP_062740	19	2	cellular_component, cytoplasm	isomerase activity, molecular_function, prostaglandin-E synthase activity	cell proliferation, fatty acid biosynthetic process, glucocorticoid receptor signaling pathway, glycogen biosynthetic process, lipid biosynthetic process, lung saccule development, prostaglandin biosynthetic process, skin development
coatomer protein complex, subunit zeta 1	Copz1	NP_062791	20	2	COPI vesicle coat, COPI-coated vesicle, cytoplasm, cytoplasmic vesicle, Golgi apparatus, membrane, membrane coat	protein binding	intracellular protein transport, protein transport, transport, vesicle-mediated transport
adhesion regulating molecule 1	Adrm1	NP_062796	42	2	cytoplasm, nucleus, proteasome complex	not classified	not classified
canopy 2 homolog	Cnpy2	NP_064337	21	2	endoplasmic reticulum	molecular_function	biological_process
START domain containing 10	Stard10	NP_064374	33	2	cell projection, cilium, flagellum	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
signal transducing adaptor family member 1	Stap1	NP_064376	35	2	cellular_component, cytoplasm	protein binding, SH3/SH2 adaptor activity	myeloid cell differentiation, transmembrane receptor protein tyrosine kinase signaling pathway
Parkinson disease protein 7	Park7	NP_065594	20	2	cytoplasm, mitochondrion, nucleus	peroxiredoxin activity, RNA binding	adult locomotory behavior, cell proliferation, dopamine uptake, hydrogen peroxide metabolic process, membrane depolarization, membrane hyperpolarization, response to hydrogen peroxide, response to stress, synaptic transmission, dopaminergic
glucosidase 1	Gcs1	NP_065644	92	2	endoplasmic reticulum, integral to membrane, membrane	hydrolase activity, hydrolase activity, acting on glycosyl bonds, mannosyl-oligosaccharide glucosidase activity	metabolic process, oligosaccharide metabolic process
epsilon subunit of coatomer protein complex	Cope	NP_067513	35	2	COPI vesicle coat, COPI-coated vesicle, cytoplasm, cytoplasmic vesicle, Golgi apparatus, membrane	binding, protein binding, structural molecule activity	protein transport, retrograde vesicle-mediated transport, Golgi to ER, transport, vesicle-mediated transport
tropomyosin 3, gamma	Tpm3	NP_071709	33	2	cleavage furrow, cortical cytoskeleton, cytoplasm, cytoskeleton, filamentous actin, growth cone, neuron projection, podosome	actin binding	not classified
ribosomal protein L23	Rpl23	NP_075029	15	2	cytosolic ribosome, intracellular, nucleolus, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	Ndufb9	NP_075661	22	2	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
ubiquitin-conjugating enzyme E2 variant 1	Ube2v1	NP_075719	16	2	nucleus	protein binding, small conjugating protein ligase activity	modification-dependent protein catabolic process, post-translational protein modification, regulation of protein metabolic process
carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	Cad	NP_076014	243	2	cytoplasm, cytosol, nucleus	aspartate carbamoyltransferase activity, ATP binding, carbamoyl-phosphate synthase (glutamine-hydrolyzing) activity, dihydroorotase activity, protein kinase activity, transferase activity, UTP binding	'de novo' pyrimidine base biosynthetic process, peptidyl-threonine phosphorylation, protein amino acid autophosphorylation
ATPase, H+ transporting, V1 subunit D	Atp6v1d	NP_076210	28	2	proton-transporting two-sector ATPase complex, catalytic domain	ATPase activity, coupled to transmembrane movement of substances, proton-transporting ATPase activity, rotational mechanism	ATP synthesis coupled proton transport, ion transport, proton transport, transport
Sec61 beta subunit	Sec61b	NP_077133	10	2	cellular_component, endoplasmic reticulum, integral to membrane, membrane	ribosome binding	biological_process, protein transport, transmembrane transport, transport
nucleolar protein 5A	Nol5a	NP_077155	64	2	nucleus	not classified	ribosome biogenesis
quinoid dihydropteridine reductase	Qdpr	NP_077198	26	2	not classified	6,7-dihydropteridine reductase activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction, tetrahydrobiopterin biosynthetic process

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RAB6A, member RAS oncogene family	Rab6	NP_077249	24	2	Golgi apparatus, membrane	GTP binding, nucleotide binding, protein binding	intracellular protein transport, peptidyl-cysteine methylation, protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
RAB5C, member RAS oncogene family	Rab5c	NP_077776	23	2	endocytic vesicle, endosome, membrane, plasma membrane	GTP binding, GTPase activity, nucleotide binding	endosome organization, protein transport, regulation of endocytosis, small GTPase mediated signal transduction, transport
small glutamine-rich tetratricopeptide repeat (TPR) containing protein	Sgta	NP_078775	34	2	cellular_component	binding, protein binding, protein heterodimerization activity, protein homodimerization activity	biological_process
succinate dehydrogenase complex, subunit C, integral membrane protein	Sdhc	NP_079597	18	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	electron carrier activity, iron ion binding, metal ion binding, succinate dehydrogenase activity	electron transport chain, transport, tricarboxylic acid cycle
ubiquinol-cytochrome c reductase, complex III subunit VII	Uqcrq	NP_079628	10	2	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	ubiquinol-cytochrome-c reductase activity	electron transport chain, transport
acylphosphatase 1, erythrocyte (common) type	Acyp1	NP_079697	11	2	not classified	acylphosphatase activity, hydrolase activity	not classified
DnaJ (Hsp40) homolog, subfamily C, member 5 beta	Dnajc5b	NP_079765	23	2	membrane	heat shock protein binding, unfolded protein binding	protein folding
DC2 protein	2310008M10 Rik	NP_079785	17	2	integral to membrane, membrane	not classified	not classified
proteasome, 26S, non-ATPase regulatory subunit 6	Psmd6	NP_079826	46	2	proteasome complex	not classified	not classified
13kDa differentiation-associated protein	Ndufa12	NP_079827	18	2	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	electron carrier activity, NADH dehydrogenase (ubiquinone) activity	electron transport chain, transport
polymerase (RNA) II (DNA directed) polypeptide E	Polr2e	NP_079830	25	2	nucleus	DNA binding, DNA-directed RNA polymerase activity	transcription
cytochrome b5 type B precursor	Cyb5b	NP_079834	16	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	heme binding, iron ion binding, metal ion binding	electron transport chain, transport
ribosomal protein L35	Rpl35	NP_079868	15	2	cellular_component, intracellular, ribonucleoprotein complex, ribosome	molecular_function, structural constituent of ribosome	biological_process, translation
NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	Ndufb3	NP_079873	12	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity	electron transport chain, transport
translocase of inner mitochondrial membrane 50 homolog	Timm50	NP_079892	40	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	interleukin-2 receptor binding, phosphoprotein phosphatase activity, protein binding	protein transport, release of cytochrome c from mitochondria, transmembrane transport, transport
UMP-CMP kinase	Cmpk	NP_079923	26	2	cytoplasm, nucleus	ATP binding, cytidylate kinase activity, kinase activity, nucleobase, nucleoside, nucleotide kinase activity, nucleotide binding, nucleotide kinase activity, phosphotransferase activity, phosphate group as acceptor, transferase activity	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, pyrimidine nucleotide biosynthetic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
signal recognition particle 72	Srp72	NP_079967	75	2	nucleolus, signal recognition particle, endoplasmic reticulum targeting	molecular_function	SRP-dependent cotranslational protein targeting to membrane
trafficking protein particle complex 5	Trappc5	NP_079977	21	2	endoplasmic reticulum, Golgi apparatus, TRAPP complex	protein binding	transport, vesicle-mediated transport
tetratricopeptide repeat domain 35	Ttc35	NP_080012	35	2	nucleus	binding	not classified
coiled-coil domain containing 47	Ccdc47	NP_080285	56	2	endoplasmic reticulum, integral to membrane, membrane, microsome	calcium ion binding	calcium ion homeostasis, embryonic development, ER overload response, post-embryonic development
small nuclear ribonucleoprotein D3	Snrpd3	NP_080371	14	2	cytoplasm, nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding	mRNA processing, RNA splicing
signal sequence receptor, gamma	Ssr3	NP_080431	21	2	endoplasmic reticulum, integral to endoplasmic reticulum membrane, integral to membrane, membrane, translocon complex	receptor activity	cotranslational protein targeting to membrane
ribosomal protein S27-like	Rps27l	NP_080743	9	2	not classified	not classified	not classified
TNF receptor-associated protein 1	Trap1	NP_080784	80	2	mitochondrion	ATP binding, nucleotide binding, unfolded protein binding	protein folding, response to stress
chitinase domain containing 1	Chid1	NP_080798	36	2	extracellular region, lysosome	catalytic activity, cation binding, chitinase activity, hydrolase activity, hydrolyzing O-glycosyl compounds	carbohydrate metabolic process, chitin catabolic process
dynein light chain LC8-type 2	Dynll2	NP_080832	10	2	cytoplasm, dynein complex, microtubule, microtubule associated complex, myosin complex	microtubule motor activity, motor activity, protein binding	intracellular transport, microtubule-based process
nucleolar protein family A, member 1	Nola1	NP_080854	23	2	dense fibrillar component, nucleus, ribonucleoprotein complex, small nucleolar ribonucleoprotein complex	RNA binding, rRNA binding, snoRNA binding	biological_process, ribosome biogenesis, rRNA processing
family with sequence similarity 98, member B	2610510H03Rik	NP_080896	45	2	not classified	not classified	not classified
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	Ndufb10	NP_080960	21	2	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	not classified	electron transport chain, transport
enoyl Coenzyme A hydratase domain containing 2	Echdc2	NP_081004	26	2	mitochondrion	catalytic activity, lyase activity	fatty acid metabolic process, lipid metabolic process, metabolic process
dolichyl-phosphate mannosyltransferase polypeptide 3	Dpm3	NP_081043	10	2	endoplasmic reticulum, integral to membrane, membrane	not classified	not classified
RAB, member of RAS oncogene family-like 2A	Rabl2a	NP_081093	26	2	not classified	GTP binding, nucleotide binding	not classified
histidine triad nucleotide binding protein 2	Hint2	NP_081147	17	2	extracellular region, mitochondrion	catalytic activity, hydrolase activity	not classified
bolA-like 1	Bola1	NP_081251	14	2	not classified	not classified	not classified
translocation protein 1	Sec62	NP_081292	46	2	endoplasmic reticulum, integral to membrane, membrane	protein transporter activity	protein transport, transmembrane transport, transport
mannosidase, beta A, lysosomal	Manba	NP_081564	101	2	lysosome	beta-mannosidase activity, catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds	carbohydrate metabolic process, glycoprotein catabolic process, metabolic process

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asparaginyl-tRNA synthetase	Nars	NP_081626	63	2	cytoplasm	aminoacyl-tRNA ligase activity, asparagine-tRNA ligase activity, aspartate-tRNA ligase activity, ATP binding, ligase activity, nucleic acid binding, nucleotide binding	asparaginyl-tRNA aminoacylation, aspartyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
golgi reassembly stacking protein 2	Gorasp2	NP_081628	47	2	Golgi apparatus, membrane	molecular_function, protein binding	biological_process
proteasome 26S non-ATPase subunit 1	Psmd1	NP_081633	106	2	proteasome complex	binding, enzyme regulator activity	regulation of protein catabolic process
hypothetical protein LOC70564	5730469M10 Rik	NP_081740	24	2	extracellular region	not classified	not classified
IQ motif containing GTPase activating protein 2	Iqgap2	NP_081987	181	2	intracellular	calmodulin binding, GTPase activator activity, protein binding	regulation of small GTPase mediated signal transduction
zinc finger protein 297B isoform a	Zbtb43	NP_082223	57	2	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, protein binding, zinc ion binding	regulation of transcription, transcription
serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 12	Serpinb12	NP_082247	48	2	cytoplasm	peptidase inhibitor activity, serine-type endopeptidase inhibitor activity	not classified
keratin 33A	Krt33a	NP_082259	46	2	cellular_component, intermediate filament	protein binding, structural molecule activity	biological_process
thioredoxin domain containing 1	Txndc1	NP_082615	31	2	endoplasmic reticulum, integral to membrane, membrane	not classified	cell redox homeostasis, electron transport chain, transport
hypothetical protein LOC73112	3110003A17 Rik	NP_082716	9	2	not classified	not classified	not classified
RNA binding motif protein 19	Rbm19	NP_083038	106	2	nucleolus, nucleus	nucleic acid binding, nucleotide binding, RNA binding	not classified
septin 14	1700016K13 Rik	NP_083102	50	2	septin complex	GTP binding, nucleotide binding, protein binding	cell cycle, cell division
fumarylacetoacetate hydrolase domain containing 2A	Fahd2a	NP_083905	35	2	not classified	calcium ion binding, catalytic activity, hydrolase activity, magnesium ion binding, metal ion binding	metabolic process
signal peptidase complex subunit 3	Spcs3	NP_083977	20	2	not classified	not classified	not classified
actin related protein 2/3 complex, subunit 2	Arpc2	NP_083987	34	2	Arp2/3 protein complex, cell leading edge, cell projection, cytoplasm, cytoskeleton, focal adhesion	actin binding, protein binding	positive regulation of actin filament polymerization, regulation of actin filament polymerization
ADP-ribosylation factor interacting protein 2	Arfip2	NP_084078	38	2	not classified	not classified	not classified
hypothetical protein LOC77006	2600009E05 Rik	NP_084108	36	2	extracellular region	not classified	not classified
transmembrane protein 33 isoform 2	Tmem33	NP_084384	28	2	cellular_component, integral to membrane, membrane	protein binding	biological_process
splicing factor 3b, subunit 2	Sf3b2	NP_084385	98	2	not classified	protein binding	not classified
V-set and immunoglobulin domain containing 1	Vsig1	NP_084457	44	2	integral to membrane, membrane	not classified	not classified
melanoma antigen family D, 2	Maged2	NP_109625	65	2	cellular_component	molecular_function	biological_process
phosphoglycerate kinase 2	Pgk2	NP_112467	45	2	cytoplasm	ATP binding, kinase activity, nucleotide binding, phosphoglycerate kinase activity, transferase activity	glycolysis
septin 8	8-Sep	NP_149156	50	2	septin complex	GTP binding, nucleotide binding, protein binding	cell cycle

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aldehyde dehydrogenase family 1, subfamily A3	Aldh1a3	NP_444310	56	2	cytoplasm	3-chloroallyl aldehyde dehydrogenase activity, aldehyde dehydrogenase (NAD) activity, aldehyde dehydrogenase [NAD(P)+] activity, NAD binding, oxidoreductase activity, thyroid hormone binding	embryonic camera-type eye development, embryonic eye morphogenesis, face development, metabolic process, nucleus accumbens development, olfactory pit development, optic cup morphogenesis involved in camera-type eye development, oxidation reduction, positive regulation of apoptosis, positive regulation of retinoic acid receptor signaling pathway, retinoic acid biosynthetic process, retinoic acid metabolic process
glutaredoxin	Glrx	NP_444338	12	2	cytoplasm	electron carrier activity, protein disulfide oxidoreductase activity, protein-disulfide reductase (glutathione) activity	cell redox homeostasis, electron transport chain, transport
phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	Pip4k2c	NP_473438	47	2	cytoplasm, membrane	1-phosphatidylinositol-5-phosphate 4-kinase activity, ATP binding, kinase activity, nucleotide binding, phosphatidylinositol phosphate kinase activity, transferase activity	phosphatidylinositol metabolic process
glyoxylate reductase/hydroxypyruvate reductase	Grhpr	NP_525028	35	2	not classified	binding, catalytic activity, cofactor binding, glyoxylate reductase (NADP) activity, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	metabolic process, oxidation reduction
SH3 domain binding glutamic acid-rich protein-like 3	Sh3bgrl3	NP_542126	10	2	cytoplasm, nucleus	electron carrier activity, protein disulfide oxidoreductase activity	cell redox homeostasis
WD repeat domain 5	Wdr5	NP_543124	37	2	histone methyltransferase complex, intracellular, nucleus	protein binding	skeletal system development
acetyl-Coenzyme A acyltransferase 1	Acaa1a	NP_570934	44	2	peroxisome	acetyl-CoA C-acetyltransferase activity, acetyl-CoA C-acyltransferase activity, acyltransferase activity, catalytic activity, transferase activity, transferase activity, transferring acyl groups other than amino-acyl groups	fatty acid metabolic process, lipid metabolic process, metabolic process
suppression of tumorigenicity 13	St13	NP_598487	42	2	cytoplasm	binding	not classified
glutaminyl-tRNA synthetase	Qars	NP_598555	88	2	aminoacyl-tRNA synthetase multienzyme complex	aminoacyl-tRNA ligase activity, ATP binding, glutamine-tRNA ligase activity, ligase activity, nucleotide binding, protein kinase binding, RNA binding	anti-apoptosis, translation
leucine rich repeat containing 59	Lrrc59	NP_598568	35	2	endoplasmic reticulum, integral to membrane, membrane, microsome	protein binding	not classified

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PDZ-domain protein scribble	Scrib	NP_598850	180	2	basolateral plasma membrane, cytoplasm, membrane	protein binding	asymmetric protein localization, cell migration, mammary gland duct morphogenesis, morphogenesis of embryonic epithelium, positive chemotaxis
transmembrane protein 109	Tmem109	NP_598903	26	2	cellular_component, endoplasmic reticulum, integral to membrane, membrane, nucleus, sarcoplasmic reticulum	molecular_function	biological_process
aldehyde dehydrogenase family 7, member A1	Aldh7a1	NP_613066	56	2	mitochondrion	L-aminoadipate-semialdehyde dehydrogenase activity, oxidoreductase activity	metabolic process, oxidation reduction
3-mercaptopyruvate sulfurtransferase	Mpst	NP_619611	33	2	cytoplasm, mitochondrial inner membrane, mitochondrion	3-mercaptopyruvate sulfurtransferase activity, thiosulfate sulfurtransferase activity, transferase activity	sulfate transport
UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	Galnt2	NP_644678	65	2	extracellular region, Golgi apparatus, Golgi lumen, integral to membrane, membrane	calcium ion binding, manganese ion binding, polypeptide N-acetylgalactosaminyltransferase activity, sugar binding, transferase activity, transferase activity, transferring glycosyl groups	protein amino acid O-linked glycosylation
biliverdin reductase B (flavin reductase (NADPH))	Blvrb	NP_659172	22	2	cytoplasm	biliverdin reductase activity, binding, catalytic activity, coenzyme binding, flavin reductase activity, oxidoreductase activity	cellular metabolic process, metabolic process, oxidation reduction
serine/threonine protein kinase 24	Stk24	NP_663440	48	2	cytoplasm	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation
methionine adenosyltransferase II, alpha	Mat2a	NP_663544	44	2	not classified	ATP binding, cobalt ion binding, magnesium ion binding, metal ion binding, methionine adenosyltransferase activity, nucleotide binding, potassium ion binding, transferase activity	one-carbon metabolic process, S-adenosylmethionine biosynthetic process
carbonic reductase 4	Cbr4	NP_663570	25	2	cytoplasm	binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
polymerase (RNA) II (DNA directed) polypeptide H	Polr2h	NP_663607	17	2	nucleus	DNA-directed RNA polymerase activity	transcription
histone cluster 1, H1d	Hist1h1d	NP_663759	22	2	chromosome, nucleosome, nucleus	DNA binding, protein binding	nucleosome assembly, nucleosome positioning
chromodomain helicase DNA binding protein 4	Chd4	NP_666091	218	2	chromatin, nucleus	ATP binding, ATP-dependent helicase activity, chromatin binding, DNA binding, helicase activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides, metal ion binding, nucleic acid binding, nucleotide binding, protein binding, transcription factor binding, zinc ion binding	chromatin assembly or disassembly, chromatin modification, regulation of transcription, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
3-hydroxyisobutyryl-Coenzyme A hydrolase	Hibch	NP_666220	43	2	mitochondrion	3-hydroxyisobutyryl-CoA hydrolase activity, catalytic activity, hydrolase activity	branched chain family amino acid catabolic process, metabolic process
thyroid hormone receptor associated protein 3	Thrap3	NP_666265	108	2	mediator complex, nucleus	ATP binding, nucleotide binding, receptor activity, transcription coactivator activity	positive regulation of transcription from RNA polymerase II promoter, regulation of transcription, transcription, transcription from RNA polymerase II promoter
actin-related protein 2	Actr2	NP_666355	45	2	cell projection, cytoplasm, cytoskeleton	actin binding, ATP binding, nucleotide binding, protein binding	not classified
4-hydroxyphenylpyruvate dioxygenase-like	Hpdl	NP_666368	40	2	not classified	4-hydroxyphenylpyruvate dioxygenase activity	aromatic amino acid family metabolic process
ubiquitin specific peptidase 9, Y chromosome	Usp9y	NP_683745	292	2	not classified	cysteine-type peptidase activity, hydrolase activity, peptidase activity, ubiquitin thiolesterase activity	modification-dependent protein catabolic process
brain glycogen phosphorylase	Pygb	NP_722476	97	2	axon	phosphorylase activity, pyridoxal phosphate binding, transferase activity, transferase activity, transferring glycosyl groups	carbohydrate metabolic process, glycogen metabolic process
pyridoxal (pyridoxine, vitamin B6) kinase	Pdxk	NP_742146	35	2	cytoplasm	ATP binding, kinase activity, metal ion binding, nucleotide binding, pyridoxal kinase activity, transferase activity, zinc ion binding	pyridoxine biosynthetic process
hypothetical protein LOC230249	AI314180	NP_759013	204	2	endoplasmic reticulum, endosome, nucleus, proteasome complex	binding	not classified
hypothetical protein LOC68832	1110057K04Rik	NP_765989	37	2	not classified	not classified	not classified
solute carrier family 25 (mitochondrial carrier, Aralar), member 12	Slc25a12	NP_766024	75	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	binding, calcium ion binding, transporter activity	malate-aspartate shuttle, transport
sushi, nidogen and EGF-like domains 1	Sned1	NP_766051	152	2	not classified	calcium ion binding	cell-matrix adhesion
translocase of outer mitochondrial membrane 22 homolog	Tomm22	NP_766197	16	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrial outer membrane, mitochondrion	receptor activity	protein transport, transmembrane transport, transport
pogo transposable element with ZNF domain	Pogz	NP_766271	155	2	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	multicellular organismal development, regulation of transcription
splicing factor, arginine/serine-rich 1 isoform 1	Sfrs1	NP_775550	28	2	cytoplasm, nucleus, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding, RS domain binding	cardiac muscle contraction, in utero embryonic development, mRNA processing, RNA splicing
ATPase, H+ transporting, V0 subunit D isoform 2	Atp6v0d2	NP_780615	40	2	early endosome, proton-transporting two-sector ATPase complex, proton-transporting domain, proton-transporting V-type ATPase, V0 domain	hydrogen ion transmembrane transporter activity	ATP synthesis coupled proton transport, ion transport, proton transport, transport
hypothetical protein LOC319675	5830418K08Rik	NP_795950	269	2	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
myosin IIIB	Myo3b	NP_796350	151	2	cytoplasm, cytoskeleton, myosin complex	actin binding, ATP binding, kinase activity, motor activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	protein amino acid phosphorylation, response to stimulus, visual perception
myosin ID	Myo1d	NP_796364	116	2	myosin complex	actin binding, ATP binding, calmodulin binding, motor activity, nucleotide binding	not classified
ATPase, H+ transporting, lysosomal V1 subunit G3	Atp6v1g3	NP_796371	14	2	cytosol, membrane, plasma membrane, vacuolar proton-transporting V-type ATPase complex	hydrogen-exporting ATPase activity, phosphorylative mechanism, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	ATP hydrolysis coupled proton transport, ion transport, proton transport, transport
amplified in osteosarcoma	Os9	NP_808282	70	2	not classified	not classified	not classified
ROD1 regulator of differentiation 1 isoform 2	Rod1	NP_835458	57	2	nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing
cystathionine beta-synthase isoform 2	Cbs	NP_835742	60	2	cytoplasm, nucleus	catalytic activity, cystathionine beta-synthase activity, iron ion binding, lyase activity, metal ion binding, pyridoxal phosphate binding	cellular amino acid biosynthetic process, cysteine biosynthetic process, cysteine biosynthetic process from serine, cysteine biosynthetic process via cystathionine, endochondral ossification, homocysteine metabolic process, metabolic process, regulation of JUN kinase activity, response to folic acid
eukaryotic translation initiation factor 5A	Eif5a	NP_853613	17	2	cytoplasm, endoplasmic reticulum, membrane, nuclear pore, nucleus	ribosome binding, RNA binding, translation elongation factor activity	apoptosis, mRNA transport, peptidyl-lysine modification to hypusine, positive regulation of translational elongation, positive regulation of translational termination, protein transport, translation, translational frameshifting, transmembrane transport, transport
NADH dehydrogenase subunit 1	ND1	NP_904328	36	2	integral to membrane, mitochondrion	NADH dehydrogenase (ubiquinone) activity, oxidoreductase activity	oxidation reduction
heterogeneous nuclear ribonucleoprotein A3 isoform a	Hnrnpa3	NP_932758	40	2	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
mitochondrial ribosomal protein S26	Mrps26	NP_997090	23	2	mitochondrion, ribonucleoprotein complex, ribosome	not classified	not classified
PREDICTED: thyroid hormone receptor interactor 11 isoform 3	Trip11	XP_001001171	226	2	not classified	receptor activity	not classified
PREDICTED: similar to 3-methylcrotonyl-CoA carboxylase alpha subunit	LOC677576	XP_001005025	28	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100048803	XP_001471667	22	2	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process
PREDICTED: hypothetical protein isoform 2	LOC100039257	XP_001472723	15	2	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein S8 isoform 2	LOC100040298	XP_001474171	24	2	not classified	not classified	not classified
PREDICTED: similar to nuclear pore complex-associated intranuclear coiled-coil protein TPR	LOC100043998	XP_001474187	149	2	not classified	not classified	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
PREDICTED: similar to 22 kDa neuronal tissue-enriched acidic protein	LOC100045716	XP_001474846	11	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100040970	XP_001475621	24	2	ribosome	not classified	not classified
PREDICTED: hypothetical protein	LOC100047609	XP_001479061	70	2	not classified	not classified	not classified
PREDICTED: similar to 60S ribosomal protein L9 isoform 1	LOC100048162	XP_001480029	22	2	not classified	not classified	not classified
PREDICTED: similar to Rab5B	LOC433464	XP_485050	22	2	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG665562	XP_915749	14	2	not classified	not classified	not classified
PREDICTED: similar to Snrpf protein	Snrpf	XP_919276	23	2	nucleus, ribonucleoprotein complex, spliceosomal complex	RNA binding	mRNA processing, RNA splicing
PREDICTED: hypothetical protein isoform 2	LOC637555	XP_929443	19	2	not classified	not classified	not classified
PREDICTED: NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11 isoform 6	Ndufa11	XP_930081	15	2	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	protein transporter activity	electron transport chain, protein transport, transport
PREDICTED: similar to hCG1816075	1700027A15Rik	XP_989739	10	2	not classified	not classified	not classified
PREDICTED: similar to zeta proteasome chain; PSMA5	LOC676113	XP_992657	26	2	not classified	not classified	not classified
hypothetical protein LOC407819	BC031181	NP_001001181	8	1	not classified	not classified	not classified
tropomyosin 4	Tpm4	NP_001001491	28	1	cortical cytoskeleton, cytoplasm, cytoskeleton, filamentous actin, podosome	actin binding, calcium ion binding, metal ion binding	not classified
nucleoporin 85	Nup85	NP_001002929	75	1	cytoplasm, membrane, nuclear pore, nucleus, plasma membrane	CCR2 chemokine receptor binding	chemotaxis, cytokine-mediated signaling pathway, lamellipodium assembly, macrophage chemotaxis, mRNA transport, protein transport, transmembrane transport, transport
type II keratin Kb14	EG406223	NP_001003670	60	1	intermediate filament	not classified	not classified
Rho guanine nucleotide exchange factor (GEF) 11	Arhgef11	NP_001003912	172	1	cytoplasm	G-protein-coupled receptor binding	G-protein coupled receptor protein signaling pathway
hypothetical protein LOC237730	AI595406	NP_001004147	33	1	nucleus, ribonucleoprotein complex	methyltransferase activity, RNA binding, transferase activity	rRNA processing, tRNA processing
zinc finger protein 366	Zfp366	NP_001004149	85	1	nucleus	not classified	not classified
signal peptide, CUB domain, EGF-like 3	Scube3	NP_001004366	109	1	extracellular region	calcium ion binding	not classified
eukaryotic translation initiation factor 2A	Eif2a	NP_001005509	64	1	not classified	translation initiation factor activity	positive regulation of signal transduction, protein amino acid phosphorylation, regulation of translation, SREBP-mediated signaling pathway, translation
pyruvate dehydrogenase phosphatase isoenzyme 2	4833426J09Rik	NP_001019777	60	1	not classified	hydrolase activity, magnesium ion binding, metal ion binding, phosphoprotein phosphatase activity	not classified
Rho GTPase activating protein 15 isoform 2	Arhgap15	NP_001020548	21	1	cytoplasm, intracellular, membrane	GTPase activator activity, protein binding, Rac GTPase activator activity	regulation of cell shape, signal transduction
hypothetical protein LOC207806	Gm608	NP_001025060	237	1	not classified	not classified	not classified
UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	Uap1l1	NP_001028465	57	1	not classified	nucleotidyltransferase activity, transferase activity	metabolic process
coiled-coil domain containing 61	Ccdc61	NP_001028486	57	1	not classified	not classified	not classified
hypothetical protein LOC241694	A230067G21Rik	NP_001028520	214	1	cytoplasm, intracellular	GTPase activator activity	regulation of small GTPase mediated signal transduction
zinc finger and SCAN domains 10	Zscan10	NP_001028597	88	1	cellular_component, nucleus	metal ion binding, molecular_function, zinc ion binding	biological_process, regulation of transcription, transcription
hypothetical protein LOC432613	4933422H20Rik	NP_001028947	71	1	not classified	metal ion binding, zinc ion binding	not classified
tubulin, alpha-like 3	Tubal3	NP_001029051	50	1	microtubule, protein complex	GTP binding, GTPase activity, nucleotide binding, structural molecule activity	microtubule-based movement, microtubule-based process, protein polymerization

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
dynamin 3 isoform 1	Dnm3	NP_001033708	97	1	cytoplasm, cytoskeleton, microtubule, mitochondrion	GTP binding, GTPase activity, hydrolase activity, molecular_function, motor activity, nucleotide binding	biological_process, endocytosis
mitogen activated protein kinase 1	Mapk1	NP_001033752	41	1	cytoplasm, cytosol, nucleus	ATP binding, kinase activity, MAP kinase 2 activity, MAP kinase activity, nucleotide binding, phosphotyrosine binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transcription regulator activity, transferase activity	B cell receptor signaling pathway, cell cycle, cytosine metabolic process, labyrinthine layer blood vessel development, lipopolysaccharide-mediated signaling pathway, MAPKKK cascade, negative regulation of cell differentiation, organ morphogenesis, peptidyl-serine phosphorylation, protein amino acid phosphorylation, regulation of transcription factor activity, response to DNA damage stimulus, response to exogenous dsRNA, response to lipopolysaccharide, T cell receptor signaling pathway
sec13-like protein isoform a	Seh1l	NP_001034177	40	1	nuclear pore, nucleus	not classified	cell cycle, cell division, chromosome segregation, mitosis, mRNA transport, protein transport, transmembrane transport, transport
TRIO and F-actin binding protein isoform 3	Triobp	NP_001034245	223	1	cellular_component, cytoplasm, cytoskeleton, nucleus	actin binding, molecular_function	biological_process
cytoplasmic linker 2 isoform b	Clip2	NP_001034251	112	1	cytoplasm, cytoplasmic microtubule, cytoskeleton, microtubule	protein binding	not classified
nucleolar and coiled-body phosphoprotein 1 isoform D	Nolc1	NP_001034442	74	1	Cajal body, nucleolus, nucleoplasm, small nuclear ribonucleoprotein complex	protein binding	nucleolus organization
La ribonucleoprotein domain family, member 2	Larp2	NP_001035489	39	1	ribonucleoprotein complex	nucleic acid binding	not classified
thioredoxin reductase 1 isoform 1	Txnrd1	NP_001035988	67	1	cytoplasm, cytosol, nucleus	FAD binding, NADP or NADPH binding, oxidoreductase activity, selenium binding, thioredoxin-disulfide reductase activity	cell proliferation, cell redox homeostasis, gastrulation, mesoderm formation, oxidation reduction
DEAH (Asp-Glu-Ala-His) box polypeptide 15 isoform 1	Dhx15	NP_001036085	80	1	nucleus	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleoside-triphosphatase activity, nucleotide binding	mRNA processing, RNA splicing
interleukin enhancer binding factor 3 isoform 4	Ilf3	NP_001036174	76	1	intracellular, nucleus	DNA binding, double-stranded RNA binding, protein binding, RNA binding	protein amino acid methylation, regulation of transcription, transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glutaryl-Coenzyme A dehydrogenase	Gcdh	NP_001038209	49	1	mitochondrial inner membrane, mitochondrion	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, glutaryl-CoA dehydrogenase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	metabolic process, oxidation reduction
clathrin interactor 1	Clint1	NP_001038985	68	1	cytoplasm, cytoplasmic vesicle, membrane	lipid binding, protein binding	endocytosis
cofactor required for Sp1 transcriptional activation, subunit 2 isoform a	Med14	NP_001041673	161	1	mediator complex, nucleus	protein binding, RNA polymerase II transcription mediator activity, transcription coactivator activity	positive regulation of transcription from RNA polymerase II promoter, regulation of transcription, regulation of transcription from RNA polymerase II promoter, transcription
GNAS complex locus isoform g	Gnas	NP_001070978	44	1	cell projection, heterotrimeric G-protein complex, membrane, membrane fraction, plasma membrane	GTP binding, GTPase activity, guanyl nucleotide binding, nucleotide binding, protein binding, signal transducer activity	activation of adenylate cyclase activity by dopamine receptor signaling pathway, activation of adenylate cyclase activity by G-protein signaling pathway, cartilage development, embryonic cranial skeleton morphogenesis, embryonic hindlimb morphogenesis, endochondral ossification, energy reserve metabolic process, G-protein coupled receptor protein signaling pathway, positive regulation of osteoblast differentiation, positive regulation of osteoclast differentiation, post-embryonic body morphogenesis, post-embryonic development, response to drug, signal transduction, skeletal system development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
protein tyrosine phosphatase, non-receptor type 6 isoform b	Ptpn6	NP_001071173	68	1	alpha-beta T cell receptor complex, cytoplasm, nucleus	hydrolase activity, phosphatase activity, phosphoprotein phosphatase activity, phosphotyrosine binding, protein binding, protein tyrosine phosphatase activity, SH2 domain binding, SH3 domain binding	B cell receptor signaling pathway, cytokine-mediated signaling pathway, dephosphorylation, intracellular signaling cascade, natural killer cell mediated cytotoxicity, negative regulation of humoral immune response mediated by circulating immunoglobulin, negative regulation of MAP kinase activity, negative regulation of MAPKKK cascade, negative regulation of peptidyl-tyrosine phosphorylation, negative regulation of T cell proliferation, negative regulation of T cell receptor signaling pathway, protein amino acid dephosphorylation, regulation of B cell differentiation
hypothetical protein LOC74854	4930402F06 Rik	NP_001074178	40	1	not classified	transferase activity, transferase activity, transferring glycosyl groups	not classified
general transcription factor II I isoform 5	Gtf2i	NP_001074218	108	1	cell projection, cell soma, cytoplasm, nucleus	DNA binding, mitogen-activated protein kinase binding	embryonic development, regulation of transcription, transcription
Ras-GTPase-activating protein (GAP120) SH3-domain binding protein 2 isoform a	G3bp2	NP_001074266	54	1	cellular_component, intracellular	nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA transport, small GTPase mediated signal transduction, transport
gastric inhibitory polypeptide receptor	Gipr	NP_001074284	53	1	integral to membrane, membrane, plasma membrane	gastric inhibitory peptide receptor activity, G-protein coupled receptor activity, receptor activity, signal transducer activity, transmembrane receptor activity	cell surface receptor linked signal transduction, G-protein coupled receptor protein signaling pathway, neuropeptide signaling pathway, signal transduction
PDZ domain containing 2	Pdzd2	NP_001074533	297	1	cell junction	protein binding	not classified
ankyrin repeat domain 26	Ankrd26	NP_001074581	192	1	actin filament	molecular_function	negative regulation of multicellular organism growth, negative regulation of organ growth, regulation of fatty acid metabolic process, regulation of feeding behavior, regulation of lipid metabolic process
dehydrogenase E1 and transketolase domain containing 1	Dhtkd1	NP_001074600	103	1	cellular_component, mitochondrion	molecular_function, oxidoreductase activity, oxidoreductase activity, acting on the aldehyde or oxo group of donors, disulfide as acceptor, oxoglutarate dehydrogenase (succinyl-transferring) activity, thiamin pyrophosphate binding	biological_process, glycolysis, metabolic process, oxidation reduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
laminin, alpha 5	Lama5	NP_001074640	404	1	basal lamina, basement membrane, extracellular matrix, extracellular region, laminin-1 complex, laminin-10 complex, proteinaceous extracellular matrix	integrin binding, protein binding, receptor binding	branching involved in salivary gland morphogenesis, branching involved in ureteric bud morphogenesis, branching morphogenesis of a tube, cell adhesion, cilium assembly, hair follicle development, lung development, morphogenesis of a polarized epithelium, morphogenesis of embryonic epithelium, muscle organ development, neural crest cell migration, odontogenesis of dentine-containing tooth, organ morphogenesis, regulation of cell adhesion, regulation of cell migration, regulation of cell proliferation, regulation of embryonic development
phosphatidylinositol glycan anchor biosynthesis, class G	Pigg	NP_001074703	108	1	endoplasmic reticulum	CP2 mannose-ethanolamine phosphotransferase activity, protein binding	GPI anchor biosynthetic process
p53-associated parkin-like cytoplasmic protein	Parc	NP_001074804	281	1	anaphase-promoting complex, cullin-RING ubiquitin ligase complex, cytoplasm	ATP binding, metal ion binding, nucleotide binding, protein binding, ubiquitin protein ligase binding, zinc ion binding	modification-dependent protein catabolic process, regulation of mitotic metaphase/anaphase transition, ubiquitin-dependent protein catabolic process
kinase D-interacting substrate of 220 kDa	C330002I19 Rik	NP_001074847	199	1	not classified	not classified	not classified
unc-13 homolog B	Unc13b	NP_001074882	182	1	cell junction, cellular_component, cytoplasm, Golgi apparatus, membrane, synapse	diacylglycerol binding, metal ion binding, non-kinase phorbol ester receptor activity, zinc ion binding	exocytosis, intracellular signaling cascade, synaptic transmission, synaptic vesicle priming
hypothetical protein LOC665775	A230054D04 Rik	NP_001074891	327	1	not classified	not classified	not classified
hypothetical protein LOC100039834	LOC1000398 34	NP_001092785	24	1	not classified	not classified	not classified
transmembrane protein 22	Tmem22	NP_001094953	46	1	not classified	not classified	not classified
pleckstrin homology-like domain, family B, member 3	Phldb3	NP_001096083	73	1	not classified	not classified	not classified
cellular nucleic acid binding protein isoform 3	Cnbp	NP_001103216	19	1	cytoplasm, cytosol, endoplasmic reticulum, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	positive regulation of cell proliferation, positive regulation of transcription from RNA polymerase II promoter, regulation of transcription, transcription
hypothetical protein LOC619288	4933417M04 Rik	NP_001103229	64	1	not classified	not classified	not classified
acid phosphatase 1, soluble isoform 1	Acp1	NP_001103709	18	1	cytoplasm	acid phosphatase activity, hydrolase activity, non-membrane spanning protein tyrosine phosphatase activity, phosphatase activity, phosphoprotein phosphatase activity, protein tyrosine phosphatase activity	protein amino acid dephosphorylation

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
splicing factor 1 isoform 1	Sf1	NP_001104261	68	1	cytoplasm, nucleus, spliceosomal complex	metal ion binding, nucleic acid binding, RNA binding, zinc ion binding	cell cycle process, Leydig cell differentiation, male sex determination, mRNA processing, regulation of steroid biosynthetic process, regulation of transcription, RNA splicing, transcription
DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	Ddx6	NP_001104296	54	1	cytoplasm	ATP binding, ATP-dependent helicase activity, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding, RNA binding	not classified
hypothetical protein LOC666274	EG666274	NP_001104748	19	1	not classified	not classified	not classified
outer dense fiber of sperm tails 2 isoform b	Odf2	NP_001106685	75	1	cell projection, centriole, cilium, flagellum, microtubule	structural constituent of cytoskeleton	cell differentiation, multicellular organismal development, spermatogenesis
ATP-binding cassette, sub-family A (ABC1), member 2	Abca2	NP_031405	271	1	integral to membrane, lysosomal membrane, membrane	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	cholesterol metabolic process, transport
acid phosphatase 2, lysosomal	Acp2	NP_031413	49	1	integral to membrane, lysosome, membrane	acid phosphatase activity, hydrolase activity	lysosome organization, skeletal system development
adenylosuccinate synthetase 1	Adssl1	NP_031447	50	1	cytoplasm, membrane	adenylosuccinate synthase activity, GTP binding, ligase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein binding	purine nucleotide biosynthetic process, purine nucleotide metabolic process
alkaline phosphatase 2, liver precursor	Alpl	NP_031457	58	1	anchored to membrane, membrane, plasma membrane	alkaline phosphatase activity, catalytic activity, hydrolase activity, magnesium ion binding, metal ion binding, phosphatase activity, zinc ion binding	metabolic process, response to antibiotic
apoptosis inhibitor 5	Api5	NP_031492	57	1	cytoplasm, nucleus, spliceosomal complex	not classified	anti-apoptosis, apoptosis
Na+/K+ -ATPase beta 3 subunit	Atp1b3	NP_031528	32	1	cytoplasm, integral to membrane, membrane	potassium ion binding, protein binding, sodium ion binding, sodium:potassium-exchanging ATPase activity	ATP biosynthetic process, ion transport, potassium ion transport, sodium ion transport, transport
NK3 homeobox 2	Nkx3-2	NP_031550	35	1	nucleus	DNA binding, sequence-specific DNA binding, transcription factor activity, transcription regulator activity	determination of left/right symmetry, embryonic skeletal system development, middle ear morphogenesis, negative regulation of apoptosis, organ formation, pancreas development, regulation of transcription, regulation of transcription, DNA-dependent, skeletal system development, skeletal system morphogenesis, spleen development
bassoon protein	Bsn	NP_031593	419	1	cell junction, cytoplasm, cytoskeleton, integral to membrane, peripheral to membrane of membrane fraction, synapse, synaptosome	metal ion binding, zinc ion binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
calcium/calmodulin-dependent protein kinase II, beta	Camk2b	NP_031621	60	1	calcium- and calmodulin-dependent protein kinase complex	ATP binding, calmodulin binding, calmodulin-dependent protein kinase activity, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	calcium ion transport, G1/S transition of mitotic cell cycle, protein amino acid autophosphorylation, protein amino acid phosphorylation
calpain 3 isoform a	Capn3	NP_031627	94	1	cytoplasm, intracellular	calcium ion binding, calcium-dependent cysteine-type endopeptidase activity, cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity, protein binding	myofibril assembly, proteolysis, sarcomere organization
catenin (cadherin associated protein), beta 1, 88kDa	Ctnnb1	NP_031640	85	1	adherens junction, apical junction complex, apical part of cell, basolateral plasma membrane, cell projection membrane, cell-cell adherens junction, cell-cell junction, cytoplasm, cytoskeleton, fascia adherens, lamellipodium, lateral plasma membrane, membrane, membrane fraction, microvillus membrane, nucleus, plasma membrane, transcription factor complex, Z disc	alpha-catenin binding, binding, cadherin binding, chromatin binding, DNA binding, double-stranded DNA binding, protein binding, protein phosphatase binding, transcription activator activity, transcription coactivator activity, transcription factor activity, transcription factor binding	anterior/posterior axis specification, apoptosis, bone resorption, camera-type eye morphogenesis, cell adhesion, cell differentiation, cell fate determination, cell fate specification, cell maturation, cell morphogenesis involved in differentiation, cell proliferation, cell-cell adhesion, cell-matrix adhesion, cellular process, cellular protein localization, dorsal/ventral axis specification, dorsal/ventral pattern formation, ectoderm development, embryonic arm morphogenesis, embryonic digit morphogenesis, embryonic hindlimb morphogenesis, endoderm formation, endodermal cell fate commitment, epithelial cell differentiation involved in prostate gland development, forebrain development, gastrulation with mouth forming second, glial cell fate determination, heart development, hemopoiesis, lung development, morphogenesis of embryonic epithelium
CD5 antigen	Cd5	NP_031676	54	1	external side of plasma membrane, integral to membrane, membrane, plasma membrane	protein binding, scavenger receptor activity	induction of apoptosis by extracellular signals, T cell costimulation
cell division cycle 25 homolog A	Cdc25a	NP_031684	58	1	intracellular	hydrolase activity, phosphoprotein phosphatase activity, protein tyrosine phosphatase activity	cell cycle, cell division, M phase of mitotic cell cycle, mitosis, protein amino acid dephosphorylation
cadherin 6	Cdh6	NP_031692	88	1	integral to membrane, membrane, plasma membrane	calcium ion binding, protein binding	cell adhesion, homophilic cell adhesion
Eph receptor B6	Ephb6	NP_031706	110	1	extracellular region, integral to membrane, membrane, plasma membrane	ATP binding, ephrin receptor activity, nucleotide binding, protein kinase activity, protein tyrosine kinase activity, receptor activity	protein amino acid phosphorylation, transmembrane receptor protein tyrosine kinase signaling pathway

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
cystatin B	Cstb	NP_031819	11	1	cytoplasm, intracellular, nucleus	cysteine-type endopeptidase inhibitor activity, endopeptidase inhibitor activity, peptidase inhibitor activity, protease binding	adult locomotory behavior
cortactin	Cttn	NP_031829	61	1	cell cortex, cell projection, cytoplasm, cytoskeleton, lamellipodium, ruffle	protein binding	not classified
phenylalkylamine Ca2+ antagonist (emopamil) binding protein	Ebp	NP_031924	26	1	endoplasmic reticulum, endoplasmic reticulum membrane, integral to membrane, membrane	C-8 sterol isomerase activity, cholestenol delta-isomerase activity, isomerase activity	cholesterol biosynthetic process, hemopoiesis, lipid biosynthetic process, steroid biosynthetic process, sterol biosynthetic process, sterol metabolic process
E74-like factor 3	Elf3	NP_031947	42	1	cytoplasm, nucleus	DNA binding, sequence-specific DNA binding, transcription factor activity	anatomical structure morphogenesis, cell differentiation, embryonic development, extracellular matrix organization, inflammatory response, mammary gland involution, multicellular organismal development, regulation of transcription, regulation of transcription, DNA-dependent, transcription
epoxide hydrolase 2, cytoplasmic	Ephx2	NP_031966	63	1	cytoplasm, peroxisome	catalytic activity, epoxide hydrolase activity, hydrolase activity, magnesium ion binding, metal ion binding	aromatic compound catabolic process, metabolic process, response to toxin
FK506 binding protein 2	Fkbp2	NP_032046	15	1	endoplasmic reticulum, membrane	isomerase activity, peptidyl-prolyl cis-trans isomerase activity	protein folding
beta-1,4-N-acetylgalactosaminyltransferase	B4galnt1	NP_032106	59	1	Golgi apparatus, integral to Golgi membrane, integral to membrane, membrane	(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups, transferase activity, transferring hexosyl groups	ganglioside biosynthetic process, glycosphingolipid metabolic process, lipid glycosylation, lipid storage, spermatogenesis
myotrophin	Mtpn	NP_032124	13	1	cytoplasm	not classified	not classified
gamma-glutamyltransferase 1	Ggt1	NP_032142	62	1	integral to membrane, integral to plasma membrane, membrane	acyltransferase activity, gamma-glutamyltransferase activity, transferase activity	glutathione biosynthetic process, glutathione metabolic process, spermatogenesis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
guanine nucleotide binding protein, alpha q polypeptide	Gnaq	NP_032165	42	1	heterotrimeric G-protein complex, membrane fraction, plasma membrane	GTP binding, GTPase activity, guanyl nucleotide binding, nucleotide binding, protein binding, signal transducer activity	activation of adenylate cyclase activity by G-protein signaling pathway, activation of phospholipase C activity by dopamine receptor signaling pathway, behavior, embryonic digit morphogenesis, forebrain neuron development, glutamate signaling pathway, G-protein coupled receptor protein signaling pathway, heart development, neuron remodeling, pigmentation during development, post-embryonic development, protein amino acid ADP-ribosylation, regulation of action potential, regulation of melanocyte differentiation, signal transduction, skeletal system development
guanylate kinase 1	Guk1	NP_032219	22	1	not classified	ATP binding, guanylate kinase activity, kinase activity, nucleotide binding, transferase activity	purine nucleotide metabolic process
host cell factor C1	Hcfc1	NP_032250	210	1	cytoplasm, nucleus	transcription coactivator activity	cell cycle, reactivation of latent virus
histone deacetylase 1	Hdac1	NP_032254	55	1	cell soma, cytoplasm, heterochromatin, histone deacetylase complex, nucleus, NuRD complex	chromatin binding, DNA binding, histone deacetylase activity, hydrolase activity, protein binding, transcription corepressor activity, transcription factor activity, transcription factor binding, transcription repressor activity	chromatin modification, endoderm development, hippocampus development, histone deacetylation, negative regulation of gene-specific transcription from RNA polymerase II promoter, negative regulation of transcription, neuron differentiation, regulation of transcription, transcription
hepatoma-derived growth factor	Hdgf	NP_032257	26	1	cytoplasm, extracellular space, nucleus	DNA binding, growth factor activity, heparin binding, nucleotide binding	cellular process, regulation of transcription, transcription
homeobox A4	Hoxa4	NP_032291	30	1	nucleus	DNA binding, sequence-specific DNA binding, transcription factor activity, transcription regulator activity	anterior/posterior pattern formation, embryonic skeletal system morphogenesis, multicellular organismal development, regulation of transcription, regulation of transcription, DNA-dependent, transcription
DnaJ (Hsp40) homolog, subfamily A, member 1	Dnaja1	NP_032324	45	1	membrane	heat shock protein binding, low-density lipoprotein receptor binding, metal ion binding, unfolded protein binding, zinc ion binding	androgen receptor signaling pathway, protein folding, sperm motility, spermatogenesis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	Ndst1	NP_032332	101	1	Golgi apparatus, integral to membrane, membrane	[heparan sulfate]-glucosamine N-sulfotransferase activity, catalytic activity, hydrolase activity, sulfotransferase activity, transferase activity	embryonic development, embryonic neurocranium morphogenesis, embryonic viscerocranium morphogenesis, fibroblast growth factor receptor signaling pathway, forebrain development, glycosaminoglycan metabolic process, inflammatory response, MAPKKK cascade, midbrain development, organ morphogenesis, polysaccharide biosynthetic process, protein amino acid deacetylation, protein amino acid sulfation, respiratory gaseous exchange, smoothened signaling pathway
potassium voltage gated channel, Shab-related subfamily, member 1	Kcnb1	NP_032446	96	1	integral to membrane, membrane, voltage-gated potassium channel complex	ion channel activity, potassium channel activity, potassium ion binding, protein binding, voltage-gated ion channel activity, voltage-gated potassium channel activity	ion transport, potassium ion transport, transport
rho/rac guanine nucleotide exchange factor (GEF) 2	Arhgef2	NP_032513	112	1	cell junction, cell soma, cytoplasm, dendritic shaft, Golgi apparatus, intracellular, microtubule, tight junction	diacylglycerol binding, guanyl-nucleotide exchange factor activity, metal ion binding, microtubule binding, protein binding, Rho guanyl-nucleotide exchange factor activity, zinc ion binding	actin filament organization, cell cycle, cell division, cell morphogenesis, intracellular signaling cascade, mitosis, regulation of Rho protein signal transduction
lipocalin 2	Lcn2	NP_032517	23	1	extracellular region	binding, transporter activity	response to virus, transport
ribosomal protein S2	Rps2	NP_032529	31	1	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, structural constituent of ribosome	translation
mannosidase 2, alpha 1	Man2a1	NP_032575	132	1	Golgi apparatus, Golgi membrane, integral to membrane, membrane	alpha-mannosidase activity, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing N-glycosyl compounds, hydrolase activity, hydrolyzing O-glycosyl compounds, mannosidase activity, mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity, metal ion binding, zinc ion binding	carbohydrate metabolic process, in utero embryonic development, liver development, lung alveolus development, mannose metabolic process, metabolic process, mitochondrion organization, N-glycan processing, respiratory gaseous exchange, vacuole organization
methylmalonyl-Coenzyme A mutase	Mut	NP_032676	83	1	mitochondrion	cobalamin binding, cobalt ion binding, intramolecular transferase activity, isomerase activity, metal ion binding, methylmalonyl-CoA mutase activity	metabolic process, post-embryonic development

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
nebulin-related anchoring protein isoform S	Nrap	NP_032759	196	1	fascia adherens, muscle tendon junction, myofibril	actin binding, metal ion binding, muscle alpha-actinin binding, protein binding, vinculin binding, zinc ion binding	actin cytoskeleton organization
tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	Tnfrsf11b	NP_032790	46	1	extracellular region, proteinaceous extracellular matrix	protein binding, receptor activity	apoptosis, extracellular matrix organization, negative regulation of odontogenesis of dentine-containing tooth, signal transduction
platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	Pafah1b2	NP_032801	26	1	cytoplasm	1-alkyl-2-acetylglycerophosphocholine esterase activity, hydrolase activity, hydrolase activity, acting on ester bonds, lipase activity	cell motion, lipid catabolic process, lipid metabolic process, spermatogenesis
p21 (CDKN1A)-activated kinase 3	Pak3	NP_032804	61	1	not classified	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, Rho GTPase binding, SH3 domain binding, transferase activity	multicellular organismal development, protein amino acid phosphorylation
peptidyl arginine deiminase, type II	Padi2	NP_032838	76	1	cytoplasm	calcium ion binding, hydrolase activity, protein-arginine deiminase activity	peptidyl-citrulline biosynthetic process from peptidyl-arginine, protein modification process
protein kinase C, theta	Prkcq	NP_032885	82	1	cytoplasm, immunological synapse, plasma membrane	ATP binding, diacylglycerol binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein binding, protein kinase activity, protein kinase C activity, protein serine/threonine kinase activity, transferase activity, zinc ion binding	intracellular signaling cascade, positive regulation of interleukin-2 biosynthetic process, positive regulation of NF-kappaB transcription factor activity, positive regulation of T cell activation, positive regulation of T cell proliferation, protein amino acid phosphorylation
DnaJ (Hsp40) homolog, subfamily C, member 3B	Dnajc3	NP_032955	57	1	not classified	not classified	not classified
aminopeptidase puromycin sensitive	Npepps	NP_032968	103	1	cytoplasm, nucleus	aminopeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
proteasome beta 4 subunit	Psmb4	NP_032971	29	1	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process
proteasome (prosome, macropain) 26S subunit, ATPase 3	Psmc3	NP_032974	49	1	cytoplasm, nucleus, proteasome complex	ATP binding, hydrolase activity, nucleoside-triphosphatase activity, nucleotide binding	blastocyst development, protein catabolic process
prothymosin alpha	Ptma	NP_032998	12	1	nucleus	not classified	not classified
ATP-binding cassette, sub-family D, member 3	Abcd3	NP_033017	75	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion, peroxisomal membrane, peroxisome	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding, protein binding	transport
RAB11B, member RAS oncogene family	Rab11b	NP_033023	24	1	cytoplasmic membrane-bounded vesicle, membrane, plasma membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
retinoic acid induced 1	Rai1	NP_033047	202	1	cytoplasm, nucleus	metal ion binding, protein binding, zinc ion binding	negative regulation of multicellular organism growth, regulation of transcription from RNA polymerase II promoter, skeletal system development
ralA binding protein 1	Ralbp1	NP_033093	75	1	intracellular, membrane	GTPase activator activity, protein binding, Rac GTPase activator activity, Ral GTPase binding	positive regulation of Cdc42 GTPase activity, signal transduction, transport
ribosomal protein L26	Rpl26	NP_033106	17	1	cellular_component, ribosome	molecular_function	biological_process
polymerase (RNA) II (DNA directed) polypeptide A	Polr2a	NP_033115	213	1	DNA-directed RNA polymerase II, core complex, nucleolus, nucleus	DNA binding, DNA-directed RNA polymerase activity, magnesium ion binding, metal ion binding, nucleotidyltransferase activity, protein binding, transferase activity, zinc ion binding	transcription, transcription from RNA polymerase II promoter
ribosomal protein S4, X-linked	Rps4x	NP_033120	30	1	intracellular, ribonucleoprotein complex, ribosome, small ribosomal subunit	RNA binding, rRNA binding, structural constituent of ribosome	translation
solute carrier family 12, member 2	Slc12a2	NP_033220	131	1	apical plasma membrane, basolateral plasma membrane, integral to membrane, membrane	cation:chloride symporter activity, potassium ion binding, protein binding, sodium ion binding, symporter activity, transporter activity	chloride transport, detection of mechanical stimulus involved in sensory perception of sound, ion transport, potassium ion transport, sodium ion transport, transport
SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	Smarcc1	NP_033237	123	1	chromatin, intracellular, nucleus, SWI/SNF complex, XY body	chromatin binding, DNA binding, protein binding	chromatin assembly or disassembly, chromatin modification, DNA packaging, organ morphogenesis, regulation of transcription, transcription
somatostatin	Sst	NP_033241	13	1	extracellular region	hormone activity	regulation of cell migration
serine (or cysteine) proteinase inhibitor, clade A, member 1b	Serpina1b	NP_033270	46	1	extracellular region	peptidase inhibitor activity, protein binding, serine-type endopeptidase inhibitor activity	acute-phase response, in utero embryonic development, protein amino acid N-linked glycosylation, response to cytokine stimulus, response to peptide hormone stimulus
spermatid perinuclear RNA-binding protein	Strbp	NP_033287	74	1	cytoplasm, cytoskeleton, intracellular, microtubule cytoskeleton	DNA binding, double-stranded RNA binding, RNA binding, single-stranded RNA binding	cell differentiation, cell motion, mechanosensory behavior, multicellular organismal development, spermatid development, spermatogenesis
zinc finger protein 143	Zfp143	NP_033307	69	1	intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	regulation of transcription, transcription
steroid sulfatase	Sts	NP_033319	67	1	endoplasmic reticulum, integral to membrane, membrane, microsome	calcium ion binding, catalytic activity, hydrolase activity, metal ion binding, steryl-sulfatase activity, sulfuric ester hydrolase activity	female pregnancy, lipid metabolic process, metabolic process, steroid metabolic process
synaptogyrin 2	Syngr2	NP_033330	25	1	integral to membrane, membrane, synaptic vesicle	not classified	protein targeting

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
tumor necrosis factor, alpha-induced protein 1	Tnfaip1	NP_033421	36	1	membrane, voltage-gated potassium channel complex	protein binding, voltage-gated potassium channel activity	embryonic development, potassium ion transport
troponin I, skeletal, fast 2	Tnni2	NP_033431	21	1	not classified	actin binding	not classified
topoisomerase (DNA) II beta	Top2b	NP_033435	182	1	chromosome, nucleus	ATP binding, DNA binding, DNA topoisomerase (ATP-hydrolyzing) activity, DNA topoisomerase activity, isomerase activity, nucleotide binding	axonogenesis, DNA metabolic process, DNA topological change, forebrain development, neuron migration
trans-golgi network protein	Tgoln1	NP_033469	38	1	Golgi apparatus, integral to membrane, membrane, plasma membrane, trans-Golgi network	not classified	not classified
uroporphyrinogen decarboxylase	Urod	NP_033504	41	1	cytoplasm, cytosol	carboxy-lyase activity, lyase activity, uroporphyrinogen decarboxylase activity	heme biosynthetic process, heme metabolic process, porphyrin biosynthetic process
X-ray repair complementing defective repair in Chinese hamster cells 5	Xrcc5	NP_033559	83	1	chromosome, cytoplasm, nucleus	ATP binding, ATP-dependent DNA helicase activity, DNA binding, helicase activity, hydrolase activity, nucleotide binding	cell proliferation, DNA recombination, DNA repair, double-strand break repair, double-strand break repair via nonhomologous end joining, hemopoietic stem cell differentiation, negative regulation of apoptosis, positive regulation of neurogenesis, response to DNA damage stimulus
activity-dependent neuroprotective protein	Adnp	NP_033758	124	1	extracellular space, intracellular, nucleus	chromatin binding, DNA binding, metal ion binding, protein binding, sequence-specific DNA binding, transcription factor activity, zinc ion binding	negative regulation of neuron apoptosis, regulation of transcription, regulation of transcription, DNA-dependent, transcription
B-cell leukemia/lymphoma 2 related protein A1a	Bcl2a1a	NP_033872	20	1	cytoplasm	not classified	apoptosis, B cell homeostasis, negative regulation of apoptosis, regulation of apoptosis
Bcl2-like 1	Bcl2l1	NP_033873	26	1	cytoplasm, cytosol, integral to membrane, intracellular, membrane, mitochondrial membrane, mitochondrial outer membrane, mitochondrial part, mitochondrion	protein binding, protein heterodimerization activity	anti-apoptosis, apoptosis, cell proliferation, fertilization, germ cell development, growth, in utero embryonic development, male gonad development, negative regulation of apoptosis, negative regulation of neuron apoptosis, ovarian follicle development, positive regulation of anti-apoptosis, positive regulation of apoptosis, positive regulation of cell proliferation, regulation of apoptosis, release of cytochrome c from mitochondria, response to cycloheximide, response to cytokine stimulus, response to protein stimulus, response to radiation, spermatogenesis

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
galactosidase, beta 1	Glb1	NP_033882	73	1	lysosome	beta-galactosidase activity, catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds	carbohydrate metabolic process, metabolic process
bone morphogenetic protein 1	Bmp1	NP_033885	112	1	extracellular space	calcium ion binding, cytokine activity, growth factor activity, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	cartilage development, cell differentiation, multicellular organismal development, ossification, proteolysis
BMX non-receptor tyrosine kinase	Bmx	NP_033889	75	1	cytoplasm	ATP binding, kinase activity, metal ion binding, non-membrane spanning protein tyrosine kinase activity, nucleotide binding, protein binding, protein kinase activity, protein tyrosine kinase activity, receptor activity, transferase activity, zinc ion binding	intracellular signaling cascade, protein amino acid phosphorylation
peripheral benzodiazepine receptor	Tspo	NP_033905	19	1	integral to membrane, membrane, mitochondrion	receptor activity	not classified
calpain 2	Capn2	NP_033924	80	1	cytoplasm, intracellular, membrane, plasma membrane	calcium ion binding, calcium-dependent cysteine-type endopeptidase activity, cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	blastocyst development, myoblast fusion, proteolysis
F-actin capping protein alpha-1 subunit	Capza1	NP_033927	33	1	cortical cytoskeleton, F-actin capping protein complex, membrane	actin binding	actin cytoskeleton organization, actin filament capping
capping protein (actin filament) muscle Z-line, beta isoform b	Capzb	NP_033928	31	1	cortical cytoskeleton, cytoplasm, cytoskeleton, F-actin capping protein complex, intercalated disc, lamellipodium, membrane, Z disc	actin binding	actin cytoskeleton organization, actin filament capping, cell projection organization, lamellipodium assembly
catalase	Cat	NP_033934	60	1	mitochondrion, peroxisomal membrane, peroxisome	aminoacylase activity, catalase activity, heme binding, iron ion binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on peroxide as acceptor, peroxidase activity	aerobic respiration, cholesterol metabolic process, hemoglobin metabolic process, hydrogen peroxide catabolic process, negative regulation of NF-kappaB transcription factor activity, oxidation reduction, positive regulation of cell division, positive regulation of NF-kappaB transcription factor activity, positive regulation of phosphoinositide 3-kinase cascade, response to oxidative stress, triglyceride metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
RB1-inducible coiled-coil 1	Rb1cc1	NP_033956	182	1	cytoplasm, nucleus	protein binding	cell cycle, heart development, JNK cascade, liver development, negative regulation of apoptosis, positive regulation of cell size, positive regulation of protein amino acid phosphorylation, regulation of transcription, transcription
chaperonin containing Tcp1, subunit 4 (delta)	Cct4	NP_033967	58	1	chaperonin-containing T-complex, cytoplasm	ATP binding, nucleotide binding, protein binding, unfolded protein binding	cellular protein metabolic process, protein folding
procollagen, type X, alpha 1	Col10a1	NP_034055	67	1	cell cortex, extracellular region, proteinaceous extracellular matrix	not classified	not classified
collagen, type VI, alpha 1	Col6a1	NP_034063	108	1	extracellular matrix, extracellular region, proteinaceous extracellular matrix, sarcolemma	platelet-derived growth factor binding, protein binding	cell adhesion
cathepsin C preproprotein	Ctsc	NP_034112	52	1	lysosome	chloride ion binding, cysteine-type endopeptidase activity, cysteine-type peptidase activity, hydrolase activity, peptidase activity	proteolysis
diacylglycerol O-acyltransferase 1	Dgat1	NP_034176	57	1	endoplasmic reticulum, integral to membrane, membrane, membrane fraction	2-acylglycerol O-acyltransferase activity, acyltransferase activity, diacylglycerol O-acyltransferase activity, transferase activity	not classified
dolichol-phosphate (beta-D) mannosyltransferase 1	Dpm1	NP_034202	29	1	dolichol-phosphate-mannose synthase complex, endoplasmic reticulum, membrane fraction, nucleus	DNA binding, dolichyl-phosphate beta-D-mannosyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups	dolichol metabolic process, GPI anchor biosynthetic process

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
dopamine receptor 2	Drd2	NP_034207	51	1	axon, dendrite, integral to membrane, membrane, plasma membrane	dopamine binding, dopamine D2 receptor activity, dopamine receptor activity, dopamine receptor activity, coupled via Gi/Go, G-protein coupled receptor activity, receptor activity, signal transducer activity	activation of phospholipase C activity by dopamine receptor signaling pathway, adenohypophysis development, adult behavior, adult walking behavior, associative learning, axonogenesis, behavioral response to cocaine, behavioral response to ethanol, branching morphogenesis of a nerve, cerebral cortex GABAergic interneuron migration, circadian regulation of gene expression, diuresis, dopamine metabolic process, dopamine receptor signaling pathway, feeding behavior, G-protein coupled receptor protein signaling pathway, grooming behavior, inhibition of adenylate cyclase activity by dopamine receptor signaling pathway, locomotory behavior, natriuresis, negative regulation of blood pressure, negative regulation of cell migration, negative regulation of cell proliferation, negative regulation of dopamine receptor signaling
eukaryotic translation initiation factor 3, subunit 10 (theta)	Eif3a	NP_034253	162	1	cytoplasm, eukaryotic translation initiation factor 3 complex, nucleus	protein binding, translation initiation factor activity	formation of translation initiation complex, translation
X-ray repair complementing defective repair in Chinese hamster cells 6	Xrcc6	NP_034377	69	1	chromosome, cytoplasm, DNA-dependent protein kinase-DNA ligase 4 complex, nucleus	ATP binding, ATP-dependent DNA helicase activity, DNA binding, helicase activity, hydrolase activity, nucleic acid binding, nucleotide binding	DNA recombination, DNA repair, double-strand break repair, double-strand break repair via nonhomologous end joining, positive regulation of neurogenesis, response to DNA damage stimulus, response to ionizing radiation, V(D)J recombination
glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	NP_034401	38	1	cytoplasm, glycerol-3-phosphate dehydrogenase complex	binding, catalytic activity, coenzyme binding, glycerol-3-phosphate dehydrogenase (NAD+) activity, NAD or NADH binding, oxidoreductase activity, oxidoreductase activity, acting on CH-OH group of donors, oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, protein homodimerization activity	carbohydrate metabolic process, gluconeogenesis, glycerol-3-phosphate catabolic process, glycerol-3-phosphate metabolic process, metabolic process, oxidation reduction
glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	NP_034404	81	1	glycerol-3-phosphate dehydrogenase complex, membrane, mitochondrial inner membrane, mitochondrion	calcium ion binding, glycerol-3-phosphate dehydrogenase activity, oxidoreductase activity	gluconeogenesis, glycerol-3-phosphate metabolic process, oxidation reduction
glial fibrillary acidic protein	Gfap	NP_034407	50	1	cell part, cytoplasm, intermediate filament, intracellular, membrane fraction	protein binding, structural molecule activity	intermediate filament-based process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
glycerol kinase-like 1	Gykl1	NP_034423	60	1	not classified	kinase activity, transferase activity	spermatogenesis
guanine nucleotide binding protein, alpha z subunit	Gnaz	NP_034441	41	1	heterotrimeric G-protein complex, membrane, membrane fraction	GTP binding, GTPase activity, guanyl nucleotide binding, nucleotide binding, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction
gonadotropin releasing hormone receptor	Gnrhr	NP_034453	38	1	integral to membrane, membrane, plasma membrane	gonadotropin-releasing hormone receptor activity, G-protein coupled receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction
glutathione S-transferase omega 1	Gsto1	NP_034492	27	1	cytoplasm	glutathione transferase activity, transferase activity	metabolic process
glucuronidase, beta	Gusb	NP_034498	74	1	endoplasmic reticulum, lysosome, microsome	beta-glucuronidase activity, catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds, hydrolase activity, hydrolyzing O-glycosyl compounds	carbohydrate metabolic process, metabolic process
histocompatibility 2, D region locus 1	H2-D1	NP_034510	41	1	external side of plasma membrane, integral to membrane, membrane, MHC class I protein complex, plasma membrane	protein binding	antigen processing and presentation, antigen processing and presentation of peptide antigen via MHC class I, immune response
hepatocyte growth factor	Hgf	NP_034557	83	1	not classified	growth factor activity, serine-type endopeptidase activity	activation of MAPK activity, anti-apoptosis, cell morphogenesis, cell proliferation, hepatocyte growth factor receptor signaling pathway, liver development, myoblast proliferation, proteolysis, regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling
ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	Elavl1	NP_034615	36	1	nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA stabilization
intercellular adhesion molecule	Icam1	NP_034623	59	1	external side of plasma membrane, immunological synapse, integral to membrane, membrane	protein binding	cell adhesion, cell adhesion mediated by integrin, cell-cell adhesion, leukocyte adhesion, regulation of cell adhesion, T cell antigen processing and presentation
integrin beta 1 (fibronectin receptor beta)	Itgb1	NP_034708	88	1	integral to membrane, integrin complex, membrane, neuromuscular junction, plasma membrane, sarcolemma, synaptosome	binding, integrin binding, protein binding, receptor activity	cardiac muscle cell differentiation, cell adhesion, cell fate specification, cell-matrix adhesion, G1/S transition of mitotic cell cycle, germ cell migration, in utero embryonic development, integrin-mediated signaling pathway, negative regulation of cell differentiation, positive regulation of cell proliferation, regulation of cell cycle, sarcomere organization

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
KH-type splicing regulatory protein (FUSE binding protein 2)	Khsrp	NP_034743	77	1	cytoplasm, nucleus	aminoacyl-tRNA ligase activity, ATP binding, DNA binding, nucleotide binding, RNA binding	mRNA processing, mRNA transport, regulation of transcription, RNA splicing, transcription, translation, transport, tRNA aminoacylation for protein translation
kinesin family member 12	Kif12	NP_034746	71	1	microtubule	ATP binding, microtubule motor activity, motor activity, nucleotide binding	microtubule-based movement
keratin complex 1, acidic, gene 12	Krt12	NP_034791	53	1	intermediate filament	structural molecule activity	not classified
keratin 13	Krt13	NP_034792	48	1	intermediate filament	protein binding, structural molecule activity	not classified
chymase 1, mast cell	Cma1	NP_034910	29	1	extracellular region, intracellular	hydrolase activity, peptidase activity, serine-type endopeptidase activity, serine-type peptidase activity	proteolysis
moesin	Msn	NP_034963	68	1	apical part of cell, apical plasma membrane, basolateral plasma membrane, cell projection, cytoplasm, cytoskeleton, extrinsic to membrane, membrane, plasma membrane, uropod	binding, cytoskeletal protein binding	not classified
NADH dehydrogenase (ubiquinone) Fe-S protein 4	Ndufs4	NP_035017	18	1	membrane, mitochondrial inner membrane, mitochondrial respiratory chain complex I, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, oxidoreductase activity, acting on NADH or NADPH	electron transport chain, regulation of protein amino acid phosphorylation, transport
sequestosome 1	Sqstm1	NP_035148	48	1	cytoplasm, endosome, nucleus	metal ion binding, protein binding, transcription cofactor activity, zinc ion binding	apoptosis, cell differentiation, immune response
procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	P4ha1	NP_035160	61	1	endoplasmic reticulum	binding, iron ion binding, L-ascorbic acid binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, procollagen-proline 4-dioxygenase activity	collagen fibril organization, oxidation reduction, peptidyl-proline hydroxylation to 4-hydroxy L-proline
phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	NP_035174	69	1	cytoplasm	carboxy-lyase activity, GTP binding, kinase activity, lyase activity, manganese ion binding, metal ion binding, nucleotide binding, phosphoenolpyruvate carboxykinase (GTP) activity, phosphoenolpyruvate carboxykinase activity, purine nucleotide binding	gluconeogenesis, glycerol biosynthetic process from pyruvate, lipid metabolic process

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
peroxisomal biogenesis factor 11b	Pex11b	NP_035199	29	1	integral to membrane, membrane, mitochondrion, peroxisomal membrane, peroxisome	not classified	peroxisome fission, peroxisome organization
proteasome (prosome, macropain) subunit, beta type 7	Psmb7	NP_035317	30	1	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process
RAN binding protein 1	Ranbp1	NP_035369	24	1	centrosome, cytoplasm	GTPase activator activity	intracellular transport, positive regulation of mitotic centrosome separation, spindle organization
RAN binding protein 2	Ranbp2	NP_035370	341	1	intracellular, nuclear pore, nucleus	binding, isomerase activity, metal ion binding, peptidyl-prolyl cis-trans isomerase activity, protein binding, zinc ion binding	intracellular transport, modification-dependent protein catabolic process, mRNA transport, protein folding, protein transport, transmembrane transport, transport
polymerase (RNA) II (DNA directed) polypeptide J	Polr2j	NP_035423	13	1	DNA-directed RNA polymerase III complex, nucleus	DNA binding, DNA-directed RNA polymerase activity, protein binding, protein dimerization activity	transcription
ribosomal protein S7	Rps7	NP_035430	22	1	intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
KH domain containing, RNA binding, signal transduction associated 1	Khdrbs1	NP_035447	48	1	membrane, nucleus	protein binding, RNA binding, SH3 domain binding, SH3/SH2 adaptor activity, transcription repressor activity	cell cycle, cell surface receptor linked signal transduction, negative regulation of transcription, regulation of RNA export from nucleus, regulation of transcription, transcription
seryl-aminoacyl-tRNA synthetase	Sars	NP_035449	61	1	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding, serine-tRNA ligase activity	seryl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
splicing factor, arginine/serine-rich 2	Sfrs2	NP_035488	25	1	nuclear speck, nucleus, spliceosomal complex	nucleic acid binding, nucleotide binding, protein binding, RNA binding	mRNA processing, RNA splicing
small proline-rich protein 2B	Sprr2b	NP_035599	11	1	cornified envelope, cytoplasm	not classified	epidermis development, keratinization, response to estradiol stimulus
testis derived transcript isoform 1	Tes	NP_035700	47	1	cell junction, cytoplasm	metal ion binding, zinc ion binding	not classified
translocase of inner mitochondrial membrane 44	Timm44	NP_035722	51	1	membrane, mitochondrial inner membrane, mitochondrial inner membrane presequence translocase complex, mitochondrion	ATP binding, nucleotide binding, P-P-bond-hydrolysis-driven protein transmembrane transporter activity	intracellular protein transport, protein transport, transmembrane transport, transport
tight junction protein 2	Tjp2	NP_035727	131	1	cell junction, gap junction, membrane, nucleus, plasma membrane, tight junction	protein binding	not classified
talin 1	Tln1	NP_035732	270	1	cell projection, cytoplasm, cytoskeleton, focal adhesion, membrane, plasma membrane, ruffle	actin binding, binding, protein binding, structural constituent of cytoskeleton	cell-substrate junction assembly, cortical actin cytoskeleton organization, cytoskeletal anchoring at plasma membrane
thymopoietin isoform alpha	Tmpo	NP_035735	75	1	chromatin, chromosome, integral to membrane, membrane, nuclear envelope, nucleus	DNA binding, protein binding	regulation of transcription

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
mesotrypsin	Prss3	NP_035775	26	1	cellular_component	hydrolase activity, molecular_function, peptidase activity, serine-type peptidase activity	biological_process
trypsin 4	Try4	NP_035776	26	1	cellular_component	hydrolase activity, molecular_function, peptidase activity, serine-type peptidase activity	biological_process
titin isoform N2-A	Ttn	NP_035782	3522	1	A band, I band, M band, muscle myosin complex, sarcomere, Z disc	protein binding, structural constituent of cytoskeleton	adult heart development, cardiac myofibril assembly, forward locomotion, heart morphogenesis, in utero embryonic development, muscle contraction, sarcomere organization, striated muscle cell development
bromodomain adjacent to zinc finger domain, 1B	Baz1b	NP_035844	171	1	centromeric heterochromatin, chromatin remodeling complex, condensed chromosome, nucleus	ATP binding, kinase activity, metal ion binding, non-membrane spanning protein tyrosine kinase activity, nucleotide binding, protein binding, protein tyrosine kinase activity, transferase activity, zinc ion binding	chromatin assembly or disassembly, chromatin remodeling, regulation of transcription, response to DNA damage stimulus, transcription
cellular repressor of E1A-stimulated genes 1	Creg1	NP_035934	24	1	extracellular region, transcription factor complex	transcription factor binding	regulation of growth, regulation of transcription, DNA-dependent
monoglyceride lipase	Mgll	NP_035974	33	1	not classified	acylglycerol lipase activity, carboxylesterase activity, hydrolase activity	not classified
5'-3' exoribonuclease 2	Xrn2	NP_036047	109	1	intracellular, nucleus	5'-3' exoribonuclease activity, exonuclease activity, hydrolase activity, metal ion binding, nuclease activity, nucleic acid binding, zinc ion binding	cell growth, DNA recombination, DNA repair, microtubule-based process, mRNA processing, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, regulation of transcription, RNA metabolic process, spermatogenesis, transcription, transcription termination
2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	NP_036063	31	1	peroxisome	2,4-dienoyl-CoA reductase (NADPH) activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
mitogen-activated protein kinase binding protein 1	Mapkbp1	NP_036071	163	1	cellular_component	protein binding	activation of JNKK activity
poly (ADP-ribose) glycohydrolase	Parg	NP_036090	109	1	cytosol, nucleus	hydrolase activity, poly(ADP-ribose) glycohydrolase activity	carbohydrate metabolic process, detection of bacterium, response to DNA damage stimulus
proteasome (prosome, macropain) subunit, alpha type 4	Psma4	NP_036096	29	1	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process, ubiquitin-dependent protein catabolic process
proteasome (prosome, macropain) subunit, beta type 2	Psmb2	NP_036100	23	1	cytoplasm, nucleus, proteasome complex, proteasome core complex	endopeptidase activity, hydrolase activity, peptidase activity, threonine-type endopeptidase activity	proteolysis involved in cellular protein catabolic process
reticulocalbin 2	Rcn2	NP_036122	37	1	endoplasmic reticulum	calcium ion binding	not classified

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eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	Eif2s3x	NP_036140	51	1	not classified	GTP binding, GTPase activity, nucleotide binding, translation initiation factor activity	translation
ribosomal protein L8	Rpl8	NP_036183	28	1	cellular_component, cytoplasm, intracellular, ribonucleoprotein complex, ribosome	molecular_function, RNA binding, rRNA binding, structural constituent of ribosome	biological_process, translation
heat shock protein 105	Hsph1	NP_038587	96	1	cytoplasm, nucleus	ATP binding, nucleotide binding, protein binding	chaperone mediated protein folding requiring cofactor, response to stress
component of oligomeric golgi complex 1	Cog1	NP_038609	109	1	Golgi apparatus, membrane	not classified	protein transport, transport
ubiquitin specific protease 5 (isopeptidase T)	Usp5	NP_038728	96	1	not classified	cysteine-type peptidase activity, hydrolase activity, metal ion binding, peptidase activity, ubiquitin thiolesterase activity, zinc ion binding	modification-dependent protein catabolic process, ubiquitin-dependent protein catabolic process
COP9 signalosome subunit 5	Cops5	NP_038743	38	1	cytoplasm, nucleus, signalosome, transcription factor complex	hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, protein binding, transcription coactivator activity, zinc ion binding	regulation of cell cycle, regulation of transcription, DNA-dependent
Nik related kinase	Nrk	NP_038752	164	1	not classified	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, small GTPase regulator activity, transferase activity	activation of JNKK activity, protein amino acid phosphorylation
zinc finger, HIT domain containing 2	Znhit2	NP_038887	43	1	cellular_component	metal ion binding, molecular_function, zinc ion binding	biological_process
ATP-binding cassette, subfamily E, member 1	Abce1	NP_056566	67	1	cytoplasm, mitochondrion	ATP binding, ATPase activity, electron carrier activity, iron-sulfur cluster binding, nucleoside-triphosphatase activity, nucleotide binding	not classified
shroom isoform 1	Shroom3	NP_056571	214	1	adherens junction, apical junction complex, apical part of cell, apical plasma membrane, cell junction, cytoplasm, cytoskeleton, microtubule	actin binding, protein binding	actin cytoskeleton organization, columnar/cuboidal epithelial cell development, multicellular organismal development, neural tube closure, pattern specification process, regulation of cell shape
exosome component 10	Exosc10	NP_057908	101	1	cytoplasm, exosome (RNase complex), intracellular, nuclear exosome (RNase complex), nucleolus, nucleus	3'-5' exonuclease activity, exonuclease activity, hydrolase activity, nuclease activity, nucleic acid binding, RNA binding	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nucleobase, nucleoside, nucleotide and nucleic acid metabolic process, RNA processing, rRNA processing
nucleosome binding protein 1	Nsbp1	NP_057919	45	1	chromatin, nucleoplasm, nucleus	chromatin binding, DNA binding	regulation of transcription, regulation of transcription from RNA polymerase I promoter, transcription

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ATPase, Ca++ transporting, ubiquitous	Atp2a3	NP_058025	114	1	endoplasmic reticulum, integral to membrane, membrane, nucleus, sarcoplasmic reticulum	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, calcium ion binding, calcium-transporting ATPase activity, catalytic activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, nucleotide binding	ATP biosynthetic process, calcium ion transport, cation transport, ion transport, metabolic process, transport
H2A histone family, member Z	H2afz	NP_058030	14	1	Barr body, chromosome, nucleosome, nucleus	DNA binding	multicellular organismal development, nucleosome assembly
peroxiredoxin 4	Prdx4	NP_058044	31	1	cytoplasm, mitochondrion	antioxidant activity, molecular_function, oxidoreductase activity, peroxidase activity, peroxiredoxin activity	biological_process, cell redox homeostasis, oxidation reduction
vesicle-associated membrane protein 8	Vamp8	NP_058074	11	1	early endosome, integral to membrane, membrane	protein binding	vesicle-mediated transport
serine/arginine repetitive matrix 1	Srrm1	NP_058079	101	1	nuclear matrix, nucleus, spliceosomal complex	DNA binding, protein binding, RNA binding, RNA splicing factor activity, transesterification mechanism	mRNA processing, nuclear mRNA splicing, via spliceosome, RNA splicing
golgi SNAP receptor complex member 1	Gosr1	NP_058090	28	1	Golgi apparatus, Golgi membrane, integral to membrane, membrane	protein binding, receptor activity	ER to Golgi vesicle-mediated transport, intracellular protein transport, protein transport, transport, vesicle-mediated transport
cleavage and polyadenylation specific factor 2	Cpsf2	NP_058552	88	1	nucleus	hydrolase activity, RNA binding	mRNA processing
keratin 35	Krt35	NP_058576	48	1	intermediate filament	structural molecule activity	not classified
phosphomannomutase 2	Pmm2	NP_058577	28	1	cytoplasm	catalytic activity, isomerase activity, phosphomannomutase activity	mannose biosynthetic process, metabolic process
regulatory factor X, 5	Rfx5	NP_059091	70	1	not classified	not classified	negative regulation of transcription from RNA polymerase II promoter
cytidine 5'-triphosphate synthase 2	Ctps2	NP_061207	66	1	cellular_component	ATP binding, catalytic activity, CTP synthase activity, ligase activity, nucleotide binding	glutamine metabolic process, pyrimidine nucleotide biosynthetic process
secreted frizzled-related sequence protein 5	Sfrp5	NP_061250	35	1	extracellular region	not classified	cell differentiation, multicellular organismal development, Wnt receptor signaling pathway
histone H1-like protein in spermatids 1	Hils1	NP_061262	19	1	chromosome, nucleus	DNA binding	cell differentiation, chromatin modification, multicellular organismal development, regulation of transcription, spermatogenesis, transcription
SAM domain- and HD domain-containing protein 1	Samhd1	NP_061339	73	1	nucleus	catalytic activity, hydrolase activity	immune response, innate immune response
sodium channel, voltage-gated, type IX, alpha	Scn9a	NP_061340	225	1	integral to membrane, membrane, voltage-gated sodium channel complex	ion channel activity, sodium channel activity, sodium ion binding, voltage-gated ion channel activity, voltage-gated sodium channel activity	behavioral response to pain, inflammatory response, ion transport, post-embryonic development, sodium ion transport, transport

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3-monooxgenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	Ywhag	NP_061359	28	1	cellular_component, cytoplasm	protein domain specific binding	protein targeting
RNA and export factor binding protein 2	Refbp2	NP_062357	24	1	cytoplasm, nucleus, spliceosomal complex	nucleic acid binding, nucleotide binding, RNA binding, single-stranded DNA binding	mRNA processing, mRNA transport, RNA splicing, transport
actin-like 6A	Actl6a	NP_062647	47	1	chromatin remodeling complex, nucleus	ATP binding, chromatin binding, protein binding	chromatin modification, chromatin remodeling, regulation of growth, regulation of transcription, transcription
DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	NP_062769	56	1	not classified	binding, heat shock protein binding	not classified
RNA binding motif protein 14	Rbm14	NP_063922	69	1	cellular_component, nucleus	molecular_function, nucleic acid binding, nucleotide binding, RNA binding	biological_process, regulation of transcription, transcription
inositol 1,4,5-triphosphate receptor 2 isoform 1	Itpr2	NP_064307	307	1	cell cortex, cytoplasm, endoplasmic reticulum, integral to membrane, membrane, microsome, sarcoplasmic reticulum	calcium channel activity, calcium ion binding, calcium-release channel activity, inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity, inositol-1,4,5-trisphosphate receptor activity, ion channel activity, phosphoinositide binding, receptor activity	calcium ion transport, ion transport, transport
microtubule associated serine/threonine kinase 1	Mast1	NP_064329	171	1	cytoplasm, cytoskeleton, membrane, plasma membrane	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	cytoskeleton organization, protein amino acid phosphorylation
deoxyribonuclease II beta	Dnase2b	NP_064341	41	1	cytoplasm, extracellular region, lysosome	deoxyribonuclease II activity, endodeoxyribonuclease activity, endonuclease activity, hydrolase activity, nuclease activity	DNA metabolic process
sortilin 1	Sort1	NP_064356	91	1	endoplasmic reticulum, endosome, Golgi apparatus, integral to membrane, lysosome, membrane, microsome, nucleus, plasma membrane, trans-Golgi network transport vesicle	receptor activity	cell differentiation, endocytosis, glucose import, multicellular organismal development, myotube differentiation, ossification, response to insulin stimulus, transport, vesicle organization
SH3-binding domain glutamic acid-rich protein like	Sh3bgrl	NP_064373	13	1	cellular_component	molecular_function, SH3 domain binding	biological_process
kaiso protein	Zbtb33	NP_064652	74	1	intracellular, nucleus	DNA binding, metal ion binding, protein binding, zinc ion binding	regulation of transcription, transcription, Wnt receptor signaling pathway
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	Atp5j2	NP_065607	10	1	membrane, mitochondrial inner membrane, mitochondrion, proton-transporting ATP synthase complex, coupling factor F(o)	not classified	ATP biosynthetic process, ion transport, proton transport, transport
interferon stimulated exonuclease	Isg20	NP_065608	21	1	intracellular, nucleus	exonuclease activity, exoribonuclease II activity, hydrolase activity, manganese ion binding, metal ion binding, nuclease activity, RNA binding	not classified

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splicing factor, arginine/serine-rich 4 (SRp75)	Sfrs4	NP_065612	39	1	nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
spectrin beta 3	Spnb3	NP_067262	271	1	not classified	actin binding	not classified
diazepam binding inhibitor-like 5	Dbil5	NP_067269	10	1	cytoplasm	acyl-CoA binding, binding, lipid binding	transport
ataxin 2 binding protein 1 isoform gamma	A2bp1	NP_067452	43	1	cytoplasm, nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
sulfide quinone reductase-like	Sqrdl	NP_067482	50	1	mitochondrial inner membrane, mitochondrion	oxidoreductase activity	oxidation reduction
THAP domain containing 11	Thap11	NP_067488	33	1	cytoplasm, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	regulation of transcription, transcription
PDZ domain containing 1	Pdzk1	NP_067492	56	1	brush border membrane, cytoplasm, membrane	protein binding	not classified
melanocyte proliferating gene 1	Myg1	NP_068359	43	1	mitochondrion, nucleus	molecular_function	biological_process
fibronectin type III domain containing 4	Fndc4	NP_071869	25	1	integral to membrane, membrane	not classified	not classified
glutaredoxin 3	Glrx3	NP_075629	38	1	cytoplasm	electron carrier activity, protein disulfide oxidoreductase activity	cell redox homeostasis
non-POU-domain-containing, octamer binding protein	Nono	NP_075633	55	1	nucleus, paraspeckles	DNA binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding	DNA recombination, DNA repair, mRNA processing, regulation of transcription, response to DNA damage stimulus, RNA splicing, transcription
protein phosphatase-1 regulatory subunit 7	Ppp1r7	NP_075689	41	1	nucleus	protein binding	not classified
hypothetical protein LOC66511	2500003M10 Rik	NP_075704	24	1	not classified	not classified	not classified
Shwachman-Bodian-Diamond syndrome homolog	Sbds	NP_075737	29	1	cellular_component, cytoplasm	molecular_function	inner cell mass cell proliferation, ribosome biogenesis
mesoderm development candidate 2	Mesdc2	NP_075892	25	1	not classified	not classified	mesoderm development
coiled-coil-helix-coiled-coil-helix domain containing 2	Chchd2	NP_077128	16	1	mitochondrion	molecular_function	biological_process
3-oxoacid CoA transferase 1	Oxct1	NP_077150	56	1	mitochondrion	3-oxoacid CoA-transferase activity, CoA-transferase activity, transferase activity	cellular ketone body metabolic process, ketone body catabolic process, metabolic process
ribosomal protein L24	Rpl24	NP_077180	18	1	cytosolic large ribosomal subunit, intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	exit from mitosis, G1/S transition checkpoint, optic nerve development, retina development in camera-type eye, retinal ganglion cell axon guidance, ribosomal large subunit assembly, translation
sorting nexin 5	Snx5	NP_077187	47	1	not classified	phosphoinositide binding, protein binding	cell communication, protein transport, transport
fucosidase, alpha-L-1, tissue	Fuca1	NP_077205	52	1	lysosome	alpha-L-fucosidase activity, catalytic activity, cation binding, hydrolase activity, hydrolase activity, acting on glycosyl bonds	carbohydrate metabolic process, fucose metabolic process, metabolic process
hypothetical protein LOC72425	2410042D21 Rik	NP_077216	34	1	not classified	not classified	not classified
hydroxyacyl glutathione hydrolase	Hagh	NP_077246	29	1	cytoplasm, mitochondrion	hydrolase activity, hydroxyacylglutathione hydrolase activity, metal ion binding, zinc ion binding	not classified
blood vessel epicardial substance	Bves	NP_077247	41	1	integral to membrane, membrane	not classified	not classified
FtsJ homolog 3	Ftsj3	NP_079586	96	1	cellular_component, nucleus	methyltransferase activity, molecular_function, nucleic acid binding, transferase activity	biological_process, methylation, rRNA methylation, rRNA processing

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ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit precursor	Atp5d	NP_079589	18	1	membrane, mitochondrial envelope, mitochondrial inner membrane, mitochondrion, proton-transporting ATP synthase complex, proton-transporting ATP synthase complex, catalytic core F(1)	hydrogen ion transmembrane transporter activity, hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism	ATP biosynthetic process, ATP synthesis coupled proton transport, ion transport, proton transport, transport
keratinocyte associated protein 2	Krtcap2	NP_079603	15	1	integral to membrane, membrane, oligosaccharyltransferase complex	dolichyl-diphosphooligosaccharide-protein glycotransferase activity	protein amino acid N-linked glycosylation via asparagine
coiled-coil-helix-coiled-coil-helix domain containing 3	Chchd3	NP_079612	26	1	mitochondrial inner membrane, mitochondrion	not classified	not classified
required for meiotic nuclear division 1 homolog	Rmnd1	NP_079619	52	1	cellular_component	molecular_function	biological_process
ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	Ube2d3	NP_079632	17	1	not classified	ATP binding, ligase activity, nucleotide binding, small conjugating protein ligase activity, ubiquitin-protein ligase activity	modification-dependent protein catabolic process, post-translational protein modification, proteasomal ubiquitin-dependent protein catabolic process, regulation of protein metabolic process
ATPase, H+ transporting, lysosomal V1 subunit F	Atp6v1f	NP_079657	13	1	proton-transporting two-sector ATPase complex, catalytic domain, proton-transporting V-type ATPase, V1 domain	hydrogen ion transporting ATP synthase activity, rotational mechanism, proton-transporting ATPase activity, rotational mechanism	ATP synthesis coupled proton transport, ion transport, proton transport, transport
transmembrane protein 14C	Tmem14c	NP_079663	12	1	integral to membrane, membrane, mitochondrion	not classified	not classified
6-phosphogluconolactonase	Pgls	NP_079672	27	1	not classified	6-phosphogluconolactonase activity, hydrolase activity	carbohydrate metabolic process, pentose-phosphate shunt
Sec11-like 3	Sec11c	NP_079744	22	1	endoplasmic reticulum, integral to membrane, membrane, microsome	hydrolase activity, peptidase activity, serine-type peptidase activity	proteolysis, signal peptide processing
keratin associated protein 3-3	Krtap3-3	NP_079800	11	1	intermediate filament, keratin filament	structural molecule activity	not classified
SAR1a gene homolog 2	Sar1b	NP_079811	22	1	endoplasmic reticulum, Golgi apparatus, intracellular, membrane	GTP binding, magnesium ion binding, metal ion binding, nucleotide binding	intracellular protein transport, protein transport, transport, vesicle-mediated transport
splicing factor, arginine/serine rich 9	Sfrs9	NP_079849	26	1	nucleus	nucleic acid binding, nucleotide binding, RNA binding	mRNA processing, RNA splicing
asparaginase like 1	Asrgl1	NP_079886	34	1	cytoplasm	asparaginase activity, hydrolase activity	asparagine catabolic process via L-aspartate
lectin, galactose-binding, soluble 2	Lgals2	NP_079898	15	1	not classified	sugar binding	not classified
ORM1-like 3	Ormdl3	NP_079937	17	1	endoplasmic reticulum, integral to membrane, membrane	not classified	not classified
phosphoglucomutase 1	Pgm1	NP_079976	69	1	not classified	phosphoglucomutase activity	glucose metabolic process
hypothetical protein LOC66763	4933425L06Rik	NP_080027	65	1	not classified	not classified	not classified
Tax1 binding protein 1 homolog	Tax1bp1	NP_080092	94	1	intracellular	protein binding, zinc ion binding	anti-apoptosis, apoptosis
prenylcysteine oxidase 1	Pcyox1	NP_080099	56	1	lysosome	oxidoreductase activity, oxidoreductase activity, acting on sulfur group of donors, oxygen as acceptor, prenylcysteine oxidase activity	oxidation reduction, prenylcysteine catabolic process
basic leucine zipper and W2 domains 1	Bzw1	NP_080100	48	1	not classified	not classified	regulation of transcription, transcription

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mannose-6-phosphate receptor binding protein 1	M6prbp1	NP_080112	47	1	cytoplasm, endosome, lipid particle, membrane	not classified	transport
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	Ndufb7	NP_080119	16	1	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity	electron transport chain, transport
succinate dehydrogenase complex, subunit D, integral membrane protein	Sdhd	NP_080124	17	1	integral to membrane, membrane, mitochondrial envelope, mitochondrial inner membrane, mitochondrion	heme binding, iron ion binding, metal ion binding	electron transport chain, transport, tricarboxylic acid cycle
CDGSH iron sulfur domain 2	Cisd2	NP_080178	15	1	cytoplasmic part, endoplasmic reticulum, integral to membrane, intracellular membrane-bounded organelle, membrane, perinuclear region of cytoplasm	2 iron, 2 sulfur cluster binding, iron ion binding, iron-sulfur cluster binding, metal ion binding, molecular_function	biological_process
arginyl-tRNA synthetase	Rars	NP_080212	76	1	cytoplasm	aminoacyl-tRNA ligase activity, arginine-tRNA ligase activity, ATP binding, ligase activity, nucleotide binding	arginyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
GTP-binding protein PTD004 isoform a	Ola1	NP_080218	45	1	intracellular	ATP binding, GTP binding, hydrolase activity, nucleotide binding	not classified
glyoxalase domain containing 4	Glod4	NP_080305	33	1	mitochondrion	not classified	not classified
dedicator of cytokinesis 7	Dock7	NP_080358	238	1	cell projection	GTP binding, GTPase binding, guanyl-nucleotide exchange factor activity, Rac GTPase binding	cell differentiation, multicellular organismal development, nervous system development, pigmentation
eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	NP_080390	36	1	cytoplasm, eukaryotic translation initiation factor 2 complex, nucleus	protein binding, RNA binding, translation initiation factor activity	protein amino acid autophosphorylation, regulation of translation, regulation of translational initiation in response to stress, translation
splicing factor 3a, subunit 1	Sf3a1	NP_080451	89	1	nucleus, spliceosomal complex	RNA binding	mRNA processing, RNA processing, RNA splicing
hypothetical protein LOC67759	5033414D02 Rik	NP_080638	17	1	integral to membrane, membrane	not classified	not classified
actin related protein 2/3 complex, subunit 5	Arpc5	NP_080645	16	1	Arp2/3 protein complex, cell projection, cytoplasm, cytoskeleton, lamellipodium	actin binding	regulation of actin filament polymerization
interleukin enhancer binding factor 2	Ilf2	NP_080650	43	1	nucleolus, nucleus	DNA binding, protein binding	biological_process, regulation of transcription, transcription
sorting nexin 2	Snx2	NP_080662	58	1	not classified	phosphoinositide binding, protein binding, protein transporter activity	cell communication, intracellular protein transport, protein transport, transport
pyrophosphatase	Ppa1	NP_080714	33	1	cytoplasm	hydrolase activity, inorganic diphosphatase activity, magnesium ion binding, metal ion binding, pyrophosphatase activity	phosphate metabolic process
Mki67 (FHA domain) interacting nucleolar phosphoprotein	Mki67ip	NP_080748	36	1	cytoplasm, nucleolus, nucleus	nucleic acid binding, nucleotide binding, RNA binding	biological_process
tubulin polymerization-promoting protein family member 3	Tppp3	NP_080757	19	1	not classified	not classified	not classified
M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	Mphosph10	NP_080759	79	1	nucleus, ribonucleoprotein complex	not classified	ribosome biogenesis, rRNA processing
dephospho-CoA kinase domain containing	Dcakd	NP_080827	26	1	not classified	ATP binding, dephospho-CoA kinase activity, nucleotide binding	coenzyme A biosynthetic process
ubinuclein 1	Ubn1	NP_080942	122	1	cell junction, nucleus, tight junction	DNA binding, transcription factor binding	chromatin modification, keratinocyte differentiation

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biliverdin reductase A	Blvra	NP_080954	34	1	cytoplasm, soluble fraction	biliverdin reductase activity, binding, catalytic activity, metal ion binding, nucleotide binding, oxidoreductase activity, zinc ion binding	heme catabolic process, metabolic process, oxidation reduction
coiled-coil domain containing 88C	Ccdc88c	NP_080957	227	1	insoluble fraction	PDZ domain binding, protein self-association	protein destabilization, protein homooligomerization, regulation of protein amino acid phosphorylation, Wnt receptor signaling pathway
SAPS domain family, member 2 isoform 1	Saps2	NP_081089	100	1	cytoplasm	protein binding, protein phosphatase binding	regulation of phosphoprotein phosphatase activity
small nuclear ribonucleoprotein D2	Snrpd2	NP_081219	14	1	nucleus, ribonucleoprotein complex, spliceosomal complex	nucleic acid binding	mRNA processing, RNA splicing
peroxisomal biogenesis factor 11c	Pex11c	NP_081227	27	1	integral to membrane, membrane, peroxisomal membrane, peroxisome	not classified	peroxisome fission
histidine triad protein member 5	Dcps	NP_081306	39	1	cytoplasm, nucleus	hydrolase activity, protein binding	deadenylation-dependent decapping of nuclear-transcribed mRNA, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
pirin	Pir	NP_081429	32	1	nucleus	iron ion binding, metal ion binding	not classified
hypothetical protein LOC69696	2310057N15 Rik	NP_081446	22	1	cellular_component	molecular_function	biological_process
golgi membrane protein 1	Golm1	NP_081583	44	1	Golgi apparatus, integral to membrane, membrane	molecular_function	biological_process
sideroflexin 1	Sfxn1	NP_081600	36	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	cation transmembrane transporter activity, iron ion binding	cation transport, erythrocyte differentiation, ion transport, iron ion transport, transport
hypothetical protein LOC70420	2610034B18 Rik	NP_081696	25	1	not classified	not classified	not classified
poliovirus receptor	Pvr	NP_081790	45	1	cellular_component, integral to membrane, membrane	protein binding, receptor activity	cell migration, cell-cell adhesion
follicular lymphoma variant translocation 1	Kdsr	NP_081810	36	1	endoplasmic reticulum, integral to membrane, membrane	3-dehydrosphinganine reductase activity, binding, catalytic activity, oxidoreductase activity	metabolic process, oxidation reduction
doublecortin-like kinase 2	Dclk2	NP_081815	83	1	not classified	ATP binding, kinase activity, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, transferase activity	intracellular signaling cascade, protein amino acid phosphorylation
synaptonemal complex central element protein 2	Syce2	NP_082230	20	1	central element, nucleus, synaptonemal complex	protein binding	cell cycle, cell division, meiosis, meiotic prophase I, synaptonemal complex assembly
germ cell-less homolog 1 (Drosophila)-like	Gmcl1l	NP_082231	58	1	nucleus	protein binding	cell differentiation, modification-dependent protein catabolic process, multicellular organismal development, spermatogenesis
epsin 3	Epn3	NP_082260	68	1	cytoplasm, cytoplasmic vesicle	lipid binding	not classified

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
acyl-Coenzyme A dehydrogenase family, member 10	Acad10	NP_082313	119	1	mitochondrion	acyl-CoA dehydrogenase activity, catalytic activity, electron carrier activity, FAD binding, hydrolase activity, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	metabolic process, oxidation reduction
hypothetical protein LOC66665	5730528L13Rik	NP_082413	32	1	cellular_component	identical protein binding	biological_process
F-box and leucine-rich repeat protein 20	Fbxl20	NP_082425	48	1	cytoplasm	protein binding	modification-dependent protein catabolic process
MMS19 (MET18 S. cerevisiae)	Mms19	NP_082428	113	1	nucleus	not classified	DNA repair, regulation of transcription, response to DNA damage stimulus, transcription
exportin 5	Xpo5	NP_082474	137	1	cytoplasm, nucleus	binding, protein transporter activity, RNA binding, tRNA binding	gene silencing by RNA, protein export from nucleus, protein transport, transport
protein phosphatase methylesterase 1	Ppme1	NP_082568	42	1	not classified	carboxylesterase activity, catalytic activity, hydrolase activity	not classified
tyrosyl-DNA phodphodiesterase 1	Tdp1	NP_082630	69	1	cytoplasm, nucleus	exonuclease activity, hydrolase activity, molecular_function, nuclease activity, phosphoric diester hydrolase activity	DNA repair, response to DNA damage stimulus, single strand break repair
NADH dehydrogenase (ubiquinone) flavoprotein 2	Ndufv2	NP_082664	27	1	membrane, mitochondrial inner membrane, mitochondrion, respiratory chain	2 iron, 2 sulfur cluster binding, electron carrier activity, iron ion binding, iron-sulfur cluster binding, metal ion binding, NAD or NADH binding, NADH dehydrogenase (ubiquinone) activity, NADH dehydrogenase activity, oxidoreductase activity	electron transport chain, oxidation reduction, transport
glutaredoxin 5	Glrx5	NP_082695	16	1	mitochondrion	electron carrier activity, protein disulfide oxidoreductase activity	cell redox homeostasis
proline-rich coiled-coil 1	Prrc1	NP_082723	46	1	cellular_component, Golgi apparatus	identical protein binding	biological_process
Nice-4 protein homolog isoform 1	Ubap2l	NP_082751	117	1	not classified	not classified	not classified
G+C-rich promoter-binding protein	Gpbp1	NP_082763	56	1	nucleus	DNA binding, protein binding, transcription factor activity	positive regulation of transcription, DNA-dependent, regulation of transcription, transcription
hypothetical protein LOC73694	2410091C18Rik	NP_082887	48	1	mitochondrion	not classified	not classified
solute carrier family 35, member B2	Slc35b2	NP_082938	42	1	Golgi apparatus, integral to membrane, membrane	not classified	transport
keratin 80	Krt80	NP_083046	51	1	intermediate filament, keratin filament	structural molecule activity	not classified
hypothetical protein LOC74528	8430406I07Rik	NP_083260	38	1	not classified	not classified	not classified
splicing factor 3a, subunit 3	Sf3a3	NP_083433	59	1	intracellular, nucleus, spliceosomal complex	metal ion binding, nucleic acid binding, zinc ion binding	mRNA processing, RNA splicing
hypothetical protein LOC228602	4930402H24Rik	NP_083708	132	1	not classified	not classified	not classified
cleavage and polyadenylation specific factor 4-like isoform 2	Cpsf4l	NP_084070	22	1	not classified	metal ion binding, zinc ion binding	not classified
tubulin-specific chaperone d	Tbcd	NP_084154	133	1	not classified	not classified	not classified
GA repeat binding protein, beta 2	Gabpb2	NP_084161	46	1	nucleus	protein homodimerization activity	regulation of transcription, transcription
zinc finger protein 142	Zfp142	NP_084164	195	1	not classified	not classified	not classified
coiled-coil domain containing 93 isoform c	Ccdc93	NP_084231	72	1	not classified	not classified	not classified

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cystatin E2	9230104L09 Rik	NP_084236	15	1	not classified	not classified	not classified
ADAMTS-like 1	Adamtsl1	NP_084243	193	1	extracellular region, proteinaceous extracellular matrix	metallopeptidase activity, zinc ion binding	not classified
methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	Mccc2	NP_084302	61	1	mitochondrion	ATP binding, ligase activity, methylcrotonoyl-CoA carboxylase activity, nucleotide binding	not classified
acyl-Coenzyme A binding domain containing 7	Acbd7	NP_084339	10	1	not classified	acyl-CoA binding, binding	not classified
GTP-binding protein PTD004 isoform b	Ola1	NP_084367	30	1	intracellular	ATP binding, GTP binding, hydrolase activity, nucleotide binding	not classified
centaurin, beta 2	Centb2	NP_084414	87	1	ruffle	ARF GTPase activator activity, GTPase activator activity, metal ion binding, zinc ion binding	actin filament-based process, regulation of ARF GTPase activity
hypothetical protein LOC78890	2310079F23 Rik	NP_084484	80	1	cytoplasm	methyltransferase activity, transferase activity	tRNA processing
WD repeat domain 76	Wdr76	NP_084510	58	1	not classified	not classified	not classified
regulator of nonsense transcripts 1	Upf1	NP_109605	123	1	cytoplasm	ATP binding, DNA binding, helicase activity, hydrolase activity, metal ion binding, nucleotide binding, zinc ion binding	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
insulin degrading enzyme	Ide	NP_112419	118	1	cytoplasm	ATP binding, catalytic activity, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, nucleotide binding, peptidase activity, zinc ion binding	proteolysis
solute carrier family 12 (potassium/chloride transporters), member 9	Slc12a9	NP_113583	96	1	integral to membrane, membrane, plasma membrane	not classified	transport
sarcolemma associated protein	Slmap	NP_114397	94	1	cytoplasm, integral to membrane, membrane, plasma membrane, prefoldin complex	unfolded protein binding	protein folding
sterol regulatory element binding factor 2	Srebf2	NP_150087	123	1	cytoplasm, cytoplasmic vesicle, endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane, nucleus	DNA binding, protein binding, sequence-specific DNA binding, transcription factor activity, transcription regulator activity	cholesterol metabolic process, lipid metabolic process, positive regulation of transcription from RNA polymerase II promoter, regulation of transcription, steroid metabolic process, transcription
suppressor of Ty 16 homolog	Supt16h	NP_291096	120	1	chromosome, nucleus	not classified	cellular process, DNA repair, DNA replication, regulation of transcription, response to DNA damage stimulus, transcription
1-acylglycerol-3-phosphate O-acyltransferase 3	Agpat3	NP_443747	43	1	integral to membrane, membrane	1-acylglycerol-3-phosphate O-acyltransferase activity, acyltransferase activity, transferase activity	metabolic process, phospholipid biosynthetic process
protocadherin beta 16	Pcdhb16	NP_444371	89	1	integral to membrane, membrane	calcium ion binding, protein binding	calcium-dependent cell-cell adhesion, cell adhesion, synapse assembly, synaptic transmission
Musashi homolog 2	Msi2	NP_473384	37	1	cytoplasm, polysome	nucleic acid binding, nucleotide binding, poly(U) RNA binding, RNA binding, single-stranded RNA binding	biological_process, stem cell development

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proline synthetase co-transcribed isoform a	Prosc	NP_473398	30	1	cellular_component	molecular_function	biological_process
metastasis associated 1	Mta1	NP_473422	79	1	cytoplasm, nucleus, NuRD complex	DNA binding, metal ion binding, protein binding, sequence-specific DNA binding, transcription factor activity, zinc ion binding	regulation of transcription, DNA-dependent
HLA-B-associated transcript 3	Bat3	NP_476512	121	1	cytoplasm, nucleus	not classified	apoptosis, regulation of apoptosis
protein O-fucosyltransferase 1 isoform 1	Pofut1	NP_536711	45	1	endoplasmic reticulum, integral to Golgi membrane	fucosyltransferase activity, manganese ion binding, peptide-O-fucosyltransferase activity, transferase activity, transferase activity, transferring glycosyl groups	angiogenesis, carbohydrate metabolic process, fucose metabolic process, heart development, nervous system development, Notch signaling pathway, protein amino acid O-linked glycosylation, somitogenesis
inositol 1,4,5-triphosphate receptor 3	Itpr3	NP_542120	304	1	cytoplasm, endoplasmic reticulum, integral to membrane, membrane, microsome, nucleolus, nucleoplasm, nucleus	calcium channel activity, calcium ion binding, inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity, inositol-1,4,5-trisphosphate receptor activity, ion channel activity, phosphoinositide binding, protein binding, receptor activity	calcium ion transport, ion transport, sensory perception of bitter taste, sensory perception of sweet taste, sensory perception of umami taste, transport
proteasome 26S non-ATPase subunit 5	Psmd5	NP_542121	56	1	proteasome complex	binding	not classified
ubiquitin-conjugating enzyme E2N	Ube2n	NP_542127	17	1	nucleus	ATP binding, ligase activity, nucleotide binding, protein binding, small conjugating protein ligase activity, ubiquitin-protein ligase activity	DNA repair, modification-dependent protein catabolic process, positive regulation of NF-kappaB transcription factor activity, post-translational protein modification, regulation of protein metabolic process, response to DNA damage stimulus, T cell receptor signaling pathway, ubiquitin-dependent protein catabolic process
zinc finger protein 87	Zfp87	NP_573491	63	1	nucleus	metal ion binding, zinc ion binding	transcription
acetyl-Coenzyme A carboxylase alpha	Acaca	NP_579938	265	1	cytoplasm	acetyl-CoA carboxylase activity, ATP binding, biotin binding, biotin carboxylase activity, catalytic activity, ligase activity, manganese ion binding, metal ion binding, nucleotide binding, protein binding	fatty acid biosynthetic process, lipid biosynthetic process, lipid homeostasis, lipid metabolic process, metabolic process, multicellular organismal protein metabolic process, tissue homeostasis
optic atrophy 1 homolog	Opa1	NP_598513	111	1	integral to membrane, membrane, mitochondrial inner membrane, mitochondrion	GTP binding, GTPase activity, nucleotide binding	apoptosis, response to stimulus, visual perception
aarF domain containing kinase 4	Adck4	NP_598531	59	1	cellular_component, integral to membrane, membrane	kinase activity, molecular_function, protein serine/threonine kinase activity, transferase activity	biological_process
nuclear pore complex-associated protein Tpr	Tpr	NP_598541	267	1	nuclear envelope	molecular_function	biological_process
NMD3 homolog	Nmd3	NP_598548	58	1	cytoplasm, nucleus	ribosomal large subunit binding	protein transport, ribosomal large subunit export from nucleus, transport

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dipeptidyl peptidase III	Dpp3	NP_598564	83	1	cytoplasm	aminopeptidase activity, dipeptidyl-peptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
histamine receptor H3	Hrh3	NP_598610	49	1	integral to membrane, membrane, plasma membrane	G-protein coupled receptor activity, histamine receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction
regulator of chromosome condensation 1	Rcc1	NP_598639	45	1	cellular_component, cytoplasm, nucleus	guanyl-nucleotide exchange factor activity, Ran guanyl-nucleotide exchange factor activity	biological_process, cell cycle, cell division, mitosis
transcriptional adaptor 3-like	Tada3l	NP_598693	49	1	nucleus, STAGA complex	ligand-dependent nuclear receptor transcription coactivator activity, protein binding	regulation of transcription, transcription
KDEL endoplasmic reticulum protein retention receptor 1	Kdelr1	NP_598711	25	1	endoplasmic reticulum, integral to membrane, membrane	ER retention sequence binding, receptor activity	protein retention in ER lumen, protein transport, transport, vesicle-mediated transport
acyl-CoA thioesterase 4	Acot4	NP_599008	46	1	peroxisome	acyl-CoA thioesterase activity, carboxylesterase activity, hydrolase activity, palmitoyl-CoA hydrolase activity, thiolester hydrolase activity	acyl-CoA metabolic process, dicarboxylic acid metabolic process, lipid metabolic process, short-chain fatty acid metabolic process, succinyl-CoA metabolic process
glycine decarboxylase	Gldc	NP_613061	113	1	mitochondrion	catalytic activity, glycine dehydrogenase (decarboxylating) activity, oxidoreductase activity, protein homodimerization activity, pyridoxal phosphate binding	glycine decarboxylation via glycine cleavage system, glycine metabolic process, oxidation reduction
translocase of outer mitochondrial membrane 70 homolog A	Tomm70a	NP_613065	68	1	integral to membrane, membrane, mitochondrial outer membrane, mitochondrion	binding, protein binding	not classified
ATPase, H+/K+ transporting, nongastric, alpha polypeptide	Atp12a	NP_619593	115	1	integral to membrane, membrane	ATP binding, ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism, catalytic activity, hydrogen:potassium-exchanging ATPase activity, hydrolase activity, hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances, magnesium ion binding, metal ion binding, monovalent inorganic cation transmembrane transporter activity, nucleotide binding, potassium ion binding	ATP biosynthetic process, cation transport, ion transport, metabolic process, monovalent inorganic cation transport, potassium ion homeostasis, potassium ion transport, proton transport, transport
hypothetical protein LOC192136	5033411D12Rik	NP_619595	48	1	cellular_component	catalytic activity, molecular_function, transferase activity	biological_process, metabolic process
pre-mRNA processing factor 8	Prpf8	NP_619600	274	1	nucleus, ribonucleoprotein complex, spliceosomal complex, U5 snRNP	protein binding, RNA binding	mRNA processing, nuclear mRNA splicing, via spliceosome, RNA splicing

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methylenetetrahydrofolate dehydrogenase 1	Mthfd1	NP_620084	101	1	cytoplasm, mitochondrion	ATP binding, binding, catalytic activity, formate-tetrahydrofolate ligase activity, formyltetrahydrofolate dehydrogenase activity, hydrolase activity, ligase activity, methenyltetrahydrofolate cyclohydrolase activity, methylenetetrahydrofolate dehydrogenase (NADP+) activity, nucleotide binding, oxidoreductase activity	cellular amino acid biosynthetic process, folic acid and derivative biosynthetic process, histidine biosynthetic process, histidine catabolic process, metabolic process, methionine biosynthetic process, one-carbon metabolic process, oxidation reduction, purine nucleotide biosynthetic process
coronin, actin binding protein 6 isoform B	Coro6	NP_624356	53	1	cellular_component	molecular_function	biological_process
chloride channel calcium activated 4	Clca4	NP_631887	113	1	not classified	not classified	not classified
pigpen	Fus	NP_631888	53	1	cytoplasm, intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, RNA binding, transcription activator activity, zinc ion binding	positive regulation of transcription from RNA polymerase II promoter
UDP-glucose pyrophosphorylase 2	Ugp2	NP_647458	57	1	cytoplasm	nucleotidyltransferase activity, transferase activity, UTP:glucose-1-phosphate uridylyltransferase activity	metabolic process
phosphoribosyl pyrophosphate synthetase-associated protein 2	Prpsap2	NP_659055	41	1	not classified	magnesium ion binding, ribose phosphate diphosphokinase activity	nucleoside metabolic process, nucleotide biosynthetic process
cat eye syndrome chromosome region, candidate 5 homolog precursor	Cecr5	NP_659064	46	1	not classified	hydrolase activity	metabolic process
cold shock domain containing E1, RNA binding	Csde1	NP_659150	89	1	cytoplasm, mitochondrial inner membrane	DNA binding, nucleic acid binding, RNA binding	regulation of transcription, DNA-dependent
cysteine sulfinic acid decarboxylase	Csad	NP_659191	55	1	cellular_component	carboxy-lyase activity, catalytic activity, lyase activity, pyridoxal phosphate binding, sulfinoalanine decarboxylase activity	carboxylic acid metabolic process, L-cysteine catabolic process to taurine, taurine metabolic process
peptidylprolyl isomerase-like 2	Ppil2	NP_659203	59	1	nucleus, ubiquitin ligase complex	isomerase activity, peptidyl-prolyl cis-trans isomerase activity, ubiquitin-protein ligase activity, ubiquitin-ubiquitin ligase activity	protein folding, protein polyubiquitination, protein ubiquitination
huntingtin interacting protein 1 related	Hip1r	NP_659507	119	1	coated pit, cytoplasm, cytoplasmic vesicle, cytoskeleton, membrane	actin binding, phospholipid binding	endocytosis, receptor-mediated endocytosis
lysophosphatidylcholine acyltransferase 3	Lpcat3	NP_660112	56	1	endoplasmic reticulum, integral to membrane, membrane	1-acylglycerophosphocholine O-acyltransferase activity, acyltransferase activity, transferase activity	phospholipid biosynthetic process
pitrilysin metallepetidase 1	Pitrm1	NP_660113	117	1	mitochondrion	catalytic activity, hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	proteolysis
hypothetical protein LOC28088	D10Wsu52e	NP_663397	55	1	cellular_component	molecular_function	biological_process
glutathione peroxidase 6	Gpx6	NP_663426	25	1	extracellular region	glutathione peroxidase activity, oxidoreductase activity, peroxidase activity	oxidation reduction, response to oxidative stress

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pyruvate dehydrogenase kinase, isoenzyme 3	Pdk3	NP_663605	48	1	mitochondrion	ATP binding, kinase activity, nucleotide binding, protein histidine kinase activity, pyruvate dehydrogenase (acetyl-transferring) kinase activity, transferase activity, two-component sensor activity	carbohydrate metabolic process, glucose metabolic process, peptidyl-histidine phosphorylation, signal transduction
centrosomal protein 290	Cep290	NP_666121	290	1	cell projection, centrosome, cilium, nucleus, photoreceptor connecting cilium	protein binding	cell projection organization, protein transport, regulation of transcription, transcription, transport
transcription factor B1, mitochondrial	Tfb1m	NP_666186	39	1	mitochondrion	DNA binding, methyltransferase activity, rRNA (adenine-N6,N6-)-dimethyltransferase activity, rRNA methyltransferase activity, transferase activity	regulation of transcription, rRNA modification, rRNA processing, transcription
splicing factor, arginine/serine-rich 7	Sfrs7	NP_666195	27	1	nucleus	metal ion binding, nucleic acid binding, nucleotide binding, protein binding, RNA binding, zinc ion binding	mRNA processing, RNA splicing
ARP1 actin-related protein 1 homolog B	Actr1b	NP_666219	42	1	cytoplasm, cytoskeleton	ATP binding, nucleotide binding, protein binding	not classified
inorganic pyrophosphatase 2	Ppa2	NP_666253	38	1	cytoplasm, mitochondrion	hydrolase activity, inorganic diphosphatase activity, magnesium ion binding, metal ion binding	phosphate metabolic process
acetyl-Coenzyme A acyltransferase 1B	Acaa1b	NP_666342	44	1	not classified	acyltransferase activity, transferase activity	not classified
olfactory receptor 121	Olfr121	NP_666840	35	1	integral to membrane	G-protein coupled receptor activity, olfactory receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, sensory perception of smell, signal transduction
T-cell activation GTPase activating protein 1	Tagap1	NP_671511	56	1	not classified	not classified	not classified
ATP-binding cassette, sub-family A (ABC1), member 5	Abca5	NP_671752	186	1	endosome, Golgi apparatus, integral to membrane, lysosome, membrane	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	transport
ATP-binding cassette transporter sub-family A member 9	Abca9	NP_671753	183	1	integral to membrane, membrane	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	transport
nodal modulator 1	Nomo1	NP_694697	133	1	not classified	not classified	not classified
angiomotin	Amot	NP_695231	95	1	cell junction, endocytic vesicle, external side of plasma membrane, lamellipodium, ruffle, tight junction	receptor activity	cell migration involved in gastrulation, chemotaxis, gastrulation with mouth forming second, in utero embryonic development, negative regulation of angiogenesis, positive regulation of embryonic development, regulation of cell migration, vasculogenesis
BCL2-like 13	Bcl2l13	NP_705736	47	1	integral to membrane, membrane, mitochondrion	not classified	apoptosis, regulation of apoptosis
transmembrane protein 41B	Tmem41b	NP_705745	32	1	integral to membrane, membrane	not classified	not classified
quiescin Q6 sulfhydryl oxidase 2	Qsox2	NP_705787	71	1	integral to membrane, membrane	oxidoreductase activity, thiol oxidase activity	cell redox homeostasis, oxidation reduction
non-imprinted in Prader-Willi/Angelman syndrome 1	Nipa1	NP_705806	34	1	integral to membrane, membrane	not classified	not classified

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CKLF-like MARVEL transmembrane domain containing 4	Cmtm4	NP_705810	23	1	extracellular space, integral to membrane, membrane	cytokine activity	chemotaxis
MHC I like leukocyte 1	Mill1	NP_715630	45	1	not classified	not classified	not classified
isoleucyl-tRNA synthetase	Iars	NP_742012	144	1	cytoplasm	aminoacyl-tRNA ligase activity, ATP binding, isoleucine-tRNA ligase activity, ligase activity, nucleotide binding, zinc ion binding	isoleucyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
ribosomal protein L32	Rpl32	NP_742083	16	1	cytosolic large ribosomal subunit, intracellular, ribonucleoprotein complex, ribosome	structural constituent of ribosome	translation
ectonucleoside triphosphate diphosphohydrolase 6	Entpd6	NP_742115	50	1	not classified	hydrolase activity	not classified
nucleoporin 93	Nup93	NP_765998	93	1	nuclear pore, nucleus	not classified	mRNA transport, protein transport, transmembrane transport, transport
THO complex 5	Thoc5	NP_766026	79	1	cellular_component, cytoplasm, nucleus	protein binding	cell differentiation, negative regulation of macrophage differentiation
solute carrier family 38, member 5	Slc38a5	NP_766067	53	1	integral to membrane, membrane, plasma membrane	not classified	not classified
RUN and FYVE domain containing 1	Rufy1	NP_766145	80	1	cytoplasm, cytosol, endosome, late endosome, membrane	lipid binding, metal ion binding, protein binding, protein transporter activity, zinc ion binding	endocytosis, protein transport, regulation of endocytosis, transport
pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	NP_766253	49	1	mitochondrion, plasma membrane	ATP binding, kinase activity, nucleotide binding, protein binding, protein histidine kinase activity, pyruvate dehydrogenase (acetyl-transferring) kinase activity, transferase activity, two-component sensor activity	carbohydrate metabolic process, glucose metabolic process, intracellular signaling cascade, peptidyl-histidine phosphorylation, signal transduction
zinc metalloproteinase, STE24 homolog	Zmpste24	NP_766288	55	1	endoplasmic reticulum, Golgi apparatus, integral to membrane, membrane, membrane fraction	hydrolase activity, metal ion binding, metalloendopeptidase activity, metallopeptidase activity, peptidase activity, zinc ion binding	nuclear envelope organization, prenylated protein catabolic process, proteolysis
DnaJ (Hsp40) homolog, subfamily C, member 11	Dnajc11	NP_766292	63	1	mitochondrial inner membrane	heat shock protein binding, molecular_function	biological_process
protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	NP_766295	37	1	cytoplasm	hydrolase activity, iron ion binding, manganese ion binding, metal ion binding, phosphoprotein phosphatase activity, protein binding, protein serine/threonine phosphatase activity	carbohydrate metabolic process, cell cycle, cell division, glycogen metabolic process, protein amino acid dephosphorylation
ubiquitin-like modifier activating enzyme 6	Uba6	NP_766300	118	1	not classified	ATP binding, binding, catalytic activity, ligase activity, nucleotide binding, small protein activating enzyme activity	metabolic process, modification-dependent protein catabolic process, protein modification process
engulfment and cell motility 3, ced-12 homolog	Elmo3	NP_766348	82	1	cytoplasm, cytoskeleton	protein binding, SH3 domain binding	apoptosis, phagocytosis
solute carrier family 9 (sodium/hydrogen exchanger), member 6	Slc9a6	NP_766368	78	1	integral to membrane, mitochondrion	antiporter activity	ion transport, sodium ion transport, transport
contactin associated protein-like 5	C230078M14Rik	NP_766439	144	1	integral to membrane, membrane	protein binding, receptor binding	cell adhesion, signal transduction

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
poly (ADP-ribose) polymerase family, member 12	Parp12	NP_766481	80	1	nucleus	metal ion binding, NAD+ ADP-ribosyltransferase activity, nucleic acid binding, transferase activity, zinc ion binding	not classified
carbonyl reductase 3	Cbr3	NP_766635	31	1	not classified	oxidoreductase activity	oxidation reduction
ubiquitin carboxyl-terminal hydrolase CYLD isoform b	Cyld	NP_775545	107	1	cytoplasm, intracellular, ribosome	cysteine-type peptidase activity, hydrolase activity, peptidase activity, protein binding, structural constituent of ribosome, ubiquitin thiolesterase activity	modification-dependent protein catabolic process, translation, ubiquitin-dependent protein catabolic process
hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	H6pd	NP_775547	90	1	endoplasmic reticulum, microsome	6-phosphogluconolactonase activity, binding, catalytic activity, glucose 1-dehydrogenase activity, glucose-6-phosphate dehydrogenase activity, hydrolase activity, oxidoreductase activity	carbohydrate metabolic process, glucose metabolic process, metabolic process, oxidation reduction, pentose-phosphate shunt
leprecan-like 1	Leprel1	NP_775555	80	1	endoplasmic reticulum, Golgi apparatus	iron ion binding, L-ascorbic acid binding, metal ion binding, oxidoreductase activity, oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen, procollagen-proline 3-dioxygenase activity	oxidation reduction
LanC lantibiotic synthetase component C-like 3	Lancl3	NP_775590	46	1	not classified	not classified	not classified
centromere protein E	Cenpe	NP_776123	286	1	chromosome, centromeric region	ATP binding, kinetochore binding, microtubule motor activity, motor activity, nucleotide binding, protein binding, protein kinase binding	attachment of spindle microtubules to kinetochore, cell cycle, cell division, establishment of protein localization, microtubule-based movement, mitosis, mitotic cell cycle spindle assembly checkpoint, multicellular organismal development, positive regulation of attachment of spindle microtubules to kinetochore, positive regulation of mitotic metaphase/anaphase transition, positive regulation of protein kinase activity, regulation of developmental process, regulation of mitosis
RAB6B, member RAS oncogene family	Rab6b	NP_776142	23	1	Golgi apparatus, membrane	GTP binding, nucleotide binding	protein transport, small GTPase mediated signal transduction, transport, vesicle-mediated transport
RCC1-like	Rcc2	NP_776292	56	1	chromosome, centromeric region, microtubule, nucleus	not classified	cell cycle, cell division, mitosis

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NIMA (never in mitosis gene a)-related expressed kinase 1	Nek1	NP_780298	137	1	cytoplasm, nucleus	ATP binding, kinase activity, magnesium ion binding, metal ion binding, nucleotide binding, protein kinase activity, protein serine/threonine kinase activity, protein tyrosine kinase activity, transferase activity	cell cycle, cell division, mitosis, protein amino acid phosphorylation, response to DNA damage stimulus, response to ionizing radiation
transmembrane protein 111	Tmem111	NP_780310	30	1	integral to membrane, membrane	molecular_function	biological_process
RAE1 RNA export 1 homolog	Rae1	NP_780321	41	1	cytoplasm, nucleus	not classified	not classified
Fe-containing alcohol dehydrogenase 1	Adhfe1	NP_780445	50	1	cellular_component, mitochondrion	hydroxyacid-oxoacid transhydrogenase activity, metal ion binding, oxidoreductase activity	oxidation reduction
EPM2A (laforin) interacting protein 1	Epm2aip1	NP_780475	70	1	cellular_component, endoplasmic reticulum	molecular_function	biological_process
acyl-Coenzyme A dehydrogenase family, member 11	Acad11	NP_780533	87	1	peroxisome	acyl-CoA dehydrogenase activity, electron carrier activity, FAD binding, oxidoreductase activity, oxidoreductase activity, acting on the CH-CH group of donors	metabolic process, oxidation reduction
lactate dehydrogenase A-like 6B	Ldhal6b	NP_780558	42	1	not classified	L-lactate dehydrogenase activity, oxidoreductase activity	glycolysis, oxidation reduction
aldehyde dehydrogenase 4 family, member A1	Aldh4a1	NP_780647	62	1	mitochondrial matrix, mitochondrion	1-pyrroline-5-carboxylate dehydrogenase activity, aldehyde dehydrogenase (NAD) activity, oxidoreductase activity	metabolic process, oxidation reduction, proline biosynthetic process, proline metabolic process
SEC14 and spectrin domains 1	Sestd1	NP_780674	79	1	not classified	protein binding	not classified
zinc finger, CCHC domain containing 11	Zcchc11	NP_780681	185	1	cytoplasm, nucleus	protein binding	cytokine production, negative regulation of NF-kappaB transcription factor activity, regulation of lipopolysaccharide-mediated signaling pathway
G protein-coupled receptor 150	Gpr150	NP_780704	47	1	integral to membrane, membrane, plasma membrane	G-protein coupled receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction
histone cluster 2, H2ac	Hist2h2ac	NP_783593	14	1	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly
Rho GTPase activating protein 18	Arhgap18	NP_789807	75	1	cellular_component, intracellular	GTPase activator activity, molecular_function	biological_process, signal transduction
fibronectin type III domain containing 7	Fndc7	NP_796065	78	1	extracellular region	not classified	not classified
hypothetical protein LOC320351	D230037D09 Rik	NP_796114	19	1	integral to membrane, membrane	not classified	not classified
LMBR1 domain containing 2	Lmbrd2	NP_796152	81	1	cellular_component, integral to membrane, membrane	molecular_function	biological_process
solute carrier family 26, member 9	Slc26a9	NP_796217	87	1	apical plasma membrane, integral to membrane, membrane	anion:anion antiporter activity, bicarbonate transmembrane transporter activity, secondary active sulfate transmembrane transporter activity, transporter activity	bicarbonate transport, chloride transport, regulation of pH, sulfate transport, transport
ankyrin repeat domain 16	Ankrd16	NP_796242	21	1	not classified	not classified	not classified
ADP-ribosylation factor-like 11	Arl11	NP_796311	19	1	intracellular	GTP binding, nucleotide binding	small GTPase mediated signal transduction

Protein Name	Gene Name	Accession No	Mw (kDa)	Peptide Count	GO Component	GO Function	GO Process
RAB5B, member RAS oncogene family	Rab5b	NP_803130	24	1	endocytic vesicle, endosome, membrane, plasma membrane	GTP binding, GTPase activity, nucleotide binding	endosome organization, protein transport, regulation of endocytosis, small GTPase mediated signal transduction, transport
hypothetical protein LOC216516	4930562D19 Rik	NP_808284	68	1	not classified	not classified	not classified
transmembrane protein 201 isoform b	Tmem201	NP_808340	44	1	integral to membrane, membrane	not classified	not classified
YTH domain containing 1	Ythdc1	NP_808348	86	1	not classified	not classified	not classified
NACHT, leucine rich repeat and PYD containing 2	Nlrp2	NP_808358	119	1	not classified	not classified	not classified
transient receptor potential cation channel, subfamily A, member 1	Trpa1	NP_808449	128	1	integral to membrane, membrane, stereocilium bundle	calcium channel activity, channel activity, ion channel activity	calcium ion transport, detection of chemical stimulus involved in sensory perception of pain, detection of mechanical stimulus involved in sensory perception of pain, ion transport, response to cold, response to drug, response to hydrogen peroxide, response to pain, response to stimulus, thermoception, transport
vacuolar protein sorting 26 homolog B	Vps26b	NP_821170	39	1	cytoplasm, membrane, retromer complex	not classified	protein transport, transport, vacuolar transport
CDC23 (cell division cycle 23, yeast, homolog)	Cdc23	NP_848124	69	1	anaphase-promoting complex	binding	cell cycle, cell division, mitosis, modification-dependent protein catabolic process, regulation of mitotic metaphase/anaphase transition
solute carrier family 6 (neurotransmitter transporter, GABA), member 1	Slc6a1	NP_848818	67	1	axon, integral to membrane, integral to plasma membrane, membrane, plasma membrane	gamma-aminobutyric acid:sodium symporter activity, neurotransmitter:sodium symporter activity, symporter activity	neurotransmitter transport, transport
BCSC-1	AW551984	NP_848852	89	1	not classified	not classified	not classified
Son cell proliferation protein	Son	NP_849211	266	1	intracellular, nucleus	DNA binding, double-stranded RNA binding, nucleic acid binding, protein binding, RNA binding, RS domain binding	not classified
AAA-ATPase TOB3	Atad3a	NP_849534	67	1	mitochondrial inner membrane, mitochondrion	ATP binding, nucleoside-triphosphatase activity, nucleotide binding	not classified
glycyl-tRNA synthetase	Gars	NP_851009	82	1	cytoplasm, secretory granule	aminoacyl-tRNA ligase activity, ATP binding, glycine-tRNA ligase activity, ligase activity, nucleotide binding, protein binding	glycyl-tRNA aminoacylation, regulated secretory pathway, translation, tRNA aminoacylation for protein translation
carbonic anhydrase 5b, mitochondrial	Car5b	NP_851832	37	1	mitochondrion	carbonate dehydratase activity, lyase activity, metal ion binding, zinc ion binding	one-carbon metabolic process
general transcription factor IIH, polypeptide 3	Gtf2h3	NP_852075	34	1	core TFIIH complex, nucleus	general RNA polymerase II transcription factor activity, metal ion binding, zinc ion binding	DNA repair, regulation of transcription, regulation of transcription, DNA-dependent, response to DNA damage stimulus, transcription
3-oxoacid CoA transferase 2B precursor	Oxct2b	NP_862907	57	1	microtubule-based flagellum, mitochondrion	3-oxoacid CoA-transferase activity, CoA-transferase activity, transferase activity	generation of precursor metabolites and energy, ketone body catabolic process, metabolic process
protein phosphatase 4, regulatory subunit 2	Ppp4r2	NP_891984	46	1	not classified	not classified	mRNA processing, RNA splicing

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structure specific recognition protein 1	Ssrp1	NP_892035	81	1	chromosome, nucleus	DNA binding	DNA repair, DNA replication, regulation of transcription, response to DNA damage stimulus, transcription
zinc finger protein 300	Zfp300	NP_899008	75	1	nucleus	metal ion binding, zinc ion binding	transcription
ring finger protein 182	Rnf182	NP_899027	27	1	integral to membrane, membrane	metal ion binding, protein binding, zinc ion binding	modification-dependent protein catabolic process
hypothetical protein LOC331529	EG331529	NP_899143	53	1	not classified	not classified	not classified
reticulon 4 isoform B2	Rtn4	NP_918942	40	1	cell projection, cell soma, endoplasmic reticulum, integral to endoplasmic reticulum membrane, integral to membrane, membrane, nuclear envelope	not classified	angiogenesis, negative regulation of anti-apoptosis, negative regulation of axon extension, nervous system development, regulation of cell migration
unc-84 homolog B	Unc84b	NP_919323	78	1	condensed nuclear chromosome, endosome, integral to membrane, membrane, nuclear chromosome, telomeric region, nuclear envelope, nucleus	protein binding	nuclear envelope organization
A kinase (PRKA) anchor protein (yotiao) 9	Akap9	NP_919444	434	1	cytoplasm, pericentriolar material	kinase activity, protein binding	not classified
SLAIN motif family, member 1	Slain1	NP_932131	61	1	not classified	not classified	not classified
slingshot homolog 1	Ssh1	NP_932777	115	1	cytoplasm, cytoskeleton	actin binding, hydrolase activity, phosphatase activity, phosphoprotein phosphatase activity, protein tyrosine phosphatase activity, protein tyrosine/serine/threonine phosphatase activity	dephosphorylation, protein amino acid dephosphorylation
neurotrophin 5	Ntf5	NP_937833	22	1	endoplasmic reticulum lumen, extracellular region	growth factor activity, neurotrophin p75 receptor binding, receptor binding	adult locomotory behavior, epidermis development, ganglion mother cell fate determination, long-term memory, mechanoreceptor differentiation, sensory organ boundary specification
eukaryotic translation initiation factor 5B	Eif5b	NP_938045	138	1	cytoplasm	GTP binding, GTPase activity, nucleotide binding, translation initiation factor activity	translation
zinc finger and AT hook domain containing	Zfat	NP_941046	136	1	cytoplasm, intracellular, nucleus	DNA binding, metal ion binding, nucleic acid binding, zinc ion binding	regulation of transcription, transcription
coiled-coil domain containing 58	Ccdc58	NP_941047	17	1	not classified	not classified	not classified
isoleucine-tRNA synthetase 2, mitochondrial	Iars2	NP_941055	113	1	cytoplasm, mitochondrion	aminoacyl-tRNA ligase activity, ATP binding, catalytic activity, isoleucine-tRNA ligase activity, ligase activity, nucleotide binding, zinc ion binding	isoleucyl-tRNA aminoacylation, translation, tRNA aminoacylation for protein translation
hypothetical protein LOC382137	D630004A14 Rik	NP_941077	70	1	cytoplasm	ATP binding, magnesium ion binding, phenylalanine-tRNA ligase activity, tRNA binding	phenylalanyl-tRNA aminoacylation, tRNA processing

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zinc fingers and homeoboxes protein 2	Zhx2	NP_955520	92	1	cellular_component, intracellular, nucleus	DNA binding, metal ion binding, protein binding, sequence-specific DNA binding, transcription factor activity, transcription regulator activity, zinc ion binding	mRNA catabolic process, negative regulation of transcription from RNA polymerase II promoter, regulation of transcription, regulation of transcription from RNA polymerase II promoter, regulation of transcription, DNA-dependent, transcription
delangin isoform B	Nipbl	NP_957684	304	1	nucleus	not classified	cell cycle
cDNA sequence BC034664	Lyrm4	NP_958746	11	1	mitochondrion	not classified	not classified
sphingosine kinase 2	Sphk2	NP_975009	66	1	cytosol, membrane fraction	ATP binding, D-erythro-sphingosine kinase activity, diacylglycerol kinase activity, kinase activity, nucleotide binding, protein binding, sphinganine kinase activity, transferase activity	activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway, anti-apoptosis, blood vessel development, brain development, positive regulation of cell proliferation, sphinganine-1-phosphate biosynthetic process, sphingosine metabolic process
immunoglobulin superfamily, member 3	Igsf3	NP_997088	135	1	integral to membrane, membrane	not classified	not classified
peptidoglycan recognition protein 4	Pglyrp4	NP_997146	41	1	extracellular region	N-acetylmuramoyl-L-alanine amidase activity, protein binding	defense response to bacterium, immune response, peptidoglycan catabolic process
oxysterol binding protein-like 1	Osbpl1a	NP_997413	108	1	cellular_component	molecular_function	lipid transport, steroid metabolic process, transport
angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 isoform 1	Ace	NP_997507	151	1	extracellular region, integral to membrane, membrane, plasma membrane	carboxypeptidase activity, hydrolase activity, metal ion binding, metallopeptidase activity, peptidase activity, peptidyl dipeptidase activity, zinc ion binding	hormone catabolic process, proteolysis, regulation of blood pressure
MARVEL (membrane-associating) domain containing 3 isoform b	Marveld3	NP_997612	44	1	integral to membrane, membrane	not classified	not classified
PREDICTED: heterogeneous nuclear ribonucleoprotein A0	Hnrpa0	XP_001001311	31	1	not classified	not classified	not classified
PREDICTED: tubulin tyrosine ligase-like family, member 7 isoform 2	Ttll7	XP_001005473	103	1	cell projection, cilium	ligase activity, tubulin-tyrosine ligase activity	cell differentiation, multicellular organismal development, nervous system development, protein modification process
PREDICTED: hypothetical protein	LOC100038847	XP_001471557	24	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100044270	XP_001471889	74	1	not classified	not classified	not classified
PREDICTED: similar to novel KRAB box and zinc finger, C2H2 type domain containing protein	LOC100039109	XP_001472332	9	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC78034	4930528H21Rik	XP_001472376	9	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG630825	XP_001472439	47	1	not classified	not classified	not classified
PREDICTED: similar to 60S ribosomal protein L38	EG633736	XP_001472500	8	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC75255	4930562F07Rik	XP_001472732	14	1	not classified	not classified	not classified
PREDICTED: similar to Thoc7 protein	LOC100044980	XP_001473492	38	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100040033	XP_001474032	96	1	not classified	not classified	not classified
PREDICTED: similar to ankyrin repeat domain 29	Ankrd29	XP_001474267	33	1	cellular_component	molecular_function	biological_process
PREDICTED: similar to coronin, actin binding protein 2A	LOC100045302	XP_001474318	60	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	EG666372	XP_001474538	19	1	not classified	not classified	not classified
PREDICTED: similar to Sm D2 isoform 2	LOC100045392	XP_001474690	13	1	not classified	not classified	not classified
PREDICTED: similar to Kifc1 protein	LOC100044006	XP_001474732	88	1	not classified	not classified	not classified

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PREDICTED: similar to ribosomal protein L37a	LOC100045996	XP_001474797	10	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100040498	XP_001474871	15	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC667147	XP_001475011	30	1	not classified	not classified	not classified
PREDICTED: similar to hippocampal cholinergic neurostimulating peptide precursor protein	LOC676548	XP_001475026	11	1	not classified	not classified	not classified
PREDICTED: similar to elongation factor SIII p15 subunit	LOC100045866	XP_001475387	12	1	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L23a	LOC100046437	XP_001475762	18	1	not classified	not classified	not classified
PREDICTED: similar to Serine/arginine repetitive matrix protein 2	LOC100046735	XP_001475797	22	1	not classified	not classified	not classified
PREDICTED: G protein-coupled receptor, family C, group 1, member B	Grm2	XP_001475864	93	1	integral to membrane, membrane, plasma membrane	calcium channel regulator activity, G-protein coupled receptor activity, group II metabotropic glutamate receptor activity, receptor activity, signal transducer activity	G-protein coupled receptor protein signaling pathway, signal transduction, synaptic transmission
PREDICTED: similar to 40S ribosomal protein S29	EG632013	XP_001476064	7	1	not classified	not classified	not classified
PREDICTED: similar to Nucleosome binding protein 1	LOC100046362	XP_001476124	24	1	not classified	not classified	not classified
PREDICTED: similar to Cngb1 protein	Cngb1	XP_001476248	147	1	integral to membrane, membrane, membrane fraction	ion channel activity	ion transport, photoreceptor cell maintenance, phototransduction, transport
PREDICTED: hypothetical protein	LOC545536	XP_001476554	28	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100046382	XP_001476881	14	1	not classified	not classified	not classified
PREDICTED: similar to sex comb on midleg-like 2 (Drosophila)	LOC100047360	XP_001476978	90	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100047128	XP_001477504	21	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100042323	XP_001477991	11	1	not classified	not classified	not classified
PREDICTED: similar to SI:zC220F6.1 (novel protein similar to human dynein heavy chain (DHC))	Dnahc6	XP_001478071	466	1	not classified	not classified	not classified
PREDICTED: similar to Pro-Pol-dUTPase polyprotein; RNaseH; dUTPase; integrase; protease; reverse transcriptase	LOC100042383	XP_001478138	125	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100047469	XP_001478262	20	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC71531	9030411M15Rik	XP_001478828	225	1	integral to membrane, membrane	not classified	not classified
PREDICTED: hypothetical protein	LOC100047800	XP_001478934	68	1	not classified	not classified	not classified
PREDICTED: regulator of G-protein signaling like 1	Rgsl1	XP_001479114	127	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC71837 isoform 2	1700003E16Rik	XP_001479836	56	1	not classified	not classified	not classified
PREDICTED: similar to 60S ribosomal protein L9 isoform 2	LOC100048162	XP_001480031	21	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC74702	4930517E11Rik	XP_001480083	22	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	LOC100048073	XP_001480112	80	1	not classified	not classified	not classified
PREDICTED: similar to mKIAA0910 protein	Synj1	XP_001481337	189	1	clathrin coat, cytoplasm, membrane coat	hydrolase activity, inositol or phosphatidylinositol phosphatase activity, nucleic acid binding, phosphatidylinositol-4,5-bisphosphate 5-phosphatase activity, phosphoinositide 5-phosphatase activity, polyphosphoinositide phosphatase activity, protein binding, RNA binding	dephosphorylation, endocytosis, learning, neurotransmitter transport, phosphoinositide dephosphorylation, phosphoinositide metabolic process, phosphoinositide-mediated signaling, synaptic vesicle endocytosis, synaptic vesicle priming, synaptic vesicle transport, synaptic vesicle uncoating
PREDICTED: gene model 969, (NCBI)	Gm969	XP_001481372	103	1	not classified	not classified	not classified
PREDICTED: flavin-containing monooxygenase 13	EG226601	XP_136366	66	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC72805	2810455K09Rik	XP_138271	91	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	Gm659	XP_195466	35	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC329739	B430201A12Rik	XP_283903	50	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	Gm1693	XP_358673	17	1	not classified	not classified	not classified

Protein Name	**Gene Name**	**Accession No**	**Mw (kDa)**	**Peptide Count**	**GO Component**	**GO Function**	**GO Process**
PREDICTED: similar to ribosomal protein L27A	EG432798	XP_484309	17	1	not classified	not classified	not classified
PREDICTED: similar to Chain C, Structure Of A Hif-1a-Pvhl-Elonginb-Elonginc Complex	EG620071	XP_889554	11	1	not classified	not classified	not classified
PREDICTED: similar to RIKEN cDNA 1110020P15 gene	EG622178	XP_891680	7	1	not classified	not classified	not classified
PREDICTED: similar to Ribosomal protein S11	EG623114	XP_892646	14	1	not classified	not classified	not classified
PREDICTED: similar to TLK2 protein	LOC627701	XP_897493	29	1	not classified	not classified	not classified
PREDICTED: similar to QM protein	EG625219	XP_899042	24	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC74307	1700092M07Rik	XP_902879	10	1	not classified	not classified	not classified
PREDICTED: hypothetical protein isoform 2	Gm70	XP_903922	47	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC75173	4930544O15Rik	XP_909948	23	1	integral to membrane, membrane	not classified	not classified
PREDICTED: hypothetical protein LOC73324 isoform 4	1700034F02Rik	XP_909961	69	1	not classified	not classified	not classified
PREDICTED: X-ray radiation resistance associated 1	Xrra1	XP_910416	88	1	cytoplasm, nucleus	protein binding	not classified
PREDICTED: similar to Proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 isoform 3	EG432448	XP_911613	94	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	Lrrc37a	XP_911630	376	1	not classified	not classified	not classified
PREDICTED: similar to Iron-sulfur cluster assembly 2 homolog, mitochondrial precursor (HESB-like domain-containing protein 1) isoform 5	Isca2	XP_913323	17	1	mitochondrion	iron ion binding, iron-sulfur cluster binding, metal ion binding, structural molecule activity	iron-sulfur cluster assembly
PREDICTED: similar to Regulator of G-protein signalling 22	LOC635821	XP_916087	129	1	not classified	not classified	not classified
PREDICTED: hypothetical protein LOC75718	4931403E03Rik	XP_919694	134	1	extracellular region	not classified	not classified
PREDICTED: hypothetical protein LOC219189	1300010F03Rik	XP_920456	213	1	extracellular region, mitochondrion	ATP binding, ATPase activity, nucleoside-triphosphatase activity, nucleotide binding	not classified
PREDICTED: similar to ribosomal protein S17	EG623169	XP_920905	16	1	not classified	not classified	not classified
PREDICTED: similar to putative pheromone receptor	LOC639943	XP_921678	59	1	not classified	not classified	not classified
PREDICTED: proline-rich polypeptide 6 isoform 4	Prr6	XP_921840	28	1	nucleus, spindle midzone	carbon-sulfur lyase activity	cell cycle, cell division, centromeric heterochromatin formation, metabolic process, mitosis, positive regulation of cytokinesis, regulation of chromosome organization
PREDICTED: similar to Chain C, Structure Of The Human Exon Junction Complex With A Trapped Dead-Box Helicase Bound To Rna	LOC641170	XP_923606	47	1	not classified	not classified	not classified
PREDICTED: similar to preserine protease	LOC641199	XP_923637	18	1	not classified	not classified	not classified
PREDICTED: similar to Fkbp15 protein	Fkbp15	XP_987350	142	1	actin filament, axon, cell projection, cytoplasm, growth cone	isomerase activity, peptidyl-prolyl cis-trans isomerase activity	protein folding
PREDICTED: similar to endothelial monocyte-activating polypeptide	EG665509	XP_988080	11	1	not classified	not classified	not classified
PREDICTED: similar to ribosomal protein L27a-like	EG666648	XP_990276	16	1	not classified	not classified	not classified
PREDICTED: similar to RIKEN cDNA 2610301G19 gene	2610301G19Rik	XP_990438	103	1	not classified	not classified	not classified
PREDICTED: hypothetical protein	4930407I10Rik	XP_991998	168	1	not classified	not classified	not classified
PREDICTED: similar to Rps15a protein	LOC676847	XP_998546	21	1	not classified	not classified	not classified